

Estimating variability and uncertainty in species diets

fastinR: a unified Bayesian framework for diet analyses

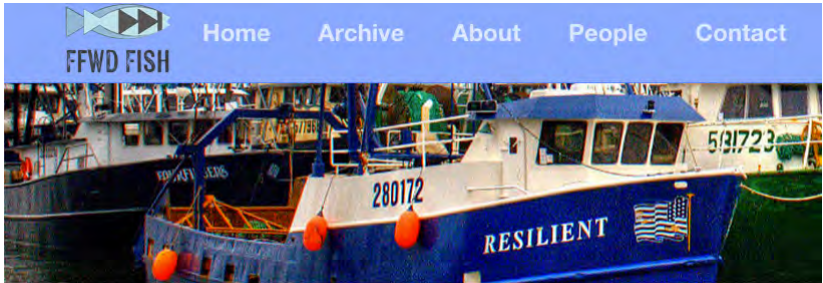
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Fast-Forward fish



Welcome

Size - based models at LME scales

Connected to regional data using Bayesian methods

Projected forward under climate change

Fast-Forward fish



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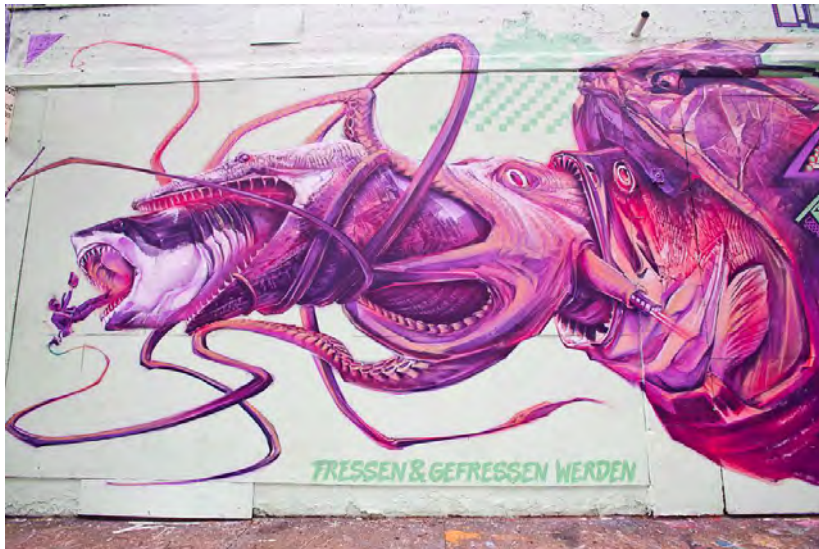


Welcome

With Ken Andersen, Nis Jacobssen, Julia Blanchard, James Watson, Malin Pinsky ...

Please see me for a chat if interested!

To eat and be eaten



Interactions are complex

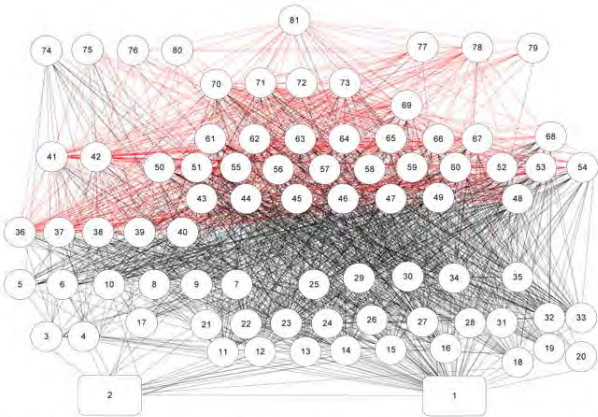
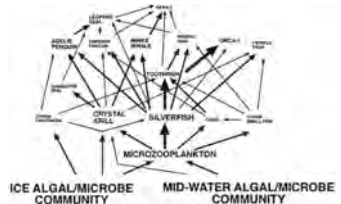


Figure 22. Food web of the northeast shelf large marine ecosystem (NES LME). Adapted from Link 2002.

Predation structures communities

- Quantifying predation is key in ecosystem models
- Many weak links increase stability
- Variability in links between
 - years
 - individuals
 - ontogeny



Empirical understanding of diets and their plasticity is a key to:

- **our understanding of food - webs**
- **projecting effects of climate change on ecosystems**

A couple of real world examples

- Effects of sardine fisheries on Marlin in Baja California, Mexico
 - How diverse are Marlin diets?
 - What is the impact of coastal sardine fisheries on pelagic Marlin?
- Endangered Hooker Sea lion in New Zealand
 - Recent population decline and reduced pup survival
 - Have their diets changed over time?
 - Out - competed by New Zealand's biggest fishery?



Quantifying predation

Marker	Pros	Cons
Stomach contents	<ul style="list-style-type: none">• straightforward• cheap	<ul style="list-style-type: none">• only a snapshot• different digestion rates
Stable Isotopes (SI)	<ul style="list-style-type: none">• integrate over time• trophic enrichment• model based statistics	<ul style="list-style-type: none">• poor discrimination• enrichment depends on prey δ_{SI}
Fatty Acids (FA)	<ul style="list-style-type: none">• potential markers• resolution	<ul style="list-style-type: none">• FAs metabolised• compositional data

Perhaps the biggest con of all: no consistent framework for estimating diets from data.

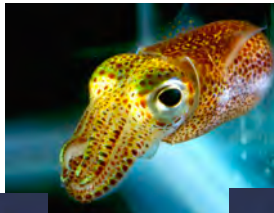
- Develop a common framework: Mixing - model based framework to estimate diet proportions.
- **Challenge 1:** Deal with proportion data: SI models not appropriate - need to use appropriate likelihood.
- **Challenge 2:** Pick from the huge amount of FAs that could be included, but make the analysis hugely inefficient.
- **Challenge 3:** Deal with metabolic conversion of FAs.
- Make assumption that the markers reflect the same overall (population level) diet, just on different timescales - combine likelihoods for each marker in a hierarchical model
- Or analyse in the model based framework with regression / group variables.

Squid experiment (Gabi Stowasser et al. 2006)

Shrimp ~ 30 d



SC ~ 15 d



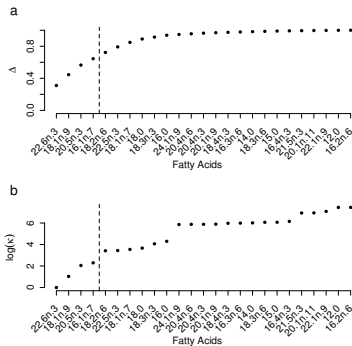
Fish ~ 30 d



SF ~ 15 d

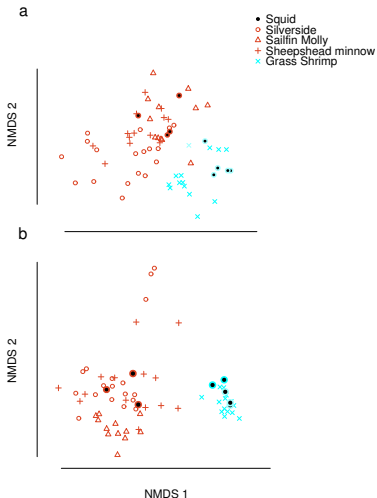


Find a subset of FAs:
contribution to source
separation in multivariate space.

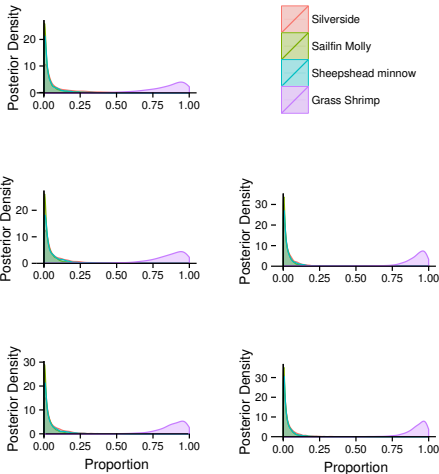


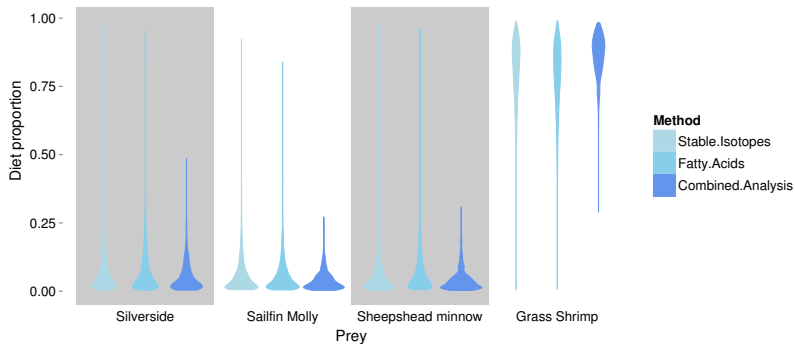
Find a subset of FAs:
contribution to source
separation in multivariate space.

Estimated conversion coeffs
from 30 day trials. Slight bias in
our favour perhaps...



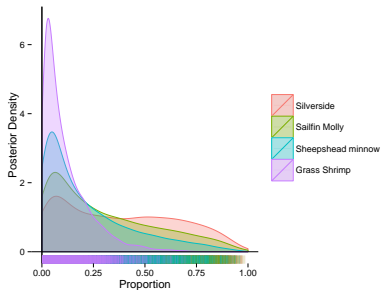
Proof of concept results



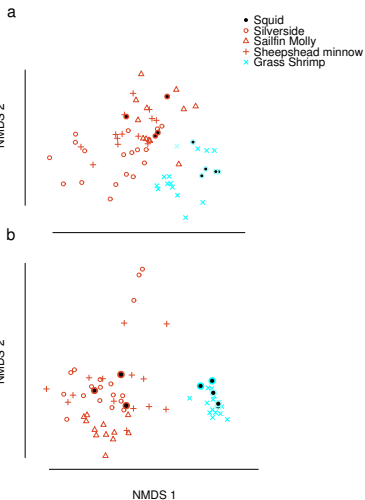


Combined markers, SC treatment

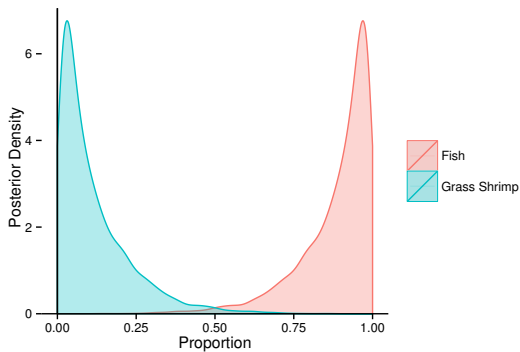
combining markers - switched treatment



Combined markers, SF treatment



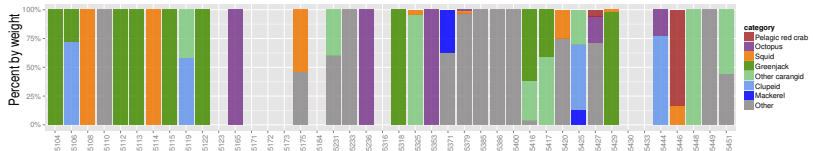
combining markers - switched treatment



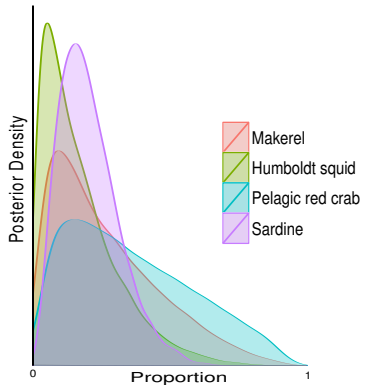
Combined markers, SF treatment

What about real systems?

Stomach contents



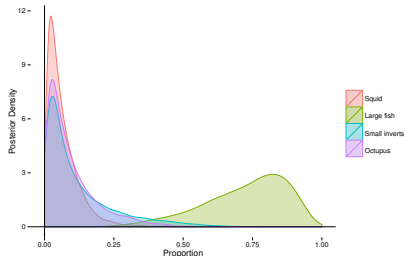
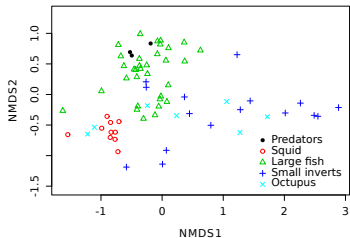
- Stomach contents suggest highly variable diets among individuals - a snapshot...
- At population level (integrated over time), diets reflect omnivory.



Sea-lion

preliminary results from early 2000's sea lion

Large fish clearly dominate diets - awaiting funding decision to look into time trends...



Plasticity and uncertainty in diets:

Plasticity in diets is important for food web stability, and hence an important aspect to consider in ecosystem models

Predictions of ecosystem responses to climate change are likely sensitive to assumptions about species interactions

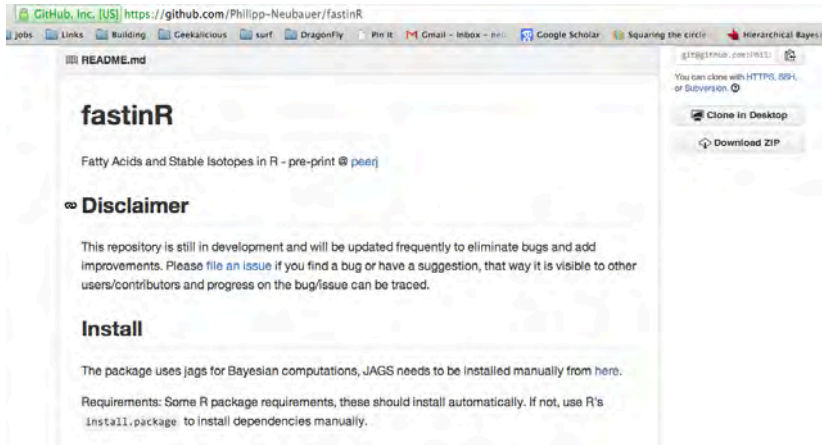
Emerging tools such as fastinR will further our empirical understanding of species diets

Need more efforts to understand fractionation / metabolic conversion to reduce uncertainties in estimates

Open source so please contribute!

Funding from NOAA co-operative grant (Olaf -> Phil), Billfish foundation (Olaf & Talia)

Thanks to the Jensen lab-group for great discussions and beta-testing!



The screenshot shows a web browser displaying the GitHub repository page for 'fastinR' by Philipp-Neubauer. The browser's address bar shows the URL 'https://github.com/Philipp-Neubauer/fastinR'. The page content includes a 'README.md' header, the repository name 'fastinR', a description 'Fatty Acids and Stable Isotopes in R - pre-print @ peerJ', a 'Disclaimer' section stating the repository is in development, and an 'Install' section mentioning the use of JAGS and R package requirements. On the right side, there are buttons for 'Clone in Desktop' and 'Download ZIP'.

GitHub, Inc. [US] https://github.com/Philipp-Neubauer/fastinR

jobs Links Building Geekalicious surf DragonFly Pin It Gmail - Inbox - help Google Scholar Squaring the circle Hierarchical Bayes

g1r@github.com:fastinR

You can clone with HTTP, SSH, or Subversion.

Clone in Desktop

Download ZIP

README.md

fastinR

Fatty Acids and Stable Isotopes in R - pre-print @ [peerJ](#)

⚠ Disclaimer

This repository is still in development and will be updated frequently to eliminate bugs and add improvements. Please [file an issue](#) if you find a bug or have a suggestion, that way it is visible to other users/contributors and progress on the bug/issue can be traced.

Install

The package uses jags for Bayesian computations, JAGS needs to be installed manually from [here](#).

Requirements: Some R package requirements, these should install automatically. If not, use R's `install.packages` to install dependencies manually.

5.1 Estimating population proportions

5.1.1 Stable Isotopes alone

Lets start with an analysis of the stable isotopes, estimating only global (population) level diets. We will use the default prior on the predator covariance matrix, and will adjust this prior subsequently. ***WARNING*** This might take a while depending on your resources, the size of the dataset and the parameters used for the MCMC.

```
Pop.SI <- run_MCMC(datas = datas.subset, nIter = 20000,  
  nBurnin = 10000, nChains = 3, nThin = 20, Data.Type = "Stable.Isotopes",  
  Analysis.Type = "Population.proportions", Rnot_SI = 0.1,  
  plott = F, spawn = F)
```

Plotting the MCMC is the easiest way to ensure that the sampler is mixing - meaning that the chain explores the posterior distribution of each parameter efficiently.

```
MCMCplot(Pop.SI)
```

Open source so please contribute!

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