?

How to control for stable isotopes baseline variation across sites

SIESTE Seminar 2018 - Benjamin Lejeune

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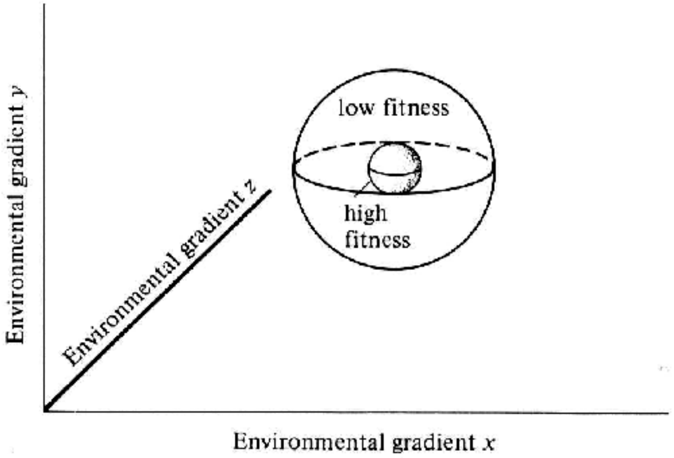
REMINDER – Stable isotopes and the ‘isotopic niche’

Concluding Remarks

G. Evelyn Hutchinson

Cold Spring Harbor symposia on quantitative biology 22: 415-427



Hutchinson’s ‘ecological niche’ (1957)

‘A hypervolume set in a n-dimensional space where each axe represents an environmental parameter’

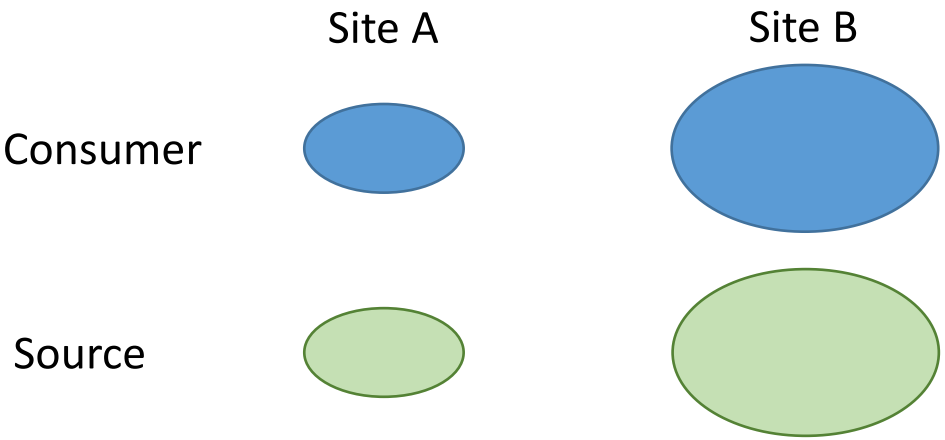
Stable isotopes and the ‘isospace’ (Bearhop et al. 2004, Newsome et al. 2007)

➔**Dimensions** to define an ‘isospace’ where **isotopic niches** = *proxy* for **trophic niches**
➔**Time and space integrative** info on trophic habits

Isotopic niche as a proxy: Problems and caveats

Measuring or comparing niches and food-web changes across sites ?

- Lack of a scale : Niche size appreciation is always relative
- Baseline variation and/or shift can be propagated across trophic levels



→ Classical **Signal :: Noise** problem

→ Solution = Rescale/Standardise isotope data

/! Standardisation ≠ Baseline correction **/!**

Rescaling isotope data ? - No single strategy

Bottom up approaches: *p*-space based on modelling from source data (concept from Newsome et al. 2007)

Replace δ_{15}N by **trophic position** estimates (ex: Quevedo et al. 2009)
Replace δ_{13}C by **source reliance** estimates (ex: Quevedo et al. 2009)

Top down approaches: Statistical, not based on source data

Rescale according to **Min-Max** (Cucherousset and Villéger, 2015)
Rescale into **Modified Z-scores** (Fry and Davis, 2015)

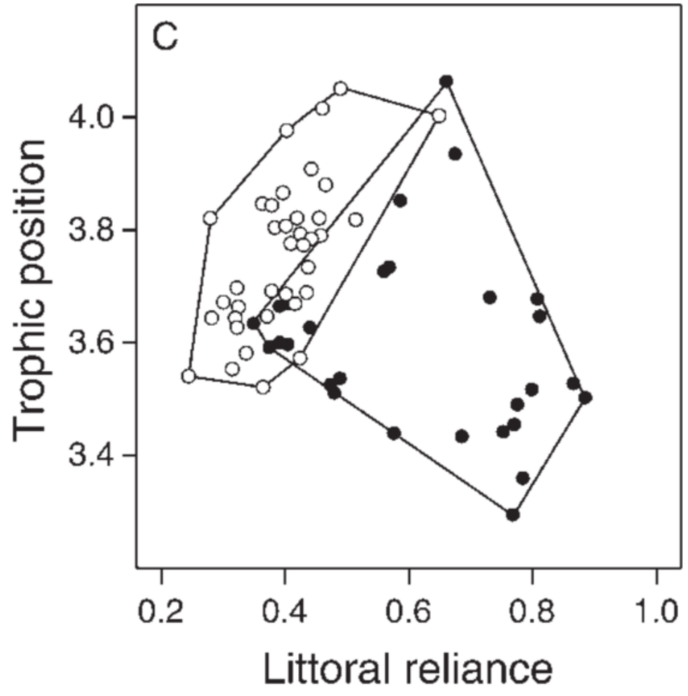
Alternative approach: Apply direct correction to the metrics

Divide niche metric by the same metric from your primary producer; e.g. divide SEA.B of consumers by SEA.B of primary producers (Warry et al. 2016)

The ‘P-space’ approach (Newsome et al. 2007; Quevedo et al. 2009)

Transform the isospace into a ‘proportional’ space:

Replace δ_{15}N by **trophic position** estimates
Replace δ_{13}C by **source reliance** estimates



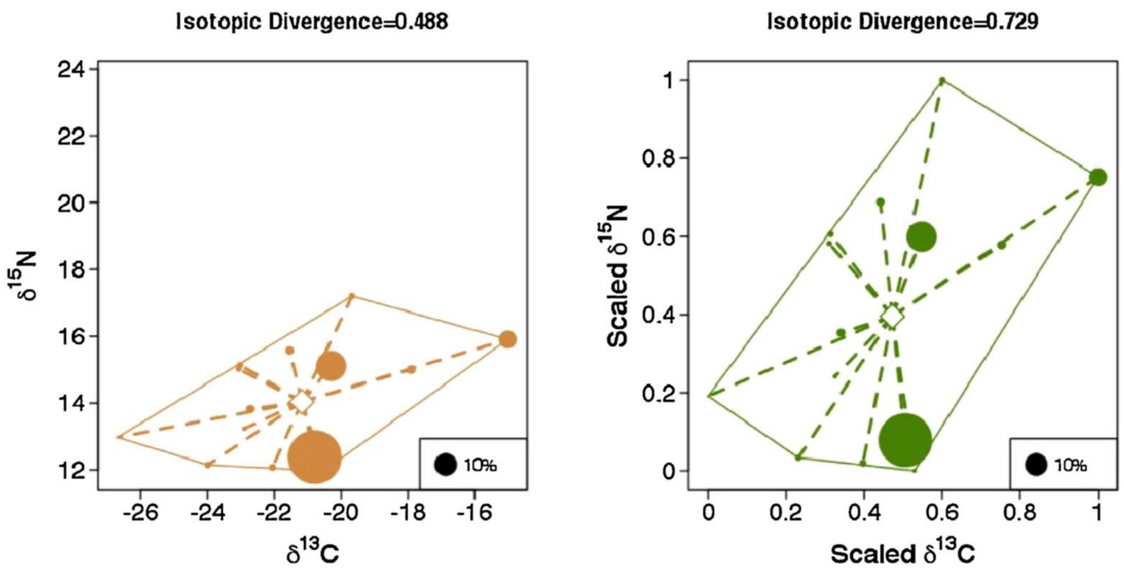
+

Easy to read and understand
Direct link to resource use
Compatible with bayesian modelling of niche metrics
Should account for baseline variation

–

Based on modelling … **/!\ Accuracy, missing information, too many baselines for TP, consumer-source isotope lag…**
Requires extensive sampling and knowledge of your system

The ‘Min-Max’ rescaling (Cucherousset and Villéger, 2015)

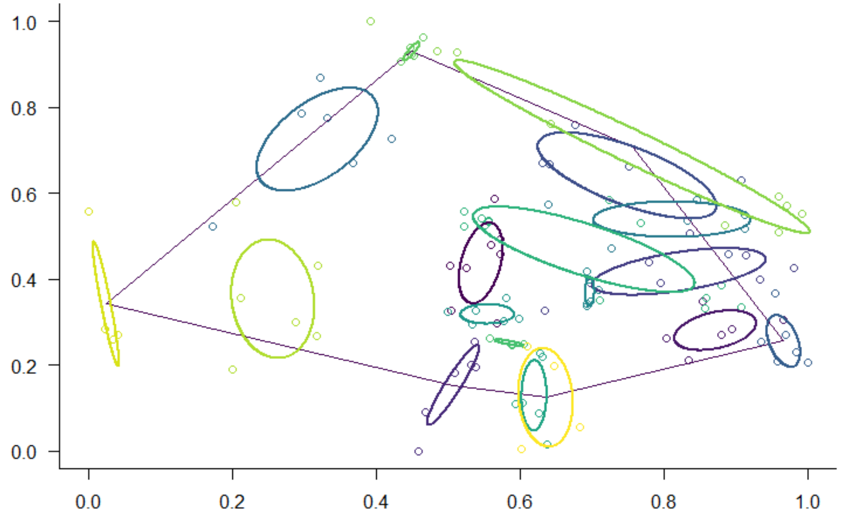


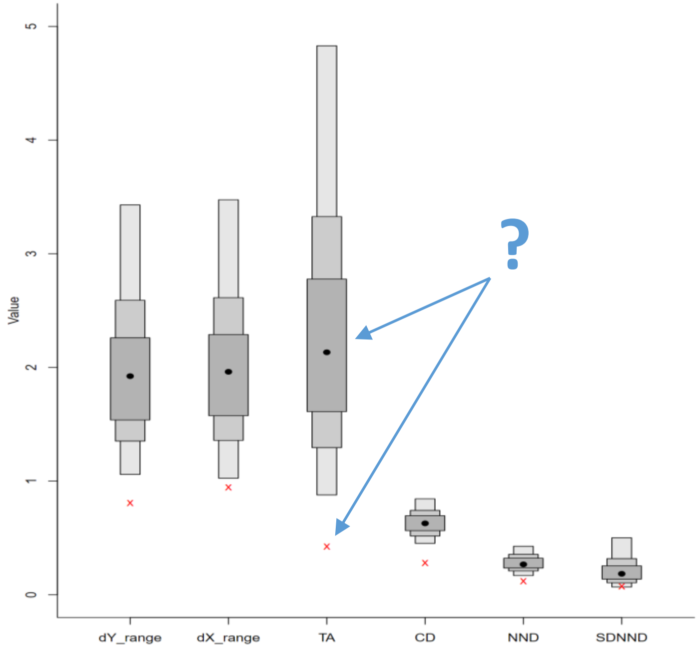
+ Easy calculation
Helps interrogating changes in food-webs topology

− Does not account for baseline variation *per se*
Sensible to extreme values

Rescale isotope data → scale of 0 to 1

The 'Min-Max' rescaling (Cucherousset and Villéger, 2015)





\+ Easy calculation

Helps interrogating changes in food-webs topology

− Does not account for baseline variation *per se*

Sensible to extreme values

Not compatible with Bayesian modelling of niche or community metrics: Too strict boundaries, break multivariate normality assumption

"Your rescaling has broken the assumption that the data are multivariate normal" Andrew Jackson

The 'Modified Z-score' approach (Fry and Davis, 2015)

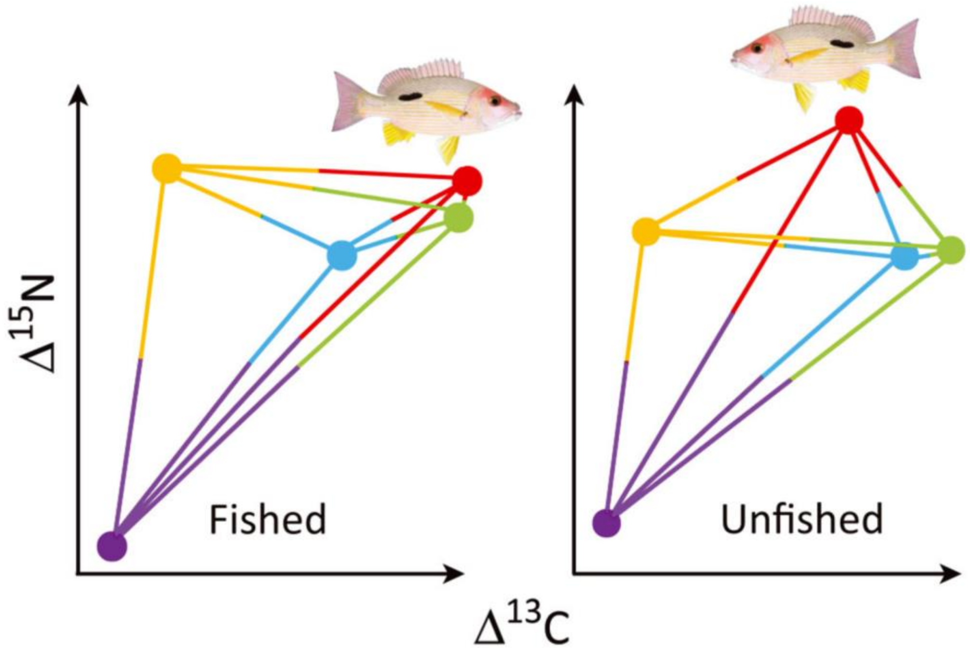
Z-score (z) = (x – μ) / σ

→ **Statistical method used to normalise data**

→ **gives differences among data in SD units**

(Turner et al. 2010)

The 'Modified Z-score' = SD rescaled * (species mean – community mean)/community SD



SD rescaled = mean SD of the communities

If rescaling of individual values → Calculation is more complicated:

Δ * X + SD rescaled * (species mean – community mean)/community SD

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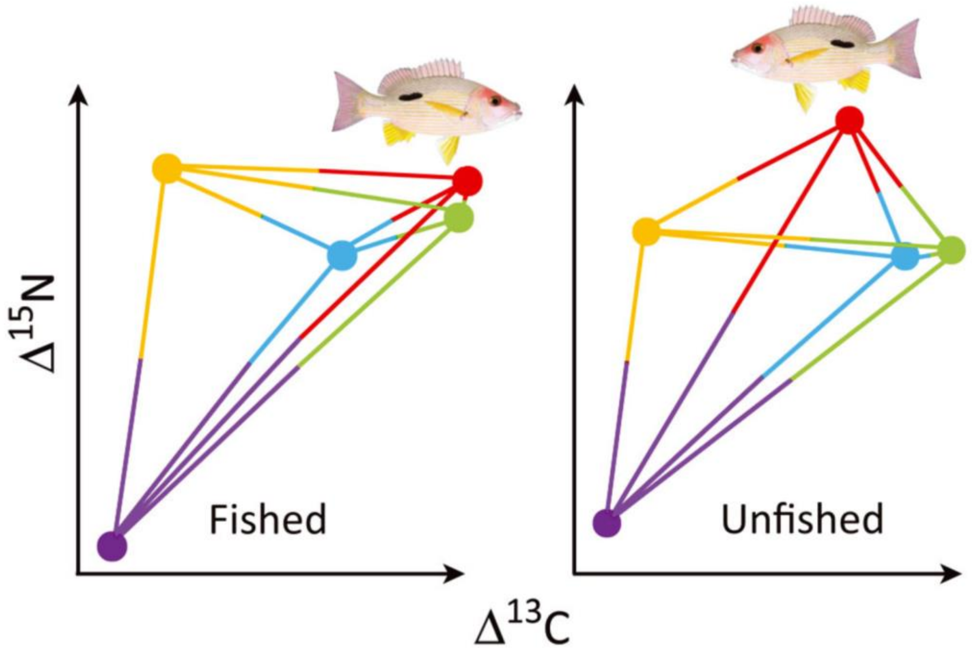


+ **Retain original units**

Helps interrogating changes in food-webs topology

Allows for bayesian modelling of pop and community metrics

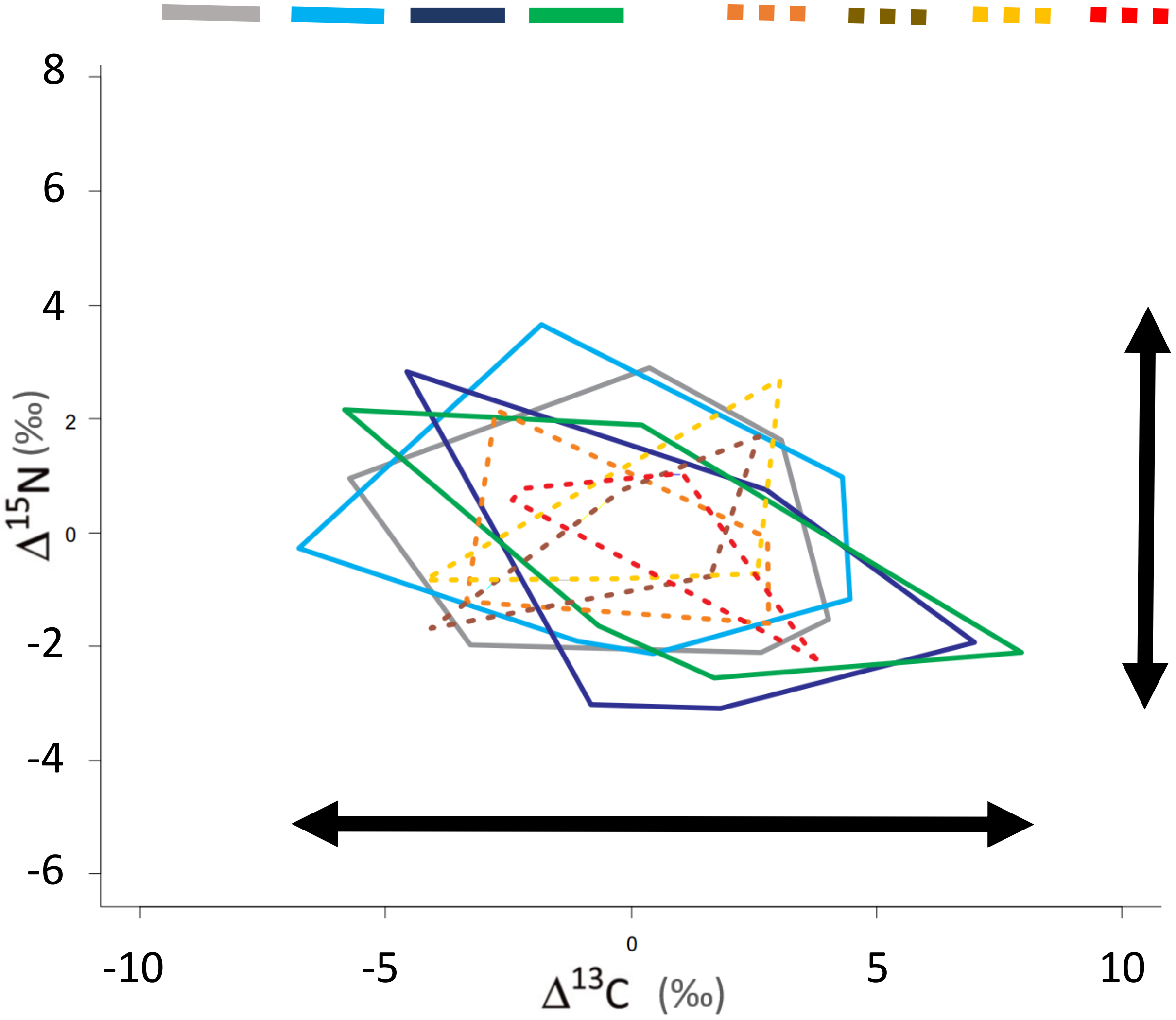
– Difficult calculation for individual rescaling

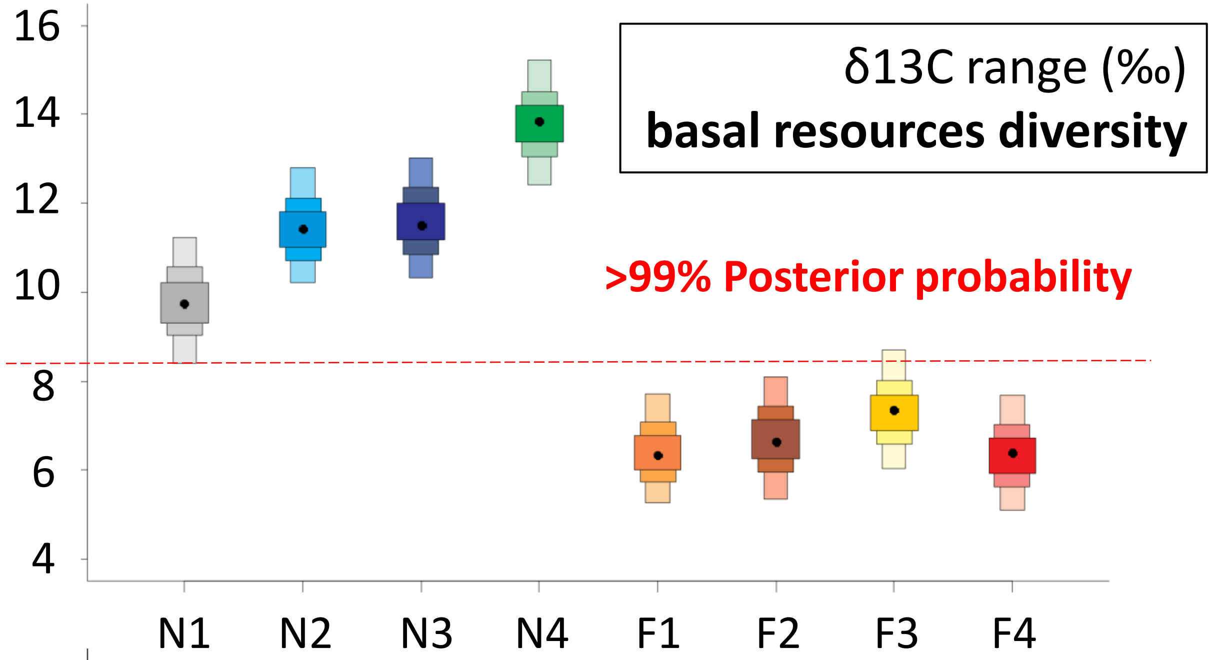
Requires data from several populations for precision

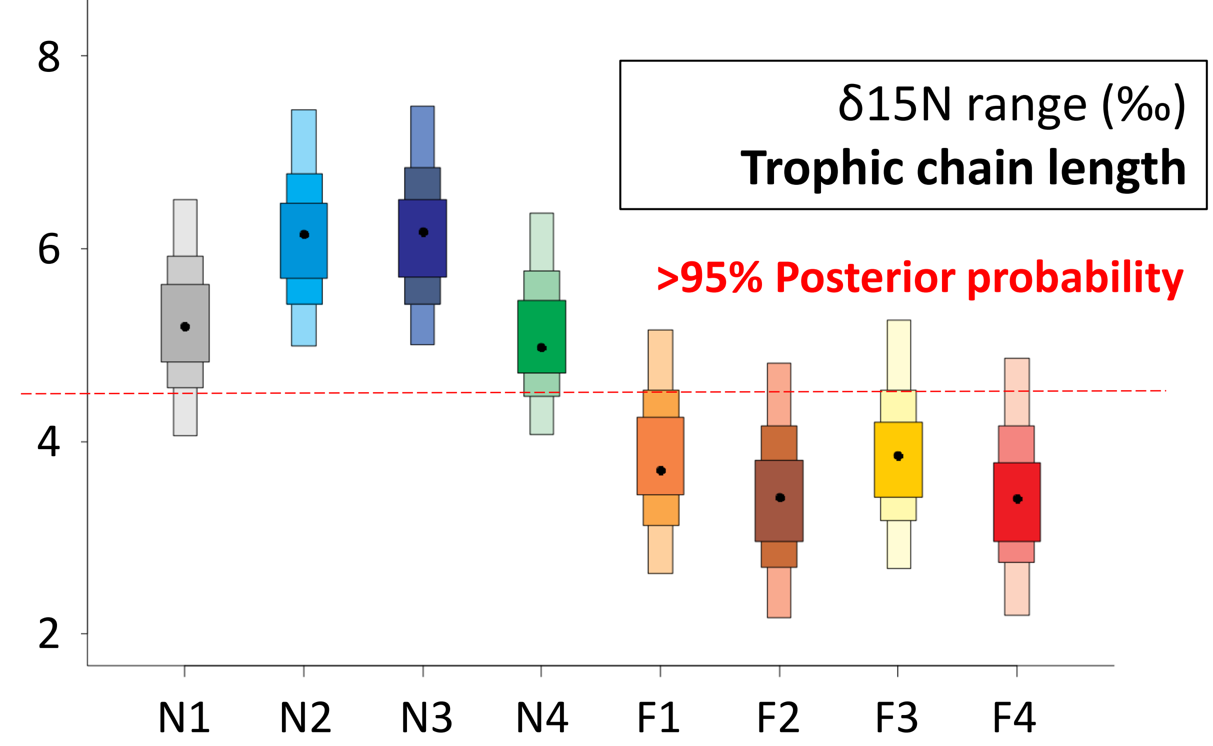
Does no account for baseline variation *per se*

Exemple for community comparisons

(SEH Congress 2017, Lejeune et al. in prep)







Exemple for community comparisons

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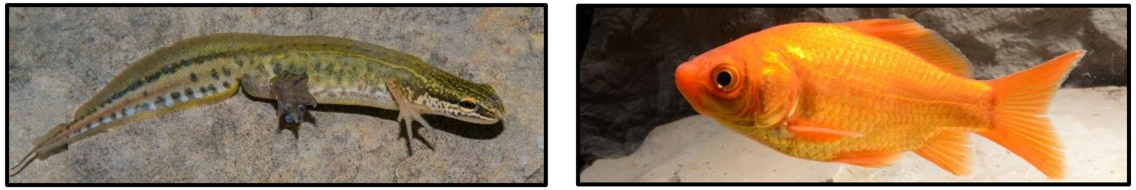
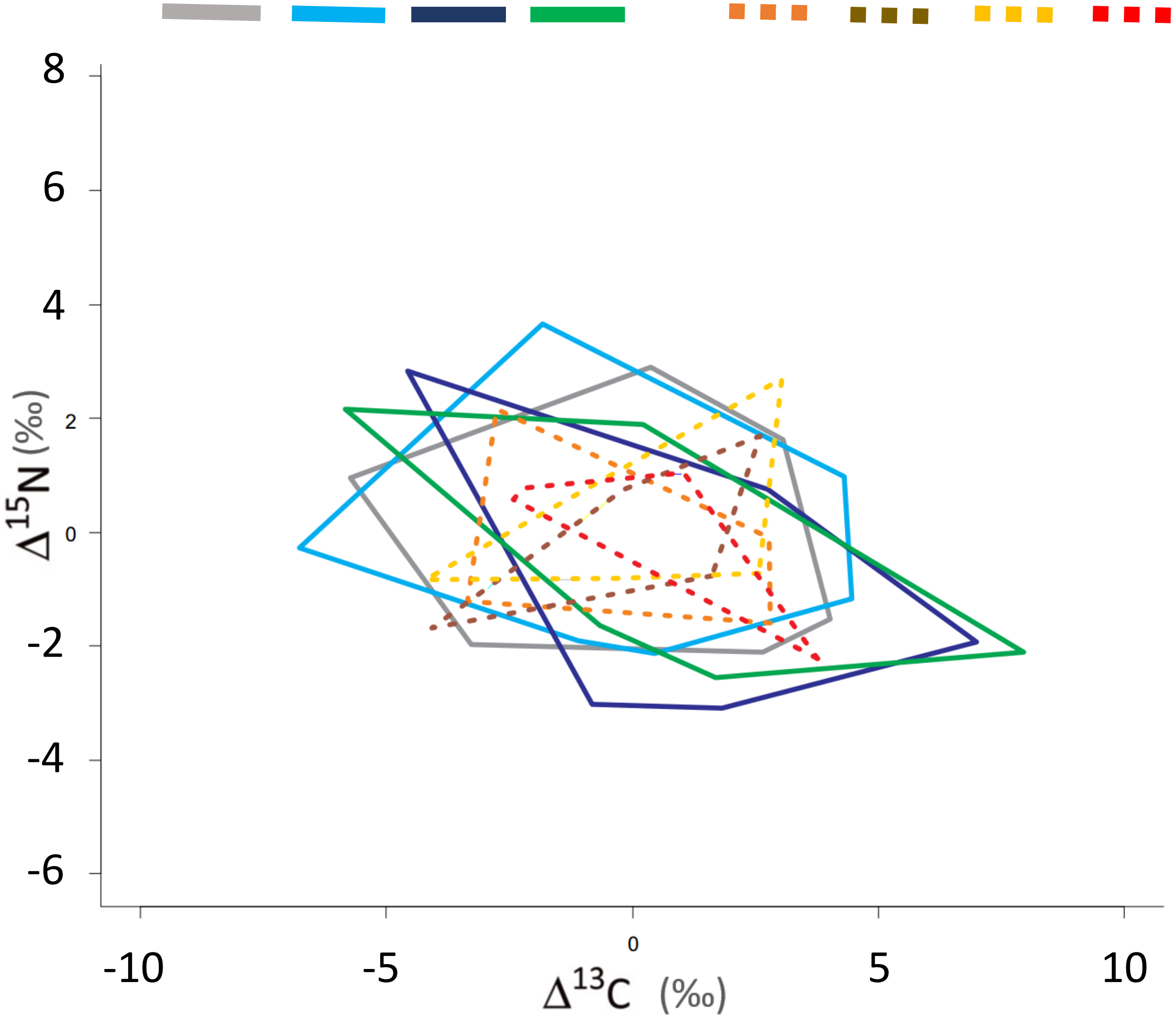
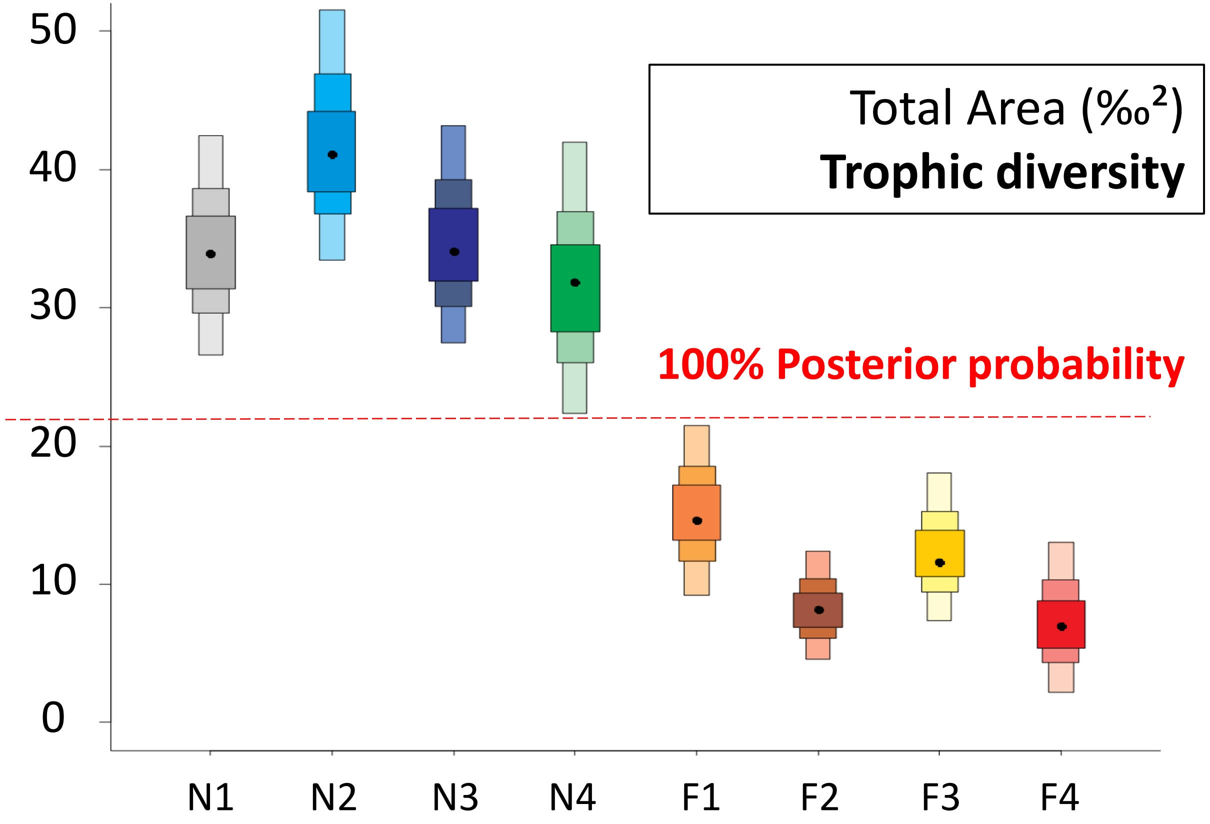
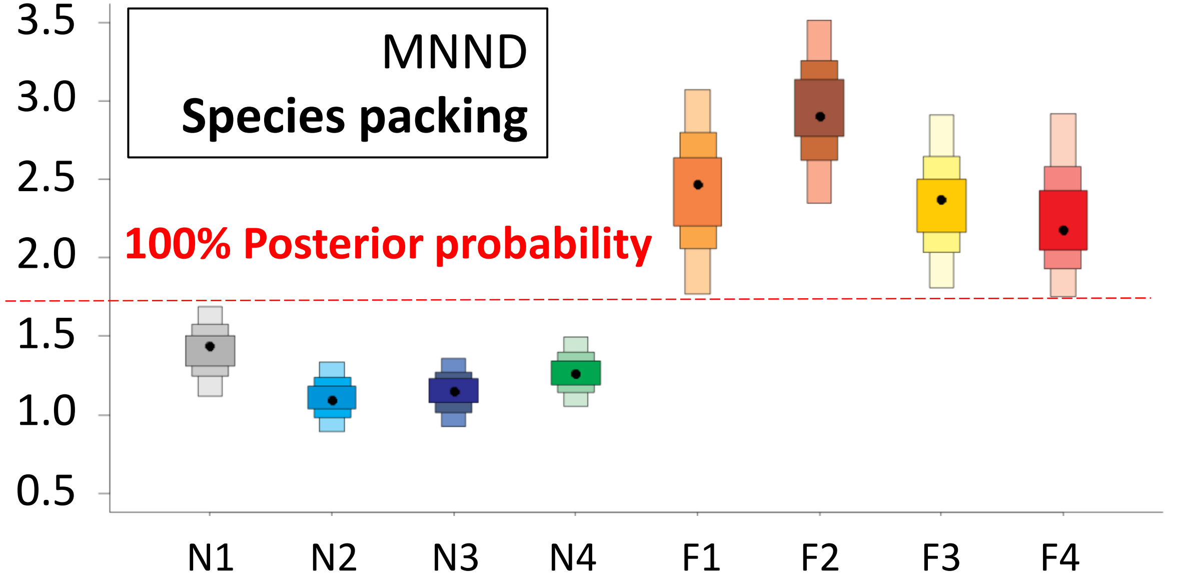




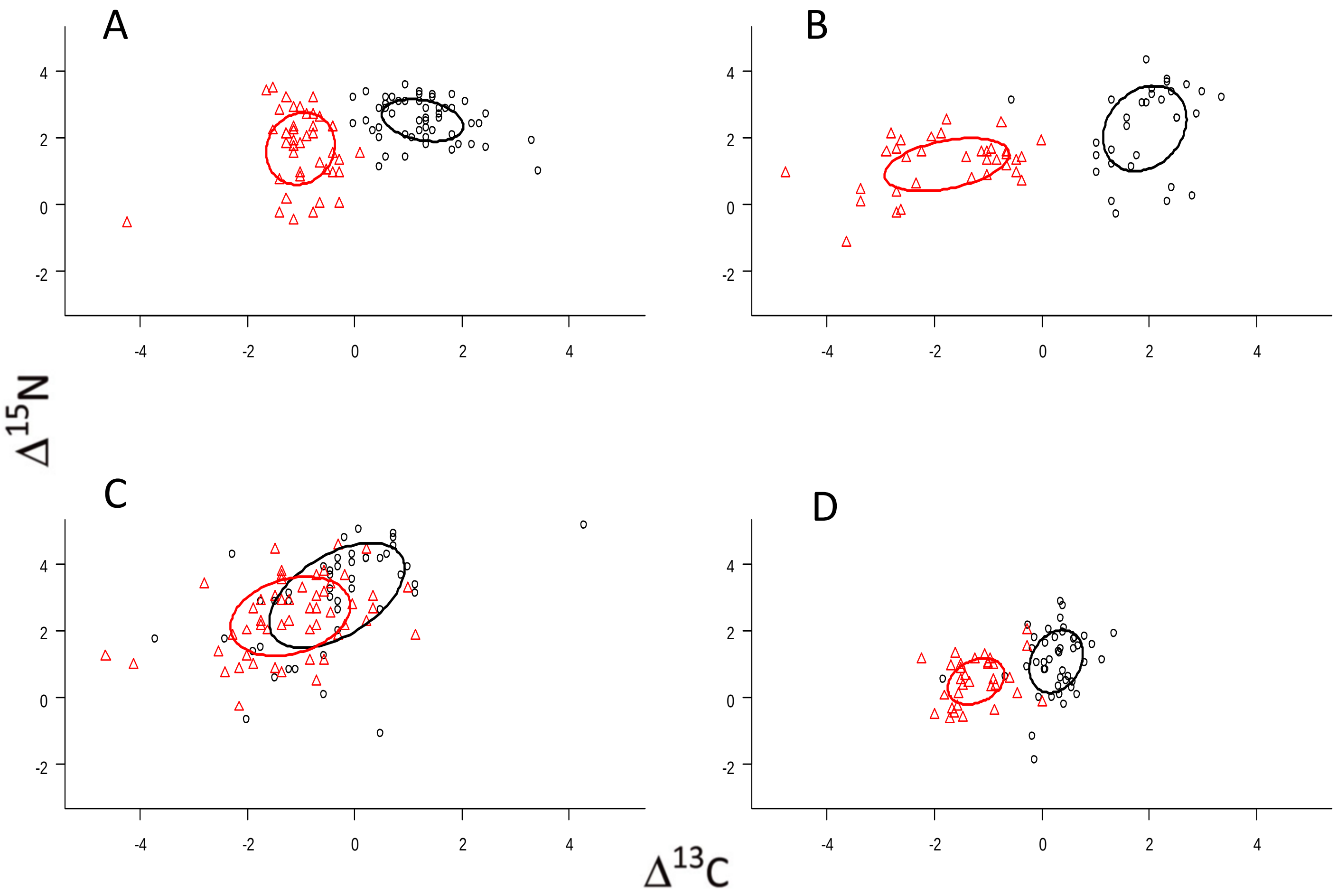




Variation of the 'Modified Z-score' approach for population comparisons (Lejeune et al. in prep)

Rescaling isotopic values of consumers based on **Mean and SD of the prey community**

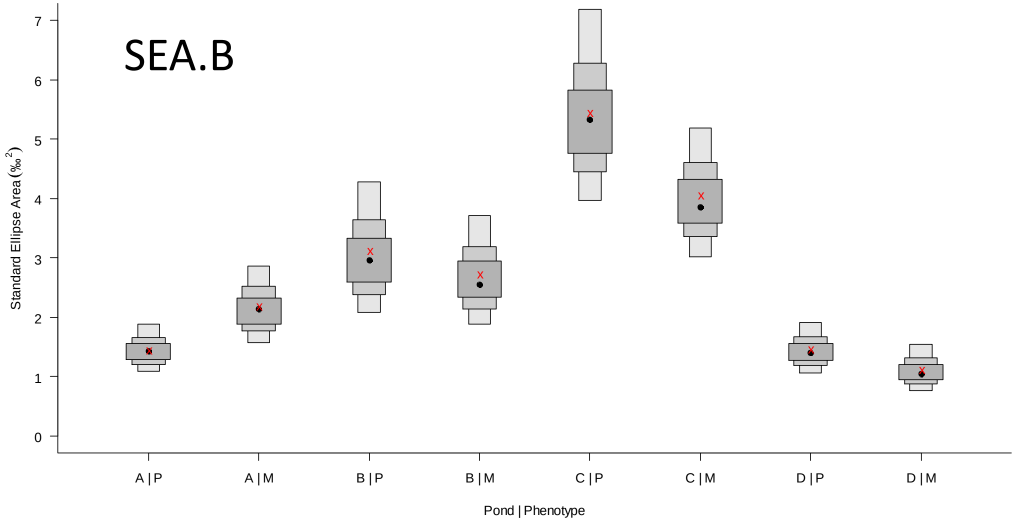
Colour code: Red = Metamorphs, Black = Paedomorphs



Incorporates isotopic variation of ressources

Isospace centered according to prey community

Position of indiv = deviation from center of ressource community



Direct correction of niche metrics (Warry et al, 2016)

Consumer metrics are corrected according to source variability and expressed as ratio (no units):

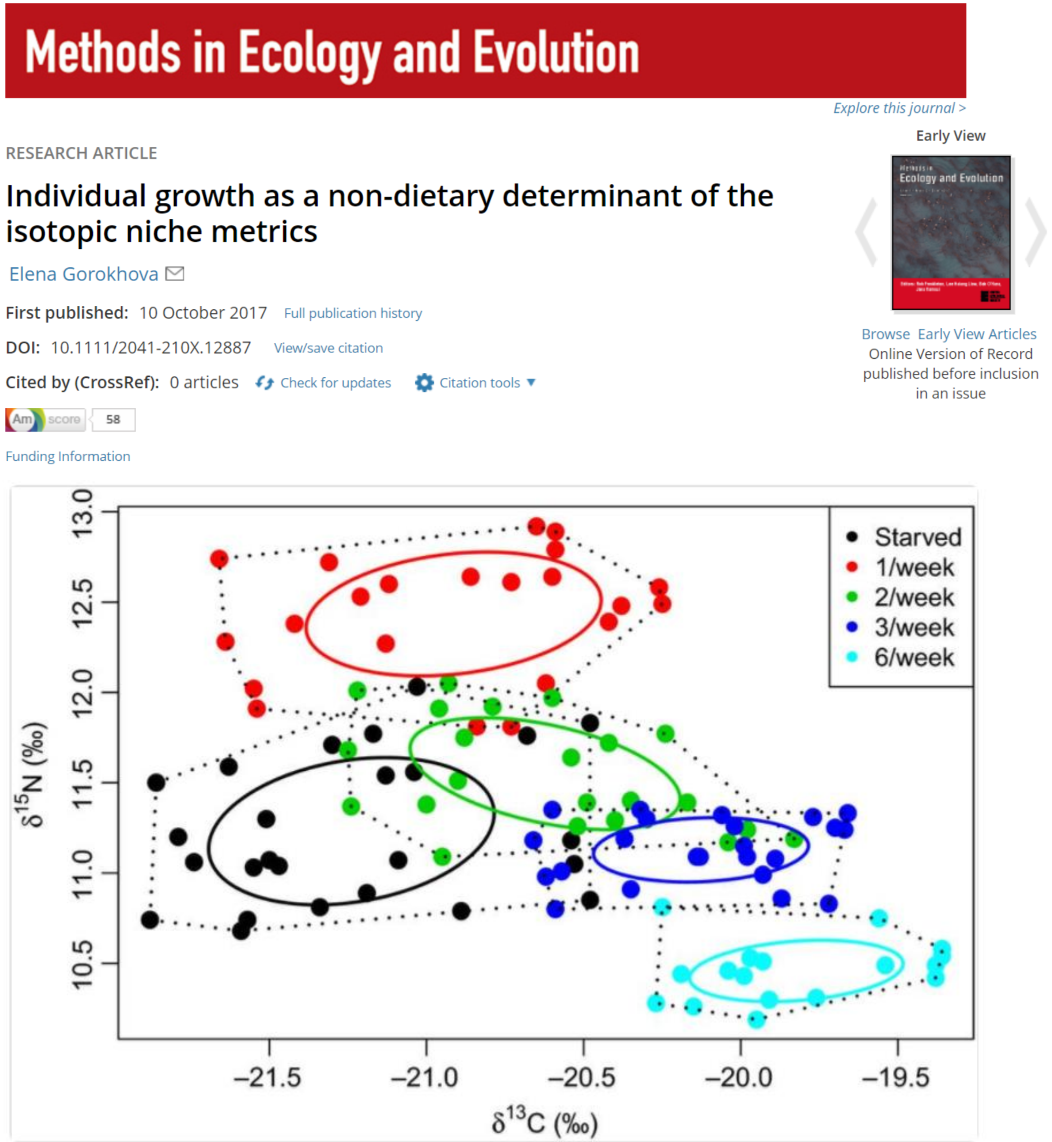
Exemples:

Corrected niche size = SEAc Consumers / SEAc Sources
Corrected d13C range = d13C range Consumers / d13C range Sources
Corrected MNND = MNND consumers / √ (SEAc sources)

Etc. …

- \+ No transformation of the raw data = straightforward
- – No rescaling of raw data, not intended to give standardized pictures of food-webs in delta space
  Calculation is more difficult if using Bayesian estimates

REMEMBER: Isotopic niche ≠ trophic niche


Methods in Ecology and Evolution

RESEARCH ARTICLE

Individual growth as a non-dietary determinant of the isotopic niche metrics

Elena Gorokhova

First published: 10 October 2017 Full publication history
DOI: 10.1111/2041-210X.12887 View/save citation
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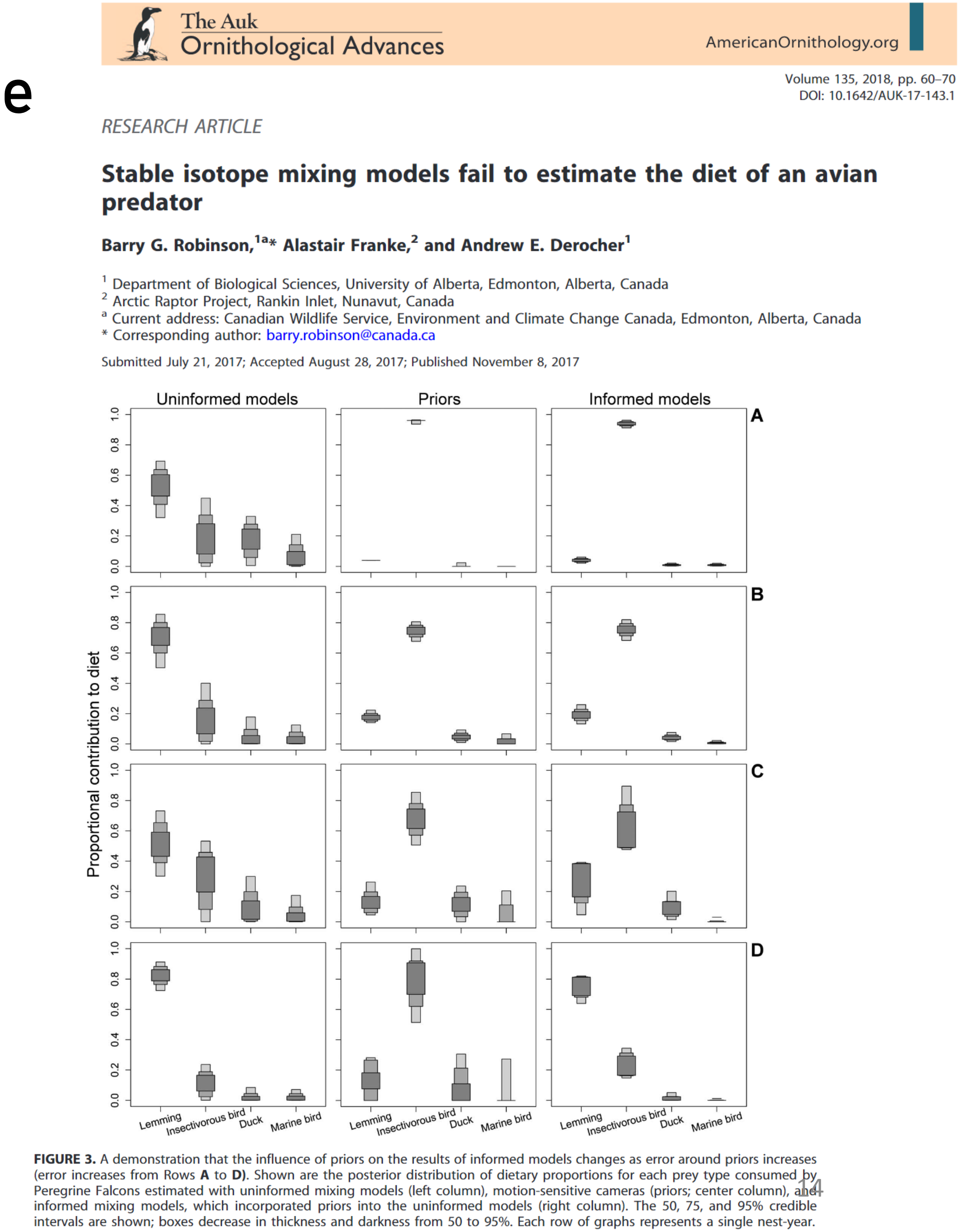
The Auk
Ornithological Advances
AmericanOrnithology.org
Volume 135, 2018, pp. 60–70
DOI: 10.1642/AUK-17-143.1

RESEARCH ARTICLE

Stable isotope mixing models fail to estimate the diet of an avian predator

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FIGURE 3. A demonstration that the influence of priors on the results of informed models changes as error around priors increases (error increases from Rows **A** to **D**). Shown are the posterior distribution of dietary proportions for each prey type consumed by Peregrine Falcons estimated with uninformed mixing models (left column), motion-sensitive cameras (priors; center column), and informed mixing models, which incorporated priors into the uninformed models (right column). The 50, 75, and 95% credible intervals are shown; boxes decrease in thickness and darkness from 50 to 95%. Each row of graphs represents a single nest-year.

REMEMBER: Isotopic niche ≠ trophic niche

TO COLLECT MORE DATA

Not only feeding! e.g. Lejeune et al. Oikos 2018

1) Know your system !

   - **Consumers:** behaviour, migration, growth, body length range, body condition,…
   - **Resources:** temporal variation in availability, external inputs

2) Try to control or acknowledge for baseline variation

   - ***p*-space** (Quevedo et al. 2009)
   - **Direct correction of each metric** (Warry et al. 2016)
   - ‘**Source based modified Z-scores**’ (Lejeune et al. in prep)

3) When relying on mixing models: Try to use multiple tracers (SI, FA…) and direct observations (stomach contents…) → *Priors*