MixSIAR:
Advanced stable isotope mixing models in R

Brian Stock, Brice Semmens, Eric Ward, Jonathan Moore, Andrew Parnell, Andrew Jackson, Donald Phillips, Stuart Bearhop, Richard Inger

Motivation

What do we mean by “estimate diet”?

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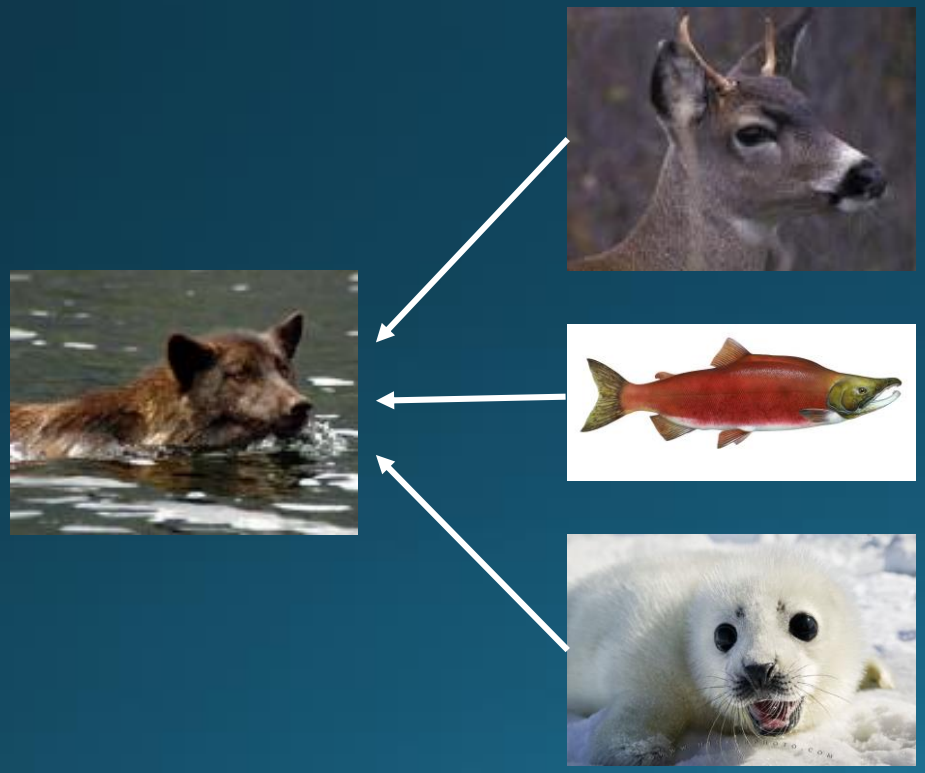

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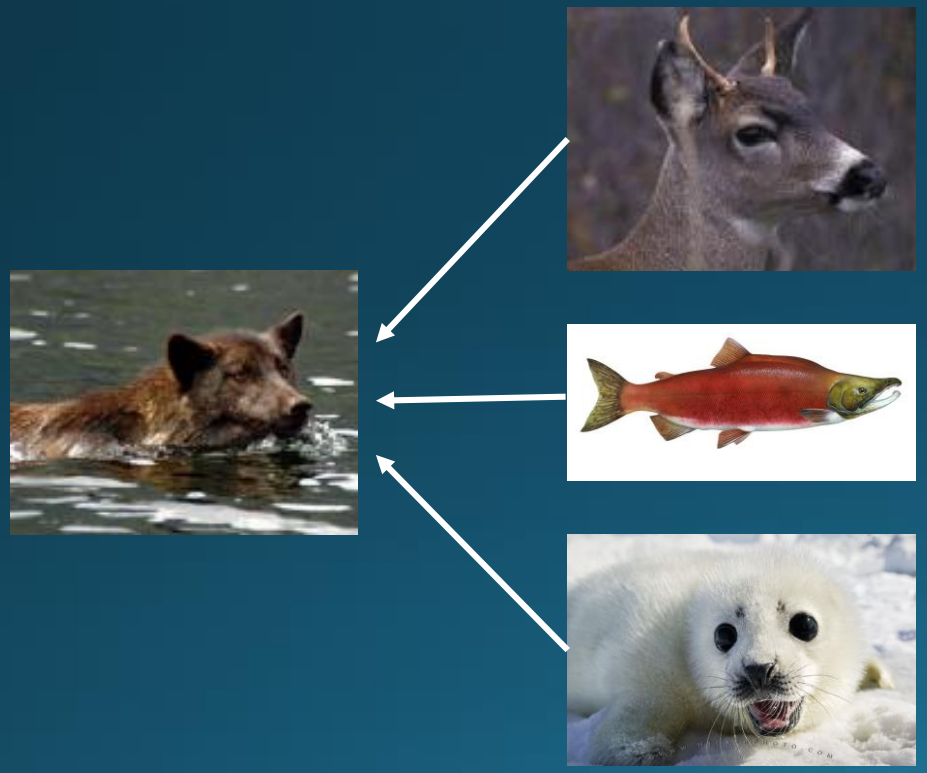

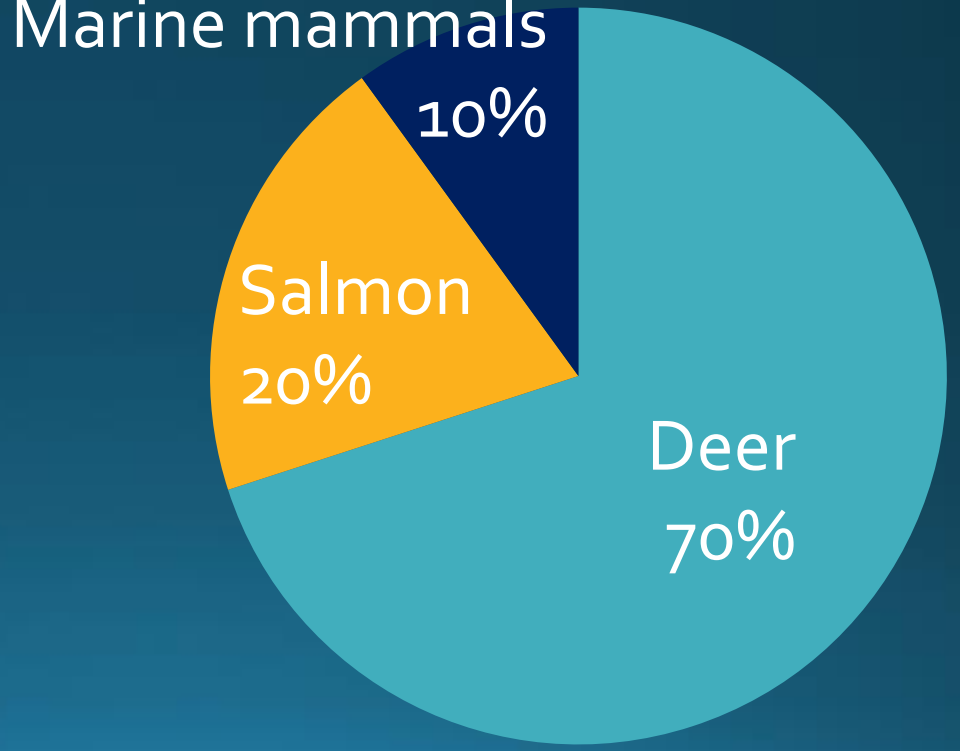

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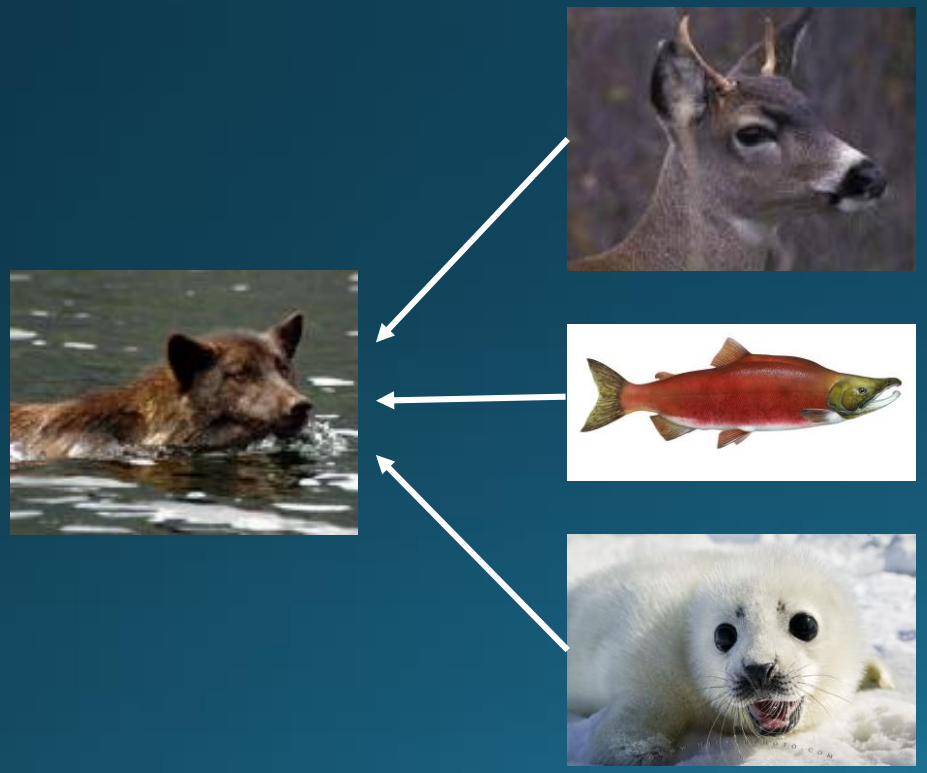
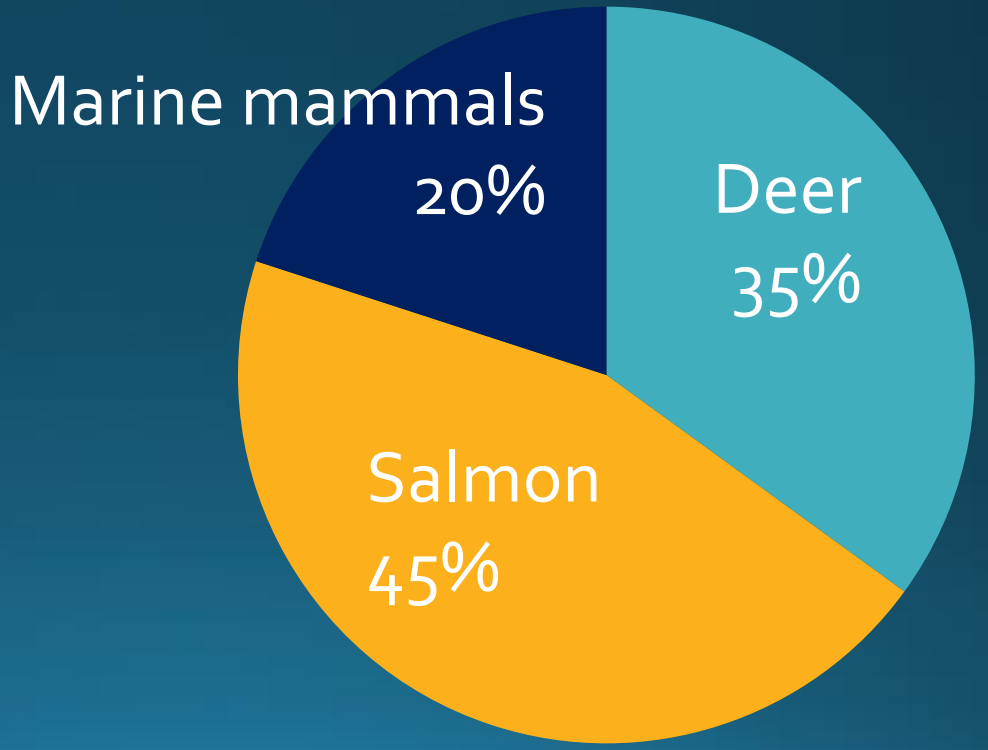
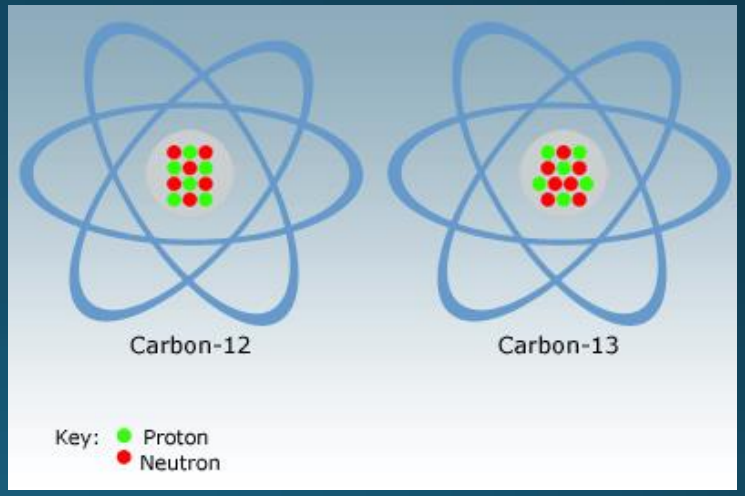




Stable isotope mixing models

What are stable isotopes?

- Elemental variants (extra neutrons) that do not decay
  - ^{12}C, ^{13}C
  - ^{14}N, ^{15}N
  - ^{16}O, ^{18}O
  - ^{32}S, ^{34}S



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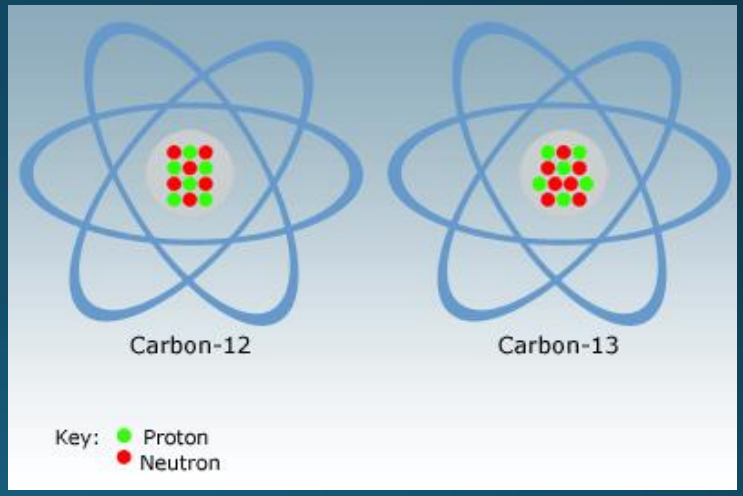

Stable isotope mixing models

Why are stable isotopes useful?

Stable isotope mixing models

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Principle #1

Variation exists

Stable isotope mixing models

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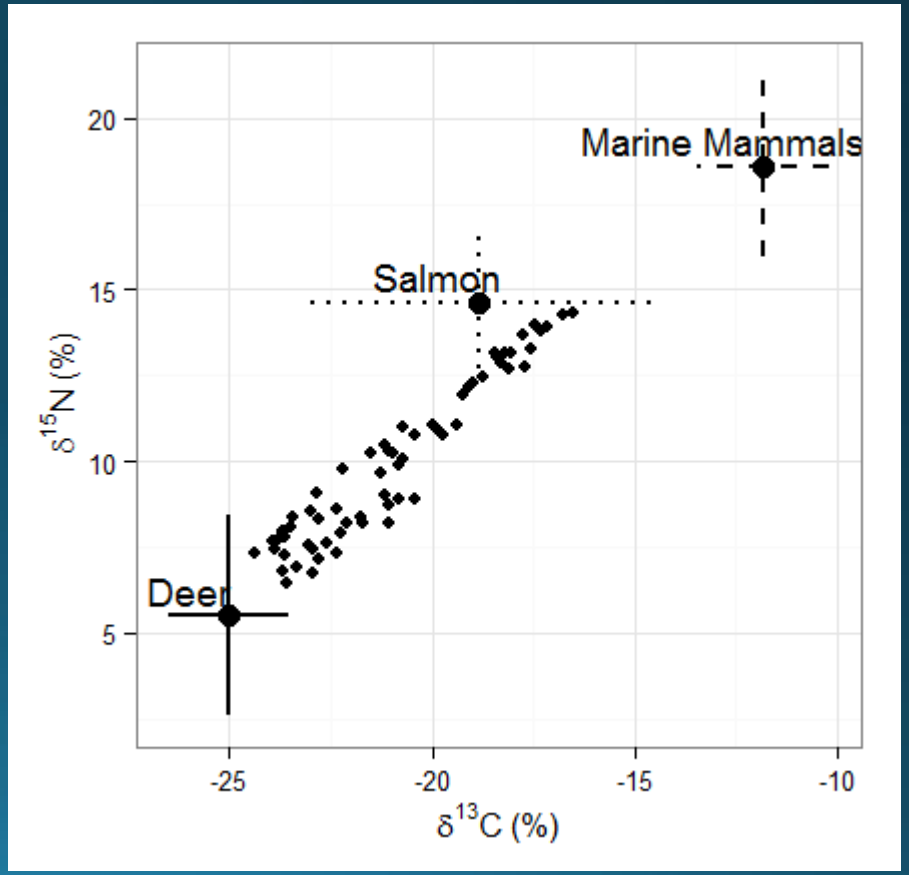
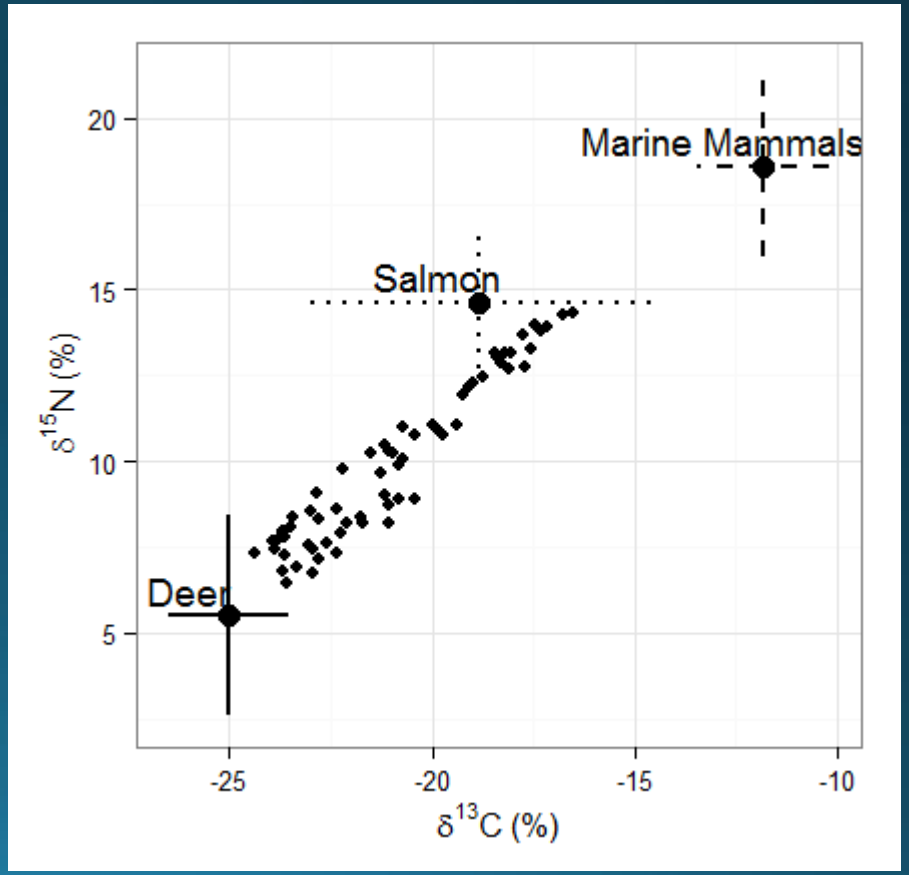


Stable isotope mixing models

Why are stable isotopes useful?

Principle #2

"You are what you eat"



Stable isotope mixing models

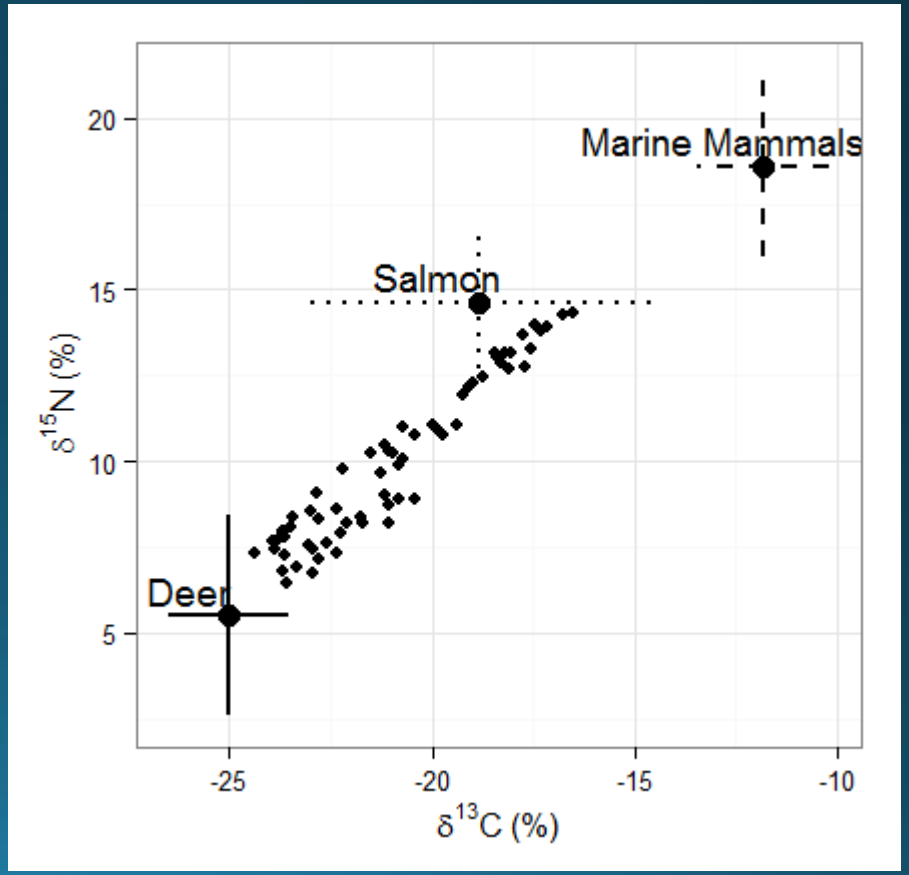
Why are stable isotopes useful?

Variation exists

+ "You are what you eat"

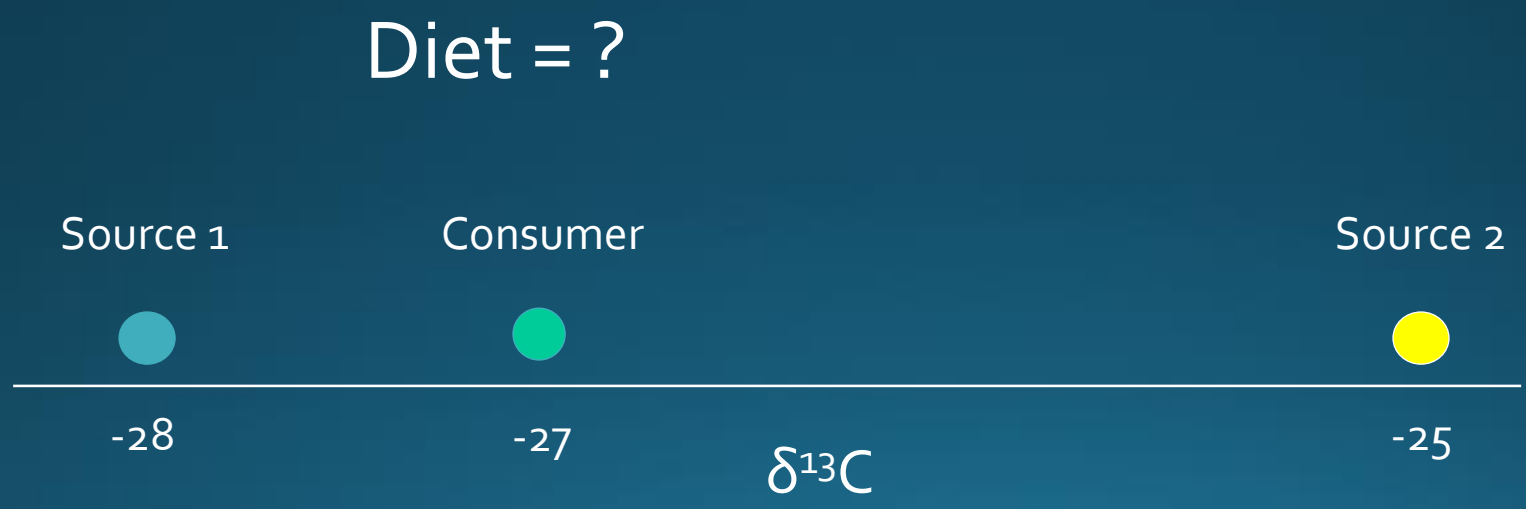
= Closer you are to a source,

the more of it you're eating



Stable isotope mixing models

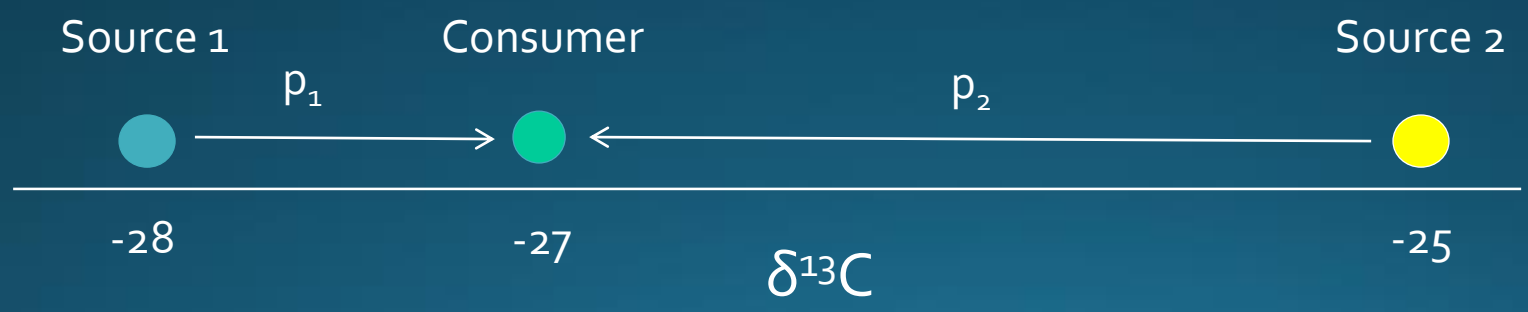
Linear mixing model:



Stable isotope mixing models

Linear mixing model:

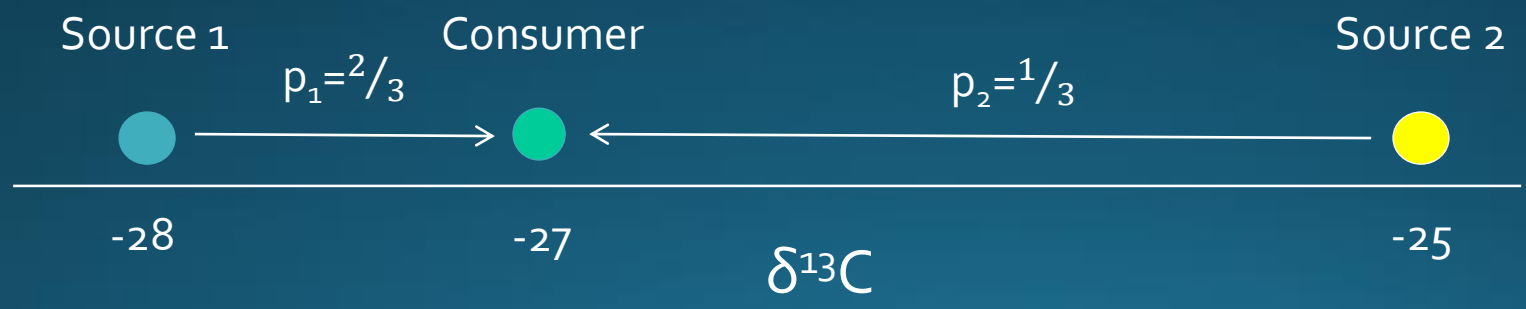
$$\text{Consumer} = p_1 * s_1 + p_2 * s_2 \qquad (p_1 + p_2 = 1)$$



Stable isotope mixing models

Linear mixing model:

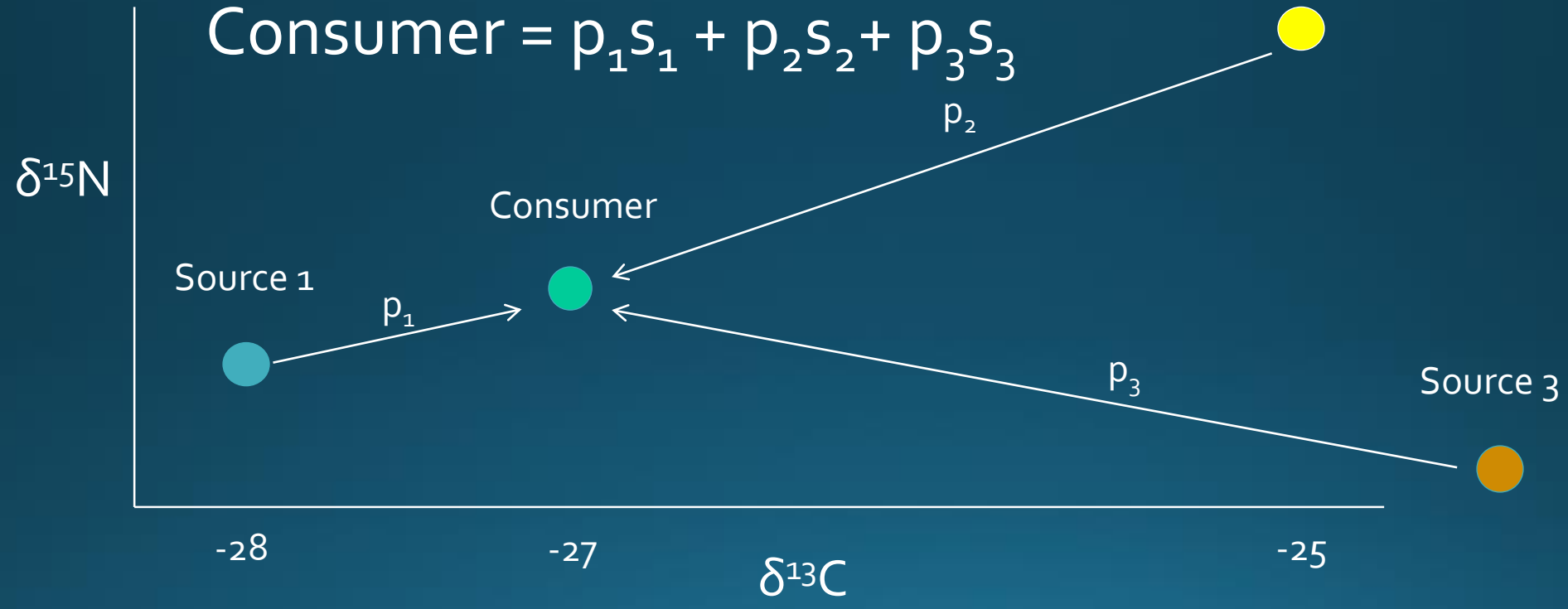
$$\text{Consumer} = 2/3\ s_1 + 1/3\ s_2$$



Stable isotope mixing models

Linear mixing model:

$$\text{Consumer} = p_1 s_1 + p_2 s_2 + p_3 s_3$$



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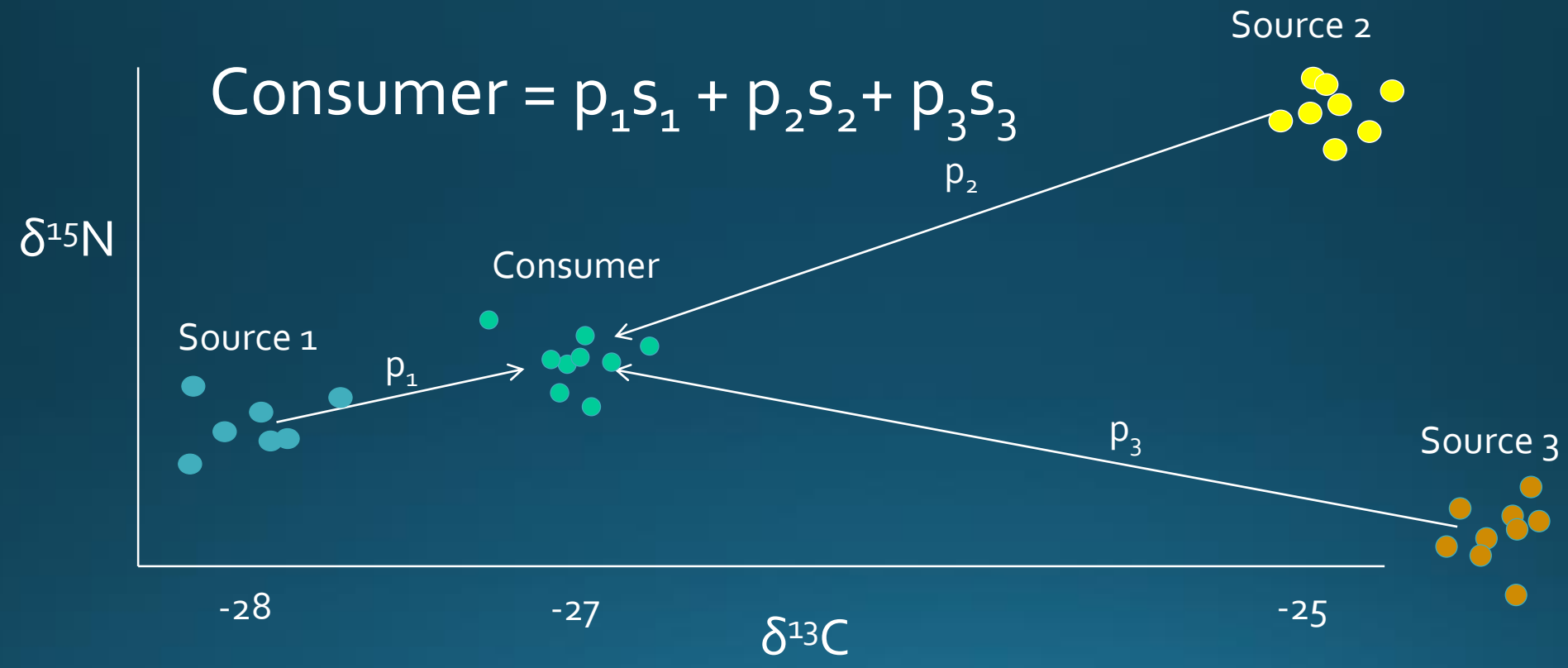

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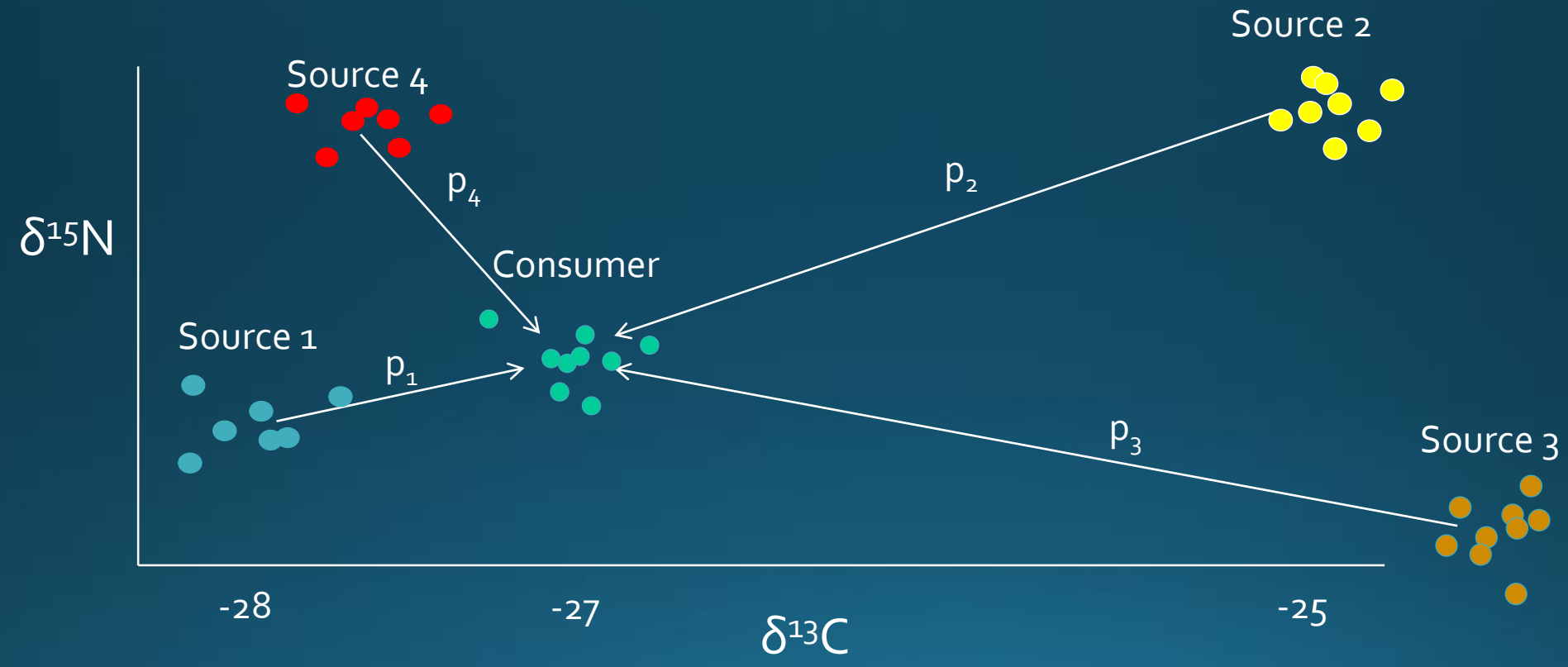

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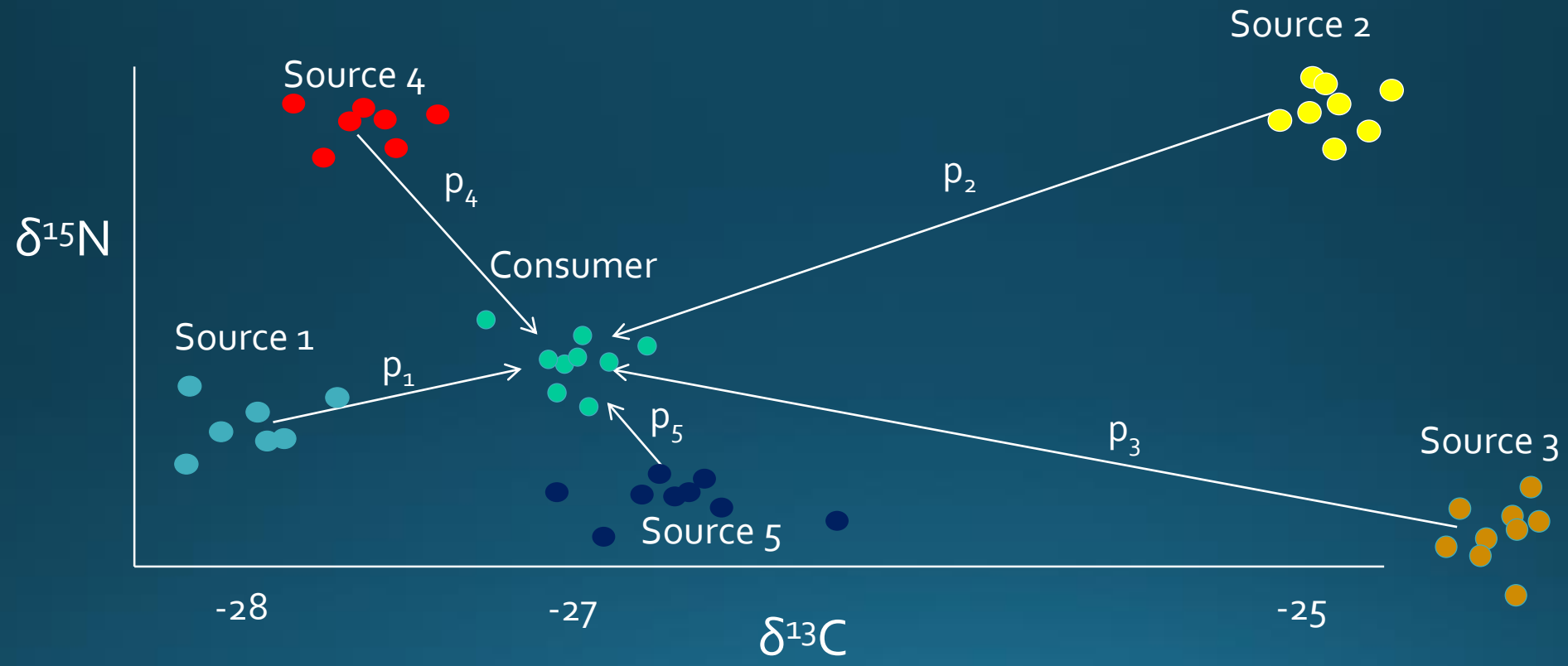

Bayesian mixing models

LETTER

Incorporating uncertainty and prior information into stable isotope mixing models

Moore and Semmens (2008)

MixSIR

Bayesian mixing models

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Erroneous behaviour of MixSIR, a recently published Bayesian isotope mixing model: a discussion of Moore & Semmens (2008)

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SIAR

OPEN ACCESS Freely available online

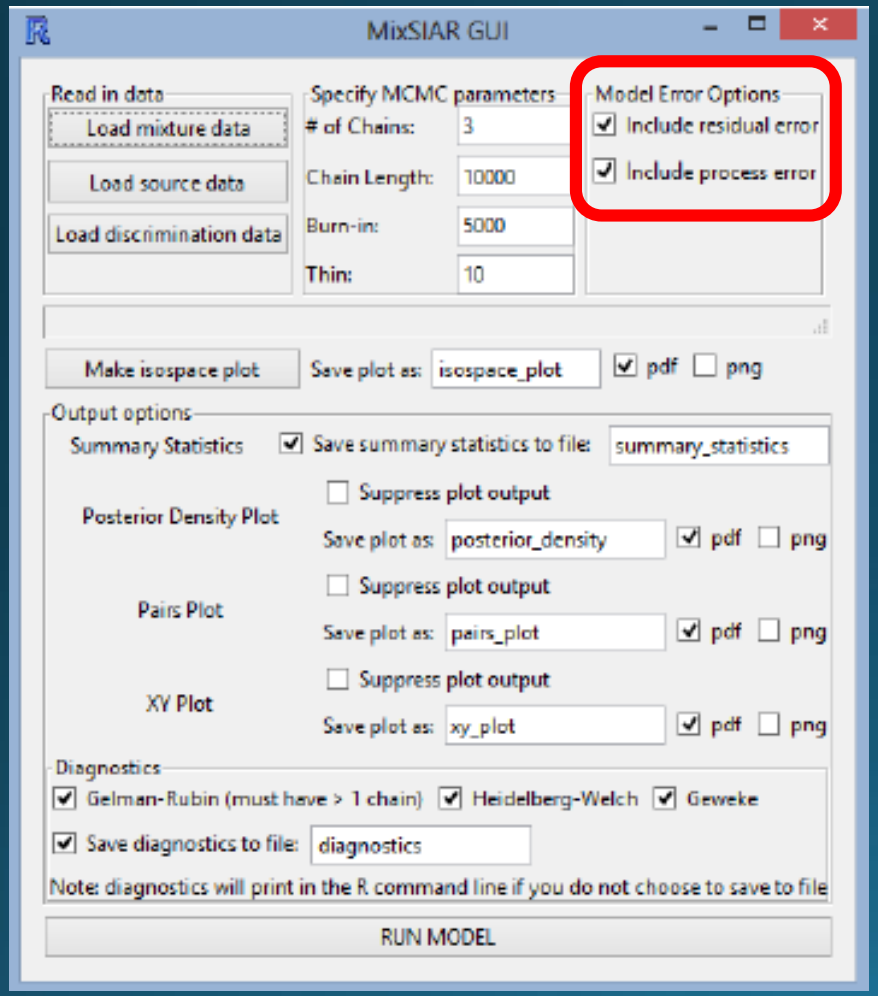
PLoS one

Source Partitioning Using Stable Isotopes: Coping with Too Much Variation

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

Parnell et al. (2010)

MixSIAR software

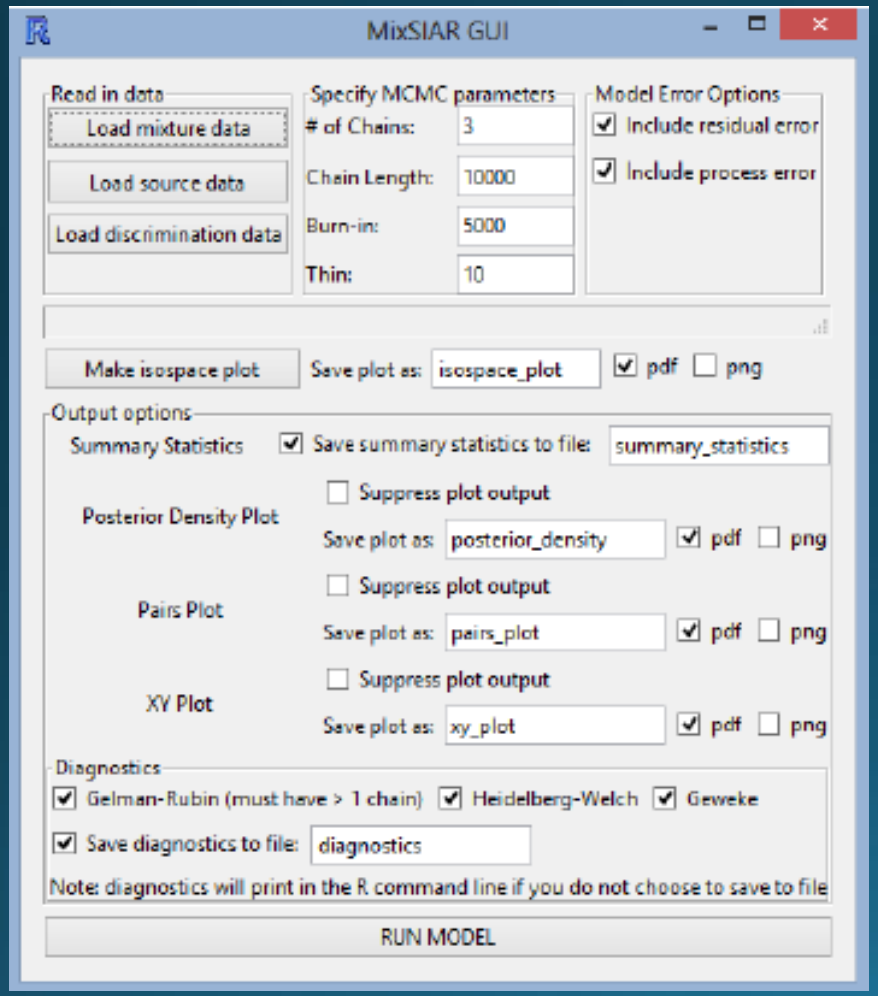


MixSIR
SIAR

Written in R and JAGS (*open source*)

Incorporates recent advances in mixing model methods

MixSIAR software

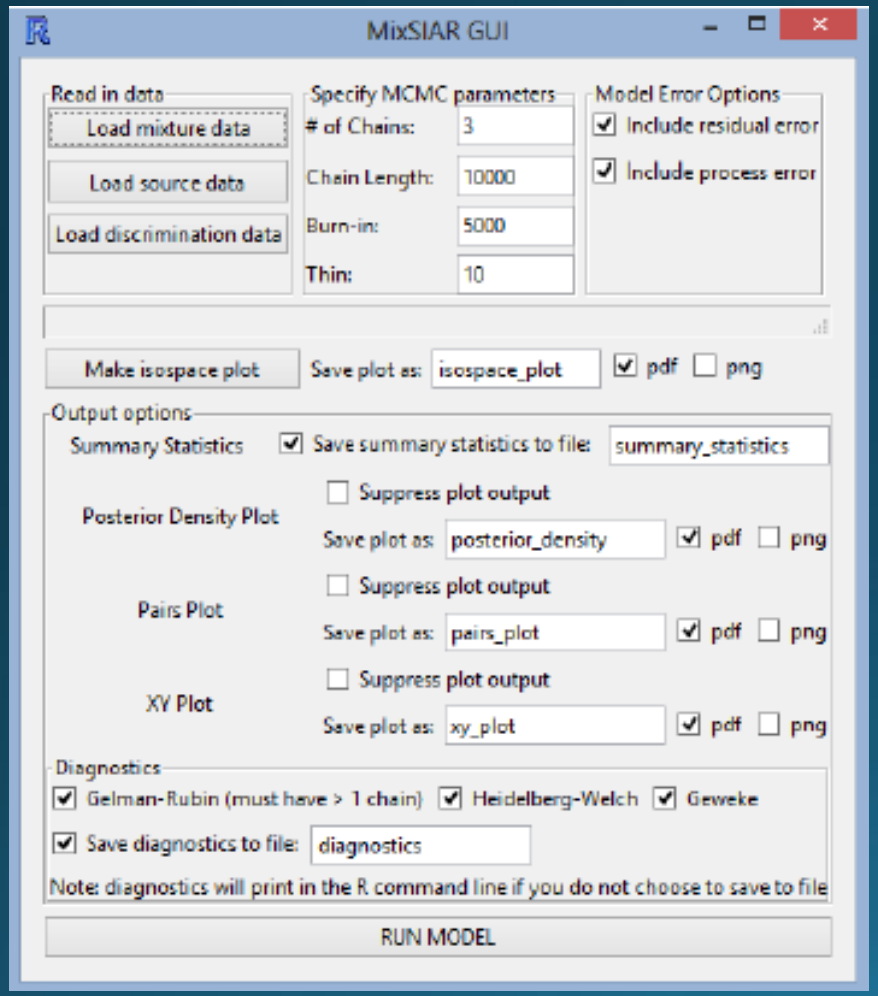


Incorporates recent advances in mixing model methods:

- **Addresses variability in source and discrimination values**
  1. **Hierarchical structure**

- Addresses variation in mixture populations:
  2. Random effects
  3. Fixed effects
  4. Continuous effects

MixSIAR software



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  4. **Continuous effects**

Source and discrimination variability

$$\text{Consumer} = \sum_k p_k (s_k + c_k)$$

p - proportion of diet
s - source
c - discrimination

Ward, E. J., Semmens, B. X., and Schindler, D. E. (2010).

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Source and discrimination variability

Consumer $= \sum_k p_k (s_k + c_k)$

$s_k \sim N(\mu_k, \omega_k{}^2)$

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Source and discrimination variability

Consumer $= \sum_k p_k (s_k + c_k)$

$s_k \sim N(\mu_k, {\omega_k}^2)$

$c_k \sim N(\lambda_k, {\tau_k}^2)$

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Consumer variability

Previously:

$$\boldsymbol{p} = [20\%, 50\%, 20\% 10\%]$$

Assumes that all consumers have the *same diet*

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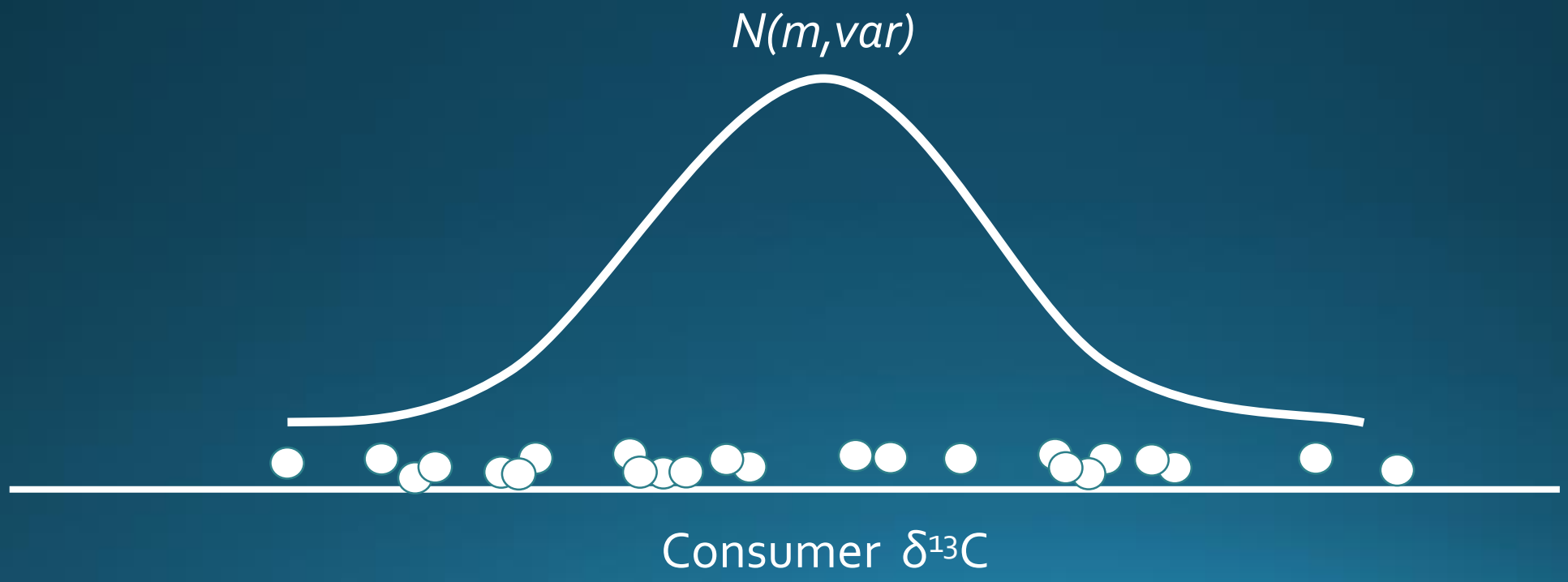
- Random effects
- Fixed effects
- Continuous effects

Consumer variability: fixed effects

Consumer $\delta^{13}C$

Consumer variability: fixed effects



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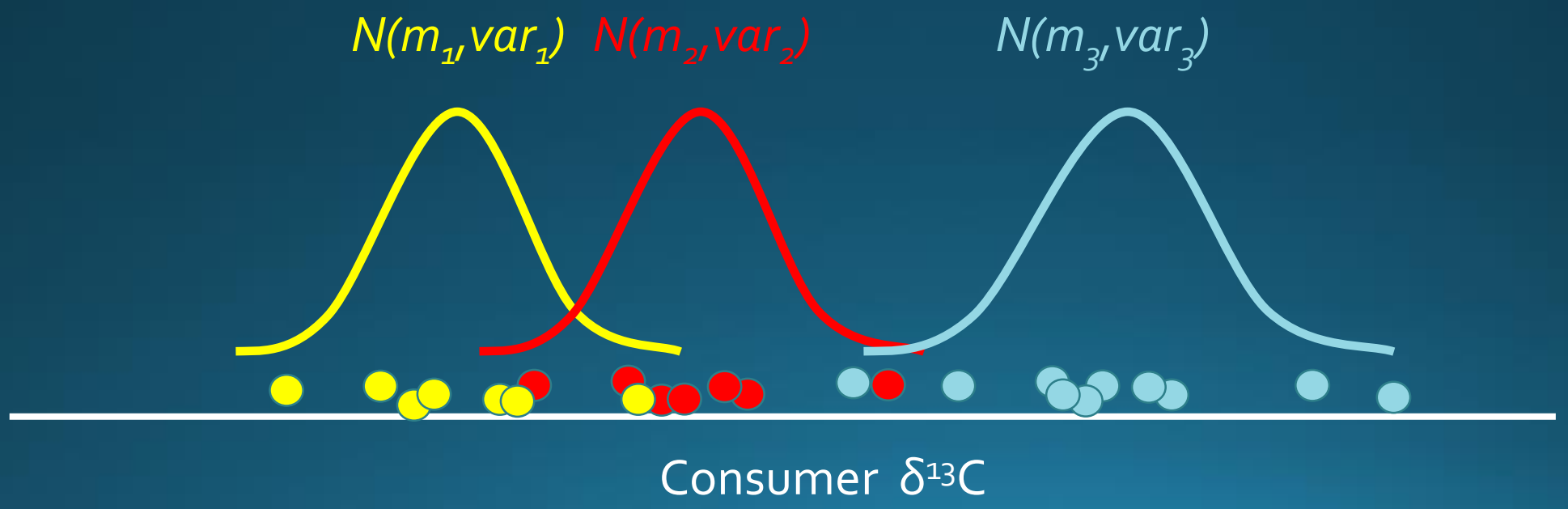
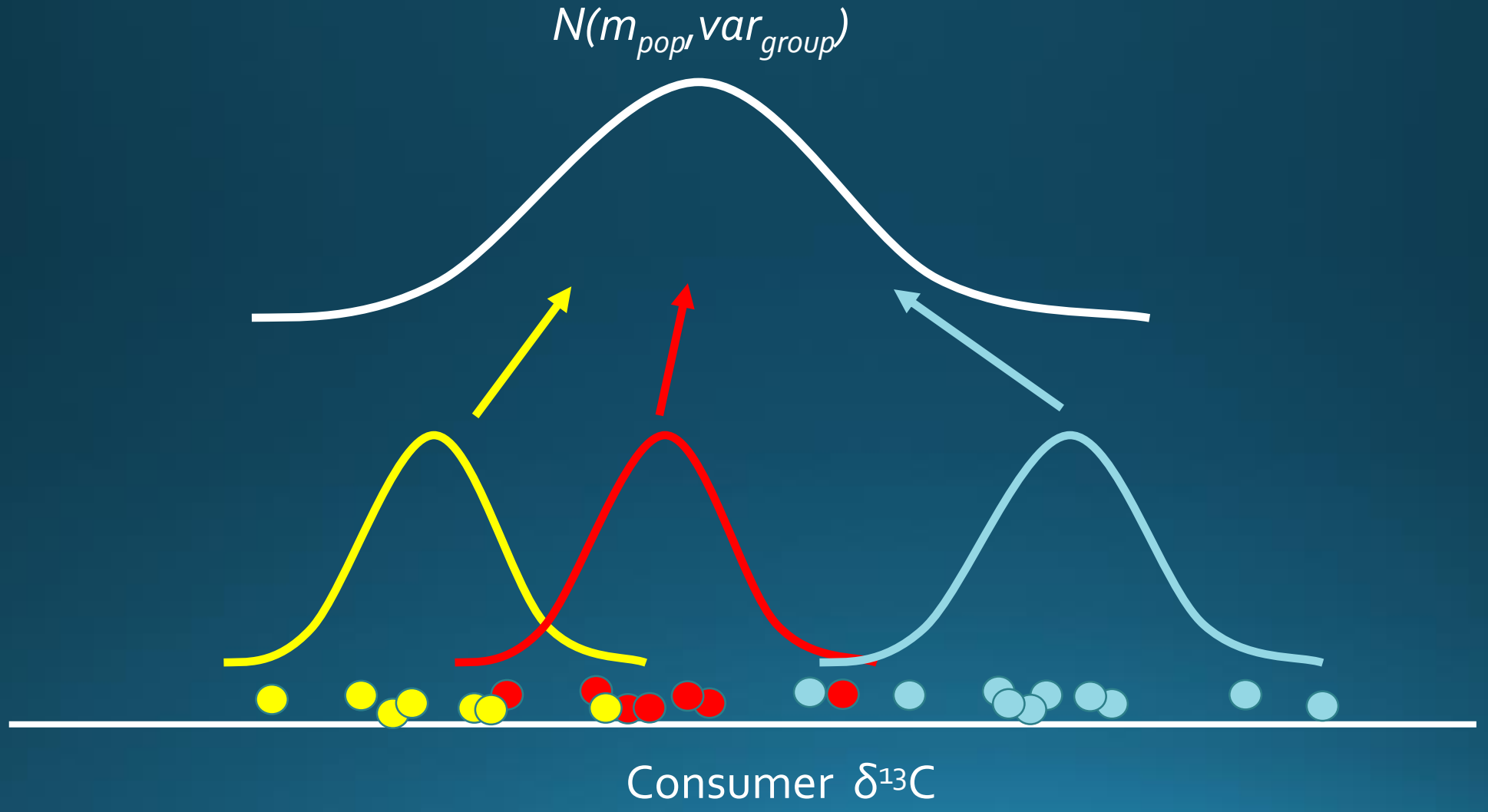


Consumer variability: random effects



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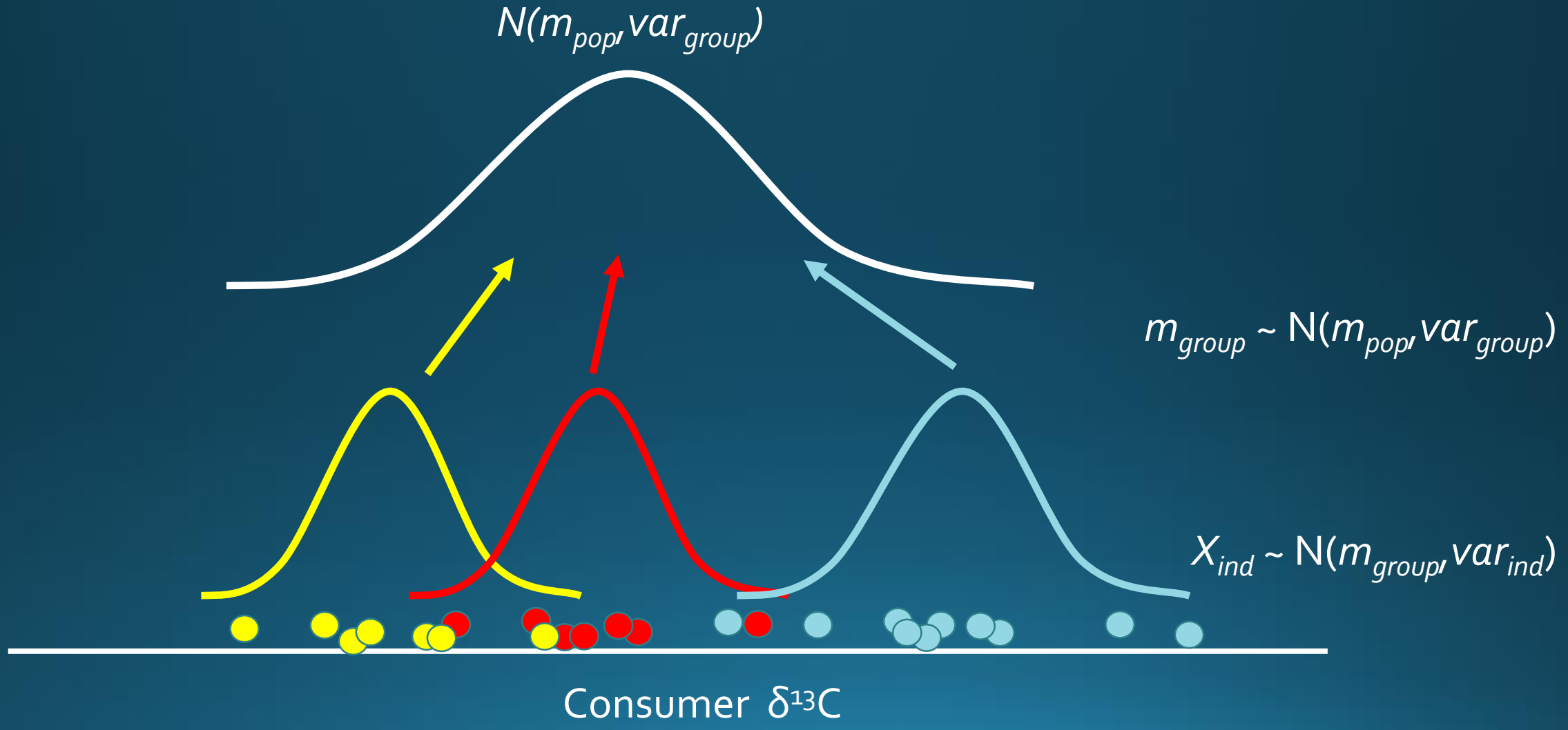
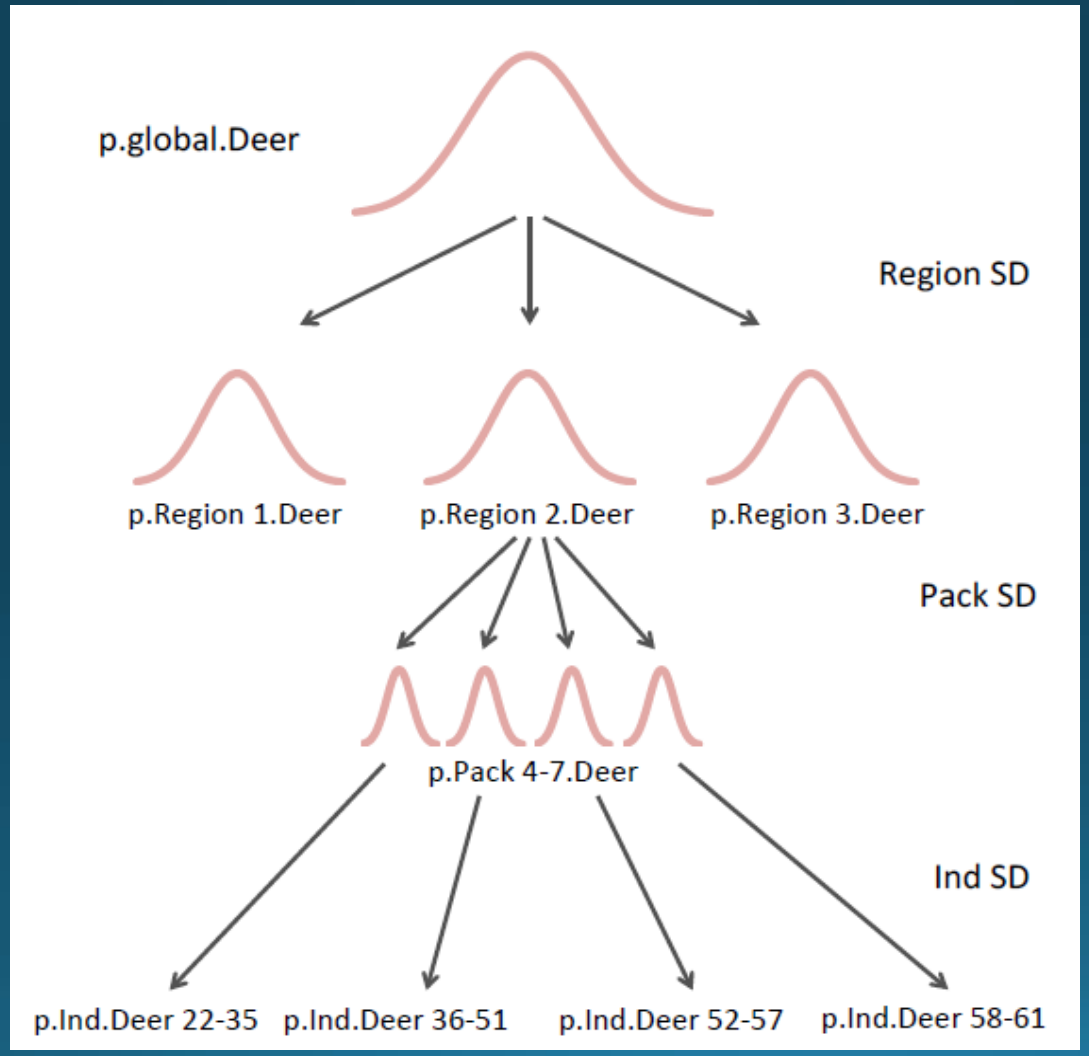


Consumer variability: random effects



Semmens et al. (2009)

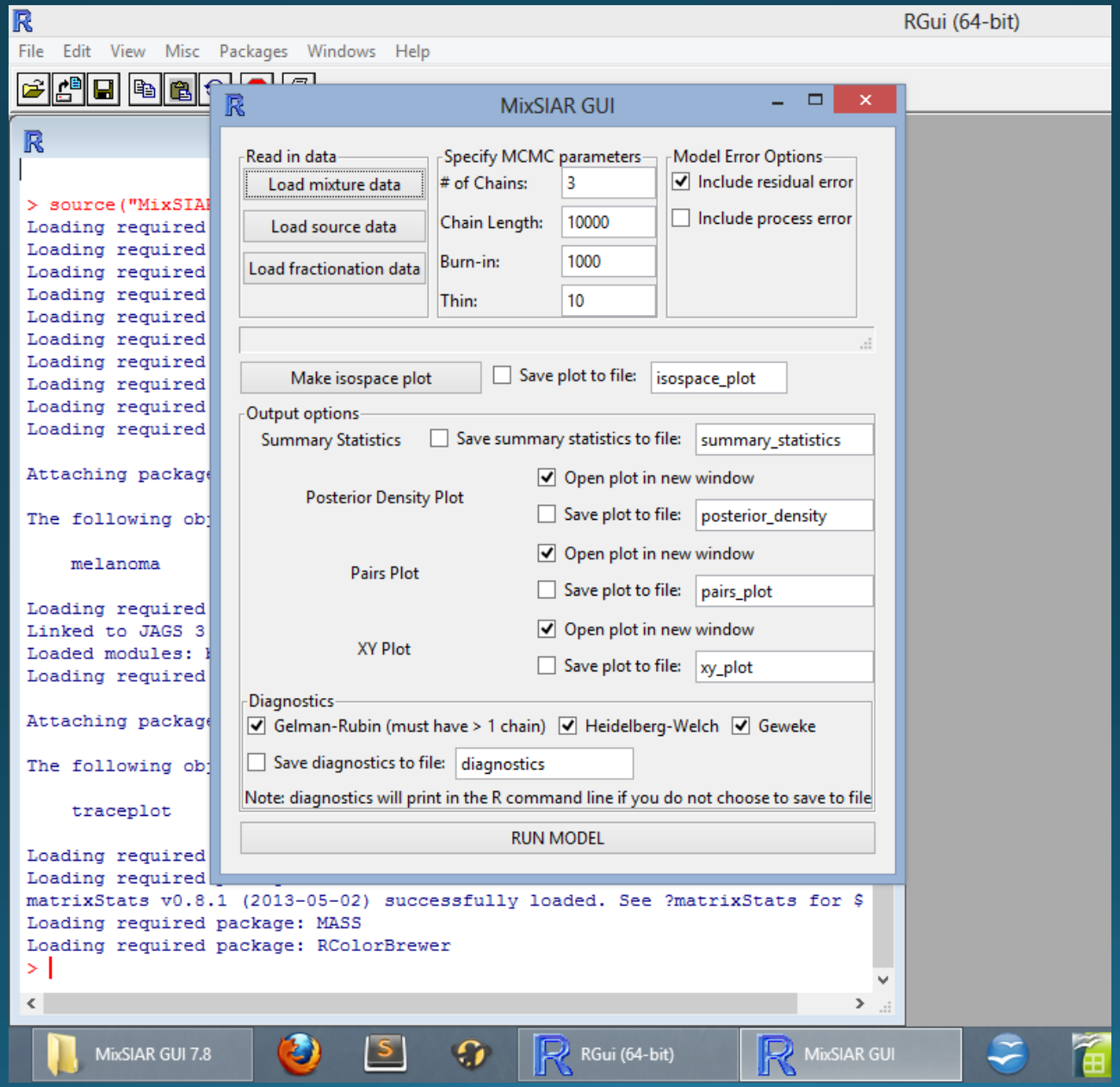
Consumer variability: continuous effects

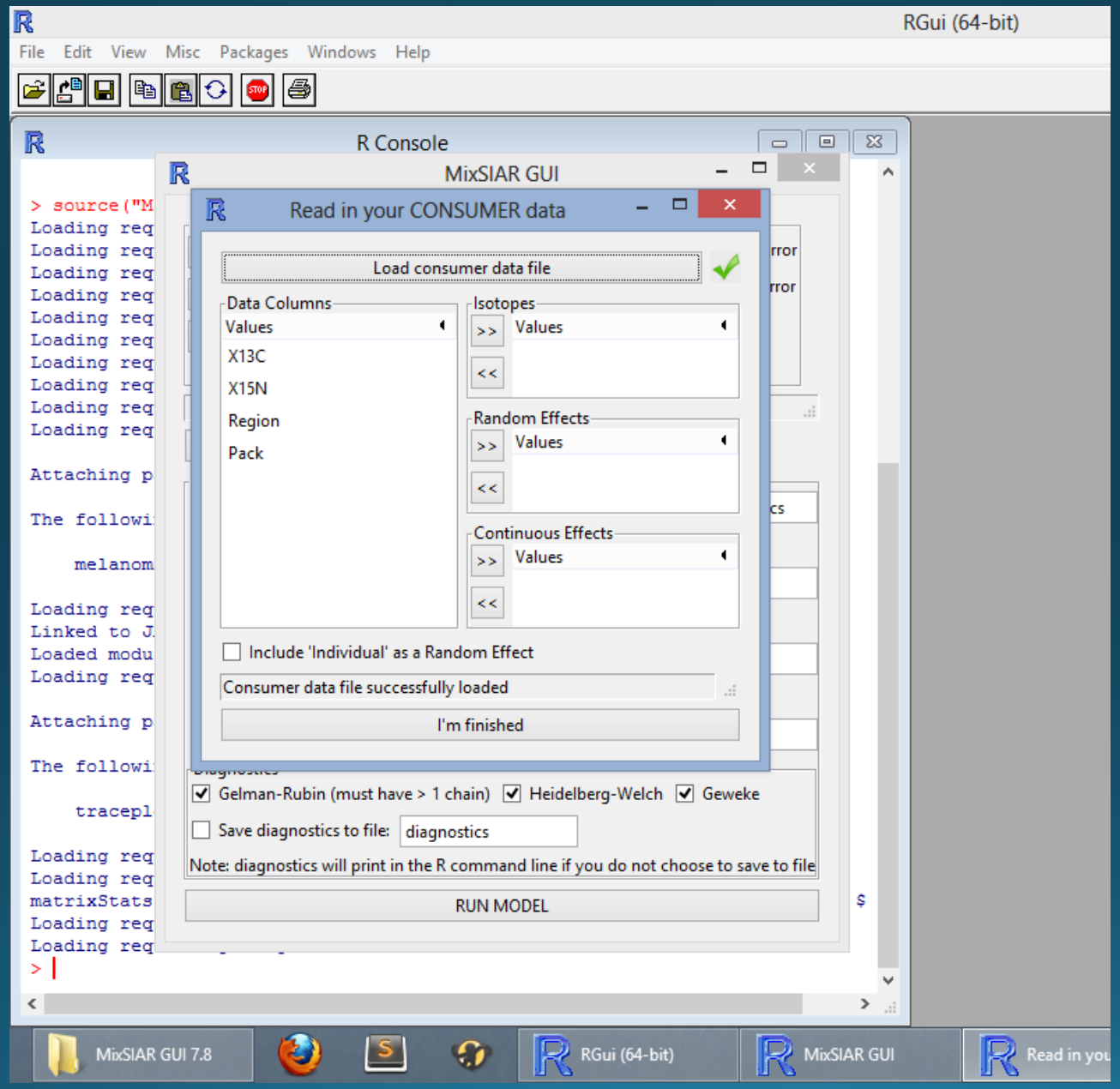
Consumer variability: continuous effects

$$\delta_c = p_1 s_1 + p_2 s_2 + \ldots p_i s_i$$

$$p_1 = B_o + B_1 * \text{Predictor}_c$$

Francis et al. (2011)


RGui (64-bit)
File Edit View Misc Packages Windows Help
MixSIAR GUI
Read in data
Load mixture data
Load source data
Load fractionation data
Specify MCMC parameters
# of Chains: 3
Chain Length: 10000
Burn-in: 1000
Thin: 10
Model Error Options
Include residual error
Include process error
Make isospace plot
Save plot to file: isospace_plot
Output options
Summary Statistics
Save summary statistics to file: summary_statistics
Posterior Density Plot
Open plot in new window
Save plot to file: posterior_density
Pairs Plot
Open plot in new window
Save plot to file: pairs_plot
XY Plot
Open plot in new window
Save plot to file: xy_plot
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
> source("MixSIAR
Loading required
Attaching package
The following obj
melanoma
Linked to JAGS 3
Loaded modules:
traceplot
matrixStats v0.8.1 (2013-05-02) successfully loaded. See ?matrixStats for $
Loading required package: MASS
Loading required package: RColorBrewer
MixSIAR GUI 7.8
RGui (64-bit)
MixSIAR GUI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File Edit View Misc Packages Windows Help
R Console
MixSIAR GUI
Read in your CONSUMER data
Load consumer data file
Data Columns
Values
X13C
X15N
Region
Pack
Isotopes
Values
Random Effects
Values
Continuous Effects
Values
Include 'Individual' as a Random Effect
Consumer data file successfully loaded
I'm finished
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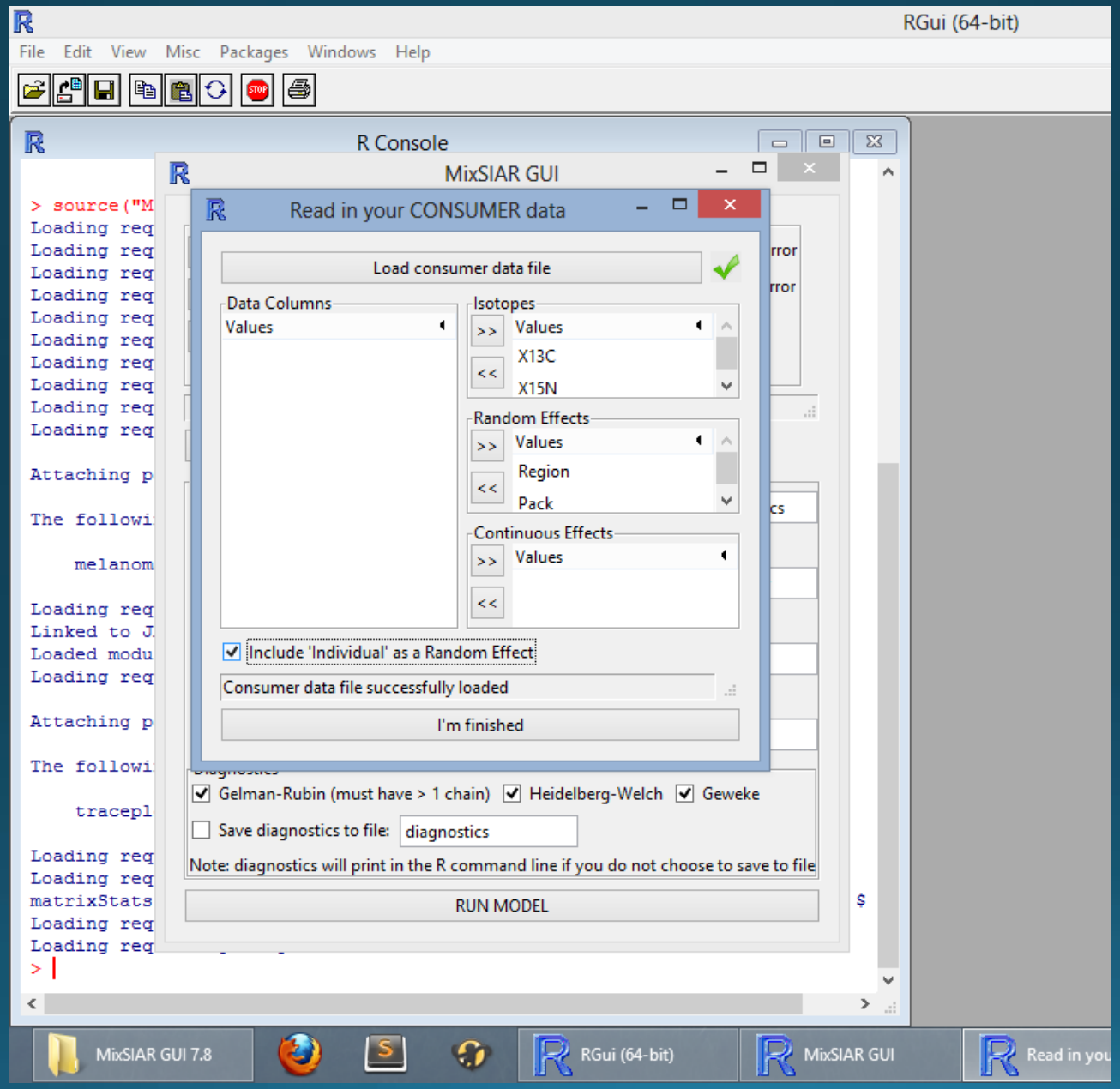
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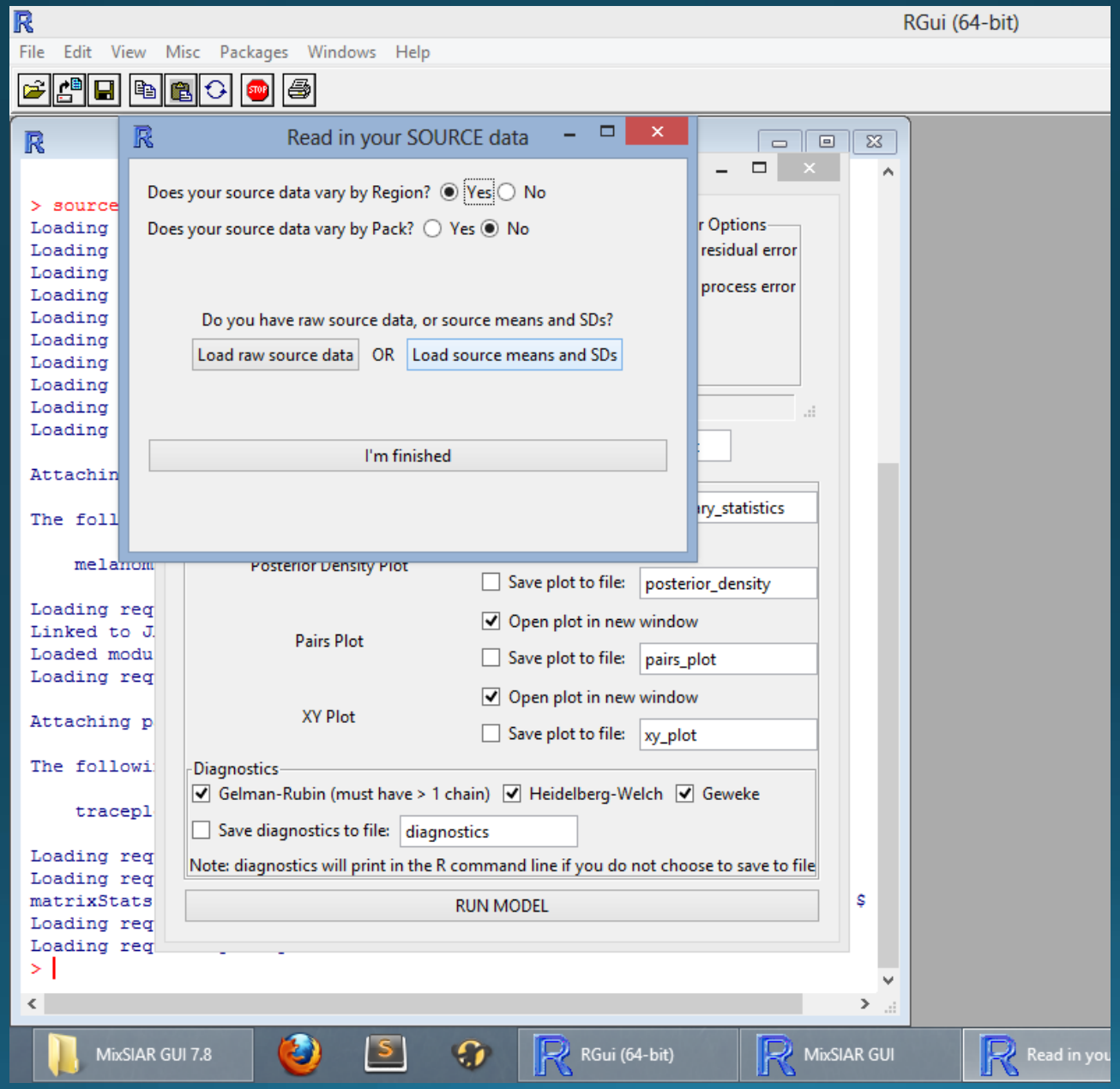
RGui (64-bit)
File Edit View Misc Packages Windows Help
Read in your SOURCE data
Does your source data vary by Region? Yes No
Does your source data vary by Pack? Yes No
Do you have raw source data, or source means and SDs?
Load raw source data
OR
Load source means and SDs
I'm finished
Posterior Density Plot
Save plot to file: posterior_density
Pairs Plot
Open plot in new window
Save plot to file: pairs_plot
XY Plot
Open plot in new window
Save plot to file: xy_plot
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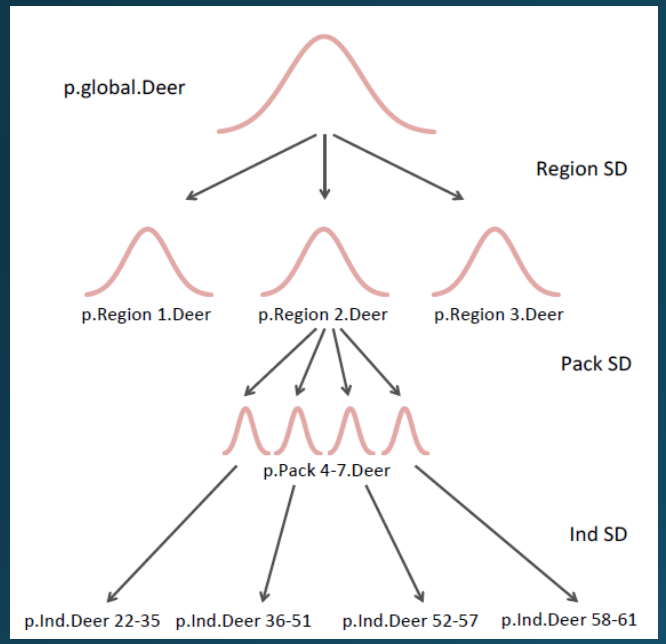
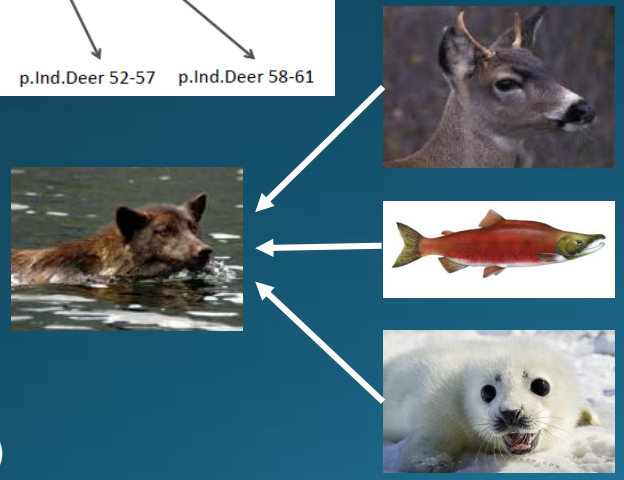
RGui (64-bit)
MixSIAR GUI

MixSIAR example: 2 random effects





Semmens et al. (2009)

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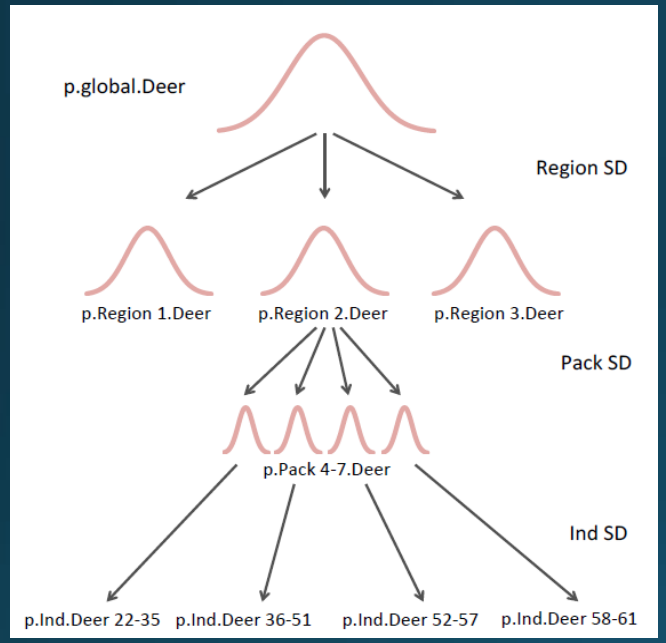

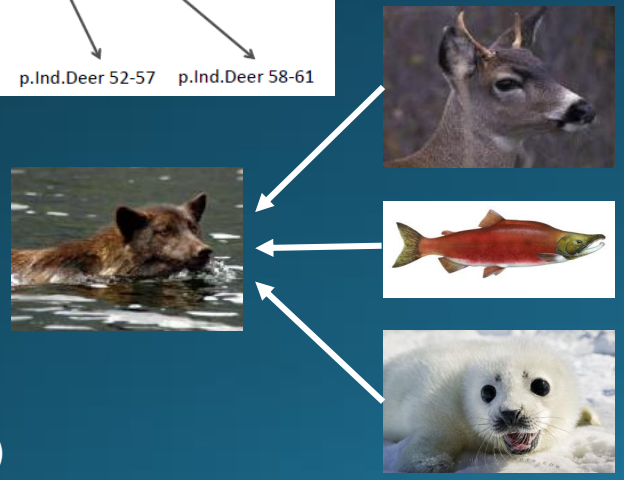

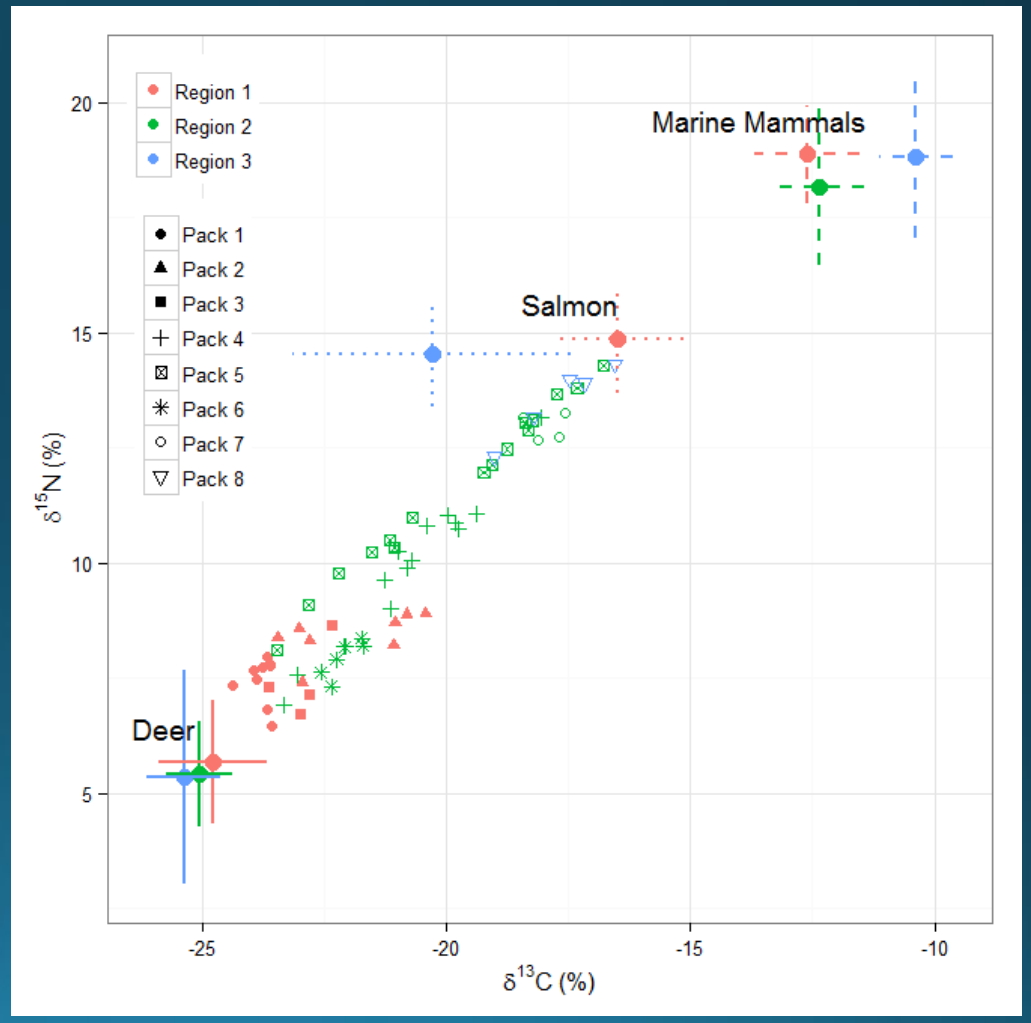

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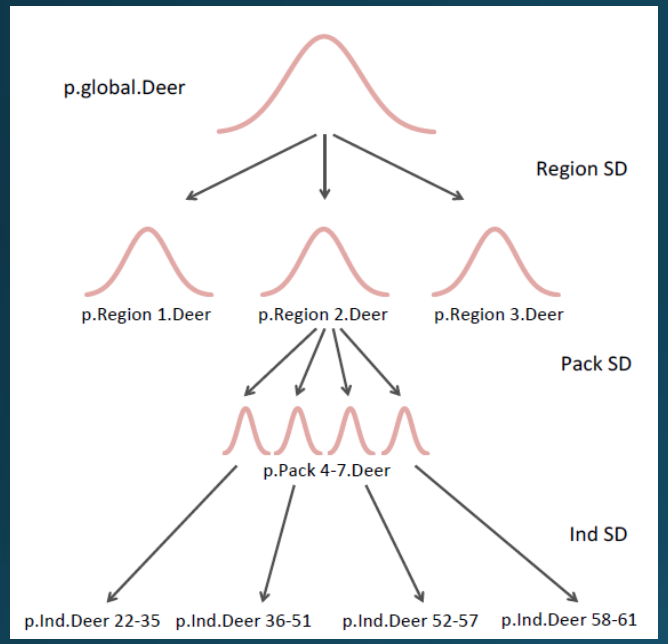

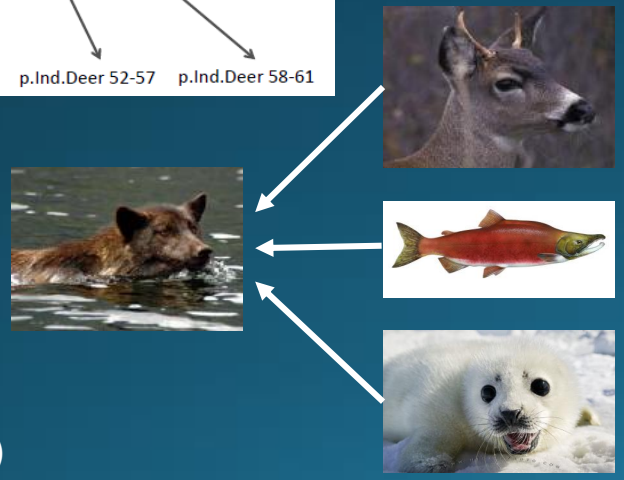

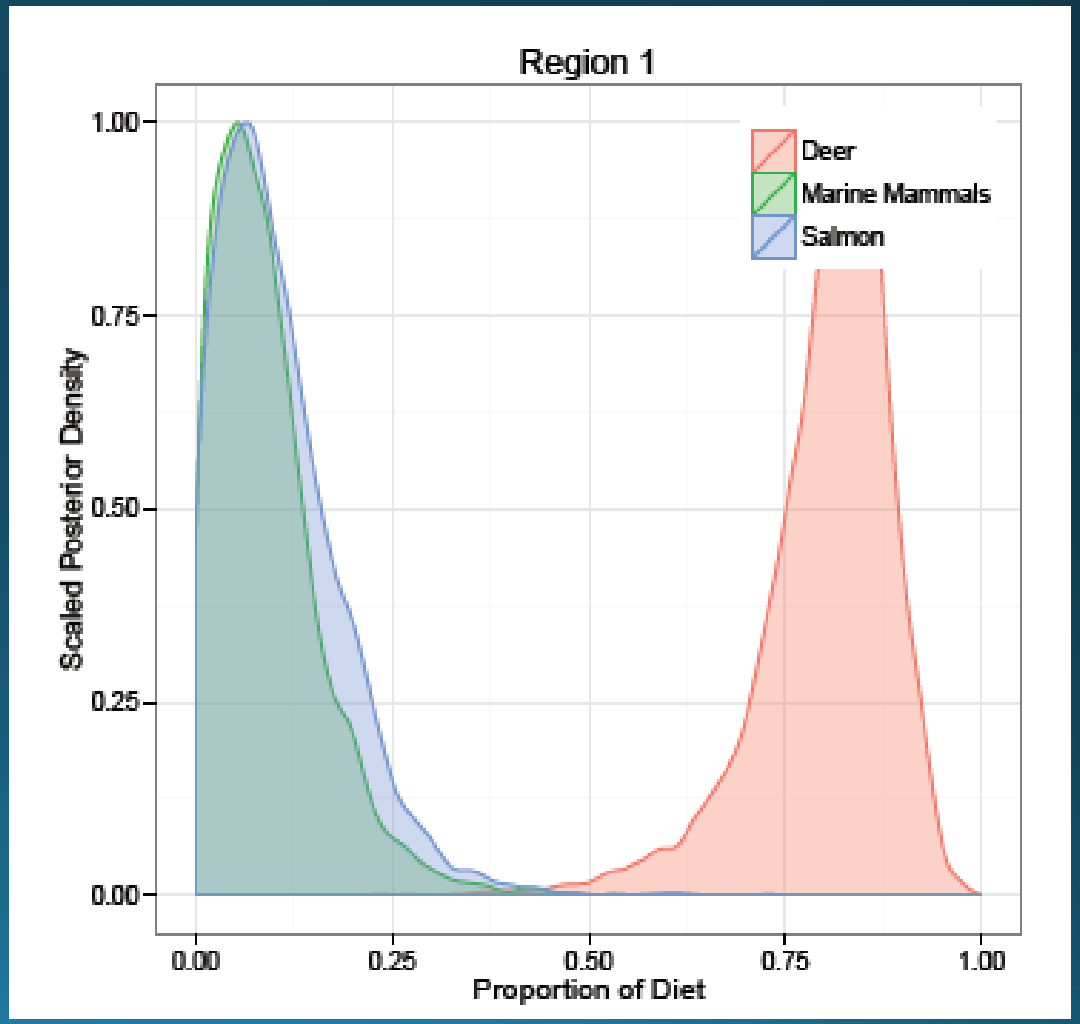

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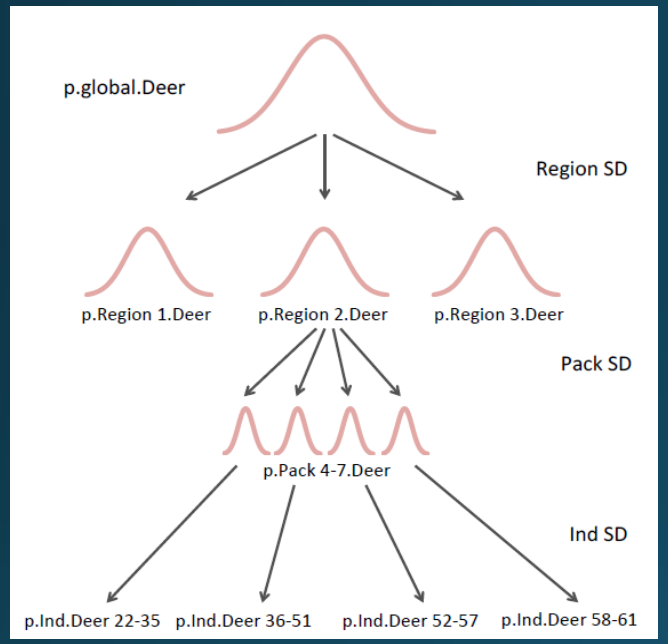
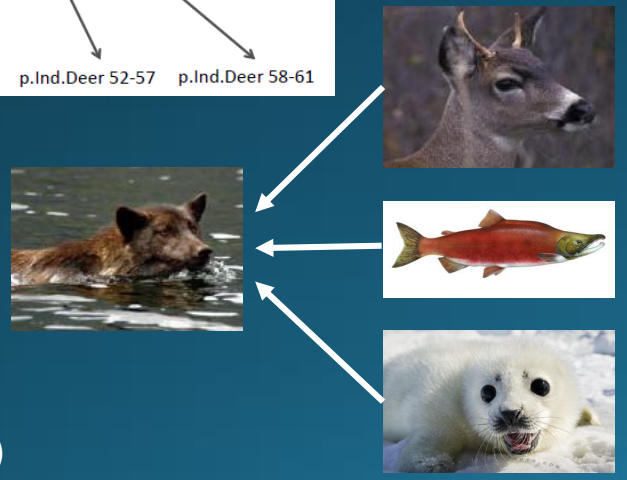
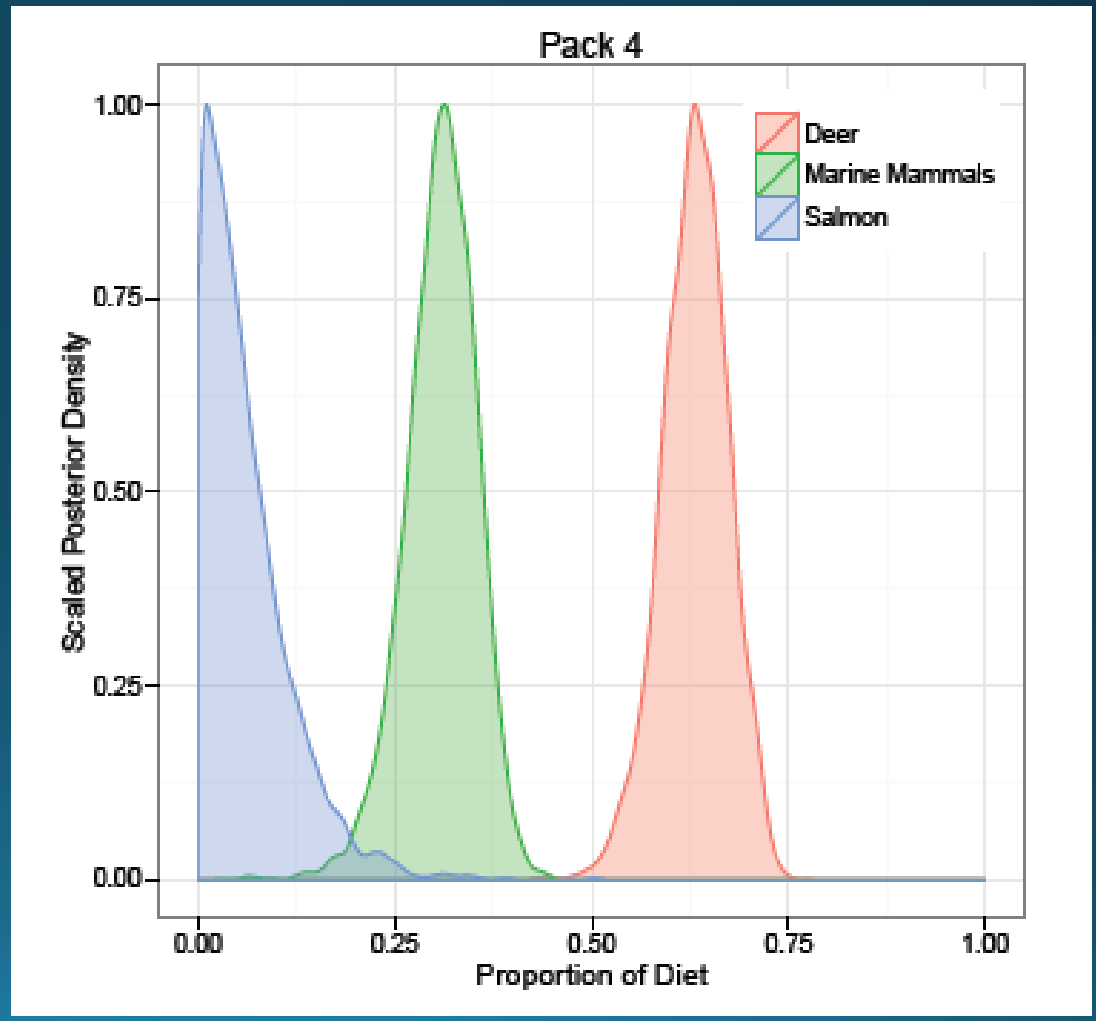
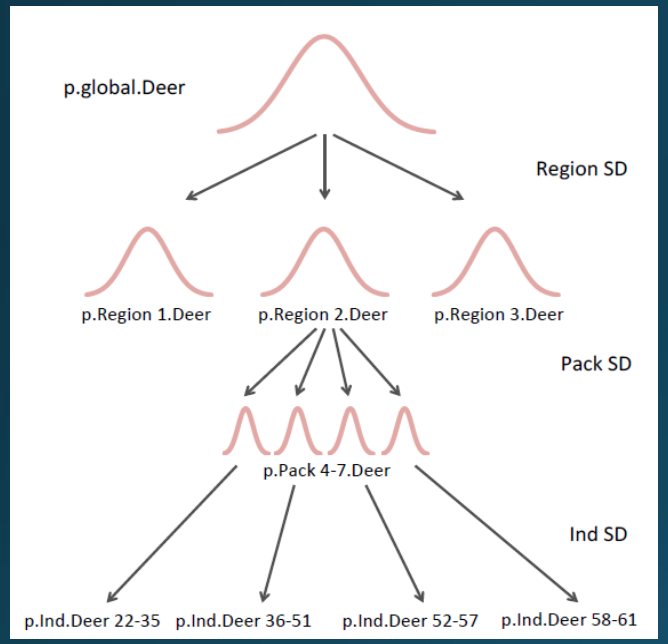


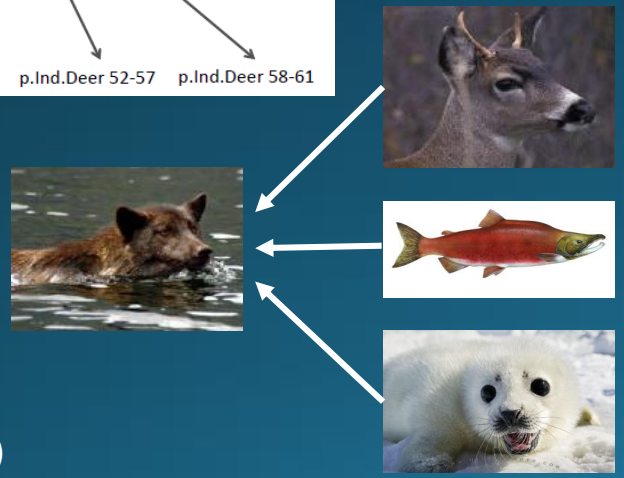


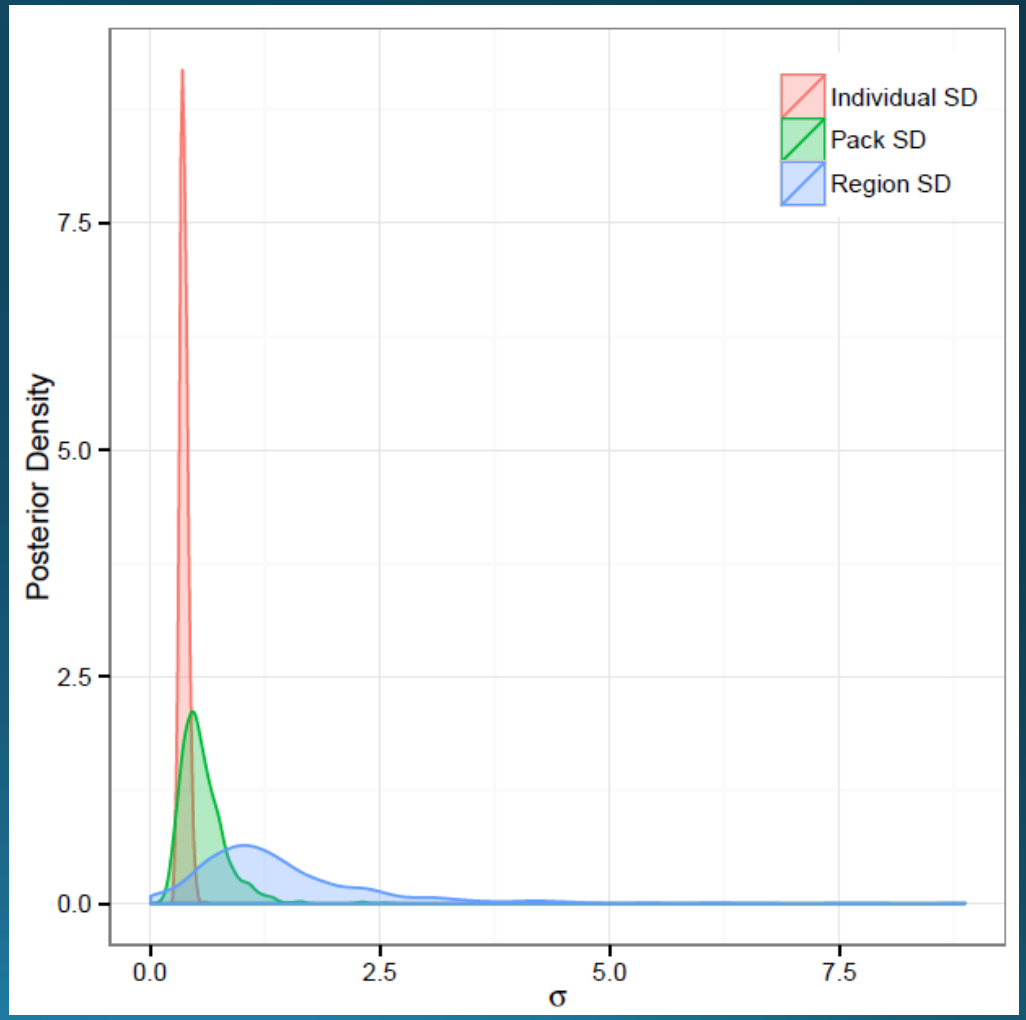


Semmens et al. (2009)

MixSIAR example: 2 random effects

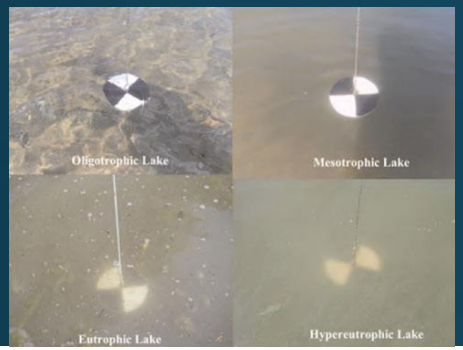


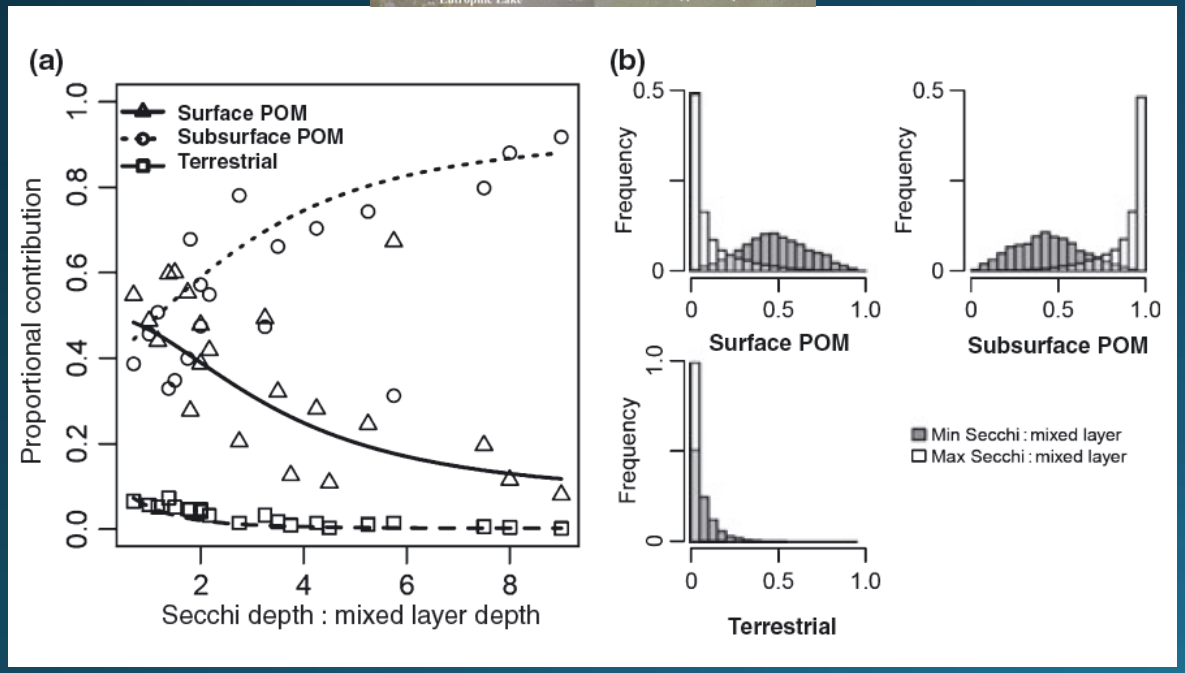




Semmens et al. (2009)

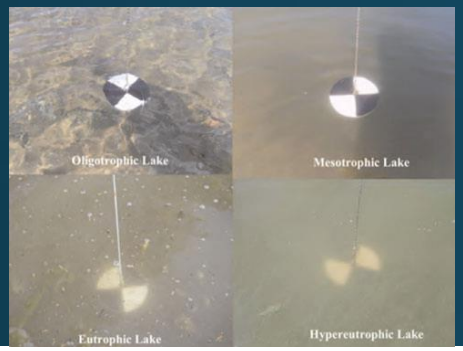
MixSIAR example: continuous effect

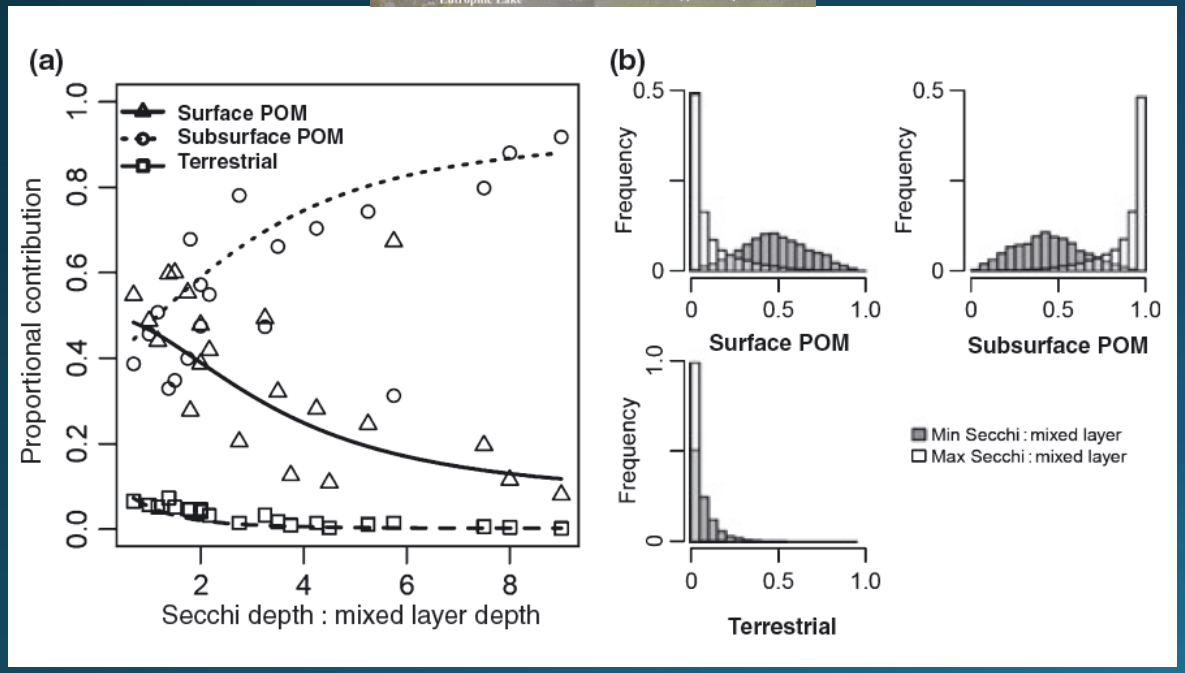


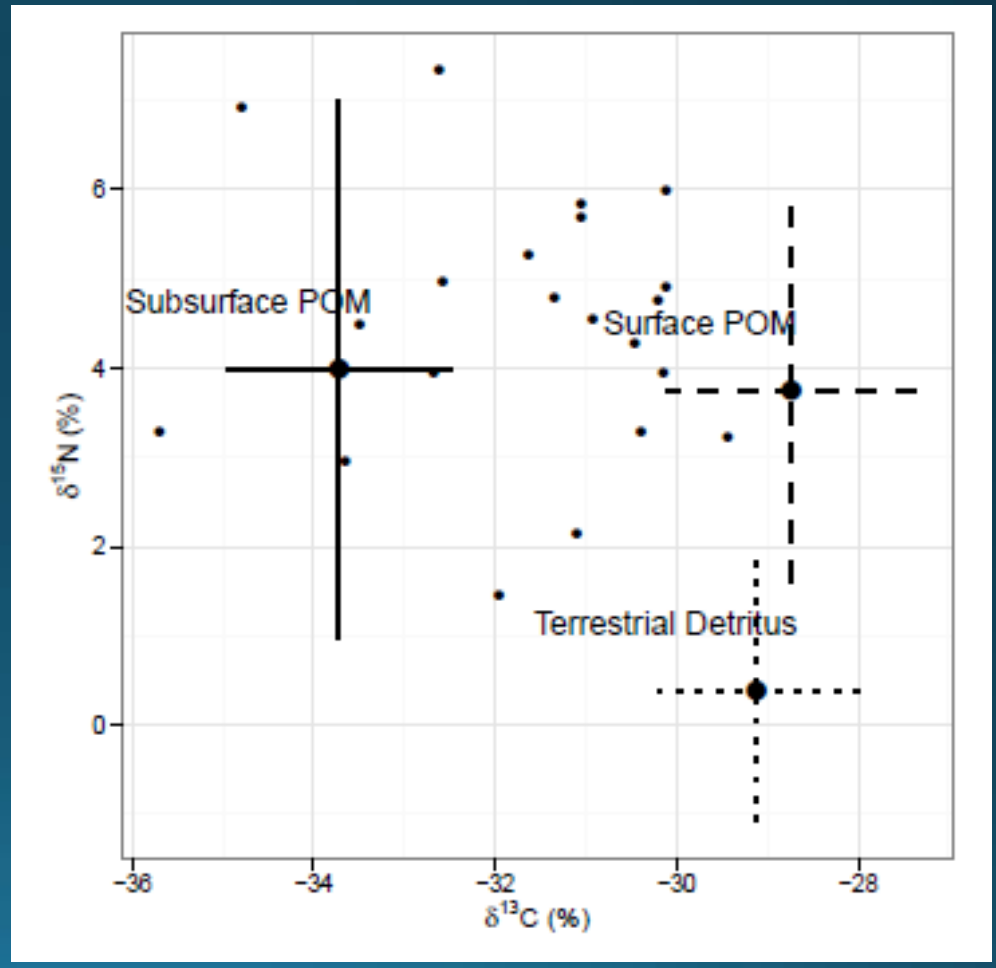


Francis et al. (2011)

MixSIAR example: continuous effect







Francis et al. (2011)

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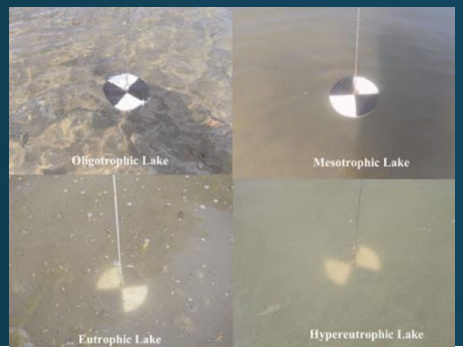

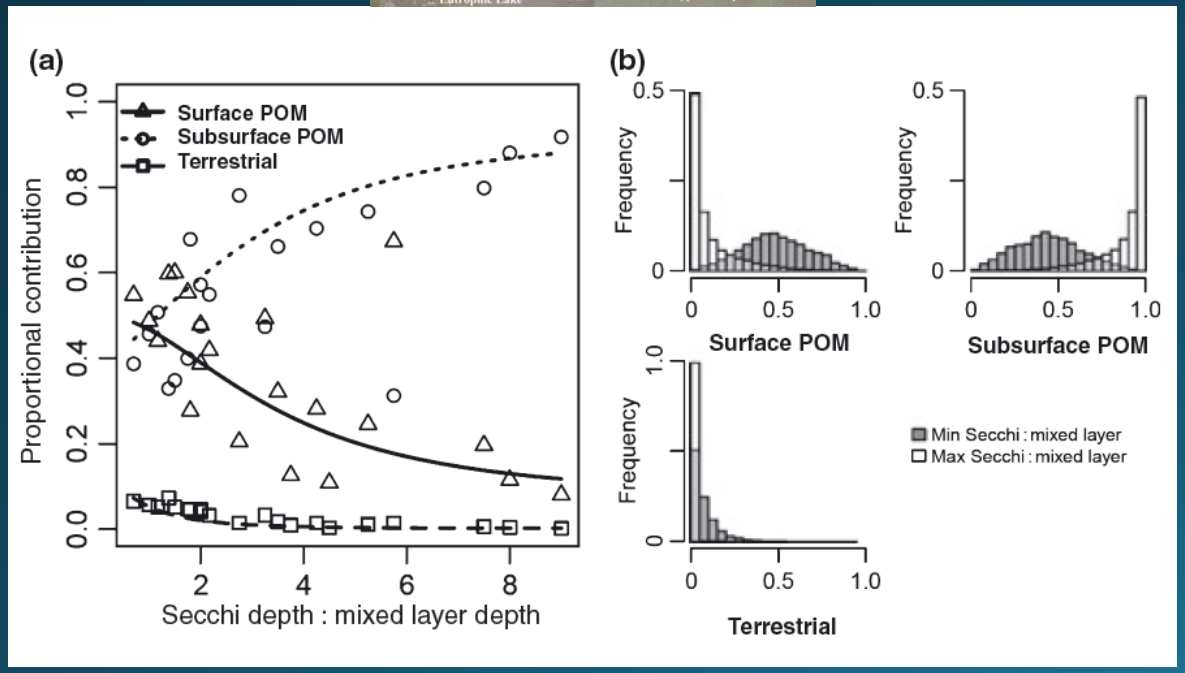

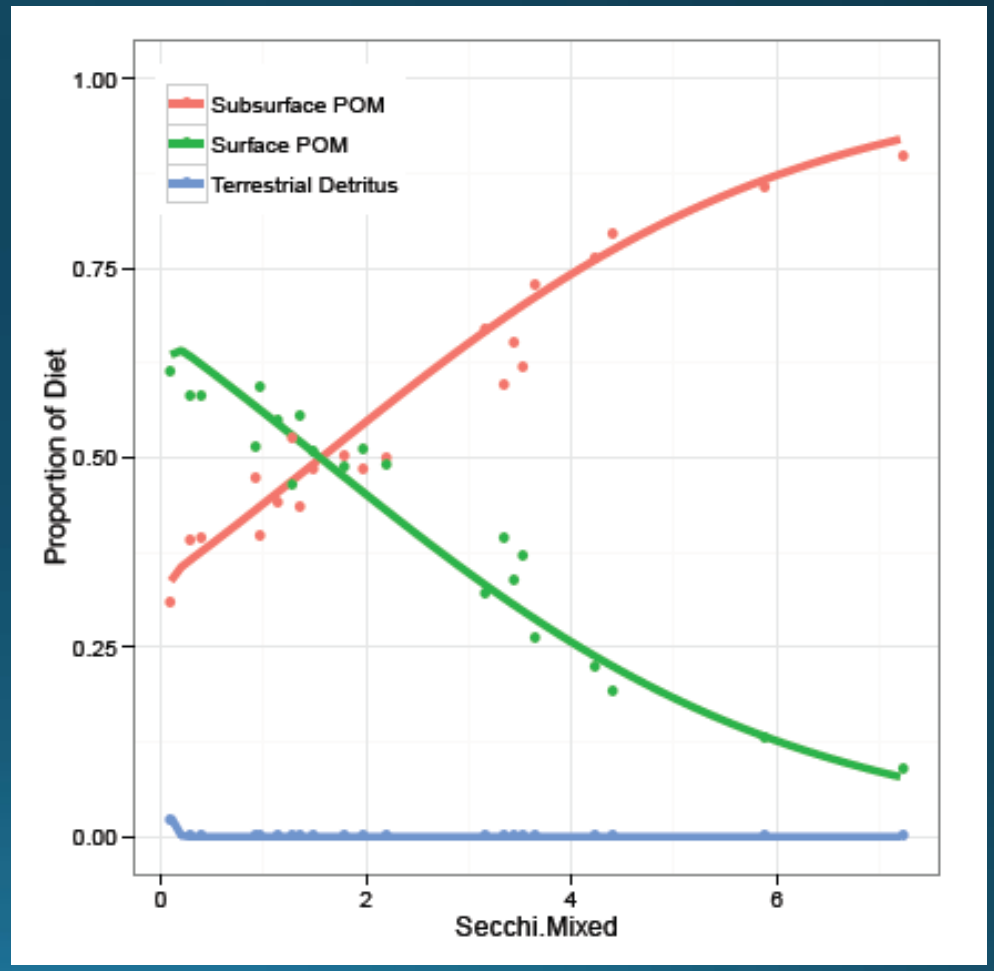

Francis et al. (2011)

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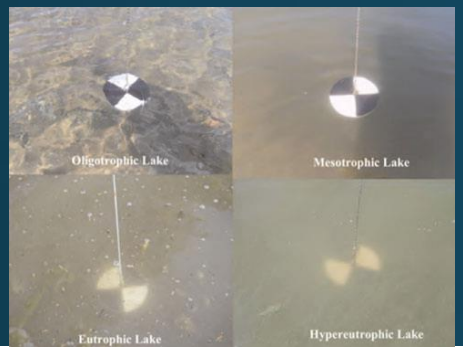

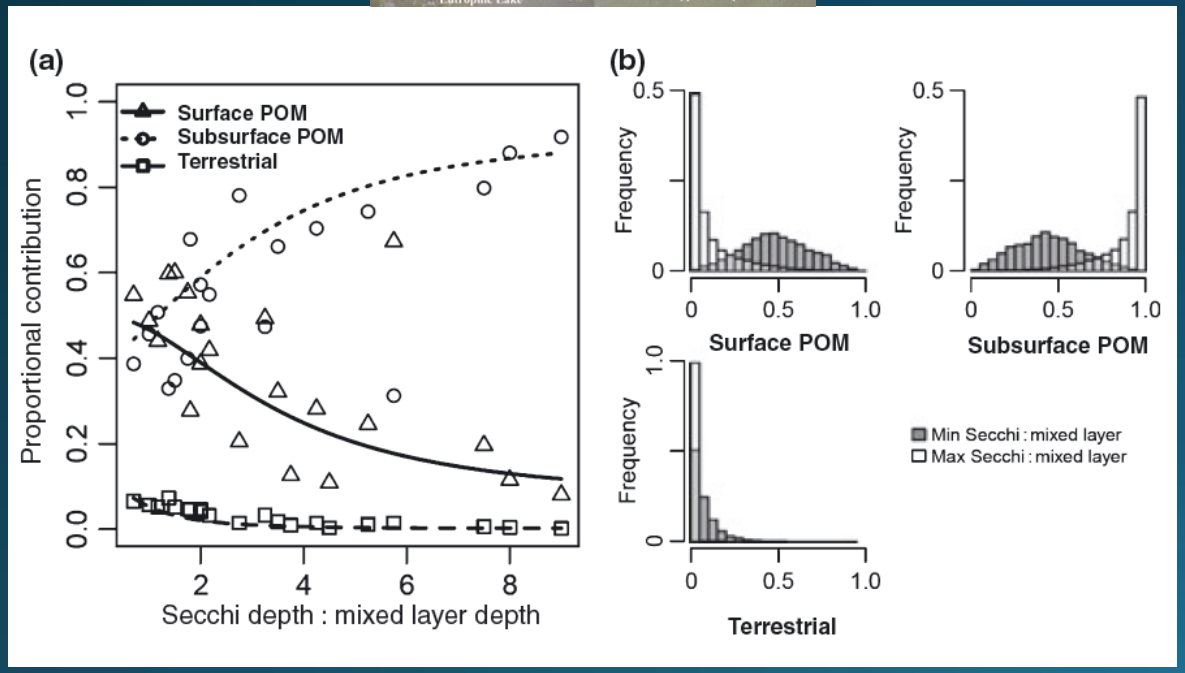

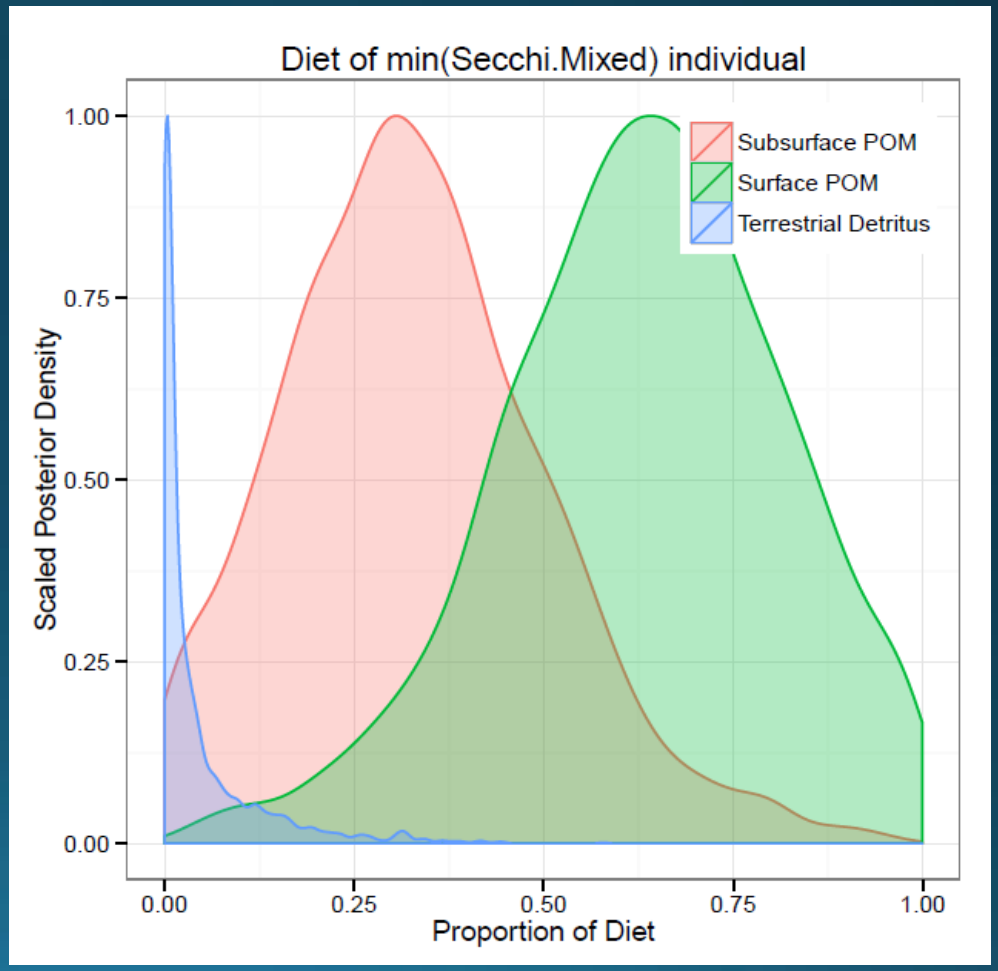

Francis et al. (2011)

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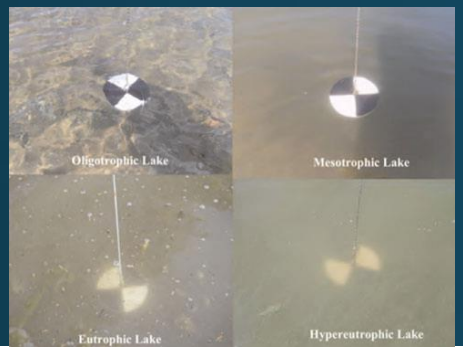
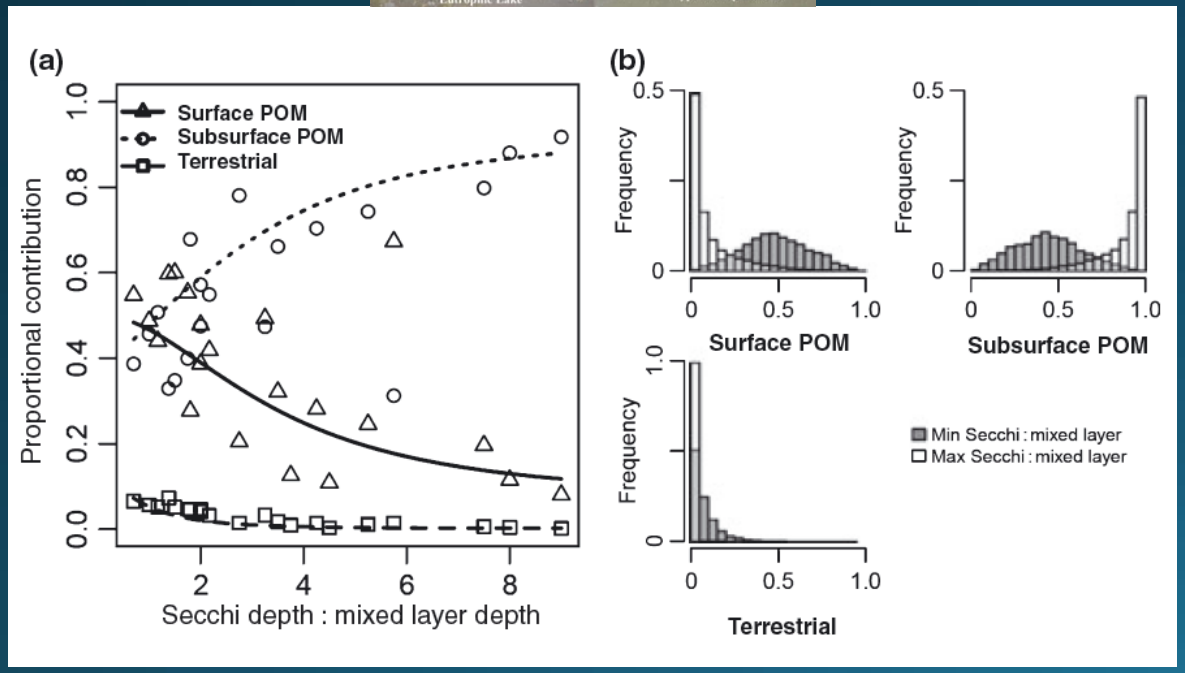
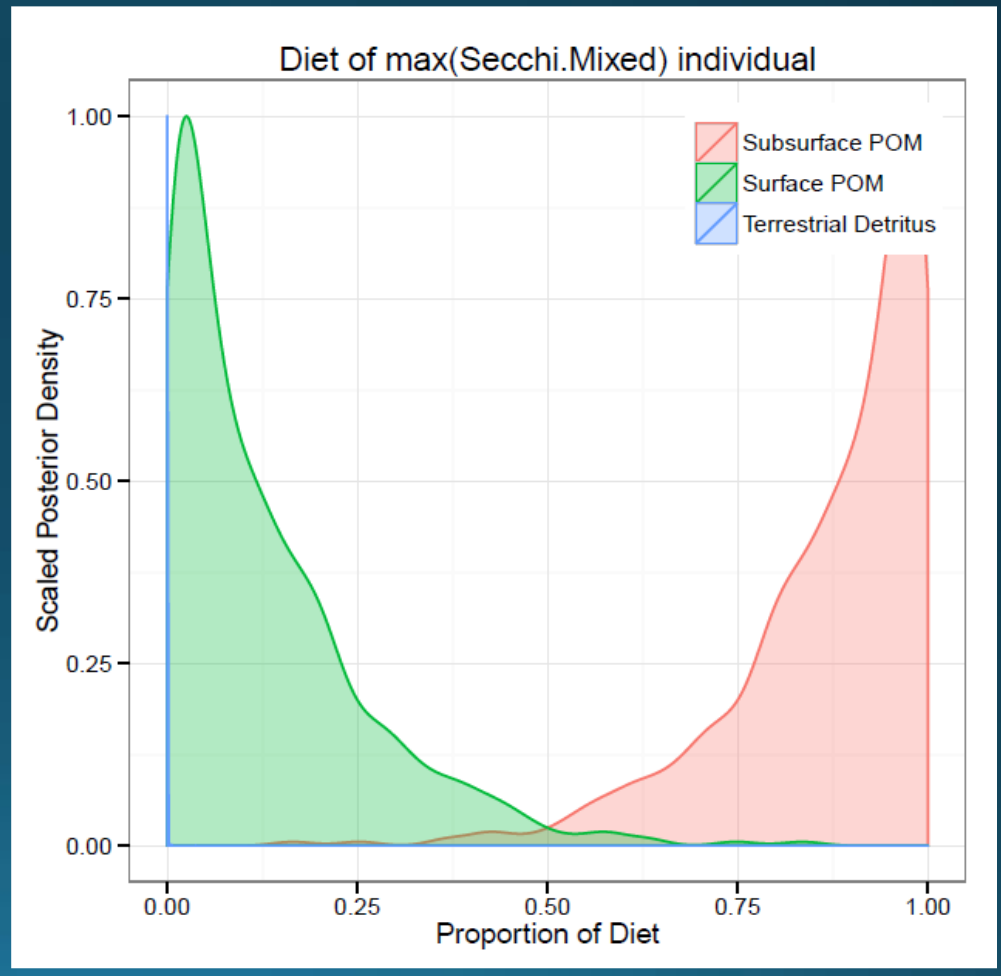


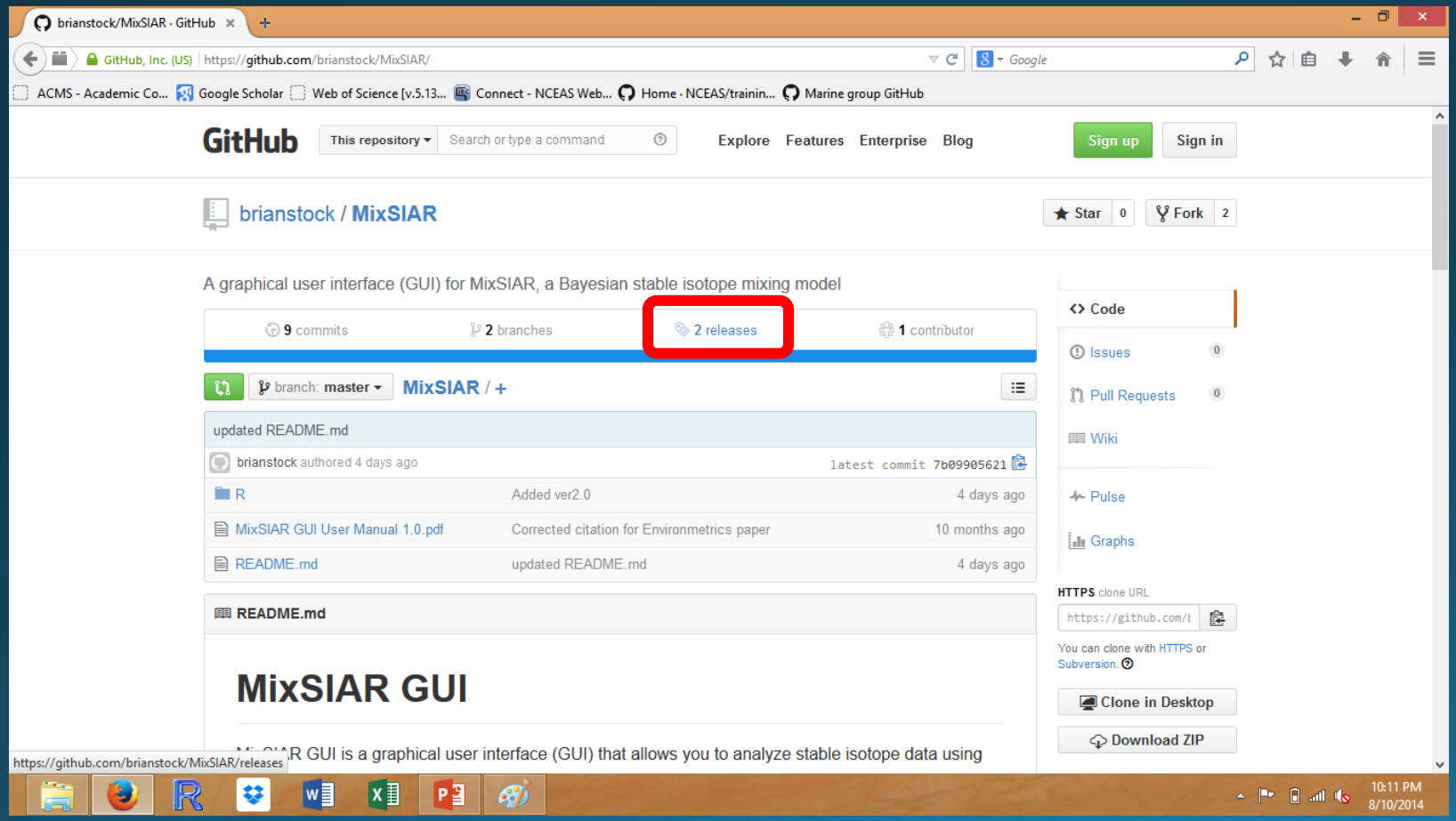




Francis et al. (2011)

Where can I get MixSIAR?

www.github.com/brianstock/MixSIAR



Releases

- Download code

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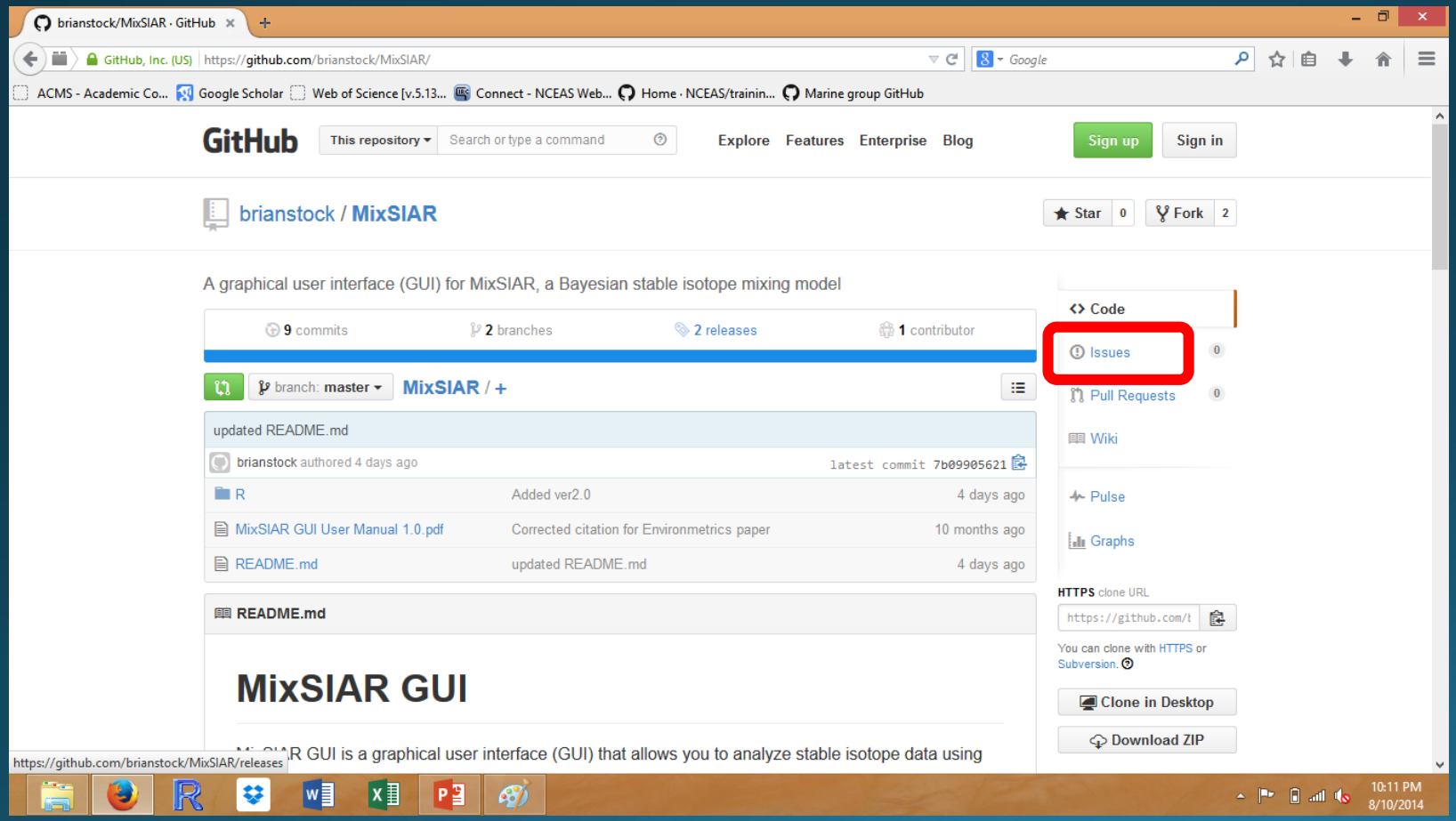

Issues

- Report bugs
- Ask questions
- Suggest changes

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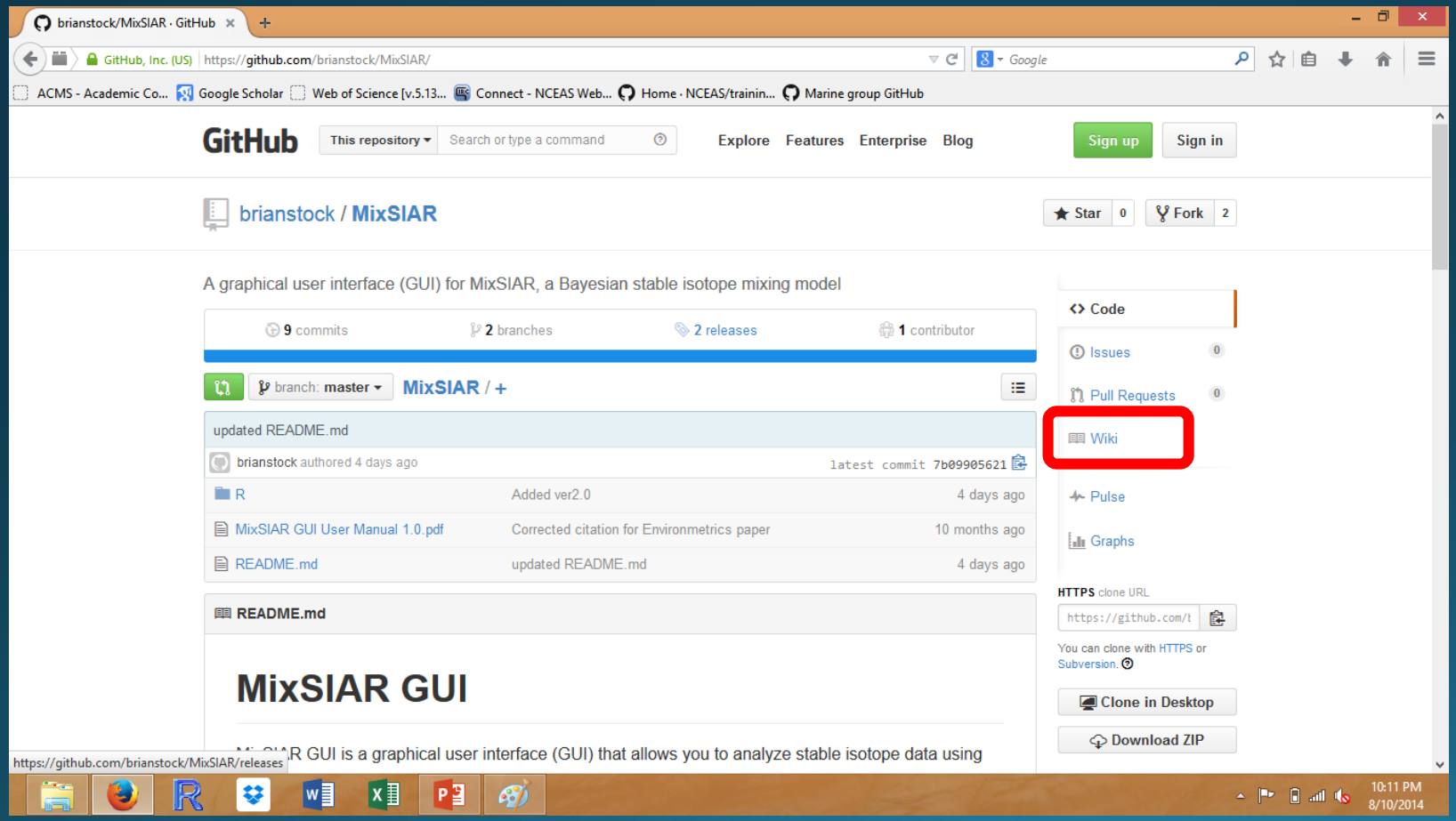
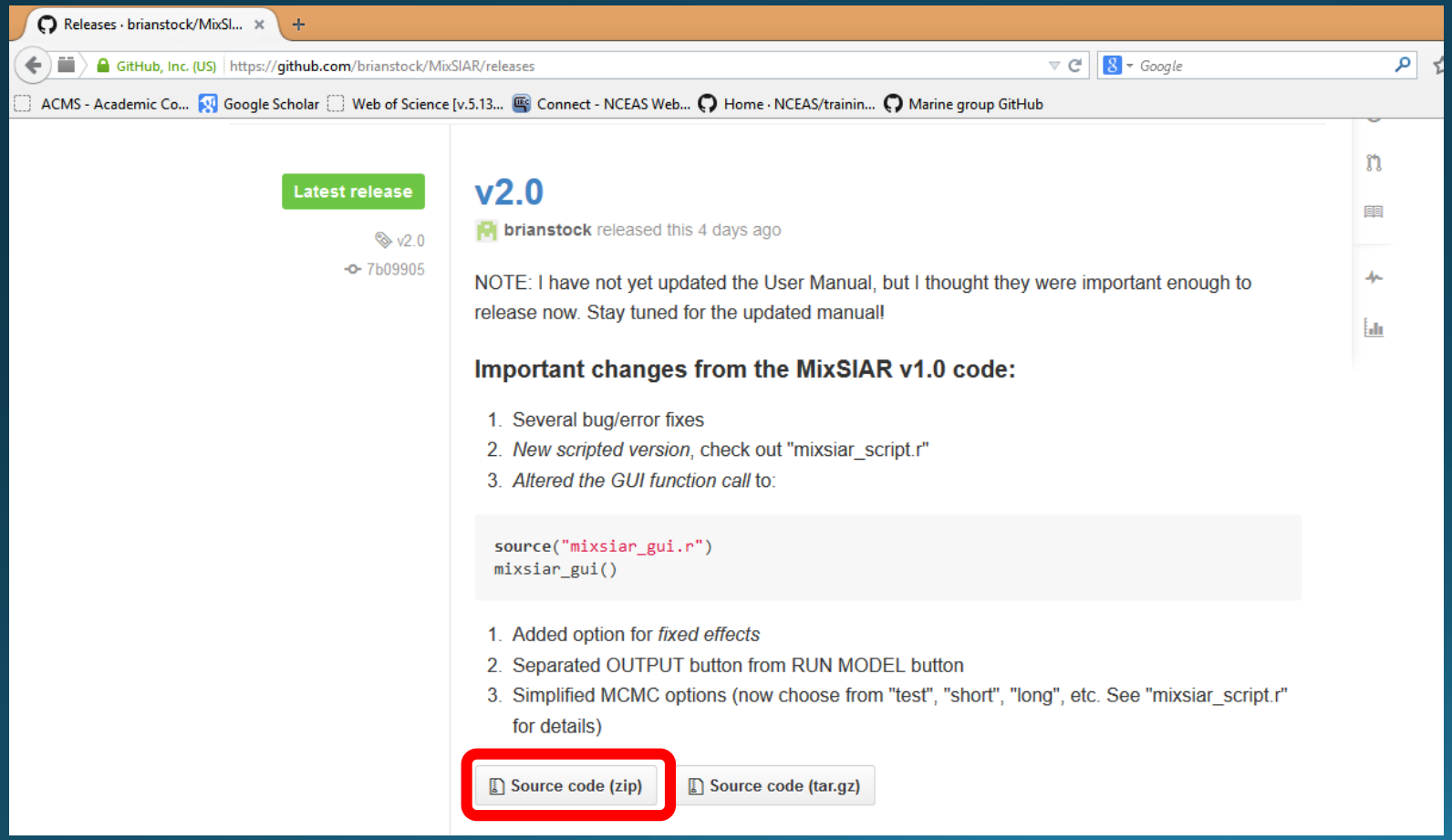


Wiki

- FAQ

Where can I get MixSIAR?

www.github.com/brianstock/MixSIAR/releases



Acknowledgements

MixSIAR team:

- Brice Semmens (SIO)
- Eric Ward (NWFSC)
- Jon Moore (Simon Fraser)
- Don Phillips (EPA)
- Andrew Parnell (University College Dublin)
- Andrew Jackson (Trinity College Dublin)
- Richard Inger (Exeter)
- Stuart Bearhop (Exeter)

Funding:

- CAPAM (CIMEC, NOAA)

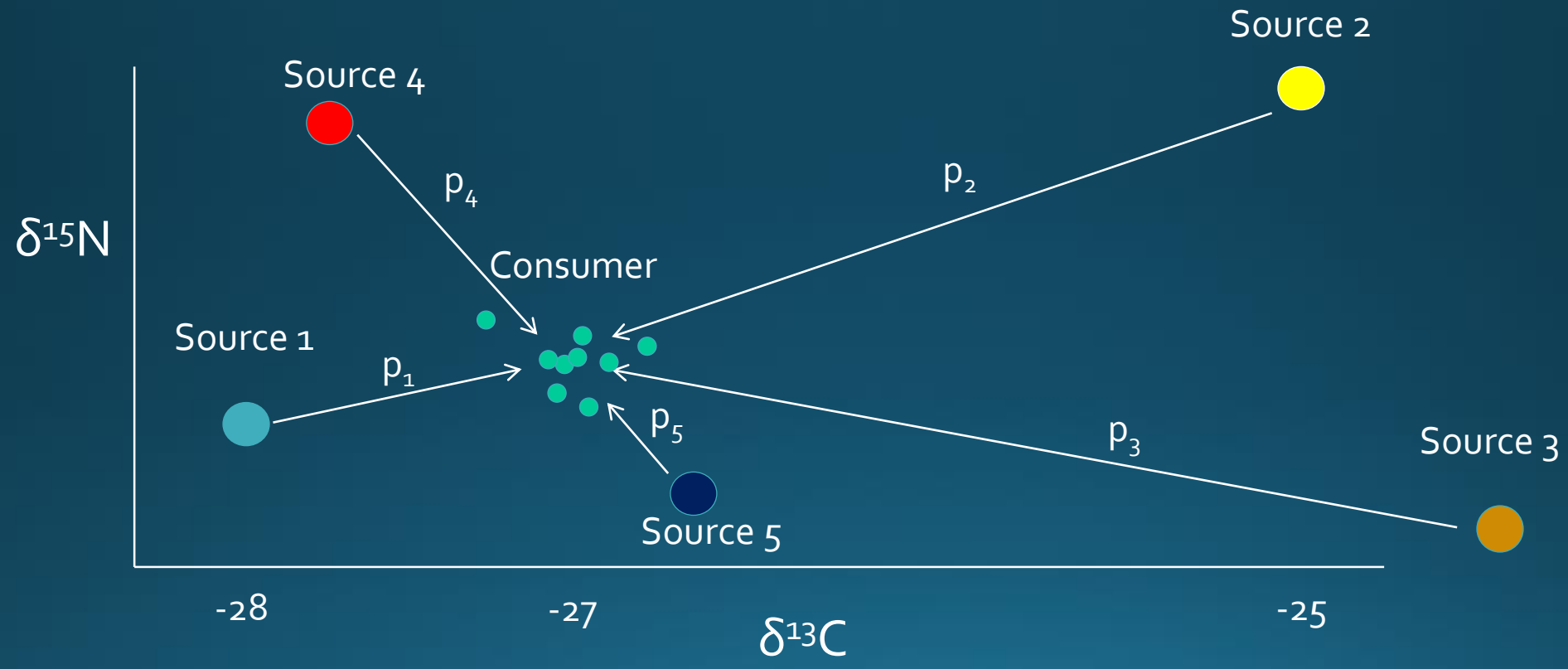
FAQ

- How many isotopes/tracers can I use?
- How many sources and effects can I include?
- Can MixSIAR handle missing data?
- What's the difference between MixSIR and SIAR? IsoSource?
- What are the model assumptions? Are they valid?
- What about normality?
- How do I compare models using DIC?
- What's the best way to model individuals?

Model assumptions

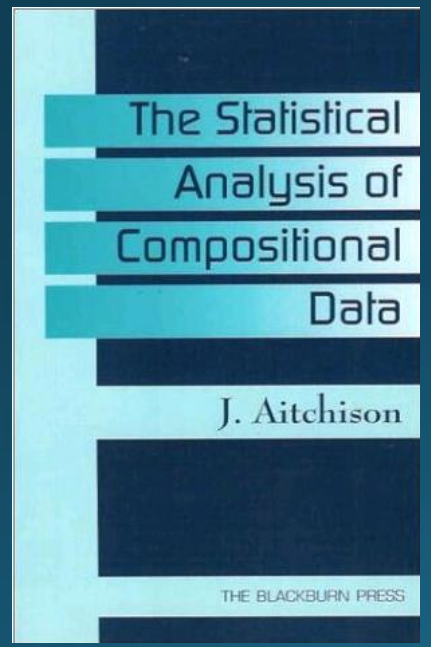
- All diet sources are included in the model
- Discrimination correctly estimated
- Isotopes are uncorrelated
- Sources are sampled across tissue turnover period

What about IsoSource?



Proportions are not normal!

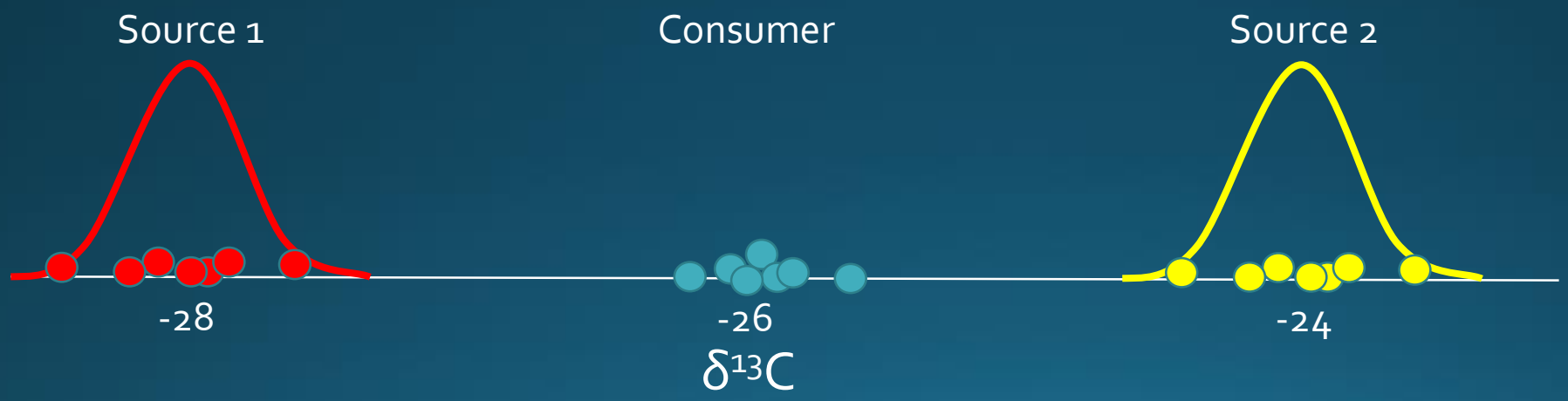
- Use the ILR (inverse log ratio) transform for compositions



Aitchison (1986)

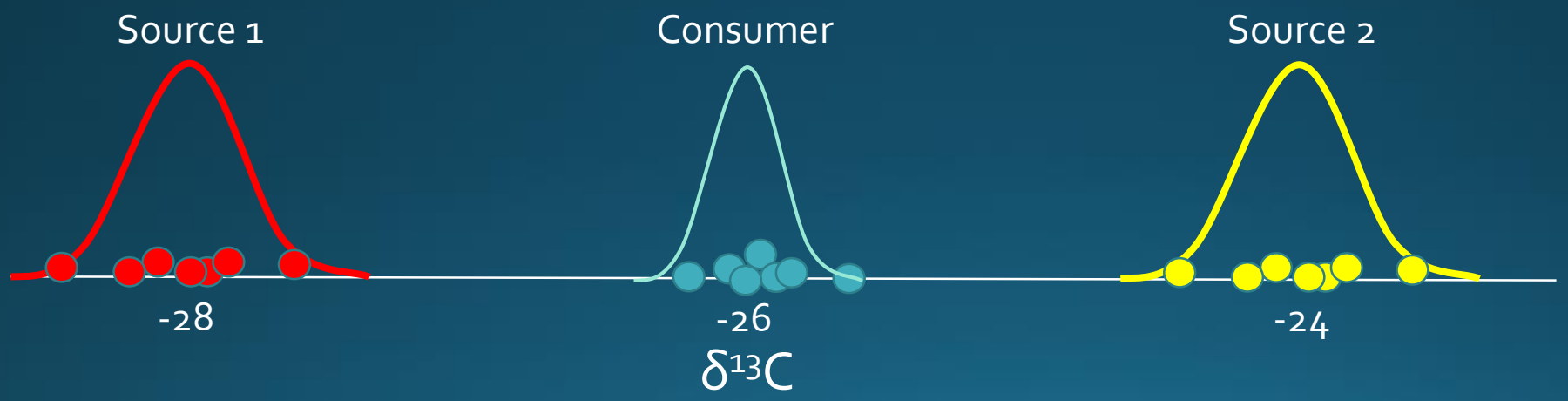
Egozcue et al. (2010)

MixSIR vs. SIAR?



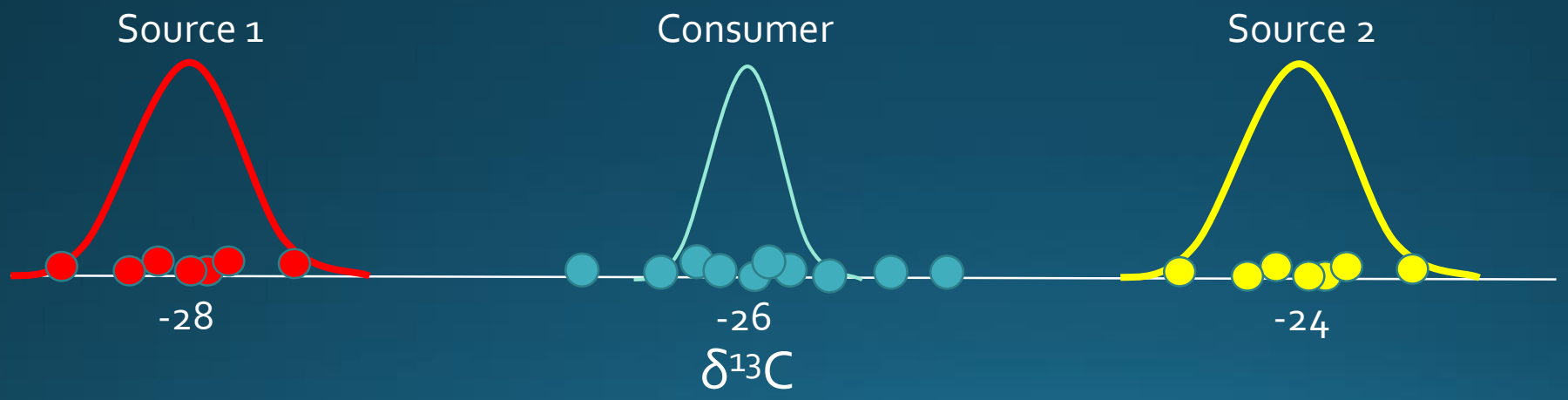
MixSIR vs. SIAR?

MixSIR $\sigma^2_{process}$ Medium variance



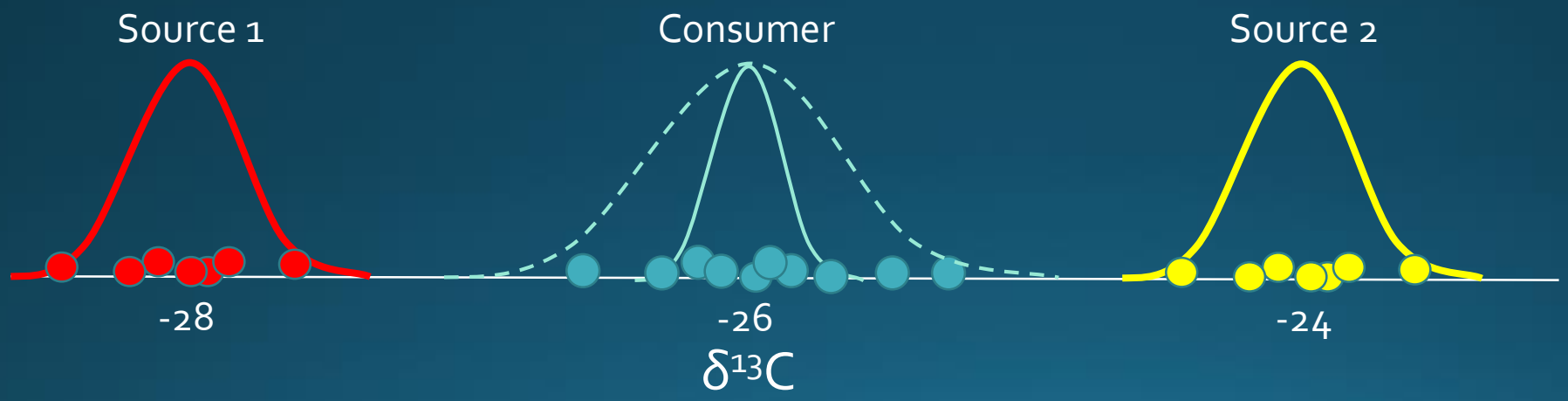
MixSIR vs. SIAR?

MixSIR $\sigma^2_{process}$ High variance



MixSIR vs. SIAR?

SIAR $\sigma^2_{process} + \sigma^2_{resid}$ High variance



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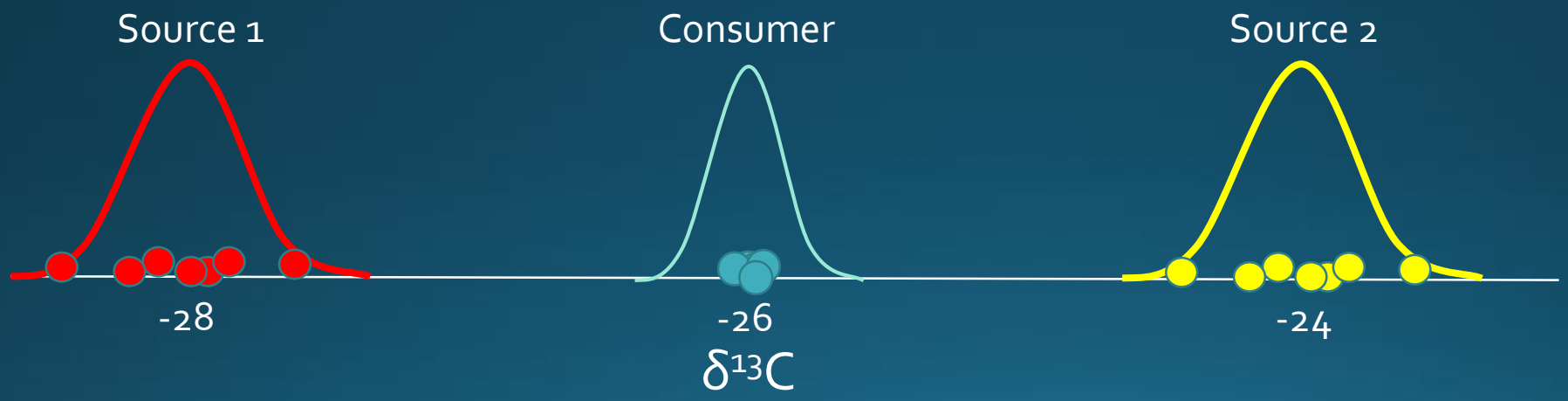

Discrimination

- Trophic enrichment factor (TEF)
- Trophic discrimination factor (TDF)

Difference between sources and mixture *due to metabolic processes*

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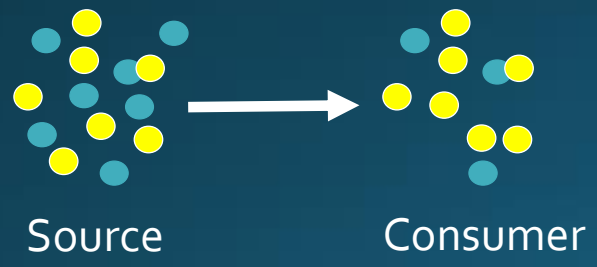

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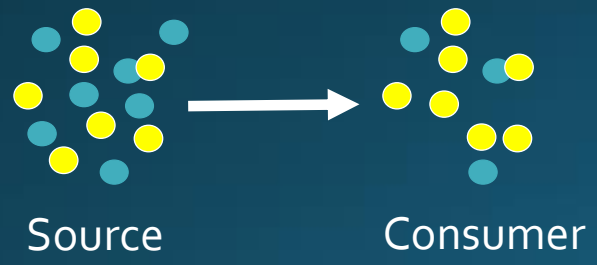

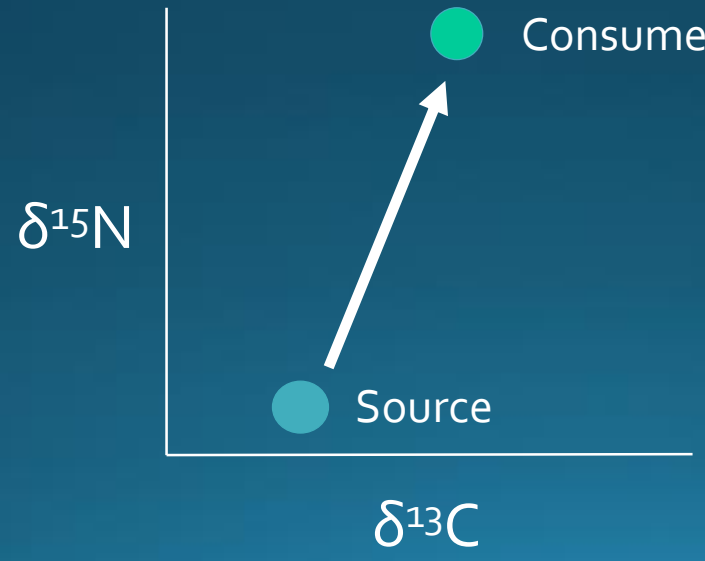

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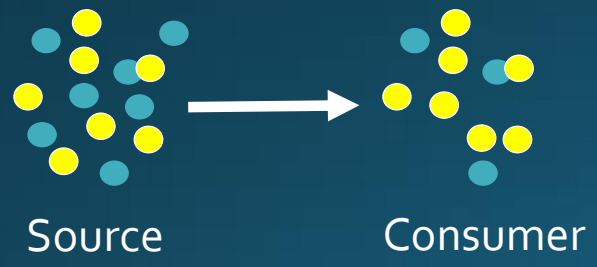

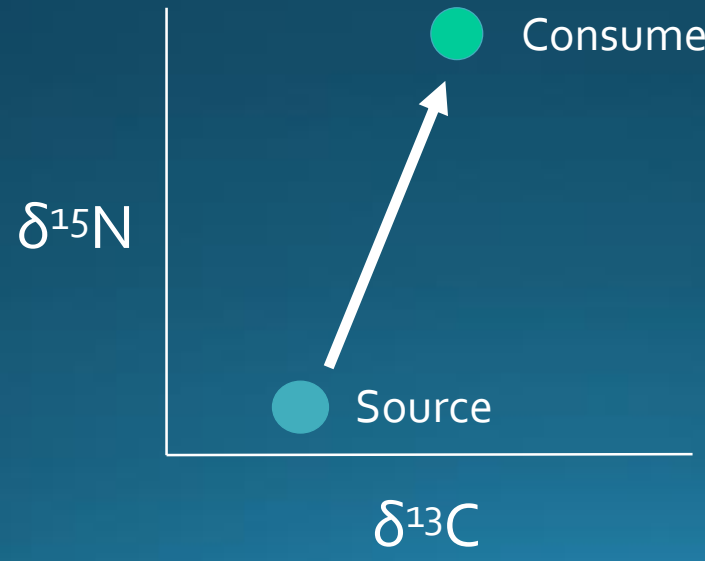

$$X_{ij} = \frac{\sum_{k=1}^{K} p_k q_{jk} (s_{jk} + c_{jk})}{\sum_{k=1}^{K} p_k q_{jk}}$$

$$c_{jk} \sim N\left(\lambda_{jk}, \tau_{jk}^2\right)$$

Concentration dependence