3rd STABLE ISOTOPE COURSE IN ECOLOGY AND ENVIRONMENTAL SCIENCES
2018

Isotopic Mixing Models (MixSIAR)

12-16 Noviembre

Joan Giménez
Estación Biológica de Doñana

Why are stable isotopes useful?

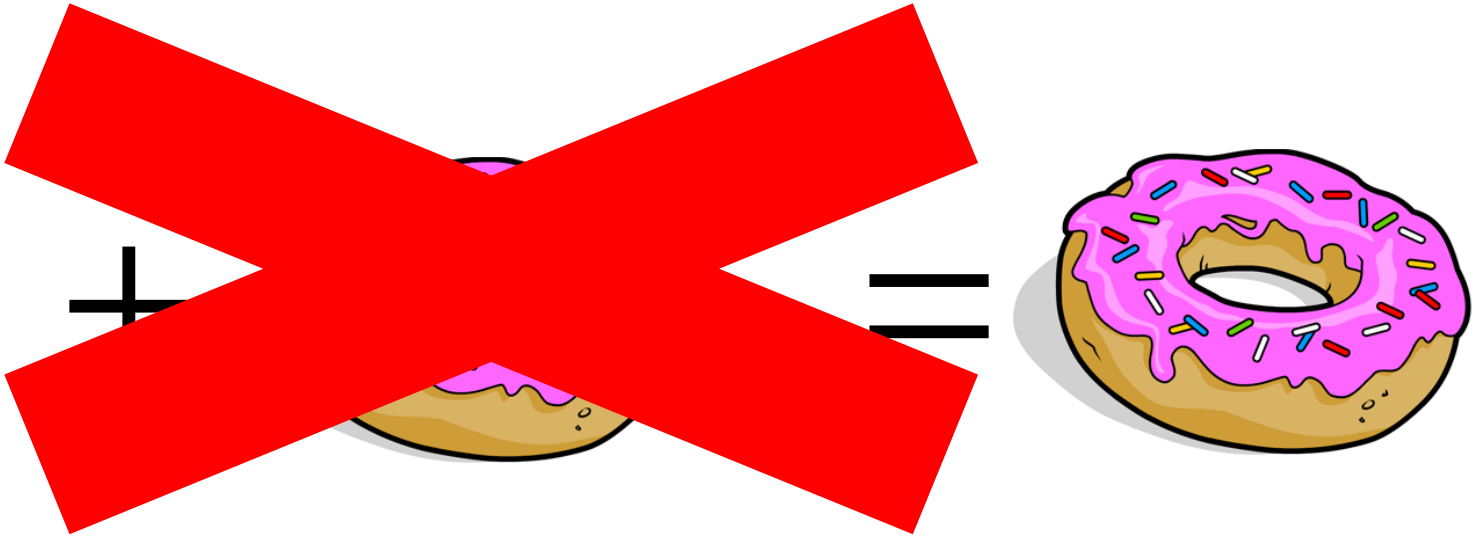
- Variation exists
- You are what you eat

+

=

Why are stable isotopes useful?

- Variation exists
- You are what you eat



Why are stable isotopes useful?

- Variation exists
- You are what you eat + something

Diet-to-tissue discrimination factors (DTDF) or Trophic Enrichment factors (TEF)

Recent Bayesian stable-isotope mixing models are highly sensitive to variation in discrimination factors

ALEXANDER L. BOND[1] AND ANTONY W. DIAMOND

Ecological Applications, 21(4), 2011, pp. 1017–1023

+1‰ for C (DeNiro and Epstein 1978)
+3‰ for N (DeNiro and Epstein 1981)

Considerable variation in isotopic discrimination factors as a function of:

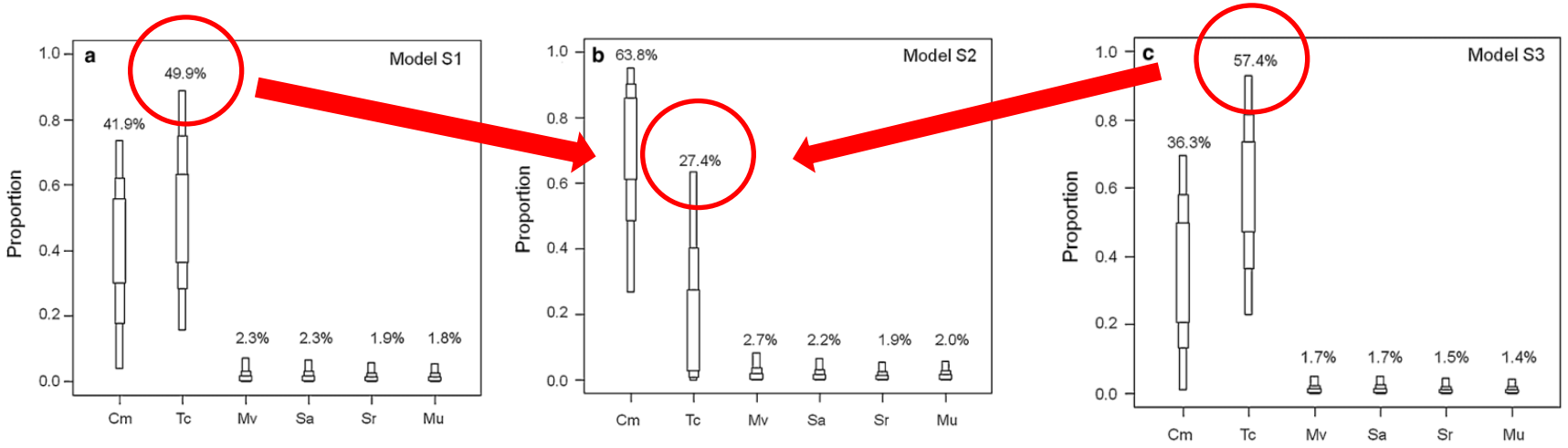
- **Extrinsic factors**
  e.g. diet quality or composition (McCutchan Jr. et al., 2003; Robbins et al., 2005)
- **Intrinsic factors**
  e.g. taxa, (Caut et al., 2009; Vanderklift and Ponsard, 2003); or age (Hobson and Quirk, 2014; Minagawa and Wada, 1984)).

	Model S1	Model S2	Model S3
	Caut et al. (2011)	Hobson et al. (1996)	Borrell et al. (2012)
$\Delta^{13}C$	2.4 ± 0.2	2.8 ± 0.1	1.3 ± 0.4
$\Delta^{15}N$	3.2 ± 0.15	2.3 ± 0.3	2.8 ± 0.3

Bottlenose dophin blood

Seals

Fin whale



***e.g.* Kiszka *et al.* (2014) Mar Biol**

APPLICATIONS

Diet recontruction

"animals are what they eat + something"

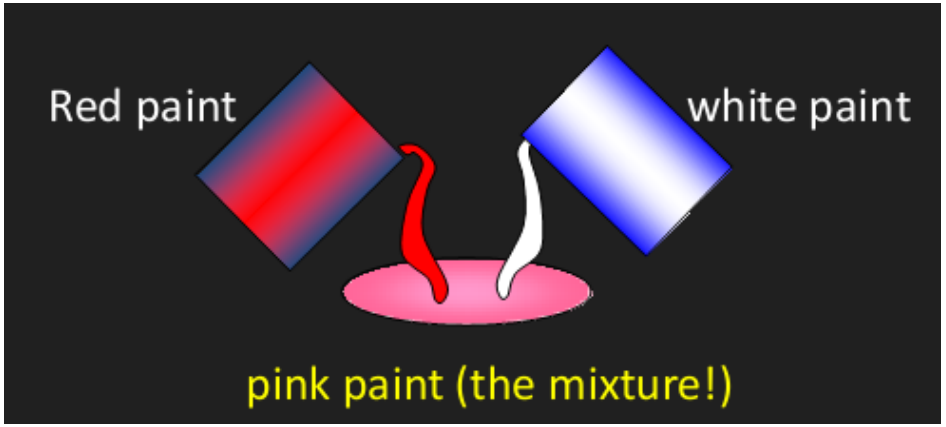
The isotopic composition of an animal tissue reflects the contribution of dietary components with different isotopic compositions

(DeNiro and Epstein, 1978, 1981)

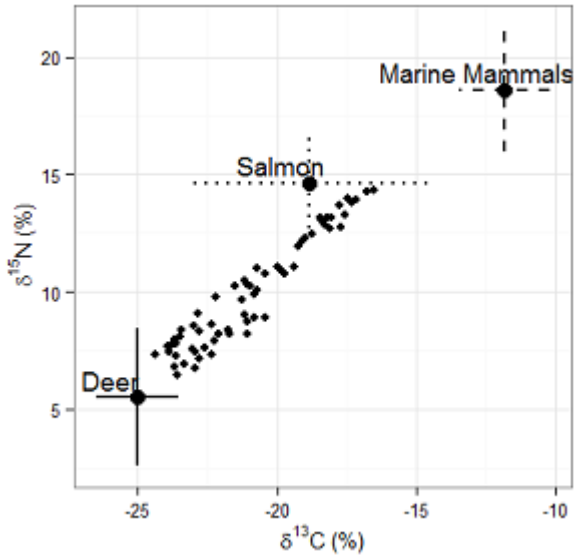
If we know:

- ***Stable isotope signature of potential preys***
- ***Stable isotope signature of the predator***
- ***We can estimate the proportion of each prey to the diet of the predator***

Mass-balance mixing models



= Closer you are to a source, the more of it you're eating



ISOTOPIC MIXING MODELS

Linear Mixing models

n isotope systems are used to determine the proportional contributions of n+1 sources to a mixture.

IsoSource

http://www.epa.gov/wed/pages/models.htm

Oecologia (2003) 136:261–269
DOI 10.1007/s00442-003-1218-3

ECOSYSTEMS ECOLOGY

Donald L. Phillips · Jillian W. Gregg

Source partitioning using stable isotopes: coping with too many sources

ISOTOPIC MIXING MODELS

IsoSource
(Phillips and Gregg, 2003)

MixSIR
(Moore and Semmens , 2008)

SIAR
(Parnell et al., 2008)

IstopeR
(Hopkins and Ferguson, 2012)

IsoWeb
(Kodoya et al, 2012)

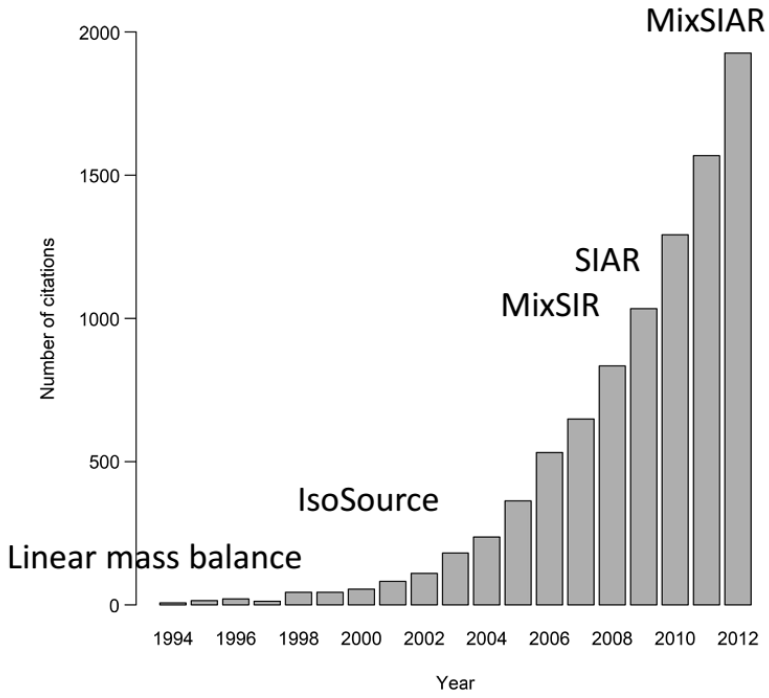
SISUS
(Erhardt et al., 2012)

FRUITS
(Fernandes et al, 2014)

MixSIAR

ISOTOPIC MIXING MODELS

- Researchers use mixing models a lot.



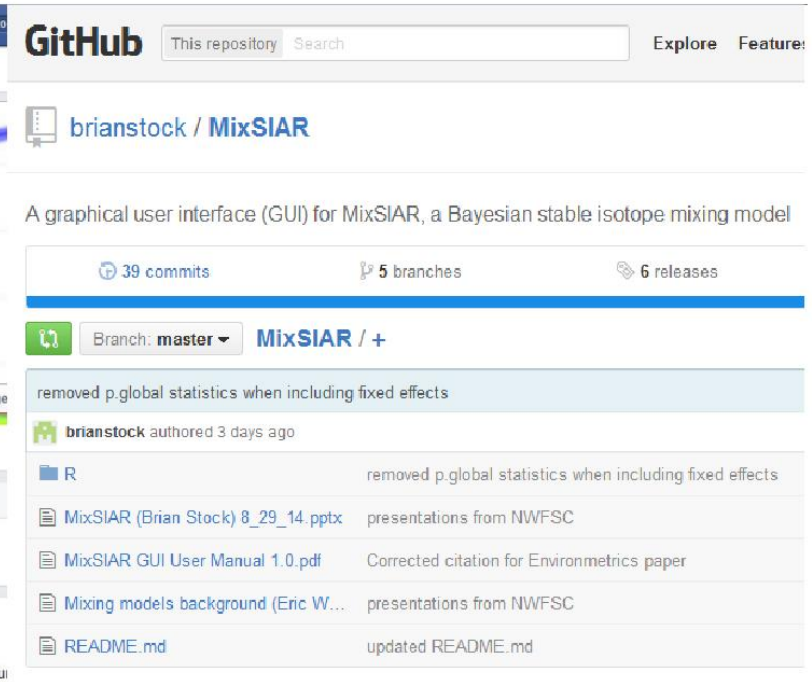
Pros of Bayesian mixing models

Firm statistical foundation
- Uncertainty in consumer, source, and TDF data

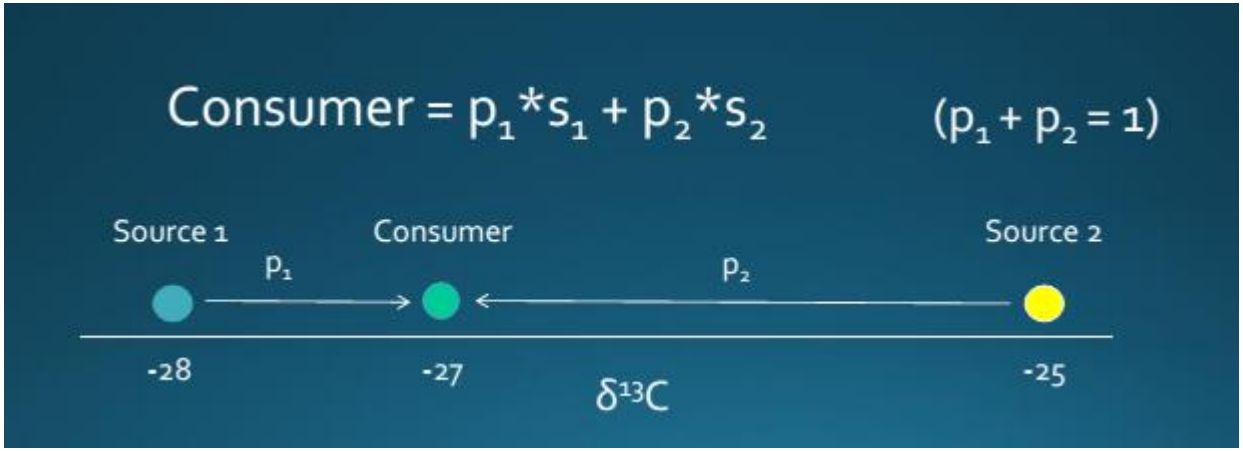
Biological complexity
- Differences due to covariates (*e.g.* sex, region, size)
- Non-biotracer data as priors (*e.g.* stomach/fecal contents, prey abundance)

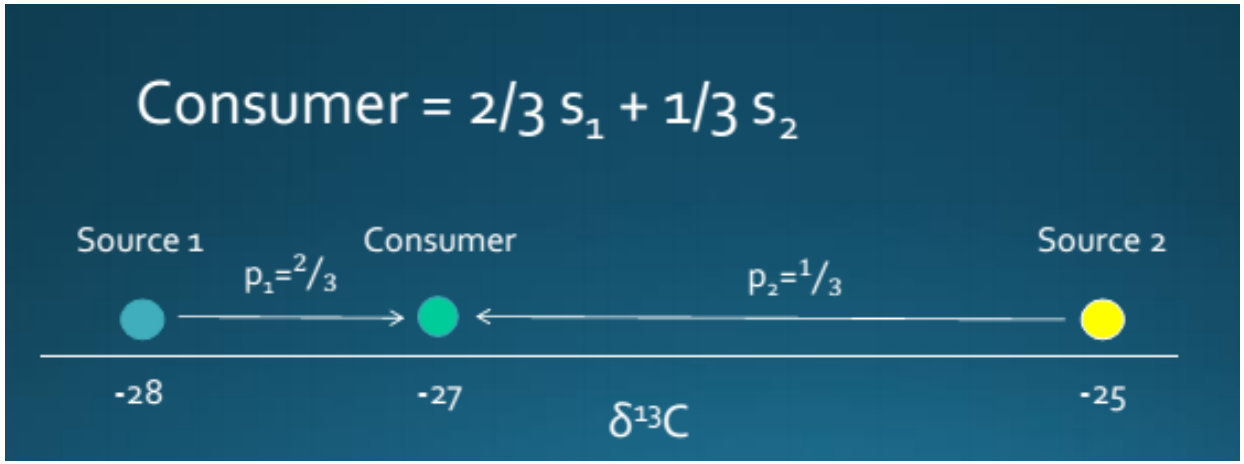
Remember:
Garbage in, garbage out (*e.g.* many sources, 2 tracers)

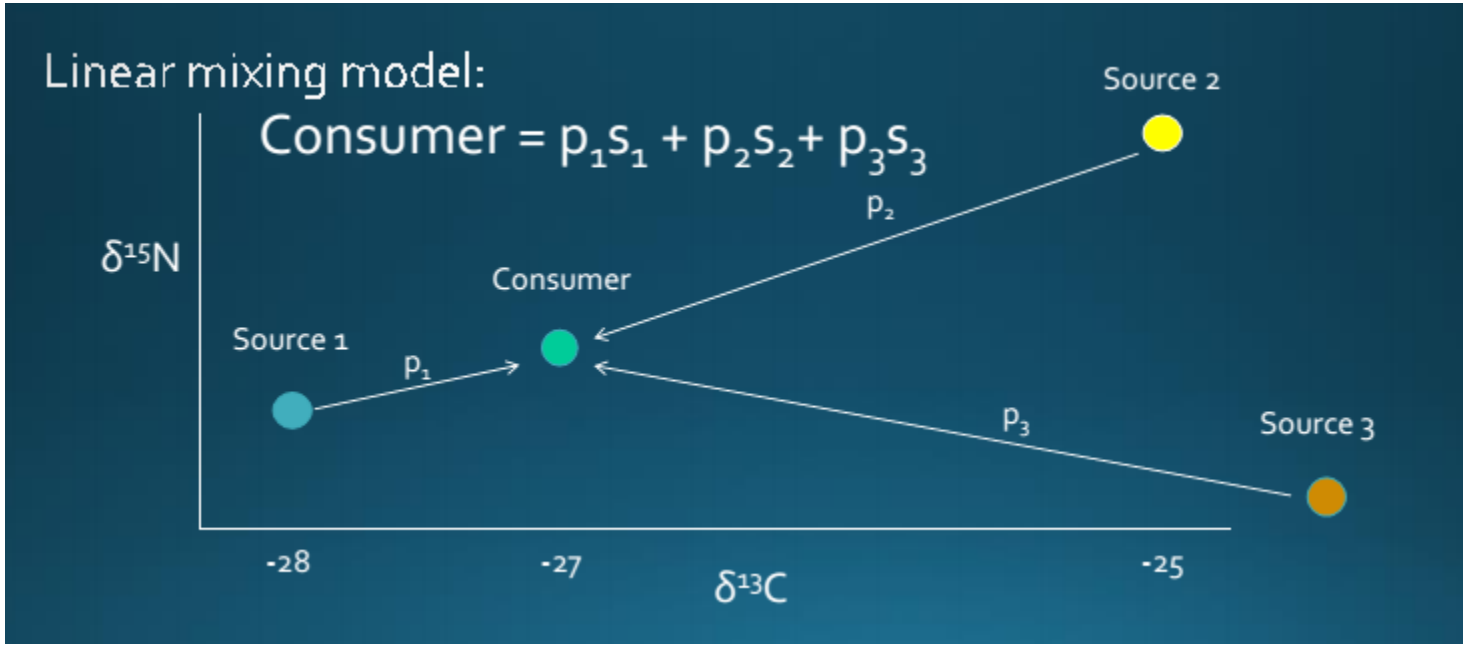
- Many researchers using mixing models
- Many questions
- Many answers

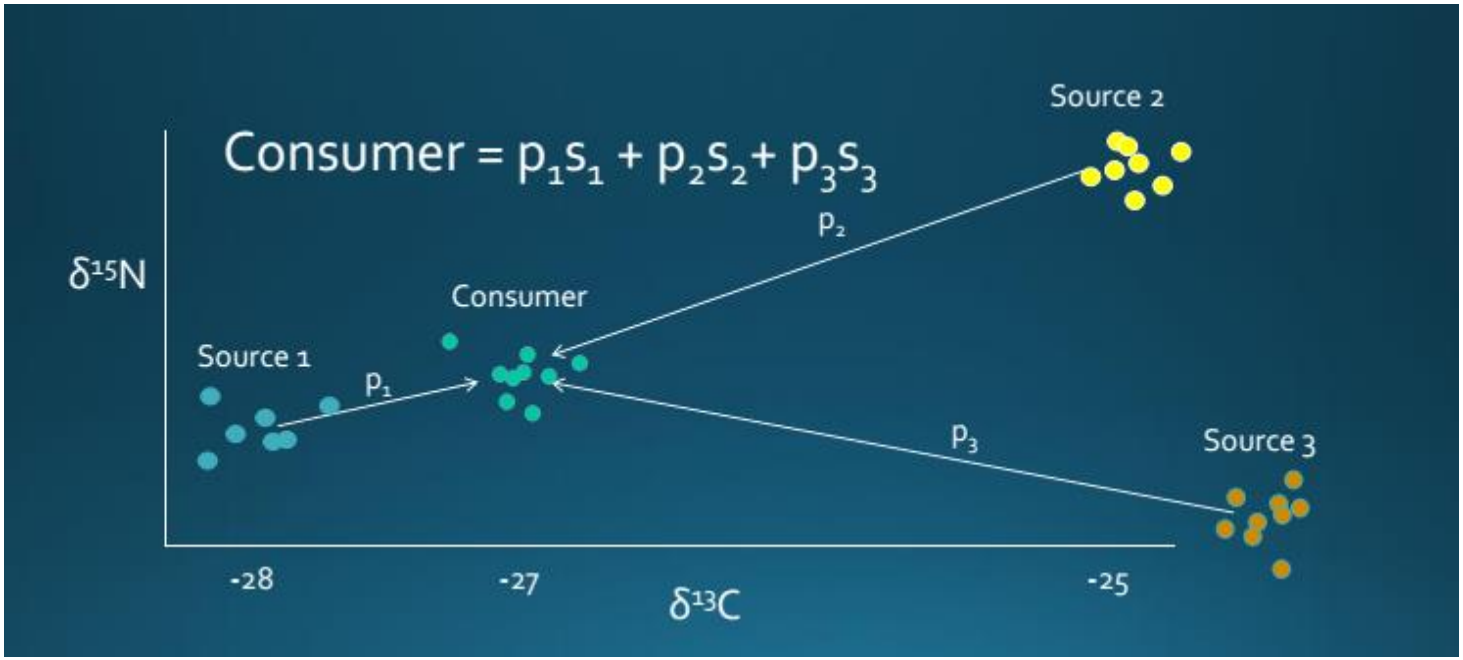


Linear mixing model






Linear mixing model:
Consumer = $p_1s_1 + p_2s_2 + p_3s_3$
Source 2
p_2
$\delta^{15}N$
Consumer
Source 1
p_1
p_3
Source 3
-28
-27
-25
$\delta^{13}C$


Consumer = $p_1s_1 + p_2s_2 + p_3s_3$
Source 2
p_2
$\delta^{15}N$
Consumer
Source 1
p_1
p_3
Source 3
-28
-27
-25
$\delta^{13}C$

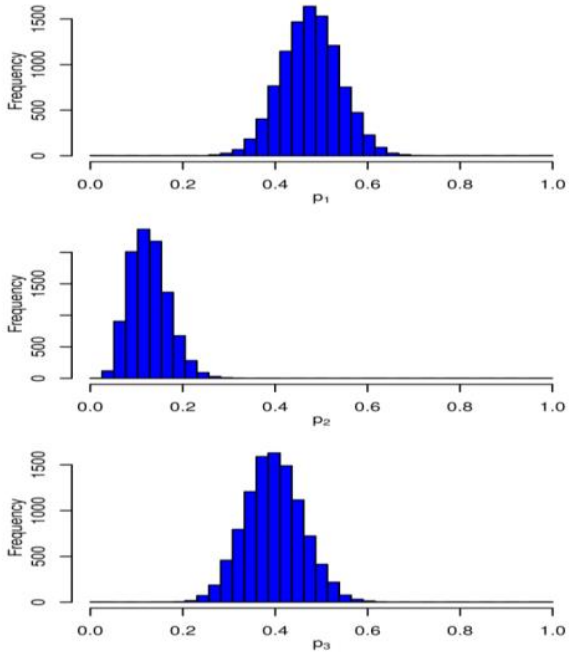
Informative priors

30  47.61 %

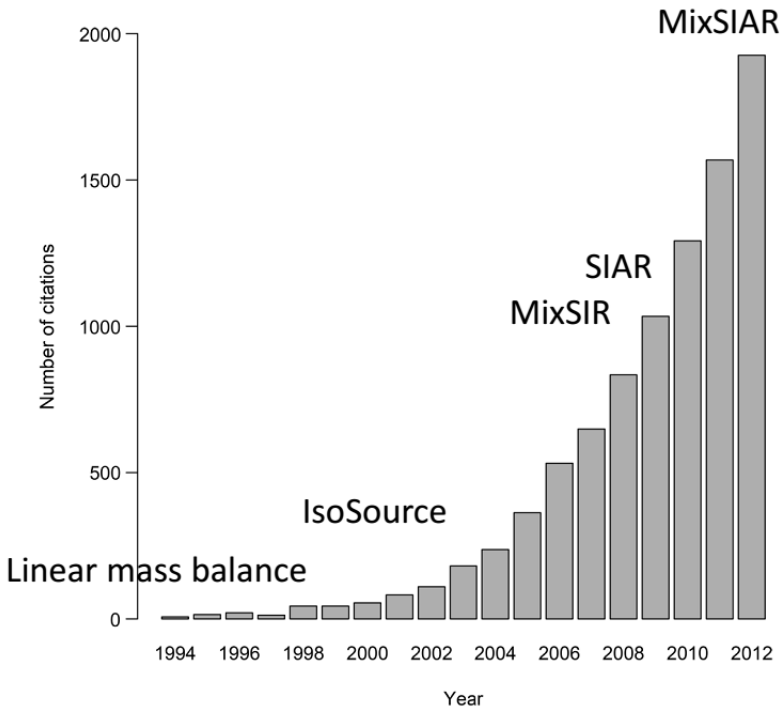
8  12.69 %

25  39.68 %

$$\alpha = (30, 8, 25)$$



ISOTOPIC MIXING MODELS



MixSIR
(Moore and Semmens , 2008)

Ecology Letters, (2008) **11**: 470–480 doi: 10.1111/j.1461-0248.2008.01163.x

LETTER

Incorporating uncertainty and prior information into stable isotope mixing models

Jonathan W. Moore[1,2*,†] and Brice X. Semmens[1,†]

Abstract

Stable isotopes are a powerful tool for ecologists, often used to assess contributions of different sources to a mixture (e.g. prey to a consumer). Mixing models use stable

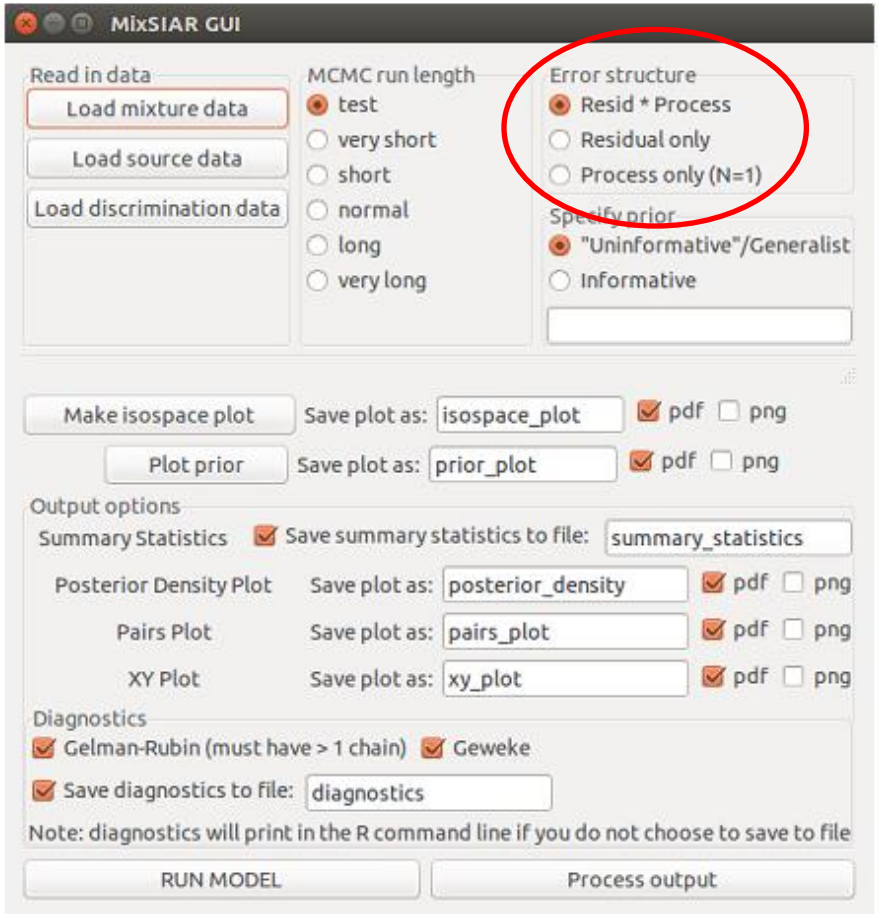
SIAR
(Parnell et al., 2008)

OPEN ACCESS Freely available online PLoS one

Source Partitioning Using Stable Isotopes: Coping with Too Much Variation

Andrew C. Parnell[1], Richard Inger[2], Stuart Bearhop[2], Andrew L. Jackson[3*]

MixSIAR software



MixSIR
SIAR

MixSIAR

- Written in R and JAGS (open source)
- Incorporates recent advances in mixing model methods

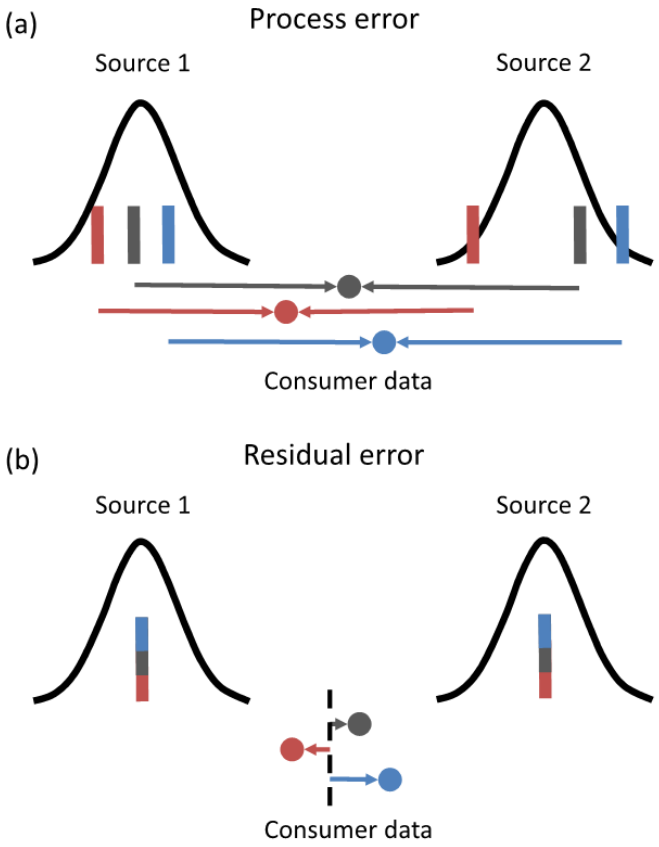
- Adresses variability in source and discrimination values
- Adresses variation in mixture population (random, fixed and continous effects)

Statistical Reports

Ecology, 97(10), 2016, pp. 2562–2569

Unifying error structures in commonly used biotracer mixing models

Brian C. Stock[1] and Brice X. Semmens



Process error (variation in consumer tracer values due to the sampling process)

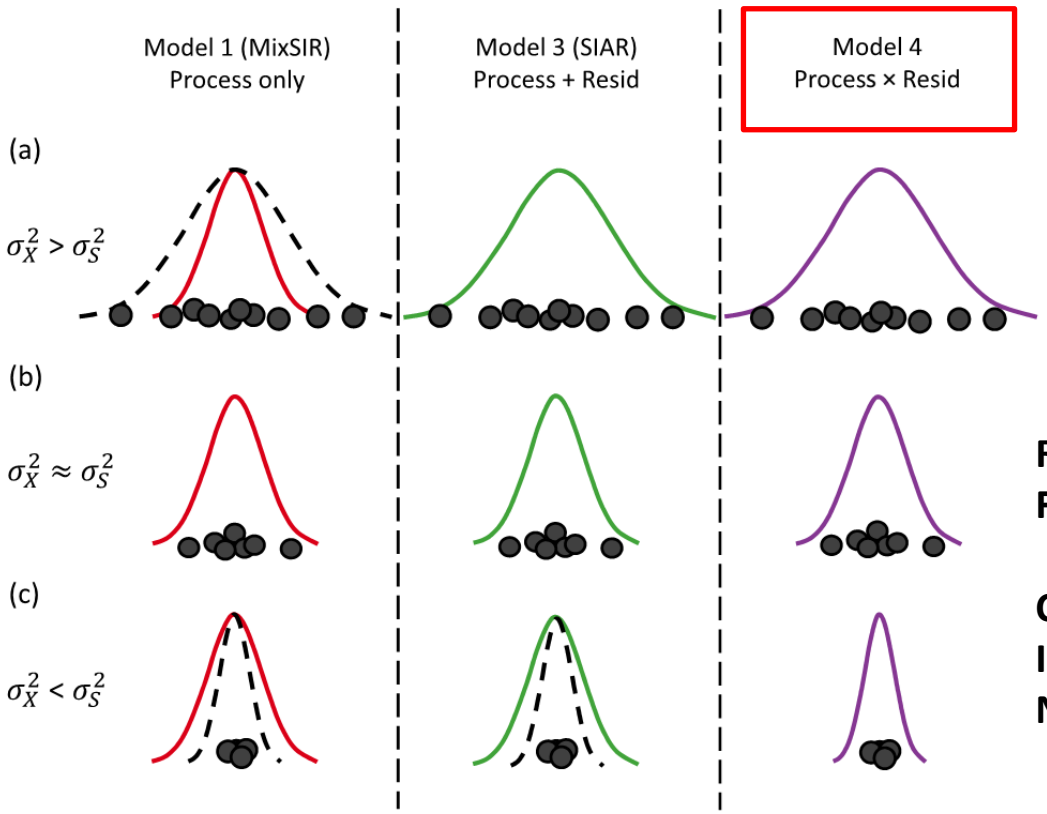
- *Sampling error:* Consumer tracer values are an average of a finite number of samples, and there will be some variability in these sample means due to chance.
- *Specialization:* Individual consumers may preferentially sample above or below the source mean, resulting in some consumers enriched or depleted.

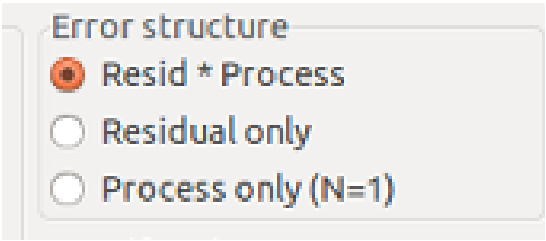
Residual error

Other agents of consumer variability, such as individual differences in digestibility, assimilation efficiency, and metabolic rates

MixSIR = Process error only
SIAR = Process + Residual error

SIAR vs MixSIR = assumption aboout consumer variability





Random effects – Resid * Process
Fixed effects - Resid * Process (taxa)
- Residual only (group)
Continuos effects – Residual only
Id as fixed effect – Process only (N=1)
Not dietary applications – Residual only

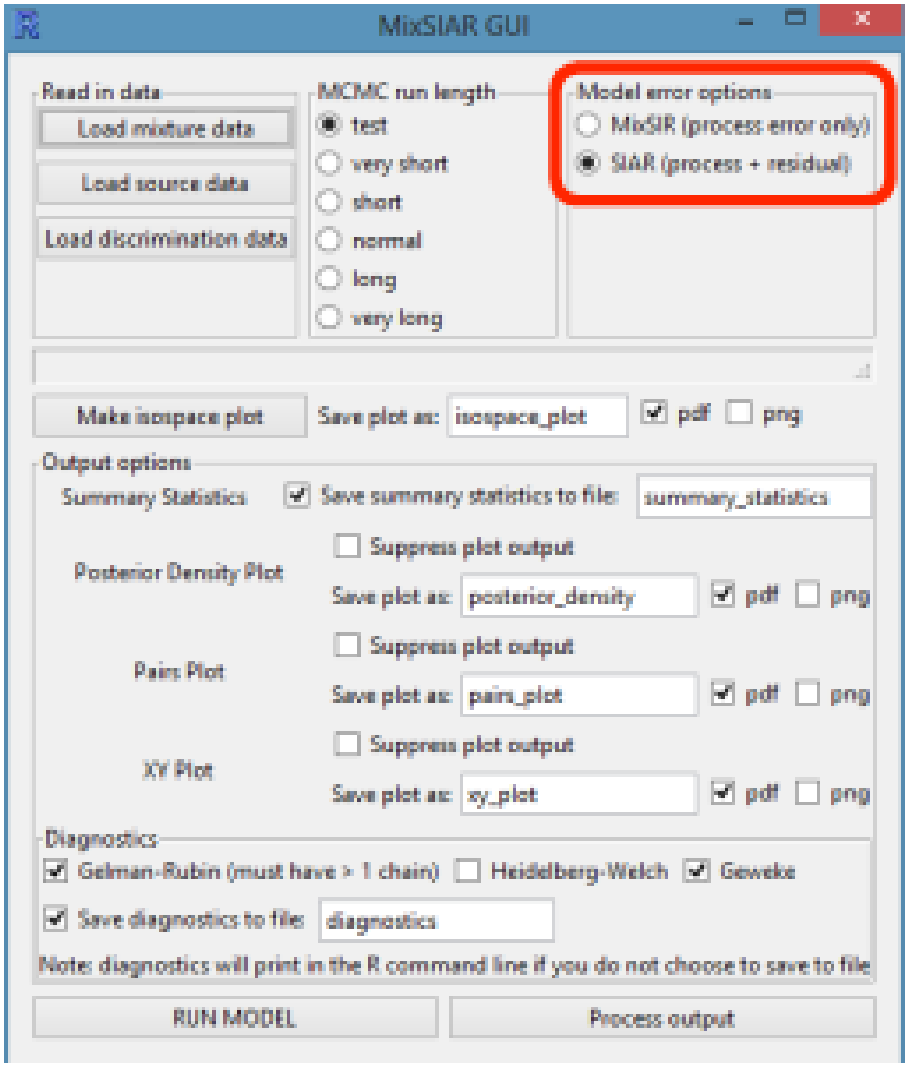
Model assumptions

- All diet sources are included in the model
- Discrimination factors correctly estimated
- Sources are sampled across tissue turnover period
- Geometry is critical

Application to other biotracers

- Fatty acids
- Compound-specific stable isotopes
- Element concentrations

More biotracers = Better performance


MixSIAR GUI
Read in data
Load mixture data
Load source data
Load discrimination data
MCMC run length
test
very short
short
normal
long
very long
Model error options
MixSIR (process error only)
SIAR (process + residual)
Make isospace plot
Save plot as:
isospace_plot
pdf
png
Output options
Summary Statistics
Save summary statistics to file:
summary_statistics
Posterior Density Plot
Suppress plot output
Save plot as:
posterior_density
pdf
png
Pairs Plot
Suppress plot output
Save plot as:
pairs_plot
pdf
png
XY Plot
Suppress plot output
Save plot as:
xy_plot
pdf
png
Diagnostics
Gelman-Rubin (must have > 1 chain)
Heidelberg-Welch
Geweke
Save diagnostics to file:
diagnostics
Note: diagnostics will print in the R command line if you do not choose to save to file
RUN MODEL
Process output


MixSIAR GUI
Read in data
Load mixture data
Load source data
Load discrimination data
MCMC run length
test
very short
short
normal
long
very long
Error structure
Resid * Process
Residual only
Process only (N=1)
Specify prior
"Uninformative"/Generalist
Informative
Make isospace plot
Save plot as:
isospace_plot
pdf
png
Plot prior
Save plot as:
prior_plot
pdf
png
Output options
Summary Statistics
Save summary statistics to file:
summary_statistics
Posterior Density Plot
Save plot as:
posterior_density
pdf
png
Pairs Plot
Save plot as:
pairs_plot
pdf
png
XY Plot
Save plot as:
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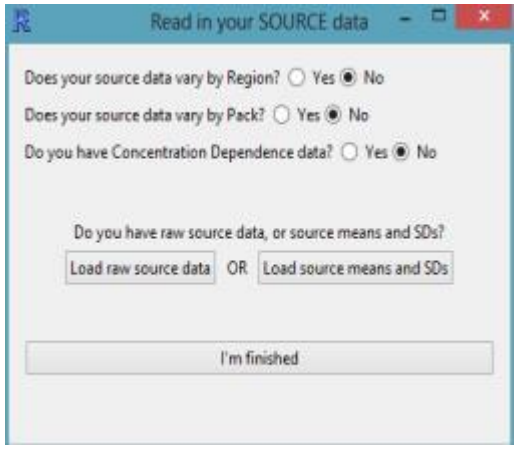
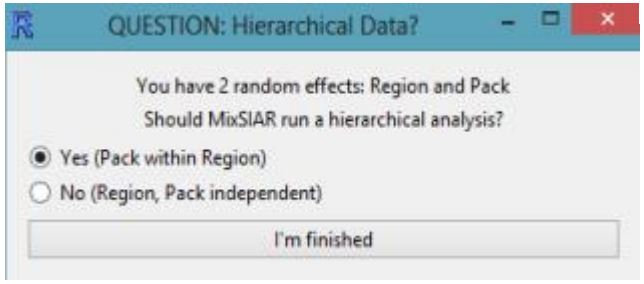
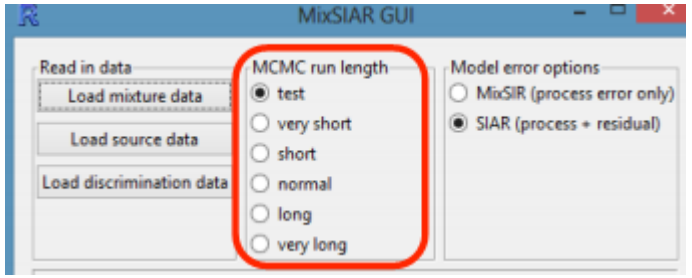
Source data options



Hierarchical/Nested data

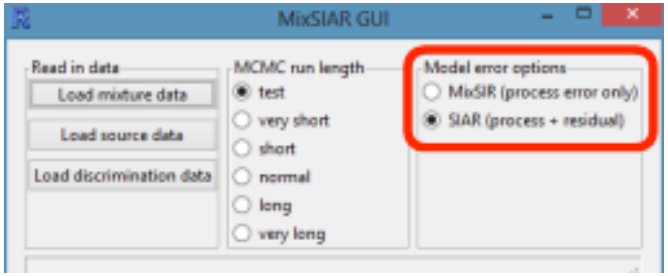


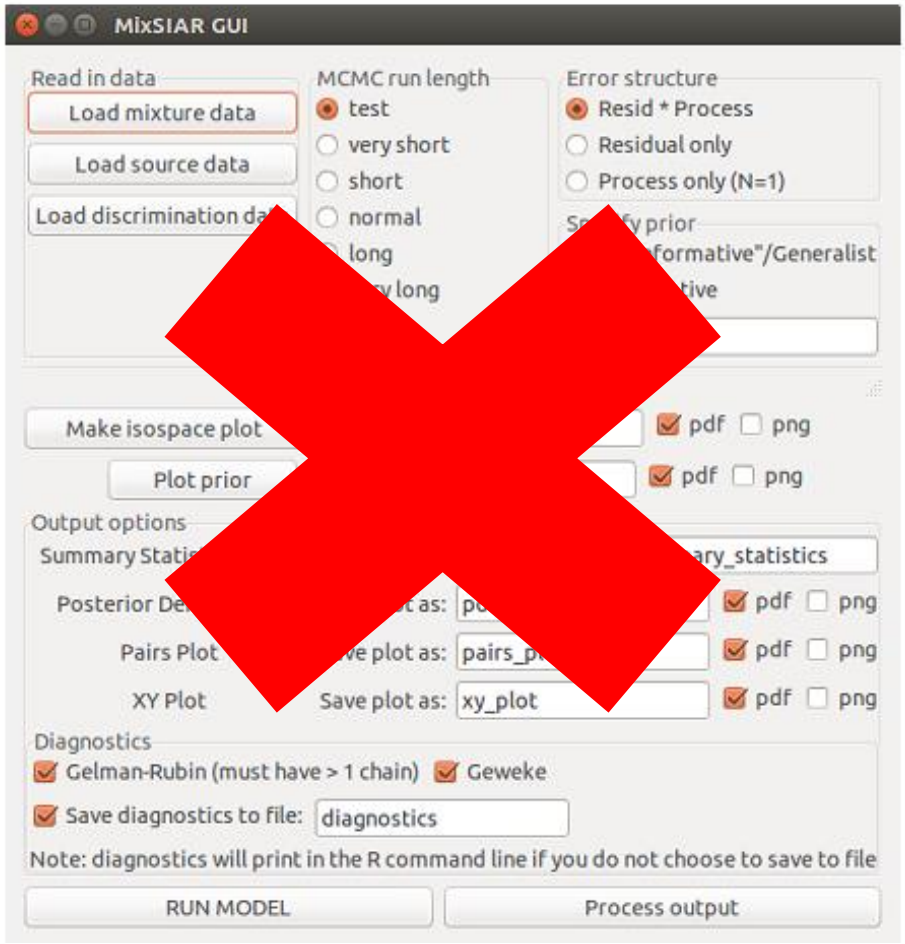
MCMC parameters



	Chain Length	Burn-in	Thin	# Chains	Est. runtime
test	1,000	500	1	3	5 sec
very short	10,000	5,000	5	3	3 min
short	50,000	25,000	25	3	15 min
normal	100,000	50,000	50	3	30 min
long	300,000	200,000	100	3	90 min
very long	1,000,000	500,000	500	3	5 hours
extreme	3,000,000	1,500,000	500	3	15 hours

Error structure





We are not going to use the GUI!!!!

The script version advantages:

1. Repeatability
2. Speed
3. Installation easy

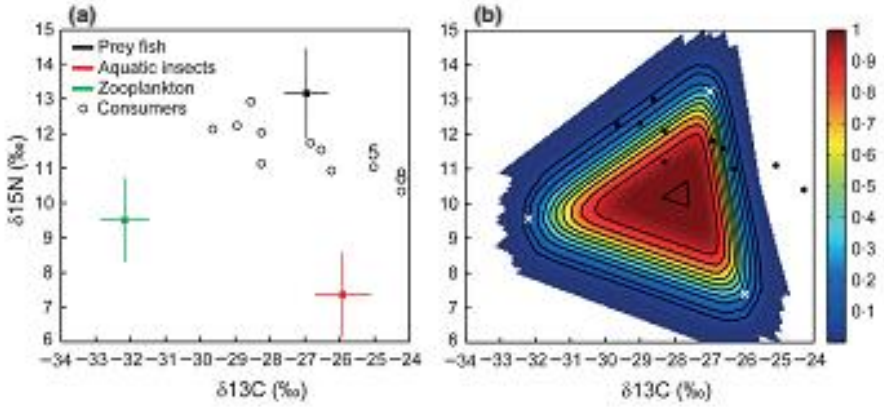
Stable Isotope Geometry

Methods in Ecology and Evolution

Methods in Ecology and Evolution 2013, 4, 612–618 doi: 10.1111/2041-210X.12048

To fit or not to fit: evaluating stable isotope mixing models using simulated mixing polygons

James A. Smith[1*], Debashish Mazumder[2], Iain M. Suthers[1] and Matthew D. Taylor[1,3]



- Quantitative method for determining whether a proposed mixing model is likely to explain the isotopic signatures of all consumers, before the model is run.
- To identify consumers for exclusion or to reject a model outright.

- This point-in-polygon assumption is not inherent in the Bayesian mixing models, because the source data are distributions not average values, and these models will quantify source contributions even when the solution is very unlikely.