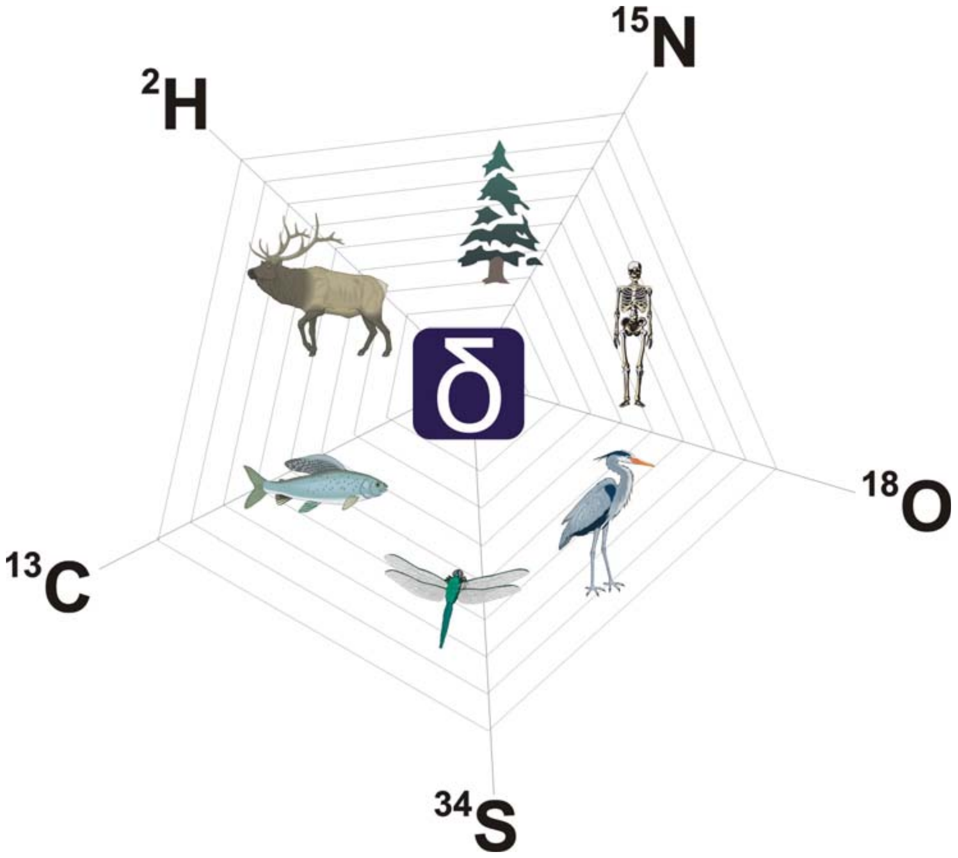
The 8th International Conference on Applications of Stable Isotope Techniques to Ecological Studies



Brest, Brittany, France - August 20th to 24th 2012

Conference Organisers

Stanislas Dubois
Jacques Grall

Organising Committee

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Location : Quartz Conference Center
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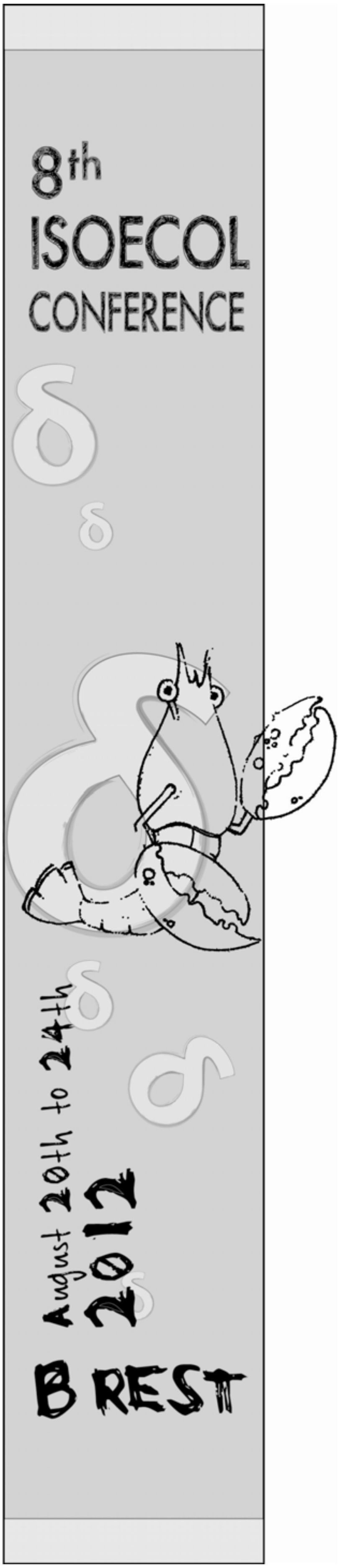

Dear Isotope lovers,

Welcome to Brest and to Brittany for the 8th International Conference on Applications of Stable Isotope Techniques to Ecological Studies. We are delighted for this eighth edition to have that unique blend of researchers and students from universities, governmental institutions and industry that has made this series so successful.

We hope that Brest will build on the success of the previous meetings, retaining the relaxed, friendly and collaborative atmosphere that sets the ISOECOL conferences apart. The ISOECOL group is growing fast. We will have this year close to 250 researchers and students attending the meeting. As you can imagine with so many delegates, we have had an extremely difficult task selecting presentations for oral slots (we could have easily run the conference twice!). However this has made for a very exciting, diverse and very full program. We didn't want to change the timetable format as the previous conference (five days with a day off in the middle), proved to be a winning formula.
This year we will have a plenary speaker to open each conference day. Plenary speakers are all international leader in their field and they will bring us new insights and new perspectives to shake things up. We will have 15 theme sessions which will run throughout the oral programme and poster evenings, as a proxy of the growing diversity of isotopic field interests.

We sincerely hope that you will enjoy your stay in Brest and that you'll find opportunities to take some time out. Brittany is one of the most beautiful part of France and we have selected several field trips so you can have a glance at our coast. If you have a chance to stay a few additional days, we are convinced that you will enjoy walking the coastal trails and wandering in old villages.

Most important of all we hope that you find this a rewarding and productive week.

Thank you for participating and helping to make this meeting a success.

On behalf of all the organising committee,

Isotopically yours,

Stan Dubois & Jacques Grall.

The Scientific Program

The program has 231 papers in total – 71 oral and 160 poster presentations. Many thanks to all the contributors.

We have four excellent plenary speakers, each a leading researcher in his field:

PLENARY SPEAKERS

■ On Monday morning **Pr Brian Fry** from the Griffith University will give a talk entitled: “*Estuarine Conservation and Restoration in the 21st century: Using Stable Isotopes to Turn the Red Dots Green Again”*
Brian said he discovered the power of stable isotopes by accident, which means accidents sometimes are a good thing. Brian has a broad interest in wetlands and marshes and has been investigating their ecological processes in the light of isotopes for years. His sense of humour and his pedagogy skills contributed to pass the love of isotopes to many students.

■ On Tuesday morning, **Pr. Sébastien Lefebvre** from the University of Lille will give a talk entitled: *“Insight from modelling into isotope ecology: love story never ends”.*
Sébastien has brought his modelling skills and unique physiology insight to isotopes to help disentangle feeding ecology from ecophysiology processes in organisms’ isotopic variations. He is a driving force to help understand isotopic fractionation mechanisms.

■ On Thursday morning, we have **Pr. Stuart Bearhop**, from the University of Exeter. Stuart will talk about *“Stable Isotopes as markers of diet and trophic structure: the good the bad and the ugly”***.**
Stuart has been using stable isotope techniques to investigate ecology and foraging behaviour of an amazingly large number of animals, in an amazingly large number of field sites all over the world. He has a pivotal role in keeping the *isoecol* group alive and making it grow.

■ On Friday, our final plenary will be given by **Dr Pascal Riera**, from the Station Biologique de Roscoff, with a presentation entitled*: “Food web ecology and stable isotopes: applications from macrofauna to microorganisms in marine and coastal ecosystems”.*
Pascal has been at the forefront of stable isotope work in France and has contributed to bring new insights in tracing carbon and nitrogen pathways in marine coastal systems, by focusing on several marine compartments.

ORAL PRESENTATIONS

Oral presentations will take place in the Petit Theatre of the Quartz Convention Center. All presenters should give their presentation files (PowerPoint) to Antoine Carlier the day before they are due to talk (this will be on Tuesday for those presenting on Thursday). Antoine will go through your presentation on a laptop in order to make sure there are no problems. Presentations should be 15 minutes in length, with 5 minutes for questions.

POSTER PRESENTATIONS

Poster presentations will be held in the Meridienne on Monday and Tuesday evenings. The sessions will begin at 8:00 pm and run until 10:00 pm. Beer and soft drinks will be provided to help you survive.
Posters can be put up from Monday (during coffee break of lunch) onwards and have to be removed by 4pm on Friday. Boards are 1 meter large and 2 meters high. We strongly recommend you to keep it as a portrait format 90 cm (35 in) large x 120 cm (47 in) high. Poster boards will be provided along with materials to attach posters to the boards (scratch).

NAME BADGES

Please wear your name badge at all times during the meeting.

STUDENT AWARDS

We have almost 100 students attending the conference and nearly all of them giving oral or poster presentations. There will be a competition for the best students' presentations. These awards consist in three cash prizes (300 euros, 250 euros and 200 euros) for the three best poster presentations and the three best oral presentations. Only Master and PhD students are allowed to compete for these awards. Presentations will be evaluated by an international committee and winners will be announced during the banquet. Good luck!

FINANCIAL SUPPORT FOR THE CONFERENCE.

We gratefully acknowledge the support of the following organisations and businesses for their financial support: Ifremer, Institut Universitaire Européen de la Mer (IUEM), Institut de Recherche pour le Développement (IRD), University of Alaska Fairbanks, CNRS, Société Française des Isotopes Stables (SFIS), Conseil Général du Finistère (CG29), Brest Métropole Océane (BMO), Région Bretagne, Sercon, Thermo Scientific, Elementar group - Isoprime, IVA Anlysentechnik, Eurovector.

Social Events

PRE-CONFERENCE MIXER *Sunday 19th August*

To expedite the process of becoming accustomed to local food and drinks, we will host a crepes-party in the famous concert-room of the Vauban hotel. Unlimited draft cider and crepes will be served. A great chance to catch up with old friends and make some new ones. Registration packages will be available here for pick up from 6:00 pm onwards (only for fully registered people).

CONFERENCE FIELD TRIPS ***Wednesday 22th August***

Several field trips are available for the day off:
Trip 1: Excursion to Ushant Island : hiking and bird watching (max 60 places)
Trip 2: Roscoff and The Bay of Morlaix (North Brittany) (max 60 places)
Trip 3: Trip landward of the Parc naturel régional d'Armorique (max 30 places)
Trip 4: Trip to Le Conquet and pointe Saint-Mathieu, the very tip of Brittany.

Details on where and when to meet will be given on arrival at the conference. Depending on the trip, we will ask you to pay at the conference the first day (Monday) or directly on site. People should bring walking boots and wet weather gear (just in case).

We might be forced to cancel Trip 4. For those who want to do something else, we are suggesting other options on the website (www.isoecol2012.com). Also note that with your badge, you will have full access to the fitness center (Physic Form) at 3 min walk from the Quartz Center (7:30 am to 11:00 pm Monday and Thursday, 8:30 am to 10:00 pm other days).

THURSDAY NIGHT FREE CONCERT ***Thursday 23th August***

A concert will be given on Brest Harbor downtown (10 min walk from the Quartz Center). This is a popular event for Brest citizens during summer time. There are a lot of people enjoying music and local food and Thursday 23th is the last concert of the summer, featuring an international famous brass band heavy funk group “*Ceux qui marchent debout*”. Feel free to join!

CONFERENCE BANQUET ***Friday 24th August***

The conference banquet will be held in Oceanopolis. A pre-dinner drinks reception will begin at 8:30 pm among aquarium of local marine fauna all around. This will be followed by a dinner at 9:15pm in a brand new reception room. There will be live music too, so you will get a chance to learn traditional dances. Buses will pick you up at the Quartz Center and bring you back around 0:30 am. You can buy “+1” tickets for the banquet only the first day (Monday) of the conference (cash only).

Conference Program

▶ Sunday 19th August

	09:30	**17:30**	**Workshop 1** (Gabe Bowen *et al.*) Isotope applications for geospatial assignment
	09:30	**17:30**	**Workshop 2** (Kirsteen MacKenzie *et al.*) Sampling animal tissues for stable isotope analysis
	18:00	**22:00**	**Ice Breaking at the Vauban Hotel** (crepes-party and cider)

(for attendees, please download the latest program on the conference website)

▶ Monday 20th August

	08:00	**09:00**	**Registration and housekeeping (conference bags can be picked up during the Sunday Ice Breaking)**	
	09:00	**09:30**	**Welcome Speach**	
K	**09:30**	**10:10**	**Brian Fry**	**Estuarine conservation and restoration in the 21st century : Using stable isotopes to turn the red dots green again**
🟫	Session 1 – Soil Ecology (p.4)			
🟫	**10:10**	**10:30**	Nicole Scheunemann	Carbon flow in the belowground food web of an agricultural field site assessed by isotope tracers: a pulse-labeling experiment
🟫	**10:30**	**10:50**	Nick Nickerson	IsoFD: A novel method for measuring the unbiased isotopic signature of surface flux
🟫	**10:50**	**11:10**	Samuel Abiven	Tracing organic matter during it decomposition in soil using ^{13}C, ^{15}N highly labelled material: the example of wood and pyrogenic matter decomposition dynamics
	Coffee Break			
🟩	Session 2 – Terrestrial Plants (p.7)			
🟩	**11:40**	**12:00**	Bruce Dudley	Groundwater and rainfall availability control soil nitrogen dynamics in a stand of invasive Mesquite (Prosopis pallida)
🟩	**12:00**	**12:20**	Kathrin Streit	Tracing carbon allocation through non structural carbon pools of *Larix decidua* exposed to elevated CO_2 and soil warming at the upper tree line
🟩	**12:20**	**12:40**	María Zunzunegui	d^{15}N pattern across sand dune systems: relevance of seawater spray in vegetation fertilization.

	Lunch			
🟧	Session 3 – Pests and Invasive Species (p.10)			
🟧	**14:10**	**14:30**	Barbara Tigar	Some truths and assumptions about using stable isotopes to trace the natal hosts of holometabolous insects in adult insects
🟧	**14:30**	**14:50**	Peter Smyntek	Isotopic niche metrics reveal the impact of an invasive species on a fish community
🟧	**14:50**	**15:10**	Jérôme Marty	Combining stable isotope and fatty acid analyses to evaluate the effects of an invader on aquatic food webs in the Great Lakes
🟧	**15:10**	**15:30**	Jessica Ives	The bloody shrimp are everywhere: spatial differences in the food sources of invasive Hemimysis anomala in the Great Lakes Basin
🟧	**15:30**	**15:50**	René Gergs	Cross-system trophic effects: Does the invasive aquatic *Dikerogammarus villosus* affect terrestrial food webs?
	Coffee Break			
🟦	Session 4 – New Recipes and Tools to Solve Isotope Mixtures (p.15)			
🟦	**16:20**	**16:40**	Pascal Boeckx	Classification of nitrate polluting activities through clustering of isotope mixing model outputs
🟦	**16:40**	**17:00**	Kevin Healy	Accounting for the process of foraging in source-level variation in isotopic mixing models
🟦	**17:00**	**17:20**	Patrick Fink	Determining trophic niche width: An experimental test of the stable isotope approach
🟦	**17:20**	**17:40**	Ryan Woodland	Evidence for seasonal shifts in the isotope composition of aquatic primary consumers and incorporating temporally dynamic baselines in mixing models
🟦	**17:40**	**18:00**	Alex Bond	A geometric method for estimating stable isotope discrimination factors
	DINER			
	20:00	**22:00**	**Poster Session 1**	

► Tuesday 21th August

	08:00	**08:30**	**Housekeeping**	
K	**08:30**	**09:10**	**Sébastien Lefebvre**	**Insight from modelling into isotope ecology: love story never ends**
🟨	Session 5 – Fractionation and Discrimination Factors; where are the damages (p.20)			
🟨	**09:10**	**09:30**	Christina Bradley	Individual amino acid turnover rates in muscle tissue from a multi-year study of captive Pacific Bluefin Tuna

09:30	**09:50**	Jens Nielsen	Trophic fractionation in compound specific stable isotopes in marine organisms.
09:50	**10:10**	Antoine Emmery	Effect of the feeding level on the dynamics of stable isotopes δ^{13}C and δ^{15}N in soft tissues of the Pacific oyster *Crassostrea gigas*
10:10	**10:30**	David Soto	Experimental quantification of hydrogen and oxygen isotopic trophic discrimination in aquatic food webs
Coffee Break			
11:00	**11:20**	Gérald Remaud	New Insights into ^{13}C fractionation obtained by isotopic NMR spectrometry
11:20	**11:40**	Christopher Sweeting	13C Concentration Dependence of the Lipid-Protein Offset: Compounding Problems for Lipid Correction of Isotope Data
Session 6 – Biogeochemistry (p.26)			
11:40	**12:00**	Nicolas Savoye	Stable isotope signatures of particulate organic matter: an inter-annual multi-site survey within the scope of the French Coastal Monitoring Network SOMLIT
12:00	**12:20**	Alex Wyatt	Isotopic insights into nutrient fluxes and trophodynamics over coral reef ecosystems
12:20	**12:40**	Muhammed N. Mullungal	Laughing Gas Plays a Serious Role in Marine Chemistry": A Stable Isotopic Voyage
Lunch			
Session 7 – A long time ago - Paleoecology (p.29)			
14:10	**14:30**	Mark Clementz	How Hot and How Wet were the Eocene Tropics? Evidence from the Stable Isotope Composition of Fossil Sirenian Tooth Enamel
14:30	**14:50**	Larisa DeSantis	Assessing mammalian responses to glacial and interglacial conditions
14:50	**15:10**	Rachel Schwartz-Narbonne	Investigating Woolly Mammoth Ecology through Compound-Specific Isotopic Analysis
15:10	**15:30**	Maura Pellegrini	Late Pleistocene animal transhumance in central Italy
15:30	**15:50**	Kena Fox-Dobbs	Grevy's zebra diet: historic and modern comparisons with co-occurring plains zebra, and the influence of livestock competition
Coffee Break			
Session 8 – Isotopes and Geospatial assignments - Isoscapes (p.34)			
16:20	**16:40**	Ashley Coutu	Mapping an East African elephant isoscape to trace historic flows of ivory
16:40	**17:00**	Gabriel Bowen	Spatiotemporal isoscapes for migration research
17:00	**17:20**	Christine Hellmann	Isoscapes to trace plant-plant-interactions at the community scale
17:20	**17:40**	Keith Hobson	A multi-isotope (δ^{13}C, δ^{15}N, δ^{2}H) isoscape for Africa: Applications to tracing animal migration

🟪	**17:40**	**18:00**	Steven Van Wilgenburg	Linking migratory populations with stable-hydrogen isotopes: improved inference through informative priors and “screening” migrants from residents
	DINER			
	20:00	**22:00**	**Poster Session 2**	

► Thursday 23th August

K	**08:30**	**09:10**	**Stuart Bearhop**	**Stable Isotopes as markers of diet and trophic structure: the good the bad and the ugly**
🟫	Session 9 – Animal Foraging Behavior (p.39)			
🟫	**09:10**	**09:30**	Thomas Bodey	Individual specialization in foraging behaviour in a wide-ranging marine predator
🟫	**09:30**	**09:50**	Yves Cherel	Stable isotopes document the effects of aging, sex and breeding status on the foraging ecology of an extremely long-lived seabird
🟫	**09:50**	**10:10**	Alyson Fleming	Standing the test of time? Why an isotopic “snapshot” of a population may form an incomplete picture of its foraging ecology.
🟫	**10:10**	**10:30**	Francesca Colombo	Seasonal variation in trophic niches of co-occurring suspension feeders
	Coffee Break			
🟫	**11:00**	**11:20**	Matthew Lattanzio	Functional consequences of disturbance for tree lizards (*Urosaurus ornatus*): Integrating isotopic evidence from multiple trophic levels
🟫	**11:20**	**11:40**	Tracey Rogers	Seal whiskers reveal long-term diet specialists: not all are top-order predators
🟫	**11:40**	**12:00**	Hannah Vander Zanden	Caribbean green turtle foraging ecology
🟫	**12:00**	**12:20**	Charlotte Evangélista	The ecological consequences of individual trophic specialization in human-altered ecosystems
🟫	**12:20**	**12:40**	Andrew Doll	Estimating temporal movements of a migratory species using stable carbon isotopes
	Lunch			
🟦	Session 10 – Freshwater and Lake Ecology (p.48)			
🟦	**14:10**	**14:30**	Marie Elodie Perga	Cyanobacterial blooms: trophic dead-end or unexpected dietary bonus?
🟦	**14:30**	**14:50**	Thomas Larsen	Can amino acid d^{13}C patterns distinguish between planktonic and benthic food pathways in alpine lakes?
🟦	**14:50**	**15:10**	Hélène Masclaux	Terrestrial subsidies of lake food webs mediated by pollen inputs
🟦	**15:10**	**15:30**	Zoraida Quiñones-Rivera	Assessing Effects of Metabolic Activity and Hydrology on Dissolved Oxygen and Dissolved Inorganic Carbon Dynamics in Hardwater Lakes using Stable Isotopes

🟦	**15:30**	**15:50**	Björn Wissel	Deconstructing the Lake: Littoral Energy Sources are of low Importance in Prairie Lakes
	Coffee Break			
🟨	Session 11 – Ecology of Fish Community (p.53)			
🟨	**16:20**	**16:40**	Gilbert Cabana	Sulfur and carbon stable isotopes as tracers of fish reliance on profundal detritic matter in lakes varying in hypoxia
🟨	**16:40**	**17:00**	Julien Cucherousset	Patterns of trophic diversity in freshwater fish communities: a stable isotope meta-analysis
🟨	**17:00**	**17:20**	Clive Trueman	Ecology, trophic structure and evolution of continental slope communities: Multi-isotope, multi-tissue investigations.
🟨	**17:20**	**17:40**	Dorothée Kopp	Body size-trophic position relationship in marine fish depends on the biological and spatial scales considered
	DINER			

► Friday 24th August

	08:00	**08:30**	**Housekeeping**	
K	**08:30**	**09:10**	**Pascal Riera**	**Stable isotopes from macrofauna to microorganisms in marine coastal ecosystem**
🟧	Session 12 – Isotopes in Scales and Otoliths (p.57)			
🟧	**09:10**	**09:30**	Kirsteen MacKenzie	Ecology and location of marine animals revealed by carbon and nitrogen isotopes
🟧	**09:30**	**09:50**	Jens Pedersen	North Atlantic ecosystem shifts revealed from δ^{15}N & δ^{13}C otolith chronologies
🟧	**09:50**	**10:10**	Chantal Huijbers	Spatial population dynamics of coral reef fish revealed by otolith stable isotopes
🟧	**10:10**	**10:30**	Jean-Marc Roussel	The use of fish scale collections to study recent changes in C and N cycles in rivers
	Coffee Break			
🟪	Session 13 – Structure of the Food Web and Community Approaches (p.61)			
🟪	**11:00**	**11:20**	Joyshree Chanam	Ants, non-ants and housing rent: interactions of a myrmecophyte host with its non-protective tenants
🟪	**11:20**	**11:40**	Jean-Charles Leclerc	Ecology in an European Kelp Forest (Laminaria hyperborea): Linking Biodiversity to Trophic Structure and Functioning
🟪	**11:40**	**12:00**	Jonathan Grey	Parasites and the isotopic integrity of individuals

	12:00	**12:20**	Gauthier Schaal	Lack of coupling between estuaries and coastal rocky shore-associated invertebrates in a semi-arid environment: Evidence through stable isotopes and fatty acid analysis
	12:20	**12:40**	Rod Connolly	Measuring resilience of aquatic ecosystems: the role of isotope labelling experiments
	Lunch			
	Session 14 – Marine Benthic Ecology (p.66)			
	14:10	**14:30**	Pierre-Yves Pascal	Trophic role of giant benthic thiobacteria in a Caribbean mangrove (Guadeloupe, FWI)
	14:30	**14:50**	Carole Decker	Contribution of chemosynthesis and nutritional patterns in Norwegian margin cold-seep communities
	14:50	**15:10**	Anne-Sophie Dubois	Transfer of organic matter sources to the macrozoobenthic food web in a semi-enclosed ecosystem: coupling fatty acids to stable isotope analyses
	15:10	**15:30**	Kelton McMahon	Unraveling carbon flow pathways on coral reefs with compound specific stable isotope analysis
	15:30	**15:50**	Antoine Carlier	What fuels the marine food web of the Banc d’Arguin (Mauritania)? New insights from isotopic analysis
	Coffee Break			
	Session 15 – Ecology in the Oceans (p.71)			
	16:20	**16:40**	Iliana Ruiz-Cooley	Amino acid d^{15}N from sperm whales (*Physeter macrocephalus*) skin indicate shifts in nitrogen cycling and food web structure in the oceanic California Current
	16:40	**17:00**	Tiphaine Chouvelon	Depicting trophic relationships through carbon and nitrogen stable isotopes ratios in a context of significant environmental variability: The Bay of Biscay case study
	17:00	**17:20**	Brian Hunt	Isotope ratios of plankton size spectra as a tool for investigating trophic dynamics
	17:20	**17:40**	Chris Harrod	Welcome to the jelly-web: using stable isotopes to understand the trophic ecology of gelatinous zooplankton
	Break			
	20:30	**23:30**		Banquet at Oceanopolis and Student Prizes

Poster Sessions Monday 20th and Tuesday 21th August

Note to presenting authors: please stay close to your poster during poster sessions so you can address questions from the audience

Session A: Soil Ecology and Biogeochemistry (p.76)

A1	Pascal BOECKX	The role of rhizodeposition for N cycling in northern fen ecosystems
A2	Andreas DEMEY	N fate of decomposing hemiparasitic plant litter: a ^{15}N tracer study
A3	Anette GIESEMANN	Using site preference of N_2O to differentiate between fungal and bacterial N_2O formation in soil
A4	Martin WERTH	13C fractionations at the root-microorganisms-soil interface and their implications for carbon partitioning studies
A5	Alessandra D´ANNIBALE	Soil mesofauna community responses to elevated CO_2 and GM barley
A6	Michael MASTERS	Restoration of soil organic carbon with cultivation of perennial biofuel crops
A7	Gervasio PIÑEIRO	Estimating carbon fluxes simultaneously in two soil fractions using ^{13}C changes after vegetation replacements
A8	Alina JASEK	Application of modified chamber method to urban river CO_2 flux and its carbon isotopic composition measurements – preliminary results
A9	Carla Roberta GONÇALVES REIS	Nitrogen dynamics in mangrove areas of Ilha do Cardoso, southeast coast of Brazil
A10	Tamara HUNJAK	δ^{18}O spatial distribution of precipitation in Croatia
A11	Saša ZAVADLAV	Seasonal variations of dissolved inorganic carbon and d^{13}C of tufa precipitating water (Krka River, Slovenia)
A12	Louise ANDRESEN	Investigating microbial responses of ^{13}C-glycine addition to dry heathland soils under elevated CO_2, drought and warming, using ^{13}C-PLFA analysis

Session B: Plant Ecophysiology (p.83)

B1	Mirjam STUDER	Dual isotope labelling (^{13}C and ^{18}O) for studying organic matter dynamics within the plant-soil system
B2	M. Paz ESQUIVIAS	Water sources used by coastal sand dune vegetation: spatial and seasonal variations
B3	Juan JÁUREGUI	Water sources isotopic analysis of the Moroccan species *Argania spinosa*
B4	Robert PANETTA	Rapid analysis of water isotope fractionation along a Pinus spp. branch: in-situ measurement of matrix-bound waters
B5	Nadia S SANTINI	Understanding the freshwater and seawater dependence of the mangrove *Avicennia marina* using oxygen isotopes as tracers for water sources

B6	Jocelyn EGAN	High-resolution $\delta^{13}CO_2$ soil efflux monitoring in tree girdling experiment exposes large temporal variability
B7	Valery TERWILLIGER	Plasticity in carbon and nitrogen use in relation to the distribution of oaks in an eastern North American deciduous forest

Session C: Fractionation & Models (p.88)

C1	Lluís JOVER	Performance of Bayesian estimation in underdetermined mixing models
C2	Vasily VAVILIN	From Rayleigh's distillation model to the dynamic model for stable isotopes fractionation based on substrate consumption and biomass growth
C3	Aline BLANCHET-AURIGNY	Linear relationship between discrimination factor and isotopic signature of food sources: myth or reality?
C4	Michelle CHAREST	Turnover Rates of Sulphur in Liver and Muscle Tissue of Brook Trout, *Salvelinus fontinalis*, determined by diet shift experiments in the field and laboratory
C5	Ashlie CIPRIANO	Experimental determination of discrimination factors and turnover rates of the ctenophore *Mnemiopsis leidyi*
C6	Sophie KOHLER	Tissue-specific variations in $\delta^{13}C$ and $\delta^{15}N$ discrimination factors of marine birds: Using chicks' tissues to infer seasonal variations in the feeding habits of adults.
C7	Antoine EMMERY	Explaining growth variability of the Pacific oyster in different coastal ecosystems: characterisation of the trophic and abiotic environment of Crassostrea gigas by the coupling of isotopic analysis and DEB modelling
C8	Pierre-Yves PASCAL	Low $\delta^{13}C$ composition of *Haplognathia* sp. in a Caribbean mangrove (Guadeloupe, FWI)
C9	Sora KIM	Differences among bulk carbon discrimination factors in a marine carnivore: a comparison of individual amino acid carbon isotope patterns
C10	Sarah BURY	Stable isotope analysis of high lipid-content notothenioid (anti-freeze) fish from the Ross Sea, Antarctica: lipid extraction issues and corrections
C11	Tamsin O'CONNELL	Carbon and nitrogen isotopic inhomogeneity of collagen from different tissues within an individual
C12	Yarnes CHRIS	Rapid Compound-Specific Stable Isotope Analysis of Amino Acids by GC-C-IRMS of Methyl Chloroformate Derivatives
C13	Lionnel MOUNIER	Latest developments and technologies in bulk and compound specific Stable Isotope Ratios Mass Spectrometry for ecological studies

Session D: Paleoecology (p.97)

D1	Nathaniel DOMINY	Antiquity and provenience of mummified baboons reveals location of Ancient Punt
D2	Rebecca FRASER	The stable isotope systematics of carbon, oxygen and nitrogen in modern koalas show plant-diet and climate interactions
D3	Olga SIDOROVA	Understanding recent and past climatic changes in the Siberian north with stable isotopes
D4	Maura PELLEGRINI	Oxygen isotope distribution of Bronze Age human populations in the British Isles
D5	Kerry SAYLE	Simultaneous $\delta^{13}C$, $\delta^{15}N$ and $\delta^{34}S$ isotope ratio determination of archaeological bone collagen.
D6	Isabella VON HOLSTEIN	Effect of diagenesis on isotope values of keratin: implications for archaeological proteins

D7	Victor FROSSARD	Chironomid abundance and carbon isotope signature as proxies for past lake-functioning
D8	Prasanta SANYAL	Intensification of monsoon, microclimate and asynchronous C4 appearance: Isotopic evidence from the Indian Siwalik sediments
D9	Vincent MOUCHI	δ^{18}O and Mg/Ca ratios in recent and fossil oyster shells: confronting thermodependant proxies
D10	Alexandra OPPELT	Chronologies in stable isotope ratios along primary and secondary growth directions of deep-sea corals
Session E: Isoscapes (p.104)		
E1	clement BATAILLE	Mapping the bioavailable strontium isotopic signature at regional scales
E2	Clive TRUEMAN	Using simple biogeochemical models as desk-based experiments to explore mechanisms driving global marine isoscapes
E3	Alexandra PEKARSKY	Using Oxygen and Hydrogen stable isotopes to determine migration connectivity between breeding and wintering populations of the Eurasian crane (*Grus grus*)
E4	Robert PANETTA	Simultaneous d^{13}C + dD combustion isotope analyser to track bird migration
E5	Suzuki YAEKO	The spatial and seasonal variations in the carbon, nitrogen and oxygen isotope values of kelp (Kombu) over three years in China, Japan and South Korea
E6	Jan DIERKING	Integrating stable isotope, otolith microchemistry, and genetic analysis to assess intra-population migration strategies of endangered anadromous North Sea houting
E7	Simona CERIANI	Satellite telemetry and stable isotopes: building isoscapes for loggerhead sea turtles in the Northwest Atlantic Ocean
E8	Patricia MANCINI	Identifying wintering areas of Sooty terns *Onychoprion fuscatus* in the Atlantic Ocean using stable isotope
E9	Gabriele STOWASSER	Does winter foraging of Southern Ocean seabirds vary between years?
E10	Fabiana SAPORITI	Complex latitudinal changes in the neritic isoscape of the south-western Atlantic shelf.
E11	Brittany GRAHAM	Aquatic isoscapes: a review of current research and future directions as it relates to fisheries science.
Session F: Animal Foraging Behaviour (p.111)		
F1	Robin NIECHOJ	Intraspecific stable isotope investigation of four temperate ant species: life stages, castes and temporal patterns
F2	Priscilla WEHI	Isotopic niches and nutrient intake: extracting foraging information from different sources
F3	Carl CLOYED	Inter- and intraspecific diet variability using stable isotopes in three species of Anura
F4	Thiago Simon MARQUES	Spatial and sexual variation in *Phrynops geoffroanus*' diet (Testudines, Chelidae) in altered habitats: a classic and isotopic approach
F5	Thiago Simon MARQUES	Sexual and ontogenetic niche variation in Caiman latirostris (*Crocodylia: Aligatoridae*) using stable isotopes of nitrogen
F6	Andrew ROBERTSON	Individual foraging specialisation in group living Badgers (*Meles meles*)

F7	Ashley STANEK	Dietary ecology of Alaskan gray wolves: integrating stable isotope and spatial analyses
F8	Rumiko NAKASHITA	Feeding ecology of brown bears of the Southern Kurils revealed by stable isotope analysis
F9	VALERIE SAUVINET	13C, ^{15}N and ^{34}S isotope abundances from human serum as diet biomarkers
F10	Frans RADLOFF	Browsing cattle? Stable isotope analysis of faecal samples reveals broad dietary type usage in Northern Namibia, Southern Africa
F11	Vivek VENKATARAMAN	Isotopic ecology of mammals in a high-altitude Ethiopian grassland
F12	Jaime RESANO	Using stable isotope mixing models as a dietary approach in a raptor species
F13	Petra QUILLFELDT	Hunting high and low – individual differences in seabird foraging behaviour revealed by stable isotope analysis
F14	Filipe R CEIA	Temporal consistency in the feeding ecology of an opportunistic species, the yellow-legged gull (*Larus michahellis*) in Portugal
F15	Carola SANPERA	Diet as a source of carotenoids for egg-yolk: link between colour and stable isotopes in the Audouin's gull
F16	Carola SANPERA	Effect of diet on the circulating and intra-clutch deposited antioxidants in near threatened Audouin's gull (*Larus audouinii*)
F17	Filipe R CEIA	Short- and long-term consistency in the foraging niche of wandering albatrosses
F18	Fabiana SAPORITI	Dietary change over winter migration in *Spheniscus magellanicus* yearlings inferred though stable isotopes analysis.
F19	Sarah NAHON	Evaluation of autotrophy versus heterotrophy in symbiotic scleractinian corals: a stable isotope study in French Polynesia Islands
F20	Jan DIERKING	Challenges of conducting stable isotope analysis on an endangered fish species: validation of results relying on novel non-lethal muscle tissue sampling
F21	Lucy SOARES	Using data from feeding habits and isotopic mixing models to understand the diet of the Blackfin goosefish *Lophius gastrophysus* from South-Western Atlantic
F22	Gislaine MANETTA	Ontogenetic change in energy sources for *Plagioscion squamosissimus* (Heckel, 1840) and *Hypophthalmus edentatus* (Spix, 1829) in the Upper Paraná River floodplain.
F23	Tony ROBINET	Trophic position during the marine life of two lampreys from the Bay of Biscay as inferred by stable isotopes in muscle and liver
F24	Niriniony Solomalala RABEHAGASOA	Vertebrae isotopic signature as a tool to depict ontogenetic trophic shifts of the blue shark (*Prionace glauca*) in the Southwest Indian Ocean
F25	Rick SCHERER	Spatial variation in the diets of female Steller sea lions inferred from ^{13}C and ^{15}N values of vibrissae from pups
F26	Lisette ZENTENO	Dispersal patterns of South American sea lions (*Otaria flavescens*) in the Atlantic revealed by oxygen isotopes from bone carbonate
F27	Lorrie REA	Using chemical feeding ecology to understand variability in mercury concentrations in western Aleutian Steller sea lions.
F28	Craig STRICKER	Carbon and nitrogen isotope discrimination factors for Steller sea lion vibrissae on milk and fish/squid diets
F29	Luis HUCKSTADT	Being a specialist in a changing environment: the diet of the crabeater seal along the western Antarctica Peninsula

F30	Tuula SINISALO	Combining carbon stable isotope ratios (δ^{13}C), fatty acid profiles (FA) and compound-specific carbon stable isotope ratios of individual fatty acids in seal muscle and blubber samples helps to build a reliable generalized picture of seal diets
F31	Katherine GAVRILCHUK	Intrapopulation isotope variation among humpback whales (Megaptera novaeangliae) summering in the Gulf of St-Lawrence, Québec, Canada
F32	Joan GIMÉNEZ VERDUGO	Stable isotope signatures in fin whales (*Balaenoptera physalus*) from the NW Atlantic coasts of Spain
F33	Veronique LESAGE	Resource partitioning among St Lawrence beluga whales: an assessment based on bayesian multisource mixing models and stable isotopes

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G2	Jean-Marc ROUSSEL	Trophic ecology of the invasive red-swamp crayfish *Procambarus clarkii* and its potential predators in the Brière Marsh, France
G3	Scott COLBORNE	Foraging ecology of native pumpkinseed sunfish (*Lepomis gibbosus*) following the invasion of zebra mussels (*Dreissena polymorpha*).
G4	Grzegorz SKRZYPEK	Flash flood and drying cycles as hydrological controls of waterhole ecosystems in semiarid zones
G5	Helen AGASILD	Biogenic methane contributes to the food web of a large shallow lake
G6	Alexis GUILPART	Land-based salmonid farm effluents enhance heterotrophy in headwater stream food webs
G7	Nicolas HETTE TRONQUART	Influence of riparian vegetation on temperate stream food web: seasonal variations along a shading gradient
G8	Jean-Michel MORTILLARO	Degradation kinetics of two Amazon floodplains macrophytes (*Paspalum repens* and *Salvinia auriculata*) from a multi-tracer approach
G9	Kaire TOMING	How δ^{13}C values reflect the origin of organic matter in a large and shallow lake in calcareous catchment?
G10	Gilles LEPOINT	Stable isotope composition spatial variability at microhabitat scale of macrofauna inhabiting a tropical freshwater stream (Pérou River, Guadeloupe)

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H1	Míriam ALBRECHT	Variation in the role of terrestrial subsidies for the ichthyofauna along the sedimentation gradient in a tropical reservoir in central Brazil
H2	Míriam ALBRECHT	Main carbon sources for primary consumer fishes in an Atlantic Forest stream along the river continuum
H3	Evanilde BENEDITO	Are fish what they eat? A review about the discrimination tissue-diet in fishes
H4	Evanilde BENEDITO	Energy sources and trophic structure of fish in neotropical streams
H5	Charlotte DROMARD	Herbivorous fishes do not share the same trophic niches on the reefs of Guadeloupe (Lesser Antilles)
H6	Charlotte DROMARD	Trophic niche of the threespot damselfish (*Stegastes planifrons*) and the dusky damselfish (*Stegastes adustus*) on Guadeloupean reefs (Lesser Antilles)
H7	Clive TRUEMAN	Using SIMS-based oxygen isotope analyses to calibrate time in incrementally-grown biominerals

H8	Mikko KILJUNEN	Otolith Isotopic Composition as Potential Indicator of Atlantic Salmon Migrations in the Baltic Sea
H9	Jyrki TORNIAINEN	Feeding migration patterns of River Simojoki salmon in the Baltic Sea: Evidence from stable isotope analysis of scales
H10	Jens NIELSEN	Large scale ocean dynamics and cod growth: Weight at age and otolith stable isotopes in Faroe shelf cod
H11	Michael POWER	Determining thermal habitat use strategies among Labrador young-of-the-year Arctic charr (*Salvelinus alpinus*) using otolith oxygen stable isotope methods
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I1	Anik BRIND'AMOUR	Community isotopic diversity indices and their ability to discriminate among trophic food web
I2	Amandine SABADEL	Mutualism/Commensalism vs. Parasitism: Using Compound Specific Stable Isotope Analysis of Amino Acids to Unravel Complex Trophic Relationships
I3	Evan DELUCIA	Elevated atmospheric CO2 alters the arthropod community in a forest understory
I4	Kristine MARALDO	The origin and fate of amino acids from producers to soil consumers in grasslands
I5	Thibaud MASCART	Trophic and specific diversity of harpacticoid copepods associated to *Posidonia oceanica* macrophytodetritus
I6	Marcelina ZIOLKOWSKA	Benthic food web structure and functioning in the Puck Lagoon eelgrass beds (southern Baltic Sea)
I7	Amandine VASLET	Spatial analysis of stable isotope data to assess primary food sources and foraging areas of juvenile fishes in mangrove and seagrass bed ecosystems
I8	Loïc MICHEL	Trophic tracers reveal considerable diversity among diets of dominant amphipods from *Posidonia oceanica* seagrass meadows
I9	Jean-Charles LECLERC	Specific assemblages and Trophic structure within microhabitats of a *Laminaria hyperborea* Forest
I10	François REMY	Leaf fall impact on diversity and trophic ecology of vagile macrofauna associated with exported *P.oceanica* litter.
I11	Francesca COLOMBO	Trophic structure of vermetid reef community: high trophic diversity at small spatial scales
I12	Pierre CRESSON	How organic matter sources are integrated into trophic networks of an artificial reef system ? A case study from French Mediterranean coastal zone.
I13	Nolwenn QUILLIEN	Eutrophication impacts of green macroalgal blooms on the benthic food webs and on the flatfish nursery function of North Eastern Atlantic fine sand beaches
I14	Sandrine LAURAND	Seasonal impact of a green macroalgal bloom on the benthic food web of an intertidal lagoon (Dublin Bay, Ireland)
I15	François GAUDIN	Food web structure of the long-term surveyed ‘Pierre Noire’ fine sand community (Bay of Morlaix, France): description and seasonal variability revealed by stable isotopes analyses
I16	Carine RIGOLET	Characterizing trophic structures of muddy soft-bottom communities
I17	Valls MARIA	Trophic structure of the Balearic Islands continental shelf and slope (western Mediterranean)

I18	Vanesa PAPIOL	Trophic web structure and seasonality of slope megafauna of the NW Mediterranean; relationship with available food sources.
I19	Emanuela FANELLI	Environmental drivers of isotopic composition variability in deep-sea megafauna over mainland and insular slopes of the Balearic Basin (W Mediterranean)
I20	marie PORTAIL	A comparative study of nutritional patterns among cold-seep and hydrothermal vent chemosynthetic communities in the deep Guaymas basin, Mexico
I21	William REID	Spatial differences in Southern Ocean hydrothermal vent food webs: influences of chemistry, microbiology and predation on trophodynamics.
I22	Kena FOX-DOBBS	The role of chemosynthetic productivity within intertidal food webs at anthropogenic hydrogen sulfide seeps in Commencement Bay, Washington
I23	Chris HARROD	An overwhelming presence: δ13C and δ15N reveal the dominance of upwelling-derived C and N in Chilean subtidal benthic fishes.
I24	Sébastien LEFEBVRE	δ13C and δ15N ratios of two benthic organisms used along with other ecological indicators
I25	Violette MARCHAIS	Trophic functioning of a temperate coastal ecosystem revealed by stable isotope analysis in oysters Crassostrea gigas
I26	Gill NOTMAN	The mutual mucus ingestion hypothesis. Stable isotope evidence for convergent resource use in intertidal grazing gastropods within experimental microcosms.
I27	Magali GOMEZ	Determination of the trophic level of *Megathura crenulata* (Sowerby, 1825) using the isotopic signal of δ 13C and δ15N.
I28	Gauthier SCHAAL	Regional scale isotopic observations : integrating stable isotope data to long-term environmental surveys
I29	Alexandra BAETA	Habitat-related diet of macrofauna consumers in intertidal areas

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J1	Anthony BICKNELL	Identifying potential dispersal mechanisms with SIA and a multi-source mixing model: individual analysis of a highly pelagic seabird.
J2	Alex BOND	Linking at-sea mortality of Flesh-footed Shearwaters (*Puffinus carneipes*) to breeding colonies of origin using multiple biochemical markers
J3	Patricia MANCINI	Using stable isotope analysis to establish trophic relationships among seabirds of Brazilian oceanic islands
J4	Dorothée KOPP	Trophic relationships in the eastern English Channel: how to simplify food web structure description for trophic niche determination?
J5	Pepe ESPINOZA	Revisiting the trophic structure of an ecosystem constrained by an intense oxygen minimum zone, the Northern Humboldt Current system
J6	MONICA YANIRA RODRIGUEZ	Stable isotope δ^{13}C and δ^{15}N as indicators of isotopic enrichment by denitrification in an antiestuarine ecosystem: the upper gulf of California
J7	Ryan WOODLAND	Trophic assimilation and fate of diazotrophic N fixed by *Nodularia spumigena* in an estuarine planktonic food web
J8	Svenja KRUSE	Trophic position and interactions between the tunicate *Salpa thompsoni* and the amphipod *Themisto gaudichaudii* in the Southern Ocean: compound-specific nitrogen isotope analysis
J9	Craig LONGMORE	Combined isotopic and genetic analyses reveal population structure, habitat use and life-history of two deep-sea teleosts in the North Atlantic
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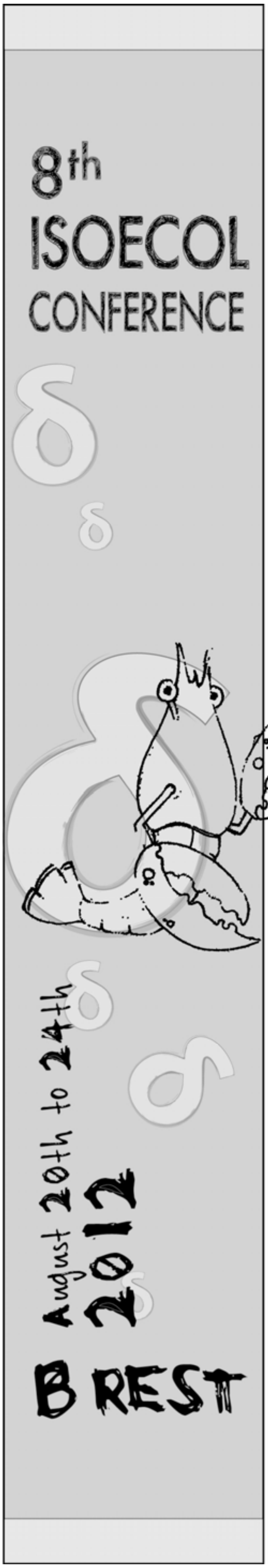
K2	Samo TAMŠE	Tracing sources of nitrate from agriculture in groundwater
K3	Ann-Lise NORMAN	A Slow Burn: Ecosystem Acidification and its effect on the Castle River in Southern Alberta, Canada using Boron, Sulfur and Oxygen Isotopes
K4	Philipp SCHUBERT	Isotopic signatures of eelgrass (*Zostera marina* L.) as bioindicator of anthropogenic nutrient input
K5	Inés G. VIANA	Stable nitrogen isotopes in coastal macroalgae: biogeographic and anthropogenic variability
K6	M.Gloria PEREIRA	Can stable isotope signatures explain changes in POP concentrations in UK gannet (*Morus bassanus*) eggs?
K7	Igor EULAERS	Combined nestling feather analysis for stable isotopes (δ^{13}C and δ^{15}N) and persistent organic pollutants reveals ecosystem-dependent bioaccumulation patterns in subarctic predatory birds
K8	Thais N. CORBISIER	Biomagnification of mercury in the trophic web off Baixada Santista continental shelf, SE Brazil



ORAL SESSIONS

Plenary Sessions

Pr. Brian Fry

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Estuarine Conservation and Restoration in the 21st century : Using Stable Isotopes to Turn the Red Dots Green Again

Human population growth is increasingly concentrated along coasts and in urban centers located along estuaries at the land-sea interface. Many types of downstream pressures result from the human activities in local watersheds, and what were once “green” ecozones in our estuaries are now becoming “red” problem spots. The theme of this talk is that isotopes can help in attempts to reverse these problematic trends, especially because extended forensic-type isotope profiles can be developed to distinguish natural system function vs. dysfunction. A review of tradition non-isotope ecosystem evaluations shows that these evaluations typically focus on bottom-up effects of nutrient loading and sediment delivery, leaving out fisheries mostly because fish seem to be too mobile easy monitoring. However, stable isotopes are strong recorders of integrated food web fisheries interactions, and this talk considers top-down or “fish-based” perspectives of ecosystem integrity. There are at least five different ways that isotopes can help evaluate estuarine functioning for fisheries food webs: 1) geolocation and residency of consumers within isoscape maps, 2) metabolic growth status and trophic level of key consumers, 3) productivity of fish measured from lipid profiles, 4) terrestrial and upland catchment-level subsidies to food webs via detrital materials, and 5) fisheries support from benthic vs planktonic sources. This talk will consider examples of these five factors within the context of the GENIE project, the Global Excellent Network of Isotopes in Estuaries. So far, GENIE is only an idea of a network rather than an actualized fact. It will take a community of isofolks to make GENIE work well and help turn those red dots green again.

Pr. Sébastien Lefebvre

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Insight from modelling into isotope ecology: love story never ends

Stable isotopes are widely used in trophic ecology. Modelling is being performed at several steps and for different purposes. This key note aims at reviewing how modelling in its broad sense helps trophic ecology using stable isotopes as tracers. Mixing models are exploited to reconstruct diets and several versions of such tools exist, the more recent ones using Bayesian statistics. The use of these models must be done in the context of three strong hypotheses: (i) organisms are in equilibrium with their food sources (ii) food source ratio is known and constant and (iii) the trophic step fractionation is known and constant. Isotope incorporation models were built to circumvent the points (i) and (ii) and were also applied to determine trophic step fractionation in experimental studies. Some of these incorporation models benefit from a parallel use with mixing models. Trophic step fractionation has been shown to vary between species and this can be determined using diet switching experiments. However, it possibly varies significantly within species depending on food level, food quality, temperature, age etc… Here, I will focus on a new generation of mechanistic and dynamic models (using the context of DEB theory) which encounter for trophic step fractionation explicitly as well as isotope incorporation through time. This kind of models are easily combined with mixing models to better reconstruct diets while fully respecting the three hypothesis above. In these models, isotope routing is fully described and this makes possible the use of organs in foraging studies. To become a “canonical” model, simplification should be undergone depending on the application and specific open source software would be built. Definitely, love story between isotope ecology and modelling never ends.

Pr. Stuart Bearhop

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Stable Isotopes as markers of diet and trophic structure: the good the bad and the ugly

The use of stable isotopes in foraging studies has been something of a "slow burner" and remains a surprisingly underused technique among animal ecologists, yet they can be very powerful tracers of nutrient flow. This presentation will briefly cover stable isotopes as dietary markers illustrating the power and breadth of the approach. This will be followed by a discussion of some more recent ideas about potential applications of stable isotope analyses such as elucidating individual specialisations and as descriptors of community structure. It will close with some ideas as to why some researchers have been hesitant about using the approach, highlighting some common errors and misconceptions that can make data interpretation equivocal.

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Food web ecology and stable isotopes; applications from macrofauna to microorganisms in marine and coastal ecosystems

δ13C and δ15N results of the trophic ecology of selected sedentary and migratory macrofauna, meiofauna and plankton larvae will be presented. In fact, different characteristics of ecosystems functioning have been highlighted through stable isotopes measurements in marine environments. For example, the trophic plasticity at a geographical scale of the oyster Crassostrea gigas was pointed out, even for a single trophic interaction namely, oysters and microphytobenthos, within similar intertidal ecosystems. When regarding migratory species, the trophic dynamic links throughout migration can be illustrated by the brown shrimp Penaeus aztecus along the South Texas coast. Here, stable isotopes showed the diversity of the feeding habitats of the juvenile brown shrimps during their migratory life cycle. Although much less applied to meiofauna as compared to macrofauna, stable isotopes provided evidence of the high diversity of food sources for different nematode communities (from microphytobenthos to detrital macroalgae) through comparisons among different intertidal mudflats. Stable isotope labelling is also increasingly used, allowing more precise investigation of food source characterisation of little organisms. For example, the importance of bacterivory in planktonic larvae of Crepidula fornicata was assessed by a dual stable isotope (13C, 15N) labeling approach, indicating that bacteria formed a significant part of the larval nutrition even in the presence of phytoplankton.

Carbon flow in the belowground food web of an agricultural field site assessed by isotope tracers: a pulse-labeling experiment

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The flow of carbon from plants to animal food webs is one of the most important transfers of organic material in soil systems, but still many details remain unclear. In the following experiment stable isotopes of carbon (^{13}C) and nitrogen (^{15}N) were used in a pulse-labeling experiment to follow the flux of these isotopes through the soil system. On an agricultural site planted with maize plexiglass chambers were installed and $^{13}CO_2$ was circulated for three hours. Further, the soil inside the chamber was watered with $K^{15}NO_3$. Soil fauna was extracted before, 2, 5, 10 and 25 days after the labeling event and analysed for ^{13}C and ^{15}N to prove if animals had fed on maize-borne resources.

25 days after labeling predators were enriched by 19 δ-units in ^{13}C compared to before the labeling, while decomposers were only enriched by 15 δ-units. Further, predators were enriched by 220 δ-units in ^{15}N, while decomposers were only enriched by 110 δ-units.

The enrichment in ^{13}C and ^{15}N indicates that transfer of organic material from plant to soil animals had taken place and was more effective in predatory species than decomposers. Therefore, soil animals rely on shortly available resources and in particular predators incorporate “fresh” organic material into their body tissue rather than “old” material.

IsoFD: A novel method for measuring the unbiased isotopic signature of surface flux

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Measurement of the isotopic composition of soil-respired CO_2 can provide a wealth of insight into soil level carbon cycle processes that cannot be achieved using measurements of bulk CO_2 emissions alone. Because of this, researchers have increasingly moved toward using natural abundance and tracer isotopic techniques in ecosystem respiration studies. However, recent experimental and theoretical evidence has called the accuracy and applicability of traditional isotopic measurement methodologies into question. Here we present a brief overview of these traditional techniques and discuss why they yield biased estimates of the soil isotopic flux, largely owing to disturbances to the soil's natural diffusive regime. We will then discuss the theory behind a new technique called Isotopic Forced-Diffusion (IsoFD) that helps eliminate these biases and offers high temporal resolution isotopic flux data. Lab benchmarking results for the method will be presented, in addition to data from preliminary field trials.

Tracing organic matter during it decomposition in soil using ^{13}C, ^{15}N highly labelled material: the example of wood and pyrogenic matter decomposition dynamics

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Soil organic matter is playing a major role in the carbon (C) cycle in terrestrial ecosystems. The C stocks in soils are 3 times higher than in the living biomass or in the atmosphere and C residence times in soils are one degree of magnitude higher than the residence time in living plants. However, the mechanisms leading to this higher stability of organic matter remain largely unknown. One main difficulty lies in the access to this organic matter without major disturbance to the system and with a specific identification of the physical, chemical and microbiological processes. The use of stable isotopes could be an adequate solution to study the decomposition of organic matter and it stabilisation in the soil.

In this study, we followed the decomposition of two types of organic matter – wood residues and pyrogenic matter (organic residues that experienced heat under oxygen-free atmosphere, for example during a wildfire) in field incubations in a forest clearing. These two types of organic matter are considered as potential important sources to stable C in soils. We applied highly labelled ^{13}C and ^{15}N labelled wood and pyrogenic matter (wood grown in a labelling chamber – half of it charred in order to prepare the pyrogenic matter) to a forest soil and followed the decomposition and C stabilisation over a year. We measured continuously the CO_2 and dissolved organic matter coming out of the soil and, after one year, we sampled the soil in order to investigate the decomposition and stabilisation processes. We particularly focussed on the microbial (microbial biomass with / without label, DNA fingerprints), physical (association of the labelled organic matter to the different particles of soils) and chemical (specific biomarkers) fate of organic matter. Thanks to stable isotope techniques, we were able to identify the main decomposition pathways as well as unexpected interactions between the organic matter already present in the soils and the newly added one (priming effect). This communication will take advantage of this experiment to present the advantages and limits of stable isotopes technique for organic matter decomposition studies.

Groundwater and rainfall availability control soil nitrogen dynamics in a stand of invasive Mesquite (*Prosopis pallida*)

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Soils in deserts and arid grasslands worldwide tend to have high $\delta^{15}N$ values, and the mechanisms that drive this pattern are not well understood. Mesquite (*Prosopis pallida*) is an N-fixing phreatophyte, introduced to Hawaii in the early 19th century, which now forms monospecific stands in many dry, leeward areas of the island chain. Stem sap $\delta^{18}O$ values indicate *Prosopis* trees in lowland areas are able to access shallow groundwater, while in upland areas they are reliant on rainfall to meet their water requirements. During periods of low rainfall, trees from upland sites showed lower leaf water potential and pre-dawn photosynthetic efficiency, and higher leaf $\delta^{13}C$ values than lowland trees, indicating seasonal water shortages where groundwater was not available. Total N content of soils was greater at lowland sites (3.1%), than at upland sites (0.8%), and mobile N pools were around seven times higher at lowland sites. *Prosopis* is the only tree species in the studied areas, and differences in soil chemistry are likely due to the presence of around four times more *Prosopis* biomass, and (> 10 times) higher N additions from litterfall at lowland sites. However, N-mineralization rates in soils at all sites appear to be strongly controlled by rainfall. $\delta^{15}N$ values of soils and *Prosopis* leaf tissues were 4-6‰ lower at lowland sites than upland sites, indicating an increased proportion of N accumulated in lowland areas from low $\delta^{15}N$ sources (e.g., N_2 fixation or low $\delta^{15}N$ groundwater nitrate), and/or a decreased ‘leakiness’ of N cycling in lowland plots, caused by a decoupling of the production and mineralization of N in lowland areas.

Tracing carbon allocation through non structural carbon pools of *Larix decidua* exposed to elevated CO_2 and soil warming at the upper tree line

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Increasing CO_2 concentrations stimulate photosynthetic C uptake of plants, but the additionally acquired carbon can only be used above a certain temperature threshold. In our experiment, we investigated the effects of nine years of elevated CO_2 exposure (FACE) and three years of soil warming on C allocation in 35-yr-old *Larix decidua* trees growing at 2180 m a.s.l. In spring 2010, after the end of the FACE experiment, we carried out a pulse labeling experiment using 99% ^{13}C enriched CO_2 to trace the pathways and translocation velocity of carbon through different pools within larch: from needles into the branch bark and branch wood. We analyzed the isotope label dynamics in non-structural carbon (NSC) pools, such as starch, lipids as well as low molecular sugars and sugar alcohols (glucose, sucrose and pinitol).

Our results showed that the combination of labeling experiment and compound-specific isotope analysis provides a high potential for studying carbon fluxes in plants. While the initial label strength in a NSC pool depends on the dilution with older carbon, the mean residence time of the label in the pool depends on the translocation speed into other tissues or transformation to other pools. Sucrose showed a high initial label (low contribution of old carbon) but a very short mean residence time (fast allocation into bark). Pinitol behaved just the opposite way: high contribution of old carbon and slow allocation. Glucose, starch and lipids were subject to transformations and showed high mixing with older carbon. The velocity of C allocation to woody tissues was comparable with larch at lower altitudes in Switzerland (Keel et al. 2007) but much faster than for larch in Siberia (Kagawa et al. 2006). We observed that neither pool sizes nor C translocation velocity were persistently affected by elevated CO_2 or soil warming. The short vegetation period (three months) left only a small number of days above the limiting threshold temperature for growth and C acquisition. Furthermore, much carbon was utilized during time without C uptake (maintenance respiration, new needle and early wood formation). Thus only small amounts of C reserves were available for the next vegetation season.

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δ^{15}N pattern across sand dune systems: relevance of seawater spray in vegetation fertilization.

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Nitrogen is a key factor controlling plant performance and its limitation is one of the main factors restricting vegetation development and species community composition. Sand dune ecosystems are characterized for being nutrient-poor, harsh environments. Therefore, allochthonous nitrogen addition is expected to play an important role in the nutrients balance. Three different inputs have been described in coastal dunes: 1) N_2 fixation, 2) atmospheric deposition and 3) marine biological sources (sea turtle nesting, seaweed remains or guano). Seawater spray could also be considered a nitrogen source for coastal dune vegetation, but until now it has not been regarded as a relevant one.

The aim of this study was to analyze δ^{15}N pattern across a sand dune system, addressing variations in plant spatial distribution from upper beach to inland depression and to assess the potential relevance of seawater spray as nitrogen input. We hypothesized, that in our dune system, δ^{15}N enrichment in plant tissues would indicate organic nitrogen from marine origin.

δ ^{15}N, and N content were measured in 8 species in 5 points across the dune system La Flecha de El Rompido (37º12'N, 7º04'W) in Huelva, Spain: 1. Upper beach, 2. Foredune crest, 3. Foredune slack, 4. Secundary dune crest, 5. Inland depression. δ^{15}N differences were found in plant tissue from upper beach to inland depression but not in nitrogen content. δ^{15}N values were high in upper beach and foredune, suggesting a marine origin, whereas lower δ^{15}N values, were recorded inversely related to sea distance. Following δ^{15}N values and spatial gradient, 3 different strategies of N uptake were found: *Poligonum maritimum*, *Euphorbia paralias* and *O. maritimum* (plants of upper beach and foredune) would use nitrogen of marine origin; *Ammophila arenaria* and *Artemisia crithmifolia* -distributed along the entire gradient- showed an inland decreasing δ^{15}N pattern that would be explained by a change in the nitrogen origin. The last strategy is that of *Retama monosperma* and *Helichrysum picardii* (the most distant to sea), using non-marine nitrogen. These results indicate the importance of seawater nitrogen income for dune system vegetation and evidenced that dune plant species display different nitrogen uptake strategies along their zonal distribution.

Some truths and assumptions about using stable isotopes to trace the natal hosts of holometabolous insects in adult insects

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Holometabolous insects undergo complete metamorphosis. At emergence from the pupa, adult tissues consist of resources obtained from the larva which frequently has a different diet from adults e.g. specialised caterpillar host plants of nectar-feeding butterflies. Larvae usually feed close to the oviposition site selected by the female. However, highly mobile adults can disperse, often by flying, to search for food, mates and oviposition sites. Therefore insect movement can be studied where adult diet is isotopically and spatially distinct from larval foods.

Mixing and turnover occur when animals change from one isotopically distinct food to another. Controlled diet switches improve the interpretation of field samples in studies of animal movement between isotopically distinct foods, but publications remain scarce (Post, 2002). During a field study of dispersal by a grain pest, we investigated δ13C and δ15N mixing and turnover in beetles reared on δ13C distinct foods. Results showed unexpectedly rapid and variable rates of isotopic mixing and turnover. We subjected our data to various scenarios, assumptions and models to better understand these processes. This included comparison with studies showing that isotopic evidence of Coleopteran larval diets, changes in adults over time.

We discuss implications for interpreting field samples of holometabolous insects using data from studies where isotopic turnover in different tissue types has been compared. For beetles, it is possible to maximise evidence of larval foods by analysing relatively metabolically inert tissues like chitinous exoskeleton, avoiding metabolically active tissues such as fat body, especially in females (Gratton and Forbes, 2006). Short intervals between dispersal and sample collection also help maximise isotopic evidence from previous diets.

Uptake of stable isotope analysis in studies of terrestrial insects has been slow compared with other taxa. Provided that assumptions are carefully examined, we believe that it has further potential for studying dispersal by pest and beneficial insects, particularly when supported by experimental diet switches. As stable isotope analysis becomes more accessible, there are also opportunities for incorporating isotopic data into multivariate modelling of insect dispersal and population ecology.

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Isotopic niche metrics reveal the impact of an invasive species on a fish community

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Within the past 20 years, increasing temperatures and the rapid expansion of the non-native fish, roach, have been exerting pressure on the ecosystem of Windermere, the largest natural lake in England. This has coincided with a decrease in zooplankton abundance and a dramatic decline in the population of Arctic charr, a protected fish species. Stable isotope analysis of archived samples of zooplankton, macroinvertebrates and fish spanning over 25 years was used in conjunction with the dietary mixing model Stable Isotope Analysis in R (SIAR; Parnell et al. 2010) to reveal changes in the diets of the main fish species in Windermere over the course of the roach invasion and zooplankton decline. The invasive roach dominate littoral food sources, and may have influenced a diet shift in the native perch population from a predominantly littoral to a pelagic diet. Arctic charr, which was previously the dominant planktivore in the lake, has also seen a decline in the contribution of littoral sources to its diet. The diet of northern pike, the top predator in the lake, was previously dominated by Arctic charr but now predominantly consists of roach and perch. Stable isotope niche modelling using Stable Isotope Bayesian Ellipses in R (SIBER; Jackson et al. 2011) indicates considerable declines in the isotopic niche space and range of carbon sources for Arctic charr, while these metrics have increased for perch. These substantial dietary changes to the main members of the fish community represent a change in the flow of energy through the lake food web and demonstrate the pervasiveness of the impact of the roach invasion on the wider ecosystem.

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Combining stable isotope and fatty acid analyses to evaluate the effects of an invader on aquatic food webs in the Great Lakes

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Invasion by non-native species is often associated with food web disruption, causing cascading effects on both lower and higher trophic levels. In the Great Lakes ecosystems, the cumulative impact of the introduction of close to 200 invasive species has resulted in a shift from pelagic production to benthic production, which in turn, has reduced primary consumers biomass and associated fisheries. Since 2006, two mysid species now inhabit the nearshore and the offshore waters of the Great Lakes, the native *Mysis diluviana* and the invasive *Hemimysis anomala*. Although the ecology of *M. diluviana* has been well described, the introduction of the invasive *Hemimysis* is raising new questions about how Great Lakes' food webs are influenced by the new mysid species. Depending on its ability to integrate into the nearshore food web and consume benthic production, *Hemimysis* could restore nearshore connectivity between pelagic and benthic food webs. If consumed by fishes, *Hemimysis* may become a valuable food resource and allow for increased coupling between nearshore and offshore food webs. The diet, trophic position, and nutritional value of both mysids species were determined here using carbon and nitrogen stable isotope values and fatty acid profiles. Significant differences in carbon pathways were observed between both species with *M. diluviana* relying on pelagic production and *Hemimysis* utilizing both benthic and pelagic food sources. Fatty acid profiles confirmed the importance of both species as a source of lipids available to higher trophic levels.

The bloody shrimp are everywhere: spatial differences in the food sources of invasive *Hemimysis anomala* in the Great Lakes Basin

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Hemimysis anomala (HA), commonly known as the bloody red shrimp, is the latest known invader of the Great Lakes basin, having first been recorded in lakes Michigan and Ontario in 2006. HA are now found in all of the Great Lakes, except Superior, and in several locations along the St. Lawrence River. High densities found in both lentic and lotic ecosystems suggest the ability of HA to integrate into contrasting food webs. As of yet, the pattern of spatial variability in HA diets is unknown, particularly differences between lentic and lotic sites. Nevertheless, such information is necessary to accurately assess the impacts of HA on the Great Lakes ecosystem. Samples of HA and concurrent food web items were collected in 2011 from several sites in lakes Ontario and Erie and along the St. Lawrence River. Stable isotope methods were used to evaluate the main food sources and trophic position of HA. Mixing models were used to evaluate the importance of benthic versus pelagic food sources entering the diet of HA at each site where appropriate endmembers were available. Trophic position was also compared using baseline corrected $\delta^{15}N$ values for each site. Results have shown significant differences in HA diet between sites, both in sources of dietary carbon and trophic position, with differences not only between lentic and lotic sites, but also between sites within the same lake or river. Mean trophic offset for all sites was 2.28‰ above primary consumers, and site specific means ranged from -1.03 to 4.12‰, with both extremes found in the river. The mean fraction of dietary carbon derived from water column production was 0.62 and site specific means ranged from 0.18 to 0.97 throughout the sites with appropriate endmembers, with both extremes found in the lake sites.

Cross-system trophic effects: Does the invasive aquatic *Dikerogammarus villosus* affect terrestrial food webs?

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Emergence of merolimnic insects has been recognized to be an important flux of energy, which subsidize the terrestrial food web. Especially riparian arthropods (i.e. spiders and ground beetles), but also bats, birds or lizards benefit from this resource, which can contribute up to 100 % to the feeding strategy of the terrestrial predators. Most of the studies on this topic were done in undisturbed running water with only low impact of anthropogenic stressors. However, most running water are affected by inter alia a wide range of invasive species. One of the most important invasive species in Europe is the predacious amphipod *Dikerogammarus villosus*, which is native in the Ponto-Caspian region and invaded aquatic systems right up to France and the British island. By successful invasion a decline of aquatic invertebrates (including merolimnic insects) was observed in many cases. We hypothesized that the invasive amphipod reduces the biomass of emergence with propagating effects to the terrestrial food web. We used $\delta^{13}C$ and $\delta^{15}N$ food web analyses of two different riparian spiders (*Tetragnatha* spp. and *Pirata piraticus*) to investigate the cross-system effect of altered emergence due to the presence of *D. villosus* on the spiders feeding strategy in the River Rhine. The overall emergence biomass of merolimnic insects was independent of the presence of *D. villosus*, because of only seasonally emerging caddisflies and mayflies. However, biomass of emerging midges (Nematocera) decreased in presence of the amphipod, indicating a strong impact of the invasive species. Dependency of feeding strategy on aquatic insect emergence reduced by the invasive amphipod differed for the two spider species. The ground-dwelling *Pirata* showed no dependency, indicating a low impact of the reduced aquatic emergence. However, the feeding strategy of the net-building *Tetragnatha* was affected by the availability of merolimnic insects and therefore on the presence of the invasive *D. villosus*. To our knowledge this is the first study showing that in invasive invertebrate is able to affect the aquatic-terrestrial food web coupling. However, to what extent riparian predators are affected on the population level needs further investigation.

Classification of nitrate polluting activities through clustering of isotope mixing model outputs

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Nitrate source apportionment and spatial classification of nitrate polluting activities could advance water quality management. The objectives of this study were 1) to test the applicability of a Bayesian isotopic mixing model (SIAR) using temporal and spatial δ^{15}N- and δ^{18}O-NO_3^- data for nitrate source apportionment of different nitrate polluting activities, 2) to use SIAR output as input to an unsupervised learning algorithm to classify nitrate polluting activities, and 3) to assess if a decision tree model using physicochemical data could retrieve the isotope-based classification. Therefore, 30 sampling points were selected in different river basins in Flanders (Belgium), which were sampled monthly during two years. Based on SIAR results and δ^{11}B data, manure or sewage was identified as major, and soil N, NO_3^- in fertilizer and NH_4^+ in fertilizer and rain as intermediate, and NO_3^- in precipitation as minor NO_3^- sources. The k-means clustering algorithm allowed for classification of nitrate polluting activities that corresponded well to an *a priori* classification based on expert knowledge. Finally, a decision tree model allowed to correctly classifying 50-100% of the sampling points as compared to the k-means clustering approach. We therefore suggest that nitrate polluting activities, defined by the relative contribution of nitrate pollution sources, can be established via clustering of SIAR analyses of δ^{15}N- and δ^{18}O-NO_3^- from water samples representative for an entire river basin. Classification of additional sampling points in the as such established classes could then potentially be done via decision tree models that use classical and easier to measure physicochemical data.

Accounting for the process of foraging in source-level variation in isotopic mixing models

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Mixing models that use a Bayesian approach such as SIAR and mixSIR have become invaluable tools in ecology for studying aspects such as food web structure. While these models excel at teasing apart the input of various sources when they are distinct and identifiable, sources with similar signatures or with overlapping uncertainties can make attributing proportional contributions to the mixture difficult. One potential cause of this difficulty is the use of fixed standard deviations on the sources as a way to quantify source variability. With this seemingly sensible assumption comes the often unrealistic and inherent assumption that consumers sample one single prey item from each source and do so freely across the full range of the distribution describing that source's signature. In reality, consumers likely sample several items from each source and in doing so tend towards the source population's mean signature with increased consumption by the consumer (i.e. sampling). One way of accounting for this foraging behaviour more accurately would be to model error with a sampling behaviour relating to the proportion of each source in the diet. This approach would result in a downward scaling of error similar to that of standard error as opposed to standard deviation. However this would also lead to problems of confounding and correlated parameters in the model, which can be difficult to identify. One method to address this problem is to restrict this otherwise free process using metabolic theory to estimate the intake rates of consumers, which hence scale the source-associated variance incorporated into the mixture downwards. By incorporating consumer behaviour more accurately, resulting models will provide a more precise and hence better description of various ecological systems.

Determining trophic niche width: An experimental test of the stable isotope approach

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Determining the trophic niche width of an animal population and the relative degree to which a generalist population consists of dietary specialists are long-standing problems of ecology. It has been proposed that the variance of stable isotope values in consumer tissues could be used to quantify trophic niche width of consumer populations. However, this promising idea has not yet been rigorously tested. By conducting controlled laboratory experiments using model consumer populations (*Daphnia* sp., Crustacea) with controlled diets, we investigated the effect of individual- and population-level specialisation and generalism on consumer $\delta^{13}C$ mean and variance values. While our experimental data follow general expectations, we extend current qualitative models to quantitative predictions of the dependence of isotopic variance on *dietary correlation time*, a measure for the typical time over which a consumer changes its diet. This quantitative approach allows us to pinpoint possible procedural pitfalls and critical sources of measurement uncertainty. Our results show that the stable isotope approach represents a powerful method for estimating trophic niche widths, especially when taking the quantitative concept of dietary correlation time into account.

Evidence for seasonal shifts in the isotope composition of aquatic primary consumers and incorporating temporally dynamic baselines in mixing models

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Stable isotopes are widely used to make inferences regarding food web structure and the phenology of diet shifts, applications that require accurate isotopic characterization of trophic resources. Most isotope mixing models require that endmembers are relatively stable; yet, there is mounting evidence that the isotopic composition of aquatic organisms often used as mixing model endmembers (i.e., baselines) can change over periods of weeks to months. To evaluate the general assumption of temporal stability in non-zooplankton aquatic invertebrates, $\delta^{13}C$ and $\delta^{15}N$ time series data from the literature were analyzed for seasonality and the influence of biotic and abiotic factors on isotope temporal patterns. We found that all size-classes displayed a winter-to-summer enrichment in $\delta^{13}C$ and depletion in $\delta^{15}N$, and that the amplitude of isotopic cycles was negatively related to body size. For $\delta^{13}C$, periphytic grazers were more variable and displayed larger temporal changes than detritivores; whereas, temporal variability and magnitude of change in $\delta^{15}N$ was most strongly related to ecosystem trophic state. Given these results, we built a dynamic baseline mixing model that allows growing consumers to track temporal gradients in the isotopic baselines of food webs (simulations show that the isotopic equilibrium of a consumer with its diet depends on both the rate of change of the isotopic baseline and equilibration rate of the consumer). In an empirical application, mixing models of varying complexity were used to estimate the relative contribution of benthic versus pelagic carbon sources *p* to juvenile fish in a fluvial lake ecosystem. Estimates of *p* derived from a static mixing model indicated broad interspecific variation in trophic niche, ranging from complete benthivory to >95% reliance on pelagic food webs. Output from the more realistic dynamic baseline mixing model increased estimated benthivory by an average of 36% among species. Our results emphasize the need for researchers to recognize the potential for temporal changes in non-zooplankton aquatic invertebrate consumers at time-scales relevant to seasonal studies and, if present, to account for temporal dynamics in isotope trophic models. Additionally, our dynamic baseline model provides a formalized framework for incorporating temporally dynamic isotope conditions in trophic studies of higher consumers.

A geometric method for estimating stable isotope discrimination factors

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Stable isotope mixing models generally require three inputs: source isotope values (prey), mix isotope values (consumers), and discrimination factors. The most recent models also allow the incorporation of error around all three of these inputs. Isotope values of prey and consumers are obtained easily, but discrimination factors can vary with species, age, diet, and other physiological or environmental factors. Because discrimination factors have only been determined for a few specific cases, there has been considerable discussion about how influential discrimination factors are to mixing model output, and how to estimate discrimination factors without controlled captive feeding studies, which are impractical for many species.

The fundamental mathematical principle implicit in all mixing models is that consumers' isotope values, once adjusted for isotopic discrimination, should fall within the convex hull polytope (an n-dimensional polygon) created by the various prey isotope values in isotopic space (e.g., $\delta^{13}C$-$\delta^{15}N$ space). When adjusted consumer values fall outside the "mixing space" created by the prey isotopic values, it is because of incomplete prey sampling, inaccurate estimation of discrimination factors, or both. More intensive sampling or additional study of the system can address the former, and here we assume that prey species have been sampled adequately.

The problem of estimating discrimination factors can be reduced to a problem in geometry – a set of points (consumers) must be translated to fit within the convex hull of another set of points (prey). We present a linear program, which, in a given system, estimates the upper and lower bounds on discrimination factors, as well as a probability distribution for discrimination factors in multiple dimensions of isotopic space. Strict unconditional bounds result in the possibility of consumers' values falling within the range of prey values, but outside the convex hull mixing space. This will allow an objective estimate of discrimination factors (and associated error) to be incorporated into mixing models and improve model output.

Session 5: Fractionation and discrimination factors, where are the damages?

Individual amino acid turnover rates in muscle tissue from a multi-year study of captive Pacific Bluefin Tuna

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We determined nitrogen turnover rates of individual amino acids from a long term (up to ~8 years) laboratory experiment using captive Pacific bluefin tuna, *Thunnus orientalis* (PBFT), a large endothermic pelagic fish fed a controlled diet. PBFT are a known migratory species, making trans-Pacific migrations between Japan and the California Current Large Marine Ecosystem (CCLME). Recent immigrants to the CCLME (δ^{15}N ~ 11.5‰) were collected in San Diego, CA and transported to the Tuna Research and Conservation Center (TRCC) where they were fed a controlled diet of a consistent mix of squid and sardine from nearby Monterey Bay (δ^{15}N ~ 14.0‰). This experiment provided an opportunity to track ^{15}N incorporation rates of individual amino acids in muscle tissue. Length and weight measurements of captive PBFT allowed rate of growth to be determined during the experiment. We will report amino acid ^{15}N incorporation rates both as a function of time and growth as well as individual amino acid trophic discrimination factors (TDFs). Changes in the δ^{15}N values of amino acids across trophic levels are the underlying drivers of the trophic ^{15}N enrichment. The rate of incorporation of amino acids into protein and its affect on the difference in δ^{15}N values of source and trophic amino acids is unknown. If rates of incorporation of source and trophic amino acids differ, amino acid-based trophic status estimates could be affected in organisms undergoing dietary changes or migrating between environments with different isotopic baselines. We will present ^{15}N incorporation rates and TDF estimates for 14 individual amino acids in white muscle tissue of 15 PBFT held in captivity ranging from 11 to 2914 days. Nearly all amino acids δ^{15}N values in this experiment changed exponentially with half lives ranging from 60 to 350 days. Significant differences in the rate of ^{15}N incorporation exist for source and trophic amino acids both within and among these groups. The implications of these results on the application of bulk tissue and amino acid compound-specific isotopic data to ecological studies will be discussed.

Session 5: Fractionation and discrimination factors, where are the damages?

Trophic fractionation in compound specific stable isotopes in marine organisms.

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A central question in marine ecology is the estimation of dietary sources and trophic positioning within food webs which is normally assessed using bulk stable isotope analysis. However fractionation patterns in bulk samples possess high uncertainty and baseline estimation is often difficult. A recent advance is the use of compound specific stable isotope (CS-SI) analysis. Isotope analysis of amino acids (AAs) are of particular interest since AAs are important biochemical compounds and carry the majority of nitrogen (N) and up to half the carbon (C) in organisms.

A primary advantage of CS-AA is that within an organism AAs reflect both the isotopic value of the dietary source and the organism itself, increasing with every trophic level. However, little is still known about the fundamental fractionation patterns in the AAs between diet and consumer. Therefore a meta-analysis was conducted to highlight similarities and general patterns in CS-AAs SI between species and/or groups of C and N in marine ecosystems, and previously published trophic estimation formulas were evaluated.

For $\delta^{15}N$ AA fractionation varied from 0‰ to high fractionation often near 10‰, making them good source and trophic markers, respectively. Interestingly, except phenylalanine and methionine, most AAs termed essential tend to show some degree of $\delta^{15}N$ fractionation. Difference between trophic and source AAs generally allowed for trophic position estimation, however underlying processes for species occupying similar trophic position and variation within single species needs further study. Evaluation of trophic estimation formulas also showed increased uncertainty for species occupying higher trophic positions. $\delta^{13}C$ AA fractionation patterns generally followed the status of being essential (source) or non-essential (trophic). Since several $\delta^{13}C$ AA showed little fractionation they seem suitable for isotope fingerprinting (dietary tracing).

Similar opportunities exist for other biochemical compound such as fatty acids. However, as with AAs information on fractionation is still scarce. Therefore a mesocosm study was performed to investigate fatty acid fractionation between phytoplankton diet and a zooplankton consumer using ^{13}C labelled bicarbonate. This study highlights the need for increased understanding of fractionation patterns and shows that CS-SI are a promising tool to investigate flux of elemental composition in marine systems.

Session 5: Fractionation and discrimination factors, where are the damages?

Effect of the feeding level on the dynamics of stable isotopes $\delta^{13}C$ and $\delta^{15}N$ in soft tissues of the Pacific oyster *Crassostrea gigas*

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Stable isotope analysis is a powerful tool used for reconstructing individual life histories, identifying food-web structures and tracking flow of elemental matter through ecosystems. However, contradictory literature results revealed that both the isotopic ratios (δ, ‰) and the trophic-shift (Δ, ‰) of organism tissues could be affected by the feeding levels and the isotopic ratios of the food sources. To investigate the effect of the feeding level on the dynamics of $\delta^{13}C$ and $\delta^{15}N$, we carried out a diet-switching experiment using Pacific oysters, *Crassostrea gigas*. Oysters were first reared under a high and low feeding levels (HF and LF respectively) over 108 d and then starved over 104 d. The feeding level had a strong and significant effect on the $\delta^{13}C$ and $\delta^{15}N$ of the whole soft body tissues of oysters W_d. At the end of the feeding experiment, tissues of oyster reared under high feeding level were depleted in ^{13}C by ≈ 6.15 ‰ and in ^{15}N by ≈ 1.66 ‰ compare to the tissues of oysters reared under low feeding level. The $\delta^{13}C$ and $\delta^{15}N$ of oyster organs, *i.e.* gills *Gi*, adductor muscle *Mu* and remaining tissues *Re* were also significantly lower in HF level compare to those in LF level. At the end of the starvation, whole soft body tissues and organs of oysters were slightly, but significantly, enriched in heavy isotopes compare to the start of the starvation. The model of *Olive, P., Pinnegar, J., Polunin, N., Richards, G., Welch, R., 2003. Isotope trophic-step fractionation: a dynamic equilibrium model. J. Anim. Ecol. 72, 608–617;* allowed us to investigate the effect of both the feeding level and the isotopic ratio of the diet on the trophic-shift. These two factors did not affect the Δ in the same way. The feeding level had a significant effect on both the $\Delta^{13}C$ and $\Delta^{15}N$. The $\Delta^{13}C$ was inversely related to the $\delta^{13}C_{XPHY}$. In addition no clear trends were observed between the $\Delta^{15}N$ and $\delta^{15}N_{XPHY}$.

Session 5: Fractionation and discrimination factors, where are the damages?

Experimental quantification of hydrogen and oxygen isotopic trophic discrimination in aquatic food webs

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The hydrogen and oxygen isotope ratios (δ^2H and δ^{18}O) of animal tissue are valuable tools in migration, forensic and terrestrial food web studies. For δ^2H in aquatic systems, large unexplained isotopic variability at the intra- and inter-specific level is observed in small freshwater systems. No systematic studies using δ^{18}O have been conducted in aquatic systems. Our objective was to implement a controlled aquatic trophic level experiment to better quantify the mechanisms that drive the H and O isotopic variation in aquatic species.

An experimental aquaria study was conducted where the isotopic composition of water and the diet of two aquatic species with different biological characteristics and trophic habits were controlled. We used an aquatic insect as prey (chironomid, *Chironomus tentans*) and a fish as predator (guppy, *Poecilia reticulata*). Both species were raised from development (hatch / fry) to a considerable growth (>30 times in weight) in order to assure that tissues were in isotopic equilibrium with all the dietary and environmental conditions (water, food, dissolved oxygen). The effect of lipids, depleted in deuterium relative to protein, and the exchangeable H with ambient water vapor was examined for δ^2H measurements. We described the inputs and outputs of H and O isotopes for the formation of tissues in aquatic organisms using a trophic modeling approach. The proportion of tissue H and O in both species derived from the environmental water was significant (30-50 % for H and >80 % for O). An apparent trophic effect of δ^2H values and an isotopic discrimination between water and protein δ^{18}O occur in aquatic food webs. Our validated model revealed new applications and some pitfalls for using hydrogen and oxygen isotopes for ecological studies of aquatic organisms.

Session 5: Fractionation and discrimination factors, where are the damages?

New insights into ^{13}C fractionation obtained by isotopic NMR spectrometry

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Isotope ratio mass spectrometry (IRMS) is commonly used to access the average isotope ratio for a given element in the target analyte. Nuclear Magnetic Resonance (NMR) spectrometry, however, offers a more refined approach because of its double intrinsic property: separation of the signal of each site of the molecule and quantification of the amount of resonating nuclei under the peak. To implement this approach for ^{13}C, some problems fundamental to ^{13}C NMR have to be solved in order to attain a target precision of 1‰, satisfactory for most applications to the transformation of natural products. The recent development of the reliable determination by NMR of ^{13}C intramolecular distributions at natural abundance has opened the door to the analysis of a wide range of products and to the determination of isotopes effects.

A major highlight of what can be learned from these investigations is illustrated by the very new information obtained on ^{13}C fractionation, unrevealed by IRMS. Only knowing the average δ^{13}C value can be misleading when interpreting isotope effects occurring during the transformation (physical, chemical or biological) of a substrate (starting material) into a product (final material) based solely on the □δ^{13}C shift. If this is equal to 0, does it mean that there is no fractionation or, rather, that there is a counteractive contribution of normal and inverse isotope effect from different carbon sites? The site-specific isotope ratios obtained by NMR allow a refinement of the data and emphasize that isotope effects may be manifest in different ways at several carbon positions.

Thus, unexpected fractionations have been shown by isotopic ^{13}C NMR. This presentation will cover some of them:

(i) Normal and inverse ^{13}C non-covalent isotope effects (NCIE), within a molecule, during sorption/desorption experiments. [1]
(ii) Evidence of non statistical isotope effects on the ^{13}C distribution in ethanol upon water stress of European vines. [2]
(iii) Differences in intramolecular ^{13}C composition in sugars from C_3, C_4 and CAM plants. [3]

It will be clearly shown that isotopic ^{13}C NMR is a very good complement to IRMS.

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^{13}C Concentration Dependence of the Lipid-Protein Offset: Compounding Problems for Lipid Correction of Isotope Data

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Lipid content varies with animal nutrition and given that lipids are commonly depleted relative to proteins (Δ_{lipid}) by ~7‰ on average, variation in lipid content can result in δ^{13}C bias and erroneous trophodynamic interpretation. Lipid extractions frequently impact δ^{15}N, necessitating separate analyses of δ^{13}C and δ^{15}N with associated increases in analytical costs or arithmetic lipid correction utilising C:N as a proxy for lipid content. However, corrections provide a poor fit when applied to diverse tissues from a wide range of taxa, analyses that are particularly common in community-scale analyses.

This study conducted extensive lipid extraction (modification of Bligh and Dyer method) and reanalysis of samples within the context of exploring invertebrate dominated hydrothermal vent food webs. This generated a dataset that had several useful characteristics including: i) diverse taxa for which lipid free C:N data were limited, ii) wide δ^{13}C ranges (-35‰ to -10‰) allowing good characterisation of extremes, iii) species found in multiple locations with variable δ^{13}C and iv) multiple tissues from numerically dominant taxa.

Lipid extraction altered δ^{15}N, δ^{13}C and C:N reinforcing requirements for species- and tissue-specific arithmetic lipid correction. A rearrangement of the isotopic mass balance lipid correction equation allowed novel exploration of Δ_{lipid}. Among multiple species, Δ_{lipid} ranged from -3‰ to -12‰ and was negatively correlated with lipid-free δ^{13}C (best fit $\Delta_{lipid} = -0.37*\delta^{13}C+0.6$) highlighting isotope concentration dependence of Δ_{lipid}. For δ^{13}C ranges conventionally considered in marine photosynthesis-based food webs (ca. -20 to -16‰), the correlation yielded Δ_{lipid} comparable to existing studies. Patterns observed across species persisted within species and tissues at different sites. Species that exhibited limited among-site differences in δ^{13}C exhibited similar Δ_{lipid}. In contrast, species exhibiting site differences in δ^{13}C had lower Δ_{lipid} when exhibiting enriched ^{13}C. Conclusions were similar regardless of tissue type although absolute Δ_{lipid} was tissue dependant.

This improved understanding of lipid bias joins an increasing number of examples of concentration dependence in fractionation processes that should lead to substantial refinement of stable isotope techniques in ecology.

Stable isotope signatures of particulate organic matter: an inter-annual multi-site survey within the scope of the French Coastal Monitoring Network SOMLIT

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Particulate organic matter (POM) is a key component of the biogeochemical cycles and constitutes the basis of the food webs. In coastal systems, POM is a mixture of many sources originating from many reservoirs. POM $\delta^{13}C$ and $\delta^{15}N$ are widely used in coastal biogeochemistry and ecology in order to estimate and even quantify the origin and composition of POM or its fate into the food webs, determine the base line of trophic levels, etc. However POM isotopic signatures are highly variable in space and time making their use restricted to snap shot studies or requiring a dense spatio-temporal sampling strategy.

The SOMLIT (Service d'Observation en Milieu Littoral, INSU-CNRS, http://somlit.epoc.u-bordeaux1.fr/fr/) is a French coastal monitoring network that gathers eight marine stations distributed along the French coastline from the eastern English Channel to the Mediterranean Sea. It aims at investigating long-term evolution of coastal systems (including estuarine, semi-enclosed and embayed systems, and open coastal waters) and the nature of their forcings based on weekly to monthly sampling of physical, chemical and biological water parameters. Since 2006 (one location) and 2010 (all locations) POM $\delta^{13}C$ and $\delta^{15}N$ have been sampled, and constitutes a unique inter-annual and multi-site time series. Data are available through the web.

A preliminary study conducted at the scale of the whole network indicates that $\delta^{13}C$ mainly depends on the continent-ocean gradient, whereas $\delta^{15}N$ mainly varies with latitude and that $\delta^{13}C$ seasonality is higher than $\delta^{15}N$ seasonality. Site-specific studies were performed. For some of them, the POM composition was estimated using mixing models. Specifically, in the Gironde Estuary, POM is largely dominated by terrestrial material (98% at the ecosystem space scale and inter-annual time scale) but phytoplankton relative contribution increases seaward; in this system, POM composition is mainly forced by hydro-dynamic and sedimentary processes. In contrast, in Arcachon Bay, POM composition is dominated by phytoplankton (*ca.* 50%) and experiences low spatial but large seasonal variations (*e.g.* higher terrestrial POM in winter *versus* higher phytoplankton POM in summer) that are again forced by hydro-dynamic and sedimentary processes in addition to phytoplankton controlling parameters like temperature and nutrient availability.

Isotopic insights into nutrient fluxes and trophodynamics over coral reef ecosystems

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Stable isotope analyses (SIA) have the potential to provide novel insights into the wide range of nutrient sources and complicated trophic relations inherent to coral reef systems. I will present a variety of SIA from reef systems in Australia, French Polynesia and Japan that greatly elucidate what was long considered a paradox: the high productivity of coral reefs despite the generally low nutrients and productivity of surrounding oligotrophic oceans. Early studies suggested that reefs were maintained by rapid internal recycling, but likely underestimated the input of organic matter from the ocean. Consistent changes in carbon isotopes ($\delta^{13}C$) of particulate organic matter (POM) in water flowing over reefs from oceanic ($\delta^{13}C$ ~ -24 ‰) to reef-derived sources (~ -16 ‰) demonstrate both the rapid metabolism of oceanic POM by reef organisms, as well as the significance of internal POM production and release. SIA thus suggests that the high productivity of reefs may depend on both oceanic inputs and internal recycling, with the balance between the two driving spatial changes in reef structure and function. As an example I will present community level changes in tissue isotopes of coral reef fishes that suggest upstream communities are supported by high quality oceanic organic matter, while downstream communities depend on lower quality recycled organic matter. Oceanic dissolved organic matter (DOM) inputs may also be important, especially in low POM locations such as mid-ocean islands and atolls, but DOM fluxes over reef systems have rarely been quantified. Reef-derived DOM may be relatively more labile than refractory oceanic DOM, with observations by myself and others suggesting that downstream supply of dissolved inorganic nutrients may result from rapid remineralisation of DOM. Previous observations of DOM depletion between the ocean and lagoon may thus reflect the relative balance between uptake of oceanic DOM and release of reef-derived DOM. SIA of DOM and specific compounds (e.g. amino acids) represent a promising path towards further elucidating the relative importance of oceanic and reef-derived organic matter in supporting coral reef communities.

Laughing Gas Plays a Serious Role in Marine Chemistry”: A Stable Isotopic Voyage

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Nitrous oxide is a biogenic trace gas in the atmosphere that plays a significant role in climate change and stratospheric chemistry. Its concentration in the ambient air has increased to the current value of 320 ppbv from 275ppbv in 1910. Oceans account for 25-30% of global N_2O emissions and 60% of its natural production; however, the biogeochemical pathways leading to its formation are poorly constrained. Nitrification and denitrification dominates N_2O production with their N_2O source output varying with oxygen availability. This study describes the dissolved nitrous oxide concentration and its relationship with dissolved oxygen (DO) through the water column at different sites (NIWAS’s sub-tropical and sub Antarctic mooring stations, Geotraces stations and Munida transect all in the South Pacific Ocean) with all other basic water parameters. Samples were collected from various voyages of the RV-Tangaroa and RV-Polaris. For the first time novel stable isotopic methods including $\delta^{15}N_{bulk}$, $\delta^{18}O$, $\delta^{15}N_{\alpha}$, site preference (SP-which is the difference between $\delta^{15}N_{\alpha}$ and $\delta^{15}N_{\beta}$) for N_2O and DO were used in these water masses around New Zealand. N_2O concentration varied from near air saturation at the surface to a maximum value in the oxygen minimum zone and its isotopic values within the mixed layer are similar to those in tropospheric values, indicating exchange with the atmosphere. Nitrification was responsible for production in oxic waters whereas the role of denitrification in the oxygen minimum zone was conspicuous from the isotopic values. From these results these water masses appeared neither as a sink nor a source for nitrous oxide.

How Hot and How Wet were the Eocene Tropics? Evidence from the Stable Isotope Composition of Fossil Sirenian Tooth Enamel

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The Early to Middle Eocene was an interval of extreme climatic warmth and humidity. Though mean sea surface temperatures (SST) were elevated globally at this time, temperature and precipitation proxies suggest that high latitudes warmed more and were relatively wetter than the tropics. However, due to variation in tropical temperature proxies and numerical simulation results as well as a dearth of information on precipitation levels at low latitudes, debate regarding these interpretations persists. Stable isotope analysis of sirenian fossils may offer one means of addressing this debate. Enamel $\delta^{13}C$ values reflect the $\delta^{13}C$ values of sirenian diets, which reflect latitudinal changes in temperature[1]; as such, sirenian enamel $\delta^{13}C$ values would be expected to respond predictably to changes in meridional SST gradients. Similarly, a constant core body temperature (~37°C) means that variation in enamel $\delta^{18}O$ values from sirenians simply reflects changes in the $\delta^{18}O$ value of the water they inhabit[2]; thus, elevated precipitation levels in the past would reduce surface water $\delta^{18}O$ values in coastal areas, resulting in lower enamel $\delta^{18}O$ values for fossil sirenians. Here we test these hypotheses by comparing enamel $\delta^{13}C$ and $\delta^{18}O$ values for Paleogene and Neogene fossil sirenians recovered from part of the Atlantic Ocean and former Tethys Sea (paleolatitudes from 10 to 55°N).

Enamel $\delta^{13}C$ and $\delta^{18}O$ values for 150 fossil and modern sirenian specimens were compiled from published and newly analyzed data. Whereas Eocene-aged specimens (n = 28) showed no significant difference in enamel $\delta^{13}C$ values for specimens sampled from low (≤ 30°N) or higher (> 30°N) latitudes, a significant difference was detected for post-Eocene-aged specimens (n = 122) sampled from these latitudes. Likewise, enamel $\delta^{18}O$ values for Eocene-aged specimens showed a greater offset relative to Oligocene and younger specimens sampled from these latitudes than the expected 1.0‰ increase due to growth in continental ice volume. This increased offset could have resulted from suppression of surface water $\delta^{18}O$ values by a tropical, annual moisture balance significantly wetter than today. Results from an atmospheric general circulation model support this interpretation as well as the hypothesis that meridional SST gradients were reduced during the Eocene.

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Assessing mammalian responses to glacial and interglacial conditions

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Stable isotopes in fossil mammal teeth record dietary and climate information that provides insight as to mammalian responses to climate change over deep time. Specifically, relative proportions of oxygen isotopes ($\delta^{18}O$) are a function of the water consumed by mammals either in food material and/or through drinking. As further demonstrated by Levin et al. (2006), an increase in $\delta^{18}O$ values of evaporation sensitive mammals can indicate increased aridity. We used the aridity index of Levin et al. (2006) to identify glacial and interglacial sites in coastal Florida. First, we determined which taxa were evaporation sensitive versus insensitive by quantifying the magnitude and frequency of greater $\delta^{18}O$ values in various extinct taxa (e.g., llamas, horses, tapirs, etc.) as compared to known evaporation sensitive proboscideans from a given site. Subsequently, we compared both the mean and total range of $\delta^{18}O$ values from inferred evaporation sensitive taxa (e.g., llamas, horses, and deer) to assess overall aridity. Serial samples of taxa with either high crowned teeth (i.e., horses and llamas) or elongated canines (i.e., peccaries) further confirmed glacial versus interglacial designations while further elucidating relative seasonality and seasonal dietary niche partitioning in primarily mixed feeding taxa. Collectively, quantitative comparisons of $\delta^{18}O$ values in evaporation sensitive taxa allow us to designate numerous sites in Florida as glacial or interglacial and along a climate continuum relative to site specific proboscideans. Thus, multi-site comparisons of Pleistocene fauna reveal greater dietary niche partitioning during interglacial periods – typically represented by more heterogeneous environments. Although mixed feeders typically consume a greater proportion of C_4 resources during interglacial periods and expand their isotopic niche with interglacial warming, individuals exhibit minimal $\delta^{13}C$ variation seasonally during both glacial and interglacial periods. These data are in contrast to mammalian isotopic records in Australia that demonstrate more homogeneous isotopic resources and decreased dietary niche partitioning with increased aridity during the Pleistocene. Improvements in our ability to classify fossil sites along a climate continuum and assess ecological responses to climate change are of relevance to current floral and faunal responses to global warming, today.

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Investigating Woolly Mammoth Ecology through Compound-Specific Isotopic Analysis

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Woolly mammoths (*Mammuthus primigenius*) were an integral part of Beringian Pleistocene environments. Understanding the causes of their extinction is one key to understanding late Pleistocene extinctions as a whole. Stable isotope analysis of woolly mammoth tissues provides insight into their behavioural and dietary vulnerabilities arising from climate change and human hunting. Still, many questions remain when interpreting such data, many of which involve the typically low $\delta^{13}C$ and high $\delta^{15}N$ of woolly mammoth collagen relative to coeval herbivores. Here, we examine the isotopic composition of individual amino acids from collagen of juvenile and adult woolly mammoths, as well as coeval species, from Old Crow, Yukon Territory, Canada. Metcalfe et al. (2010) have reported bulk collagen and carbonate isotopic compositions for these samples previously. In these woolly mammoths, non-essential amino acids synthesized from the energy portion of the diet had relatively low $\delta^{13}C$, supporting the hypothesis that they were particularly reliant on fat reserves to survive winter. This would have caused these mammoths to be particularly susceptible to climatic changes that decreased plant productivity and left less food for winter consumption, since their winter diets were already well below subsistence levels. The high $\delta^{15}N$ of phenylalanine, which does not undergo significant transamination in an animal, may suggest feeding of woolly mammoths on ^{15}N-enriched plants, rather than a metabolic enrichment. If the high plant $\delta^{15}N$ resulted from dung fertilization, it may indicate that mammoths maintained regular habitats or migration routes, making them vulnerable to human hunting. Alternatively, such compositions may reflect increased aridity, supporting the interpretation of Old Crow as an extremely dry site. The mammoths may have fed in particularly dry microenvironments, leaving them sensitive to the increasingly mesic conditions at the terminal Pleistocene.

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Late Pleistocene animal transhumance in central Italy

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Transhumance of domestic herds from coastal (lowlands) to inner (uplands) areas has historically been a common practice in peninsular Italy. It has been suggested that the same routes may have been exploited since the Last Glacial by animals moving seasonally in search of fresh pasture. Hunter-gatherer would have followed these movements chasing their prey animals.

We tested this proposition using sequential $\delta^{18}O$, $\delta^{13}C$ and $^{87}Sr/^{86}Sr$ in *equid* and *cervid* tooth enamel from five late glacial Epigravettian coastal and Apennine sites to assess whether these animals moved seasonally from lowlands to highlands. The combination of consecutive stable ($^{18}O/^{16}O$ and $^{13}C/^{12}C$) and radiogenic ($^{87}Sr/^{86}Sr$) isotopes in tooth enamel should allow us to assess an animal's approximate location in the seasons. The former are proxies for climate and vegetation, which can indicate seasonal shifts, while the latter are associated with the underlying geology and thus provide information about ranging behaviour.

In order to establish the distribution of strontium isotopes available to flora and fauna across the landscape we first carried out a study of rocks, soils, plants, water and modern fauna. We investigated a grazing-based (*Equus hydruntinus*) and a browsing-based (*Cervus elaphus*) species in order to assess ecological and transhumance differences. Samples were obtained from layers in the archaeological sequences that were associated both with colder (stadial) and warmer (interstadial) phases in the Late Glacial (c.a. 20-10 ky BP), to allow comparisons under different conditions. Here we present the first set of data comprising the intra-tooth sequences in archaeological fauna, which are evaluated against the results for bioavailable $^{87}Sr/^{86}Sr$. We show that $^{87}Sr/^{86}Sr$ variability recorded in the geosphere is strongly attenuated in animal tooth enamel, suggesting a dampening effect in the routing of these isotopes from the landscape to the tooth. Nevertheless, in combination, the $^{18}O/^{16}O$ and $^{13}C/^{12}C$ and $^{87}Sr/^{86}Sr$ values obtained within tooth sequences show coherent patterns that can be associated with movements across the geographical settings. However, the movements appear not to be consistent and there is no evidence that movement habits changed with time in spite of the large climate oscillations associated to this period.

Grevy's zebra diet: historic and modern comparisons with co-occurring plains zebra, and the influence of livestock competition

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Two species of zebra coexist in north central Kenya; the plains zebra (*Equus burchelli*), and Grevy's zebra (*Equus grevyi*). The world population of Grevy's zebra is <3,000 individuals, and they only found today in Kenya and Ethiopia. The Grevy's is a species of conservation importance, and ongoing population decline is not fully understood. Co-occurring plains zebra populations have remained relatively stable over the same time period. Zebras (both species) primarily consume grass in savanna ecosystems, and they are routinely classified as hypergrazers - they are adapted to eat protein-poor, fibrous, silica-rich grass leaves and stems. Yet studies of zebra habitat choice and foraging dynamics have shown that both species do spend time in closed habitats (woodland or brushland). Predator and human avoidance, competitive exclusion by livestock, forage quantity/quality, and reproductive status are all known to influence zebra habitat use. It is still unclear is how important the non-grass (browse) resources encountered in closed habitats are to zebra diet. The contribution may be cryptic; foraging can be difficult to observe in closed habitats, and current isotopic estimates of diet are time-averaged, and largely reflect grazing. We collected short (N=3 samples per individual) $\delta^{13}C$ and $\delta^{15}N$ chronologies from zebra tail hairs removed from modern animals and historic museum specimens in order study fine scale dietary patterns. First, we investigated the diets of the two zebra species where they coexist – we made this comparison for the present, and a century ago (~1910) in north central Kenya. In both the past and today, the majority of Grevy's diet was grass, yet they consumed significantly more browse than plains zebras. Second, we explored the relative influences of livestock competition and seasonal changes in primary productivity on modern Grevy's diet. The proportion of grass in Grevy's diet decreased with high livestock competition, and this effect was generally stronger than the effect of seasonal changes in primary productivity.

Mapping an East African elephant isoscape to trace historic flows of ivory

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As part of the Historical Ecologies of East African Landscapes (HEEAL) project, isotope analysis was utilised as a tool to provenance 19th and early 20th century ivory artefacts to elephant hunting grounds in East Africa. These ivory artefacts included material from museum collections, such as ivory piano keys in the US and cutlery handles in the UK, and worked ivory found in archaeological deposits in southeastern Kenya. In order to use isotope analysis to provenance this material, it was necessary to build a baseline database of East African elephants by collecting tissue samples from both modern and historic elephants and using a combination of isotope analyses ($\delta 13C$, $\delta 15N$, $\delta 18O$, and $^{87}Sr/^{86}Sr$). Part of this research also included the collection of climate data from the region to further understand the isotopic signatures of these elephants, as well as archival data such as trade records and elephant hunting accounts. By using mapping tools such as ArcGIS, it is possible to layer these different sources of information to create an East African elephant isoscape, relating the biological and environmental information about the elephant and its landscape with historical information documenting how it was hunted and traded for its ivory. Mapping the data in this way facilitates an understanding of the patterns and connectivity of trade relations between people and elephants in the past, while also understanding at a molecular level through the isotope analysis the distribution and habitat preferences of elephants in the region from the 19th century until today. East Africa is a particularly ideal region for this type of research due to the diverse climate, geological, and vegetation zones, which can be mapped and linked to elephant habitat and distribution patterns at a landscape level. This paper will therefore discuss the challenges and future research directions of using isotope analysis not only as a provenancing tool, but also as an ecological tool for understanding diet and habitat changes between historic and modern East African elephant populations.

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Spatiotemporal isoscapes for migration research

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Light stable isotope tracers have become a popular and widely used source of information on the regional to continental scale migration patterns of many animal groups. This work is founded on a quantitative understanding of the spatial distribution of environmental isotopes (isoscapes) that are assimilated in animal tissues, providing a basis for assigning animals to locations or regions based on retrospective analysis of their tissues. To date, almost all studies have developed interpretations on climatological, or 'static', isoscapes, because models allowing accurate estimation of isotope distributions for specific calendar years or seasons have often not been available. This situation creates a disconnect between the temporal support of biological samples and environmental isoscapes. Developing stronger temporal connections between biological samples and environmental isoscapes is especially important in systems where the isoscapes exhibit a high degree of temporal variability. We report here on new analyses characterizing temporal variation in environmental water (H and O) isotope ratios and testing our ability to accurately model short-term (individual months and seasons) water isoscapes using existing datasets. We implement the resulting data products in a case study using previously published data from monarch butterfly wing chitin and compare the accuracy and sensitivity of Bayesian geographic assignments for these samples using different climatological and time-specific isoscapes. Combined with a continued emphasis on environmental isotope monitoring, the modeling tools used here should support continued improvement in the precision and accuracy of geographic assignments. The data and data analysis methods have been implemented in the IsoMAP web portal and are freely available to the migration research community in support of their research.

Isoscapes to trace plant-plant-interactions at the community scale

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Isoscapes have greatly improved our ability to understand biogeochemical processes on continental to global scales. However, the isoscapes framework may also bear a significant potential to resolve the spatial component of within-community interactions. For example, exotic plant invaders often exert strong impacts on ecosystem functioning, particularly regarding water-, carbon- and nutrient-cycles, but the spatial extent of such alterations is largely unknown. Here we show that massive N input by the N_2-fixing exotic invasive *Acacia longifolia* to a Portuguese dune system can be traced using spatially resolved information on native plants' leaf $\delta^{15}N$. We found isotopic signatures of N to differ strongly between the native system ($\delta^{15}N \approx -10‰$) and the atmospherically derived N in *A. longifolia* phyllodes ($\delta^{15}N \approx 0‰$)[a]. Thus, sources of N for native plants could be readily distinguished. Leaf $\delta^{15}N$ of a native, non-fixing species was increasingly enriched the closer the plant grew to the invader, indicating uptake of N derived from decaying *A. longifolia* litter. The enrichment was evident far beyond the stands of the invader, demonstrating that *A. longifolia* affected N budgets of native species up to a distance of 8 m exceeding the margin of the canopy. Furthermore, using the isoscapes approach, we were able to quantify the total area of N enrichment and could thus show that the area affected by invasion was at least 3.5 times larger than the area actually occupied by the invader[b]. However, a native N_2-fixing species had no such effects.

Thus, downscaling isoscapes to the community level opens new frontiers in quantifying the spatial dimension of functional changes associated with plant invasions. Moreover, considering the feasibility and applicability of this approach, it may provide a promising tool to identify, quantify and monitor different types of functional plant-plant interactions within communities at a spatially explicit scale.

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A multi-isotope (δ^{13}C, δ^{15}N, δ^{2}H) isoscape for Africa: Applications to tracing animal migration

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A universal challenge in methodology used to study the ecology, conservation and evolutionary biology of migratory species is the quantification of connectivity among breeding, wintering and stopover sites. For the avian Eurasian-Afrotropical migratory system, knowledge of geographical wintering areas used by migrants that breed in Europe remains deficient, despite the advent of satellite transmitters and geolocators. Here we explored the use of theoretical plant δ^{13}C and δ^{15}N landscape distributions coupled with δ^{2}H hydrologic models to construct multi-isotopic avian foodweb clusters for Africa. The cluster analysis identified four distinct regions of Africa based on all three isotopes (^{13}C,^{2}H,^{15}N), and five regions based only on ^{13}C and ^{15}N. We applied known isotopic diet-tissue discrimination factors to map equivalent feather isotopic clusters for Africa. The validity of these feather isotopic clusters was tested by examining how well known- and unknown-origin species were placed in regions of Africa using previously published feather isotope data and the analysis of a new set of feathers from Barn Swallows (*Hirundo rustica*) breeding throughout Europe. The success of this multi-isotopic cluster model depended upon the species of interest and additionally on how well potential winter molt origins in Africa were constrained by prior information. Ground-truthing data suggested this approach will be useful for first-order approximation of overwintering regions for Afrotropical migrants and will be improved as our understanding of the nature of isoscapes for Africa is refined.

Linking migratory populations with stable-hydrogen isotopes: improved inference through informative priors and “screening” migrants from residents.

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Establishing linkages between breeding and wintering populations of migratory species can greatly enhance our ability to inform conservation efforts, particularly for threatened species. The use of stable-hydrogen isotope analysis of feathers (δ^2H_f) has provided an important tool to make these connections, however a number of issues can complicate assignment to origins. Recent work has highlighted the use of likelihood approaches to address sources of uncertainty in assignments to geographic origin. In addition to assignment uncertainty, other factors such as the biology of the species under study can also complicate inference; for example, the existence of overlapping migratory and resident populations on the wintering grounds will complicate assessments of connectivity. Loggerhead Shrike (*Lanius ludovicianus*) is one such species with resident populations overlapping with migrants on the wintering grounds. Using data collected during both the breeding and wintering seasons, we developed species and age-class specific isoscapes and demonstrate the use of likelihood-based approaches to assigning birds to the isoscapes that incorporate informative prior information from Bayesian analysis of microsatellite markers. Furthermore, we demonstrate how likelihood-based approaches can be used to assess whether individuals were migrants versus residents, and how this can influence conclusions about migratory connectivity.

Individual specialization in foraging behaviour in a wide-ranging marine predator

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Treating all animals in a population as ecological equivalents, particularly in studies of resource use, can mask individual level effects that have important implications for our understanding of demographic, ecological and evolutionary processes. Indeed, individual specialization appears to be a feature of many organisms, yet the causes and consequences of this phenomenon remain surprisingly under-investigated. For example, the generation and persistence of specializations is likely to be strongly influenced by interactions with conspecifics, and with the availability of additional anthropogenic resources. These effects should be especially apparent when densities are highest, for example as among centrally placed foragers such as breeding seabirds.

Here we combine stable isotopic analysis of different tissue types with information from remote tracking technologies to examine the degree of specialization in the diets and foraging behaviours of individual Northern Gannets *Morus bassanus* from a suite of colonies of varying size. Gannets are one of the few UK seabirds exhibiting consistent breeding success, and their ability to take a wide variety of prey sources, including fisheries discards, is believed to be a key reason behind this. We were able to examine this hypothesis using $\partial^{15}N$ and $\partial^{13}C$ to distinguish between scavenged benthic and hunted pelagic prey. However, there is also evidence that consumption of discards is a specialized technique with potential fitness consequences, and so proposed legislative changes to fisheries discards may result in disproportionate impacts across colonies.

We found that individual birds showed repeatable patterns of prey consumption and behaviour, and that consistent differences between individuals also existed. However, these patterns varied with colony size, suggesting an important role for competition in generating the observed results. This demonstrates that interactions between apex predators and anthropogenic resources are complex, but individualistic responses to resources and environmental variation suggest that distinct preferences may interrelate with competitive interactions to provide a mechanism by which specializations can be maintained over large spatial scales.

Stable isotopes document the effects of aging, sex and breeding status on the foraging ecology of an extremely long-lived seabird

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Although a large body of literature reports that foraging skills improve at a young age, there is a surprising lack of information on the potential links between feeding behaviour and aging. Here, age-related variations in foraging ecology were investigated in a unique data set of known-aged individuals (3-47 years) of a long-lived seabird, the wandering albatross (*Diomedea exulans*) at the Crozet islands (Southern Indian Ocean). Firstly, the use of a latitudinal $\delta^{13}C$ gradient to depict the birds' foraging areas was validated by combining satellite tracking of a large number of albatrosses (n = 45) and subsequent measurement of their plasma isotopic signature. Secondly, $\delta^{13}C$ and $\delta^{15}N$ values were measured in blood cells and body feathers of albatrosses as reflecting their foraging habitat and trophic level during the breeding and moulting (inter-nesting) periods, respectively. The main results are the following. (i) Immature birds presented no significant sex-related isotopic differences. (ii) In breeding birds, blood and feather $\delta^{13}C$ values (and blood $\delta^{15}N$ values) were overall lower in males than in females, thus indicating that adult males foraged in colder waters than their mates and suggesting a southern shift in the foraging areas of males (but not females) when they recruit into the breeding population. (iii) The blood isotopic signature of breeding females (n = 53) does not change with age, but (iv) blood $\delta^{13}C$ values of breeding males (n = 54) decreased, indicating that older males foraged in colder waters than younger individuals. (v) In contrast to blood, feather $\delta^{13}C$ and $\delta^{15}N$ values of both breeding females (n = 87) and males (n = 110) were related to age, with older birds foraging at more southern latitudes than younger albatrosses during the inter-nesting period. In conclusion, this cross-sectional investigation reveals a complex pattern of latitudinal segregation at sea of birds according to their age, sex and breeding status. It confirms and considerably expands the previous information provided by short-term satellite tracking (Lecomte et al. PNAS 107:6370-6375, 2010), with the wandering albatross being the first species, to our knowledge, to document a pattern of segregation by adult age in foraging areas.

Standing the test of time? Why an isotopic “snapshot” of a population may form an incomplete picture of its foraging ecology.

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Many marine ecosystems and food webs are known to be highly variable over monthly to decadal time scales. Although this environmental heterogeneity influences the availability of prey sources and predator foraging behavior, few studies have been conducted on the temporal consistency of an apex predator’s prey base and resulting isotopic signature. As a result, there is little understanding of how ecological controls impact prey availability and the frequency of prey switches by top predators.

In this study, the temporal variability of humpback whale diet and the resulting stable nitrogen and carbon isotopic signatures were examined over an eleven-year period (1999-2010). Analysis was conducted at the population level, using skin biopsies from 173 individuals and at the individual level, using samples along the length of a baleen plate and repeatedly-biopsied individuals. All samples were collected from a population of humpback whales that feed in the California Current. Baleen plate isotopic signatures revealed significant enrichment in $\delta^{15}N$ during winter months suggesting metabolism of blubber reserves during the breeding season, which has not been observed in other biopsy-only studies of humpback whales. Repeatedly-biopsied individuals showed an increase in signature variability with time. Annual variation in the population’s diet was greater than seasonal variation. Isotopic signatures of skin biopsies from 2001-2003 reflected measured carbon and nitrogen values of krill. These signatures were significantly different from 2004-2006 samples which reflected measured isotopic values of schooling fish. The sample timeframe coincides with a cool-to-warm phase-shift in the Pacific Decadal Oscillation and an accompanying ecosystem shift in the dominance of prey from krill to schooling fish. The combined isotopic and oceanographic data indicate a probable prey switch in the sampled humpback population. The resulting temporal isotopic variability within this population was comparable to the spatial isotopic variability previously observed across all humpback whale populations in the North Pacific. This work provides evidence that top predators may significantly alter their diet in response to environmental variability and prey availability. In addition, this work has significant ramifications for population structure and migration studies that assume relative consistency in a population’s isotopic signature.

Seasonal variation in trophic niches of co-occurring suspension-feeders

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The filter feeder honeycomb worm (*Sabellaria alveolata*) builds reefs between the mid level to the lower level of the intertidal zone, where others suspension feeders naturally co-occur (for example mussels and barnacles) being able to establish inter-specific competition relationships for space and food resources. The aim of this study was to investigate the temporal dynamics of feeding relationships among co-occurring benthic suspension feeders, by mean of stable isotopic ratio analyses ($\delta^{13}C$, $\delta^{15}N$). The reef-builder *S. alveolata*, blue mussels (*Mytilus edulis*), barnacles (*Chthamalus montagui*), and organic matter sources, were surveyed seasonally in the Bay of Douarnenez (Brittany, France). In order to assess the individual specialization within populations and to evaluate both inter-specific and intra-specific differences in the food exploitation, specimens from each species were analyzed separately. The results of this study showed, during the investigated seasons, constant differences in $\delta^{13}C$ and $\delta^{15}N$ signatures between consumers, suggesting that inter-specific competition was limited among co-occurring suspension-feeders. Suspension feeders can potentially utilize the same food resources without having similar isotopic signatures by consuming the food items in different proportions. *M. edulis* and *C. montagui* exhibited unvarying diet in all seasons, relying mainly on sedimentary organic matter and on phytoplankton, respectively. *S. alveolata* exhibited more opportunistic behavior, feeding largely on phytoplankton during bloom period, and shifting on green macroalgae (*Ulva* spp.) in the other seasons. Indeed, the Bay of Douarnenez is affected by large and recurrent green tides, with large biomass of *Ulva* spp. growing in the water column and stranding on the intertidal area. As intra-specific differences in the diet, the width of trophic niche and the degree of differences between individuals varied seasonally. Whatever the season, *S. alveolata* population exhibited the larger diet spectrum and the higher degree of trophic plasticity, with high variability between individuals. This study supports the hypothesis that trophic plasticity allows suspension-feeders to adapt to seasonal availability of food items and to minimize the trophic niche overlapping between co-occurring species.

Functional consequences of disturbance for tree lizards (*Urosaurus ornatus*): Integrating isotopic evidence from multiple trophic levels

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Changes in resource diversity and number, mediated by trophic interactions, ultimately shape species responses to disturbance. At the heart of the species response to these changes is the individual stress response to the disturbance itself: to disperse, adapt, or go extinct. For many individuals, the most viable option is to adapt, which usually requires some level of plasticity in trophic (functional) relationships. In arid grassland habitats of the southwestern US, prescribed fire is a common practice intended to mimic historical episodes of wildfire and maintain ecosystem structure and function. However, the changes to the environment incurred by this disturbance mimic those predicted by recent models of climate change: an increase and spread of grass cover and non-native grass species. The functional consequences of this structural reorganization of dominant vegetation types remain unknown. Here we model changes in habitat and trophic linkages during a three-year period in southeastern Arizona (2009-2011). We monitor three study sites: an unburned control, and two treatment sites varying in burn history. We focus on ornate tree lizards (*Urosaurus ornatus*), a meso-predator, and model their trophic linkages at each site using dual-isotope (carbon and nitrogen) mixing models. We apply these models to tissue samples collected from multiple trophic levels (i.e., primary producers, arthropod consumers, and lizards) to illustrate broad changes in trophic connectedness across sites. We then utilize structural equation modelling to delineate the strength of the various ecological, morphological, and demographic parameters characterizing lizard populations at each site towards predicting their dietary variation among sites. Preliminary findings highlight both 1) significant variation in resource availability and use among sites and 2) increased morphological differentiation among lizards at more frequently-burned sites (all $P < 0.05$). Ultimately, we will provide a synergistic model of the functional consequences of disturbance for lizard species that can inform future studies and conservation efforts alike.

Seal whiskers reveal long-term diet specialists: not all are top-order predators

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Apex predators are assumed to be dietary generalists but there is increasing evidence that individual-level dietary specialization may be common in many species. The leopard seal is considered to be an Antarctic generalist and is reported to use a diverse prey base including seals, penguins, fish and krill. We examined whether this was the case. We used stable isotope signatures of the keratin of seal whiskers to examine foraging behaviour. As whiskers grow progressively and are isotopically inert, they reflect an individual's dietary choice over the period of growth. Through trials with captive leopard seals we calibrated growth patterns to model the time periods that sections of whisker represent. For an individual whisker this could be up to several years. Using linear mixed-effects models we examined the influence of sex, region and individual on the variance in stable isotope signatures (δ15N and δ13C) of serially sampled whisker segments from 75 individual wild leopard seals. We found a wide species-level isotopic niche breadth but showed that this was explained by variation among specialist individuals; for any individual seal the isotopic values showed remarkably stable patterns across whisker segments, that is, across time. There was enormous difference in dietary specialization between populations, the Eastern Antarctic leopard seal population was composed predominantly (26/29) of warm-blooded prey specialists, with few individuals specialising on krill, while the Western Antarctic Peninsula (WAP) population were almost entirely (41/46) krill specialists with few individuals specialising on warm-blooded prey. The environmental changes occurring off the WAP are well documented and it is tempting to speculate whether the krill-specialisation of the WAP leopard seals is a behavioural shift in response to the recent events occurring in the region. Our findings show that using archived keratinous tissues, like whiskers, can open up the study of progressive changes in behaviour over periods of many years. This could be an important tool in understanding trophic dynamics of highly mobile marine top predators in environments that are logistically difficult to work within, such as the Antarctic.

Caribbean green turtle foraging ecology

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The green turtle (*Chelonia mydas*) is a highly migratory species found in tropical and subtropical waters worldwide. We used bulk tissue (epidermis) and compound-specific amino acid stable isotope analysis from a green turtle nesting population at Tortuguero, Costa Rica to investigate the trophic ecology and spatial distribution of foraging of green turtles in the Greater Caribbean. Adult green turtles were thought to be solely herbivorous as adults, though primarily carnivorous foraging strategies have been observed in Pacific adult green turtles. We explore the possible presence of this alternative foraging strategy among green turtles in the Greater Caribbean. A wide range of $\delta^{13}C$ and $\delta^{15}N$ values of bulk epidermal tissue in the green turtle nesting population at Tortuguero could indicate that these turtles feed over several trophic levels. However, the isotopic niches varied among the five foraging populations examined, and the isotopic niche of the Tortuguero nesting population mimics the geographic variability observed in the isotopic compositions of the primary producer *Thalassia testudinum* seagrass throughout the Greater Caribbean. Compound-specific nitrogen isotope analysis of amino acids revealed that amino acid biosynthesis in seagrass is more similar to that of terrestrial C_3 plants than to macroalgae and phytoplankton. Based on this observation, we calculated trophic position of individuals of the green turtle nesting population using the isotopic composition of specific amino acids. These results indicate that despite different bulk epidermal $\delta^{15}N$ values, these turtles feed at the same trophic position. The combined results indicate that spatial differences in the isotopic compositions at the base of the food web, rather than dietary differences, contribute to the isotopic variation in the nesting population. Therefore, there is no evidence of carnivory in the nesting population. These spatial differences in $\delta^{13}C$ and $\delta^{15}N$ values of bulk epidermal tissue allow us to estimate the proportion of the nesting population migrating from specific foraging areas, and provide a complementary method to some of the more traditional methods of estimating connectivity through tag returns and genetic mixed stock analysis. Results of this study can be useful in better understanding the foraging ecology of highly dispersed and migratory populations.

The ecological consequences of individual trophic specialization in human-altered ecosystems

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Ecologists have widely demonstrated the ecological and evolutionary importance of individual trophic specialization (ITS), i.e. that natural populations are composed of specialized individuals that use a narrower trophic niche than the total population. ITS is promoted by reduction in interspecific competition, predation and/or ecological opportunities that favor the utilization of unexploited resources. Since human activities are increasingly affecting ecological opportunities such as subsidies fluxes between ecosystems, it is of upmost importance to determine how human-induced habitat perturbations affect ITS. As opposed to gut stomach analysis (GCA), the recent development of models based on stable isotope analyses (SIA) allows to account for the temporal consistency of ITS. The aim of the present study was i) to determine how habitat perturbations, by creating ecological opportunities, drive ITS and ii) to quantify the subsequent ecological consequences at different levels of biological organization. Using in conjunction individual tagging, GCA and SIA ($\delta^{13}C$ and $\delta^{15}N$), we quantified the trophic niche structure (population wide metrics, Layman *et al.,* 2007) and individual diet (mixing model, Parnell *et al.,* 2010) of brown trout (*Salmo trutta*) in 10 populations along a gradient of human alterations (i.e. canopy cutting). By combining both GCA and SIA, we also applied a new method that converted isotopic data into a standardized index of ITS (Araùjo *et al.,* 2007). Our results suggested that trophic niche structure and ITS varied among populations, were driven by habitat perturbation that modified ecological opportunities (i.e. terrestrial allochtonous inputs), and were correlated to individual growth and body condition. Additionally, some individuals were more specialized on allochtonous prey and functionally-important aquatic invertebrates (e.g. herbivorous), indicating some potential cascading effects on ecosystem functioning. In conclusion, the alteration of reciprocal subsidies fluxes between adjacent ecosystems can modify prey-consumer dynamics and we demonstrated here the importance of considering inter-individual variability in trophic niche since it interacts with the effects of habitat perturbations.

Estimating temporal movements of a migratory species using stable carbon isotopes

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Dunlin (*Calidris alpina arcticola*) are a species of long distance migratory shorebirds that breed terrestrial environments in the high Arctic and winter in coastal environments in temperate and equatorial zones. Dietary species occur across a gradient in ^{13}C space such that their diet is relatively enriched in ^{13}C during winter and depleted in summer. This means we can use isotopic methods to estimate time since diet switch for individual dunlin, which can be interpreted as time since arrival on the breeding grounds. The temporal window for breeding is narrow and breeding success is generally maximized when nests hatch just prior to the seasonal peak in arthropod abundances. As such, we are interested in estimating arrival times for individual dunlin. We solved a set of equations for a widely used exponential decay model for $\delta^{13}C$ in blood from recaptured individuals to find (1) the isotopic turnover rate of blood tissue and (2) time since diet switch for free-ranging wild dunlin that nest near Barrow, Alaska. We assumed the solutions from these sets of equations represent the individually “true” rates and dates; that is, each bird has a single known turnover rate and a single known arrival date. Our estimated blood tissue turnover rates (beta mean: 0.0959; 95% CI: 0.0495, 0.1553) were higher than previously published estimates (beta mean: 0.0663; 95% CI: 0.0311, 0.1134; Evans-Ogden *et al.* 2004) for captive dunlin. This difference may be due in part to increased metabolic demands associated with post-migration tissue repair and reproduction in our study population. We then quantified the potential bias in estimated arrival dates that can be attributed to the application of (1) the population mean for our individual turnover rates, and (2) a previously published population mean turnover rate. Bias ranged from -15 to 23 days for (1) above and -31 to 13 days for (2) above. The methods implemented here demonstrate how to assess the individual variability in the isotopic dynamics of a population. Our results support the theory that stable isotope techniques provide a minimally invasive approach for determining the phenology of migration events on an individual level.

Cyanobacterial blooms: trophic dead-end or unexpected dietary bonus?

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Cyanobacterial blooms induce significant ecological and economical costs that are expected to increase in the near future. Cyanobacterial resistance to zooplankton grazing is one of the factors thought to promote these bloom events. Yet, numerous studies on zooplankton ability to graze upon cyanobacteria have been producing conflicting results and such a puzzle might arise from the lack of direct observations *in situ*. The objective of this work was to track, using fatty acids and fatty acid stable isotope analyses (FA-SIA), the fate of cyanobacterial organic matter in the food web of a lake subjected to summer blooms of *Planktothrix rubescens*.

A metalimnetic bloom of *P. rubescens* occurred in the lake during the study period and was shown to be especially rich in □-linolenic acid 18:3(n-3). None of the zooplankton taxa exhibited spiking content in 18:3(n-3), precluding any intense grazing on *P. rubescens*. FA-SIA revealed however that up to a third of small zooplankton's 18:3(n-3) was provided by the *P. rubescens* bloom while large cladoceran grazers did not benefit from it. The food chain constituted of small zooplankton and predatory cladocerans conveyed the 18:3(n-3) of cyanobacterial origin to the lipids of juvenile perch, to which it contributed to ~10-25% of total 18:3(n-3).

Overall, *P. rubescens* biomass was transferred with a low trophic transfer efficiency to higher trophic levels and thus constituted a trophic dead-end. Nevertheless, *P. rubescens* bloom provided the food web with components of high nutritional values. Thus, from the consumers' perspective, *P. rubescens* bloom represented a significant dietary bonus.

Can amino acid $\delta^{13}C$ patterns distinguish between planktonic and benthic food pathways in alpine lakes?

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Quantifying the relative contributions of different food sources for animals feeding on mixed habitats is often challenging using bulk stable isotope compositions. In lakes, different habitats can to some degree be differentiated based on d13C since there is general gradient of d13C enrichment from planktonic to benthic food sources. However, confounding d13C values between these habitats can lead to large uncertainties in mixing models and therefore more informative tools are needed. A study by Larsen et al (2009) recently demonstrated that organisms originating from a terrestrial environment such as bacteria, fungi and plants, could be identified to their respective phylogenetic groups based on the relative amino acid d13C ($\delta^{13}C_{AA}$) differences. The groups could be discriminated because of their different biosynthetic amino acid pathways. To investigate the extent it would be possible to draw more specific conclusions on the origin and fate of carbon in different lake habitats we analysed $\delta^{13}C_{AA}$ as well as bulk d13C and d15N from plankton and benthos (both epilithon and sediment biofilms) of high mountain lakes and ponds of the Pyrenees with contrasting ecological characteristics. We used the marker pigment composition to characterise the relative importance of each algal or cyanobacterial groups in each habitat. We found that the dominant algal groups in the epilithon were cyanobacteria and to lesser extent diatoms, while in sediment diatoms and chlorophytes dominated in most lakes. Seston was mainly composed by chrysophytes, cryptophytes and chlorophytes. Probably due to the differences in algal compositions, we found that a discriminant analysis of $\delta^{13}C_{AA}$ was able to distinguish among the three different habitats in almost all lakes sampled. However, by using only the essential amino acids, the degree of differentiation was less robust, yet sufficient to distinguish among the different habitats. These results suggest that $\delta^{13}C_{AA}$ patterns have a good scope for distinguishing between plankton and benthic food sources along the food chain of lakes.

Terrestrial subsidies of lake food webs mediated by pollen inputs

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Huge amounts of pollen can end up in aquatic ecosystems during the floral bloom of wind pollinated trees and can accumulate at the air-water interface. We hypothesized that such pollen rains could enhance the development of a neustonic microbial food web and be of benefit to aquatic secondary production. Our results show indeed that a pine pollen rain event on an oxbow lake created a strong vertical heterogeneity of food resources and consumers in the water column, with significantly more microorganisms in the neuston than in the seston, and an uneven distribution of zooplankton species in the two compartments. Bulk isotope and isotopes of fatty acids analysis revealed trophic partitioning among these zooplankton species and showed that some taxa forage specifically on neuston, where they benefit from pollen-derived carbon. Microorganisms seem to be a key element in the trophic upgrading of pollen food quality and in the transfer of pollen carbon to metazoan consumers. Pollen rains may thus not only act as an external input of nutrients but also as a structuring factor supporting consumers' production in aquatic ecosystems. The accentuation of habitat heterogeneity and the induction of a new trophic niche could also play an important role by supporting consumers' diversity. Our results emphasize that future investigations on the contribution of terrestrial organic matter to aquatic productivity should account for the form under which this allochthonous carbon enters the system and consider the role of micro-organism mediation in transferring this carbon to metazoan consumers.

Assessing effects of metabolic qctivity and hydrology on dissolved oxygen and dissolved inorganic carbon dynamics in hardwater lakes using stable isotopes

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Dynamics of dissolved oxygen (DO) and dissolved inorganic carbon (DIC) are affected differently by metabolic and hydrologic processes. Oxygen responds quickly to ambient productivity levels, and the majority of fluxes occur between water column and atmosphere. While in softwater lakes DIC and DO dynamics are similar, in hardwater lakes DIC is largely controlled by watershed processes. To evaluate the relative importance of metabolic and watershed processes on DO and DIC dynamics, as well as their coupling, we analyzed seasonal changes of both concentrations and stable isotopes of DO and DIC in seven Qu'Appelle Valley lakes, a chain of hardwater lakes in western Canada. Oxygen dynamics indicated a clear seasonality with one to two periods of high productivity and high P:R, followed by low productivity and P:R<1. In contrast, DIC dynamics in three lakes showed continuous depletion of DIC with time due to photosynthetic activity, while in other lakes this effect was not detected, which was probably a result of DIC influx from the watershed. Ultimately, this method will help determine the importance of hardwater lakes in the global carbon cycle.

Deconstructing the lake: Littoral energy sources are of low importance in prairie lakes

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The importance of pelagic vs. littoral energy supporting higher trophic levels in inland lakes has received an increasing degree of attention. Work in boreal systems has resulted in a recent paradigm shift; refuting the previous belief that pelagic phytoplankton is the dominant energy source in lakes. Instead, terrestrial material and benthic or epiphytic algae significantly contribute to the energy demands of higher trophic levels. Here, we tested if this new paradigm is also appropriate for hardwater lakes on the Great Plains. The study was conducted over a four-year period across 15 lakes in southern Saskatchewan, Canada. We analyzed $\delta^{13}C$ and $\delta^{15}N$ of pelagic zooplankton, littoral macro-invertebrates and fish assemblages to quantify the contributions of pelagic and littoral prey to the diets of fishes. Based on stable isotope mixing models (and stomach content analysis), we recognized that higher trophic levels in prairie lakes were predominantly reliant on pelagic primary production, while littoral energy sources were largely limited to support habitat specialists, such as crayfish and benthivorous fishes. Terrestrial sources are likely trivial as well due to non-forested watersheds and a strong hydrological isolation of lakes. This contrast to boreal lakes is likely due to the naturally high nutrient contents of these lakes, where high phytoplankton biomass reduces light availability for littoral primary producers. Accordingly, food-web dynamics in lakes across the Great Plains and other arid regions worldwide are controlled differently than boreal systems. In addition, we observed significant interannual shifts in $\delta^{13}C$ and $\delta^{15}N$ baselines that occurred at the landscape level as a response to climate-related hydrological changes. The subsequent mismatch in predicted energy sources between stable-isotope and stomach-content approaches highlighted not only the importance of different turn-over rates for such models but also the risk of erroneous results derived from short-term studies.

Sulfur and carbon stable isotopes as tracers of fish reliance on profundal detritic matter in lakes varying in hypoxia

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Growing evidence suggests that benthic prey from the hypolimnion (*e.g.* chironomid larvae) constitute a potentially important food source to lake food webs. These organisms can have very negative $\delta^{13}C$, distinct from benthic littoral and pelagic food sources, which have been hypothesized to be related to microbial recycling of methane. “Traditional” two-end member models cannot resolve this three food-source problem, leaving the interpretation of data ambiguous. We show that the $\delta^{34}S$ of primary consumers can be used to successfully distinguish deep sedimentary food sources from zooplanktonic or littoral sources in a three-source and two-isotope model. In a study of twelve boreal lakes we observe a large range of contribution (0-71%) of hypolimnetic sedimentary matter to fish communities. S and C recycling are evident in lakes with important hypolimnetic oxygen deficits. Inclusion of both C and S in the mixing model leads to very different inferences about the relative importance of pelagic vs littoral sources compared to the previously used model based on C alone.

Patterns of trophic diversity in freshwater fish communities: a stable isotope meta-analysis

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Understanding how biodiversity affect ecosystem functioning is a central question in modern ecology. Trophic diversity of communities strongly affects ecosystem functioning via trophic interactions between species (e.g. predation, competition) that can subsequently control ecosystem functioning through bottom-up and/or top-down forces. However, the natural and anthropogenic broad scale determinants of trophic diversity in animal communities remained poorly understood. Here, we used a meta-analysis approach to investigate the role of natural (i.e. biodiversity, ecosystem characteristics) and anthropogenic (i.e. biological invasions) parameters on the trophic diversity of freshwater fish communities. Specifically, we aim at determining *i*) if the relationship between biodiversity (i.e. taxonomic diversity) and trophic diversity in communities (i.e. quantitative metrics based on stable isotope analyses) differs between ecosystems and *ii*) whether this relationship is affected by biological invasions. We compiled from the literature the stable isotope values ($\delta^{13}C$ and $\delta^{15}N$) of freshwater fish species (> 2000 occurrences, > 650 unique species), the status of the species (native and non-native) and the characteristic of the ecosystem (type, size, latitude) in more than 300 food webs located worldwide. For each food web, we assessed the complementary facets of trophic diversity based on the stable isotope values of each fish species. Our results first confirm that lentic ecosystems (lakes) have longer food chain than lotic ecosystems (streams). Irrespective to the number of species, we observed that the trophic diversity is higher in lentic than in lotic ecosystems but that food chain length increases more rapidly with increased biodiversity in lotic than in lentic ecosystems. The presence and the proportion of non-native species in the communities interact with these patterns. Specifically, the presence of non-native species decreases the relationship between biodiversity and trophic diversity in all ecosystem types. To our knowledge, this study represents one of the first cases where trophic diversity of communities, determined using stable isotope analyses, are analysed at a broad spatial scale. Our results provide new insights into the relative contributions of natural and anthropogenic parameters in the relationship between biodiversity and ecosystem functioning through the analyses of the multiple facets of trophic diversity.

Ecology, trophic structure and evolution of continental slope communities: Multi-isotope, multi-tissue investigations.

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Bentho-pelagic fish communities on the continental slopes are separated from primary production by the overlying water column. Slope communities receive energy either through passive rain of nutrients or via intercepting diurnally-migrating organisms. Differences in the origin of fuelling nutrients result in isotopic separation between differing functional components of the ecosystem, providing a tool to study ecosystem-scale influences of depth on nutrient cycling and ecosystem structure. We applied a community-scale sampling approach, sampling species representing more than 50% of biomass in 5 discreet mass classes at three depth intervals, and, using basic carbon and nitrogen isotope analyses, demonstrate depth-dependent changes in ecosystem function that explain depth-dependent gradients in diversity and biomass.

At 500m depth, primary production and benthic production are tightly coupled, presumably via diurnal vertical migrations. With increasing depth, mass-specific trophic level increases in the benthic but not bentho-pelagic community, resulting in increased trophic separation. Benthic fish biomass decreases with depth but more slowly than predicted based on the depth-trophic level relationship, indicating an additional source of nutrient transfer. We hypothesise that this represents the active transfer of nutrients by the bentho-pelagic fish community, whose connection to primary production is invariant with depth between 500 and 1500m and whose absolute and proportional contribution to biomass increases over the depth over the same range. At bottom depths greater than 1500m, vertical interception is difficult, active nutrient transfer is reduced and benthic fish biomass decreases rapidly.

Continental slope bentho-pelagic fish communities are relatively speciose, but ecosystem trophic function is maintained independently of taxonomic composition. Fish diversity and biomass is dominated by a small number of higher taxa, and we have used a combination of otolith and muscle-based isotope proxies to explore behavioural, ontogenetic and dietary specialisations in an attempt to explain the success of particular groups in colonizing slope ecosystems.

Body size-trophic position relationship in marine fish depends on the biological and spatial scales considered

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The structure, dynamics and productivity of marine ecosystems depend mainly on their underlying food webs. Marine food web structure can be partly characterized by fish species' trophic level. Trophodynamics studies often highlight size-related ontogenetic shifts in the diet of marine fishes, implying an increase of the trophic level according to fish size and/or body mass both throughout an individual's life cycle and across individuals within a population or a community. However, few studies have addressed how size-dependence of trophic position varies according to spatial scale, i.e. whole maritime basin vs. habitat, and whether observed community-scale patterns hold at lower biological scales, i.e. guild and population levels. Here we used individuals' $\delta^{15}N$ and $\delta^{13}C$ signatures within the fish community from the eastern English Channel to estimate body size-trophic level relationships at different spatial scales and biological organisation levels and proposed some hypotheses for the underlying mechanisms contributing to the observed patterns. Different patterns of trophic position variation according to fish body size were detected depending on the scale considered. A positive trend in $\delta^{15}N$ at the community level suggested that individuals feed at higher trophic level with increasing body size. However, at lower biological organization levels, a similar positive trend was found for the demersal guild and a few species only. Furthermore, decreasing trophic level with increasing body size was observed for some species like thornback ray suggesting an ontogenetic change in food preferences whereas no change in trophic level according to body size was observed for the benthic guild and pelagic species. Examination of body size-trophic level relationships at large (whole eastern English Channel) and low (within habitats) geographical scales revealed no consistent pattern across spatial scales. This study reveals that the relationship between fish body size and trophic level is highly variable and depends on the scale considered, be it spatial or biological. Consequently, using a generic positive relationship to describe trophic relationships within marine food webs without accounting for variation across the spatial scales or levels of biological organization might lead to an oversimplification of the trophic links and hide some specific properties of the food webs.

Ecology and location of marine animals revealed by carbon and nitrogen isotopes

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Direct monitoring of animals at sea is difficult and expensive. The isotopic composition of carbon and nitrogen in tissues such as fish scales provides information on both the trophic level and nutritional status of the fish and the state of primary production at feeding sites, which can be used to infer migration patterns. Archives of salmon scales dating back decades exist around Europe and may be used to assess historical trends in ecology.

We use carbon stable isotope data from scale tissues to identify marine feeding grounds for separate salmon populations, and therefore the extent of population-specific geographic separation. We also test isotopically whether climatically-driven changes in ocean conditions are related to marine mortality in the returning fish. The results are compared both within and between populations, in particular assessing differences in marine behaviour of fish that return as 1 sea-winter or as multi sea-winter fish.

Fluctuations in $\delta^{13}C$ data are not consistent between archives, and can be used in conjunction with coeval sea surface temperature records as a novel means to determine the areas in which the tissues were grown. Results show a complex, population-specific relationship between ocean productivity, climate indices, migration and fish survival. We use these results to produce maps showing strengths of covariation between $\delta^{13}C$ values in these salmon scales and oceanographic variables, providing a method of inferring marine feeding areas for different salmon populations, and many other pelagic animals, based on temporal variability in $\delta^{13}C$ values.

North Atlantic ecosystem shifts revealed from $\delta^{15}N$ & $\delta^{13}C$ otolith chronologies

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Changes in climate and exploitation have caused large fluctuations in the productivity of many North Atlantic cod populations and the collapse of many cod fisheries. These fluctuations are most likely due to a combined effect of physical processes and changes in ecosystem trophic structure.

To study the link between environmental changes and ecosystem trophic structure we developed $\delta^{15}N$ & $\delta^{13}C$ chronologies by analyzing the organic matrix of cod otoliths from the Nuuk Fjord cod population (1927-2009) and the Faroe Shelf cod population (1950-2010). Significant correlations between $\delta^{15}N$ & $\delta^{13}C$ annual mean values over time were seen in both ecosystems, suggesting $\delta^{15}N$ & $\delta^{13}C$ values were affected by the same overall processes. There was a significant effect of climate variables (temperature, Arctic Multidecadal Oscillation (AMO) and sub polar gyre index) on $\delta^{15}N$ & $\delta^{13}C$ chronologies in both ecosystems. Fast Fourier Transformations showed the same periodicity in climate variables, $\delta^{15}N$ & $\delta^{13}C$ chronologies and cod size-at-age. In the Nuuk Fjord ecosystem discontinuity analyses (STARS) found coinciding shifts in both $\delta^{15}N$ & $\delta^{13}C$ chronologies, climate variables, cod size-at-age and inshore cod catches. This indicates a large ecosystem shift in the Nuuk Fjord around 1970 and a smaller in 1995 and is further supported by the $\delta^{15}N$ & $\delta^{13}C$ bi-plot that shows a clear separation in signatures before and after 1970. To take baseline effects into account new $\delta^{15}N$ & $\delta^{13}C$ chronologies of organic matrix of otolith core material (Nuuk Fjord) and annual growth increments in Ocean Quahog *(A. Islandica)* shells will be included.

Spatial population dynamics of coral reef fish revealed by otolith stable isotopes

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In tropical coastal ecosystems, several fish and invertebrate species utilize inshore seagrass beds and mangroves during their juvenile stage before migrating as adults to coral reefs. Measuring the actual contribution of these nursery habitats to reef populations remains a major challenge. Fish otoliths (earbones) are very useful as natural tags due to their permanent recordings of environmental factors. Signatures of stable carbon and oxygen isotopes that are incorporated into otoliths vary regionally in surface waters, and thus reflect differences in water composition among habitats, making them suitable to trace earlier residence areas of fish. In this study, we determined the stable carbon and oxygen isotope signatures in the juvenile margin of otoliths of adult yellowtail snappers (*Ocyurus chrysurus*) from coral reefs, and compared these to the signatures in otoliths of juvenile fish collected in different nursery embayments harboring seagrass beds, to trace the origin of individual reef fishes. Unique in our approach is that our experimental reef fish represent a complete population on the scale of an entire island, and that all potential nurseries were sampled. Of all adult reef fish caught, 97% were identified as having resided as juveniles in one of the seagrass nurseries, yet different bays contributed unequally to the adult population. Additionally, we combined these data with a spatial simulation model that showed that adult dispersal away from reef areas near the mouth of bays was limited. These findings show that the spatial distribution of nursery areas and their productivity are important drivers of population dynamics, and can lead to a source-sink structure in a closed demersal fish population on the reef. Understanding source-sink dynamics of marine animals is of major importance for the design and placement of marine reserves, especially when life stages utilize spatially different habitats and source-sink dynamics occur within life stages.

Session 12: Isotopes in Scales and Otoliths

The use of fish scale collections to study recent changes in C and N cycles in rivers

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Stable isotope analysis of organic matter in sediment records has long been used to track historical changes in carbon (C) and nitrogen (N) cycles in marine and lacustrine ecosystems. While flow dynamics preclude stratigraphic measurements of riverine sediments, retrospective analysis is challenging in running waters. Archived biological material could be an alternative option. Notably, it has been shown that δ^{13}C and δ^{15}N of archived fish scales can reveal temporal variations in fish diet and aquatic food webs functioning. However, available collections of riverine fish scales mostly involve migratory anadromous adults returning to freshwater to spawn. The inner portion of the scales corresponds to the juvenile period in freshwater but also includes collagen formed later during the oceanic period of their life, precluding rigorous reading of environmental conditions experienced in the natal river.

In this work, we use unique scale collections of juvenile Atlantic salmon (*Salmo salar*) and brown trout (*S. trutta*) that grew up in rivers that underwent various anthropogenic pressure over the past 4 decades. The Teno River catchment (70°N, Finland) is a pristine area where human activities have had negligible impacts on water quality. δ^{15}N values remains remarkably stable, and a slight decrease in δ^{13}C matches with recent change observed in atmospheric δ^{13}C. Conversely, intense agricultural activities have developed in the Scorff River catchment (47°N, France) such that the aquatic ecosystem suffered unbalanced loads of N. High δ^{15}N values reflect anthropogenic inputs to the riverine food webs, and a parallel increase of δ^{13}C values and dissolved inorganic N load suggests the enhancement of autotrophic production. Finally, archived scales from rivers of the Kerguelen Archipelago (49°S, French Southern and Antarctic Territories) reveal that both δ^{13}C and δ^{15}N values dramatically decreased over the last 40 years. A major change in marine nutrient transfers to freshwaters is suggested, and the role of invasive mammal species intentionally introduced in the archipelago is pointed out in such a process.

Our results show the value of analysing C and N stable isotopes on riverine fish scales collections to study anthropogenic pressure on stream ecology. Potential weaknesses in ecological interpretations are also identified.

Ants, non-ants and housing rent: interactions of a myrmecophyte host with its non-protective tenants

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Humboldtia brunonis (Fabaceae) is a unique myrmecophyte (plant housing ants) endemic to the wet evergreen forests of the Indian Western Ghats. Although all individual trees produce ant food as extrafloral nectar (EFN) on young leaves and bracts, only some bear ant shelters (domatia) in the form of swollen hollow stems. This myrmecophyte, therefore, provides an excellent natural experimental system to understand the evolutionary benefits of bearing domatia whose traditional function is believed to be for housing ants that provide protection against herbivory. However, *H. brunonis* domatia are occupied by ants and myriad invertebrates. Only one of the eleven species of ant occupants protects the plants against herbivory, and that too only over a limited geographical area. In the absence of a universal protection mutualism, we investigate the possibility of trophic interaction between host plant and tenants, and whether trophic benefits, if any, translate into fitness benefits for the plant.

We obtained natural values of $\delta^{15}N$ of plant and invertebrates, and performed pulse-chase experiments with ^{15}N labelled glycine to investigate nutrient transfer in this system. To determine fitness benefits to the domatia-bearing host plant, we performed hand-pollination of inflorescences on domatia- and non domatia-bearing branches, and compared their fruit set. We studied domatia anatomy to understand mechanisms of nutrient absorption. Using natural values of $\delta^{13}C$ we also determined dependence of resident ants on EFN compared to other available sugar sources such as honeydew.

We confirmed the ability of domatia to absorb nutrients from its inner lining. The ^{15}N label was transferred via domatia-resident ants to the plant and was not only absorbed by the domatia wall, but was also traced along domatia-bearing branches. Fruit set was affected by domatia presence. Our results also show that EFN is an important dietary component of resident ants.

Because of its high abundance in its range, and association with myriad invertebrate species, this myrmecophyte forms an important component of the Western Ghats forest ecosystem. Our findings of trophic mutualism will add to understanding the evolution and maintenance of myrmecophytism in the absence of protective ant species, and provide new perspectives on the evolution of myrmecophytism.

Ecology in a European kelp forest (*Laminaria hyperborea*): linking biodiversity to trophic structure and functioning

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Kelp forests in European subtidal areas are commonly dominated by *Laminaria hyperborea*, and shelter an important diversity of species, including sessile and mobile organisms. *L. hyperborea* plant can be considered on its own with preferential assemblages of species distributed on the holdfasts, the stipes, the epiphytes, and the fronds. Each of these kelp parts may constitute a microhabitat. Up to now, most studies focused on the fauna directly associated with the different parts of kelps but overlooked the surrounding diversity.

The present study aims to describe the whole structure of a Northern Brittany *L. hyperborea* forest in a pristine area and to determine the main trophic pathways involved by the dominant species using stable isotopes. At two seasons, samples of each part of the kelp and of the surrounding area were collected separately by scuba. The abundance and biomass of the macroalgae and invertebrate species were measured to characterize community and trophic structures within each microhabitat. These results were coupled to $\delta^{13}C$ and $\delta^{15}N$ values in order to characterize the associated food web. Biomasses were dominated by suspension feeders which seemed to select their food sources within the organic matter pool. More than 100 seaweed and 300 fauna species were determined, differently distributed among stipe, holdfast and the surrounding substratum. Trophic structures established by both biomass and isotopic analyses suggested different functioning according to microhabitats and seasons.

Parasites and the isotopic integrity of individuals

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Stable isotope analysis has been used for many years now to characterise trophic interactions within, between and among organisms at scales from the individual to the ecosystem. Early studies used bi-plots to qualitatively map food webs in x-y space, and trophic links were established using mixing-models based on mathematical proportions; hence, a lot of useful information was discarded. Within the last five years, the way that we analyse isotope data has been revolutionised by the development of community and population metrics to assess the 'isotopic niche' occupied in x-y space (either as convex hulls or Bayesian standard ellipse areas), and other metrics such as nearest neighbour distance and mean distance to centroid are now used to infer the feeding ecology and strategies of organisms; e.g. specialists or generalists. How individuals behave and interact is currently a hot topic in ecology and an isotopic approach is one of the tools driving this forward; for example, Jackson et al (2012) used isotope analysis to assess how an established population niche changes when a functionally similar invasive species enters the habitat.

An implicit assumption within these metrics is that the expression of isotope signal by individuals solely reflects diet. However, and as with many aspects of ecology, the potential effects of parasites are completely overlooked. Parasites by definition incur a physiological cost to their host by competition for resource or by direct feeding upon the host, and often alter the behaviour of the host, causing them to reduce or even cease feeding, or to occupy a different habitat and hence feed on different prey items. Both physiology and a change in diet may affect isotope integrity and hence have a knock on effect to isotope-derived metrics. The majority of published parasite studies using stable isotopes have tended to focus on relating the parasite to its host rather than on how that parasite may be affecting the isotope signal of the host. Using a number of well documented host-parasite relationships, and both field and experimental data, I will discuss how parasites make everything just a little more complicated as usual.

References :
Jackson MC, Jackson A, Britton JR, Donohue I, Harper DM & Grey J. 2012 Population-level metrics of trophic structure derived from stable isotopes and their application to invasion ecology. *PLoS One* 7(2): e31757

Lack of coupling between estuaries and coastal rocky shore-associated invertebrates in a semi-arid environment: Evidence through stable isotopes and fatty acid analysis

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Understanding the effects of estuarine inputs on their nearby habitats is crucial to assess the role played by estuaries in the ecological functioning of coastal ecosystems. In particular, estuaries are known to deliver large amounts of dissolved and particulate organic matter that may enter coastal food webs and support coastal communities. In South Africa, the high evaporation rates associated with semi-arid climate together with the numerous impoundments in the catchments for agricultural uses result in a low freshwater runoff into the sea from the rivers. Consequently, it is expected that estuaries may have very limited supporting roles for coastal communities, and that this support will decrease even further with the increased prevalence of arid conditions expected as a result of global climate change. In this study, we describe food web structure and functioning at different rocky sites close to the mouths estuaries along the South African coastline. These estuaries were representative of different freshwater runoff and surrounded by coastal waters from oligotrophic (eastern coast) to eutrophic (western coast). The most abundant benthic consumers and their potential food sources (i.e. estuarine and marine particulate organic matter, macroalgae) were sampled at different distances from each estuary mouth, and their stable isotope ratios ($\delta^{13}C$, $\delta^{15}N$) and fatty acid profiles measured. We observed very limited impact of estuarine-derived organic matter on the food webs of southern and western coast rocky shores (intermediate to eutrophic conditions). In contrast, significant estuarine signals were found in invertebrates inhabiting rocky shores at the vicinity of eastern coast estuaries (oligotrophic conditions). This study points out the general low impact of organic matter delivered by estuaries in semi-arid conditions, and the importance of coastal hydrologic features in controlling the interactions between estuaries and their nearby coastal environment. The need for sustainable management of freshwater resources, guaranteeing sufficient runoff into the sea to support coastal invertebrate populations is also emphasized.

Measuring resilience of aquatic ecosystems: the role of isotope labelling experiments

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Ecosystem resilience has become something of a holy grail for environmental managers. Resilience theory has advanced rapidly over the last decade but real-world applications of measurement and maintenance of resilience have been restricted by the need to measure processes rather than structure. Experimental spiking of components of the ecosystem with labelled isotopes overcomes several limitations of natural-abundance isotope surveys. Examples from Australian coastal systems show the breadth of hypotheses that can be resolved with labelling experiments: e.g. whether seagrass is important in the nutrition of juvenile prawns; whether the nutrition of animals in mangrove forests can be based solely on benthic microalgae. More recently, the usefulness of these isotope experiments in supporting management has become clear. The processes important in ecosystem resilience include rates of transfer of energy and nutrients in food webs. Isotope labelling experiments are very useful for this purpose. Isotope labelling allows precise measurements over periods of a few days; actual rates of energy transfer can therefore be assayed as part of monitoring programs. Recent advances demonstrate how the techniques of isotope labelling and food web modelling can be combined to provide a mobile field laboratory. The effectiveness of this strategy is demonstrated using examples that detect effects of organic enrichment and physical disturbance in estuaries.

Trophic role of giant benthic thiobacteria in a Caribbean mangrove (Guadeloupe, FWI)

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Marine benthic bacteria are abundant and highly productive, however their role in food webs remains uncertain. In some part of mangroves from Guadeloupe (FWI), giant benthic thiobacteria form a thick white mat on sediment surfaces. This large amount of bacteria could constitute a good supply of food resource, as they are abundant and easily accessible. In this environment, thiobacteria are characterised by highly depleted $\delta^{13}C$ (-31.7‰), as compared to $\delta^{13}C$ of other available resources: microphytobenthos (-16.6‰) and benthic detritus (-24.3‰). This uniqueness was used in the present study to determine the trophic role of thiobacteria in mangroves food web. Most mats dwelling grazers were identified as members of meiofauna (polychaeta, nematode, copepod, rotifer, turbellaria and vorticel) with isotopic composition ($\delta^{13}C$) fluctuating from -33.2‰ to -16.7‰. This variability suggests different contributions of thiobacteria to the diet of each grazer. A spatial study run in the mat and in its surrounding sediment (*i.e.* 1m, 20m and 100m away from the mat) revealed a similar trend for all studied grazers: turbellaria, nematode and copepod communities, as well as the macrofaunal sea hare (*Bursatella leachii*) presented decreasing $\delta^{13}C$ with proximity to the mat. This trend suggests an increasing trophic role of thiobacteria in location where this resource is more easily available. Thiobacteria would consequently play an important role as complementary or unique food source for organism inhabiting the mat, hence evidencing trophic specialization in several investigated taxonomic groups.

Contribution of chemosynthesis and nutritional patterns in Norwegian margin cold-seep communities.

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The relative contribution of chemosynthesis in heterotrophic fauna associated with cold-seep ecosystems is known to be influenced by depth and habitat. Using stable carbon and nitrogen isotopes, we investigated macro- and megafaunal nutritional patterns in Norwegian margin cold seeps by comparing food webs among habitats within a seep site and between different sites. The Håkon Mosby mud volcano (HMMV, 1250 m depth) is characterized by a concentric zonation of successive biogenic habitats related to an activity and a geochemical gradient decreasing from its centre to its periphery. Along the Storegga Slide (600–900 m depth), some pockmarks with patchy less active seeps, also showed such concentric habitat zonation, but at a much smaller spatial scale. Both sites were accurately sampled for macro- and megafauna by the ROV Victor 6000 during the VICKING cruise (IFREMER, 2006) in the framework of the European project HERMES.

At HMMV, food chains were clearly separated according to habitats, with significantly lighter $\delta^{13}C$ signatures on microbial mats and adjacent sediment (-33.06 to -50.62 ‰) than in siboglinid fields (-19.83 to -35.03 ‰). Mixing model outputs revealed that the contribution of methane derived carbon was low in the siboglinid fields (0–17%) but significantly higher (39–61%) in the microbial mats. However, the variability of $\delta^{13}C$ and $\delta^{15}N$ signatures of the macrofauna within this habitat suggested the co-occurrence of two food chains, one based on sulphur-oxidation and the other one based on aerobic or anaerobic methanotrophy. The length of the food chains also varied among habitats, with at least one more trophic level in the siboglinid fields, which were located at the periphery of the volcano. Conversely, in Storrega pockmarks, faunal $\delta^{13}C$ signatures did not vary among habitats but yes among species. Separate food chains also seemed to co-occur. The small size of the seepage areas and their lower fluxes, when compared to HMMV, allowed more background species to penetrate the seep area, increasing the range of $\delta^{15}N$ and the trophic level number. Probably due to the higher flux of photosynthetic particulate organic carbon, the overall chemosynthesis based carbon contribution in invertebrate nutrition was lower at Storrega than at HMMV.

Transfer of organic matter sources to the macrozoobenthic food web in a semi-enclosed ecosystem: coupling fatty acids to stable isotope analyses

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Coastal ecosystems hosts a wide diversity of primary producers — phytoplankton, microphytobenthos, macroalgae, seagrasses, epiphytes, saltmarshes plants — of autochthonous and allochthonous origins. Because of their biochemical composition all primary producers are not similarly bioavailable for primary consumers. Consequently, easily digestible phytoplankton and microphytobenthos, in contrast to seagrasses, often constitute the main trophic resources for macrozoobenthos in many coastal ecosystems. However it may not be the case in semi-enclosed systems where seagrass beds are very extensive such as in Arcachon Bay, a coastal semi-enclosed lagoon with shallow depths and tidal regime which hosts the largest intertidal seagrass meadow (*Zostera noltii*) of Europe.

In coastal ecosystems, primary production is the basis of a complex food web due to the multiplicity of primary producers and to the numerous pathways of element and energy through trophic levels. This complexity requires the use of multi-tracers approach in order to discriminate at best all the primary producers.To investigate the use of primary producers as trophic resource for macrozoobenthic primary consumers, primary producers and consumers were sampled in September 2009 for stable isotopic ($\delta^{15}N$ and $\delta^{13}C$) and fatty acids analyses.

This study was performed at the Arcachon Bay space scale — 31 stations covering subtidal channels,intertidal mudflats and seegrass meadows. Six groups of primary producers and four main groups of macrobenthic primary consumers were discriminated by stable isotopes. Use of fatty acids profiles lead to more precision within these groups with two and three sub-groups for grazers and interface feeders, respectively.

Results showed that among the six groups of primary producers considered, microphytobenthos and decayed seagrasses were the main food sources supporting the macrozoobenthic secondary production (mainly represented by interface feeders and sub-surface deposit feeders) at the scale of the Bay.

Unraveling carbon flow pathways on coral reefs with compound specific stable isotope analysis

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Quantifying carbon flow on coral reefs is fundamental to the development of models capable of predicting the response of reef ecosystems to threats, including overfishing and global climate change. For instance, it is often assumed that water column-based phytoplankton production is the dominant carbon source fuelling large predatory fish, such as snapper and grouper, on coral reefs. However, recycled carbon passing through microbial/detrital pathways may also supply significant amounts of carbon to higher trophic levels. We used amino acid $\delta^{13}C$ values to examine diet and food web structure supporting commercially and ecologically important fishes on coral reefs along a cross-shelf gradient in the northern Farasan Banks, Red Sea. Our results highlight the remarkable complexity of food webs on coral reefs. Coralivorous butterflyfish, planktivorous damselfish and herbivorous damselfish plotted close to coral tissue, zooplankton and macroalgal profiles, respectively. One of the more fascinating observations in this system was the apparent prey resource partitioning of two congeneric snapper species (*Lutjanus kasmira* and *L. ehrenbergii*) that commonly occur together in mixed species schools. While *L. kasmira* apparently feeds on C derived from phytoplankton, *L. ehrenbergii* relies almost entirely on C that has been recycled through a macroalgal/detritus pathway. Non-essential amino acid $\delta^{13}C$ values showed quite different patterns from the essential amino acids, with evidence of biosynthesis and isotopic routing. The herbivorous damselfish, *Stegastes nigricans*, had an essential amino acid profile very similar to that of its farmed algae, *Womersleyella setacea*; however, there was a significant fractionation between diet and consumer for several non-essential amino acids associated with the glycolysis cycle. The high degree of biosynthesis of non-essential amino acids likely reflects that *S. nigricans* was feeding on a low protein, low quality diet. Conversely, the planktivorous damselfish, *Amblyglyphidodon indicus*, and the carnivorous snappers, *L.kasmira* and *L. ehrenbergii*, showed tight correlations between diet and consumer for essential and non-essential amino acids, suggesting a higher quality diet and enhanced isotopic routing of dietary proteins. Compound-specific stable isotope analyses represent a powerful new tool for tracing the origin of nutrients fuelling reef ecosystems.

What fuels the marine food web of the Banc d'Arguin (Mauritania)? New insights from isotopic analysis

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Banc d'Arguin (BA), Mauritania is a nationally protected shallow gulf of over 10,000 km^2 located between the Sahara desert and the large upwelling system off the Mauritanian coast. On its southeastern part, BA consists of a 500 km^2, seagrass-covered intertidal flat area, which is the most important wintering site for shorebirds using the East Atlantic Flyway. So far, very little is known about the influence of offshore primary production from the upwelling to the inshore BA food web functioning.

Here, we aimed to identify the main trophic pathways that fuel the BA ecosystem. In particular, we assessed to what spatial extent the northwestern upwelling's production is assimilated by the inshore benthic consumers and motile predatory fishes. For these purposes, suspended particulate organic matter, dominant benthic invertebrate's taxa (mostly suspension-feeders) and various species of fish were characterised for $\delta^{13}C$ and $\delta^{15}N$ along a northwest to southeast gradient. Additionally, the spatial extent of upwelling entering BA was monitored over the year 2008 by remote sensing sea surface temperature and chlorophyll *a* data.

By these two complementary approaches, our results suggested that benthic invertebrates living in the northwestern edge of BA (close to Cape Blanc) assimilate the upwelling's primary production, whereas this food source does not benefit to consumers living close to the tidal flats in the southeast of the gulf. Possible mechanisms explaining such a rapid decreasing trophic role of upwelling's food source over the BA will be discussed. Furthermore, isotopic signatures of fish suggested only a weak trophic connectivity between the northern and the southeastern BA. Our results reinforced the hypothesis that the tidal flat area functions as a distinct ecosystem whose food web is mainly supported by local benthic primary production. This knowledge seems crucial for effective management of the pristine BA national parc.

Amino acid δ ^{15}N from sperm whales (*Physeter macrocephalus*) skin indicate shifts in nitrogen cycling and food web structure in the oceanic California Current

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The California Current continues to experience changes in temperature, oxygen and nutrient concentrations due to natural and anthropogenic perturbations that may have altered biochemical processes, primary productivity, and the structure of food webs. Measuring the magnitude of such changes at the ecosystem level is very difficult for mesopelagic systems. Because apex predators integrate various ecosystem properties through predation, we tacked, for first time, shifts at the base of the food web and top trophic level by measuring δ^{15}N from bulk and individual amino acids from skin samples of sperm whales. Although bulk δ^{15}N values declined from 1972 to 2004 by 2.9 ‰, we couldn't distinguish if the effect was driven by shifts in primary producers and/or trophic structure. Source amino acids declined in δ^{15}N values by 1.5 ‰ indicating that the entire ecosystem has suffered a shift in nitrogen biochemical cycling, while trophic amino acids followed this trend and only exhibited a slight decrease post-2002 indicating a reduction in the length of the food web. We suggest the progressive decline in δ^{15}N from primary producers is related to changes in the physical environment such as the shoaling of the nutricline and the sources of new nitrogen available in the euphotic zone, but the mechanisms are still unknown.

Depicting trophic relationships through carbon and nitrogen stable isotopes ratios in a context of significant environmental variability: The Bay of Biscay case study

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The knowledge of species' trophic ecology is a critical aspect for the assessment of their role in marine food webs or for the comprehension of the recruitment drivers. Stable isotopes analysis (SIA) of carbon and nitrogen in consumers' tissues may constitute reliable indicators of their trophic position and/or their feeding zone. However in open marine ecosystems, a high biological diversity as well as oceanic and terrigenous influences may lead to an important heterogeneity in consumers' isotopic values, constraining the use of these markers or even leading to misinterpretations of isotopic field data for the study of trophic relationships. In the case of the Bay of Biscay (North-East Atlantic), a simplistic interpretation of nitrogen signatures could lead to conclude that small sepiolids (15.1‰) feed on sperm whales (11.1‰), which is total nonsense. Therefore in the present study, we first aimed at investigating the environmental variability that lead to peculiar signatures measured in the different food webs components of this marine ecosystem. The second objective was to highlight the trophic links between mesozooplankton and adults of two pelagic fish of ecological and economical importance in this area (the European sardine *Sardina pilchardus* and European anchovy *Engraulis encrasicolus*) through SIA, as a case study in a context of potentially highly significant environmental variability. Isotopic values of more than 140 species including marine mammals, fish, molluscs and crustaceans are thus reported, as well as $\delta^{13}C$ and $\delta^{15}N$ values of identified mesozooplanktonic organisms and of sardine and anchovie individuals. Significant and constant spatial variations of isotopic signatures along the inshore-offshore gradient in particular were revealed for all the taxa and trophic levels considered, including mesozooplankton. Results particularly suggested the importance to account for nitrogen variability when deriving trophic levels from $\delta^{15}N$ values. Mixing models taking into account this environmental variability (as well as the biological variability) were finally applied to depict foraging areas and potential diet overlapping of sardine and anchovy in this area. Sardine seemed limited to neritic waters and associated mesozooplankton species for feeding, while anchovy showed a greater trophic plasticity, by foraging likely offshore and on a wider range of mesozooplanktonic prey.

Isotope ratios of plankton size spectra as a tool for investigating trophic dynamics

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Marine planktonic food webs are highly complex, characterised by a diverse array of trophic guilds and interactions. Community stable carbon and nitrogen isotope analyses have served to highlight this complexity while also identifying considerable between species trophic level overlap. The high taxonomic diversity and trophic complexity of plankton food webs makes comparison of between ecosystem dynamics difficult without generic trophic categories. It is well established that marine food webs are strongly size structured, with a typically positive relationship between organism size and trophic level, suggesting that size classes may present useful community categories for analysis of both within and between ecosystem trophic dynamics. Here we test the applicability of community size classes to plankton trophic studies using samples collected from Chatham Rise in the austral spring of 2011. Chatham Rise, a shallow sub-marine plateau to the east of New Zealand, is bounded to the north and south by the Sub-Tropical Front (STF) and Sub-Antarctic Front (SAF) respectively. These fronts separate distinct biogeographic zones, differing in sea surface temperature by > 4°C, nutrients availability to primary producers, and plankton species composition.

Using a MOCNESS zooplankton net, depth stratified sampling between 0 and 1000m was conducted across the rise. The zooplankton community was subsequently split into logarithmic size classes between 0.25 and 4mm, before analysis of C and N isotope ratios. Plankton $\delta^{13}C$ and $\delta^{15}N$ both showed strong positive relationships with temperature. In the case of $\delta^{15}N$ this most likely reflected nitrate limitation and higher primary production in the northern sub-tropical waters (Delizo et al. 2007). Trophic level was generally positively correlated with size in the epipelagic zone (0-200m depth). At mid depths (200-600m), however, the smallest size class (0.25-0.5mm) was frequently $\delta^{15}N$ enriched relative to larger size classes, indicating a different trophic dynamic to 0.25-0.5mm plankton in the epipelagic. Mean size class N isotope ratios across depth zones indicated a daily migration of higher trophic level (carnivorous) zooplankton between mid-depths and the surface. The utility of plankton isotope size spectra to trophic studies are discussed in the context of Chatham Rise, and further compared with data from other regions.

Welcome to the jelly-web: using stable isotopes to understand the trophic ecology of gelatinous zooplankton

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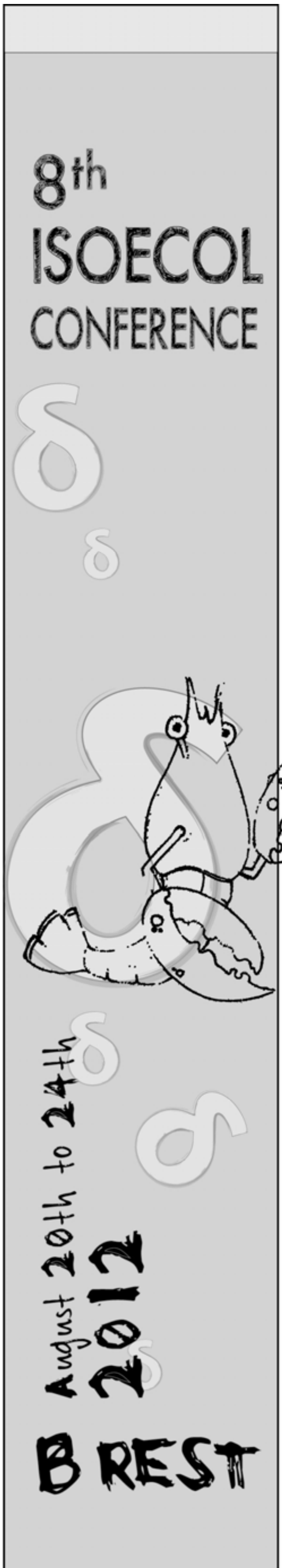
Gelatinous zooplankters are now acknowledged to play a more complex role within marine ecosystems than previously thought. However, due to the limitations of traditional dietary analysis, their trophic ecology is difficult to characterise, e.g. intra-guild predation between gelata is difficult to quantify. Furthermore, there have been repeated suggestions that gelatinous zooplankton may display trophic overlap with, or even act as major predators of fishes. Stable isotope analysis is gaining momentum as a tool for investigating the trophic ecology of gelatinous species and to complement existing dietary studies. Here we report isotopic data from six abundant species of gelatinous zooplankton (ctenophores and cnidaria) and the fish community of Strangford Lough, Northern Ireland. This large, semi-enclosed marine embayment is characterised by an elevated diversity of gelatinous zooplankton. As such, it represents an excellent location to examine the functional role of these taxa and their interactions with fish. To understand the role of these taxa in coastal marine waters, we use information on individual size, $\delta^{13}C$ and $\delta^{15}N$ stable isotope values and Bayesian mixing models to examine: (1) intra-guild predation amongst gelata, (2) allometric shifts in diet, and (3) how temporal shifts in community structure alter the combined impact of gelatinous zooplankton on temperate coastal food webs. Finally, (4), we demonstrate limited trophic overlap with the fish community and the apparent existence of a distinct gelatinous trophic-web.



POSTER SESSIONS

Poster session A
“Soil Ecology and Biogeochemistry”

A1	Pascal BOECKX	The role of rhizodeposition for N cycling in northern fen ecosystems
A2	Andreas DEMEY	N fate of decomposing hemiparasitic plant litter: a ^{15}N tracer study
A3	Anette GIESEMANN	Using site preference of N_2O to differentiate between fungal and bacterial N_2O formation in soil
A4	Martin WERTH	^{13}C fractionations at the root-microorganisms-soil interface and their implications for carbon partitioning studies
A5	Alessandra D´ANNIBALE	Soil mesofauna community responses to elevated CO_2 and GM barley
A6	Michael MASTERS	Restoration of soil organic carbon with cultivation of perennial biofuel crops
A7	Gervasio PIÑEIRO	Estimating carbon fluxes simultaneously in two soil fractions using ^{13}C changes after vegetation replacements
A8	Alina JASEK	Application of modified chamber method to urban river CO_2 flux and its $^{-}$ carbon isotopic composition measurements – preliminary results
A9	Carla Roberta GONÇALVES REIS	Nitrogen dynamics in mangrove areas of Ilha do Cardoso, southeast coast of Brazil
A10	Tamara HUNJAK	δ^{18}O spatial distribution of precipitation in Croatia
A11	Saša ZAVADLAV	Seasonal variations of dissolved inorganic carbon and d^{13}C of tufa precipitating water (Krka River, Slovenia)
A12	Louise ANDRESEN	Investigating microbial responses of ^{13}C-glycine addition to dry heathland soils under elevated CO_2, drought and warming, using ^{13}C-PLFA analysis

The role of rhizodeposition for N cycling in northern fen ecosystems

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Belowground plant C allocation is reported to have great influence on nitrogen (N) cycling and can consequently affect net ecosystem productivity and nutrient dynamics. In this study we investigated *in situ* for a northern (Biebrza, Poland) pristine fen ecosystems the ecological paradigm that rhizodeposition increases when soil N turnover is limited. The role of rhizodeposition in regulating both gross N mineralization and gross NH_4^+ immobilization and the allocation of rhizodeposit C by diverse microbial groups; i.e. Gram-negative bacteria, Gram-positive bacteria, fungi have been evaluated concurrently. *In situ* measurements were made in three undisturbed fens along an eco-hydrological gradient using component specific stable isotope tracing techniques.

The proportion of newly assimilated rhizodeposit C in the soil microbial biomass increased in the poor fen with low gross N mineralization and gross NH_4^+ immobilization relative to the other two fens: gram negative bacteria: 338%, gram positive bacteria 171% and fungi 393%. Equal net N mineralization rates in all three fen ecosystems indicate that rhizodeposition also influences the balance between gross N mineralization and gross NH_4^+ immobilization. The abundance and rhizodeposit C allocation of Gram-negative bacteria and Gram-positive bacteria showed significant differences along the eco-hydrological gradient as a consequence of their different resilience to moisture changes. The proportion of rhizodeposit C in fungi as compared to bacteria was higher when N turnover was lower, indicating the role of fungi for organic mater de-polymerization.

N fate of decomposing hemiparasitic plant litter: a ^{15}N tracer study

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Parasitic angiosperms are represented in the majority of ecosystems worldwide and are considered keystone species in many ecosystems worldwide. Parasitic plants affect population dynamics, community structure and plant diversity through (1) direct 'parasite effects' on the host community and (2) indirect 'litter effects' through the redistribution of nutrients in the ecosystem. (1) Hemiparasitic infection directly reduces host and total aboveground biomass production. If a host preference exists for dominant graminoids, hemiparasitic infection can alter the competitive balance in favour of forbs. This reduced competition may in turn increase species richness and accelerate the restoration of species-rich grasslands. (2) Most parasites shed their leaves or die of early in the season and produce high quality litter that mineralizes faster. This can enhance nutrient cycling and could indirectly reduce species richness when higher nutrient availability favours competitive species.

Here we focus on the indirect effect of litter of two hemiparasitic plants (*Rhinanthus angustifolius* and *Pedicularis sylvatica*) on the composition of their host communities. In a tracer experiment we determined which co-occurring species profit most of the addition of hemiparasitic litter labelled with nitrogen-15 (^{15}N). We found tenfold differences between species. For *Rhinanthus* litter, we found a significant positive relation between the N derived from the applied litter (Ndfl) and specific leaf area (SLA). We suggest that plants with a higher SLA have less root biomass (and thus less N storage), but a higher N uptake rate. Because of N stored in root biomass, plants with a lower SLA would take up relatively less N from the soil (and the added litter). Legume species have relatively low Ndfl values, which is due to biological N fixation from the air. On the other hand, saplings and dwarf shrubs have relatively high Ndfl values.

Using site preference of N_2O to differentiate between fungal and bacterial N_2O formation in soil

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The site preference (SP) of ^{15}N in N_2O is a clue to whether fungal or bacterial metabolism was involved in its production. This is important for the potential mitigation of N_2O emission. Pure culture studies with bacteria and fungi yielded different SP of N_2O (e.g. Sutka et al. 2008, Frame & Casciotti 2010). Most fungi lack N_2O reductase, resulting in N_2O rather than N_2 as the endproduct of denitrification. N_2O reduction, however, is part of the bacterial denitrification pathway. The ^{14}N-O bond is preferentially broken compared to the ^{15}N-O bond of N_2O, resulting in increasing SP in residual N_2O with ongoing N_2O reduction.

In this study, the method of substrate induced respiration with selective inhibition (Anderson & Domsch 1975) was modified to determine the fungal contribution to N_2O production in a soil and to verify the results of pure culture studies by analyzing the SP from N_2O produced by soil microorganisms in situ.

We conducted an incubation experiment with a sandy soil under anaerobic conditions with NO_3 as substrate for denitrification.

Four treatments were established: a) control without growth inhibition, b) inhibition of bacterial growth, c) inhibition of fungal growth and d) inhibition of bacterial and fungal growth. All treatments were analyzed with and without blocking the N_2O reductase by acetylene to investigate the effect of N_2O reduction on SP.

N_2O production was largest in the control (a), followed by the treatment with bacterial growth inhibition (b). Treatments (c) and (d) resulted in smallest N_2O production. These results indicate that fungal N_2O production was relevant.

Blocking the N_2O reductase led to larger N_2O production in all treatments (a,b,c,d). As expected, the largest effect was observed in bacteria-dominated treatments (c).

SP was positive in control (a) and fungi-dominated treatments (b). Blocking N_2O reductase resulted in positive SP in the control (a) and bacteria-dominated treatments (c). SP was negative when fungi dominated (b).

Our results differed from SP reported for pure culture studies. For the soil community present in the soil under evaluation, SP could not be verified as a tool for distinguishing between bacterial and fungal pathways of N_2O production.

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^{13}C fractionations at the root-microorganisms-soil interface and their implications for carbon partitioning studies

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Carbon sources and fluxes between plants, microorganisms, and soil can be easily traced using natural variations of the ^{13}C/^{12}C ratio including changes from C_3 to C_4 vegetation. In this presentation, we focus on ^{13}C fractionation in the main soil processes root respiration, microbial respiration, formation of dissolved organic carbon, as well as microbial uptake and utilization of soil organic matter (SOM). Based on literature data and our own studies (Werth & Kuzyakov 2010), we estimated that roots of C_3 and C_4 plants are ^{13}C enriched compared to shoots by +1.2±0.6‰ and +0.3±0.4‰, respectively. CO_2 released by root respiration was ^{13}C depleted by about –2.1±2.2‰ for C_3 plants and –1.3±2.4‰ for C_4 plants compared to root tissue. In soils developed under C_3 vegetation, the microbial biomass was ^{13}C enriched by +1.2±2.6‰ and microbial CO_2 was also ^{13}C enriched by +0.7±2.8‰ compared to SOM. These ^{13}C fractionations suggest preferential utilization of ^{13}C-enriched substances by microorganisms, but a respiration of lighter compounds from this fraction. The δ^{13}C signature of the microbial pool is composed of metabolically active and dormant microorganisms; the respired CO_2, however, derives mainly from active organisms. This discrepancy and the preferential substrate utilization explain the δ^{13}C differences between microorganisms and CO_2 by an 'apparent' ^{13}C discrimination.

In the framework of standard isotope mixing models (Phillips & Gregg 2001), we calculated CO_2 partitioning using the natural ^{13}C labelling approach at a vegetation change from C_3 to C_4 plants assuming a root-derived fraction between 0% and 100% to total soil CO_2. Disregarding any ^{13}C fractionation processes, the calculated results deviated by up to 10% from the assumed fractions. Accounting for the above identified ^{13}C fractionations in the standard deviations of the C_4 source and the mixing pool did not improve the exactness of the partitioning results; rather, it doubled the standard errors of the CO_2 pools. Including ^{13}C fractionations directly into the mass balance equations reproduced the assumed CO_2 partitioning exactly. At the end, we therefore give recommendations on how to consider ^{13}C fractionations in studies on carbon flows in terrestrial ecosystems.

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Soil mesofauna community responses to elevated CO_2 and GM barley

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Rising levels of atmospheric carbon dioxide (CO_2) in future scenarios are recognized to have major impacts on soil ecosystems. At the same time, the increasing use of genetically modified (GM) crops in agriculture represents another factor affecting soil functions and below-ground processes.

In order to investigate the individual and interactive effects of elevated CO_2 and a GM barley line (C-hordein antisense barley) on soil fauna, a mesocosm experiment was set up. Each mesocosm unit contained the same mesofauna community (five collembolans, one enchytraeid and one predatory mite species), but different barley varieties (GM and non-GM) and were exposed to either ambient or elevated (+80 ppm) CO_2 in a greenhouse. Crushed maize leaves, mixed in the top layer, were used in the mesocosmos as an isotopic marker, having a higher $\delta^{15}N$ and $\delta^{13}C$ respect to barley. In order to study the trophic structure and changes caused by the action of the two experimental factors, soil, plants (roots, shoots and leaves) and animals were collected after five and 11 weeks. At both time occasions their ^{13}C and ^{15}N content were determined.

The isotopic analyses revealed information about trophic relations between Collembola, Enchytraeidae and the predatory mite. Crushed maize leaves directly and indirectly influenced the isotopic signatures of collembolans, enchytraeids and predatory mites. Collembolans presented intermediate $\delta^{13}C$ values between maize leaves and barley roots signatures, showing a shift during time towards more depleted values, i.e. closer to roots signatures, indicating changes in the diet. The result was also reflected in the predatory mite signatures. The depleted injected CO_2 had the same role as isotopic marker, as the different $\delta^{13}C$ values were reflected in barley plants and in some Collembola species. No effects on soil community resulted from the presence of the GM line.

The experiment confirmed the potentialities of a multi-factorial mesocosm experiment combined with stable isotopes analysis, as a tool to detect and track changes in the soil food web.

Restoration of soil organic carbon with cultivation of perennial biofuel crops

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The amount of carbon that is sequestered in bioenergy cropping systems is an important ecosystem service that varies among temperate crop species. Perennial grasses that are proposed as cellulosic feedstock sources have the potential to store greater soil C than annual crops. We compared soil organic carbon (SOC) storage and bacterial communities in *Zea mays* L. (corn), *Panicum virgatum* L. (switchgrass), *Miscanthus x giganteus* Greef et Deuter (miscanthus), and native prairie sites at seven locations that spanned a range of temperatures, precipitation, and soil types in Illinois, USA. By comparing annually harvested switchgrass and miscanthus plots to conventional corn agro-ecosystems and native prairies, we calculated the potential for perennial biofuel crops to restore SOC in intensively managed soils of the Midwest. We also calculated SOC accumulation using the ^{13}C isotope composition of the soil as a tracer for C_4 plant-derived SOC additions. On average, the change in total SOC and the δ^{13}C of the soil in the miscanthus and switchgrass plots indicated an accumulation of SOC after establishment of perennial grasses, but the accumulation of SOC with each crop species varied among sites. Differences in plant species and SOC explained 39-62% of the variation in bacterial communities across sites. Bacterial communities associated with annually harvested switchgrass and miscanthus differed from communities found in conventional corn-soybean agriculture and prairies. Thus, the potential to restore SOC to agriculturally depleted soils of the Midwest is not dependent on a soil bacterial community that mimics prairie soil communities. Soil organic carbon of conventional agricultural soils could be restored over time if miscanthus or switchgrass crops were planted and harvested annually, but the restoration potential varies with geographic location.

Estimating carbon fluxes simultaneously in two soil fractions using ^{13}C changes after vegetation replacements

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For more than two decades soil researchers have estimated the proportion of C_3 and C_4 derived carbon in the soil organic matter based on ^{13}C changes occurred after a vegetation shift or after ^{13}C labelling. Carbon outputs from the soil and soil organic carbon (SOC) decomposition rates (*k*) have been also estimated based on this approach. Although, this method applies to a single pool model with known $^{13}C/^{12}C$ inputs, it has been also erroneously applied to models with multiple pools or data collected for multiple soil fractions. Here we present a new approach to estimate C inputs from vegetation to the soil and C fluxes from a labile to a recalcitrant soil fraction. Our method is easy to apply and is based on two simple equations based on mixing models. We use data collected in Uruguay grasslands (mostly C_4 grasses) that have been replaced by Pine and Eucalyptus plantations. We collected soil a litter samples at five independent sites and fractionated soil samples using a common physical fractionation protocol that separates the more labile particulate organic matter fraction (POM) and the recalcitrant mineral associated organic matter fraction (MAOM). Our method gave estimates of decomposition rates of the POM and MAOM fraction and also maximum and minimum estimates of the amount of POM carbon that was transferred to the MOAM fraction after vegetation replacement. Our data suggest that in the top 5 cm of the soil and after approximately 25 years nearly all the carbon in the POM fraction is derived from trees and more than 60% of the MOAM fraction. In deeper soil layers these proportions decrease, but most of the POM is still derived from trees while the MAOM fraction has only 5 to 10% of C derived from plantations.

Application of modified chamber method to urban river CO_2 flux and its $^-$ carbon isotopic composition measurements – preliminary results

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Surface water, including watercourses, in most cases is the source of CO_2 released into the atmosphere. This is due to CO_2 partial pressure excess in water, related to the atmosphere cased by CO_2 release processes (respiration and organic matter decomposition) occurring in the water. Intensification of processes related to the mutual transformations of organic and inorganic forms of carbon in watercourses is promoted by anthropogenic factors, such as agriculture or conversion of the river channel. Few existing estimates of river CO_2 flux show that it can be comparable with the amount of CO_2 released from soils. CO_2 released from the urbanized sections of large rivers may therefore contribute significantly to the local balance of this gas.

The research object in this work is Vistula, the largest Polish river of length of 1047 km and annual runoff of $6.2\text{x}10^{10}\text{m}^3$, flowing through Krakow. Vistula urban section receives a large amount of organic matter in highly urbanized catchments.

Chamber method several times proved to be an effective tool in the field measurements of various gas fluxes into the atmosphere. In this work, a modified chamber method was used for measurements of CO_2 emissions from water surface of the Vistula river passing the Krakow city. In the frame of this work, a floating chamber was build and tested. Thanks to a set of floats and an anchor the chamber remains steady on the surface of flowing water making possible the flux measurement. For better control of conditions inside, the chamber is equipped with pressure, relative humidity and temperature sensors. A measurement system consists of water-chamber coupled with two types of CO_2 analyzers (VAISALA CarboCAP sensor and Cavity Ringdown Mass Spectrometer Picarro G2101i), Vistula CO_2 fluxes and its carbon isotopic signature were measured on approximately monthly basis starting from October 2011 in three locations inside the administrative city area representing inflow, intermediate state and outflow from the city. Additionaly, physicochemical properties of the water were investigated. In this work some preliminary results are presented and discussed.

Nitrogen dynamics in mangrove areas of Ilha do Cardoso, southeast coast of Brazil

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Nitrogen isotope ratio ($\delta^{15}N$) is an integrative measurement of N dynamics in ecosystems. Aiming to contribute to a better understanding about N dynamics in mangrove forests that can be useful to predict impacts of N enrichment in mangrove areas, we tested the hypothesis that a more nutrient limited and less productive mangrove formation (Basin compared to Fringe), which is expected to have lower rates of N transformation in the soil and losses for atmosphere, would exhibit lower foliar $\delta^{15}N$ values.

We collected leaf samples of individuals of *Rhizophora mangle* L. (Rhizophoraceae), *Avicennia shaueriana* Stapf & Leechm. ex Moldenke (Acanthaceae) and *Laguncularia racemosa* (L.) C.F. Gaertn. (Crombetaceae) in Fringe and Basin mangrove formations in the State Park of Ilha do Cardoso, São Paulo state and measured their leaf N and C concentrations and leaf $\delta^{15}N$. We also measured the soil redox potential (Eh) near sampled individuals.

The $\delta^{15}N$ was higher in Fringe (5.62 ± 1.00 ‰) than in Basin (0.61 ± 0.72 ‰). The formations did not differ in leaf N concentration (Fringe: 16.12 ± 4.19 g. kg^{-1}; Basin: 15.34 ± 1.63 g. kg^{-1}) and C/N ratio (Fringe: 28.06 ± 6.89; Basin: 29.00 ± 2.61). Soil Eh was more strongly reducing in Basin (-543 ± 145 mV) than in Fringe (-134 ± 89 mV).

The $\delta^{15}N$ and Eh differences between the formations indicate that nitrogen dynamics in Basin seems to be more conservative than in Fringe forests. Fringe showed less reducing soil Eh values, which is expected to support higher rates of N transformation in mangroves soil and losses to the atmosphere than soils with stronger reducing potential, as observed in Basin. Higher N losses to the atmosphere results in ^{15}N enrichment of all N pools of the system, which includes vegetation and are reflected in the higher foliar $\delta^{15}N$ values. Because Fringes are less nutrient limited and may exhibit higher rates of N losses, these systems may be less responsive to N enrichment than the more N conservative Basin forests.

Influence of riparian vegetation on temperate stream food web: seasonal variations $\delta^{18}O$ spatial distribution of precipitation in Croatia

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The precipitation as the input into the water system and its stable isotope composition is a basic part of the knowledge that is required for proper use and management of water resources. Thus there is an increasing need for research programs that use spatial precipitation data to identify and characterize regional water resource issues that have the potential to severely impact large sectors of society in the coming decades. The light stable isotope ratios of water (δ^2H, $\delta^{18}O$) are parameters that can be easily and routinely measured for almost any water sample and which can preserve information on the climatological source (i.e., the location, time, and phase of precipitation) and the history of water after precipitation. Environmental water resources, including ground and surface water, derive their H and O isotopic composition primarily from the meteoric precipitation [Gat, 1981; Kendall and Coplen, 2001; Smith et al., 2002; Dutton et al., 2005].

Croatia is not well represented in the GNIP data set, and the geomorphology of the country can cause specific local conditions. Therefore, at the Stable Isotope Laboratory (SILab Rijeka)we monitor the stable isotopic composition ($\delta^{18}O$ and $\delta^{2}H$) of precipitation in a large number of stations in various locations all over Croatia at different altitudes and latitudes. The $\delta^{18}O$, $\delta^{2}H$ and d-excess altitude effects have been extracted from the measured data and provide a data base of precipitation isotope ratios.The diverse climate conditions in Croatia are seen e.g. in the altitude-$\delta^{18}O$ relationship. Spatial analysis of $\delta^{18}O$ data in a GIS environment is a new endeavor, and developments in this area are well-timed to take advantage of the recent emphasis on catchment to basin-scale hydrology.

Seasonal variations of dissolved inorganic carbon and $\delta^{13}C$ of tufa precipitating water (Krka River, Slovenia)

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The main objective of this study was to evaluate dissolved inorganic carbon (DIC) dynamics in Krka River watershed (Slovenia). Isotopic composition of DIC and other chemical properties (temperature, pH, conductivity and major ion concentrations) were measured on monthly to seasonal scale during 2008 and 2010 on several sampling points located in the main stream of Krka River and its tributaries. The water chemistry is mainly influenced by chemical weathering of limestone and dolomite with minor anthropogenic influence. Interaction of soil waters with carbonate bedrock results in high concentrations of DIC (3.3 – 5.7 mM) and pCO_2 levels (800 - 15000 ppm). Seasonal variations of DIC and pCO_2 in river water can be mostly attributed to changes in soil respiration, disturbances from tributaries and rainwater input. Moreover, a clear distinction in carbon chemistry and its isotopic characteristics between the headwaters and stream water was revealed. The annual total DIC flux exported by Krka River was estimated to be between 45 to 86 × 10^3 t of C/year. CO_2 evasion estimates were highest for warm periods (average 4600 t of C/year) which coincide with base flow conditions in the Krka River stream. With increasing water discharges and decreasing temperatures the CO_2 fluxes decreased (average 2900 t of C/year).

Analysed water samples had $\delta^{13}C$ values of DIC between -15.6‰ and -8.8‰. Lowest $\delta^{13}C_{DIC}$ values were measured in the headwaters, reflecting variable contributions of different carbon sources, such as soil respiration and carbonate dissolution. The $\delta^{13}C_{DIC}$ values of stream water were higher than those measured in the headwaters. Seasonal and spatial variations of $\delta^{13}C_{DIC}$ in stream water result from in-river processes of CO_2 evasion and aquatic metabolism. Highest $\delta^{13}C_{DIC}$ values in the lower reaches result from photosynthesis during warmer periods whereas respiration activity dominates during winter. CO_2 evasion is more pronounced in the upper reaches, where water is more turbulent due to occurrence of tufa barriers and narrower channel.

Poster session B
"Plants Ecophysiology"

B1	Mirjam STUDER	Dual isotope labelling (^{13}C and ^{18}O) for studying organic matter dynamics within the plant-soil system
B2	M. Paz ESQUIVIAS	Water sources used by coastal sand dune vegetation: spatial and seasonal variations
B3	Juan JÁUREGUI	Water sources isotopic analysis of the Moroccan species Argania spinosa
B4	Robert PANETTA	Rapid analysis of water isotope fractionation along a Pinus spp. branch: in-situ measurement of matrix-bound waters
B5	Nadia S SANTINI	Understanding the freshwater and seawater dependence of the mangrove *Avicennia marina* using oxygen isotopes as tracers for water sources
B6	Jocelyn EGAN	High-resolution $\delta^{13}CO_2$ soil efflux monitoring in tree girdling experiment exposes large temporal variability
B7	Valery TERWILLIGER	Plasticity in carbon and nitrogen use in relation to the distribution of oaks in an eastern North American deciduous forest

Dual isotope labelling (^{13}C and ^{18}O) for studying organic matter dynamics within the plant-soil system

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Combined δ^{18}O and δ^{13}C analysis has been widely used for studying plant physiological processes and to reconstruct past climates (Werner et al. 2011). Further, ^{18}O and ^{13}C stable isotopes have been applied in artificial labelling experiments to study carbon and water dynamics within the plant-soil system. But even though organic molecules consists mainly of carbon and oxygen atoms, their stable isotopes have, to our knowledge, never been applied simultaneously to artificially label organic matter in ecosystem studies. We suggest a dual labelling technique using ^{13}C and ^{18}O stable isotopes for studying organic matter dynamics within the plant-soil system.

To test this novel labelling approach a short-term experiment was conducted. Young poplar trees (*Populus deltoides x nigra*, 6 weeks old) were exposed to an atmosphere containing CO_2 enriched in ^{13}C (10atom%) and water vapour depleted in ^{18}O (δ^{18}O = -365‰) for 14 days. One day before and after 1, 2, 8 and 14 days of continuous labelling the plant-soil systems were sampled destructively and isotopic analysis have been performed for their compartments (leaves, petioles, stems, roots, bulk soil, microorganisms, soil CO_2 efflux).

The results show that new assimilates can be labelled simultaneously with ^{13}C and ^{18}O by adding the stables isotopes in the gaseous phase to the plants atmosphere, whereat the label uptake is dependent on environmental conditions controlling photosynthesis and stomatal conductance. The label can then be traced from the leaves to the roots and into the soil system. The relative allocation of ^{18}O vs.^{13}C varied in between plant-soil compartments. After 2, 8 and 14 days of labelling the $^{18}O_{(new)/}{}^{13}C_{(new)}$ ratio was significantly different in leaf, stem and root tissue (0.0024, 0.0011 and 0.0007, respectively), suggesting a change in OM quality towards more C-rich compounds (e.g. sugars -> lignin).

Dual isotope labelling is a new promising tool, which can be used to study organic matter dynamics within the plant-soil system and which is providing in addition information on leaf gas exchange.

Werner, C., Badeck, F., Brugnoli, E., Cohn, B., Cuntz, M., Dawson, T., Gessler, A., et al. (2011). Linking carbon and water cycles using stable isotopes across scales: progress and challenges. Biogeosciences Discussions, 8, 2659-2719.

Water sources used by coastal sand dune vegetation: spatial and seasonal variations

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The aim of this study was to know the water sources used by a coastal plant community using stable isotopes, addressing variations in spatial (zonal distribution across the dune from high beach to the inland) and seasonal (spring, summer and winter) patterns. The study was conducted in El Rompido spit dune system (37º12'N, 7º04'W) in Huelva province, SW Spain. Climate is Mediterranean with Atlantic influence, and mean annual rainfall is 583 mm with a marked dry period in summer.

δ^{18}O values of potential water sources (air, rain, soil, ground and ocean water) were measured seasonally, concurrently with stem water of eight representative plant species. Three parallel transects were laid out across the dunes (130, 130 and 110 m length), in which plant samples were taken from 5 points determining spatial pattern: 1. Upper beach (proximal to the foredune); 2. Foredune crest; 3; Foredune slack; 4. Secondary dune crest; 5. Inland depression. Nine stem samples per species and point were collected for xylem water extraction (3 stem replicates x 3 transects = 9 stems per point and species).

Results showed isotopic evidence that dune plant species display different use of water sources along their zonal distribution, with a high seasonal influence. The dune vegetation used a mixture of soil and ground water, characterized by the ocean influence spatially and temporally heterogeneous. In seasons with low water availability, spatial patterns arised as plants closest to the ocean were independent of groundwater and standed better seawater influence, whereas inland plants and species still relied on groundwater and deeper soil layers. Under higher water availability, spatial pattern across the dunes was less pronunciated and plant sources relied basically on groundwater. Water use patterns were also related to the type of radical system of the species: shallow rooted changed the main water source used depending on the season and its water availability, while those species with deepest root systems (present especially in the inner points) kept using groundwater the whole year. In conclusion, spatial patterns arised, but highly dependent on the seasonal pattern.

Water sources isotopic analysis of the Moroccan species *Argania spinosa*

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In south-western Morocco, water scarcity and high temperature are the main factors determining species survival. *Argania spinosa* is a Moroccan endemic tree species subjected to a constant regression. This tree plays essential local ecological and economical roles: it protects soils from erosion, it shades different types of crops, it helps maintain soil fertility, and its seeds are used for oil production, with valuable nutritional, medicinal and cosmetic purposes.

The main purpose of this study was to identify the sources of water used by this species and to asses the effect of water availability on the photosynthetic rate and leaf water potential in two populations: one growing in the coast and other one 10 Km inland. Both populations were located, in the Agadir region, the core of the species' main distribution area, where mean annual precipitation is 215 mm y^{-1}. Ten trees per site were marked and the following variables were seasonally monitored: leaf water potential, photosynthetic rate, xylem water isotopic composition ($\delta^{18}O$), carbon isotopic signature ($\delta^{13}C$), stomatal density, and leaf mass area.

Trees from both populations showed a similar strategy in the use of the available water sources, which was dependent on rainfall distribution. The results indicated that during the wet season the main water source was precipitation, while during dry periods or under low precipitation it was soil water. No evidence was found of use of neither groundwater nor atmospheric water in this species. Despite the similar water use strategy, Argania trees from inland population showed a better physiological status with higher photosynthetic rates and leaf water potential than coastal trees, hence suggesting that coastal population of *Argania spinosa* was subject to higher stress.

Rapid analysis of water isotope fractionation along a Pinus spp. branch: in-situ measurement of matrix-bound waters

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Matrix-bound water found in soils and plant tissue provides very detailed information on the flow and uses of water through ecological systems. However, conventional analytical techniques employed to measure these isotopes are long, tedious, complex, costly, and require hazardous materials and dangerous operating conditions not amenable to field studies in a process can take weeks, if not months to complete. Cavity ring-down spectroscopy (CRDS) is already a proven technology for the measurement of stable isotopes in liquid and vapour water. In an effort to make the isotopic analysis of matrix-bound water amenable to field studies, we have developed a simple peripheral that uses heat generated via electric induction to extract water from a small sample, and immediately sends that water to a CRDS analyzer for immediate isotopic analysis. The system is used to probe the variations in δD and $\delta^{18}O$ of water in a *Pinus spp.* from branch through leaf tip. A branch of ~40 cm in total length (including leaves) was sliced (~0.05 mm thick, 7 mm diameter, at 1 cm intervals) and each slice analyzed immediately. A total of 11 samples were prepared and analyzed in a clock time of 99 minutes (9 minutes per sample). The slope of the *Pinus spp.* water line (δD vs. $\delta^{18}O$) was 2.7, which is in agreement with a previous study of pine leaves showing increased evaporation compared to the Global Meteoric Water Line. From branch to leaf tip, δD and $\delta^{18}O$ are enriched by 75.11 and 27.39 ‰, respectively. The enrichment is linear with distance away from the branch with δD increasing by 2.75 ‰ cm^{-1} ($r^2 = 0.99$) and $\delta^{18}O$ by 1.06 ‰ cm^{-1} ($r^2 = 0.98$). Evapotranspiration of water through stomatal openings of the leaf explain this enrichment profile.

Understanding the freshwater and seawater dependence of the mangrove *Avicennia marina* using oxygen isotopes as tracers for water sources

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Mangrove forests are distributed along the tropical and subtropical riverine and coastal shores. Mangroves are highly adapted to saline environments although maintaining water uptake and tissue homeostasis under highly saline conditions increases energetic costs for mangrove trees. Therefore salinity has been widely recognized as an important factor that limits mangrove growth and productivity.

Mangroves can access a range of water sources such as soil pore-water, rainwater and tidal water from the adjoining rivers, creeks or sea. Freshwater sources, such as rainwater and groundwater are important in reducing the water salinity in mangrove ecosystems therefore increasing mangrove productivity. Given changes in rainfall patterns are predicted with climate change, it is important to know the extent of freshwater utilization by mangroves in order to better predict current and future mangrove distributions and productivity.

We used the abundance of ^{18}O isotopes in xylem sap water 1) to identify the relative contribution of different water sources used by the mangrove *Avicennia marina* in different hydrological settings and 2) we assessed whether mangrove growth, measured as increments in stem circumference, is sensitive to variation in rainfall availability.

We found that the $\delta^{18}O$ isotopic composition of xylem water was similar to more than one source of water indicating that mangroves used a mix of rainwater/groundwater and tidal water/seawater for metabolic processes. In addition, we found that mangrove growth is enhanced by rainfall availability ($r^2 = 0.4$, $p < 0.005$). Our results corroborate previous findings that mangrove productivity relies on access to freshwater, whether rainwater or groundwater. This study predicts mangrove productivity and distribution will be highly sensitive to changes in patterns of rainfall with climate change.

High-resolution $\delta^{13}CO_2$ soil efflux monitoring in tree girdling experiment exposes large temporal variability

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Carbon stable isotopes ($\delta^{13}C$) provide an abundance of information that can help in understanding physical and biological processes that control soil respiration. In the past few years, we have seen rapid advances in the way we measure $\delta^{13}CO_2$, using Tunable Diode Lasers (TDL) or Cavity Ring Down Spectroscopy (CRDS), which has helped make us aware of the high isotopic variability in natural soils. There is also growing recognition that most sampling strategies induce gas transport fractionations, which can be of high magnitude. Previous high profile studies using $\delta^{13}CO_2$ are increasingly being called into question for these reasons, as variability or transport fractionations may have overprinted the biologic variability of interest. Our aim in this study was to conduct a girdling experiment similar to other widely cited girdling experiments, where we were interested in identifying isotopic signatures and magnitudes of respiration associated with autotrophic and heterotrophic activity and the spatial variation within treatment plots. Our study is different from previous studies in that it relies on automated continuous CRDS measurements from several locations, using a sampling methodology that we developed specifically to address previous fractionation issues. The new methodology, called isotopic-Forced Diffusion (Iso-FD), measures $\delta^{13}CO_2$ efflux. The field study took place in two 400-m^2 pine plots in Antigonish County, NS, Canada. In addition to Iso-FD continuous data, spatial $\delta^{13}CO_2$ data from gas chambers, and meteorological data were also collected in growing seasons of both 2010 and 2011. Variation was seen in bulk flux rates between the plots, and girdling both resulted in increased CO_2 fluxes and decreased temporal variability in $\delta\ ^{13}CO_2$ as compared to the control plot. Overall it was clear that girdling did not have the characteristic effect of decreasing respiratory activity, or shifting the isotopic signature cleanly in one direction. The resolution of the Iso-FD technique was useful, however, in exposing substantial temporal variability, which allowed us to investigate the drivers of $\delta^{13}CO_2$ biologically sourced variation by avoiding possible errors that could have accounted for the variation observed in other oft-cited studies.

Plasticity in carbon and nitrogen use in relation to the distribution of oaks in an eastern North American deciduous forest

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The range of habitats in which a plant species can maintain a population may be influenced not only by its average responses to environmental conditions but also by the variability of these responses within and among individuals. Functional characters such as carbon and nitrogen use play principal roles in shaping plant responses to environment but can be challenging to measure in sufficient numbers of trees to quantify variability. We used carbon and nitrogen isotopic analyses as part of an effort to examine the hypothesis that tree species distributed in the widest range of environments exhibit the greatest variation in resource use characters. We studied three oak species with differing distributions in a dry and wet year where they co-occurred along a moisture gradient in a deciduous forest in Maryland, USA. Of these, *Quercus falcata* is least widespread and tolerates the driest conditions, *Quercus palustris* tolerates the wettest conditions, and *Quercus alba* is most widespread. Leaves were analyzed for $\delta^{13}C$ and $\delta^{15}N$ from first emergence to senescence. Soils of various depths were analyzed for $\delta^{15}N$ values of total nitrogen, ammonium, and nitrate. Although the $\delta^{13}C$ values of autotrophic leaf growth are shaped by the ratio of the partial pressures of CO_2 in the photosynthesizing leaf to atmospheric CO_2 (p_i/p_a), initial leaf growth following budburst is largely heterotrophic with a ^{13}C enrichment that does not reflect p_i/p_a. Our sampling scheme enabled us to estimate both investment of stored organic carbon in early leaf growth and p_i/p_a --which plays a role in water use efficiency—in autotrophic leaf growth. Integrated p_i/p_a did not differ significantly on average between species. The coefficients of variations during the dry year did differ, however, being highest in *Q. alba* and lowest in *Q. falcata*. P_i/p_a was not related to soil moisture, however. At lower soil moistures, $\delta^{15}N$ values were higher in leaves of *Q. palustris* than in the other species. This may reflect differences in depths of nitrogen acquisition. $\delta^{15}N$ values of nitrate at the soil surface did not differ enough from those of ammonium to explain the differences. $\delta^{15}N_{NH4+}$ increased with depth, however.

Poster session C
“Fractionation & Models”

C1	Lluís JOVER	Performance of Bayesian estimation in underdetermined mixing models
C2	Vasily VAVILIN	From Rayleigh’s distillation model to the dynamic model for stable isotopes fractionation based on substrate consumption and biomass growth
C3	Aline BLANCHET-AURIGNY	Linear relationship between discrimination factor and isotopic signature of food sources: myth or reality?
C4	Michelle CHAREST	Turnover Rates of Sulphur in Liver and Muscle Tissue of Brook Trout, Salvelinus fontinalis, determined by diet shift experiments in the field and laboratory
C5	Ashlie CIPRIANO	Experimental determination of discrimination factors and turnover rates of the ctenophore Mnemiopsis leidyi
C6	Sophie KOHLER	Tissue-specific variations in δ^{13}C and δ^{15}N discrimination factors of marine birds: Using chicks’ tissues to infer seasonal variations in the feeding habits of adults.
C7	Antoine EMMERY	Explaining growth variability of the Pacific oyster in different coastal ecosystems: characterisation of the trophic and abiotic environment of Crassostrea gigas by the coupling of isotopic analysis and DEB modelling
C8	Pierre-Yves PASCAL	Low δ^{13}C composition of *Haplognathia* sp. in a Caribbean mangrove (Guadeloupe, FWI)
C9	Sora KIM	Differences among bulk carbon discrimination factors in a marine carnivore: a comparison of individual amino acid carbon isotope patterns
C10	Sarah BURY	Stable isotope analysis of high lipid-content notothenioid (anti-freeze) fish from the Ross Sea, Antarctica: lipid extraction issues and corrections
C11	Tamsin O'CONNELL	Carbon and nitrogen isotopic inhomogeneity of collagen from different tissues within an individual
C12	Yarnes CHRIS	Rapid Compound-Specific Stable Isotope Analysis of Amino Acids by GC-C-IRMS of Methyl Chloroformate Derivatives
C13	Lionnel MOUNIER	Latest developments and technologies in bulk and compound specific Stable Isotope Ratios Mass Spectrometry for ecological studies

Performance of Bayesian estimation in underdetermined mixing models

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One of the most common applications of SIA is to reconstruct diets of consumers that use two or more resources in order to estimate their relative importance or to elucidate patterns of resource acquisition and allocation. Over the past 15 years several procedures of increasing complexity have been proposed to carry out such analysis on stable isotope data, although the isotopic mass-balance mixing model is shared by all the procedures. The most recent methods are based on Bayesian approaches, with several differences in the specific models to be fitted. The option to include known information through the priors, the incorporation of uncertainty and variability in input parameters and the capacity to cope with problems were the mixing model is underdetermined are viewed as a clear methodological advantages of such procedures, although accuracy of estimations are always relying on fulfilment of model assumptions and data quality (sources used and isotope discrimination and element concentration values). Nevertheless, low effort has been addressed to evaluate accuracy and precision of estimations in problems where the number of sources exceeds the number of isotope signals by more than one, so that the underlying linear mixing model is underdetermined.

Through a simulation study we tried to evaluate two different Bayesian approaches that are currently available in R: SIAR (Parnell et al, 2010) and IsotopeR (Hopkins & Ferguson, 2012) in underdetermined scenarios using two and three isotopes and up to six different resources. The mean squared error and coverage of credible intervals were used to evaluate their performance. Two different coverage metrics are used, the first evaluates the percentage of simulated runs in which all the source's credible intervals cover the simulated proportion values and the second one, evaluates the percentage of total source proportions in which credible intervals cover simulated values. Additionally, we explore the relationships between the observed performance of the estimations and some characteristics of the configuration of the isotopic resource space.

From Rayleigh's distillation model to the dynamic model for stable isotopes fractionation based on substrate consumption and biomass growth

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Rayleigh's equation (1896) is commonly used for calculation of stable isotope fractionation. In fact, "mechanism" of substrate biological transformation is ignored by Rayleigh's approach. Besides, this approach is restricted by log phase of biomass growth. However, substrate consumption and biomass growth can be easily described by traditional mathematical models based on Monod functions with corresponding kinetic coefficients. Usually, an isotopic composition of substrate is not taking into account in such models. In order to consider this issue, the following equation was developed by describing dynamics of heavier stable isotope accumulation in product as well as in biomass (Vavilin, 2012):

$$\begin{aligned}\frac{df^{P}}{dt} &= \frac{1}{P}\frac{d\,{}^{IsHav}P}{dt} - \frac{{}^{IsHeav}P}{P^{2}}\frac{dP}{dt}\\ &= \frac{dP/dt}{P}\left\{\frac{d\,{}^{IsHeav}P/dt}{dP/dt} - f^{P}\right\}\\ &\approx \frac{dP/dt}{P}\left(\frac{1}{\alpha}f^{S} - f^{P}\right)\end{aligned}$$

where $f^{S} = {}^{IsHeav}S/S$, $f^{P} = {}^{IsHeav}P/P$ are the fractions of heavier isotope in substrate and product, respectively; S and P are the total substrate and product concentrations; dP/dt is the production rate of P; α is the kinetic fractionation coefficient of heavier isotope transferring from substrate to product. Isotope fractionation was not taking into account for the totally labeled substrate (Vavilin, 2010). Mass balance equation of heavier isotope should be considered in order to describe changes of isotopes ratio in substrate.

The metabolic pathways of substrate transformation by biological community can be revealed by involving the isotopic equations into the dynamic model in order to describe substrate consumption and biomass growth. As a result, for the following batch systems we were able to describe the changes in isotopic values of:

(*i*) $\delta^{15}N$ during the uptake and assimilation of ammonium, nitrate, nitrite, and urea by cultures of

Thalassiosira pseudonana where it was shown that fractionation of ^{15}N and ^{14}N decreased at decreasing current concentration of *N*-substrate and it stopped after substrate depletion (data: Waser et al., 1998);

(*ii*) $\delta^{13}CH_4$ and $\delta^{12}CDH_3$ during anaerobic methane oxidation by sulfate with inoculum originated from three different sea and ocean areas. In this study, it was shown that fractionations of ^{13}C and ^{12}C as well as ^{2}H and ^{1}H were dependent on the kinetic coefficients, such as maximum methane uptake rate and half-saturation coefficient, at similar initial methane concentration (data: Holler et al., 2009);

(*iii*) $\delta^{13}CH_4$ during methanization of peat organic material from three boreal peatland ecosystems where it was confirmed that non-canonical pathway of peat methanization occurred for the nutrient poor peat with a dominance of hydrogenotrophic methanogenesis (data: Galand et al., 2010);

(*iv*) $\delta^{13}CH_4$ during methanization of cellulosic wastes where it was shown that a significance of acetoclastic and hydrogenotrophic methanogenesis changes in time (data: Qu et al., 2009).

In contrast to Rayleigh's approach, our dynamic model based on substrate consumption and biomass growth showed that stable isotope fractionation was dependent on metabolic scheme of substrate transformation and the corresponding kinetic coefficients. It stopped after substrate depletion.

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Linear relationship between discrimination factor and isotopic signature of food sources: myth or reality?

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Stable isotopes have proven to be a successful tool to investigate animal diets and trophic relationships within food webs. However, a crucial point is the a priori knowledge of tissue-diet discrimination factors (TDDFs) that is the enrichment process of the heavy elements (^{13}C or ^{15}N for example) in consumers relative to their diet. Numerous studies showed evidence that discrimination factor is not only species-specific but strongly related to the quality and quantity of the food sources and also ultimately to the physiology of organisms. Surprisingly, several recent studies (Caut et al., 2009) revealed a negative linear relationship between isotopic signature of the food and $\Delta\delta^{13}C$ and $\Delta\delta^{15}N$, showing that the more enriched the diet in ^{15}N and ^{13}C, the lower the TDDF. This relationship has been strongly debated by several authors advocating possible mathematical artifact or experimental bias (Auerswald et al, 2010; Perga and Grey, 2010). We estimated TDDFs for carbon and nitrogen for two ophiuroids species (echinoderms), in tissues of two body compartments (disk and arms) according to different diet qualities (fish muscle, mussel and macroalgae) and in the light of physiological changes (gonadal rest and gonadal maturation).

Our results showed the average TDDF values ranged from -4.1±0.2 to 1.5±0.2‰ and from -1.8±0.2 to 4.0±0.3‰ for $\Delta\delta^{13}C$ and $\Delta\delta^{15}N$ respectively. TDDF values showed some unexpected values, especially for $\Delta\delta^{13}C$ with macroalgae diet and $\Delta\delta^{15}N$ with fish muscle diet. TDDFs were plotted against the isotopic value of diets and revealed significant linear relationships. The explanation of such a relationship is still unexplained but this experiment brings additional evidences that this debate is worth investigating, since such a relation would provide – if proven right – a useful proxy in ecological isotopic studies. More attention will be necessary to demonstrate whether this relation is a myth or a reality.

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Turnover rates of sulphur in liver and muscle tissue of brook trout, *Salvelinus fontinalis*, determined by diet shift experiments in the field and laboratory

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The number of published studies on the turnover rate and trophic discrimination factor (TDF) of δ^{34}S analysis in fish is limited relative to those published for δ^{13}C and δ^{15}N analysis. The objectives of this study are to determine the turnover rate of sulphur in fish muscle and liver tissues, and the TDF of brook trout (*Salvelinus fontinalis*), using laboratory and field experiments. A diet shift experiment will be performed on brook trout (*Salvelinus fontinalis*) at the aquaculture fish facility at the University of New Brunswick, Canada. At the start of the experiment, brook trout will be fed a diet with a low δ^{34}S value, relative to their previous diet that had a high δ^{34}S value. For the field experiment, hatchery-reared brook trout will be introduced to Otter Brook, a tributary of the Miramichi River, New Brunswick, Canada, where their sulphur turnover rate and TDF will be monitored *in situ*. These trout will have an initial δ^{34}S value that is high (i.e., due to the marine feed used at the hatchery) relative to their natural diet in the stream. Subsequent sampling over several months will permit a comparison of natural and laboratory-derived turnover rates and lead to the most robust values to be used in future studies. Both laboratory and field experiments will begin in early summer 2012. The results of this study will facilitate the use of sulphur SIA to be used as a third ecological tracer in food web studies, and to successfully track fish movements.

Experimental determination of discrimination factors and turnover rates of the ctenophore *Mnemiopsis leidyi*

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Knowledge of the discrimination factors and turnover rates of an organism is important when conducting foodweb analysis based on stable isotope data. For many groups of animals such data are already available; however, to date, they are completely lacking for gelatinous zooplankton. In 2006, the ctenophore, *Mnemiopsis leidyi* was first documented in the Baltic Sea. The recent invasion of northern Europe has raised concerns about potentially harmful impacts of *M. leidyi* on native species and on the Baltic Sea ecosystem structure. In order to assess these effects, studies of the feeding ecology of *M. leidyi* will be essential and require information on the discrimination factors and turnover rates. The goal of our experiment was to provide species specific estimates of these parameters (δ^{13}C and δ^{15}N) for *M. leidyi*.

For this experiment, a *M. leidyi* laboratory culture (33PSU,18ºC) was established from individuals collected in the Eastern Skagerrak, southwestern Swedish coast (58º15´N, 11º 24´E). The newly hatched larvae were equally divided into two 50-L buckets with filtered sea water and fed *ad libidum* twice a day with *Acartia tonsa* (δ^{13}C: -21.35‰ ± 0.36‰; δ^{15}N: 0.48‰ ± 0.7‰) raised on *Rhodomonas salina*; both from laboratory cultures (33PSU,18ºC). After week three, the food source was switched to newly hatched *Artemia salina* (δ^{13}C: -22.75‰ ± 0.04‰; δ^{15}N: 12.95‰ ± 0.15‰) in one of the 50-L buckets. The other bucket was continued on *A. tonsa* diet and served as a control. Starting after two weeks, five replicate samples from each bucket were taken every two days until the end of the experiment four weeks later. In parallel to *M. leidyi* sampling, both diet sources were sampled at each time point to control for fluctuations in the isotopic values of dietary sources. After freeze-drying, isotopic analysis (δ^{13}C and δ^{15}N) was then carried out at the UC Davis Stable Isotope Facility.

The discrimination factors and turnover rates for δ^{13}C and δ^{15}N will be provided at the conference for the first time. At present, this will represent the first such dataset for any jellyfish or ctenophore species that we know of.

Tissue-specific variations in δ^{13}C and δ^{15}N discrimination factors of marine birds: Using chicks' tissues to infer seasonal variations in the feeding habits of adults.

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Trophic enrichment factors (TEF) vary among species or taxa, but also with the type of nitrogen excretion, trophic guilds and the consumer tissues into which the material is incorporated. In trophic studies focusing on marine birds using stable isotopes, researchers have favoured the combined use if blood and feathers for two reasons: first, their sampling is non-destructive and secondly, , their isotopic compositions represent diets integrated during different time-periods when sampled simultaneously in adult birds. Blood gives information on the diet integrated over the few weeks prior to the sampling while feathers inform on the moulting period, often occurring during the non-breeding season. Comparison of different tissues sampled from one organism is, however, complicated by TEF differences among consumer tissues, depending on their metabolic and physiological features. In chicks, blood and newly grown feathers both reflect the diet integrated over the same period, i.e. the few weeks between hatching and sampling. Therefore differences between blood and feathers will only reflect differences between the diet-blood and diet-feather enrichment factors. Consequently, blood-feather isotopic differences in chicks could theoretically be used as a baseline for interpreting tissue differences in adults. We used blood and feathers collected on chicks and adults African Black Oystercatchers (*Haematopus moquini*) sampled during the breeding season, to investigate this theory. Feathers were strictly enriched in ^{13}C and δ^{15}N compared to blood in chicks: $\Delta\delta^{13}C_{\text{blood-feathers}}$= +0.9±0.6‰ and $\Delta\delta^{15}N_{\text{blood-feathers}}$=+1.3±0.5‰ and both tissue variations were highly correlated (R^2_{carbone}= 0.92, R^2_{nitrogen} = 0.79). These isotopic steps between tissues were slightly different from adults ($\Delta\delta^{13}C_{\text{blood-feathers}}$=+0.6±0.6‰ and $\Delta\delta^{15}N_{\text{blood-feathers}}$=+1.5±0.4‰) and could result from intrinsic physiological differences between the two age groups (ex: chicks growth). Nevertheless the consistence of blood-feathers isotopic shifts in chicks indicate that it could be used to aid in the interpretation of blood-feathers differences in adults: large deviations of adults $\Delta\delta^{13}$C and $\Delta\delta^{15}$N from those of chicks are most likely related to changes in diet composition or foraging locations between breeding and winter for adults. Combined used of blood and feathers for both chick and adult, can therefore give information on temporal changes of adults feeding ecology.

Explaining growth variability of the Pacific oyster in different coastal ecosystems: characterisation of the trophic and abiotic environment of *Crassostrea gigas* by the coupling of isotopic analysis and DEB modelling

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Growth performances of the Japanese oyster (*Crassostrea gigas*) mainly rely on environmental factors, *e.g.* water temperature and food resources. However, French oyster culture is still lacking both explicative and reliable tool to characterize the trophic functioning of marine ecosystems and some relevant indicators to quantify and explain the variability in growth performances of oysters among culture sites. In this context, three different approaches, *i.e.* growth *in situ* monitoring, diet switching experiment and modelling, were considered to better understand the effect of the environment (*i.e.* diversity/quality and quantity of the food sources) on the growth and stable isotope composition (C and N) of the oyster whole soft tissues. In the growth *in situ* monitoring, two populations of oysters (originating from the same batch) were transplanted in two contrasted environment in term of food availability. Results revealed different isotopic dynamics in whole soft tissues and organs of oysters that can be partly explained by oyster metabolism. Our diet-switching experiment, carried over 108 d, demonstrated a significant effect of the feeding level on both the dynamic of stable isotopes and on the trophic-shift Δ. Results also revealed that the isotopic ratio of the food source could also potentially influence the trophic-shift. Modelling approach (DEB model) makes possible to present new framework and mechanisms for the understanding of isotope dynamic and fractionation processes in oyster tissues. The model, which was calibrated on experimental and literature data set, provide a tool to investigate to contribution of the different food sources to the growth of organisms, considering variations of the environment (temperature, food quantity and food isotopic ratios) and oyster physiological state.

Low $\delta^{13}C$ composition of *Haplognathia sp.* in a Caribbean mangrove (Guadeloupe, FWI)

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Gnathostomulidae have been first described in 1956 and are considered as a rare taxa in marine benthos. About 100 species are currently known worldwide, predominantly from the North Sea, the Mediterranean, the Caribbean and the South Pacific. Those basic acoelomates move by ciliary gliding through the interstices of anoxic marine sediments. They are supposed to feed on bacteria, protists and fungi but their exact diet remains unknown. In mangrove sediment of Guadeloupe (FWI), thiobacteria form a thick white mat visible with naked eyes. Compared to other available food resources, those bacteria present the lowest $\delta^{13}C$ (-31.7‰). Nevertheless the gnathostimulidae *Haplognathia sp*. present a $\delta^{13}C$ even lower (-33.2‰). The use of Scan Electron Microscopy did not reveal any ectosymbiont, and other methods (Fluorescence *in situ* hybridation and Transmission Electron Microscopy) did not showed endosymbiont. Energy Dispersive X-ray analyses did not detected sulphur, a specific compound of sulfur-oxidizing bacterial symbiont. So we can reject symbiotic interactions with autotrophic bacteria to explain such depleted $\delta^{13}C$. This low $\delta^{13}C$ would consequently be due to a diet exclusively based on thiobacteria and to a negative isotope discriminating factor. When diet presents a low $\delta^{13}C$, discrimination factors are supposed to be higher (Caut *et al*. 2008). However *Haplognathia* discrimination factor would be low even with low $\delta^{13}C$ resource. Result of the present study reminds that standard isotope discrimination factors should be used with caution in mixing models.

Differences among bulk carbon discrimination factors in a marine carnivore: a comparison of individual amino acid carbon isotope patterns

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Discrimination factors are an important biological parameter to interpret the ecological significance of stable isotope data. Studies often use average values gleaned from the literature, but these values may vary among taxa, individuals, diet, and habitat. For example, a review of 107 studies revealed an average carbon discrimination factor of 0.4‰, but a range from -3 to 4‰ (Post 2002). We conducted a feeding study with leopard sharks (*Triakis semifasciata*) and fed two groups either squid or tilapia. The bulk carbon discrimination factors ($\Delta^{13}C = \delta^{13}C_{shark} - \delta^{13}C_{prey}$) for the squid and tilapia diets were 1.7‰ and 3.5‰, respectively (Kim et al. *in press*). To better understand the source of this variation, we analyzed the carbon isotope value of individual amino acids in shark muscle and whole prey. Previous studies have demonstrated that 1) essential amino acids have little trophic differentiation and reflect baseline carbon isotope sources and 2) non-essential amino acids are either biosynthesized or routed from diet.

Some patterns for carbon isotope values of amino acids from shark muscle were as expected. Glycine and Serine were the most ^{13}C-enriched amino acids and Valine, Phenylalanine, and Leucine were the most ^{13}C-depleted amino acids. However, carbon isotope values of essential amino acids in shark muscle and prey differed by greater than 1‰. Among the non-essential amino acids, Proline, Aspartic Acid, and Glutamic Acid, had similar discrimination factors for the two diets but Glycine had different discrimination factors for the two diets. This difference between the Glycine discrimination factors among diets likely contributes to the difference in bulk carbon discrimination factors. Trophic discrimination of carbon isotopes in essential amino acids in shark muscle is surprising and currently unexplained. One potential source of variation to trophic discrimination factors is the abundance of amino acids in the two diets. Differential ^{13}C-enrichment among non-essential amino acids based on diet has been reported for animals consuming mixed plant-animal diets, but may occur, as well, for animals that are entirely carnivorous.

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Stable isotope analysis of high lipid-content notothenioid (anti-freeze) fish from the Ross Sea, Antarctica: lipid extraction issues and corrections

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Ross Sea fish are dominated by a single family, the notothenioids, which comprise half of Antarctic marine fish species and 95% of all fish biomass in the region. Notothenioids characteristically lack swim bladders and the majority of species are benthic or demersal. However, a depth-related diversification has given rise to some species attaining increased buoyancy by concentrating lipid deposits in tissues and reducing skeletal mineralisation: examples being Antarctic toothfish (*Dissostichus mawsoni*), Patagonian toothfish (*Dissostichus eleginoides*), Antarctic silverfish (*Pleuragramma antarticum*), and icefish (*Chionobathyscus dewitti*). Antarctic toothfish are particularly lipid-rich with on average 10% of their body mass derived from lipids. These lipid-rich species can present problems for the accurate determination of δ^{13}C values with regard to appropriately addressing the δ^{13}C lipid contamination issue. We discuss modifications made to our lipid extraction methods (after trailling methods on a series of internal laboratory fish standards from the Ross Sea, which were also analysed non-lipid extracted) and present isotopic corrections applied to ensure reliable δ^{15}N and δ^{13}C values.

Carbon and nitrogen isotopic inhomogeneity of collagen from different tissues within an individual

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The use of stable isotope techniques to study animal diets requires knowledge of the diet to tissue offsets, or trophic level effects. Studies have shown that these offsets depend on an number of parameters, including tissue type, environment, taxon and dietary type.

Isotopic variation between tissues has been ascribed to differential tissue composition, in particular to variation in differential amino acid composition. Large differences in carbon and nitrogen isotopic values between component amino acids have been observed within the same protein (Gaebler, Vitti & Vukmirovich, 1966; Macko *et al.* 1987; Hare *et al.* 1991, Howland *et al.* 2003), reflecting different metabolic, synthetic and catabolic processes. Thus it is assumed that differences in amino acid composition between proteins will in turn translate to differing isotope values of the entire protein. Since similar patterns have been found in single amino acid isotopic values of different tissues, it is frequently assumed that individual amino acids have the same value in all tissues.

This study tested this assumption, by investigating the isotopic homogeneity of collagen throughout the body. We compared the isotopic values of collagen samples isolated from samples of muscle, skin, heart and bone from four species, sheep, pig, goat and rabbit, raised on controlled diets. Results showed that collagen is not isotopically homogenous throughout the body of these species, but instead shows statistically significant differences between both the δ13C and δ15N values, with the collagens clustering into two pairs of skin and bone, and muscle and heart. Reasons for this are suggested, and implications of these finds are considered for dietary reconstruction using isotopic analyses: it must not be assumed that proteins are isotopically homogeneous both within and between individuals. Internal physiological variation as well as external factors affecting isotope values must be considered during isotopic analyses.

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Rapid Compound-Specific Stable Isotope Analysis of Amino Acids by GC-C-IRMS of Methyl Chloroformate Derivatives

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Compound-specific stable isotope analysis of amino acids (AA-CSIA) has become an informative tool in ecological studies. Currently, gas chromatography/combustion/isotope-ratio mass spectrometry (GC/C/IRMS) is the prevailing method for AA-CSIA, especially for δ_{15}N analysis. For AA-CSIA via GC/C/IRMS, amino acids are required to be derivatized to enhance their volatility. Several derivatization procedures have been utilized in AA-CSIA using GC/C/IRMS, with esterification/acylation being most widely utilized. However, these derivatives can be time-consuming to produce and the resulting derivatives may have undesirable qualities. For example, the products of a popular derivativization agent, triflouroacetic acid (TFAA), can poison the oxidation reactor through the irreversible conversion of Cu and Ni into stable metal halides. Additionally, many derivatives contain an excessive amount of non-analyte carbon, thus reducing the precision of δ_{13}C analysis isotope analysis and/or impeding δ_{15}N analysis.

Despite the recent popularity of derivatization using alkyl chloroformates in GC-MS studies because of its rapid one-step preparation, this method has rarely been applied to AA-CSIA. We established a derivatization procedure using methyl chloroformates (MCF) that can be applied to CSIA of both δ_{13}C and δ_{15}N in amino acids. Compared to currently popular derivatization procedures, MCF derivatives have the lowest carbon contribution from the derivatization agent and are quite amenable to δ_{15}N analysis. Additionally, we demonstrate that on a polar GC column, e.g. VF-23, MCF amino acid derivatives exhibit excellent resolution sufficient for CSIA. This method has been successfully used in the analysis of δ_{13}C and δ_{15}N in amino acids from animal tissues, blood plasma and plants; data from several studies is presented.

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Latest developments and technologies in bulk and compound specific Stable Isotope Ratios Mass Spectrometry for ecological studies

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Recent years have shown an increasing demand for multi-element isotope analysis for ecological studies in both bulk stable isotope analysis (BSIA) and compound specific isotope analysis (CSIA) modes.

We developed a new BSIA system which combines two furnaces in a single elemental analyzer and is equipped with an Automatic Switching Valve to automatically switch between the two modes of operation,

Dynamic Flash Combustion for C, N and S and HighTemperature Conversion for O and H isotope analysis. This is enabling conversion reactions in either of the two reaction lines with subsequent separation of the gases in two dedicated isothermal GC columns. Two autosamplers and optimized chromatography allow the analysis of up to five isotopes with two sample drops in reduced time giving maximum benefit for multi-element isotope ratio analysis.

The growing interest and appreciation in CSIA required new features and functionalities of the instrumentation. We developed a new concept for an automated multi-element irm-GC/MS. The combustion reactor and heater have been redesigned to determine C and N isotope ratios using identical reactor conditions. The system includes automated switching between the combustion reactor and the high temperature conversion reactor for unattended analysis of C, N and H isotopic ratios within the same batch of samples. The high temperature conversion also enables O isotopic ratios determinations.

We will present this new workflow solution for Multi Element Isotope Analysis and describe the principles, operation modes and switching times. Examples and results will be shown.

Poster session D
“Paleoecology”

D1	Nathaniel DOMINY	Antiquity and provenience of mummified baboons reveals location of Ancient Punt
D2	Rebecca FRASER	The stable isotope systematics of carbon, oxygen and nitrogen in modern koalas show plant-diet and climate interactions
D3	Olga SIDOROVA	Understanding recent and past climatic changes in the Siberian north with stable isotopes
D4	Maura PELLEGRINI	Tooth enamel d^{18}O distribution in Bronze Age human populations from the British Isles
D5	Kerry SAYLE	Simultaneous δ^{13}C, δ^{15}N and δ^{34}S isotope ratio determination of archaeological bone collagen.
D6	Isabella VON HOLSTEIN	Effect of diagenesis on isotope values of keratin: implications for archaeological proteins
D7	Victor FROSSARD	Chironomid abundance and carbon isotope signature as proxies for past lake-functioning
D8	Prasanta SANYAL	Intensification of monsoon, microclimate and asynchronous C4 appearance: Isotopic evidence from the Indian Siwalik sediments
D9	Vincent MOUCHI	δ^{18}O and Mg/Ca ratios in recent and fossil oyster shells: confronting thermodependant proxies
D10	Alexandra OPPELT	Chronologies in stable isotope ratios along primary and secondary growth directions of deep-sea corals

Antiquity and provenience of mummified baboons reveals location of Ancient Punt

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Punt was a celebrated place in antiquity. For Ancient Egyptians, it was the primary source of valuable commodities such as ebony, myrrh, electrum, and exotic pets (leopards and baboons). The importance of the Egypt-Punt relationship is twofold. First, it is one of the earliest examples of peaceful commerce between neighbouring political states. Second, it represents the longest trading alliance in human history, spanning more than 1200 years. Yet the location of Punt is a mystery. Scholarly debate during the past century has resulted in six hypothetical regions: (1) Eritrea-Ethiopia, (2) Mozambique, (3) Sinai, (4) Somalia, (5) western Uganda, and (6) Yemen. To test among these competing geographic hypotheses, we sampled the hair and bone tissue of modern and mummified baboons. The oxygen isotope composition of one mummified baboon, an 18th Dynasty royal pet, indicates a prolonged life in Ancient Thebes (Luxor), whereas the oxygen isotope composition of a mummified baboon from the Temple of Khons (20th Dynasty) indicates an origin in modern-day Eritrea. The strontium isotope compositions of Ptolemaic-era mummified baboons are also instructive, but indicative of improved maritime technologies and wider trading relationships in the millennium that followed recorded expeditions to Punt.

The stable isotope systematics of carbon, oxygen and nitrogen in modern koalas show plant-diet and climate interactions

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Australia's marsupial koala (*Phascolarctos cinereus)* is a conservative consumer. Their browsing diet consists solely of *Eucalyptus* leaves, and they have small (~2 ha) home-ranges. We present an investigation of the $\delta^{13}C$, $\delta^{15}N$ and $\delta^{18}O$ values in modern koalas inhabiting woodlands in different climate zones. Our isotopic case-study has the view to support palaeoecological reconstruction.

First we examine the levels of isotopic variability in wild koala populations and how this relates to the isotopic variability in their C_3 leaf-diet. Understanding the variability observed in modern populations is often made difficult because of individual feeding habits, seasonal migration and/or changing food availability. Opportunely, koalas' feed exclusively on *Eucalyptus*, so we enquire how much isotopic variation exists in koala bone collagen and enamel considering their diet is much standardised? Whilst the intra-population range in collagen $\delta^{13}C$ values was ~1.3±0.6‰, the range in $\delta^{15}N$ and $\delta^{18}O$ values were up to 6‰. Correspondingly high variations in *Eucalyptus* leaf $\delta^{15}N$ values at some sites partly explain this observation.

Secondly, we examine the isotopic fractionation ($\delta^{13}C$ and $\delta^{15}N$) between the *Eucalyptus* leaf-diet and the koalas' bone collagen, dentine and enamel. The data show a consistent mean offset of 7‰ exists between the $\delta^{13}C$ values of leaves and collagen. This figure is larger than the 3-5‰ fractionation observed between the diet and collagen of other herbivorous mammals and humans. Koalas have a unique digestive physiology that enables them to survive on *Eucalyptus* leaves, which are extremely low in nitrogen yet high in oils, phenols and tannins. Digestive processes and diet quality combined may explain this larger than 'normal' $\delta^{13}C$ fractionation.

Finally, we examine the relationships between koala stable isotopes and metrological variables; rainfall, moisture balance, temperature and humidity. Contradictory findings are observed. The inverse relationship commonly observed between mammalian collagen $\delta^{15}N$ and rainfall is not evident, in fact it is reversed. As an alternative, we suggest koala $\delta^{15}N$ values may correlate with the openness of the N-cycle. The most significant relationship is the inverse correlation between collagen $\delta^{13}C$ and moisture balance (r^2=0.95). This parallels similar relationships between *Eucalyptus* leaf $\delta^{13}C$ values and moisture previously observed across continental Australia.

Understanding recent and past climatic changes in the Siberian north with stable isotopes

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The application of stable isotope analysis in combination with the classical dendrochronology is steadily increasing because $^{13}C/^{12}C$ and $^{18}O/^{16}O$ in wood or cellulose provide complementary information to tree-ring width about climatic variabilities.

Siberian forests are important to study because of their vast extension and the severe ongoing and anticipated climate changes in this region. Our study is focused at the high latitude regions, in northeastern Yakutia (YAK) [70°N, 148°E] and eastern Taimyr (TAY) [70°N, 103°E]. Stable carbon and oxygen isotope analyses were performed for the samples from larch trees.

The climatological analysis for the calibration period from 1900 to 2004 revealed that the stable isotope data (C, O) show a significant relationship with July precipitation, which is not observed in tree ring widths.

We found that the isotope chronologies from the Northern Siberian sites carry information on large-scale climate patterns. In particular, the $\delta^{18}O$ signal from the eastern site (YAK) proved to have many wide-ranging connections, reaching as far as to Greenland, responding to the North Atlantic Oscillation. This indicates that this location is ideal for capturing a representative climate signal for a large area, which is important in the context of climate reconstructions over millennia, which are possible for this site due to the good preservation of dead trees.

For obtaining quantitative and reliable information about climatic changes in the past the use of a multidisciplinary approach by analyzing multi proxy data as performed in this study is needed.

Tooth enamel $\delta^{18}O$ distribution in Bronze Age human populations from the British Isles

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The oxygen isotope ratios of phosphate bioapatite ($\delta^{18}O_p$) have been employed in archaeological and forensic studies as a means to trace human mobility. The technique is based on the principle that skeletal oxygen isotopes are inherited, after species-specific metabolic filters, from ingested food and drink oxygen isotopes and, ultimately, in the case of obligate drinkers such as humans, from local water sources.

Many studies have compared the $\delta^{18}O_p$ values measured in single individuals with water isotope values gathered from global distributions of meteoric precipitations. This approach, however, often neglects the natural inter-individual variability that might affect specimens from the same locations. Such variability can be due to a number of factors: for instance the use of different teeth for analysis, short-term climatic variations during the formation of the investigated teeth, the use of specific cooking techniques or brewing practices, which may lead to an ^{18}O-enrichment of the oxygen isotopic values, or the use of water sources originated in other areas or that might have undergone evaporation. Additionally, another possible source of variation may come from the employment of one of the several regression equations available for the $\delta^{18}O_p$-$\delta^{18}O_w$ relationship, which may alone be responsible for some of the observed variability.

We present the results of a study in which $\delta^{18}O_p$ have been measured in teeth of 258 individuals from Britain, mostly ranging in age from 2500 to 1500 BC. This study is part of larger investigation on individual burials coming from the British Isles where skeletal $\delta^{13}C$, $\delta^{15}N$ and $\delta^{34}S$ and $^{87}Sr/^{86}Sr$ have also been analysed by a consortium of investigators. The $\delta^{18}O_p$ results show a large variability, even in individuals coming from the same locations. In some areas, such spread of results may be as large as the environmental water (i.e. drinking water) $\delta^{18}O$ range across the entire British Isles.

The observed $\delta^{18}O_p$ variability and the relationship between the $\delta^{18}O_p$ values and the $\delta^{18}O_w$ from the same location are discussed. Finally, we compare the observed $\delta^{18}O_p$-$\delta^{18}O_w$

relationship with the most widely used $\delta^{18}O_p$-$\delta^{18}O_w$ conversion equations available in the literature.

Simultaneous $\delta^{13}C$, $\delta^{15}N$ and $\delta^{34}S$ isotope ratio determination of archaeological bone collagen.

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For more than 30 years, $\delta^{13}C$ and $\delta^{15}N$ measurements on human bone collagen have been used to infer information about the diets of our ancestors. Increasingly over the past decade, $\delta^{34}S$ has been measured in conjunction with $\delta^{13}C$ and $\delta^{15}N$ to evaluate the location in which individuals resided for the greater part of their lives, as well as to determine the source of their foodstuffs.[1] In order to quantify the quality of the bone collagen being analysed, DeNiro[2] introduced the use of the C:N atom ratio; samples that fall between 2.9 and 3.6 are deemed to be of acceptable quality whilst those outside that range are considered unacceptable due to possible collagen degradation in the post-depositional environment. In a similar manner, Nehlich and Richards[3] measured $\delta^{13}C$, $\delta^{15}N$ and $\delta^{34}S$ values in a variety of archaeological bone collagen samples from several species and used atomic C:S and N:S ratios to define the standard for sulphur isotope analysis.

With advancements in technology has come the capability to measure $\delta^{13}C$, $\delta^{15}N$ and $\delta^{34}S$ simultaneously. This poster describes: 1. the hardware modifications that were applied to our existing isotope ratio mass spectrometer and elemental analyser and 2. the method development work that enabled us to undertake multi-isotope analyses on a single archaeological bone collagen sample. For comparison, an alternative method was developed that solely measures $\delta^{34}S$ values. The results from this case study, and the wider implications that they may have with respect to the criteria laid down by Nehlich and Richards are discussed.

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Effect of diagenesis on isotope values of keratin: implications for archaeological proteins

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Hair is fast-growing tissue which not remodelled once formed, and therefore has the potential for sampling at high temporal resolution from archaeological remains. However it is much more seldom preserved than collagen and dentine in archaeological conditions, and most palaeo-focused isotope work has focused on these tissues, because of their reliability and ease of recovery. Previous work on keratin material (e.g. archaeological human hair, fur, wool) has focused on samples preserved by desiccation or in permafrost. However in the temperate waterlogged conditions in which keratin samples are typically preserved in Europe, microbiological and hydrolytic processes cause degradation of the hair fibres.

This presentation will discuss the effects of these processes on the integrity of isotopic properties of wool fibres, which are largely composed of keratin proteins, using two models of degradation: experimental burial (up to 8 years, at three different Northern European sites) and isothermal hydrolysis (80°C, 110°C or 140°C). The discussion will integrate amino acid content and racemisation rate data (determined by RP-HPLC), elemental composition, and bulk $\delta^{13}C$, $\delta^{15}N$, (un-exchangeable) $\delta^{2}H$, and $\delta^{18}O$. Implications for isotope analysis of other archaeological proteins (other keratins, leather collagen, silk protein) will be explored.

Chironomid abundance and carbon isotope signature as proxies for past lake-functioning

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A series of sediment cores covering the last 150 years were taken at several depths in two French peri-Alpine lakes (Lake Annecy and Lake Bourget).

Long -term trends in the head capsules (HC) $\delta^{13}C$ values of *Micropsectra contracta-type* have been compared to (i) past abundance of this species group and (ii) organic matter content (TOC) of sediment.

During the studied period, HC $\delta^{13}C$ values decreased at all depths and were negatively related to the TOC in sediments. This result suggests a ^{13}C depletion in the food sources that sustained *M. contracta* –type larval growth. This finding supports the assumption of an increase in lake respiration processes from the 1850's to the 2000's.

The relationships between *M. contracta-type* abundance and both TOC and HC $\delta^{13}C$ values were non-linear and were therefore characterized by tiping-points. This implies complex thresholds and resilience processes in the response of *M. contracta-type* to environmental changes.

In each lake, the HC $\delta^{13}C$ values trends differed between depths. It provides new insights of the spatial variability in lake metabolism and benthic community responses to changes in trophic state (i.e eutrophication and reoligotrophication).

Long-term trends of the HC $\delta^{13}C$ values as well as their depth-related differences offer promising developments to understand long-term changes in lake functioning and ecological state.

Intensification of monsoon, microclimate and asynchronous C4 appearance: Isotopic evidence from the Indian Siwalik sediments

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Analysis of the D/H ratio of pedogenic clay and the $^{18}O/^{16}O$ ratio of carbonate nodules collected from Siwalik sediments in India indicates three episodes of monsoon intensification at ~11 Ma, 6 Ma and 3 Ma. These episodes coincide with major pulses of tectonic uplift in the Himalayas suggesting causal link between monsoon intensity and uplift. In addition, variation in the carbon isotope ratio of carbonate nodules and residual organic matter indicates a change in vegetation regime from pure C3 type to a mix of C3–C4 type during this time span. Isotopic analysis of samples collected from different locations of the Himalayan Siwalik shows that the late Miocene C4 appearance was locally asynchronous (by ~3 Ma), similar to what is seen on a global scale. The lack of synchronous emergence of C4 plants in various parts of Siwalik probably indicates a combined effect of microclimate (e.g. varying monsoon intensity) and habitat disturbance (e.g. forest fire). In contrast, subsequent expansion of C4 plants during the late Miocene–Pliocene time could be entirely due to monsoon intensification that favoured C4 respiration in a warm and seasonally variable rainfall regime

Insight into the trophic web of *Cystoseira balearica* forests of the Bay of Calvi $\delta^{18}O$ and Mg/Ca ratios in recent and fossil oyster shells: confronting thermodependant proxies

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One of the main goals in recent paleoclimate research proposes the use of sclerochronology, consisting in the geochemical study of bivalve shells. This material allows reaching infra-annual time resolution of the environmental conditions evolution throughout the life of the organism. Exclusively thermodependant proxies, as Mg/Ca in carbonates, have been developed for a few decades in order to replace oxygen isotope ratios, which also fluctuates with salinity, an environmental parameter not always properly constrained in ancient times. However calibration of proxies lack of precise chronological time-scale in the shell biomineralization.

In this study, we investigate Mg/Ca and isotope ratios from time-calibrated oyster shells according to mark and recapture experiments. Shells bred during two years and stained every month with manganese were analyzed by electronic microprobe for elemental ratios measurements (spatial resolution of 25µm on a 1cm long transect corresponding to more than a year) and micromill samplings for stable isotope ratios (0.3mm for samples diameter). The analyses were conducted in the foliated structure from the umbo region, which corresponds to the area where biomineralization is the most continuous for these species.

We developed a temperature model of Mg/Ca in modern oyster shells (*Crassostrea gigas*), which can be used to infer high-resolution seawater temperatures (Mouchi et al., accepted). Although Mg/Ca fluctuations present more obvious vital effects than $\delta^{18}O$ variations, most are easily removable. Overall, it seems necessary to use only the youngest cycles for thermal seasonal contrasts reconstruction using Mg/Ca.

The Mg/Ca model was applied on fossil shells from affiliated species and compared with the temperatures deduced from the oxygen isotope composition, estimated using $\delta^{18}O_w$ provided in literature for corresponding ages and locations. An age model developed in previous studies based on cathodoluminescence observations (Lartaud et al., 2006) helps us to check on the seasonal pattern of geochemical fluctuations.

Results show that seasonal cycles observed in $\delta^{18}O$ records are more stable than those in Mg/Ca profiles, in which an ontogenic trend is visible throughout the growth of some shells. Nevertheless, seasonal cycles (highlighted by the age model) are not always present in the $\delta^{18}O$ variations, but visible in the Mg/Ca record.

Chronologies in stable isotope ratios along primary and secondary growth directions of deep-sea corals

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Although researchers have been aware of the existence of deep sea corals (especially in the North Atlantic) for a while, it is only since the 1990s that many aspects of their biology and importance as reef habitat builders have been investigated. More recent research focuses on the response of cold-water corals (CWC) to environmental change, and in particular to ocean acidification.

Records of high-resolution (i.e. seasonal) variations are scarce in the deep. Therefore, an archive like corals skeletons that have been mineralized for up to 8000 years in locations that are in contact with important ocean currents is very valuable.

Various metabolic mechanisms can be recorded in the biomineralized structures and complicate the deciphering of physicochemical incorporation. To detect these, the growth pattern has to be understood. The aragonitic skeleton of the CWC *Lophelia pertusa* displays several distinct radial layers of alternating white and beige colour, different transparency and thickness. Live observations in situ show that the growth takes place along the main axis as well as radially (to a lower extent).

We mapped the stable isotope compositions along single layers in time over a cross section of the calyx wall. The results show that the influence of metabolic effects on isotopic compositions varies considerably between different stages of growth. Clear differences in $\delta^{18}O/\delta^{13}C$ correlations and wavelength of the isotopic variations along the growth axis between layers and in their mineral structure are visible. Those indications of varying growth rates are directly connected to the impact of vital effects on stable isotope ratios (fast growth equals low impact of vital effects). A combination with trace element analysis improves the distinction between metabolic and environmental effects.

This method helps selecting the most suitable layer to isolate vital effects and consequently retrieve the recorded environmental information.

Poster session E
“Isoscapes”

E1	Clement BATAILLE	Mapping the bioavailable strontium isotopic signature at regional scales
E2	Clive TRUEMAN	Using simple biogeochemical models as desk-based experiments to explore mechanisms driving global marine isoscapes
E3	Alexandra PEKARSKY	Using Oxygen and Hydrogen stable isotopes to determine migration connectivity between breeding and wintering populations of the Eurasian crane (*Grus grus*)
E4	Robert PANETTA	Simultaneous d^{13}C + dD combustion isotope analyser to track bird migration
E5	Suzuki YAEKO	The spatial and seasonal variations in the carbon, nitrogen and oxygen isotope values of kelp (Kombu) over three years in China, Japan and South Korea
E6	Jan DIERKING	Integrating stable isotope, otolith microchemistry, and genetic analysis to assess intra-population migration strategies of endangered anadromous North Sea houting
E7	Simona CERIANI	Satellite telemetry and stable isotopes: building isoscapes for loggerhead sea turtles in the Northwest Atlantic Ocean
E8	Patricia MANCINI	Identifying wintering areas of Sooty terns Onychoprion fuscatus in the Atlantic Ocean using stable isotope
E9	Gabriele STOWASSER	Does winter foraging of Southern Ocean seabirds vary between years?
E10	Fabiana SAPORITI	Complex latitudinal changes in the neritic isoscape of the south-western Atlantic shelf.
E11	Brittany GRAHAM	Aquatic isoscapes: a review of current research and future directions as it relates to fisheries science.

Mapping the bioavailable strontium isotopic signature at regional scales

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Although variation in strontium isotope ratio ($^{87}Sr/^{86}Sr$) has been widely pursued as a tracer of provenance in ecology, environmental studies, forensics, archaeology and food traceability, methods for mapping variations in bioavailable $^{87}Sr/^{86}Sr$ at regional scale are still debated. Maps developed by interpolation of bioavailable $^{87}Sr/^{86}Sr$ datasets are limited in scale and number because they rely on time consuming and expensive sampling campaigns and measurements. These empirically based $^{87}Sr/^{86}Sr$ maps could greatly benefit from the parallel development of more cost-effective process-oriented $^{87}Sr/^{86}Sr$ models. Bataille and Bowen (2012) made a step in this direction by developing a method to map $^{87}Sr/^{86}Sr$ variations in bedrock and water. In this GIS-based model, they fitted lithology-specific model parameters for generalized equations accounting for both: 1) the combined effects of lithology and time on $^{87}Sr/^{86}Sr$ variations in bedrock and 2) the influence of weathering and Sr content on $^{87}Sr/^{86}Sr$ variations in water. While this method does not explicitly predict $^{87}Sr/^{86}Sr$ variations in bioavailable Sr, validation datasets showed promising results in predicting $^{87}Sr/^{86}Sr$ variations at large scale in a variety of substrates. Here, we present a new version of this model that includes: 1) an improved quantification of the flux of soluble Sr from bedrock based on an empirical process-oriented chemical weathering model (Jansen et al., 2010), 2) sub-models representing the contribution of Sr fluxes from atmospheric sources (sea salt and mineral dust) and 3) a mixing model of the multiple sources of Sr into the soluble Sr pool in soil to explicitly predict bioavailable $^{87}Sr/^{86}Sr$ variations. We document the model performance through quantitative comparisons with several observational bioavailable $^{87}Sr/^{86}Sr$ datasets from the circum-Caribbean region where large atmospheric deposition occurs. For this area, the predictive power of the new model for bioavailable $^{87}Sr/^{86}Sr$ variations is largely improved in comparison with Bataille and Bowen (2012) and can be used to constrain provenance. More generally, we show that this process-oriented isoscape that explicitly considers the different components of the Sr cycle can help refine the interpretation of $^{87}Sr/^{86}Sr$ datasets for provenance at both local and regional scale.

Using simple biogeochemical models as desk-based experiments to explore mechanisms driving global marine isoscapes

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The spatial distribution of carbon, oxygen and nitrogen isotopes within marine ecosystems potentially provide geographic tracers similar to those used effectively by terrestrial isotope ecologists. However, marine ecosystems are extremely dynamic in terms of isotope distributions, significantly complicating the interpretation of stable isotopes in marine systems. Global biogeochemical models provide tools to explore likely distributions of stable isotopes (particularly carbon). While these models are insufficiently accurate to predict actual stable isotope compositions, they provide useful desktop tools to test the likely stability of isotopic gradients between seasons or years, and assess the relative feasibility of using stable isotopes to identify location in specific marine systems.

Here I outline some basic modelling approaches that could potentially be used to predict the scale and stability of spatial distributions in the carbon isotope compositions of particulate organic matter prior to designing expensive, time consuming, and (for the subjects at least) possibly lethal studies.

Using Oxygen and Hydrogen stable isotopes to determine migration connectivity between breeding and wintering populations of the Eurasian crane (*Grus grus*)

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Establishing the links between different habitats occupied by migratory species throughout their annual cycle is essential for understanding population ecology and dynamics, life-history strategies and critical for designing effective conservation plans. Over the last two decades, Eurasian cranes (*Grus grus*) have used the Hula valley (north Israel) as one of the most important wintering and stopover sites along the "Eastern Migratory Flyway". However, despite substantial efforts in banding and satellite tracking, little is known about the origins of the cranes migrating through and wintering in Hula valley. We thus applied stable isotope techniques to elucidate if wintering vs. migrating populations of Eurasian cranes in Hula valley are originated from different breeding areas.

Previous studies have shown that natural abundance of hydrogen (δD) and oxygen ($\delta^{18}O$) stable isotopes in avian tissues can be used to infer geographic origins of molt. Eurasian cranes undergo flight feather molt during the summer. This molting pattern ensures that the wing feathers record the isotopic composition of diet and water in the breeding areas. We analyzed δD and $\delta^{18}O$ signatures of primary flight feathers collected across the breeding areas in Eastern Europe and Russia, and during the wintering and migration seasons in Hula valley.

We found no latitudinal pattern in the feathers collected in the breeding areas. Yet, our results showed a strong negative relationship between the longitude of the collection site and the δD or $\delta^{18}O$ isotope values in the feathers. Furthermore, stable isotopes values in the feathers were not correlated as expected to the pattern in precipitation during summer, but rather they were strongly correlated to the precipitation pattern during winter. There was no difference in the isotope ratios in feathers collected during the wintering and migration seasons, suggesting that the decisions regarding the route and timing of migration are not driven by strong migration connectivity of the cranes populations.

Simultaneous $\delta^{13}C$ + δD combustion isotope analyser to track bird migration

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Isotope ratios provide detailed knowledge useful in a variety of fields, in particular ecology. Information on spring migration routes, geographic linkages among winter, spring, and breeding locations, and potential geographic effects on arrival body condition of a variety of avian species is so far little known. Stable isotope ratios are exquisitely sensitive to the biochemistry of living organisms and the nutrients available to them. It has long been known patterns in bird migration and behavior can be discerned using a combination of stable-isotope ratio measurements, including carbon ($^{13}C/^{12}C$) for dietary information and hydrogen (D/H) for geographical information. The dual isotope can reveal associations among specific geographic areas, habitat use, and arrival condition through the measurement of these dual isotopes. We report here on the development of a novel laser spectroscopy based system for the simultaneous analysis of the stable isotope ratios of carbon ($^{13}C/^{12}C$) and hydrogen (D/H) that is robust, easy-to-use, and is the first stable isotope ratio analysis system to combine the measurement of $^{13}C/^{12}C$ and D/H in one simple analysis from a bulk organic sample with an application to bird migration. The system comprises a combustion module to convert the organic sample into CO_2 and H_2O and a Cavity Ring-Down Spectrometer (CRDS) that analyzes the combustion species inside an optical cavity based on the molecular absorption of individual isotopomers. This CRDS uses dual lasers to target the four isotopomers of interest: $^{12}CO_2$, $^{13}CO_2$, H_2O and HDO. The system delivers a typical precision of 0.1 permil for $\delta^{13}C$ and 1.5 permil for δD that parallels that achieved by IRMS, but with an unprecedented simplicity that allows ecologists to leverage the orthogonal information provided by these isotopes and elucidate avian migration patterns.

The spatial and seasonal variations in the carbon, nitrogen and oxygen isotope values of kelp (Kombu) over three years in China, Japan and South Korea

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Kelp grows in large forests underwater and provides food, structure, habitat, and protection for many ecologically and economically important species. On the other hand, kelp has also traditionally been harvested by humans as a food vegetable in Asian. Kombu is edible kelp from the family *Laminariaceae* widely eaten in East Asia. Most kombu is from the species *Saccharina japonica* (*Laminaria japonica*), extensively cultivated on ropes in the seas of China, Japan and Korea. Kombu is widely consumed in Japan and is commonly used to make dashi soup stock in Japanese cooking. Japanese Kombu is very expensive compared with from South Korea and China. Unfortunately, it has been targeted for the mislabeling.

Stable isotope analysis has widely been used to trace the origin of organic materials in various fields, such as geochemistry, biochemistry, archaeology, and petroleum chemistry. The isotope values of kelp mainly reflect physiological status and the source of nutrients in photosynthesis process1). In this study, we investigated the spatial and seasonal variations in the $\delta^{13}C$, $\delta^{15}N$ and $\delta^{18}O$ values of kombu over three years in China, Japan and South Korea to trace their geographical origin.

The reliable samples (n=265) of kombu were collected from Hokkaido (Japan), Wando (South Korea), Yantai (China), Weihai (China) and Fujian (China). The 30 cm lengths segment from the root was used to investigating the spatial and seasonal variations. The kombu from Yantai and Weihai, located in the Yellow River estuary, had relatively higher nitrogen isotope values than the other areas over three years. The high nitrogen isotope values of these Chinese kelps would be depending on the nutrient enrichment of the water of the Yellow River estuary. On the other hand, there was no significant difference in the stable carbon, nitrogen and oxygen isotope values between Japanese and South Korean kelps.

In Hokkaido (Japan), 165 reliable samples of kombu were collected from 4 area, Donan (n=100), Hidaka (n=5), Rausu (n=10) and Rishiri (n=50). The kelp from Rishiri has relatively lower carbon and nitrogen isotope ratios than other area in Hokkaido. On the other hand, the kelp from Hidaka has relatively higher carbon and nitrogen isotope ratios. Moreover, the $\delta^{18}O$ values of Hidaka are relatively lower than other area. The $\delta^{13}C$, $\delta^{15}N$ and $\delta^{18}O$ values would thus be probably useful in discriminating geographical origin of kombu within Hokkaido.

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Integrating stable isotope, otolith microchemistry, and genetic analysis to assess intra-population migration strategies of endangered anadromous North Sea houting

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Knowledge of migration patterns is essential for the effective conservation of diadromous fishes. Our goal here was to provide the first detailed characterization of the migration behaviour of the endangered anadromous North Sea houting (NSH). Specific aims were to (1) *describe migration patterns and habitat use of NSH individuals over their lifetime*, (2) *assess whether NSHs maintain anadromous migrations despite the presence of potential migration barriers*, and (3) *assess intra-population differences in migration patterns, and the potential genetic basis thereof.*

Stable isotope analysis (SIA) has become an important tool in animal migration studies, though it faces its limits when the focus lies on individual migration behaviour over the lifetime of long-lived species. We therefore complemented muscle tissue SIA ($\delta^{13}C$, $\delta^{15}N$) (n ≈ 400) with otolith microchemistry (Sr/Ca, Ba/Ca) (n = 26) to analyze individuals from the Treene and Elbe River, two of three extant German populations, obtained by electrofishing during the spawning seasons 2009-2011. Because of frequent hybridization of NSH with Baltic houting, which in contrast to NSH purportedly does not tolerate fully marine water, we also quantified the proportion of admixture from Baltic houting in all individuals using 17 microsatellite markers.

A difference of ~+10‰ in $\delta^{13}C$ between most NSH individuals and freshwater fishes from the spawning rivers showed that NSH feeding occurred mostly outside of this system, in marine habitat. Otolith transects confirmed marine habitat use during most of the year outside the spawning period. Moreover, it showed that spawning migrations generally occurred annually once individuals had reached sexual maturity. Interestingly, both methods consistently identified a small number of NSH with a divergent migration strategy, namely, the extended or even exclusive use of freshwater habitat. In contrast to expectations, these differences were unrelated to hybrid or pure status of individuals, and thus likely represented phenotypic plasticity.

This study demonstrated the usefulness of integrating ecological and genetic data. From a conservation standpoint, the finding that NSH manages to regularly pass potential migration barriers between North Sea feeding and river spawning habitats, and the maintenance of an anadromous lifestyle even by NSH-BH hybrids, should represent positive news for resource managers.

Satellite telemetry and stable isotopes: building isoscapes for loggerhead sea turtles in the Northwest Atlantic Ocean

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The use of intrinsic markers such as stable isotopes to link breeding and foraging grounds of migratory species has increased. However, several assumptions still must be tested to interpret isotopic patterns found in the marine realm in order to develop robust geospatial assignment models for the organisms of interest. We used stable isotope analysis and satellite tracking to (i) identify key foraging grounds used by loggerheads from the second most important nesting aggregation in the world and (ii) develop isoscapes for this species along the U.S. Atlantic coast. Between 2008 and 2011, we collected tissue samples from 22 nesting females equipped with satellite tags and an additional 180 untracked females. Telemetry revealed three main migratory routes and associated foraging/residency areas: (1) a northward continental shelf-constrained path to waters off the coast of North Carolina and Virginia, (2) a southern path to waters surrounding the Bahamas and Florida Keys and (3) a short eastward path to waters immediately adjacent to the Central Florida breeding area. Isotopic variability in both $\delta^{13}C$ and $\delta^{15}N$ among individuals allowed discrimination of these three distinct feeding aggregations. We attributed differences among females in $\delta^{13}C$ and $\delta^{15}N$ to a latitudinal gradient in primary producers' isotopic signatures. To test the latitudinal gradient hypothesis and build isoscapes, we collected tissue samples from loggerheads at feeding areas along the southeast U.S. Atlantic Coast and in the Bahamas. We used the isotopic patterns identified in the satellite-tagged loggerheads and found at the foraging grounds to assign putative post-nesting migration destinations of the untracked females. Our findings support the use of stable isotopes as a promising tool to unravel migratory connectivity in this vagile endangered species and offer insights for future management efforts. We provide a tool to scale-up knowledge obtained from a limited number of tracked individuals to sample sizes that are more representative of the population level and offer a basic framework for loggerhead isoscapes in the north western Atlantic Ocean.

Identifying wintering areas of Sooty terns *Onychoprion fuscatus* in the Atlantic Ocean using stable isotope

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The Sooty tern, *Onychoprion fuscatus*, is an abundant tropical seabird whose largest colony in the Atlantic Ocean is at Atol das Rocas, northwestern Brazil. Wintering areas (non-breeding grounds), where they spend most of the year are unknown. Tracking with remote sensing devices is difficult or even impossible due to the small size of these birds. The possibility of tracing changes in habitat used by birds using stable isotope occurs due to distinct isotopic areas in the ocean. Thus, we used carbon and nitrogen ($\delta^{13}C$ and $\delta^{15}N$) stable isotopes to obtain information about the Sooty tern wintering areas by comparing stable isotope values in tern feathers with isoscapes available based on zooplankton. We collected the S1 feather (grown during the wintering period) from 33 adults breeding at Atol das Rocas, as well as blood from the tarsal vein for molecular sexing. In order to compare with the existing baseline isotopic landscapes of the Atlantic Ocean, maps of probable areas for each bird were made and overlapped with baseline isotopic areas, with values of $\delta^{13}C$ and $\delta^{15}N$ corrected for isotopic discrimination between the basal values of plankton and the trophic level of birds. There was no sexual segregation during the wintering period: $\delta^{15}N$ (females average 10.87 ± 0.65‰ SD, n = 15 and males average 10.71 ± 0.74‰ SD, n=18, $t = 0.64$, df = 31, $p = 0.52$) and $\delta^{13}C$ (females average -15.56 ± 0.28‰ SD, n=15 and males average -15.62 ± 0.38‰ SD, n=18, $t = 0.5$, df = 31, $p = 0.62$). Maps showed five distribution patterns, and the majority of individuals (18 birds, 55%), wintered in pelagic areas to the north-northwest of Atol das Rocas, between the Caribbean to the west, the Mid-Oceanic Ridge to the east and the Sargasso Sea to the north. Other patterns (15 individuals, 45%) also indicated that birds wintered to the north of the atoll, but in a smaller area, and a few birds also showing a probable wintering area south of the atoll in addition to the north area mentioned above.

Does winter foraging of Southern Ocean seabirds vary between years?

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Procellariiform seabirds are among the world's most threatened taxa of birds and knowledge of their winter distribution and foraging areas are critical to their conservation and thus future survival. Stable carbon and nitrogen isotopes have already proven useful in describing migration strategies and habitat preferences of seabirds during non-breeding periods. Many procellariiform species nesting on the South Georgia archipelago are known to exhibit considerable inter-annual variability in their diets during the breeding season, yet little knowledge exists if similar variation occurs in their winter foraging. In order to assess inter-annual patterns in migration and diet during the non-breeding period we compared stable isotope ratios from feather samples of ten albatross and petrel species from five austral winters (2000-2001 and 2006-2008) collected on Bird Island (South Georgia).

White-chinned petrel and wandering and black-browed albatrosses always occupied the highest isotopic niches and showed carbon isotope ratios indicative of foraging on the continental shelf. In contrast, small petrels and light-mantled albatrosses occupied lower isotopic niches and seemed to feed in predominantly Antarctic waters. A consistently wide foraging distribution was only evident for grey-headed albatrosses, with inferred foraging areas ranging from Antarctic to subtropical waters. In addition carbon isotope ratios revealed significant inter-annual differences in inferred habitat preferences for light-mantled and black-browed albatrosses and white-chinned and southern giant petrels.

Complex latitudinal changes in the neritic isoscape of the south-western Atlantic shelf.

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The use of stable isotopes analysis to study the ecology of top predators has grown exponentially during the last decade and currently is considered a standard method in marine biology. Detailed isoscapes are critical for an accurate interpretation of stable isotope ratios in top predators, but many researchers do not generate their own isoscapes and relay on previously published data sets, ignoring that general patterns observed in oceanic areas cannot be extrapolated to coastal regions. This is well illustrated by the situation in the south-western Atlantic, where modelling of data derived from oceanic sampling has been used to suggest a decrease of the $\delta^{13}C$ values and an increase of the $\delta^{15}N$ values of neritic species inhabiting the continental shelf of South America from latitude 35ºS to 55ºS. To test this hypothesis, we collected samples of small schooling fishes and pelagic squids from southern Brazil (26º-30ºS; 46º-50ºW), Mar del Plata (38º'S; 58ºW), northern Patagonia (43ºS; 62ºW) and southern Patagonia (49º-51ºS; 63º-69ºW) and analyzed $\delta^{13}C$ and $\delta^{15}N$ of the dorsal muscle of fish and mantle of squids. As the composition of the assemblage changed with latitude, we used nested ANOVA to test the hypothesis that average $\delta^{13}C$ decreases and the average $\delta^{15}N$ increases with latitude. Statistically significant differences were observed for the average $\delta^{15}N$ of the assemblage (ANOVA, $F_{16,3}=102.021$, $p<0.001$) but no latitudinal gradient was found. Instead, the lowest values were observed in southern Brazil and northern Patagonia, and the highest values in Buenos Aires and southern Patagonia. Differences in the average $\delta^{13}C$ of the assemblage in the four areas were in the verge of statistical significance (ANOVA, $F_{16,3}=4.860$, $p=0.004$), but patterns varied among species. For instance, the $\delta^{13}C$ of young hake (*Merluccius hubbsi*) increased southward, opposite to the expected pattern, whereas the $\delta^{13}C$ of anchovies (*Engraulis anchoita*) from Brazil was higher than that of anchovies from Buenos Aires or northern Patagonia. Therefore, we conclude that the latitudinal variation of stable isotope ratios in the area is more complex than previously described on the basis of modelling of oceanographic data and that local isoscapes should always be reconstructed.

Aquatic isoscapes: a review of current research and future directions as it relates to fisheries science.

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The inability to directly observe marine and freshwater fish in their dynamic environment has limited our understanding of their movements and distribution. This challenge has been met with the development of new methods, including radio- and satellite tag technologies. Stable (C, N, O, H, and S) isotope ratios of fish tissues are intrinsic tags that can be used to study fish movements in and between marine and freshwater habitats. In addition to applying this method to elusive and highly migratory species, this method works well to track the movements of juvenile fish that are not suitable for current tagging technologies. In addition, stable isotope analysis of scales and otoliths can provide information on fish movements in both modern and extinct species. Here we review the current knowledge of how this technique has been successfully applied to fish movements in a) marine ecosystems, and how it can be applied to b) large river systems. We discuss the strengths and weaknesses of the method and its most promising future directions in fisheries research.

Poster session F
“Animal Foraging Behaviour”

F1	Robin NIECHOJ	Intraspecific stable isotope investigation of four temperate ant species: life stages, castes and temporal patterns
F2	Priscilla WEHI	Isotopic niches and nutrient intake: extracting foraging information from different sources
F3	Carl CLOYED	Inter- and intraspecific diet variability using stable isotopes in three species of Anura
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Intraspecific stable isotope investigation of four temperate ant species: life stages, castes and temporal patterns

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This study provides information on the trophic relations of four sympatric ant species, the myrmicine *Myrmica sabuleti* and the formicines *Formica lemani, Lasius flavus* and *L. platythorax*, from an isolated limestone pavement in the West of Ireland derived from natural abundances of ^{13}C and ^{15}N determined using EA-IRMS. Differences in ^{13}C and ^{15}N levels were found between the species at every life stage. The highest ^{15}N levels were found for *L. flavus*, suggesting that its large involvement in the belowground food web, determines the ^{15}N enhancement, rather than its trophic level. Both, ^{12}C/^{13}C and ^{14}N/^{15}N isotopic ratios of larvae and pupae of the four ant species were different from those of the imagines, supporting the metamorphic shift hypothesis. A methodical agreement to include the abdomen in determinations for the comparison of life stages would help verifying this result and future comparative studies. The castes of workers and females (alatae) of formicines showed no differences in C:N ratios nor in their isotopic composition of ^{12}C/^{13}C and ^{14}N/^{15}N, suggesting that trophallaxis in ants must be seen as feeding all castes equally, and this could also apply for larvae and pupae. Interestingly, ant workers do not show seasonal differences regarding ^{14}N/^{15}N but *L. flavus* and *M. sabuleti* show a depletion of ^{13}C during the active season.

Isotopic niches and nutrient intake: extracting foraging information from different sources

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Tree weta (*Hemideina* spp.) are large, sexually dimorphic crickets that are widely distributed in New Zealand, inhabiting environments that range from lowland forest to alpine herbfields. Few direct observations of foraging in the wild have been recorded for any of the seven species, in large part because they are nocturnal. Foraging differences between the sexes also remain unexamined. Nonetheless, previous stable isotope evidence indicates that the lowland tree weta *H. thoracica* is largely herbivorous[1]. This finding, however, contrasts with the high degree of omnivory suggested for the alpine weta *H. maori*, based on invertebrate fragments in their frass. It thus appears that omnivory varies across the genus. To quantify omnivory and diet in a more consistent way, we analysed C and N stable isotope values from tissues in three species, the alpine *H. maori*, and lowland forest *H thoracica* and *H crassidens.* We then analysed the crop contents from these same individuals for nutrients, including protein. We discuss the results of these analyses, as well as those obtained from frass analyses, in relation to both size and sex. We comment on the consistency between the methods and the information gained from each. Finally, we discuss how identifying both isotopic niche and nutrient intake in these species can inform our understanding of foraging and life history.

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Inter- and intraspecific diet variability using stable isotopes in three species of Anura

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Studies have shown that many species that appear to be generalist foragers are actually composed of individuals that specialize on subsets of the species' resource spectrum. We used stable isotope analysis from bone and whole blood to investigate individual diet variability in three anuran species that are well recognized as dietary generalists (*Lithobates catesbeiana, L. clamitans,* and *Anaxyrus americanus*). We compared the diets among the study species and then tested whether diet variability is related to resource diversity and niche width. We predicted that variation in individuals' diets would increase when resource diversity is high and when the species niche is wide. Prey were grouped into the following three categories: aquatic herbivores and predators; terrestrial herbivores; and terrestrial predators. *L. catesbeiana* took the highest proportion of aquatic prey (0.17±0.06), followed by *L. clamitans* (0.14±0.02) and *A. americanus* (0.11±0.02). *A. americanus* had the highest proportion of predators in their diet (0.63±0.06). However, both *L. catesbeiana* and *L. clamitans* took more predators (0.61±0.11 and 0.57±0.04, respectively) than herbivores (0.22±0.06 and 0.28±0.05, respectively). Our estimates of individual diet variability are very conservative because of the broad classification of prey groups we used. Both *A. americanus* and *L. clamitans* showed very little individual specialization. However, *L. catesbeiana* did show specialization and was significantly more variable among individuals than *L. clamitans* (F=4.21, df=1,13, *p*=0.047). Our hypothesis that individual variation in diet would increase with increasing resource diversity was supported. Within *L. catesbeiana,* individuals that were captured at ponds with higher resource diversity were more specialized (F=5.71,df=1,30, R^2=0.37, *p*=0.0072). Our second hypothesis was also supported: species that had wider niches also had more individual diet variation. This study shows that *L. catesbeiana* exhibits individual specialization, while *L. clamitans* and *A. americanus* individuals act more as generalists.

Spatial and sexual variation in *Phrynops geoffroanus*' diet (Testudines, Chelidae) in altered habitats: a classic and isotopic approach

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Phrynops geoffroanus is widely distributed throughout South America and commonly found in polluted rivers. This freshwater turtle species can stand different types of environmental stressors, including high levels of heavy metals in its tissues. Although anthropogenic habitat alterations seem to benefit the species, it is still unknown the magnitude of such changes on species life story trait. Diet is probably one important ecological attribute for species capacity in thriving in polluted rivers and streams. In such context, stable isotopic analyses in dietary studies are more currently common and they can minimize problems from stomach flushing technique (e. g. different digestibility levels of ingested items and accidental ingestion). The goal of this study was to evaluate spatial and sexual differences in *P. geoffroanus*'s diet from two polluted rivers in Sao Paulo State, Brazil, using two complementary techniques: stomach flushing and stable isotopes analyses. Turtle were captured between August 2006 and June 2007 in Piracicaba River (active search using hand dip nets), and between May 2006 and June 2007 in Piracicamirim stream (fishing nets). We used stomach flushing in addition to turtle claw samples to evaluate $\delta^{13}C$ and $\delta^{15}N$ composition. The stomach flushing samples indicated a diet based on larvae and pupae of *Chironomus inquinatus* (Chironomidae) as well as smaller amounts of plant material, fish and terrestrial and aquatic invertebrates. $\delta^{13}C$ was different between study sites and sexes, but there was no difference in relation to $\delta^{15}N$. The $\delta^{13}C$ and $\delta^{15}N$ signatures for *C. inquinatus* were different between sites and developmental stages (pupae and larvae). The isotopic signatures for the diet's main item from both study sites did not reflect the isotopic sign found in the turtles, suggesting that items with lower frequency of occurrence (not analyzed by the technique of isotopic or not recorded by our sampling methods) may be important. We suggest future investigation on dietary items not detected in our samples (soil, dissolved organic matter from sewage and rural areas, particles associated with consumed items such as cocoons and microorganisms) or with lower frequency of occurrence which were probably ingested and absorbed this being important items in turtle's diet.

Sexual and ontogenetic niche variation in *Caiman latirostris* (Crocodylia: Aligatoridae) using stable isotopes of nitrogen

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Strategies like the use of different food resources at different levels in the foodchain are common in wild animals in order to minimize intraspecific competition. The isotope of nitrogen is useful to determine the trophic structure of a given environment, because there is a progressive enrichment of ^{15}N atoms from the bottom to the top of the chain. The transfer of trophic usually occurs with an increase 3-5 ‰ in $\delta^{15}N$ value. However, studies are practically nonexistent with this methodology in neotropical crocodilians. The broad-snouted-caiman can be considered a generalist predator able to colonize anthropogenic habitats, but males and females appear to occupy different ecological niche. This study aimed to verifying the occurrence of sex and ontogenetic variation in trophic level in *C. latirostris* using stable isotopes of nitrogen in a silvicultural landscape in the Alto Paranapanema watershed, State of São Paulo, Brazil. The caimans were captured overnight in the period from February to April 2011. The isotopic ratios of nitrogen ($\delta^{15}N$) were determined for claw samples collected from 24 juveniles, 8 adults and 16 hatchlings totaling 48 individuals. Adults and hatchlings had higher enrichment of ^{15}N compared with juveniles (mean $\delta^{15}N$ respectively, 7.3 ± 0.9 ‰, 5.6 ± 0.1 ‰ and 2.6 ± 1.3 ‰). No difference was found between adults males and females, but young females had more enrichment of ^{15}N than young males (average $\delta^{15}N$ for females and males respectively, 4.2 ± 0.9 ‰ and 2 ± 0.8 ‰). The average $\delta^{15}N$ of hatchlings was closer to the isotopic signature of the adults. A possible explanation for the pattern is that the hatchlings are reflecting the trophic status of their mother. The results of this study may indicate a possible exploitation of different food resources, with consequent reduction in competition among age classes and between sexes. Ontogenetic differences in diet have been documented in several species of crocodilians. Juveniles feed mostly on invertebrates whereas as the size of animals increases the importance of vertebrate prey grows.

Individual foraging specialisation in group living Badgers (*Meles meles*)

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Individual specialisation, where individuals exploit only a narrow range of the total population niche, has been recorded in a large number of species, with important evolutionary and ecological implications. However, to date the causes and consequences of this behaviour remain poorly understood in the majority of cases where it is documented. This is not surprising, as investigating individual specialisation requires data on individual long term foraging variation, combined with detailed ecological and life history data, which may be difficult to obtain.

Our research uses stable carbon and nitrogen isotope analysis to quantify and investigate individual foraging variation in a long-term study population of Eurasian badgers (*Meles meles*) which has been studied using mark-recapture techniques for over thirty years. Badgers are omnivorous social carnivores which live in groups of 2-30 individuals occupying a shared territory with a centrally located main sett (burrow). However, within social groups, individual badgers forage predominantly alone. Individual foraging variation within this species has important ecological implications as badgers are a reservoir of bovine tuberculosis (TB) and individuals foraging in pastures or farm building may come into close contact with cattle. Despite this, few studies have investigated individual foraging variation in this species, primarily due to the limitations of traditional methods such as faecal and gut analysis.

We combine individual foraging data derived via stable isotope analysis of badger vibrissae, with data on individuals, to quantify the degree of individual niche variation within our study population. We find that individuals within social groups differ markedly and consistently in their isotope values indicating that individuals within territories differ in their utilisation of shared resources. These differences are not age or sex related, and in some instances are remarkably consistent across years, suggesting long term individual foraging specialisation. In addition, we utilise data on social group and territory composition to answer whether individual differences are the result of competition or resource availability. These results not only have implications for understanding how badgers interact with their environment, potentially influencing disease risk and management, but also shed light on how ecological factors may drive niche variation in wild populations.

Dietary ecology of Alaskan gray wolves: integrating stable isotope and spatial analyses

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The dietary ecology of gray wolves (*Canis lupus*) is of great interest to researchers and wildlife managers throughout Alaska. While wolves are traditionally considered to rely primarily on terrestrial prey, such as ungulates like moose (*Alces alces*) and caribou (*Rangifer tarandus*), they are opportunistic feeders and have been observed to use alternative resources, including marine derived resources, such as salmon (*Oncorhynchus sp.*). Despite these observations of alternative resource use, the seasonal or interannual variation and the relative importance of different protein sources has not been studied in animals currently using the landscape. Our research combines stable isotope analysis ($\delta^{13}C$, $\delta^{15}N$) of wolf guard hair and blood, and GPS collar data to examine how wolf feeding ecology is reflected in their landscape use patterns.

Lake Clark National Park and Preserve in southwestern Alaska is an ideal location for such an examination because it exhibits a large variation in landscape types with different degrees of access to marine derived nutrients. Our results demonstrate that wolf packs in the Lake Clark region differ in their use of marine resources both spatially and temporally. Salmon may be a substantial part of the diet of some packs with relatively smaller home ranges, while those with larger home ranges and less access to salmon have stable isotope values representative of a primarily terrestrial diet and may be less reliant on salmon. Additionally, some packs have distinctly terrestrial diets throughout the year while other packs consume substantial amounts of salmon seasonally. The variation in spatial patterns and in diet shows a wide range of landscape and resource use in the wolf packs of the Lake Clark region.

Feeding ecology of brown bears of the Southern Kurils revealed by stable isotope analysis

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White-colored brown bears (*Ursus arctos*) are found on the Kunashiri and Etorofu islands located among the Southern Kuril Islands[1)]. Although a certain number of such bears are reported only from these two islands around the world, their ecology is not well clarified. In September 2010, we conducted an ecological survey of brown bears on the Kunashiri Island and collected the hair samples of white- and brown-colored brown bears. We determined carbon and nitrogen stable isotopic compositions of these hair samples to estimate the feeding habit of brown bears on the Kunashiri Island.

Although we anticipated that white hair may be advantageous for catching salmon, as Klinka and Reimchen (2009) have reported for the white morph of the American black bear[2)], no significant difference was found in the isotopic compositions between the white and brown bears on the Kunashiri Island. A strong positive correlation between carbon and nitrogen isotopic compositions was observed, indicating a small variation in food sources. Moreover, every bear showed a similar isotopic pattern from hair root to tip, which suggests that bears have a similar feeding history; consume plants in spring and salmons from summer to autumn. Compared to brown bears on the nearby Shiretoko Peninsula, which consumed not only plants and salmons but also sika deer (*Cervus nippon*) and anthropogenic crops, Kunashiri bears highly depended on abundant salmon resources under an environment without influences of human activities. We are planning to conduct a same survey also on the Etorofu Islands for further information.

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^{13}C, ^{15}N and ^{34}S isotope abundances from human serum as diet biomarkers

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Measurements of natural isotopic abundance are used to reconstruct diet in animal ecology. In human, the evaluation of diet mainly relies on self-reported surveys that are often biased by memorisation problems. The aim of this study was to evaluate if serum ^{15}N/^{14}N, ^{13}C/^{12}C and ^{34}S/^{32}S ratios could be useful biomarkers of diet composition.

Data from 286 adolescents (17.5±0.5 years) of the French ICAPS cohort, an intervention aiming at preventing overweight, were obtained two years after the end of the intervention. Weight and height were measured. Diet was evaluated using a semi-quantitative food-frequency questionnaire with a set of photographs to estimate portions. Dietary data were analysed as food items and groups, energy and nutrients (using the French General Directory of Food), and dietary patterns identified by a principal component analysis (PCA). ^{15}N/^{14}N, ^{13}C/^{12}C and ^{34}S/^{32}S ratios were measured by elemental analysis-isotope ratio mass spectrometry on fasting, delipidated serum samples. The relationships between isotope ratios and food data were analyzed using general linear models and reduced-rank regressions analyses (RRR).

Univariate analyses showed that serum ^{15}N/^{14}N (mean=9.41±0.30‰) and ^{13}C/^{12}C (mean=-22.48±0.49‰) were positively associated with animal proteins and meat intakes ($p<0.05$ for all). Serum ^{15}N/^{14}N was further associated with fish consumption ($p<0.001$), while ^{13}C/^{12}C was related to dairy products ($p\leq 0.01$) but not to sugar-sweetened beverages consumption. RRR indicated that ^{15}N/^{14}N was associated with a diet rich in fish, meat and milk, and ^{13}C/^{12}C with a diet rich in meat, poultry, milk, cereals, fruit and deserts. Using a PCA combining food data and isotopes enrichments, we identified a dietary pattern combining high ^{15}N/^{14}N and ^{13}C/^{12}C ratios with high meat, fish and milk consumption that was inversely associated with body mass index ($p=0.02$).

Our results indicate that serum ^{15}N/^{14}N and ^{13}C/^{12}C measurements may be useful to objectively assess consumption of specific food items of animal origin. Contrasting with previous US data, ^{13}C/^{12}C was not related to sugar-sweetened beverages consumption, probably due to a lower level of corn-sugars in Europe. By distinguishing marine and terrestrial dietary resources, ^{34}S/^{32}S measurements, still on-going, should lead to a more complete food isotope signature and to additional information on diet habits.

Browsing cattle? Stable isotope analysis of faecal samples reveals broad dietary type usage in Northern Namibia, Southern Africa

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Intraspecies variation in diet type consumption (graze vs. browse) has received scant attention in dietary studies of herbivores. This is despite growing evidence of substantial dietary variability within and between populations of especially bovine species traditionally classified as either browsers or grazers. Understanding the extent to which local vegetation composition can influence bovine dietary type choice is important in the face of growing anthropogenically induced habitat changes experienced across the African continent.

Here we report on a study that looks at cattle diet across seasons (wet, early dry and late dry) in two physiognomically different communal pasture areas in Northern Namibia. We use stable isotope analysis of faecal samples obtained during the respective seasons from both areas to quantify the proportional use of grass vs. browse by the cattle. Both areas have high livestock densities but vastly different vegetation structures. The King Nehale area is open grassland, while the Okongo area is dense woodland believed to have been converted, from grassland, to its current state due to overgrazing and the suppression of fire. We determined δ^{13}C values for both C_3 (trees, shrubs and herbs; average δ^{13}C = -27.5‰) and C_4 (grass; average δ^{13}C = -14.2‰) plants commonly consumed by the cattle to accurately calibrate the dual end-point mixing model used in the calculation of the percentage grass consumed.

Results indicate that vegetation structure strongly influence diet type consumption in the two areas. Only 28% of the Okongo woodland cattle diet comprise of grass during the early dry season. This is in stark contrast to the King Nehale grassland cattle that consume 96% grass during this time. At the end of the dry season the grass intake of Okongo woodland cattle increase to 58% as they supplement their diet with post-harvest maize remains made available from small subsistence farming plots. At the same time KN cattle increase their browse intake to 18%, possibly to compensate for the reduction in grass quality at the time. Results of the wet season diet composition will be available at the time of the conference where we will also discuss the ecological significance of our findings.

Isotopic ecology of mammals in a high-altitude Ethiopian grassland

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The Ethiopian highlands harbor a diversity of endemic, insular, and ecologically specialized mammals. Characterizing the dietary ecology of these species by direct observation has proven difficult given their low population densities and shyness toward humans. As a result, it is not well understood how Afroalpine mammalian communities might cope with climate change and habitat destruction. Accordingly, we investigated the isotopic ecology of several mammals inhabiting an ecologically intact high-altitude (3500 m) grassland, the Guassa Plateau, in northern Ethiopia. Carbon, nitrogen, and oxygen values were documented for hair (keratin), and bone (collagen and carbonate) from six mammal species: gelada baboons (*Theropithecus gelada*), Ethiopian wolves (*Canis simensis*), klipspringer (*Oreotragus oreotragus*), Starck's hare (*Lepus starcki*), rock hyrax (*Procavia habessinica*), and yellow-spotted brush-furred rat (*Lophuromys flavopunctatus*). We found that δ^{13}C values were uniformly depleted, a result consistent with the prevalence of C3 vegetation at high altitudes. Few significant differences in δ^{13}C values were found between species. Intra-individual variation in keratin δ^{15}N values from gelada baboons suggests seasonality of protein consumption. We also report the first isotopic values for the critically endangered Ethiopian wolf: δ^{15}N values in Ethiopian wolves exhibit little variation and are enriched relative to those of its rodent prey items. Variation in δ^{18}O values among species indicates differences in water consumption habits among species but is also consistent with differential consumption of above-ground versus below-ground food items.

Using stable isotope mixing models as a dietary approach in a raptor species

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The trophic ecology of top predator species has been broadly studied. In birds of prey, the pellet analysis has been the most common approach to study the dietary habits of several species, both in terms of prey frequency consumption and prey biomass ingested. During the breeding seasons of 2008 to 2010, we studied the diet of Bonelli's Eagle *Aquila fasciata* nestlings at 28 territories (i.e. breeding pairs) in Catalonia, northeastern Spain. The diet study involved both conventional pellet analysis and stable isotope analysis (SIA) of δ^{13}C, δ^{15}N and δ^{34}S in nestling's feathers. Our main objectives were: 1) to estimate the percentage of prey biomass assimilated by the nestlings by using stable isotope mixing models (SIAR), and 2) to assess whether those results were in concordance with different approaches of the conventional pellet analysis (i.e. prey percentage consumption, total prey biomass, and fraction of prey biomass delivered to the chicks). Main prey categories were identified based on the pellet analysis. Samples from main prey collected at the eagles' territories were analysed to assess for isotopic differences at the species level. Main prey species were sampled in the eagles' territories, and for some of them we found significant isotopic differences related with habitat coverage and marine proximity. Stable isotope mixing models showed marked dietary differences between breeding pairs. Finally, we compared the diet assessment based on SIAR and that from the pellet analysis through the concordance correlation coefficient (CCC) index. Our results highlight the importance of distinguishing between prey consumption and prey assimilation in dietary studies, and the use of Bayesian mixing models such as SIAR is showed as a useful tool to cope with trophic studies of top predator species as birds of prey.

Hunting high and low – individual differences in seabird foraging behaviour revealed by stable isotope analysis

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Seabirds use a number of foraging strategies to exploit the full range of marine environments, pelagic (offshore), neritic (nearshore or over shelf areas) and coastal. Pelagic seabirds carry out large-scale movements, often crossing ocean fronts and entering different ecological zones. Most species studied to date use a number different areas, both for foraging in the breeding season and during migration. Often, the prey found in these different areas is isotopically distinct, and stable isotope analyses (SIA) can thus be used to determine the use of these areas. We show examples from Wilson's storm-petrels Oceanites oceanicus and Thin-billed Prions Pachyptila belcheri, and discuss how different areas are used in relation to environmental conditions and faithfulness of individuals to individual strategies. We compare SIA data with data collected at sea by geolocation (GLS). In contrast to the pelagic seabirds, species such as the Dolphin Gull Larus scoresbii are restricted to coastal habitats, where they find food either scavenging from other seabirds or seals, or feeding on coastal invertebrates in the intertidal. We used stable isotopes and GPS loggers, and found that individuals specialize on one strategy consistently over time. In conclusion, we suggest SIA can represent individual strategies in many seabird species of different ecological backgrounds. SIA can be used to monitor individuals across time, and to plan tracking work in seabirds, as sample sizes can be adjusted according to the individual strategies detected by SIA.

Temporal consistency in the feeding ecology of an opportunistic species, the yellow-legged gull (*Larus michahellis*) in Portugal

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Populations of yellow-legged gull (*Larus michahellis*) have increased dramatically throughout Europe in the recent decades, with several ecological and social impacts. The successful management and conservation of gull population numbers depends on a good understanding of its foraging and trophic ecology. The aim of this study was to evaluate the consistency in the feeding ecology (trophic level and resource/habitat use) of yellow-legged gulls during different stages of their breeding and non-breeding periods, using stable isotope analysis ($\delta^{13}C$ and $\delta^{15}N$) of red blood cells and plasma (both corrected for fractionation), to represent the pre-laying and incubation periods, 1st primary, representing the post-breeding season, 8th secondary and breast feathers, both representing the wintering season. During the breeding period, May – June 2011, 26 breeding adults were sampled in the larger breeding colony of the species in Portugal (Berlenga Island).

The results for $\delta^{15}N$ suggest that during the breeding season the gulls explored resources from a higher trophic level than in the non-breeding season. Moreover, lower significant values in $\delta^{13}C$ after the breeding season indicate that birds changed their carbon source, suggesting a modification on the resource/habitat use during this period. Nevertheless, our results suggest a high short- and long-term individual consistency in the trophic level throughout the year, with exception of the wintering season, when birds apparently became less consistent, and a strong short-term consistency in the resource/habitat use during the breeding season.

The feeding ecology of the sampled individuals confirms the plasticity of this species throughout the year. However, a high degree of short- and long-term foraging niche consistency was detected at the individual level, suggesting individual preferences in the feeding ecology of this highly opportunistic and generalist species.

Diet as a source of carotenoids for egg-yolk: link between colour and stable isotopes in the Audouin's gull

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Egg-yolk has yellow-reddish colours because of the presence of dietary carotenoids. It has been hypothesized that carotenoids act as antioxidants preventing the developing embryo from the action of free-radicals. For this reason, higher carotenoid content has been related to a higher breeding success and fledging survival rates.

Seabirds get carotenoids from the fish and crustaceans they consume. Audouin's gulls inhabiting the Ebro Delta mainly exploit two foraging habitats associated to these two kinds of prey. Being mainly a marine piscivorous (both on pelagic and discarded fish) they feed at some extend, on the less valuable American crayfish that they obtain from the surrounding rice fields paddies, which however, are rich in asthaxantin.

There are few studies in the wild assessing the influence of diet on egg-yolk colour. In this study we analyzed stable isotopes (N, C) in 60 egg-yolks corresponding to twenty 3-egg clutches of Audouin's gull from the Ebro Delta. We also described the characteristics of carotenoid-based marks of the yolk using a portable spectrophotometer Konica Minolta (CM-2600D) and the CIELab method by means of descriptors [L* (lightness), a* (red-green axis), b* (blue-yellow axis)]. We found that in the yolk, colour varies depending on the female, the laying order, yolk weight, and female diet. The highest carotenoid associated-coloration was found to be in the first laid egg, the colour descriptors of the remaining eggs were staggered from the first. The weight of the yolk proved to be another feature related to the brightness of the yolk, L*, being higher in heavier yolks. Finally, the descriptors a* and b* revealed a link between carotenoid coloration of the yolk and its isotopic signature, mediated by crayfish consumption.

Effect of diet on the circulating and intra-clutch deposited antioxidants in near threatened Audouin's gull (*Larus audouinii*)

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The diet is a source of antioxidants primarily synthesized by the plants which are assimilated by the animals and can strongly affect their antioxidant levels. These antioxidants compounds play an important role against oxidative stress. Most of the studies relating diet and antioxidant capacity in birds have been conducted in captivity conditions administrating different diet qualities, and mainly focused on carotenoids. At this point emerges the need to study the relationship between diet and the total antioxidant capacity (not only carotenoids) in the plasma of breeding females and in their clutches (i.e. egg compartments -albumen and yolk-). In this way, stable isotopes analysis stands as a very useful tool to trace the diet of birds in the wild.

In our work we assess diet-antioxidant relationship in Audouin's gull (*Larus audouinii*), a medium-sized species catalogued as Near Threatened at global level by the IUCN. About two thirds of the world Audouin's gull breeding population nest in the Ebro Delta Natural Park (NE Spain). In this area, the species show a great dependence on trawling discards from fisheries, but they can also exploit resources from the neighbouring ricefields, especially the American crayfish (*Procambarus clarkii*). It has been suggested that the relevance of ricefield resources is higher during trawling moratorium years. Sampling was conducted at two breeding nucleuses (saltpans and coastal dunes) which show differences in nest density and breeding success which were higher in the saltpan's nucleus. 11 females (6 from the saltpans and 5 from the dunes) and 20 clutches of three eggs (10 per nucleus) were analyzed. Our results pointed to a greater plasticity of the albumen intra-clutch pattern compared to yolk. Moreover, when comparing both nucleuses we found that in the saltpan's clutches albumen antioxidants and proteins decline through the laying order, whereas in the coastal nucleus tends to maintain or even increase the investment. Nearly all the antioxidant measures (in plasma, albumen and yolk) presented a negative relation with the δ^{15}N, probably indicating that marine fish diets (depleted in $\delta^{15}N$) are better than rice fields in terms of increasing the antioxidant capacity.

Short- and long-term consistency in the foraging niche of wandering albatrosses

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The wandering albatross (*Diomedea exulans*) is regarded as a generalist predator, but can it be consistent in its foraging niche at an individual level? This study tested short- and long-term consistency in the foraging niche in terms of habitat use, trophic level and, by inference, prey selection. Fieldwork was carried out at Bird Island, South Georgia, in May-October 2009, during the chick-rearing period. Blood (plasma and cells) and feathers for stable isotope analyses ($\delta^{13}C$ and $\delta^{15}N$) were sampled from 35 adults on their return from a foraging trip during which they carried stomach temperature, activity and Global Positioning System loggers. Results suggest short-term consistency in foraging niche in relation to both oceanic water mass and trophic level, and long-term consistency in use of habitat. Consistent differences among individuals partly reflected sex-specific habitat preferences. The proportion of consistent individuals (i.e. with a narrow foraging niche) was estimated at c. 40% for short-term habitat and trophic level (prey) preferences, and 29% for longer-term habitat preference, suggesting this is an important characteristic of this population and potentially of pelagic seabirds in general. Foraging consistency was not related to body condition or level of breeding experience, instead it may reduce intra-specific competition.

Dietary change over winter migration in Spheniscus magellanicus yearlings inferred though stable isotopes analysis.

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Stable isotope analysis is a powerful tool to infer and compare trophic relationships and diets between different habitat types during animal movements. Feathers have been the most widely used tissue to the track the migration of seabird species with a well known patter of sequential molt. This is not possible, however, with penguins, as they moult all their feathers simultaneously. In order to solve this problem we measured the stable isotope ratios of carbon and nitrogen along the claws of yearlings of Magellanic penguin (*Spheniscus magellanicus*) to infer the existence of ontogenic dietary changes and gain a further insight into the poorly know winter throphic ecology of young Magellanic penguins. A capture-tag-recapture experiment conducted in a nesting colony in Península Valdes revealed a mean growth rate of 0,11 ± 0,02 mm day $^{-1}$. These results show that an entire penguin claw represents an average time span of 6 months and hence the claws of yearling penguins collected in Brazil during the winter months would inform about the diet offered by parents while in the nesting colonies (claw tip), the diet consumed during fall off Argentina (claw center) and the diet consumed during winter off southern Brazil (claw base).. The results indicate that there is a significant change in the isotope signatures between the portions of the claw corresponding to the breeding season and the wintering period (MANOVA, $p<0.001$). However, these differences are not explained by an ontogenic change in diet as a result of a shift in prey selection when yearlings begin to forage independently as has been suggested by stomach contents analysis studies, but are the consequences of shifting baselines. The general pattern of diet of yearling penguins found in the three study areas was basically the same: the most important prey item was the anchovy, *Engraulis anchoita,* followed by a group of four cephalopods species.

Evaluation of autotrophy *versus* heterotrophy in symbiotic scleractinian corals: a stable isotope study in French Polynesia Islands

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Tropical scleractinian reef corals are extremely well adapted to oligotrophic conditions through their endosymbiosis with dinoflagellates (zooxanthellae). Although it is widely accepted that photoautotrophic processes provide the primary source of fixed carbon and nitrogen for symbiotic scleractinian corals, the relative contribution of heterotrophic diet has rarely been quantified. The aim of this study was to investigate the relative contribution of heterotrophy *versus* autotrophy in scleractinian corals from contrasted fringing reefs in the Moorea lagoon (Society Island, French Polynesia). Twelve species of corals from 7 genera were sampled at three sites (Vaiare, Maharepa and Tiahura) during both hot-wet and cold-dry seasons. Coral host tissues and microalgae (zooxanthellae) were separated by centrifugation and $\delta^{13}C$ and $\delta^{15}N$ were determined on both fractions. Seawater physical and chemical parameters were monitored at the three sites.

Density of zooxanthellae and chlorophyll *a* concentrations in coral tissues varied with environmental parameters. The highest concentrations of suspended particulate matter and nutrients in the water column were measured at Vaiare site during both seasons. Stable isotope ratios of the holobiont tissues were ^{13}C and ^{15}N-enriched at Vaiare compared to the two other sites regardless to species and seasons. Stable isotope ratios of coral hosts and zooxanthellae were ranged from -17.90 to -9.99 ‰ and from -18.14 to -9.98 ‰ for $\delta^{13}C$ and from 3.43 to 8.75 ‰ and from 1.70 to 7.89 ‰ for $\delta^{15}N$ respectively. Differences between coral hosts and zooxanthellae averaged 0.34 ± 0.89 ‰ and 1.97 ± 1.05 ‰ for $\delta^{13}C$ and $\delta^{15}N$ respectively. Our data indicated that the origin of dietary carbon and nitrogen varied between species among sites and seasons.

SIAR mixing models will be run with autochthonous and allochtonous sources available for corals in order to determine the degree of heterotrophy *versus* autotrophy under contrasted environmental parameters.

Challenges of conducting stable isotope analysis on an endangered fish species: validation of results relying on novel non-lethal muscle tissue sampling

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Working with endangered species poses the challenge that lethal sampling is oftentimes not an option. At the same time, knowledge of the feeding ecology and habitat use/migrations of such species may be essential for conservation efforts, and can be obtained via stable isotope analysis (SIA) if tissue samples are available. One way around this dilemma is the use of non-lethal sampling techniques. In salmonid fishes, clipping the adipose fin has been a way to obtain tissue for analysis, but most other fishes do not possess this fin. In addition, recent research shows that it may play a role as sensory organ, and its high fat content can negatively affect SIA results. In principle, use of muscle tissue would therefore be more desirable.

For isotopic analyses of the endangered North Sea houting (Coregonidae), a close salmonid relative that has an adipose fin, we therefore tested the use of biopsy punches (5 mm diameter, yielding ~3-4 mg dry mass) to non-lethally sample small amounts of muscle tissue of 50 individuals (body mass 350 – 2000 g). To assess the validity of SIA results ($\delta^{13}C$, $\delta^{15}N$) obtained from these samples, we compared them with results obtained from larger (~1 cm^3), homogenized muscle fillet samples (requiring sacrificing), as well as with results based on adipose fin samples of the same individuals. Furthermore, 30 additional fish were monitored over 6 weeks after biopsy punching to assess wound healing.

Wounds healed completely and without visible inflammation. Pairwise t-tests incidated that SIA results based on biopsy and “traditional” muscle samples did not differ significantly from each other, nor did variability increase when using biopsy samples (assessed using Bartlett’s test). In contrast, results based on adipose fin tissue showed significant shifts in both $\delta^{13}C$ and $\delta^{15}N$

compared to muscle tissue. Although a correction for these shifts may be possible, they prevent a direct comparison with published fish SIA studies based on muscle tissue. In conclusion, the novel use of biopsy punches to obtain muscle samples for SIA of fishes appears ideally suited in all cases where non-lethal sampling is required.

Using data from feeding habits and isotopic mixing models to understand the diet of the Blackfin goosefish *Lophius gastrophysus* from South-Western Atlantic

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Two of the main approaches to study the natural diet of marine species are the stomach content and stable isotopes analysis. In the current work, we compared data of stomach content analysis by Pucci (2004) with results of three isotopic mixing models: IsoSource, MixSIR and SIAR (Parnell et al., 2010). We used $\delta^{15}N$ and $\delta^{13}C$ data and an enrichment factor of about 2.2‰ nitrogen and 0.4‰ carbon at each trophic level, estimated for marine fish species.

The possible food sources considered in the models were Algae, Asteroidea, Crustacea, Bivalvia, Gastropoda, High-N Fish, Low-N Fish, Teuthida, Polychaeta and Zooplankton. There is morphological evidence that some of these groups should not be food sources for *L. gastrophysus*, and the models were run with and without these groups, showing little difference in the results. Overall, the models predicted the main food sources as Fish, Teuthida and Crustacea, totalling 68 to 80 percent of the diet (result from SIAR, first and third quartiles), which are in good agreement with the data from the stomach content analysis.

However, the models were sensitive to variations in the enrichment factors, producing strikingly different profiles for the main food items when run with other enrichment factor estimates. Also, the width of the posterior distributions was sensitive to the standard deviations used on the enrichment term, with lower standard deviations producing much “flatter” profiles.

Our work thus confirms the models to be adequate for the investigation of feeding habits, highlights the importance of using adequate enrichment factor estimates in the utilization and interpretation of these models, and points out that the models are robust to the addition of improbable food sources.

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Ontogenetic change in energy sources for *Plagioscion squamosissimus* (Heckel, 1840) and *Hypophthalmus edentatus* (Spix, 1829) in the Upper Paraná River floodplain.

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The present study aimed to determine the autotrophic sources that sustain food chain of the piscivorous*Plagioscion squamosissimus* and of the zooplanctivorous *Hypophthalmus edentatus*, during ontogenetic development of both species, in order to verify whether the primary producer assimilated in the initial periods of development continues being the same one required by the adults. The larvae and juvenile had been captured in the spawning period of the fishes, from October/2002 to March/2003 in the Ivinheima River sub basin, and the adults in November/2004 in the Upper Paraná River floodplain. The specimens were separated according to the notochord development degree: preflexion, flexion, postflexion, juvenile and adult. The primary sources of energy used were phytoplankton, riparian vegetation, C_3 macrophytes, periphyton and C_4 macrophytes. For the estimation of isotopic sources SIAR package was used (Stable Isotopes Analysis in R) in the computer program R.2.11.1. For both species, the phytoplankton was the source most assimilated with a contribution above 50% (credibility interval of 95%) in all development stages. Nevertheless, it is worth to highlight the importance of phytoplankton as source of energy for the early stages of flexion and post-flexion of both species, being these values 88% and 94% for *P. squamossissimus*, and 81% and 78% for *H. edentatus*, respectively. Only for the juvenile of *H. edentatus* was not possible to separate the primary sources that were incorporated. Thus, both species used the same source of energy (phytoplankton) throughout the ontogenetic development and the adult only differ from them in the proportion of the assimilated resource. Therefore, the antropic interventions that affect the phytoplankton community should be minimized in order to preserve the autotrophic sources which sustain the food chains from *P. squamosissimus* and *H. edentatus*.

Trophic position during the marine life of two lampreys from the Bay of Biscay as inferred by stable isotopes in muscle and liver

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The marine lamprey (*Petromyzon marinus*) and the river lamprey (*Lampetra fluviatilis*) are jawless vertebrate species (Agnathes) native from Western Europe. Both reproduce in coastal brooks and upstream in rivers, where they live as larvae for years and feed on organic matter. After metamorphosis, they migrate at sea to achieve their life-cycle by a marine growth phase. This marine life is characterized by a parasitic blood-feeding mode on marine vertebrates for *P. marinus*, and a fish-predator mode for *L. fluviatilis*. However this marine period is extremely poorly documented, and we don't know exactly on which preys they feed nor where they go.

To bring information on their trophic position during the marine life, *ca*. 250 specimens have been collected from estuaries and coastal areas in the Bay of Biscay, on the French Atlantic. The objective is to estimate their trophic position before the capture, as inferred by stable isotopic ratios (dC and dN) in their muscle and liver. Some samples have been delipidized to correct the potential lipid-effect. The results are interpreted in regard of the stable isotopic ratios of their potential preys among sharks, rays, bony fishes and marine mammals.

Vertebrae isotopic signature as a tool to depict ontogenetic trophic shifts of the blue shark (*Prionace glauca*) in the Southwest Indian Ocean

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Ontogeny of the trophic ecology of the blue shark was investigated using longitudinal stable isotope analysis ($\delta^{15}N$ and $\delta^{13}C$) along individual vertebrae of six individuals (FL ranged from 194cm to 276cm). Results highlighted a distinct ontogenetic trophic shift from the embryonic stage (ranged from the birth date to the first growth ring, GR) marked by a placenta dietary to the active feeding on preys by juveniles, subadults and adults (GR from 2 to 13). This shift is well underlined by an astonishing higher trophic level at the growth ring #1 (early juveniles) than for the other growth rings. For the 6 studied individuals a decrease in $\delta^{15}N$ values is observed from GR#1 to GR#5, the GR#5 (back calculated fork length = 150cm) being the limit between subadults and adults. This trend might be explained by a metabolic reworking in vertebrae. From the GR#5 to GR#13, $\delta^{15}N$ values increases according to the individual size. The global augmentation corresponds nearly to one trophic level (i.e. a difference of 2‰ for fish). Regarding the trophic habitat and the source of food informed by $\delta^{13}C$ values, a mean decrease up to 1‰ is observed between GR#1 and GR#2. From the GR#3 to GR#13, $\delta^{13}C$ values pattern displays a slowly increase following the individual growth. However, these $\delta^{13}C$ results did not allowed us to decipher different foraging habitats and migration through age due to (i) inadequate sampling resolution or (ii) small variations in $\delta^{13}C$ values of the baseline in this region. Simultaneous analysis of $\delta^{15}N$ and $\delta^{13}C$ stable isotope in muscles for both embryos and their mother revealed significant higher level of $\delta^{15}N$ and $\delta^{13}C$ for embryos with an average difference of +1.6‰ and +0.7‰, respectively..

Spatial variation in the diets of female Steller sea lions inferred from ^{13}C and ^{15}N values of vibrissae from pups

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Populations of apex predators have experienced declines and extinctions around the world, and changes in diet have been identified as a possible cause. The Steller sea lion (*Eumetopias jubatus*) is an apex predator in the North Pacific Ocean, and subpopulations of the species in Alaska (USA) are exhibiting different temporal trends in abundance. Abundance of subpopulations in the western part of the region has dramatically declined over the last 40 years, while abundance in the east has increased. Prey data from scats suggest diets vary among subpopulations. The differences in diet have been proposed as a possible cause of the variation in population growth rates, but biases associated with the use of scats to infer diet preclude robust conclusions.

The objective of our study is to characterize the diets of five subpopulations of Steller sea lions using stable isotopes. From 1998 to 2009, we collected vibrissae from pups, cut the vibrissae into segments for stable isotope analyses, and used the $\delta^{13}C$ and $\delta^{15}N$ values from segments of the vibrissae while the pup was *in utero* to make inference regarding the diets of the pups' mothers. Vibrissae segments from westernmost subpopulation, the Central Aleutians, are depleted in $\delta^{13}C$ and $\delta^{15}N$ relative to subpopulations to the east. On average, $\delta^{13}C$ values are depleted by 1.3 ± 0.5‰, and $\delta^{15}N$ are depleted by 3.0 ± 0.3‰. These results are consistent with the patterns inferred from the spatially and temporally limited scat data. We are compiling a database of $\delta^{13}C$ and $\delta^{15}N$ values of putative prey species in the region and have estimated discrimination factors for both nursing pups and developing fetuses. We will use stable isotope mixing models to estimate the composition of prey in Steller sea lion subpopulations and compare the estimates to frequency of occurrence of prey from scat data. Diet estimates from vibrissae will provide a more energetically meaningful description of the prey species important to Steller sea lions and a more complete understanding of the diets of adult females during gestation and the subsequent nursing period.

Dispersal patterns of South American sea lions (*Otaria flavescens*) in the Atlantic revealed by oxygen isotopes from bone carbonate

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Bone apatite grows at a constant temperature in mammals and, hence, variations in the $\delta^{18}O$ of apatite carbonate reflect changes in the $\delta^{18}O$ of ingested water. As in marine mammals food is the only relevant source of water, the $\delta^{18}O$ of their apatite bone is expected to reflect that of their food, which in turn reflects that of the surrounding water mass. Thus, the $\delta^{18}O$ of apatite in marine mammal bone is a potentially useful habitat tracer for marine ecosystems and we used it to investigate dispersal patterns of South American sea lions in the south-west Atlantic. Samples were collected from the skulls of individuals that were found dead stranded in Brazil (32 males), northern Patagonia (39 males and 39 females) and Tierra del Fuego (19 males). Bone samples were grinded and soaked into a hydrogen peroxide solution to oxidize organic matter, the original structural carbonate was isolated from potential contaminants using a solution of acetic acid buffered with calcium acetate, and its O isotopic signal analysed using a mass spectrometer. A statistically significant correlation was found between the latitude of the stranding point and the $\delta^{18}O$ value of mature males (n=58, r_p= -0.285, $p <$ 0.030), which agrees with the latitudinal gradient of $\delta^{18}O$ in the ocean. This correlation suggests limited dispersal of adult males along the coast of South America. On the other hand, variability in the $\delta^{18}O$ values of young and immature sea lions of both sexes from northern Patagonia is much wider than that of adults from the same region, which suggests that young and immature sea lions disperse more widely than adults.

Nevertheless, the dispersal period of females was much shorter (<3 years) than that of males (<8 years), consistently with the female philopatry revealed by genetic markers.

Using chemical feeding ecology to understand variability in mercury concentrations in western Aleutian Steller sea lions.

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One hypothesis for the lack of recovery of endangered Steller sea lions (SSLs, *Eumetopias jubatus*) in Alaska is low natality. Although there is no direct evidence mercury contamination causes adverse effect in SSLs, it is known high mercury exposure is neurotoxic to humans and other piscivorous mammals. Young pups have higher total mercury concentrations ([THg]) in hair than older SSLs, suggesting pups are exposed to mercury *in utero* during late gestation when lanugo (natal pelage) is grown. With limited direct information regarding the foraging habits of adult females in the western Aleutians, we utilized patterns of $\delta^{13}C$ and $\delta^{15}N$ deposited in the vibrissae (or whiskers) of young pups to help us understand how diet variations between gestating females might impact mercury exposure during this critical period of fetal development.

Hair and a vibrissa were collected from 22 SSL pups (newborn to 6 weeks old) on their natal rookery at Agattu Island, in the western Aleutian Islands, Alaska. Hair was washed, freeze-dried and analyzed on a direct mercury analyzer (Milestone DMA-80). We measured $\delta^{13}C$ and $\delta^{15}N$ in approximately 0.1 cm sections selected every 0.5 cm along the length of the vibrissa from the tip (earliest *in utero*) to the root (present nursing signature). Five to 8 sections estimated to represent the growth during late gestation were selected for each pup to establish a mean $\delta^{13}C$ and $\delta^{15}N$ of the fetal vibrissa tissue during that period.

Hair [THg] was highly variable among pups, ranging from 3.7 to 63.9 µg/g dwt. Pups born with the highest [THg] in their hair (above 40 µg/g) showed significantly higher $\delta^{15}N$ in vibrissa tissue grown during late gestation ($F_{2,25}=8.61$, $p=0.0019$) suggesting that their mothers may have incorporated higher trophic level fish into their diet. The wide distribution of both $\delta^{13}C$ and $\delta^{15}N$ seen in late gestation vibrissae segments of these pups illustrates the diverse nature of the isotopic signature of the diet of adult females, whether that be driven by trophic level of the prey species, the geographic location of foraging, or both.

Carbon and nitrogen isotope discrimination factors for Steller sea lion vibrissae on milk and fish/squid diets

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Nutritional constraints have been proposed as a contributor to population declines of the endangered Steller sea lion (*Eumetopias jubatus*) in some regions of the North Pacific. Isotopic analysis of vibrissae (whiskers) is a potentially useful approach to resolving the nutritional ecology of this species because long-term (up to 24 months) dietary information is sequentially recorded and metabolically inert once formed. Additionally, vibrissae are grown in utero, potentially offering indirect inference on maternal diet. However, diet reconstruction using isotopic techniques requires a priori knowledge of tissue-diet discrimination factors (DFs), which can vary as a function of diet quality. We refined vibrissa DFs for free ranging nursing pups and provide new estimates for captive sub-adults maintained on complex fish/squid diets. In a previous study, we reported vibrissa-milk DFs based on the analysis of 14 animals and now extend that to an additional 58 animals with age distributions ranging from 1 to 20 months. Lipid-free $\delta^{13}C$ and bulk $\delta^{15}N$ vibrissa-milk DFs are 2.5‰ (+/- 0.9) and 2.0‰ (+/- 0.8), respectively, and did not differ among the Aleutian Island, Prince William Sound, and Southeast Alaska regions. In contrast, vibrissa-fish/squid DFs were 1.5‰ (+/- 0.4) and 1.6‰ (+/- 0.3) higher for lipid-free $\delta^{13}C$ and bulk $\delta^{15}N$ respectively. DF differences between milk and fish/squid diets are consistent with expectations based on the nutritional quality of the former. Empirically determined DFs are critical for accurate retrospective diet modelling, particularly for evaluating the hypothesis of nutritional deficiency contributing to the lack of recovery of Steller sea lions in some regions of Alaska.

Being a specialist in a changing environment: the diet of the crabeater seal along the western Antarctica Peninsula

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Despite being one of the most abundant consumers of Antarctic krill *Euphausia superba*, the diet of crabeater seals *Lobodon carcinophaga* has been rarely studied throughout most of its range. Using $\delta^{13}C$ and $\delta^{15}N$ values in vibrissae from 53 seals, we examined the trophic ecology of crabeater seals from the western Antarctica Peninsula (wAP) in 2001, 2002 and 2007. We observed a wide variability in individual seal mean $\delta^{13}C$ values, which ranged between -24.9‰ and -19.8‰, whereas mean $\delta^{15}N$ value varied between 5.39‰ and 7.9‰. We identified a positive significant effect of seal mass on $\delta^{13}C$ values, as well as a significant seasonal effect (higher in winter), likely a consequence of changes in the composition of the community of primary producers. Crabeater seals $\delta^{15}N$ values, on the other hand, were affected by year, with individuals in 2002 having higher $\delta^{15}N$ values. The median (range) contribution of Antarctic krill to the diet of crabeater seals, as estimated using the Bayesian mixing model MixSIR, was 87.9% (81.2 – 94.8%). During 2002, krill biomass in the wAP was at one of its lowest levels during the last two decades, coinciding with a slight reduction in the importance of krill to the diet of the seals that year, which reached 84.5% (75.1 – 92.4%). Despite the relative plasticity observed in the diet of crabeater seals, it is unknown to what extent, and at what rate, crabeater seals might be able to switch to a more generalized diet, which might impact their fitness given the ongoing environmental change along the wAP.

Combining carbon stable isotope ratios ($\delta^{13}C$), fatty acid profiles (FA) and compound-specific carbon stable isotope ratios of individual fatty acids in seal muscle and blubber samples helps to build a reliable generalized picture of seal diets

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Previous diet studies of seals have used muscle tissue for stable isotope (SI) analysis and blubber for fatty acid (FA) analysis. In this study we evaluated if muscle tissue could be used for both FA and SI analyses to study the inter-individual feeding of Baltic ringed seals (*Phoca hispida botnica*) in the brackish Bothnian Bay. We analyzed the carbon stable isotope ratios ($\delta^{13}C$) from muscle and from two blubber layers of ringed seals. The $\delta^{13}C$ value of seal muscle did not statistically differ from blubber closest to the muscle, but differed significantly from blubber closest to skin. We also determined the fatty acid profiles of these three seal tissues and their potential prey items and used principal component analysis (PCA) to identify possible differences in FA profiles. The principal component analysis (PCA) clustered muscle and the closer blubber together whereas the blubber sample from closest to the skin separated clearly from the other tissues. Finally we analyzed the compound-specific carbon stable isotope ratios of individual fatty acids from muscle, from blubber closest to muscle and from the potential prey items to define the status of carbon resources in ringed seal diets. Compound-specific carbon isotope signals of seals reflected their diet sources, but yielded only small differences in $\delta^{13}C$ values between seals. $\delta^{13}C$ of fatty acids differed between muscle and blubber in some seals. Our SI and FA analyses from ringed seals indicate that muscle and blubber closest to muscle similarly reflect diet assimilation but differ significantly from blubber closest to skin. The fractionation during the conversion of diet material to muscle or blubber is also discussed.

Intrapopulation isotope variation among humpback whales (*Megaptera novaeangliae*) summering in the Gulf of St-Lawrence, Québec, Canada

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Individuals within a population have been long considered ecologically equivalent, however there has been a renewed interest in intrapopulation trophic niche variation since this type of trophic variation may have interesting consequences for adaptability. Humpback whales are known as generalist predators worldwide, feeding on a combination of euphausiid crustaceans and small pelagic fish. However, little information is available regarding sources of intrapopulation trophic variation or individual-level trophic consistency. From 1995 to 2010, a total of 206 photo-identified individual humpbacks were remotely biopsied to obtain epidermal tissue in the Gulf of St-Lawrence in Eastern Canada. Carbon and nitrogen stable isotope ratios were measured and gender was determined using DNA-amplification techniques. Age class (calf, juvenile, adult) and reproductive status (resting, pregnant, lactating) of mature females was deduced from photo-identification records. A subset of individuals (n = 14) were resampled 3 - 4 times over a 10 - year period to gain insight into the degree of individual dietary consistency. Mean overall $\delta^{13}C$ and $\delta^{15}N$ were measured at -18.55 ‰ (SD ± 0.39) and 13.88 ‰ (± 0.81), respectively. Males and females had very similar C and N values. Age class had no significant effect on C or N values; however adults and juveniles were on average 0.2 ‰ N-enriched over calves. The reproductive status of mature females had no significant influence on C or N values; however, pregnant females were the most N-enriched and lactating females the least N-enriched, suggesting that pregnant females may be feeding at a slightly higher trophic position. The ratio of within-individual N variance to total population N variance of resampled individuals ranged from 0.05 to 1.0 (mean = 0.7). Only 35 % of the resampled population used less than half of the total population niche width, suggesting a low degree of individual dietary consistency. Estimation of the population's diet composition revealed an average diet of 60 % small pelagic fish (sand lance, capelin, herring) and 40 % euphausiid zooplankton. Intra-individual diet estimation suggests a population consisting primarily of individual generalists.

Stable isotope signatures in fin whales (*Balaenoptera physalus*) from the NW Atlantic coasts of Spain

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Research on baleen plates, an inert tissue that keeps a permanent chronological record of the isotopic signature in body circulating fluids, has produced contrasting results in different species of baleen whales and even in different populations of the same baleen whale species. The variation has been associated to differences in migratory regime, changes in diet composition, alternation between feasting and fasting periods, or a combination of these factors. We investigated signature variation in both muscle and baleen plates from fin whales inhabiting the waters off NW Spain. From the regular pattern observed in the baleen plates, baleen growth rate was calculated. This allowed to establish the chronology of deposition in the various segments of the baleen plates, while in the muscle such chronology was determined directly from the date of sampling. The observed pattern of variation differed from that found in individuals of the same species but sampled in the Mediterranean Sea and in the British Isles, suggesting some degree of isolation between putative stocks or subpopulations. Potential causes for the observed variation in patterns are discussed.

Resource partitioning among St Lawrence beluga whales: an assessment based on bayesian multisource mixing models and stable isotopes

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Individual specialization may reduce potential competition for food or space among and within species. In the St Lawrence Estuary, Canada, beluga occupy a small area (2800 km^2) during summer, where large adults, likely males, segregate spatially from adult females with juveniles. This spatial segregation likely results in access to different prey communities and thus,

should be reflected in sex-specific diets. Muscle isotopic ratios were determined for 137 beluga sampled between 1988 and 2008 to examine variability in isotopic signature and diet composition using a bayesian approach to multisource mixing models. A hierarchical cluster analysis identified eight beluga groups within our sample, which were used as independent mixtures in mixing models. Young-of-the-year segregated from other beluga based on high $\delta^{15}N$ values, reflecting *in utero* development and lactation. Among older beluga, male as a group occupied significantly higher trophic positions and were ^{13}C-enriched relative to females. Using potential prey as sources in mixing models, we found that most beluga (n = 85) consumed a mixture of sandlance, capelin and tomcod, with variable contributions of sandworm, redfish and squid. The cluster analysis also revealed some structure within sex classes, as two groups of females were significantly ^{13}C-depleted compared to other beluga, probably from exploiting resources from the Upper Estuary such as smelt and tomcod (as well as sandlance and capelin), where carbon inputs from terrigenous origin are larger. A group comprised exclusively of males had higher $\delta^{15}N$ values than other groups as a result of a greater consumption of groundfish species such as Atlantic cod and white hake. No seasonal trend was observed in isotopic signatures, a result somewhat expected given the 2-3 mo integration time for muscle and diversity of beluga diet. These results confirm food partitioning not only occurs between male and female beluga, but also within these groups.

Poster session G
“Freshwater Ecology”

G1	Fabio ERCOLI	Do the native noble crayfish and introduced signal crayfish occupy similar trophic niches in small boreal lakes?
G2	Jean-Marc ROUSSEL	Trophic ecology of the invasive red-swamp crayfish *Procambarus clarkii* and its potential predators in the Brière Marsh, France
G3	Scott COLBORNE	Foraging ecology of native pumpkinseed sunfish (*Lepomis gibbosus*) following the invasion of zebra mussels (*Dreissena polymorpha*).
G4	Grzegorz SKRZYPEK	Flash flood and drying cycles as hydrological controls of waterhole ecosystems in semiarid zones
G5	Helen AGASILD	Biogenic methane contributes to the food web of a large shallow lake
G6	Alexis GUILPART	Land-based salmonid farm effluents enhance heterotrophy in headwater stream food webs
G7	Nicolas HETTE TRONQUART	Influence of riparian vegetation on temperate stream food web: seasonal variations along a shading gradient
G8	Jean-Michel MORTILLARO	Degradation kinetics of two Amazon floodplains macrophytes (*Paspalum repens* and *Salvinia auriculata*) from a multi-tracer approach
G9	Kaire TOMING	How $\delta^{13}C$ values reflect the origin of organic matter in a large and shallow lake in calcareous catchment?
G10	Gilles LEPOINT	Stable isotope composition spatial variability at microhabitat scale of macrofauna inhabiting a tropical freshwater stream (Pérou River, Guadeloupe)

Do the native noble crayfish and introduced signal crayfish occupy similar trophic niches in small boreal lakes?

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The introduction of exotic species is recognized as one of the greatest biological threats to global biodiversity, since introduced species affect the distribution and abundance of native species. The North-American signal crayfish (*Pacifastacus leniusculus* Dana) is an introduced species that has become widespread throughout Europe. Signal crayfish was introduced to Finland in the late 1960s to 1970s and thereafter has been spreading rapidly into Finnish lakes where it has often replaced the native noble crayfish (*Astacus astacus* L.). Its rapid growth and reproduction and its more aggressive behaviour compared to the native noble crayfish threatens the stability of Finnish lake ecosystems.

This study aimed to compare the trophic niches of the introduced signal crayfish and the native noble crayfish in small to medium sized boreal lakes using stable isotope data of carbon and nitrogen. We studied 8 lakes with signal crayfish and 8 lakes with noble crayfish. For each lake, stable isotope analyses were made from samples of crayfish as well as from their potential food sources (periphyton, detritus, macrophytes and macroinvertebrates).

We used mixing models to analyse the stable isotope data to quantify the food sources used by the two species of crayfish and to describe their respective feeding niches. We also compared niche widths between the two species considering the same basal resource isotope signature found in every lake.

Our data suggest that signal crayfish and noble crayfish populations do not show differences in within-lake niche widths, although there were indications of signal crayfish having a somewhat wider overall niche at the species level. Nevertheless, isotope niches of the two species strongly overlapped suggesting that the introduced species essentially uses the same resources and hence occupies a trophic niche very similar to that of the native species. This inference is also supported by the fact that the estimated proportions of basal resources (profundal, littoral and terrestrial) used by crayfish varied considerably among individual populations but did not differ consistently between species.

Trophic ecology of the invasive red-swamp crayfish *Procambarus clarkii* and its potential predators in the Brière Marsh, France

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Freshwaters are threatened by the expansion of non-native species. While adverse effects on local biodiversity are widely reported, ecological mechanisms that may constrain or promote the invasion process are still poorly documented. The red-swamp crayfish *Procambarus clarkii* has become a successful aquatic invaders worldwide as a result of numerous intentional and accidental introductions. It has been accidentally introduced in 1981 in the Brière Marsh, one of the largest wetland in France (190 Km^2), and rapidly extended throughout the marsh. High abundances are currently recorded in both permanent waters (canals) and seasonally flooded habitats (reed beds and grasslands) of the marsh.

The objectives of this study are 1) to examine trophic ecology of red-swamp crayfish in various habitats of the marsh, and 2) to detect aquatic predators that could contribute to the reduction of its abundance. Stable C and N isotope analyses were used to identify energy sources and trophic links from primary producers to aquatic predators. Depending on the habitat, the trophic position (TP) of red-swamp crayfish varies from primary to secondary consumer (TP=2 in reed bed; TP=2.9 in grassland), showing that this opportunist and omnivorous species can adjust its diet to available resources in the marsh. Mixing models reveal that benthic organic matter is the major carbon source contribution to *P. clarkia*, and that crayfish is the main food source for most fish species in the marsh. Therefore, it appears that the “invader” has become a key species of the decomposer pathway and the aquatic food web functioning in the Brière Marsh.

Foraging ecology of native pumpkinseed sunfish (*Lepomis gibbosus*) following the invasion of zebra mussels (*Dreissena polymorpha*).

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The existing balance within ecosystems is often disturbed following the introduction and establishment of non-native species. The ecological changes in an ecosystem can include the decline, and possibly extinction, of native species, changes in resource availability, and alterations to the physical features of the habitat. However, the presence of non-native species may also present an opportunity for native species that are able to adapt to the changing ecosystem. We focused on zebra mussels (*Dreissena polymorpha*) that were introduced to freshwater lakes and rivers in North America during the late 1980s and their impact on the foraging ecology of a native fish species, the pumpkinseed sunfish (*Lepomis gibbosus*). Past studies of this fish have shown that they feed primarily on snails, being one of only three sunfish species to have the pharyngeal jaw structures and musculature required to crush the hard shells of the snails. Given these adaptations, we predicted that pumpkinseed sunfish might be best able to incorporate zebra mussels into their diet. We sampled pumpkinseed sunfish from Lake Opinicon, Ontario, and used both stomach content and stable isotope analyses of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) to estimate the proportion of sunfish diet made up of zebra mussels, snails, and other benthic invertebrates. In the short period since the invasion of zebra mussels into Lake Opinicon, pumpkinseed sunfish have changed their foraging behaviour such that zebra mussels now represent more than 70% of all resources consumed. While pumpkinseed sunfish likely will not eradicate zebra mussels from the ecosystem, they may be on their way to establishing a population equilibrium with zebra mussels that could decrease the overall abundance of the mussels. Diet shifts like the one we document can help to combat the spread or impact of non-native species and help to establish a new balance within altered ecosystems.

Flash flood and drying cycles as hydrological controls of waterhole ecosystems in semiarid zones

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Isolated waterholes in dryland rivers play a critical role during periods of no-flow in supporting the ecological functioning of arid regions and acting as refugia for aquatic biota. Waterholes in the arid, sub-tropical northwest of Australia are periodically flushed during large rainfall events such that the hydrochemistry and aquatic biota of previously isolated waterholes are unified. However, as surface water recedes, individual pools differentiate from each other geochemically and biologically, resulting in aquatic ecosystems that reflect local hydro-ecological regimes. The source of water maintaining each waterhole during dry periods can vary (rain, creek bank storage, groundwater) and therefore may influence their biogeochemistry and overall food web structure.

We measured the stable isotope composition of water (δ^2H, $\delta^{18}O$), $\delta^{13}C_{DIC}$, hydrochemistry and fluorescence of dissolved organic matter (DOM) from pools across the Hamersley Basin of Western Australia. We sought to determine the origin of surface water, which would help elucidate pool hydrological regimes, and to link these regimes with DOM biogeochemistry. Evaporation models using δ^2H and $\delta^{18}O$ showed three different hydrologic regimes of waterholes: 1) pools isolated from shallow alluvium groundwater that generally had high evaporative water loss; 2) pools with consistent alluvium water throughflow that resulted in low evaporation; and 3) pools constantly fed by groundwater. In addition to a conventional ion mass balance model, we used stable isotope mixing models to better explain variation in salinity. Nutrient concentrations and total DOM fluorescence were generally greater in waterholes isolated from groundwater with high evaporative loss. In contrast, nutrients were lower in waterholes fed by bank storage or groundwater inputs. Isotope signatures were also significantly correlated with DOM fluorescence characteristics and C, N, and P concentrations, confirming the hydrological influence on DOM biogeochemistry (Fellman et al., 2011).

Our findings suggest that dryland river waterholes receiving inputs of shallow alluvium water may retain surface water during the most extended of dry periods and act as refugia for aquatic biota between flush-flood events. This novel and promising approach is currently being applied to understand how changes in land use may alter catchment hydrology, which will enable the development of more effective freshwater management strategies.

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Biogenic methane contributes to the food web of a large shallow lake

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Recent studies have highlighted carbon subsidies from biogenic methane via methanotrophic bacteria to consumers in aquatic food webs. In freshwaters, such evidence has mostly arisen from stratified lakes with strong hypolimnetic anoxia. However, anoxic conditions can occur also in the organic sediments of shallow lakes where dense macrophyte beds prevent oxygen diffusion from the water column, hence providing potentially suitable conditions for methane production and utilization.

Here we present data from a wider food web investigation in large and shallow (270 km^2, mean depth 2.7m), eutrophic Lake Võrtsjärv, Estonia. The CH_4 emissions from the lake surface and the oxygen depletion in the water column in the shallow macrophyte-covered part of the lake indicated suitable conditions for methane oxidation in the sediment and in the overlying water during most of the vegetation period. Therefore, we addressed the question of whether biogenic methane could help fuel both the pelagic and benthic food webs in the plant dominated area of a large shallow lake.

Stable isotope analyses of zooplankton showed a strong seasonal variation of $\delta^{13}C$ signature with the lowest values co-occurring the period of oxygen depletion in the water column. Spatial analyses of chironomid larvae (*Chironomus plumosus*) indicated high isotopic variability within the lake (up to 21‰ in $\delta^{13}C$ and 7.3 $\delta^{15}N$‰ between the sampling sites) and those larvae with significantly depleted values (down to -64‰ in $\delta^{13}C$ and -2.6‰ in $\delta^{15}N$) were recorded from the macrophyte lake part. In addition, a difference of 3.9‰ in $\delta^{13}C$ of the dominant fish species roach (*Rutilus rutilus*), perch (*Perca fluviatilis*) and pike (*Esox lucius*) indicated a change in carbon source between the plankton and macrophyte dominated lake parts. The results suggest that methane-derived carbon can seasonally contribute to the food web in this large shallow lake.

Land-based salmonid farm effluents enhance heterotrophy in headwater stream food webs

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Land-based salmonid fish farms discharge quantity of organic matter and dissolved nutrients to streams, resulting from faeces, unconsumed feed pellets and dissolved inorganic nitrogen from fish excretion. Because salmonid farming requires cool waters of fairly good quality, the farms are located in headwater streams. In such streams, autotrophy is usually low and aquatic food webs are mostly fuelled by allochtonous organic matter from adjacent terrestrial ecosystems. Therefore, the effect of fish farm effluents on river food web can be twofold: inputs of allochthonous suspended solids can enhance heterotrophy and the decomposer pathway, or dissolved inorganic nutrients can boost primary production and the algal-grazer pathway, leading to a shift toward autotrophy downstream of the outlet.

In this work, we aim at studying the effect of land-based salmonid farm effluents on trophic ecology in rivers. More particularly, we focus on how this anthropogenic source of energy may promote autotrophy (dissolved nutrients, primary producers and the algal-grazer pathway) or heterotrophy (solid organic matter, primary consumers and the decomposer pathway) in aquatic food web downstream of the fish farm output. To that end, benthic invertebrates of various trophic groups and fish samples were collected upstream and downstream of the fish farms effluents in 3 rivers belonging to different geological and hydrochemical contexts in France. Stable C and N isotope analyses were performed on samples, and mixing models with 3 end-members (primary producers, organic matter collected upstream from the farms, and feed pellets) were run on data.

Feed pellets were significantly ^{13}C-enriched (from 4-9 ‰) compared with the isotopic background in the river upstream of the outlets. $\delta^{13}C$ values in benthic food web significantly increased downstream of the outlets (from 2-7‰), indicating assimilation of organic matter from the effluents by benthic invertebrates and transfer to fish. However, a slight decrease in $\delta^{15}N$ values of primary producers and grazers suggests that the algal-grazer pathway was also enhanced by dissolved N-NH_4^+ from the effluents. Mixing models give evidence that organic matter from the effluents becomes a major contribution to riverine food web (reaching 40-60%), especially at the expense of autochthonous sources (primary producers).

Influence of riparian vegetation on temperate stream food web: seasonal variations along a shading gradient

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Riparian vegetation is of paramount importance for stream ecology. For instance, riparian vegetation plays a key role in determining to what extent autochthonous and allochthonous organic matter contribute to stream food webs. In temperate regions, these contributions are strongly affected by the seasonal patterns displayed by riparian vegetation: i.e. leaf emergence in spring and leaf fall in late autumn. Here, we shed light on these seasonal effects on stream food web.

Using stable isotope analysis of nitrogen, carbon and hydrogen, we studied stream food webs in four sites with varying degree of shading (from 0 to 100%) at four different dates (before leaf emergence, just after leaf emergence, before leaf fall and just after leaf fall). All sites were located maximum 50 km from each others, so that they display quite homogenous environmental conditions. Following a quantitative sampling, we estimated the biomasses of macroinvertebrates and fish. Accordingly, we analysed the isotope ratios of the representative taxa (1531 values) from basal resources (algae, macrophytes, biofilm, suspended organic matter and leaf litter) to consumers (macroinvertebrates and fish).

In a first step, we described the food web trajectories across seasons, using circular statistics on different food web metrics (CircStats package for R sofware). In a second step, we estimated the contributions of autochthonous and allochthonous organic matter to the food webs, running isotopic Bayesian mixing models (SIAR package for R software).

Given riparian vegetation differences between sites, we expect to see a sharp contrast in terms of food web functioning, with sites mainly influenced by aquatic primary production (open-canopy sites), and sites mainly influenced by allochthonous organic matters (forested sites). Besides, we expect to find trophic differences between seasons at each site. In forested sites, we posit, that aquatic primary production provides the major part of energy to the food web before leaf emergence; after that, the food web would mostly rely on allochthonous organic matter with a maximum after leaf fall. On the contrary, open-canopy sites would mainly depend on autochthonous organic matter with an optimum in summer and a minimum in winter.

Degradation kinetics of two Amazon floodplains macrophytes (*Paspalum repens* and *Salvinia auriculata*) from a multi-tracer approach

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One of the greatest challenges in understanding the Amazon basin functioning, is to ascertain the role played by floodplains in the organic matter cycle. There remains, however, a lack of understanding about organic carbon dynamics, particularly on the contribution of aquatic macrophytes to organic matter and to the food web. Indeed, in Amazon floodplains, food webs are dependent on C_3 aquatic plants and planktonic productions. It suggests a lower utilization of C_4 aquatic phanerogam, although their biomass is dominant in comparison to C_3 plant species.

In this study, two macrophytes, *Paspalum repens* and *Salvinia auriculata* (a C_4 and C_3 macrophyte, respectively), were collected in Camaleão Lake (Manaus, Brazil) and incubated into different treatments (high and low biomass), in order to estimate their degradation kinetics. The transfer of organic compounds to particulate organic matter was investigated through stable isotopes and fatty acids composition. In addition, the role played by bacteria was investigated through bacterial activities and quantification of extracellular polymeric substances.

The similar fatty acids and stable isotopes composition of particulate organic matter in *S. auriculata* and control treatments do not permit to conclude, after 23 days of experiment, on an impact of degradation on this macrophyte. However, a rapid degradation of *P. repens* has been evidenced through fatty acids and stable isotopes, where an increase in bacterial fatty acid markers and $\delta^{13}C$ enrichment was recorded. The degradation of *P. repens*, also evidenced through bacterial activities, suggest a larger contribution of these macrophytes to dissolved organic matter. Based on preliminary conclusions on degradation kinetics, these C_4 macrophytes may contribute mainly to the detrital pathway and potentially sustain primary production in Amazon floodplains.

How $\delta^{13}C$ values reflect the origin of organic matter in a large and shallow lake in calcareous catchment?

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Allochthonous DOM of terrestrial origin typically has $\delta^{13}C$ values around -27‰. Basing on many previous lake studies we expected that also in large (270 km^2) shallow (mean depth 2.8 m) eutrophic Lake Võrtsjärv in Estonia carbon stable isotopes (SI) of dissolved organic matter (DOM) are more ^{13}C-depleted in allochthonous than in autochthonous material. Our study revealed that this was not the case in Võrtsjärv, where autochthonous DOM had lower $\delta^{13}C$ values than allochthonous DOM.

Our 3-year (2008-2010) dataset of DOM characteristics included SI values, fluorescence index, normalized specific ultraviolet absorption ($SUVA_{254}$), absorption ratio (a_{250}/a_{365}), total carbon and total nitrogen ratio.

The $\delta^{13}C$ values of the DOM of the main inflow varied from -28.2‰ to -25.4‰ (mean -26.7‰) and those of in-lake DOM varied from -28.4 ‰ to -26.1‰ (mean -27.2‰). Low signatures of autochthonous DOM were caused by relatively ^{13}C-depleted values of its precursors (mainly phytoplankton) with mean $\delta^{13}C$ of -28.9‰. The signatures of dissolved inorganic carbon in the main inflow and in the lake represented also relatively low values ($\delta^{13}C$ range -5.0‰ to -14.0‰). Therefore, the DOM originating from phytoplankton that is using the ^{13}C depleted DIC is expected to have also low $\delta^{13}C$ values. Moreover, the main inflow of Lake Võrtsjärv has notable phytoplankton and primary production that increases the isotopic values of DOM entering Võrtsjärv from its catchment area.

In Võrtsjärv SI values were lower during the active growing season from May to September and higher from October to April, when the average proportions of allochthonous DOM were 68% and 81%, respectively. The high share of allochthonous DOM in Võrtsjärv confirms the strong influence of the catchment area on the Võrtsjärv ecosystem. It also shows that even in this highly productive ecosystem labile autochthonous DOM is rapidly utilized and degraded by micro organisms and thus has relatively low contribution to the instantaneous in-lake DOM pool. The proportion of allochthonous DOM decreases with increasing water temperature, chlorophyll *a* and pH (increasing autotrophy of ecosystem) and increases with increasing water level and concentration of yellow substances (increasing heterotrophy of ecosystem).

Stable isotope composition spatial variability at microhabitat scale of macrofauna inhabiting a tropical freshwater stream (Pérou River, Guadeloupe)

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The spatial variability of isotopic (C and N) composition of freshwater fauna was assessed in a small and pristine tropical stream (Pérou River, Guadeloupe). In order to assess this variability, a section of 80 m was mapped and divided in quadrate (n= 132). Microhabitats (i.e. depth, hydrodynamic facies, presence of litter) were defined for each quadrate. Electric fishing was performed in each quadrate and individual isotopic measurements using EA-IRMS were done using abdominal muscles for crustaceans and lateral muscles for fishes. Isomap was generated for each species. Potential food sources (green ripisylve, macrophytodetritus, epilithic biofilm and deriving organic material) were sampled and analyzed for their isotopic composition. SIAR mixing model was applied to try to delineate isotopic and trophic variability in relation to microhabitat in this river section.

Nine species were recorded belonging to four decapod families (n= 8 species) and one fish family (n= 1 species). This fauna, dominated by crustaceans, is typical of high and medium elevations of Caribbean rivers in relatively pristine area. In these turbulent biotopes, species encountered are strongly linked to the hydrological characteristics of their microhabitat and have well defined preferenda.

Isotopic compositions of ripisylve material, of deriving matter and of autochtonous biofilm were significantly different for both $\delta^{13}C$ values and $\delta^{15}N$ values, allowing to discriminate their respective contributions to consumer diet. Epilithic and epiphytic biofilm appeared to contribute significantly to these diets, but most of the species showed evidence for litter material contribution too. Species repartition and their respective diet were evident at microhabitat scale and strongly related to hydrological regime.

Poster session H
"Fish Ecology and Otoliths"

H1	Míriam ALBRECHT	Variation in the role of terrestrial subsidies for the ichthyofauna along the sedimentation gradient in a tropical reservoir in central Brazil
H2	Míriam ALBRECHT	Main carbon sources for primary consumer fishes in an Atlantic Forest stream along the river continuum
H3	Evanilde BENEDITO	Are fish what they eat? A review about the discrimination tissue-diet in fishes
H4	Evanilde BENEDITO	Energy sources and trophic structure of fish in neotropical streams
H5	Charlotte DROMARD	Herbivorous fishes do not share the same trophic niches on the reefs of Guadeloupe (Lesser Antilles)
H6	Charlotte DROMARD	Trophic niche of the threespot damselfish (*Stegastes planifrons*) and the dusky damselfish (*Stegastes adustus*) on Guadeloupean reefs (Lesser Antilles)
H7	Clive TRUEMAN	Using SIMS-based oxygen isotope analyses to calibrate time in incrementally-grown biominerals
H8	Mikko KILJUNEN	Otolith Isotopic Composition as Potential Indicator of Atlantic Salmon Migrations in the Baltic Sea
H9	Jyrki TORNIAINEN	Feeding migration patterns of River Simojoki salmon in the Baltic Sea: Evidence from stable isotope analysis of scales
H10	Jens NIELSEN	Large scale ocean dynamics and cod growth: Weight at age and otolith stable isotopes in Faroe shelf cod
H11	Michael POWER	Determining thermal habitat use strategies among Labrador young-of-the-year Arctic charr (*Salvelinus alpinus*) using otolith oxygen stable isotope methods
H12	Li Ling HAMADY	Ecogeochemistry techniques for shark age, movement, and trophic dynamics

Variation in the role of terrestrial subsidies for the ichthyofauna along the sedimentation gradient in a tropical reservoir in central Brazil

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Reservoirs are complex systems with features which are intermediate between those of rivers and lakes. In the longer term, the water column becomes stratified, especially near the dam. This has implications on food web structure, with autochthonous productivity expected to be more important as water transparency increases. To determine if food webs are predominantly auto- or heterotrophically driven along the sedimentation gradient in the 15-year-old Serra da Mesa reservoir (upper Tocantins River, Brazilian Pre-Cambrian Shield) we evaluated the proportion of allochthonous and autochthonous resources consumed and assimilated by fish species belonging to distinct trophic guilds: detritivore (*Hypostomus emarginatus*), omnivore (*Hemiodus unimaculatus*), invertivore (*Auchenipterus nuchalis*) and piscivore (*Plagioscion squamosissimus* and *Serrasalmus rhombeus*). The assimilation was assessed through isotopic signatures of $^{13}\delta$C and $^{15}\delta$N in food resources and in muscle tissue of fish specimens from three areas (upstream, transition, reservoir) and two seasons (dry and rainy) in 2010. As expected, baseline species indicated a shift along the environmental gradient, with an increasing role of algal carbon relative to detrital carbon at the food web base. Piscivores did not reflect this change through the isotopic signatures, but had a zooplanktivorous engraulid as the main prey in the reservoir. Terrestrial resources, however, were also shown to contribute significantly for most species. Allochthonous and autochthonous resources might play a complementary role to the fish fauna either through direct consumption or the diet of their prey. Food-chain length (FCL) is one of the emergent properties of communities, which has complex interactions with abiotic factors. The ‘productivity hypothesis’ predicts that FCL will lengthen along gradients of increasing productivity. FCL was given by the ^{15}N signature of top predators, using *H. emarginatus* to provide baseline values. The prediction that FCL is longer near the dam was not confirmed. This contrasts with studies in lakes and might be due to the large amounts of flooded terrestrial biomass and/ or tributaries that provide an input of terrestrial subsidies near the dam. If this represents a common pattern to tropical reservoirs should be resolved, as knowledge about food webs and energy sources for fish are required for management strategies.

Main carbon sources for primary consumer fishes in an Atlantic Forest stream along the river *continuum*

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Theoretical models that predict the longitudinal gradient of biotic and physical characteristics in streams have shown inconsistencies between the availability of food resources for consumption and what is in fact assimilated by organisms. In headwaters, where algal production is constrained by low incidence of light and high water velocity, detrital carbon is expected to sustain primary consumers. Fishes of the Neotropical family Loricariidae are usually recognized as detritivores and/or grazers, and might represent an essential link for the understanding of nutrients cycling in aquatic ecosystems, as they feed directly on a detrital mixture composed of several sources. In the Macaé River (Biogeographical Region of the Eastern Basins, Southeastern Brazil), loricariids occur in different locations along the headwater-delta vector: Pareiorhaphis garbei is restricted to headwaters (1090m), where it is dominant, whereas Rineloricaria sp1 and Rineloricaria sp2 co-occur in the intermediate stretch (700-590m). A mixture of different proportions of detritus, sediment, plant remains and scarce insect larvae was found in gut contents. Muscle tissue of fish and their resources (sediment, litter, macrophytes, epilithon, terrestrial C4 and C3 plants, insects) were collected during dry seasons (2008-2011) and analyzed for 13δC and 15δN. Mixing models revealed that epilithon was the most assimilated resource by P. garbei, whereas terrestrial C4 plants (grass) were the main resource for both Rineloricaria species, contradicting our initial expectations. Stoichiometry (high C:N ratio) might explain dominant epilithon assimilation for P. garbei despite its supposedly lower availability in headwaters, but not the higher assimilation of grass by Rineloricaria spp. which was the most refractory of all resources analyzed. This suggests that these species might have associations with microorganisms that aid in the breakdown of refractory components.

Are fish what they eat? A review about the discrimination tissue-diet in fishes

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The stable isotope analysis (SIA) has been employed in several areas in Ecology and with different taxonomic groups. This tool has been very important to trophic ecology studies. The basic principle of the SIA is that the proportion of a stable isotope in an animal tissue could be related with the diet, and is described by the discrimination factor (DF). The DF is one of the most important parameters in stable isotope analysis. Accurate estimates of the DF are extremely important because they are used in mixture models and to determine the species trophic level. The goals of this study were quantify, by a scientometrics analysis, the research that investigates the sources of variability of the discrimination factor, focusing in fishes, and to synthesize the results obtained until the moment.

A survey in the ISI Web of Science was performed to find articles investigating the source of variation of the DF in fishes. The majority of research was led by United States, United Kingdom and Germany. Muscle was the tissue most utilized. Recently, fin and scale have been used because represent non-lethal samples. Besides the use of $\delta^{13}C$ and $\delta^{15}N$, interest in using δD (deuterium) as a food web tracer has been applied in studies with fish. Diet, trophic group, metabolic and growth rate appeared to be important sources of variability. The protein content in diet appears to contribute to the variation in DF values. In this way, the compound-specific isotope analysis of amino acids, offers an opportunity to reduce the variation related to the protein content.

We believe that there is a need in investigate (i) DF in tropical areas, (ii) the effect of temperature in the DF, (iii) the variation of the DF in different trophic groups. We call for a standardization of the methods to obtain the DF. This could help researchers to gather the results obtained and improve the understanding of the sources of variation of the DF.

Energy sources and trophic structure of fish in neotropical streams

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The contribution of allochthonous and autochthonous resources for food chains of fish in tropical streams is not well documented as do to temperate streams. In this research, we tested the hypothesis that the main energy sources that sustain the food chain of fish assemblages inhabiting Neotropical first order stream are allochthonous. To quantify the contribution of these resources we analyzed stomach contend (diet) and stable isotopes (SIA) in fish flesh. According to the diet, the most consumed autochthonous resources by fish were the immature forms of aquatic insects, mainly Chironomidae, Ephemeroptera and Trichoptera. However, it was not possible to quantify the contribution of resources with the analysis of stable isotopes (carbon and nitrogen), because the isotopic signatures of primary producers were very similar. This result was also proved in study conducted in rivers and lakes along the same basin, which suggests that carbon isotopic signatures of primary producers are inherent characteristics of the studied region. We emphasized that the food chain is mainly autochthonous, although it was not possible to determine the carbon flow in this study. The use of methodologies such as fatty acids analysis and stable hydrogen isotope can answer questions with more efficiency about resources investigation that are incorporate to consumers biomass.

Herbivorous fishes do not share the same trophic niches on the reefs of Guadeloupe (Lesser Antilles)

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Herbivorous fishes are key species in the coral reef ecosystem that play a major role in controlling the algal dynamics of the reef benthic communities. They are often globally considered as a same homogenous functional group. In fact, the different species can display various diet patterns. To investigate this fact, a study was conducted on ten species of herbivorous fishes (Three Acanthurid and seven Scarid species) currently found on the coral reefs of Guadeloupe Island (Lesser Antilles). Stomach and gut content analyses were coupled with stable isotope analyses (^{13}C/^{12}C and ^{15}N/^{14}N ratios) to determine their trophic niches. Food assimilation was estimated using the concentration-weighted linear mixing model.

Among Acanthurids, the three species presented different diet preferences. That can explain why this species forage in mutispecific schools, without exploiting the same trophic niche. The highest values of δ^{15}N were found for this three fishes, due to specific food sources.

Considering Scarids, three diet patterns were found: a group of fishes mostly grazing on algae, another one scraping hard substrate and ingesting a high quantity of sediment and a last group the guts of which contained an important part of ground amorphous organic matter. These fishes presented small δ^{15}N differences whereas they showed more scattered δ^{13}C values, which imply the use of diversified sources of carbon.

Trophic niche of the threespot damselfish (*Stegastes planifrons*) and the dusky damselfish (*Stegastes adustus*) on Guadeloupean reefs (Lesser Antilles)

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Stegastes planifrons and *Stegastes adustus* are two abundant territorial damselfishes of Caribbean coral reefs. Though much is known about territoriality, composition of territories, and their control on benthic communities, no study to date has been done on their trophic status.

In this study, we compare the trophic niche of the two fish species at two contrasted sites, by stomach contents and stable isotopes analyses (^{15}N/^{14}N and ^{13}C/^{12}C ratios). At the first site, *S. planifrons* was located deeper than *S. adustus*, whereas the two species were found at the same depth at the second site, sharing the same environment.

While ingested food items were significantly different between both species, the assimilation of each food source (macroalgae, algal turf, benthic invertebrates and detritus) calculated with concentration-weighted linear mixing model was similar.

Detritus and macroalgae, which presented higher nutritional quality, contributed respectively for 30.8% and 33.1% of the diet. Stable isotope signatures indicate a similar trophic structure on a territory scale at both sites. However, *S. adustus* presented a reduced territory size at the site where fish were found at the same depth, showing a possible competition for space between the two species.

Using SIMS-based oxygen isotope analyses to calibrate time in incrementally-grown biominerals

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Incrementally-grown biominerals such as otoliths and mollusc shells are extremely effective repositories of ecological and environmental information. Typically time is marked in incremental tissues on annual or seasonal scales. Calibrating time within biomineralised tissues, however, is challenging, particularly at higher, sub-annual resolutions. As the precision and accuracy of ion-beam techniques improves, oxygen isotopes can be used to mark time in biominerals grown in temperate environments with known temporal changes in temperature and salinity.

Here we show results of an experiment where plaice (*Pleuronectes platessa*) were maintained in a tank with continuously-flowing coastal seawater over a single year. At the start of the experiment, fish were marked with a fluorescent dye to indicate experiment onset within the otolith. Temperature and salinity measurements were taken throughout the duration of the experiment. At the end of the year otoliths were removed and oxygen isotope compositions determined in situ by SIMS. Using a 20□m beam diameter, we obtained an external precision of c.0.2 per mil. Measured values were compared to oxygen isotope compositions predicted from measurements of tank temperature and salinity.

While absolute isotope values may differ from predicted values due to inaccuracies in the otolith fractionation equation and measurement error, temporal patterns should coincide. We used ‘wiggle matching’ algorithms to align predicted and measured profile shapes based on inflection points to produce a calendar date for each 20μm spot on the otolith. After temporal matching, correlation coefficients between measured and predicted oxygen isotope values exceeded 0.8, and SIMS-based measurements were typically within plus/minus 0.5 per mil of predicted values. Critically, the isotope-based temporal chronology corrected time estimates based on interpolation between two annual check marks by up to 3 months. We expanded the same approach to calibrate otolith growth in wild fish fitted with data storage tags, and achieved similar correlation coefficients between predicted and temporally corrected measured oxygen isotope values.

These results demonstrate the increasing precision and accuracy of SIMS-based in-situ isotopic analyses, but caution against simplistic interpretations of growth dynamics in biomineralised tissues.

Otolith Isotopic Composition as Potential Indicator of Atlantic Salmon Migrations in the Baltic Sea

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Migrations have been studied mostly for fish using mark-recapture methods. However, due to several limitations in these methods, the outcomes of such studies have been somewhat limited. Revolution in the use of intrinsic migration markers, such as stable isotopes (SIs), has opened up new possibilities to study fish migration in more comprehensive way. These techniques are especially appropriate in the Baltic Sea, where there is a progressive north to south increase in salinity. In theory this gradient should also create distinctive differences in oxygen and carbon isotope ratios of the inorganic components of the water. Further, this gradual change in isotopic signatures is retained in fish bony structures which can be used to reconstruct migration paths from environmental data.

Using fish otolith (fish ear bones) stable isotope chemistry, we investigate feeding migration areas used by Baltic salmon originating from one natal river. Otoliths of ascending salmon as well as water samples around the Baltic Sea and rivers were determined for stable isotope ratios. Otoliths were analyzed for oxygen and carbon ($\delta^{18}O$ and $\delta^{13}C$) by micromilling technique, wherein very small samples (<25 µg) are taken from an otolith using a computerized micro-dental drill. The methodology allows samples to be taken continuously at very high spatial resolution (>30 samples from one otolith) by following otolith growth increments. This profile will reflect the isotopic composition of ambient water in those locations in the Baltic Sea occupied by a fish at the times that each zone of the otolith was laid down.

Due to its heterogeneity in water chemistry the Baltic Sea seems to be excellent environment to study salmon feeding migrations. Main salmon feeding areas where well separated especially by oxygen isotopes. Comparing these isotopic base maps to otoliths isotope values obtained from ascending salmon we were able to reconstruct Baltic salmon feeding migration paths in individual level. Better knowledge of the significance of salmon migratory behaviour will improve the scientific basis for restoring wild Baltic salmon stocks in the future.

Feeding migration patterns of River Simojoki salmon in the Baltic Sea: Evidence from stable isotope analysis of scales

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Migratory connectivity can be considered one of the main concepts in conservation biology. Populations with strong migration connectivity have been hypothesized to be most vulnerable against population perturbations. Although weakly connected populations may be relatively safer, they are also more difficult to conserve because management units are usually not large enough to cover a significant proportion of the population of interest. In contrast strongly connected populations may benefit more from the conservation efforts.

River Simojoki salmon (*Salmo salar*) breeding population is river specific. Instead, the connectivity of the population varies annually during the feeding migration in the Baltic Sea. For the reference We collected archived scales of feeding salmons from three different sea areas between years 1989-2011. Likewise, scales of ascending salmons from the river mouth of River Simojoki from the same years were collected. The last year growth of scales from both sets of salmon were analyzed for stable isotopes (SIs)($\delta^{13}C$, $\delta^{15}N$). By comparing the ascending salmon scale SI-values to those reference individuals caught from the sea, using canonical discriminant analysis (CDA) as an assignment method, the estimation of the most likely feeding area where each salmon individual has spent the last feeding season can be defined. This allows us to assess the annual variation of migratory connectivity of River Simojoki salmon.

Abundance of salmon main prey species (sprat and herring) in feeding areas is considered as one of the main influences for variation of migratory connectivity. Evaluating the amount of suitable prey fitting the foraging window of salmon helps us to assess the prey effect on migratory connectivity of River Simojoki salmon.

Large scale ocean dynamics and cod growth: Weight at age and otolith stable isotopes in Faroe shelf cod

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The relationship between oceanographic variation and cod growth in the Faroe shelf ecosystem in the Eastern North Atlantic was studied using nitrogen and carbon stable isotopes. Cod otoliths were used for analysis of $\delta^{15}N$ and $\delta^{13}C$ in the organic matrix of the otolith using a novel approach. Otoliths from 5 year old cod were used to create a time series, covering a 20 year period (1991-2010). A significant positive relationship was seen between values of $\delta^{15}N$, the sub polar gyre index, and sea temperature, while a significant negative relationship was seen between isotopes of $\delta^{15}N$ and fish weight. Fish weight also showed a strong negative relationship with the temperature and gyre index indicating, that years with high growth is associated with low temperature regimes. The annual variation is believed to be caused by either a change in prey availability (i.e. benthic invertebrates or zooplanktivorous fish), and / or a change in the primary production source in the ecosystem. There also seemed to be a clear link between the physical environment experienced during the 5th growth year and the isotopic signature from the whole otolith.

Determining thermal habitat use strategies among Labrador young-of-the-year Arctic charr (*Salvelinus alpinus*) using otolith oxygen stable isotope methods

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Archived otoliths from young-of-the-year Arctic charr captured in the 1983-85 in the Ikarut River, Labrador, were used to test the correspondence between monitored water temperatures and those used by the fish and study within season patterns of thermal habitat use. Here we report on historical patterns of thermal habitat use as inferred from otolith oxygen stable isotope measures known to vary predictably with the water temperatures at which otolith aragonite precipitates during formation. Young-of-the-year Arctic charr were found to consistently use warmer temperatures than those measured at 1m depth in the main channel of the river, particularly in the earliest part of the growing season. Evidence of behavioural thermoregulation was also observed in the latter part of the growing season, with fish tending to move to cooler, deeper waters than those measured at 1m, but adjusting to shallower warmer waters in the year in which end of growing season temperatures fell. Individuals were also found to pursue dichotomous strategies, with some fish tending to maximize exposure to optimum growth temperatures and others tending to maximize exposure to temperatures known to optimize growth efficiency. Results are consistent with theories of habitat selection where individuals minimize the predation-foraging gain ratio via the “asset protection principle”. The behavioural bias in otolith-derived estimates of thermal environments requires that derived temperatures must be interpreted with caution when used to infer historical conditions as they represent the portion of the habitat used and are not general indicators of environmental conditions. Nevertheless, studies of otolith temperatures provide insights into the use of available thermal habitat and point to patterns of behaviour which may become constrained as environments change.

Ecogeochemistry techniques for shark age, movement, and trophic dynamics

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Accurate age estimation is critical to population assessment and conservation strategies for sharks; management decisions based on under aging can inadvertently lead to overexploitation. The primary method for estimating shark ages relies on counting distinct layers of tissue, assumed to be annual, that are laid down sequentially over an individual's lifetime in bands, like fish otoliths, and that similarly may preserve a chemical record of environmental exposure. While it is widely acknowledged that the assumption of annual deposition should be tested by an independent method, most shark species lack this. Determining metabolic stability is also critical if vertebrae are to be used as lifetime chemical records. We present new radiocarbon data taken from analyses of shark vertebrae with the intent of determining banding periodicity, and thus age, as well as metabolic stability. Two shark species, white sharks *(Carcharodon carcharias)*, and basking sharks (*Cetorhinus maximus*), are compared; both are listed as vulnerable on the IUCN Red List of Threatened Species due to a history of overfishing, and also lack age validation. Additionally, we present preliminary ∂^{13}C and ∂^{15}N data from specific amino acids in the vertebrae and attempt to interpret these values with the help of isoscapes and tagging data. We hope that this work will inform and assist with conservation efforts for both species

Poster session I
“Food Web Structure & Community Approach”

I1	Anik BRIND'AMOUR	Community isotopic diversity indices and their ability to discriminate among trophic food web
I2	Amandine SABADEL	Mutualism/Commensalism vs. Parasitism: Using compound specific stable isotope analysis of amino acids to unravel complex trophic relationships
I3	Evan DELUCIA	Elevated atmospheric CO2 alters the arthropod community in a forest understory
I4	Kristine MARALDO	The origin and fate of amino acids from producers to soil consumers in grasslands
I5	Thibaud MASCART	Trophic and specific diversity of harpacticoid copepods associated to *Posidonia oceanica* macrophytodetritus
I6	Marcelina ZIOLKOWSKA	Benthic food web structure and functioning in the Puck Lagoon eelgrass beds (southern Baltic Sea)
I7	Amandine VASLET	Spatial analysis of stable isotope data to assess primary food sources and foraging areas of juvenile fishes in mangrove and seagrass bed ecosystems
I8	Loïc MICHEL	Trophic tracers reveal considerable diversity among diets of dominant amphipods from Posidonia oceanica seagrass meadows
I9	Jean-Charles LECLERC	Specific assemblages and Trophic structure within microhabitats of a *Laminaria* hyperborea Forest
I10	François REMY	Leaf fall impact on diversity and trophic ecology of vagile macrofauna associated with exported *P.oceanica* litter.
I11	Francesca COLOMBO	Trophic structure of vermetid reef community: high trophic diversity at small spatial scales
I12	Pierre CRESSON	How organic matter sources are integrated into trophic networks of an artificial reef system ? A case study from French Mediterranean coastal zone.
I13	Nolwenn QUILLIEN	Eutrophication impacts of green macroalgal blooms on the benthic food webs and on the flatfish nursery function of North Eastern Atlantic fine sand beaches
I14	Sandrine LAURAND	Seasonal impact of a green macroalgal bloom on the benthic food web of an intertidal lagoon (Dublin Bay, Ireland)
I15	François GAUDIN	Food web structure of the long-term surveyed ‘Pierre Noire’ fine sand community (Bay of Morlaix, France): description and seasonal variability revealed by stable isotopes analyses
I16	Carine RIGOLET	Characterizing trophic structures of muddy soft-bottom communities

I17	Valls MARIA	Trophic structure of the Balearic Islands continental shelf and slope (western Mediterranean)
I18	Vanesa PAPIOL	Trophic web structure and seasonality of slope megafauna of the NW Mediterranean; relationship with available food sources.
I19	Emanuela FANELLI	Environmental drivers of isotopic composition variability in deep-sea megafauna over mainland and insular slopes of the Balearic Basin (W Mediterranean)
I20	marie PORTAIL	A comparative study of nutritional patterns among cold-seep and hydrothermal vent chemosynthetic communities in the deep Guaymas basin, Mexico
I21	William REID	Spatial differences in Southern Ocean hydrothermal vent food webs: influences of chemistry, microbiology and predation on trophodynamics.
I22	Kena FOX-DOBBS	The role of chemosynthetic productivity within intertidal food webs at anthropogenic hydrogen sulfide seeps in Commencement Bay, Washington
I23	Chris HARROD	An overwhelming presence: $\delta^{13}C$ and $\delta^{15}N$ reveal the dominance of upwelling-derived C and N in Chilean subtidal benthic fishes.
I24	Sébastien LEFEBVRE	$\delta^{13}C$ and $\delta^{15}N$ ratios of two benthic organisms used along with other ecological indicators
I25	Violette MARCHAIS	Trophic functioning of a temperate coastal ecosystem revealed by stable isotope analysis in oysters *Crassostrea gigas*
I26	Gill NOTMAN	The mutual mucus ingestion hypothesis. Stable isotope evidence for convergent resource use in intertidal grazing gastropods within experimental microcosms.
I27	Magali GOMEZ	Determination of the trophic level of *Megathura crenulata* (Sowerby, 1825) using the isotopic signal of $\delta^{13}C$ and $\delta^{15}N$.
I28	Gauthier SCHAAL	Regional scale isotopic observations : integrating stable isotope data to long-term environmental surveys
I29	Alexandra BAETA	Habitat-related diet of macrofauna consumers in intertidal areas

Community isotopic diversity indices and their ability to discriminate among trophic food web structures

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Recently revisited concepts of niche ecology has lead to the definition of different niches and particularly the isotopic niche using stable isotope ratios. The latter are commonly presented as biplots (i.e. $\delta\ {}_{13}C$ – $\delta\ {}_{15}N$ plots) to analyse/understand the trophic structure of the food web. Isotopic diversity indices (IDI) derived from a set of measures assessing the dispersion/distribution of points in the δ-space was suggested and increasingly used in the literature. However, four main critics/limitations emerge from the use of these IDI: 1) they fail to account for the isotopic composition of the sources, 2) the lack of standardization prevent any spatial and temporal comparisons, and 3) some indices are highly sensitive to the number of species and/or the presence of rare species. Using simulations we investigated the ability of eight routinely used IDI to discriminate among different trophic food web structures, thereby focusing on two of the four limitations (n°1 and n°3). More precisely we tested the sensitivity of the IDI to four food web structures along a gradient of isotopic redundancy, varying from very low isotopic redundancy with two distinct food webs with differentiated sources to very high isotopic redundancy, with two superimposed food webs (50% superimposition) sharing two sources. For each of the food web structures we varied the number of species (from 10 to 100 species) and the type of species interactions (i.e. random or patchy distribution of species). Values of IDI are generally larger in food webs with distinct basal sources and tend to decrease as the superimposition of the food webs increases. This was more pronounced when species displayed food preferences (i.e. patchy distribution) in comparison to food webs where species fed randomly on any preys. The number of species composing the food web also had strong effects on the indices. A threshold of ~ 20 species was observed below which certain indices were either overestimated or underestimated. In all cases, analysing food webs with low numbers of species increases the uncertainty of the indices.

Mutualism/Commensalism vs. Parasitism: Using Compound Specific Stable Isotope Analysis of Amino Acids to Unravel Complex Trophic Relationships

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Unravelling complex relationships between species to understand ecological patterns and processes remains a very challenging aim for ecologists worldwide. Symbiosis is the most common consumer strategy among organisms, and yet little has been done in order to trophically distinguish between mutualistic, commensalistic and parasitic relationships within an ecological system. This differentiation is essential to constructing accurate food webs, as parasitism might affect their stability, interaction strength and energy flow. Identifying complex trophic relationships is therefore a critical step in this process.

Traditional stable isotope analyses on bulk samples have shed considerable light on such systems but can lack specificity. Stable isotopic analysis of individual amino acids (CSI-AA) provides the means of identifying nutrient sources, and allows inferences about the spatial and temporal distribution of variability in nutrition.

In this paper we apply this technique to unravel the trophic relationship and nitrogen exchanges between a sand scarab *Percoptus truncatuslarvae* and its guest: Laelapid mite (Acari: Mesostigmata). A new version of the *N*-acetylmethyl ester (NACME) derivatization procedure is used to prepare amino acids for gas chromatographic separation. The CSI-AA $\delta^{15}N$ values indicate an increase of 2-3 trophic levels for the mite over its host, implying a commensalistic relationship within this ecosystem.

Elevated atmospheric CO$_2$ alters the arthropod community in a forest understory

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The objective of this study was to determine the extent to which overall population sizes and community composition of arthropods in a naturally occurring forest understory are altered by elevated CO$_2$. The Free Air Concentration Enrichment (FACE) method was used to fumigate large, replicated plots in the Piedmont region of North Carolina USA to achieve the CO$_2$ concentration predicted for 2050 (~580 □l l^{-1}). In addition, the extent to which unrestricted herbivorous arthropods were spatially delimited in their resource acquisition was determined. Stable isotope data for spiders (δ^{13}C and δ^{15}N) were collected in ambient and elevated CO$_2$ plots and analysed to determine whether their prey species moved among plots. Elevated CO$_2$ had no effect on total arthropod numbers but had a large effect on the composition of the arthropod community. Insects collected in our samples were identified to a level that allowed for an assignment of trophic classification (generally to family). For the groups of insects sensitive to atmospheric gas composition, there was an increase in the numbers of individuals collected in primarily predaceous orders (Araneae and Hymenoptera; from 60% to more than 150%) under elevated CO$_2$ and a decrease in the numbers in primarily herbivorous orders (Lepidoptera and Coleoptera; from -255 to more than -50%). Isotopic data gave no indication that the treatment plots represented a “boundary” to the movement of insects or that there were distinct and independent insect populations inside and outside the treatment plots. A simple two-ended mixing model estimates 55% of the carbon and nitrogen in spider biomass originated external to the elevated CO$_2$ plots. In addition to changes in insect performance, decreases in herbivorous arthropods and increases in predaceous arthropods may also be factors in reduced herbivory under elevated CO$_2$ in this forest.

The origin and fate of amino acids from producers to soil consumers in grasslands

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Amino acids are considered a limited resource for soil consumers both as a nitrogen source and as a biochemical compound because animals cannot biosynthesize about half of the 20 amino acids. Thus, amino acids can function as markers for linking food web processes and carbon and nitrogen cycling in response to environmental changes. Since soil fauna function as regulators of soil decomposition processes it is essential to know their dietary amino acid sources.

Here I present a new approach for tracking the origin and fate of amino acids from producers to soil consumers based on naturally occurring δ 13C variations among amino acids. The study was conducted on an agricultural grass field in Denmark dominated by a mixture of grass-clover To understand the vegetational influence on nitrogen cycling we collected plants, soil, earthworms and enchytraeids from plots with clover only, grass only and with a mixture of both. Earthworm was significantly affected by the plant composition, whereas enchytraeids were not affected. The amino acids δ13C patterns reveal clear differences in feeding habit for the different earthworm species as well as the enchytraeids. Using δ13C amino acids fingerprints can therefore give a clear idea of the soil fauna’ food-source and thus their role in the N-cycling.

Trophic and specific diversity of harpacticoid copepods associated to *Posidonia oceanica* macrophytodetritus

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Extended meadows of living *Posidonia oceanica* plants in the Mediterranean Sea produce large amounts of detritus of dead seagrass plants that are packed at the bottom of the sea. In spite of their large quantities, these phytodetritus are of low nutritional quality (high C:N:P ratio). However, these detritus are massively colonised by bacterial communities, fungi, diatoms, meiofauna and macrofauna. This leads to the assumption that those associated communities enrich the litter and play an important role in the energy transfer to higher trophic levels like macrofauna and juvenile fish that use these accumulations as nursery and feeding grounds.

In these litter accumulations harpacticoid copepods (Crustacea) are the main meiofauna players (metazoans in the size range of 38µm – 1mm). Their families are characterised by different specialized morphologies (body form and appendages). Nonetheless their morphological differences they are all grazers and seem to feed on similar sources. Ecological theories state that diversity of trophic niches is an essential parameter to explain specific diversity. Therefore subtle trophic niches may occur among species assemblages, linked to the complexity of the phytodetritus.

In order to unravel the ecological function, trophic relations, seasonal fluctuations and habitat interactions in these litter accumulations, a bulk stable isotope analysis (SIA) is conducted. The isotopic composition of C and N of the potential food sources and the most dominant harpacticoid copepod families are measured using an EA-IRMS coupling. The results are run in a SIAR Beyesian mixing model to calculate the approximate contributions of each potential food sources towards the composition of different families of harpacticoid copepods present in the macrophytodetritus.

Benthic food web structure and functioning in the Puck Lagoon eelgrass beds (southern Baltic Sea)

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The Puck Lagoon (western part the Gulf of Gdansk, southern Baltic Sea) is a very shallow and unique water-basin of Polish marine waters. In 1970s, the ecological balance of Puck Lagoon was disturbed by a huge amount of drained sewage which caused dramatic changes in its environment. Among others the decline of eelgrass beds (*Zostera marina*, *Fucus vesiculosus* and *Furcelaria fastigata*) being a habitat, food resource and shelter for numerous organisms (e.g. economically important fish) was observed. Currently, the last two vascular plant species are not observed in the region, whereas the *Zostera marina* beds occur rarely. However, the diversity of flora and fauna is regarded as the highest in the Polish coastal zone. In the present years, the lagoon was designated as Nature 2000 site and incorporated in the EU network of protected areas (*Baltic Sea Protected Area – BSPA)*.

In a presentation we present the results of a study on the food web of eelgrass beds using stable carbon and nitrogen isotope analysis. We focused on the description of dietary input and trophic relationships in order to increase the understanding of the system and help in sustainable management of the very unique habitat in question. In particular, the investigation addressed food chain length (*FCL*), assessment of differences in the potential food source and trace of principal flows of organic matter. Samples of benthic macroalgae, vascular plants and epiphytes, meiofauna, macrozoobenthic, fish and potential food source were collected once a season between July 2010 and August 2011. Investigated site was dominated by *Zostera marina* and *Potamogeton pecticunatus*. The taxonomical richness in macrozoobenthic communities was higher in summer (15 taxa) than in winter (11 taxa). The total biomass of macrozoobenthic species was the highest in autumn (29 $g{\cdot}m^{-2}$) due to presence of alien species estuarine mud crab *Rhithropanopeus harrisi* (19 $g{\cdot}m^{-2}$) while the lowest biomass was observed in spring (1.7 $g{\cdot}m^{-2}$). The food webs of eelgrass beds consisted of four trophic levels with top predators such as the legally protected species straigtnose pipefish *Nerophis ophidion*.

Spatial analysis of stable isotope data to assess primary food sources and foraging areas of juvenile fishes in mangrove and seagrass bed ecosystems

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Mangrove and seagrass ecosystems are characteristic environments in tropical coastal areas and represent suitable fish habitats as shelters, nurseries or feeding areas. Yet, the relative importance of mangroves as fish foraging habitats seems to be site-specific and to depend mainly on habitat configuration. A spatial study was therefore conducted in a tropical lagoon in Guadeloupe (Lesser Antilles) to assess primary food sources and foraging areas for mangrove transient fishes, which occur in mangroves during their juvenile life stages. Three study sites were considered: one seagrass bed and two mangrove areas, consisting of one fringing mangrove along the coast and an offshore mangrove islet. A total of 12 species of juvenile transient fishes, belonging to five different trophic guilds, were sampled in the three sites with a selection of similar fish size ranges. Stable isotope analyses (SIA) of carbon and nitrogen were performed on fish muscles and potential prey to examine fish foraging habitats.

Carbon isotopic signatures of potential prey consisting of primary producers and invertebrates were statistically distinct between mangroves ($\delta^{13}C_{mean}$ = -19.2 ± 1.1 ‰) and seagrass beds ($\delta^{13}C_{mean}$ = -12.9 ± 0.4‰) allowing the examination of fish foraging areas. Most transient fish species from the three sites presented carbon signatures ranging from -14.2 to -12.0‰. SIAR mixing model indicated that these fishes derived most of their food from seagrass beds and their associated epiphytic community. Patterns in $\delta^{13}C$ of two planktivores (*Harengula clupeola, Anchoa lyolepis*) and two carnivores (*Lutjanus apodus, Centropomus undecimalis*) presented depleted carbon values ranging between -17.1 to -16.2‰. Mixing models indicated an increased reliance on mangrove prey in the diets of the species cited above. However, mangrove-derived organic matter contributed only marginally to these fish diets as mangrove carbon was derived indirectly through the pelagic (i.e. zooplankton) or benthic food web (i.e. crabs and shrimps). This study revealed that carbon signatures of invertebrates and transient fishes did not vary substantially with different mangrove habitats (i.e. offshore islet, coastal fringing mangroves) and that transient species sheltering in mangroves appeared to derive most of their food from adjacent seagrass beds.

Trophic tracers reveal considerable diversity among diets of dominant amphipods from *Posidonia oceanica* seagrass meadows

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Mediterranean *Posidonia oceanica* meadows shelter a high biomass and an important biodiversity of amphipod crustaceans. In other temperate meadows, the amphipods play an important part in the functioning of the ecosystem, notably in organic matter transfers from producers to higher level consumers. However, the situation in *Posidonia oceanica* meadows remains unclear, and little is known about the trophic ecology of amphipods, which are generally regarded as generalist herbivores/detritivores despite the lack of precise studies.

Here, we combined gut content examination and trophic markers (fatty acids, stables isotopes of C and N) to delineate the diet of the dominant species of amphipods from *Posidonia oceanica* seagrass meadows and to highlight trophic diversity among this community. Our results indicate that contribution of microepiphytic diatoms and of benthic and suspended particulate organic matter to the diet of amphipods were anecdotal. On the other hand, all dominant species heavily relied on macroalgal epiphytes, suggesting a certain extent of overlapping in the diets of the dominant species. Considerable interspecific differences nonetheless existed, notably concerning grazing preferences towards epiphytes from leaves or litter fragments vs. epiphytes from rhizomes. In addition, the use of the SIAR isotopic mixing model showed that most species had a mixed diet, and relied on several food items. None of the examined species seemed to graze on their seagrass host, but *Gammarus aequicauda* partly relied on seagrass leaf detritus. Overall, our findings demonstrate that amphipods have the potential to be key-items in trophic and functional interactions occurring among Mediterranean *Posidonia oceanica* meadows.

Specific assemblages and Trophic structure within microhabitats of a *Laminaria hyperborea* Forest

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Kelp forests in European subtidal areas are commonly dominated by *Laminaria hyperborea*, and shelter an important diversity of species, including sessile and mobile organisms. *L. hyperborea* plant can be considered on its own with preferential assemblages of species distributed on the holdfasts, the stipes, the epiphytes, and the fronds. Each of these kelp parts may constitute a microhabitat. Up to now, most studies focused on the fauna directly associated with the different parts of kelps but overlooked the surrounding diversity.

The present study aims to describe the whole structure of a Northern Brittany *L. hyperborea* forest in a pristine area and to determine the main trophic pathways involved by the dominant species using stable isotopes ($\delta^{13}C$ and $\delta^{15}N$). At two seasons, samples of each part of the kelp and of the surrounding area were collected separately by scuba. The abundance and biomass of the macroalgae and invertebrate species were measured to characterize community and trophic structures within each microhabitat. These results were coupled to isotopic analyses in order to characterize the associated food web. Biomasses were dominated by suspension feeders which seemed to select their food sources within the organic matter pool. More than 100 seaweed and 300 fauna species were determined, differently distributed among stipe, holdfast and the surrounding substratum. Trophic structures established by both biomass and isotopic analyses (supported by Layman metrics) suggested different functioning according to microhabitats and seasons.

Leaf fall impact on diversity and trophic ecology of vagile macrofauna associated with exported *P.oceanica* litter.

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In the Mediterranean Sea, *Posidonia oceanica* meadows produce a huge amount of detritus, evaluated up to 300 to 2000 g dry wt m^{-2} yr^{-1}. This litter is mainly composed of dead leaves but also of uprooted *P.oceanica* shoots and drift macro-algae from adjacent rocky bottoms. Although rich in refractory materials (lignin) and poor in P and N, these underwater accumulations of leaves are colonised by fungi, micro-algae (like diatoms), bacteria, but also by micro and macrofauna assemblages. These organisms could play an important role in leaf litter degradation and enrichment, but also in energy and carbon transfer from *P.oceanica* to higher trophic levels in adjacent coastal ecosystems.

In this study we focus on the vagile macro-fauna (invertebrates with a size > 500µm) inhabiting the exported litter accumulations of the Calvi Bay (France). We took standardised samples at two different sites (a sheltered one and an exposed one) before and after leaf fall. We emphasised that crustaceans represent 65 – 85% of the biodiversity, followed by annelids and molluscs, representing respectively 10-20% and 10-15% of the diversity. That general pattern differs between sampling sites and we highlighted changes after leaf fall at both sites. In order to assess the impact of the autumn period litter input on the trophic structure of these invertebrates, we conducted gut contents observations and “bulk” stable isotope analysis. The isotopic compositions of C and N stable isotopes of the potential detritic food sources and of the most abundant invertebrate’s species were measured using EA-IRMS. We finally focused on the two most abundant Gammaridean Amphipoda species representing up to about 60% of the vagile macrofauna found in litter accumulations: *Gammarella fucicola* and *Gammarus aequicauda*. The results of their isotopic measurements were used in the “SIAR” Bayesian mixing model to calculate the potential contribution of their potential food sources.

Trophic structure of vermetid reef community: high trophic diversity at small spatial scales

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Within rocky intertidal Mediterranean habitats, vermetid reefs are unique and highly diverse biogenic constructions, which host a highly diverse associated community from several taxa (e.g. molluscs, polychaetes, crustaceans). Stable isotopes were used to investigate respective contributions of autochthonous and allochthonous organic matter sources to the diet of suspension-feeders, grazers and predators associated to small reef-pools (*cuvettes*) created but the reef-building species *Dendropoma petraeum*. Organic matter sources and consumers from a vermetid reef *cuvette* from the northwestern coast of Sicily (Italy) were collected, and analysed for carbon and nitrogen stable isotope composition. Contributions of potential food sources were calculated using Bayesian mixing-models and integrated to a multivariate approach. Both pelagic and benthic compartments are exploited by benthic consumers although clear differences were revealed in the various species depending on their feeding strategy. Three different trophic pathways were identified within the *cuvettes*. Suspension-feeders seemed to rely mainly on allochthonous organic matter sources while grazers showed a wider diet spectrum. Top predators revealed a high specialization in each of the three food chains and showed a distinct reliance on organic matter originated from benthic sources or phytoplankton,. Stable isotopes evidenced here a marked differentiation of the trophic niche within the *cuvette*-associated community, which allow minimizing competition in very space-limited.conditions.

How organic matter sources are integrated into trophic networks of an artificial reef system ? A case study from French Mediterranean coastal zone.

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Located between earth and sea, coastal zones are essential for the global functioning of marine ecosystems. In addition to local primary production, they also receive diverse allochtonous organic matter (OM) inputs from continental and anthropogenic origins. Understanding the trophic relationships in coastal zones is thus a complex task, particularly in the Bay of Marseilles, the second largest city in France, due to numerous anthropogenic influences.

Through the “RECIFS PRADO”, the largest artificial reef program in the Mediterranean Sea, 400 structures were deployed in the Bay of Marseilles, representing a unique opportunity to better understand the trophic functioning of an artificial reef system.

Three methodological approaches were used in this work to determine the main characteristics of OM pools and their use by consumers at various trophic levels. Stable isotopes of C and N are powerful tools commonly used to follow the origin and fate of OM, as they can discriminate between OM sources and estimate the trophic level of organisms. Biochemical characterization of OM pools provides an estimation of their nutritional quality and can evidence the factors controlling their integration in trophic networks. Eventually, stomach content analyses allow explaining the trophic position of fishes living in the artificial reefs and their variations.

Differences between sedimentary (SOM) and suspended particulate (POM) organic matter were recorded for both isotopic and biochemical signatures. Biochemical compounds’ concentrations and $\delta^{15}N$ values were higher in POM with marked spatio-temporal variations, while $\delta^{13}C$ values were higher in SOM with low variations in space and time. These values were mainly linked with fluctuating phytoplanctonic production and occasional terrestrial inputs for POM and with permanent OM inputs of settling phytoplankton and *P. oceanica* detritus for SOM. Based on stable isotope and stomach content analyses, the 24 fishes species sampled in the artificial reef area appeared to occupy at least 3 trophic levels, from zooplankton-feeder fishes (with lowest $\delta^{13}C$ and $\delta^{15}N$ ratios) to piscivorous fishes. They relied mainly on artificial reef fauna

for their diet, with low spatial and seasonal variations of stable isotope ratios. These patterns were related to fish feeding behaviors and prey isotopic ratios.

Eutrophication impacts of green macroalgal blooms on the benthic food webs and on the flatfish nursery function of North Eastern Atlantic fine sand beaches

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Coastal ecosystems are currently suffering, directly or indirectly, from the increasing influence of anthropogenic activities, among which one of the most important is the release of nitrogen and phosphorus in excess. One of the direct symptoms of such enrichment of coastal zones may be, according to local hydrodynamic conditions, the quick and important development of assemblages of short life cycle macroalgae. Some of these exceptional blooms are constituted by green macroalgae, whose frequency and intensity are increasing worldwide.

In Brittany, more than 50 bays, which have the characteristic of being shallow and with low water turnover, are affected by this phenomenon. In parallel, these bays constitute nursery areas for many flatfish species (soles, turbots, plaice…). This is the case of the Bay of Douarnenez (Western Brittany) harbouring an extraordinary variety of flatfishes (sixteen species), and that has been, for 20 years under the influence of severe green macroalgal blooms.

The presence in excess of macroalgae, results in significant changes in biogeochemical cycles and the structure of animal communities living there (transient hyperoxias and hypoxias, organic matter in excess, loss of biodiversity). These physical and biogeochemical changes affect the system and can potentially impact higher trophic levels including fish in their most vulnerable stages, i.e. juveniles. To date, we have not identified any literature measuring the impact of green tides on NE Atlantic coastal systems functioning, either on the diversity and structure of benthic communities, on food webs structure or on the flatfish nursery function.

We will here present the sampling strategy and very first results of an *in situ* integrative approach aiming to better understand the effects of green tides on areas of ecological importance (interactions between primary producers, carbon transfers within food webs, impacts on key role ecological functions, in the bay of Douarnenez. In particular we give results on food web structure analysis, including stable isotopes ($\delta^{13}C$, $\delta^{15}N$) for all biological compartments (POM, SOM, Macroalgae, benthic fauna and fish), in association with quantitative benthic sampling (meio- and macrofauna) with fish growth and community structure.

Seasonal impact of a green macroalgal bloom on the benthic food web of an intertidal lagoon (Dublin Bay, Ireland)

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Coastal and estuarine ecosystems are nowadays largely affected by anthropogenic inputs of high nutrient loads from land. This increasing eutrophication of coastal waters can induce excessive developments of green opportunistic macroalgae, often named as green tides. This phenomenon may engender strong changes of the local biogeochemical conditions, alter the structure of the benthic communities and, potentially, the trophic functioning of the ecosystems. The real effects on the food web and the processes involved are however poorly known.

Surrounded by a conurbation of over 1,8 million inhabitants, Dublin bay is particularly affected by the nutrient fuelling of its waters via riverine and treated sewage inputs. This result in the annual occurrence of heavy green macroalgae blooms (*Enteromorpha* spp.) in a semi-enclosed estuarine lagoon, classified as a special area of conservation by numerous European and international designations.

A seasonal study of the food web was carried out in this lagoon, aiming to identify the main trophic pathways driving the food web structure and their eventual temporal dynamics as a response to the changing environmental conditions induced by the green tide occurrence. In this end, the benthic invertebrates, fishes and the various sources of organic matter (suspended and sedimented particulates, fresh and detrital primary producers) were characterized for their $\delta^{13}C$ and $\delta^{15}N$ signatures. Our results show that consumers do not rely on particulate organic matter (POM) from allochtonous origin (river, sewage) but on marine types of sources such as suspended POM, sedimented POM, microphytobenthos and green macroalgae. While partially incorporated in spring-summer, the bloom forming macroalgae became a major source of food in early winter, while at a detrital stage, for deposit and interface feeders and some omnivorous invertebrates, as determined by the bayesian mixing model SIAR. This resulted in seasonal variations in the $\delta^{15}N$ of primary consumers of up to 4‰. The incorporation of the green macroalgae in the food wed could not be detected at higher trophic levels. This study is to our knowledge the first assessing the impact of green tides on the food web of coastal ecosystems and also highlighted the need to couple it with an extensive study of the structure of the benthic marine community.

Food web structure of the long-term surveyed ‘Pierre Noire’ fine sand community (Bay of Morlaix, France): description and seasonal variability revealed by stable isotopes analyses

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Strongly affected by the Amoco Cadiz oil spill in 1978, the ‘Pierre Noire’ fine sand community in the Bay of Morlaix benefits from a long term survey of its composition since 1977. In order to better understand the functioning of this benthic subtidal community, the food web structure was studied at two different seasons (i.e. summer 2010 and winter 2011) through the carbon and nitrogen isotopic characterization of the main macrobenthic invertebrate species and their potential food sources. Consisting of suspended particulate organic matter (SPOM) and sedimented organic matter (SOM), these potential food sources were in a narrow $\delta^{13}C$ range at both seasons. By contrast, the large distribution of primary consumers (suspension-feeders and surface deposit-feeders) $\delta^{13}C$ signatures suggests that they preferentially use distinct fractions within the SPOM and SOM pools and, consequently, exhibit a high level of trophic specialization. Differences in isotopic signatures were also observed within the upper trophic levels which include a large set of invertebrate species (surface deposit-feeders, sub-surface deposit feeders, omnivorous and predators) displaying a high degree of omnivory. Most top predators are characterized by a large $\delta^{13}C$ range suggesting a non-selective feeding behaviour. Assuming the classical mean ^{15}N-enrichment factors (2.5 ‰ for primary consumers and 3.4 ‰ for higher trophic levels) we estimated that the benthic food web of the ‘Pierre Noire’ fine sand community was composed of 4 trophic levels. The results also pointed out a significant seasonal variation of the $\delta^{13}C$ signatures between the summer and the winter seasons for both sources and consumers with a shift of about 2 ‰, confirming their close relationship. The use of community-wide metric indices highlighted the seasonal stability of the food web structure. Generally, mean stable isotopic ratios overlap and cover a large range within feeding types, suggesting feeding selectivity for many primary consumers, omnivory of the upper trophic level species and a high degree of complexity of the food web. Long-term changes in the biomass of the main benthic invertebrates suggest different energy pathways over time in response to variations in the macrobenthic community structure.

Characterizing trophic structures of muddy soft-bottom communities

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Haploops nirae are gregarious tubiculous amphipods spreading over thousands of hectares in two embayments of South Brittany. As an engineer species, they strongly structured their habitat by consolidating the sediment and modifying niche space.

The main objective of this study is to compare the trophic structure of this particular habitat with two adjacent benthic food webs structures. We equally investigated temporal changes in food webs structures to understand how each benthic community studied trophically changed across seasons. For this purpose, stable isotopes (carbon and nitrogen) were used to describe and characterize community-wide aspects of trophic structure of soft-bottom muddy communities from the bay of Concarneau. In 2010, six stations located in three benthic communties (*Amphiura filiformis* sandy mud community, *Owenia fusiformis* muddy sand community and *Haploops* consolidated mud community) were seasonally sampled. More than one hundred species were analysed, allowing to precisely describe trophic structures of communities studied.

Using quantitative metrics derived on similar approaches from ecomorphology research, we used and modified indices such as the convex hull area (TA) occupied by species in a δ^{13}C - δ^{15}N biplot space as a representation of the total extent of trophic diversity within a food web, or the mean nearest neighbor distance (NND) among all species pairs as a measure of species packing within trophic niche space and an indication of redundancy in trophic structure. We used a randomization bootstrap routine to cope with differences in species diversity in each community.

The results showed if major changes in structure of the food web and in species trophic niches occurred across seasons. Moreover, the findings enabled to understand consequences of *Haploops* presence on the food web functioning.

Trophic structure of the Balearic Islands continental shelf and slope (western Mediterranean)

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We describe the trophic structure of three different assemblages, on the shelf (250 m) and the slope (650 and 850 m) off the Balearic Islands (western Mediterranean). A wide range of taxa (83 species) of benthic, pelagic and bentho-pelagic defined *a priori* were analysed at two locations with contrasting water masses and benthic and mesopelagic assemblages, to the north (Sóller) and south (Cabrera) of Mallorca.

The *a priori* hypothesis was that the food web structure as indicated by δ^{15}N and δ^{13}C data differs among depths and between locations. Mean species δ^{15}N signatures ranged from 3.67‰ for *Pyrosoma atlanticum* to 12.44‰ for *Nezumia aequalis*. Mean δ^{13}C ranged from -21.8‰ for *Ophiura* spp. to -14.02‰ for *Gryphus vitreus* with the latter species consistently occuring as an outlier. δ^{15}N and δ^{13}C were frequently strongly positively correlated with each other, indicative of single production sources sustaining all the marine food webs, and ultimately based on plankton.

A micro-meso zooplankton baseline exhibited δ^{15}N and δ^{13}C differences between the locations. These were reflected in mean δ^{15}N and δ^{13}C of macroinvertebrate and fish species present at both locations (shelf 18 species, upper slope 13 species, mid-slope 17 species). Trophic level of particular species based on δ^{15}N and zooplankton baseline varied with depth; longer food chains were indicated for the deepest slope assemblages. Four trophic levels were present at all depths and the majority of organisms sampled were at the third trophic level. Data dispersion as indicated by convex hull parameters shows overall structural similarities between locations. Broad isotopic differences between benthic and pelagic species indicated somewhat distinct food webs with bentho-pelagic species intermediate between them.

Trophic web structure and seasonality of slope megafauna of the NW Mediterranean; relationship with available food sources.

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Temporal changes in δ^{13}C and δ^{15}N isotopic composition of deep-sea benthic-boundary layer megafauna (decapods and fishes), macrofauna (infauna, suprabenthos and zooplankton) and primary producers were studied on a seasonal basis at bathyal depths (at 600-800 m depth) off Catalan coasts, NW Mediterranean. A wide range of sedimentary organic compounds (e.g. total lipids, total organic carbon, phytoplanktonic pigments) were analysed on the same seasonal basis. Main segregation in the megafaunal community was observed between the two taxa under analyses, fishes and decapods, the former usually with higher trophic levels and more depleted δ^{13}C. Within each taxocenosis, main structuration was function of both the position of each predator along the benthos–plankton gradient, and of prey and predator size. Benthofagous species were located at the top of the trophic web while planktofagous species were at the other extreme. These results were strongly consistent with previous information on diets of species, and suggest development of different feeding strategies probably related to resource partitioning for food competition avoidance. Temporal changes in isotopic signatures of species were observed, most generalised pattern being of both δ^{13}C and δ^{15}N depletion from winter to spring and/or to summer and probably driven by changes in pelagic prey availability. In oligotrophic environments, seasonal changes in trophic guild in order to take advantage of particularly abundant prey have been documented. Increase in specific food sources shall increase overlap of resource use temporarily, causing changes in the ecological interactions among species. Nevertheless, almost species-specific strategies were observed, and community restructured gradually maintaining high levels of resource partitioning.

Strong $\delta^{15}N$ and $\delta^{13}C$ correlations observed in periods of water column homogeneity (February and April) indicate a single type of primary source material supporting deep-sea communities, likely marine snow derived from surface production. Weak correlations found in autumn imply several sources of OM, and may relate to advective fluxes in the study area. Total organic carbon and fluorescence above the bottom were explanatory variables for dynamics in isotopic signatures of benthivorous fishes and decapods. Total lipids, total chlorophylls and $\delta^{13}C$ of sediments were important for macroplankton feeders.

Environmental drivers of isotopic composition variability in deep-sea megafauna over mainland and insular slopes of the Balearic Basin (W Mediterranean)

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Stable carbon and nitrogen isotope signatures were determined for deep-sea benthopelagic species (fish, decapods and cephalopods) and other large invertebrates (echinoderms, sponges, jellyfish etc.) from two contrasting settings of the NW Mediterranean for trophic assessment. Samples for SIA were collected during an experimental trawl survey carried out in summer 2010, between 450 and 2200 m in the Catalan-Balearic basin encompassing stations located on the mainland slope (Catalonian coasts, hereafter named "mainland") and others on the insular slope (North of Mallorca, Balearic Archipelago, hereafter "insular"). Thus our main objective was to compare the isotopic composition of benthopelagic species and large invertebrates along two gradients: i) bathymetric, from 450 to 2200 m and ii) geographic, contrasting mainland *vs*. insular area. Simultaneously, environmental data were collected on surface production, near-bottom physical parameters, and elemental and isotopic composition of sediments. $\delta^{13}C$-$\delta^{15}N$ correlations were stronger for species inhabiting middle (1000-1300 m) and lower (1400-2200 m) slopes than for those from upper slope (450-690 m) at both sites, indicating that at higher depths mainly marine snow support marine communities, while at shallower depths more than one carbon sources occurred. Overall $\delta^{13}C$ and $\delta^{15}N$ values were always more enriched in species from mainland than from insular, although significant differences in the isotopic composition between the two areas were only observed on the upper slope (450-690 m). Among environmental/trophic variables, at mainland deep-sea communities were mainly driven by salinity, and chlorophyll *a* recorded on the bottom and gelatinous plankton biomass, while at insular turbidity, $\delta^{13}C$ in the sediments and euphausiids biomass were the best explanatory variables based on DISTLM models. However variances explained were quite low in both cases due to the complexity of Deep Sea trophic webs analyzed.

A comparative study of nutritional patterns among cold-seep and hydrothermal vent chemosynthetic communities in the deep Guaymas basin, Mexico

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Hydrothermal vents and cold-seeps are among the most recently discovered marine habitats. They sustain huge faunal densities and biomass, contrasting with the background deep-sea floor environment. These ecosystems mainly rely on primary production by microbial chemosynthesis using the chemicals present in the fluids such as methane and hydrogen sulphide. These extreme environments generally sustain low species diversity, and are dominated by highly specialised taxa that are either associated in endo- or ecto-symbiosis with bacteria or simply consume free-living chemolithotrophic microbes. However, cold seep benthic communities, located on continental margins, can also partly derive their diet from photosynthetically-derived material originating from the surface. Analyses of δ13C and δ15N signatures of animal tissues can be used to assess the relative importance of chemosynthetic vs. photosynthetic food sources in these ecoystems. Past studies have revealed a highly variable dependence on chemosynthetic food sources along different depth and chemical gradients. Diets and trophic levels have been identified in a number of studies, highlighting the presence of several food chains and variable number of trophic levels.

The present study is based on recent investigation of hydrothermal vent and cold-seep ecosystems located at 2000m depth in the Guaymas Basin, the deepest parts of the highly productive Gulf of California. These sites, separated by 60 miles, have been sampled by the submersible Nautile during the BIG cruise in 2010. Faunal similarities among both ecosystems likely favoured by geographic proximity and depth were revealed. To investigate trophic relationships and food source pathways, a total of 25 macro- and megafauna epibenthic species were sampled at cold seeps, 13 at hydrothermal vents and 9 at a reference site. Three biogenic habitats encountered both at seeps and vents were selected: microbial mats, vesicomyid bivalve clusters, and siboglinid polychaete (tubeworms) bushes.

Stable isotopic ratios (δ13C, δ15N) were estimated for species and sediment, as well as δ13C for methane from near bottom and pore-waters. We compared the relative contributions of chemosynthesis vs photosynthesis nutritional sources among taxa, biogenic habitats and ecosystems, and investigated differences in the different food webs in the light of environmental conditions.

Spatial differences in Southern Ocean hydrothermal vent food webs: influences of chemistry, microbiology and predation on trophodynamics.

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Hydrothermal vents are ephemeral habitats sustained by chemoautotrophic primary production. The newly discovered hydrothermal vents on the East Scotia Ridge (ESR), Southern Ocean, are the first to be explored in the Antarctic and lack the characteristic fauna of other oceans. Instead they are dominated by yeti crabs (*Kiwa* n. sp.), stalked barnacles (*Vulcanolepas* n. sp) and large peltospiroid gastropods (Peltospiroidea n. sp.). Samples were collected at venting sites (E2, E9) with contrasting vent fluid chemistries on the ESR. It was hypothesised that the combination of varying vent fluid chemistry and a new species assemblage would produce novel trophic interactions. Stable carbon, nitrogen and sulphur analysis was used to describe trophic interactions and identify potential energy sources. Peltospiroidea n. sp. had the lowest and similar $\delta^{13}C$ values at all sites, around -30.5‰, indicative of carbon fixed via the Calvin-Benson-Bassham (CBB) cycle. Similar $\delta^{13}C$ values among sites were in agreement with the single species of gamma-Proteobacteria housed within the gills. *Kiwa* n. sp. had the highest $\delta^{13}C$ values at each site, with large differences in $\delta^{13}C$ observed between E2 (-19.2‰) and E9 (-10.6‰). *Kiwa* $\delta^{13}C$ tracked that of its epibiont community attached to the setae on its ventral surface. At E9 *Kiwa* epibionts were dominated by epsilon-Proteobacteria and this in conjunction with heavier $\delta^{13}C$ values suggests carbon was fixed via the reductive tricarboxylic acid (rTCA) cycle. In contrast, the epibiont community at E2 was a mix of gamma- and epsilon-Proteobacteria, which may result in *Kiwa* n. sp. assimilating carbon fixed via the rTCA and CBB cycles. Site differences in carbon fixation pathways were traced into higher trophic levels e.g. to a sea star (Stichasteridae n. sp.) that predates on *Kiwa* n. sp. $\delta^{34}S$ values indicated that sponges and anemones at the periphery of E2 assimilated a proportion of photosynthetic primary production but this was not observed in vent fauna from E9. The differences in $\delta^{13}C$ and $\delta^{34}S$ values of vent fauna at E2 and E9 sites suggest possible differences in the relative contribution of photosynthetic primary production and chemoautotrophic carbon fixation via CBB and rTCA cycles to the hydrothermal vent food webs.

The role of chemosynthetic productivity within intertidal food webs at anthropogenic hydrogen sulfide seeps in Commencement Bay, Washington

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Organic pollution from wood waste produced by the lumber industry between 1869 and 1977 resulted in >30 feet of subsurface debris in Commencement Bay, Washington. Woodchip decomposition by sulfate-reducing bacteria generates a hydrogen sulfide (H_2S) rich environment, similar to the anoxic and H_2S-rich environments found at marine hydrothermal vents and cold methane seeps. The H_2S-rich intertidal areas support extensive mats of free-living chemoautotrophic bacteria that form on hard substrates, such as rocks and the carapaces of shore crabs (*Hemigrapsus oregonensis*) that live under the rocks. The food web dynamics within this unique micro-ecosystem are not well understood. We aimed to test whether shore crab presence in intertidal seep areas was driven by access to a novel food source (bacterial mats), or other factors such as physical habitat (shelter provided by unoccupied space under rocks). Carbon, nitrogen and sulfur stable isotope and elemental data, as well as fluorescence *in situ* hybridization analysis, revealed that crabs eat green algae in both control and seep sites, and consumption of bacteria appears to be incidental. Crab muscle $\delta^{34}S$ values at the seep sites were intermediate between the values of control site intertidal samples and seep bacterial filaments. The high concentration of sulfur in the bacteria (wt % = 80) suggests that even minimal bacterial intake can influence crab $\delta^{34}S$ values. Unlike crustaceans that persist in deeper marine H_2S-rich areas the shore crabs found at localized seeps in Commencement Bay do not derive substantial energy from chemosynthetic productivity. Additional behavioral research has shown that intertidal shore crabs will choose H_2S-rich water if shelter is available (and not present in a clean site), indicating that physical habitat is likely a limiting factor.

An overwhelming presence: $\delta^{13}C$ and $\delta^{15}N$ reveal the dominance of upwelling-derived C and N in Chilean subtidal benthic fishes.

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Chile is extremely diverse in terms of its geography, and the ecology and biogeochemistry of its marine zones. Although this natural variation represents an opportunity with regards to Chile's capacity to develop diverse fishery and aquaculture sectors, it also complicates the management of natural resource exploitation, as managers require locally-relevant information. This is particularly relevant in the north of Chile, where the marine ecosystems supporting wild-capture fisheries are strongly influenced by the offshore Humboldt Current. The strength of this influence varies both temporally, due to interannual variation in the strength of the El Niño-Southern Oscillation and spatially, due to the effect of local geographical features. This is manifested by marked spatiotemporal variation in the intensity of marine upwelling, resulting in significant temporal (interannual and seasonal) and spatial (regional and local) differences in the ecological processes and communities that support fisheries production.

Although northern Chile is famous for its large-scale pelagic fisheries, the majority of fishes consumed by human populations in the region are benthic and are associated with inshore sub-tidal rocky/macroalgal reefs. These localised, artisanal fisheries represent an important regional source of food and employment, and as such, require sustainable, science-based management. There is very little information regarding the basic ecological processes that support these ecosystems. For instance, they are typically treated as classical benthic systems, even though offshore production is of such a scale to make a significant contribution to inshore habitats.

We sampled coastal filter-feeding and grazing benthic invertebrates and benthic fishes from a series of locations spanning ca. 1000 km of the north Chilean coast in the Austral summer and winter of 2010. Benthic fishes had $\delta^{13}C$ and $\delta^{15}N$ characteristic of a phytoplankton-based foodweb, even though they were captured from inshore reefs dominated by benthic- and macroalgae. Furthermore, mixing models indicated that almost all (> 90%) fish production was associated with upwelling-derived pelagic C and N.

Our results reveal a pelagic subsidy of inshore habitats in the region of previously unknown proportions that necessitates new thinking in ecosystem management. Furthermore, our results provide another example of the power of stable isotope analysis to reveal cryptic energetic subsidies.

$\delta^{13}C$ and $\delta^{15}N$ ratios of two benthic organisms used along with other ecological indicators

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Coastal ecosystems exhibit complex spatio-temporal patterns due to their position at the interface between land and sea. This is particularly the case of temperate ecosystems where exploitation of coastal resources (fisheries and aquaculture) and intensive agricultural use of watersheds further complicate our understanding of their dynamics. Our objective was to determine the spatio-temporal dynamics of contrasted megatidal coastal ecosystems located at the same regional scale (i.e. under the same regional climate), but under different kinds of human pressure. For this purpose, we use two kinds of ecological indicators which were assessed over several years at 11 locations along the coast of the Cotentin peninsula (Normandy, France). A first set of hydrobiological variables (dissolved nutrients, Chl a, temperature, salinity, etc.) was measured fortnightly in the water column. A second set of variables were the carbon and nitrogen stable isotope ratios of two organisms. i) Isotope ratios of the adductor muscles of cultured *Crassostrea gigas* introduced every year were used to typify the bentho-pelagic coupling at each location. ii) Whole body of *Arenicola marina* was used to typify the sediment organic matter reservoir at some location. Food sources were also investigated using a mixing model with data on the isotopic composition of the food sources obtained previously. To identify which environmental variables played a significant role in determining the organism diet, the contributions of oyster food sources were combined with environmental variables in a canonical correspondence analysis (CCA). Isotopic values of *C. gigas* or *A. Marina* varied significantly between the different locations. The PCA distinguished two groups of coastal ecosystems that differed in their coastal hydrology, nutrient inputs, and the size of their respective watershed, irrespective of the year. In each zone, different spatial patterns in the measured variables were observed depending on the year showing that local impacts differed temporally. As revealed by CCA, food sources used by the oysters were mainly explained by salinity suggesting regional differences between ecosystems. On the west coast of the peninsula, climatic factors act in synergy with anthropogenic factors (i.e. nutrient enrichment) whereas on the east coast, climatic factors appear to be dampened by anthropogenic factors.

Trophic functioning of a temperate coastal ecosystem revealed by stable isotope analysis in oysters *Crassostrea gigas*

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The purpose of this study was to improve our knowledge of a temperate coastal ecosystem functioning (the Bay of Brest) through carbon and nitrogen stable isotope analysis of an intertidal suspension feeder. Thereby, we analyzed oyster muscles together with 3 potential food sources of the oyster *Crassostrea gigas* i.e. particular organic matter (POM), benthic biofilm and macroalgae along an estuarine/open sea gradient (19 stations). The contribution of each food source was investigated by SIAR analysis (Stable Isotope Analysis with R) which uses Bayesian probabilities together with measured isotopic data.

Nitrogen isotope ratios of oyster muscles decreased significantly along the sampling gradient (from 12.1‰ for the estuarine stations to 9.7‰ for the open sea stations). This result suggested that *C. gigas* muscles allowed to show anthropogenic pollution (such as nitrate input) bring to the Elorn water. Conversely, carbon isotopic ratios do not vary much (values between -20.0 and -18.2‰). A hierarchical clustering analysis discriminated 2 major stations groups (estuarine *vs* open-sea stations). SIAR supported these observations indicating that oysters mainly fed on benthic biofilm and biofilm contribution increased along the estuarine/open sea gradient, 30% to 71% in the mean. Macroalgae contribution in *C. gigas* diet follows opposite trend: decline of 41% to 18% in the mean. POM contribution is variable through this gradient. Finally, oysters were good candidates to investigate the functioning of a temperate ecosystem at the intertidal level concerning both the suspension-feeder diet and the anthropic influences.

The mutual mucus ingestion hypothesis. Stable isotope evidence for convergent resource use in intertidal grazing gastropods within experimental microcosms.

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According to traditional food web and ecological theory, niche differentiation and complementary resource use are mechanisms by which species are able to coexist by reducing competition for available resources. In this study a manipulative experimental approach was used to examine whether species coexistence induces dietary niche differentiation and partitioning of available food resources in a coastal marine environment. Three species of grazing gastropod found on British rocky shores (*Littorina littorea, Patella vulgata* and *Patella depressa*) were held under differing conditions in experimental cages.

Three main hypotheses were evaluated using natural abundance stable carbon and nitrogen isotope analyses:

1. The diet of caged animals, forced to forage only on biofilms, differs from that of uncaged conspecifics free to forage naturally.
2. The diet of animals caged with interspecific competitors shows dietary divergence, differing from that of animals in single-species treatments.
3. Food availability influences diet in grazing gastropods and that interspecific competition further affects food choice.

Animals were held in experimental cages for a period of six months. Species number and food availability were manipulated to test the articulated hypotheses. Stable carbon and nitrogen isotope analyses were used to examine grazer diets. The results showed that food availability and species identity were important factors controlling diet choice in intertidal grazing gastropods but no evidence for niche differentiation or divergent resource use was observed. In fact, *L. littorea* and *P. vulgata* caged together on bare rock exhibited dietary convergence: the diets of the two species were more similar when caged together than when caged separately. A number of possible explanations for this interesting phenomenon were proposed including the 'mutual mucus ingestion hypothesis'.

Determination of the trophic level of *Megathura crenulata* (Sowerby, 1825) using the isotopic signal of δ^{13}C and δ^{15}N.

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Megathura crenulata is a native gastropod of the rocky shores from California, USA to Baja California Sur, Mexico. This species has economic and pharmacological importance because its hemocyanin is used in the treatment of some types of cancer, allergy and immunosuppression. It has been reported that in nature is a specialist predator that feeds on seaweeds and tunicates, mainly. We study the major components of *M. crenulata* food and its trophic level using the isotopic signal of δ^{13}C and δ^{15}N. Gastropods and food sources (*Eisenia arborea*, *Macrocystis pyrifera*, *Gelidium robustum*, articulated coralline algal mats and seagrass *Phyllospadix torreyi*) were collected in Bahia Tortugas, Baja California Sur, Mexico, in 2009 and 2010. Mean isotopic signatures of the tunicates were -9.38 ‰ (± 0.55) for the δ^{13}C and 8.18 ‰ (± 1.11) for the δ^{15}N. In the case of macroalgae, the overall average for δ^{13}C and δ^{15}N of *M. pyrifera* were -15.26 ‰ (± 0.11) and 9.78 ‰ (± 1.68), for *E. arborea* -19.78 ‰ (± 0.68) and 8.95 ‰ (± 0.46), for coralline algae -11.54 ‰ (± 0.21) and 10.55 ‰ (± 0.58), for *G. robustum* -22.31 ‰ (± 0.85) and 8.35 ‰ (± 1.68). In the case of *P. torreyi*, the overall average was -18.15 ‰ (± 0.52) for δ^{13}C and 8.09 ‰ (± 1.83) for δ^{15}N. The mixing models showed that the contributions of food sources vary by year and sampling site. Overall gastropod isotope signal reflects mainly the isotopic signature of *G. robustum* which contributes 24.6% of the signal while the tunicate contributes a 7.6%. The calculated trophic level of *M. crenulata* was 3.25.

Regional scale isotopic observations: integrating stable isotope data to long-term environmental surveys

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The increasing awareness on global changes affecting the biosphere has recently led to an increasing demand of long-term data to better understand the effects of man-induced disturbances on natural ecosystems. In Brittany, the program REBENT (Réseau Benthique, Benthic Network) aims, on a yearly basis, to characterize the evolution of macrobenthic communities associated to a variety of coastal habitats (intertidal and subtidal fine sands, intertidal and subtidal rocky habitats, maerl beds, seagrass beds). Although providing precious data on the structural evolution of coastal communities facing global changes, complementary measurements could help identify the actual factors that may lead to the observed changes. In the past 15 years, stable isotopes have proven to be powerful tools to early detect anthropogenic modifications of the environment (eutrophication, atmospheric CO_2 increase). A new program, concurrent to and completing the REBENT, aiming at following long-term evolution of stable isotope ratios ($\delta^{13}C$, $\delta^{15}N$) on selected macrobenthic species, has therefore started in 2012. Different species, belonging to various trophic groups (i.e. suspension-feeders, deposit-feeders, carnivores) will be sampled on a yearly basis at 12 sampling stations (maerl beds and subtidal fine sands) around Brittany. This poster will present the general framework of this project and some preliminary results for the first year of this survey. These data will be compared with previous ones acquired in the area, and will represent a basis for the future investigation of long term variability of macrobenhtic fauna's stable isotope ratios.

Habitat-related diet of macrofauna consumers in intertidal areas

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Seagrasses increase the availability and diversity of food sources, thereby changing trophic structure of their associated communities as well as the ecosystem goods and services regulated by the food web. We studied the benthic trophic structure of the eelgrass *Zostera noltii* and of bare sediments using stable isotopes ($\delta^{13}C$ and $\delta^{15}N$). We expected that (i) there would be differences in the isotopic signatures between the consumers inhabiting the bare sediments and the eelgrass and that (ii) such differences would be related to changes in the contribution of primary producers and detritus to their diet. Primary producers and detritus showed distinct $\delta^{13}C$ signatures, which allowed for a powerful discrimination of carbon sources. Our data suggested that detritus of *Z. noltii* were of limited importance to macrofauna consumers. Microphytobenthos was a major source of nutrition for the gastropod *H. ulvae* regardless of habitat. Diet composition of *S. plana* varied among habitats, reflecting the availability of food in the surroundings, and between juveniles and adults specimens reflecting mostly feeding shifts from microphytobenthos to phytoplankton. Green macroalgae and *Z. noltii* detritus were preferentially used as food sources by the grazer *Littorina littorea*. The polychaets *Heteromastus filiformis*, *Hediste diversicolor, Tharix marioni* and oligochaetes relied mainly on macroalgae and detritus in the *Zostera* habitat. At the bare sediments, microphytobenthos, phytoplankton and organic matter appeared to contribute in the same proportion to the annelids diet. Overall, macrofauna in theses systems relied on detritus and microphytobenthos as dominant food resources, and dietary contributions from primary producers varied among species and habitats.

Regional scale isotopic observations: integrating stable isotope data to long-term environmental surveys

Poster session J
“Ecology in the Oceans”

J1	Anthony BICKNELL	Identifying potential dispersal mechanisms with SIA and a multi-source mixing model: individual analysis of a highly pelagic seabird.
J2	Alex BOND	Linking at-sea mortality of Flesh-footed Shearwaters (*Puffinus carneipes*) to breeding colonies of origin using multiple biochemical markers
J3	Patricia MANCINI	Using stable isotope analysis to establish trophic relationships among seabirds of Brazilian oceanic islands
J4	Dorothée KOPP	Trophic relationships in the eastern English Channel: how to simplify food web structure description for trophic niche determination?
J5	Pepe ESPINOZA	Revisiting the trophic structure of an ecosystem constrained by an intense oxygen minimum zone, the Northern Humboldt Current system
J6	Monica YANIRA RODRIGUEZ	Stable isotope $\delta^{13}C$ and $\delta^{15}N$ as indicators of isotopic enrichment by denitrification in an antiestuarine ecosystem: the upper gulf of California
J7	Ryan WOODLAND	Trophic assimilation and fate of diazotrophic N fixed by Nodularia spumigena in an estuarine planktonic food web
J8	Svenja KRUSE	Trophic position and interactions between the tunicate Salpa thompsoni and the amphipod Themisto gaudichaudii in the Southern Ocean: compound-specific nitrogen isotope analysis
J9	Craig LONGMORE	Combined isotopic and genetic analyses reveal population structure, habitat use and life-history of two deep-sea teleosts in the North Atlantic
J10	William REID	Intra-population variation in stable isotope values explained by body size for Rockall Trough deep-sea fish

Identifying potential dispersal mechanisms with SIA and a multi-source mixing model: individual analysis of a highly pelagic seabird.

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Highly fragmented populations are reliant upon dispersal to maintain demographic and genetic connectivity, and isolation of these subpopulations can make them particularly vulnerable to extinction. Dispersal between populations can be directly identified using tagging and tracking techniques, however these approaches are unsuitable for some species due to their size, cryptic nature and/or low encounter rate. Therefore indirect methods are required to characterise dispersal behaviour in these species. Multi-source stable isotope mixing models are typically used for dietary reconstruction (Inger and Bearhop, 2008), but here we adapt the method to estimate the contribution of isotopically distinct regions (sources) within an individual's tissue (mixture) to identify recent regional movement and a potential dispersal mechanism in a pelagic seabird. In combination with stable isotope analysis of baseline primary consumers, the $\delta^{13}C$ and $\delta^{15}N$ values of red blood cells from breeding and immature (non-breeding) Leach's storm-petrel *Oceanodroma leucorhoa* were incorporated into the SIAR multi-isotope mixing model (Parnell et al., 2010) to identify changes in individual foraging location during the breeding period. The colonial breeding behaviour of this seabird naturally creates a fragmented north Atlantic population but recent genetic analysis suggests high gene flow among colonies (Bicknell et al., In press). However, the source of this connectivity had not been established. The ~3% of immature birds found to have model estimates that clearly indicate recent movement from other Atlantic regions indicate prospecting at distant colonies and supports the theory that natal dispersal is an important dispersal mechanism in this seabird. A clear benefit of the mixing model approach is the analysis of isotope values, and therefore movement, of individuals rather than a traditional group average analysis, which in this case would not have identified this important behaviour.

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Linking at-sea mortality of Flesh-footed Shearwaters (*Puffinus carneipes*) to breeding colonies of origin using multiple biochemical markers

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Stable isotopes are being used more and more to assign migratory animals of unknown provenance to an origin, but to date, the vast majority of avian assignment studies have used terrestrial species and $\delta^{2}H$. In the marine environment, however, there is generally less spatial variability in isotope values, and a poorer understanding of what drives this variation. Combining stable isotope analysis ($\delta^{13}C$, $\delta^{15}N$) with analysis of spatially variable trace elements could therefore improve the assignment of migratory marine organisms to a breeding colony of origin.

An emerging issue in wildlife conservation is the ability to link mortality incidents (which for seabirds typically occur at sea and are thus difficult to quantify) with observed demographic changes at the breeding colony. Recent advances in modelling and biochemical techniques have allowed wildlife managers to associate mortalities of unknown provenance to their breeding site of origin. Establishing the linkage between mortalities and breeding origins can ensure conservation actions can be targeted at those colonies that are most heavily impacted by the source of mortality. Flesh-footed Shearwaters (*Puffinus carneipes*) are trans-equatorial migrants, breeding in colonies in New Zealand's North Island, on Lord Howe Island in the Tasman Sea, on islands in South and Western Australia, and on

Île Saint-Paul in the Indian Ocean, and wintering in the North Pacific and North Indian Oceans. Their at-sea distribution overlaps significantly with fishing operations in Australian and international waters, where they are subject to high levels of fisheries bycatch. At their largest colony (Lord Howe Island), shearwater populations have declined by 1% per year from 1978-2002, and 3% per year from 2003-present, in part because of mortality associated with fishing bycatch in the North Pacific.

We combined analysis of stable C and N isotopes with geographically varying trace element concentrations in feathers from adults breeding across the species' range to identify colony-specific criteria against which birds of unknown origin from fisheries bycatch could be assigned. We show the advantages of combining stable isotope with trace element data in assigning marine birds to a colony of origin, and estimate the magnitude of at-sea mortality for this declining species.

Using stable isotope analysis to establish trophic relationships among seabirds of Brazilian oceanic islands

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Tropical marine ecosystems have low productivity, negligible seasonality and prey are patchily distributed. Resource partitioning among seabirds, whether by diet or foraging grounds, is presumably a major factor allowing several species to coexist. We used δ^{13}C and δ^{15}N analysis of seabird blood and prey muscle samples to investigate how seabirds partition the oceanic resources around tropical Atlantic Ocean islands off Brazil during 2007 to 2012. Seabird communities breeding in Brazilian oceanic islands are composed of 12 species from the orders Procellariiformes, Pelecaniformes and Charadriiformes. Preliminary results are presented for five seabird species breeding at Trindade Island (Brown Noddy *Anous stolidus,* White Tern *Gygis alba,* Sooty Tern *Onychoprion fuscatus,* Trindade Petrel *Pterodroma arminjoniana* and Masked Booby *Sula dactylatra*). There was no isotopic segregation by age except by juveniles of the petrel for δ^{13}C. Petrels had higher δ^{15}N values (average 11.3 ± 0.59‰ SD) than other species, probably because they consume high trophic level squid. Boobies which have body mass 10 times that of Sooty Terns and Brown Noddy, did not differ in δ^{15}N. However, all species differed from the small White Tern that feeds on smaller fish and squids close to the island. The latter three species overlapped in their pelagic foraging areas, as shown by the narrow range of δ^{13}C (-17.3 ± 0.12‰ to -17.3 ± 0.11‰). Boobies had higher δ^{13}C (-16.5 ± 0.11‰) than other seabirds, possibly due differences in foraging area. Results from mixing models (SIAR) will be used to determine the contribution of various prey to species' diets.

Trophic relationships in the eastern English Channel: how to simplify food web structure description for trophic niche determination?

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Determining the organisation of natural communities as well as their ability to face environmental changes are at the core of many ecological studies. In that aim, many studies tried to describe trophic interactions between species and quantify their strength in ecological networks, the multiplicity of trophic links being assumed to promote the stability and persistence of communities. In marine ecosystems, the study of trophic relationships has extensively benefited from the development of analytical tools like stable isotopes analysis (SIA) as dietary tracers. Particularly, δ^{15}N values are useful in estimating intra- and inter-specific trophic level variations while δ^{13}C values will indicate variation in the source of organic matter. Here, we proposed to use stable isotope data to establish relevant functional groups in order to simplify food web description and to further determine species' isotopic and trophic niche. SIA signatures of marine species from the eastern English Channel were used as a case study. Particulate organic matter, zooplankton, invertebrates and fish were collected during two scientific surveys conducted in October 2009 and January 2010 in the area. Trophic positions were determined using stable isotopes of δ^{15}N and δ^{13}C and were then aggregated into functional groups using clustering analysis coupled to a bootstrap procedure. The food web of the eastern English Channel is characterized by 10 functional groups: one group of primary producers, 4 groups of primary consumers, and 5 groups of higher-order consumers. It is composed of two main trophic pathways, one pelagic and one benthic, and forms a continuum of four tropic levels. This procedure allows us to produce a simplified description of the food web structure that could be directly used as input in trophic modelling and isotopic niche determination (i.e. SIAR mixing model and SIBER niche width calculation) for which association of species were necessary to reduce the number of potential source pools and to constrain model outputs.

Revisiting the trophic structure of an ecosystem constrained by an intense oxygen minimum zone, the Northern Humboldt Current system

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The northern Humboldt Current system (NHCS) off Peru produces more fish per unit area than any other region in the world oceans. This system is subject to the world largest fluctuations in climate, ecosystem and fisheries and encompasses an intense and shallow oxygen minimum zone (OMZ). However, the secret of the NHCS fish productivity has still not been elucidated. An important step was the determination that the dominant forage fish, anchovy (*Engraulis ringens*), prey on much higher trophic level than previously supposed (macrozooplankton instead of phytoplankton-mesozooplankton). This finding, based on stomach content analyses, challenged current understanding of anchovy position in the foodweb, and more generally the functioning and trophic models of this system. To provide a new vision of the NHCS trophic structure, we analysed carbon and nitrogen stable isotopes of >550 individuals of different trophic levels (mainly zooplankton, squat lobster, mesopelagic fish, anchovy, jumbo squid and seabirds) collected during 2008-2011. Results show that variable anoxic conditions along the Peruvian coast contribute to remarkable latitudinal gradients in the δ^{15}N baseline level (nearly 8‰ δ^{15}N difference from 3ºS-18ºS) that are reflected in organisms at higher trophic levels. A clear cross-shore gradient appeared in the δ^{13}C baseline but also in the ecosystem structure with for instance squat lobster (*Pleuroncodes monodon*) distributed close to the coast while the jumbo squid (*Dosidicus gigas*) predate more offshore. Results also confirm the recent results on anchovy trophic level. Interestingly we show that the squat lobster, that became very abundant in the system since the mid 1990s, has a trophic level similar or higher than anchovy. This species is thus a probable competitor of anchovy and even a predator of anchovy first life stages. All species showed a high variability in δ^{15}N values even when the OMZ and size effects were removed indicating a high plasticity of these species that needs to cope with the world highest climate variability. This study proposes a comprehensive vision of the trophic structure in the NHCS that will provide a new basis to understand its functioning.

Stable isotope of δ^{13}C and δ^{15}N as indicators of isotopic enrichment by denitrification in an antiestuarine ecosystem: the upper Gulf of California

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The stable isotopes analysis of carbon and nitrogen on top predators allows us to use them as monitors of the ecosystem. In this study we propose the use of δ^{13}C and δ^{15}N signals in order to accomplish two main objectives: 1) To determine the cause of δ^{15}N enrichment in the Upper Gulf of California, 2) To define the influence of regenerated productivity on the trophic web of the vaquita marina (*Phocoena sinus*). To achieve this we took sediment samples (n= 59), we also performed an isotopic analysis on skulls of vaquita marina (n = 31) and several components from its ecosystem. The obtained results show high δ^{15}N values in *P. sinus* (21.0 ± 0.8‰) in comparison to other marine mammals from different areas in the Gulf of California and the Pacific Ocean, which show a range of values from 13.3‰ to 19.4‰. This enrichment is also observed in fishes, gastropods, bivalves and zooplankton from the west area (20.3 ± 1.6‰, 19.9 ± 0.3‰, 15.2 ± 0.4‰, 15.9 ± 1.2‰, respectively) and the east area (16.9 ± 2.0‰, 13.5 ± 1.8‰, 12.1 ± 0.9‰, 14.8 ± 1.0‰, respectively). The mentioned differences are observed from the baseline (sediment) of the trophic web, finding a direct relationship (r^2=0.52 $p<0.05$) between two granulometric provinces, given by the cluster analysis, with the $\delta^{15}N$ signals, having the highest enrichment for the west region (10.7 ± 2.0‰), that presented a high predominance on silt-clay, in contrast to the east region, that presented fine sand (7.2 ± 2.3‰). In terms of $\delta^{13}C$ the highest values in sediment were obtained for the coastal zone (-16.4 ± 3.8‰), in contrast to the east (-21.2 ± 4.4‰) and the west area (-21.4 ± 3.4‰). The found differences especially for $\delta^{15}N$ and slightly for $\delta^{13}C$ are the result of four main factors: 1) The hydrography of the region, 2) The influx of organic matter, 3) The denitrification processes that take place in the west region and 4) The predominant primary productivity (phytoplankton and macrophyta).

Trophic assimilation and fate of diazotrophic N fixed by *Nodularia spumigena* in an estuarine planktonic food web

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Blooms of the toxic diazotrophic cyanobacterium *Nodularia spumigena* have caused ecological and economic disruption in coastal ecosystems. Due to their ability to fix atmospheric N_2, *Nodularia* do not rely on the availability of dissolved inorganic nitrogen forms to stimulate growth; however, the light $\delta^{15}N$ signature of atmospheric N_2 and lack of significant fractionation during uptake by *Nodularia* provides a convenient isotopic ‘tag’ for tracing the fate of *Nodularia* biomass in aquatic food webs. We investigated the assimilation and fate of atmospheric nitrogen fixed during a *Nodularia* bloom in the planktonic food web of the estuarine Gippsland Lakes (Australia). *Nodularia* and zooplankton were sampled at multiple locations from the surface at 2-week intervals before, during, and after a *Nodularia* bloom event during the austral summer of 2011-12. Isotopic evidence clearly showed that atmospheric N_2fixed by *Nodularia* was eventually assimilated by multiple size-classes of zooplankton. Concurrent laboratory incubations of the phytoplankton community indicated that *Nodularia*: 1) were not heavily grazed; and 2) were phosphorus-limited during the initial and peak stages of the bloom. Conversely, diatoms experienced heavy grazing and were nitrogen-limited during the same period. A diatom bloom, closely following the cessation of the *Nodularia* bloom, suggests a mechanism whereby *Nodularia* blooms can stimulate secondary production via release and recycling of diazotrophic nitrogen into the planktonic food. The routing of nitrogen fixed by *Nodularia* through other phytoplankton (e.g., diatoms), rather than directed grazing, could explain the light $\delta^{15}N$ of the zooplankton observed during this study.

Trophic position and interactions between the tunicate *Salpa thompsoni* and the amphipod *Themisto gaudichaudii* in the Southern Ocean: compound-specific nitrogen isotope analysis

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The pelagic tunicate *Salpa thompsoni* and the hyperiid amphipod *Themisto gaudichaudii* are two conspicuous macrozooplankton species that occur in high numbers in the Polar Frontal Zone of the Southern Ocean. The trophic position of both species, and particularly that of *Themisto*, is not however clearly understood. While *S. thompsoni* is often considered to represent the first consumer level feeding directly on phytoplankton, bulk stable isotope measurements on *T. gaudichaudii* have generally shown highly variable $\delta^{15}N$ signatures, suggesting a highly opportunistic feeding behaviour and flexible trophic level. Recent observations of both species’ population dynamics near the Polar Front during austral summer 2012 suggest that in some instances *T. gaudichaudii* may control *S. thompsoni* populations through predation, thus preventing the development of the “salp bloom”. To more closely assess the trophic dynamics of *S. thompsoni* and *T. gaudichaudii*, we analysed the nitrogen isotopes ($\delta^{15}N$) of their amino acids by gas chromatography/combustion/isotope ratio mass spectrometry (GC/C/IRMS). The trophic positions of both species in the Southern Ocean food web as well as their potential trophic interactions are discussed by comparing these compound-specific stable isotope measurements with bulk values. In addition, the trophic niche differences between the two forms of *Themisto*, *T. gaudichaudi compressa* and *T. gaudichaudi bispinosa* are examined.

Combined isotopic and genetic analyses reveal population structure, habitat use and life-history of two deep-sea teleosts in the North Atlantic

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The study of the chemical characteristics of otoliths is quickly establishing itself as a fundamental tool in fish stock identification. Specifically, the isotopic composition of otolith aragonite can be used to reveal fish location (water temperature) retrospectively and thus infer ontogenetic migratory behaviour.

Deep sea fish are difficult to observe directly, but are increasingly threatened through vertical expansion of fishing and other industrial activities. Information about basic biological characteristics of deep sea fish such as ontogenetic migrations and population structure and connectivity are urgently needed to evaluate their susceptibility to ecosystem perturbation. In this study, the isotopic composition of oxygen and carbon was assessed in the otoliths of two highly exploited deep sea fish (Roundnose grenadier & Black scabbardfish). Otolith isotope analyses were conducted in parallel with trace element and micro-satellite DNA analyses to assess patterns of spatial and temporal population segregation, movements and habitat use in the NE Atlantic.

For both species, stable isotope analysis (SIA) revealed a consistent pattern of elevation of both $\delta^{18}O$ and $\delta^{13}C$ values with age. Analysis of $\delta^{18}O$ values at larval, mid and adult life stages in the roundnose grenadier revealed significant differences between and within life stages, suggesting that this species conducts consistent ontogenetic depth migrations, and the population is comprised of geographically distinct population units that persist throughout their life-history. By contrast, $\delta^{18}O$ values in the black scabbardfish revealed weak geographic separation at each life stage. Absolute $\delta^{18}O$ values in the juvenile portions of black scabbardfish otoliths collected from adults from a wide geographic range indicate extensive lateral migrations and common water conditions during larval growth. Both observations imply a relatively high degree of population connectivity. The stable isotope results for both species are corroborated by both otolith microchemical analysis and microsatellite DNA, and provide behavioural explanations for the genetic results.

Collectively, the results of the present study contribute new information on the stock structure and life histories of the selected deep-sea species providing a strong foundation for improved management of the respective species fisheries.

Intra-population variation in stable isotope values explained by body size for Rockall Trough deep-sea fish

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Understanding the role of body size within a community and how this affects food web structure has been a long-term theme in ecology and is now recognised as pertinent in successful fisheries management. Stable carbon and nitrogen isotopes are frequently utilised to elucidate trophodynamics, providing information on energy source (carbon) and trophic position (TP) (nitrogen). Intra-population variation in TP is often positively correlated with individual body size in shallow water fish. This is the main descriptor of stable nitrogen isotope variability and in conjunction with changes in stable carbon isotope values can describe whether perceived increases in TP are in fact changes in energy source or habitat use. But investigations into these relationships are currently lacking in deep-sea fish. Rockall Trough (Northeast Atlantic) demersal fish were collected along the continental slope and Rosemary Bank 1000 m contour. Stable isotope analysis (SIA) was undertaken to examine the role of body size in intra-population trophodynamics on species which covered over 30% of their maximum length range. Body size accounted for intra-population variability in stable nitrogen isotopes in all species. However, not all relationships were linear. In some species this was due to size-based trends in stable carbon isotopes, which indicated a size-dependent switch in habitat utilisation, while in other species stable nitrogen isotope values stopped increasing at a certain body size. Gape limitation, prey availability and competition are potential causes for the variability in body-size stable isotope trends, reflecting differences in foraging behaviour and diet among species and at different life history stages within species. SIA presents compelling evidence that intra-population trophic roles are strongly size dependant and vary between species of deep-sea fish. The information becomes important when trying to understand community dynamics as size-spectra and predator-prey interactions change as a result of fishing.

Poster session K
“Human Impacts”

K1	Irene FERNANDEZ	Unexpected δ^{13}CO2 atmospheric changes recently imprinted in tree-ring isotope records from temperate Atlantic ecosystems
K2	Samo TAMŠE	Tracing sources of nitrate from agriculture in groundwater
K3	Ann-Lise NORMAN	A Slow Burn: Ecosystem Acidification and its effect on the Castle River in Southern Alberta, Canada using Boron, Sulfur and Oxygen Isotopes
K4	Philipp SCHUBERT	Isotopic signatures of eelgrass (*Zostera marina* L.) as bioindicator of anthropogenic nutrient input
K5	Inés G. VIANA	Stable nitrogen isotopes in coastal macroalgae: biogeographic and anthropogenic variability
K6	M.Gloria PEREIRA	Can stable isotope signatures explain changes in POP concentrations in UK gannet (*Morus bassanus*) eggs?
K7	Igor EULAERS	Combined nestling feather analysis for stable isotopes (δ^{13}C and δ^{15}N) and persistent organic pollutants reveals ecosystem-dependent bioaccumulation patterns in subarctic predatory birds
K8	Thais N. CORBISIER	Biomagnification of mercury in the trophic web off Baixada Santista continental shelf, SE Brazil

Unexpected δ^{13}CO2 atmospheric changes recently imprinted in tree-ring isotope records from temperate Atlantic ecosystems

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Information about the evolution of the chemical composition of the Earth's atmosphere during the last decades can be especially relevant to adopt appropriate guidelines for climate change strategies. It is well known that the atmospheric CO2-C fixed by trees during photosynthesis remains within the growing tree-ring tissues, providing a proper chronological fingerprint of the momentary atmospheric composition. Also, it is widely accepted that accurate C isotope natural abundance determinations are critical to track atmospheric C, since competently determined 13C changes can be powerful indicators of biochemical transformations. Although isotopic dendrochronology can successfully attest long-term atmospheric trends, such us the 13C Suess effect, C-isotope variability among individual trees often frustrated the exact interpretation of 13C atmospheric changes from tree-rings at short or medium time-scales. However, is this research we demonstrate that climatic and genetic dendrochronological variability can be methodologically absorbed, hence allowing the deconvolution of past anthropogenic impacts in order to improve the accuracy of atmospheric global warming models. By providing a reliable mirror of 13C atmospheric changes for the last quarter of the twentieth century, our isotopic assessment of coniferous growing-rings from temperate ecosystems in the SW of Europe was not only useful to illustrates the resilience capacity of the Earth's system but also to reveal a consistent temporary interruption of the air 13C declining trend during the mid-nineties that matched the brief decrease of global CO2 emissions during that the last decade of the 20th century.

Tracing sources of nitrate from agriculture in groundwater

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The potential health hazards posed by nitrates from agricultural activity in drinking water supplies encourage us to find new ways to study the mobility of nitrate in shallow hydrological systems. Nitrogen and oxygen isotope (δ^{15}N, δ^{18}O) data can provide information about nitrate sources and sinks in groundwater. Our research was performed at 7 wells which represent the drinking water supply in the Ljubljana region. Water samples were taken monthly through one hydrological cycle in 2010 and 2011. The δ^{18}O and δD values show that the main source of groundwater is precipitation mixed with a small amount of upstream river water, and that a significant recharge between groundwater and river water occurs. Near the Sava river bed and in the central pumping station of Ljubljana city, more than 90% of the groundwater comes from the river, while in wells situated further from the pumping station the proportion of river water decreases to as much as 19%. The δ^{15}N values of nitrate ranged between 1.4‰ and 9.7‰, while δ^{18}O values in nitrate ranged from 6.3‰ to 34.6‰. The strong correspondence of δ^{15}N and δ^{18}O values during the changing river flow conditions suggests that the groundwater nitrate composition could be explained by varying proportions of three end-member sources, one dominated by atmospheric nitrate and the other one by a well-mixed combination of sewage and other nitrate sources. Atmospheric nitrate represented between 10 to 40% of groundwater nitrate, depending on the location of the well. Wells located closer to the Sava River were less polluted and almost 50% of nitrate was from pristine soils.

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A Slow Burn: Ecosystem Acidification and its effect on the Castle River in Southern Alberta, Canada using Boron, Sulfur and Oxygen Isotopes

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Quantitative measures to assess pollutant deposition on the environment, and the ability to separate current from long-term effects, are necessary to create a scientific basis for decisions on current and future land use practices. Long-term acid deposition and its effect on sulfur and boron distributions in a major waterway within a relatively remote ecosystem is examined using stable isotopes. Spatial and temporal variations recorded in vegetation (moss, tree needles, tree cores) as well as air, soil and water were used to assess environmental impacts within a 60 x 60 km region encompassing an area of complex topography neighbouring the Rocky Mountains of southern Alberta. This multi-receptor approach was compared to sulfur deposition based on atmospheric deposition modeling using the Lagrangian-Gaussian puff California Puff model (CALPUFF). Short and long-term impacts from industrial sulfur emissions on the eastern slopes of the Rocky Mountains north of Waterton National Park in southern Alberta, Canada will be discussed.

Isotopic signatures of eelgrass (*Zostera marina* L.) as bioindicator of anthropogenic nutrient input

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Eutrophication is a global problem for coastal ecosystems. An important driver of this process is the input of anthropogenic nitrogen from human sewage. However, quantifying the contribution of this nitrogen source to eutrophication is hindered by its high variability in the water column and quick uptake by phytoplankton and filamentous macroalgae. Recently, stable isotope analysis (SIA) of long-lived macrophytes has emerged as useful tool to provide time-integrated quantifications of sewage derived nutrient inputs, exploiting the high $\delta^{15}N$ of nitrogen from sewage in the environment.

Our goal here was to establish the viability of the widely distributed eelgrass *Zostera marina* in the western Baltic Sea sampled by high resolution spatial sampling (instead of predefined locations) for spatial screens of sewage derived anthropogenic nitrogen inputs. Assuming a positive test outcome, our ultimate aim was to use SIA of an existing eelgrass sample library covering >600 locations along 400 km of coastline to provide a coastal-wide screen of such inputs.

Heiligenhafen Bay, a small bay inside a spit (Graswarder) with an important sewage outfall and well described current patterns, served for the initial assessment. Eelgrass shoots were sampled in 500 m intervals along a continuous transect parallel to the shore covering 6 km upstream and 6 km downstream of the outfall, and along 7 additional transects perpendicular to the shore (total grid space ~40 km^2). SIA ($\delta^{13}C$, and in particular $\delta^{15}N$) values were then used to predict baywide sewage nutrient availability.

Predicted and expected availability agreed very well. Specifically, $\delta^{15}N$ values were low upstream of the outfall, with a sharp, highly significant increase near the outfall, followed by a gradual and significant decrease back over the 6 km downstream. Corresponding clines in $\delta^{13}C$ and C/N ratios pointed to the biological relevance of sewage nutrient availability. Based on this test, we are currently proceeding with the full-scale SIA of Kiel Bight eelgrass libraries, and will present conclusions of this screen for the first time at this conference. Based on results to date, we conclude that high resolution eelgrass sampling coupled with SIA has high potential as spatial bioindicator of sewage derived nitrogen inputs in the Baltic Sea.

Stable nitrogen isotopes in coastal macroalgae: biogeographic and anthropogenic variability

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Coastal areas are exposed to increasing nitrogen loads due to the growing human population. The excess nitrogen is readily incorporated in new biomass as done for natural sources (e.g. coastal upwelling) and the different nitrogen sources can be identified by the measurement of the ratio between stable nitrogen isotopes ($\delta^{15}N$). In this study $\delta^{15}N$ was determined in two species of macroalgae (*Ascophyllum nodosum* and *Fucus vesiculosus*) and in nitrate and ammonium in water to determine the relative importance of anthropogenic versus natural sources of nitrogen along the coast of NW Spain. The size of the human population in the watershed of each sampling site was also recorded.

The largest nitrate inputs were associated with discharges of freshwater while ammonium concentrations were unrelated to salinity, suggesting a potential major role of terrestrial nitrogen sources. Both algal species and nitrogen sources showed similar isotopic enrichment to a given site, but algal $\delta^{15}N$ was not related to either inorganic nitrogen concentrations or $\delta^{15}N$. The latter suggest that inorganic nitrogen inputs are largely variable and do not always leave an isotopic trace in macroalgae. However, a significant linear decrease in macroalgal $\delta^{15}N$ along the coast is consistent with the differential effect of upwelling.

Besides this geographic variability, the influence of anthropogenic nitrogen sources is evidenced by higher $\delta^{15}N$ in macroalgae from rias and estuaries compared to those from open coastal areas and in areas with more than $15x10^3$ inhabitants in the watershed. These results indicate that, in contrast with other studies, macroalgal $\delta^{15}N$ is not simply related to either inorganic nitrogen concentrations or human population size but depends on other factors as the upwelling or the efficiency of local waste treatment systems.

Can stable isotope signatures explain changes in POP concentrations in UK gannet (*Morus bassanus*) eggs?

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We measured stable isotope (δN^{15} and δC^{13}) signatures in the eggs of the Northern gannet (*Morus bassanus*), a sentinel for marine pollution.The eggs were from two colonies (Ailsa Craig and Bass Rock), representing birds foraging in the Western Atlantic and North Sea respectively. Between 1977-2007, gannet eggs had been monitored for persistent organic pollutants (PBDEs, PCBs, dieldrin, DDE) and mercury. The aim of this study was to determine if diet, as measured by proxy using stable isotopes, can explain some of the temporal and inter-colony variation in contaminant burdens that have previously been reported in these eggs.

Eggs from Ailsa Craig were significantly more enriched in δC^{13} and δN^{15} than those from Bass Rock, suggesting increased consumption by Ailsa Craig gannets of higher trophic level prey and/or an increased proportion of demersal fish discards in the diet. This difference may account to some extent for the higher levels of some PCB congeners, ΣPCB concentrations, DDE and Hg concentrations in eggs from Ailsa Craig compared with those from Bass Rock, although ΣPBDE concentrations were similar in eggs from the two colonies.

The δC^{13} signature decreased significantly over time in the eggs from both colonies, indicating a likely change in food source (lower trophic level) in both foraging areas. For gannet eggs from Ailsa Craig, there was a significant positive correlation between δC^{13} and δN^{15} and concentrations of Hg, ΣPBDE and ΣPCB and, to a lesser extent, DDE and individual PCB congeners. In eggs from Bass Rock, δC^{13} correlated significantly but inversely with BDE 49, 153 and 154, and positively with DDE and dieldrin, but no significant trends were found with Hg, ΣPBDE and ΣPCB. Our results therefore suggest that diet may also be a significant factor explaining some of the temporal variation in contaminant burdens in eggs from both colonies but its importance varies between colonies and different contaminants.

Combined nestling feather analysis for stable isotopes ($\delta^{13}C$ and $\delta^{15}N$) and persistent organic pollutants reveals ecosystem-dependent bioaccumulation patterns in subarctic predatory birds

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Predatory birds living at their northernmost distribution limit are subject to high natural stress. In addition, they are increasingly exposed to anthropogenic stressors, such as organohalogenated pollution. Experimental studies have indicated that a combination of natural and anthropogenic stressors may interact synergistically and compromise fitness and overall health. Furthermore, recent studies on the blood biochemistry of subarctic predatory bird nestlings have suggested that persistent organic pollutant (POP) exposure may cause endocrine and homeostatic disruption. As POP exposure in predatory birds primarily stems from food ingestion, the quantification of feeding ecology, through stable isotope analysis, is a promising method to assess exposure pathways.

During three subsequent breeding seasons (2008-2010), we sampled nestlings from three subarctic predatory bird species: Northern Goshawk (NG; *Accipiter gentilis*; woodland ecosystem), Golden Eagle (GE; *Aquila chrysaetos*; mountainous ecosystem), and White-tailed Eagle (WTE; *Haliaeetus albicilla*; marine ecosystem). The nestling body feathers were analysed for δ^{13}C, δ^{15}N and POPs. The combination of pollutant and stable isotope analysis in the same feather samples is a unique non-destructive method that provides an integrated ecological and toxicological assessment.

Mean (±2*SE) δ^{13}C (NG: -21.53±0.22 ‰; GE: -22.14±0.29 ‰; WTE: -16.47±0.44 ‰) and mean (±2*SE) δ^{15}N (NG: 7.04±0.65 ‰; GE: 5.83±0.81 ‰; WTE: 14.34±0.27 ‰) in the nestling feathers agree with dietary information from the literature. In addition, δ^{13}C and δ^{15}N indicate geographical variation in trophic level and origin of preys that could logistically not have been determined in the field. While δ^{13}C and δ^{15}N correlate in WTE ($r=0.58$; $P<0.01$), they do not in the terrestrial species ($P\geq0.05$). Furthermore, relationships between stable isotopes and POPs seem to be ecosystem-dependent. Linear regressions indicate POP biomagnification in terrestrial ecosystems ($r^2=0.16$-0.48; $P<0.05$), while WTE nestlings feeding on higher trophic level prey contained lower POP concentrations ($r^2=0.12$; $P=0.04$). Furthermore, δ^{13}C is only a useful predictor for POP concentrations in the marine ecosystem ($r^2=0.14$-0.16; $P<0.03$).

In conclusion, the combined analysis for stable isotopes and POPs in nestling body feathers seems promising as δ^{13}C and δ^{15}N effectively reveal ecosystem-dependent POP bioaccumulation. Furthermore, the use of nestling feathers eliminates potential confounding caused by different half-lives of pollutants and stable isotopes.

Biomagnification of mercury in the trophic web off Baixada Santista continental shelf, SE Brazil

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Anthropogenic mercury (Hg) contamination has been a major concern in Santos estuarine system, mainly because of the presence of an industrial complex and intense harbor activities. Nevertheless, it remains unclear whether this contamination is magnified throughout the food web of the adjacent shelf system. We studied the total mercury (THg) concentrations in 23 fish species representing four trophic groups (zooplanctivore, piscivore, teuthophagous, and benthic invertebrate feeder), which were sampled on board of the RV “Prof. W. Besnard” in eight areas encompassing the Santos Bay, inner and middle shelf. Zooplanktonic crustaceans, shrimp, crabs, swimming crabs, polychaetes, mollusks (bivalves, gastropods, octopus, and squids), ophiuroids, and sea stars were also sampled, representing a gradient of trophic positions in the marine food web. THg (μg.g^{-1}, d.w.) was measured in muscle and/or whole specimens. Stable isotope of nitrogen (δ^{15}N) was used to determine the organisms’ trophic levels and the rate of biomagnification of mercury in the food web. The biomagnification factor (BF) of Hg was calculated following Rolff et al. (1993).

A linear relationship between mercury levels and trophic position was observed ($p<0.0001$). Low [THg] levels were found in zooplankton (0.002 μg g^{-1}), and surface depositivore polychaetes (0.011 μg g^{-1}). High [THg] levels occurred in the largest fishes: Brazilian flathead (1.189 μg g^{-1}), cutlassfish (1.416 μg g^{-1}), and lesser guitarfish (2.200 μg g^{-1}). Few fish specimens had values that exceeded the national limit for human consumption (ANVISA, 1998: 0.500μg g^{-1} w.w., ~1.3-2.5 μg g^{-1} d.w.). Biomagnification of Hg was detected in the trophic web, being higher in the pelagic system. The high complexity of the benthic trophic web related to the high diversity of feeding habits, and the different metabolism between benthic and pelagic organisms, might be affecting the magnitude of the BF of Hg. The higher [THg] basal value in the benthic trophic web is probably associated to the high Hg bioavailability in this system. The δ^{15}N as trophic level indicator is a promising tool to evaluate the behavior of contaminants in food webs, giving support to long term monitoring in environments under intense anthropogenic activities.

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(presenting authors underlined)