

Fatty acid based dietary estimation when calibration coefficients are unavailable

Jennifer McNichol ¹ Connie Stewart ² Jory Cabrol ³ Véronique Lesage ³

¹University of Victoria

²University of New Brunswick

³Fisheries and Oceans Canada, Québec Region

Motivation



- Dietary estimation is a research hotspot of quantitative ecology, providing key insights into predator–prey relationships.
- Fatty acids (FAs) are fundamental components of lipids that are used to store energy and contain information about diet.
- Quantitative fatty acid signature analysis (QFASA) [Iverson et al., 2004].
- Given a prey database and a predator's FA signature, QFASA estimates the proportion of each species in the predator's diet.

Motivation

- Dietary set (typically 29 FAs).
- Compositional data.
- FAs are stored with little modification and can be used to identify consumed prey.
- To account for the difference in FA signatures between predator and prey, we adjust the prey FAs by **calibration coefficients (CCs)**.

Table 1: Example of FA signatures.

FA	seal 1	seal 2	seal 3
16:2n-6	0.00	0.00	0.00
16:2n-4	0.00	0.00	0.00
16:3n-6	0.03	0.03	0.03
16:3n-4	0.02	0.02	0.02
16:4n-3	0.00	0.00	0.00
⋮	⋮	⋮	⋮
22:5n-6	0.00	0.00	0.00
22:4n-3	0.00	0.00	0.00
22:5n-3	0.07	0.07	0.08
22:6n-3	0.20	0.20	0.21

- Quantitative fatty acid signature analysis [Iverson et al., 2004] estimates the proportion α of prey type i in the diet by minimizing

$$\text{dist}(\mathbf{Y}, \sum_{i=1}^I \alpha_i \bar{\mathbf{X}}_i)$$

where \mathbf{Y} = predator FA signature

$\bar{\mathbf{X}}_i$ = mean FA signature of prey type i

- QFASA R package [Stewart et al., 2021]

MLE approach to FASA

- Maximum unified fatty acid signature analysis (MUFASA) [Steeves, 2020] assumes

$$\mathbf{Y} = \left(\sum_{i=1}^I \alpha_i \mathbf{Z} \right) \circ \epsilon$$

where \mathbf{Z} is a random effect representing the unobserved FA signatures of they prey.

- \mathbf{Y} , \mathbf{Z} and ϵ are isometric log-ratio (ilr) transformed and assumed to be multivariate normal.
- A marginal likelihood was obtained by integrating the joint likelihood with respect to the random effects using the R package TMB.



- CCs are used to account for the potential metabolization of FAs.
- May be obtained from long-term controlled diet feeding studies.
- We should have a set of CCs for every species of predator.

SQFASA

- Simultaneous QFASA (SQFASA)[Bromaghin et al., 2017] is an extension of QFASA which estimates CCs alongside diet.

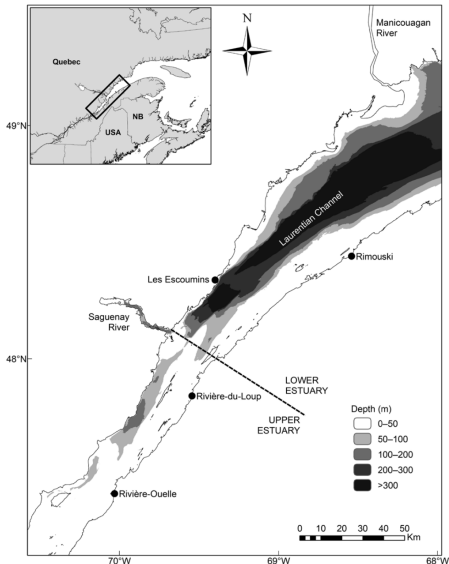
- Simultaneous maximum unified fatty acid signature analysis (SMUFASA) extends MUFASA to estimate CCs and diet.
- Predator FAs are modelled by

$$\mathbf{Y} = \mathbf{C} \circ \left(\sum_{i=1}^I \alpha_i \mathbf{Z} \right) \circ \epsilon$$

where \mathbf{Z} is a random effect representing the unobserved FA signatures of their prey.

- \mathbf{Y} , \mathbf{Z} and ϵ are ilr transformed and assumed to be multivariate normal.
- Marginal likelihood obtained using the R package TMB.
- α and \mathbf{C} are parameters to be estimated in the optimization.

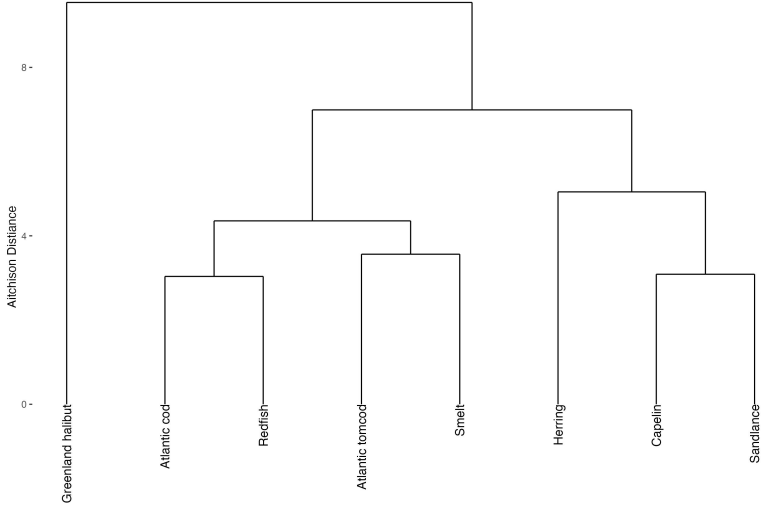
Real life example: Beluga whales



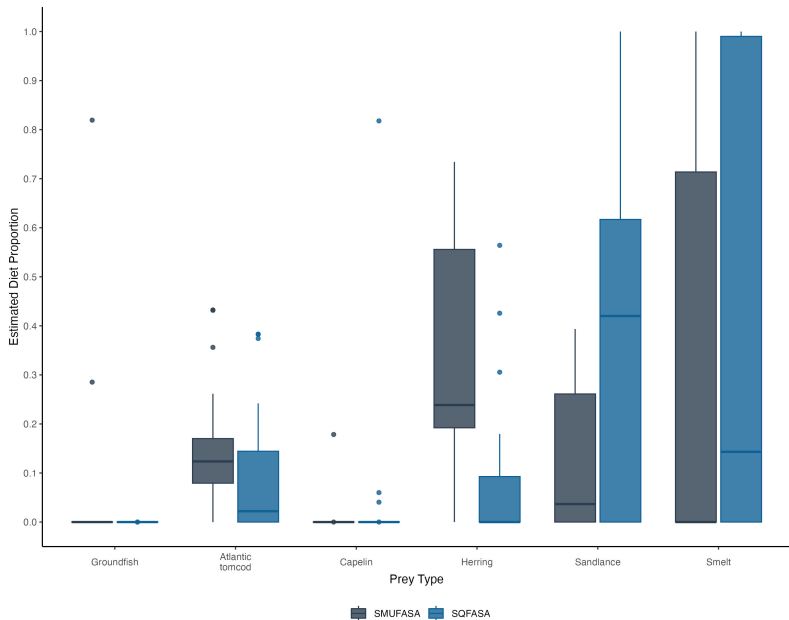
Beluga data

- Sample of 20 beluga whales in the St. Lawrence Estuary
- Reliable CCs are not available.
- Some dietary insight from stomach content analysis [Lesage et al., 2020] and stable isotope analysis.

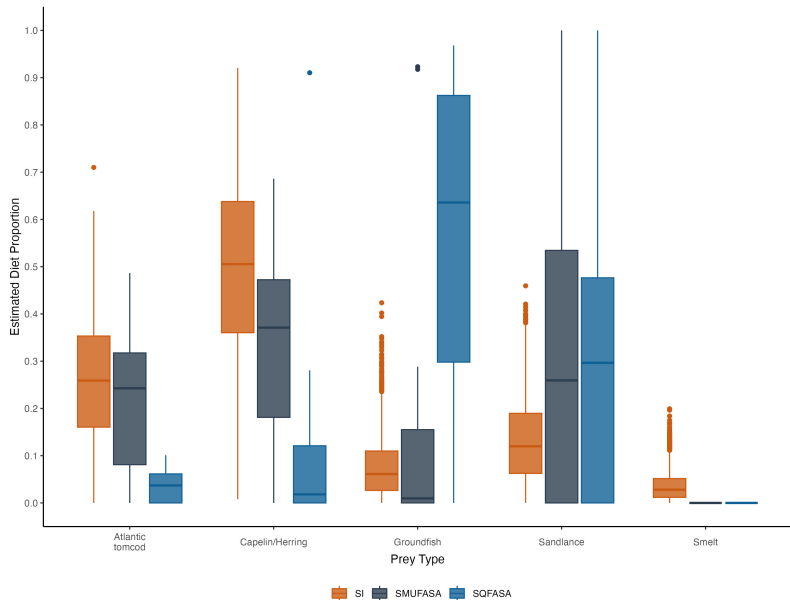
Dendrogram of Beluga Prey



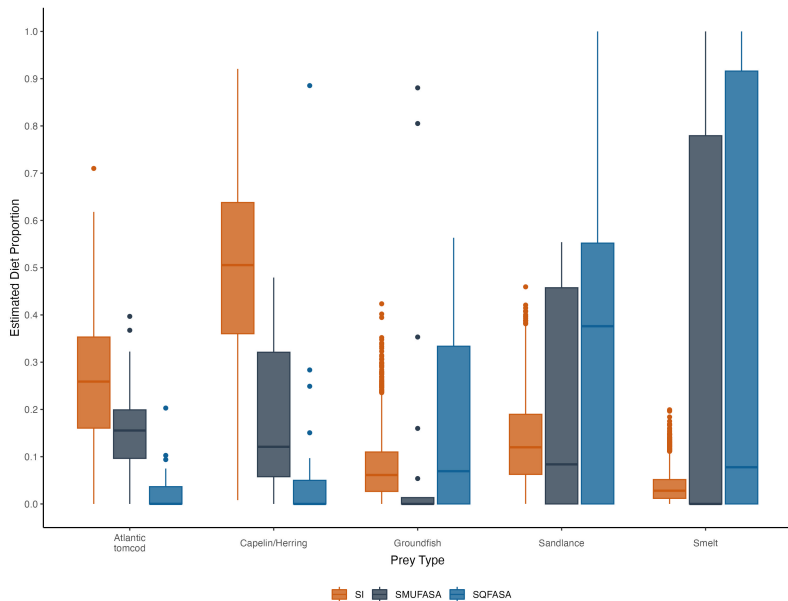
Beluga diet estimates



Comparison to Stable Isotope Analysis

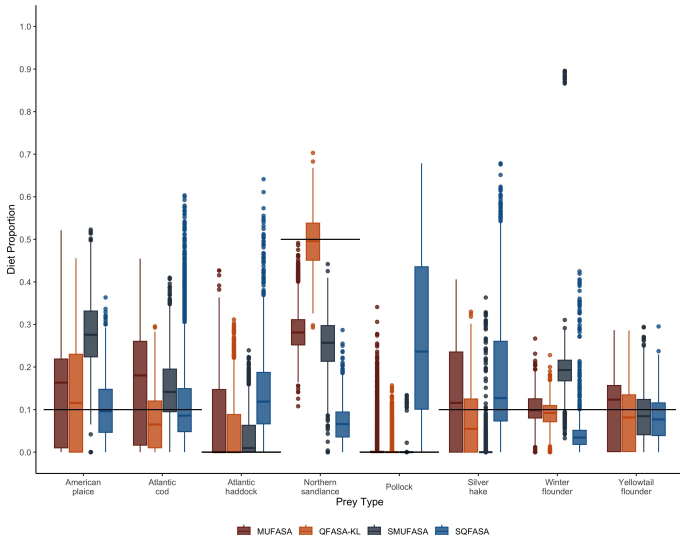


Comparison to Stable Isotope Analysis



Simulations

Create “pseudo-predators” (seals, $n=20$) based on real-life prey data set (fish) and realistic diet. Number of simulations = 100



SMUFASA trade-offs

- Computationally intensive.
- Highly sensitive to choice of FA set used and confounding between prey types.
- Often not as accurate as QFASA with *known* CCs.

Thank you!





Bromaghin, J., Budge, S., Thiemann, G., & Rode, K. (2017).
Simultaneous estimation of diet composition and calibration coefficients with fatty acid signature data.
Ecology and Evolution, 7(16), 6103–6113.



Iverson, S., Field, C., Bowen, W., & Blanchard, W. (2004).
Quantitative fatty acid signature analysis: A new method of estimating predator diets.
Ecological Monographs, 74(2), 211–235.



Lesage, V., Lair, S., Turgeon, S., & Beland, P. (2020).
Diet of st. lawrence estuary beluga (*delphinapterus leucas*) in a changing ecosystem.
The Canadian Field-Naturalist, 134(1), 21–35.



Steeves, H. (2020).

Maximum likelihood approach to diet estimation and inference based on fatty acid signatures.

PhD thesis, Dalhousie University.



Stewart, C., Iverson, S., Field, C., Bowen, D., Blanchard, W., Lang, S., Kamerman, J., Steeves, H., & McNichol, J. (2021).

QFASA: Quantitative Fatty Acid Signature Analysis.

R package version 1.1.1.