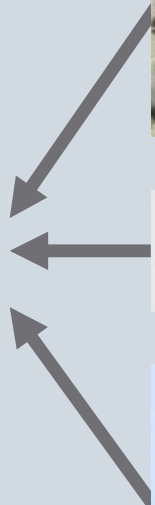


Bayesian (stable isotope) mixing models: MixSIAR

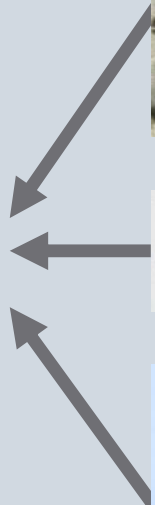
BRIAN STOCK

MAY 22, 2017

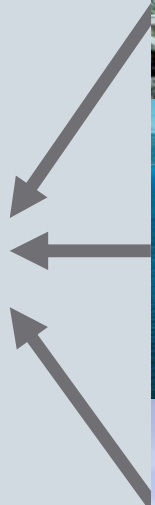
Calculate source % to a mixture



Calculate prey % to a diet



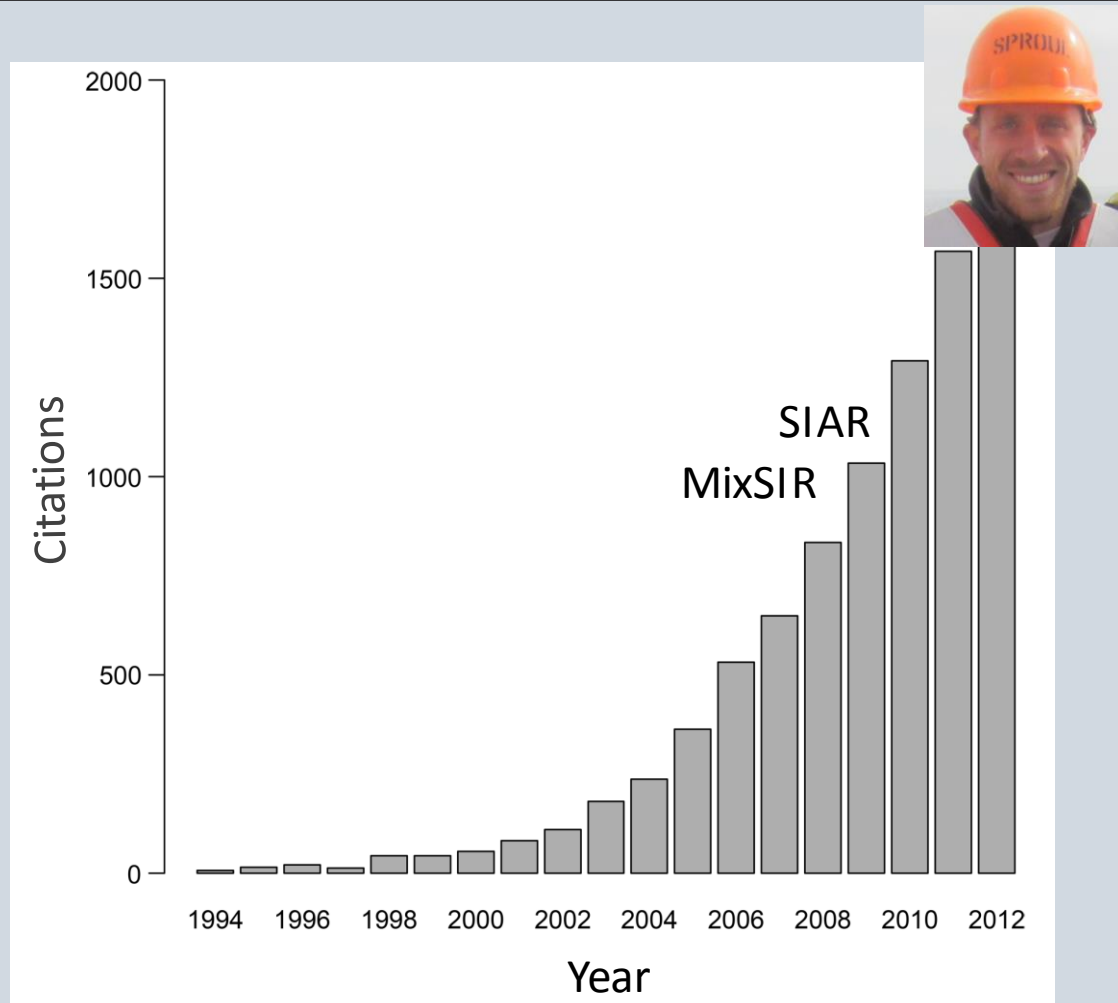
Calculate colony % to a bird



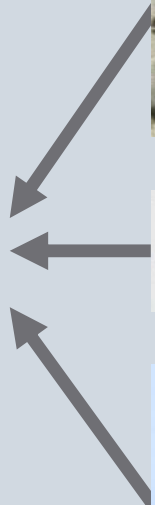
Calculate **soil** % to a **sediment**



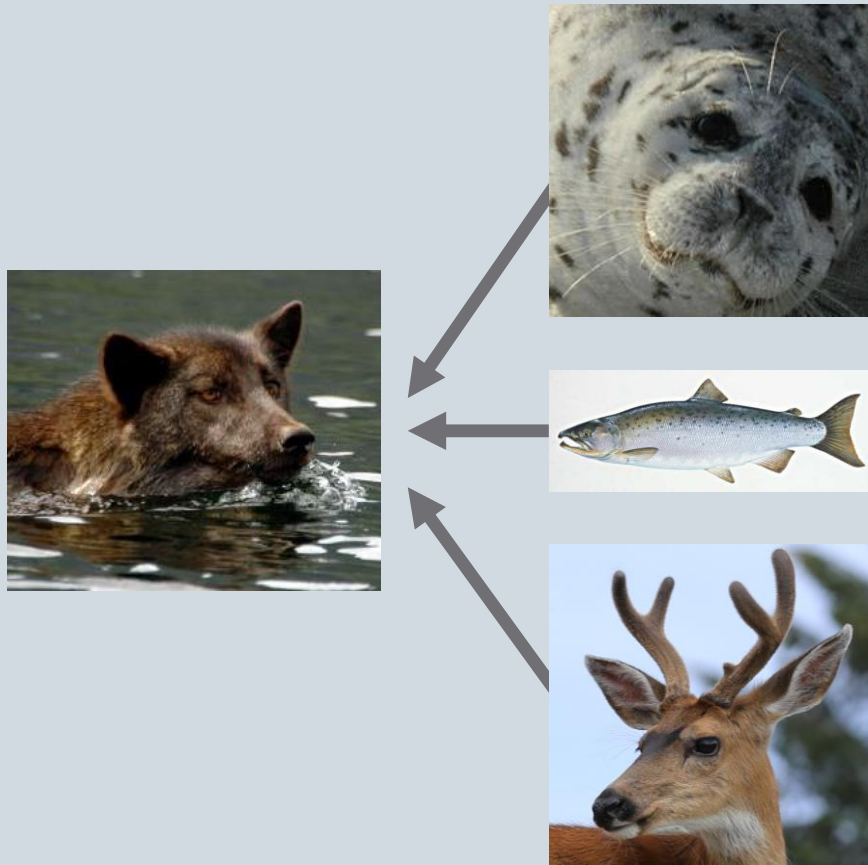
Scientists use mixing models a lot



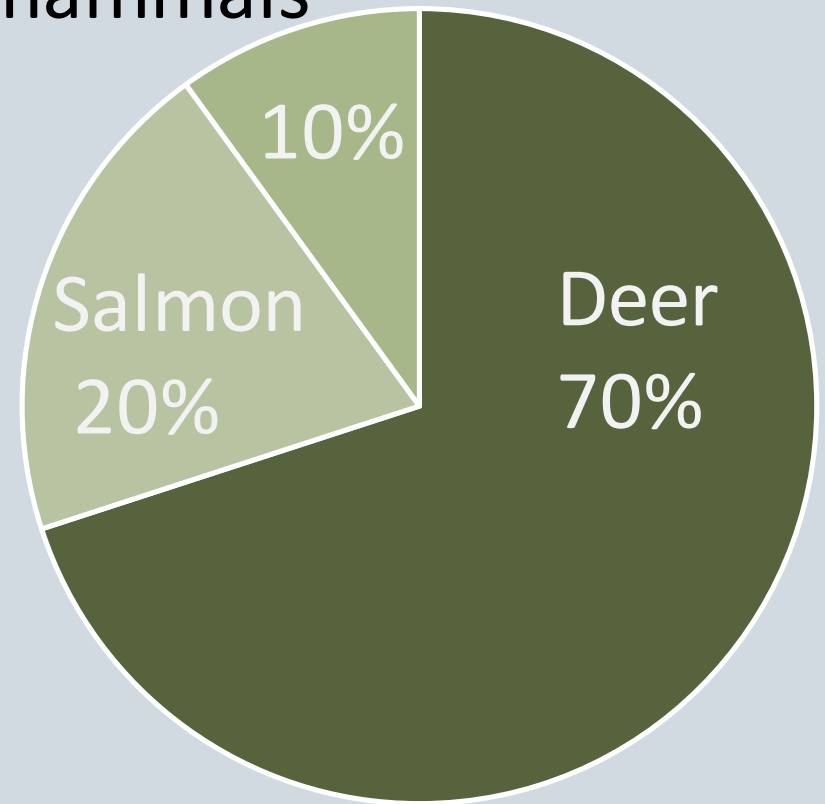
Calculate **prey** % to a **diet**



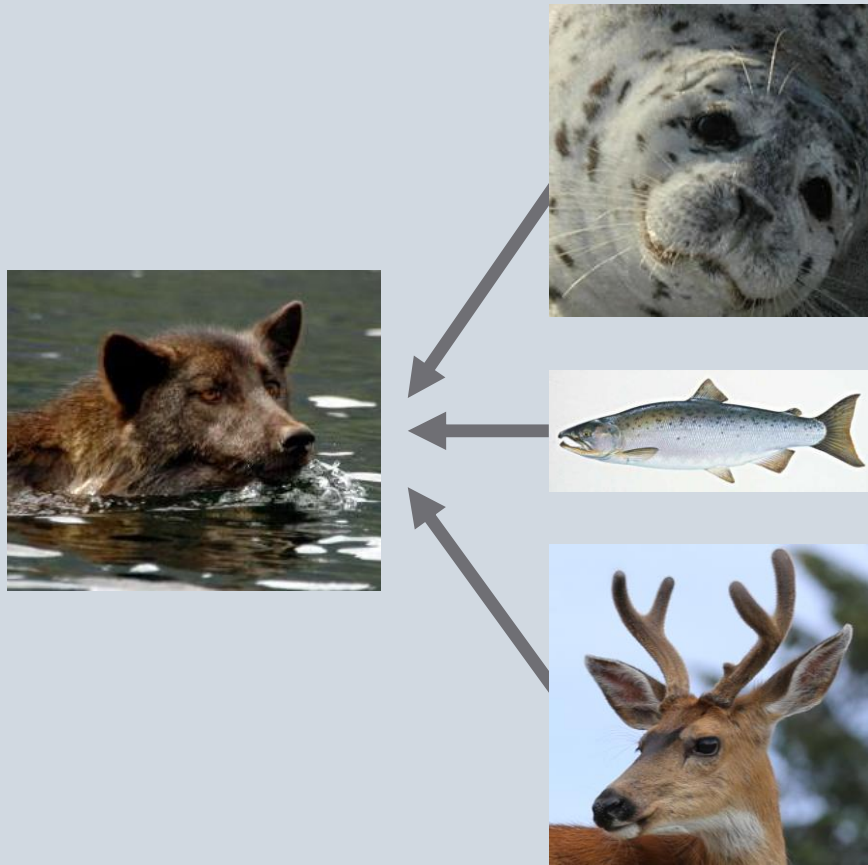
Calculate prey % to a diet



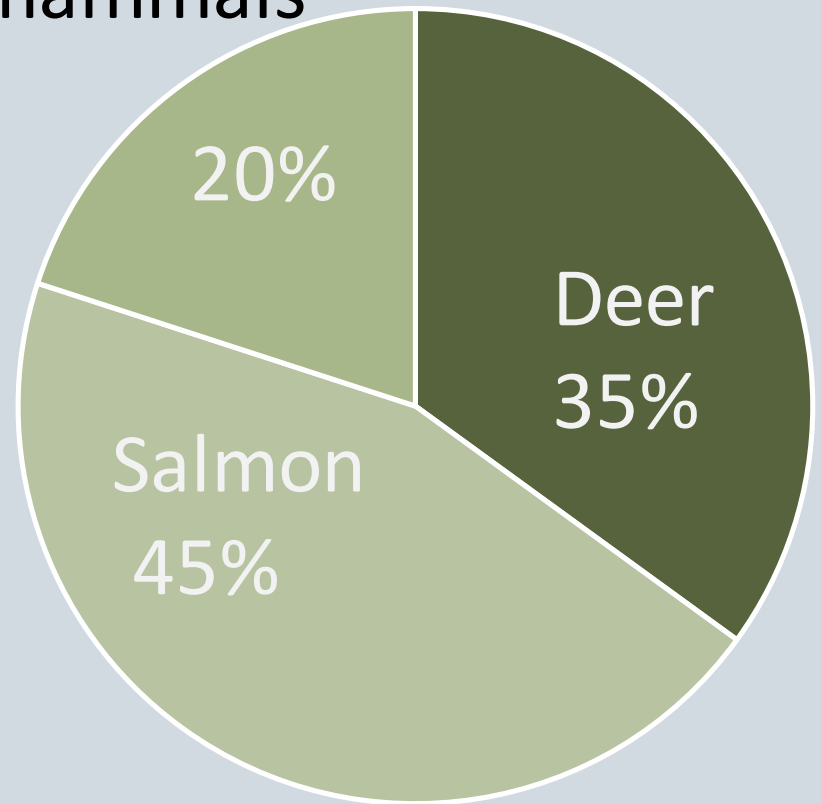
Marine mammals



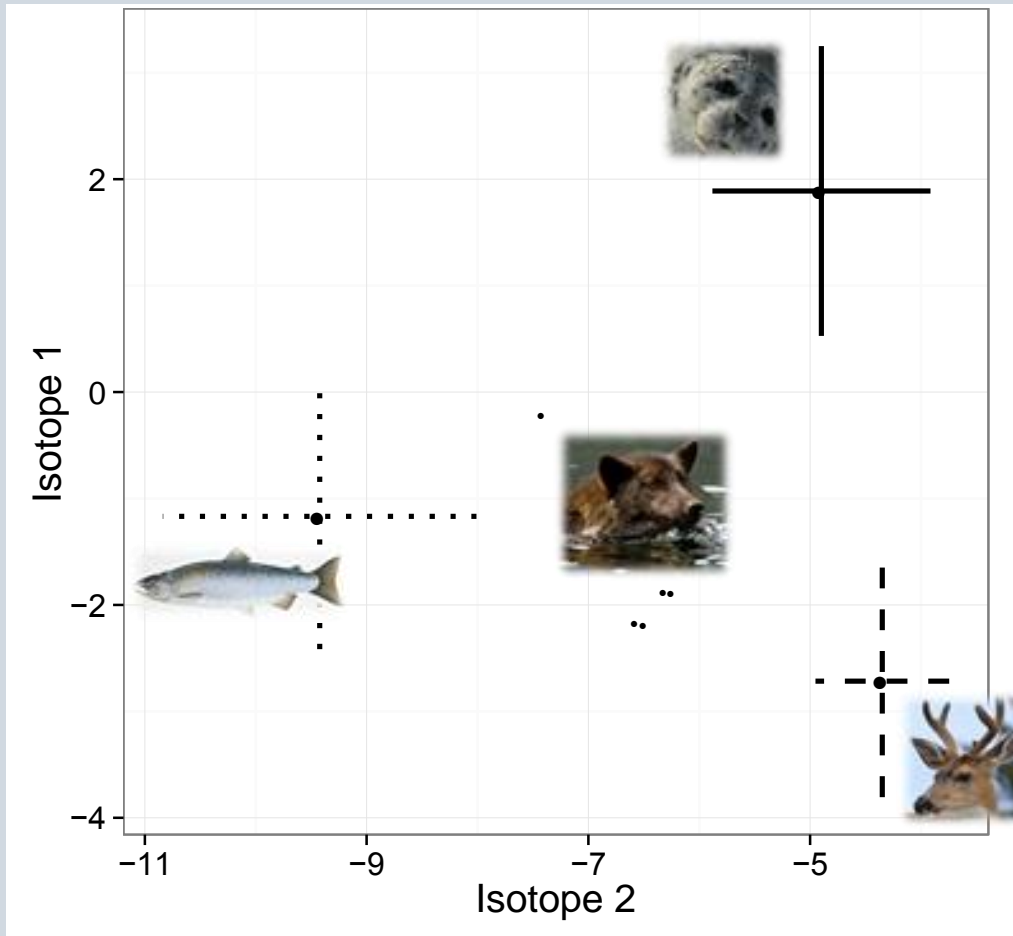
Calculate prey % to a diet



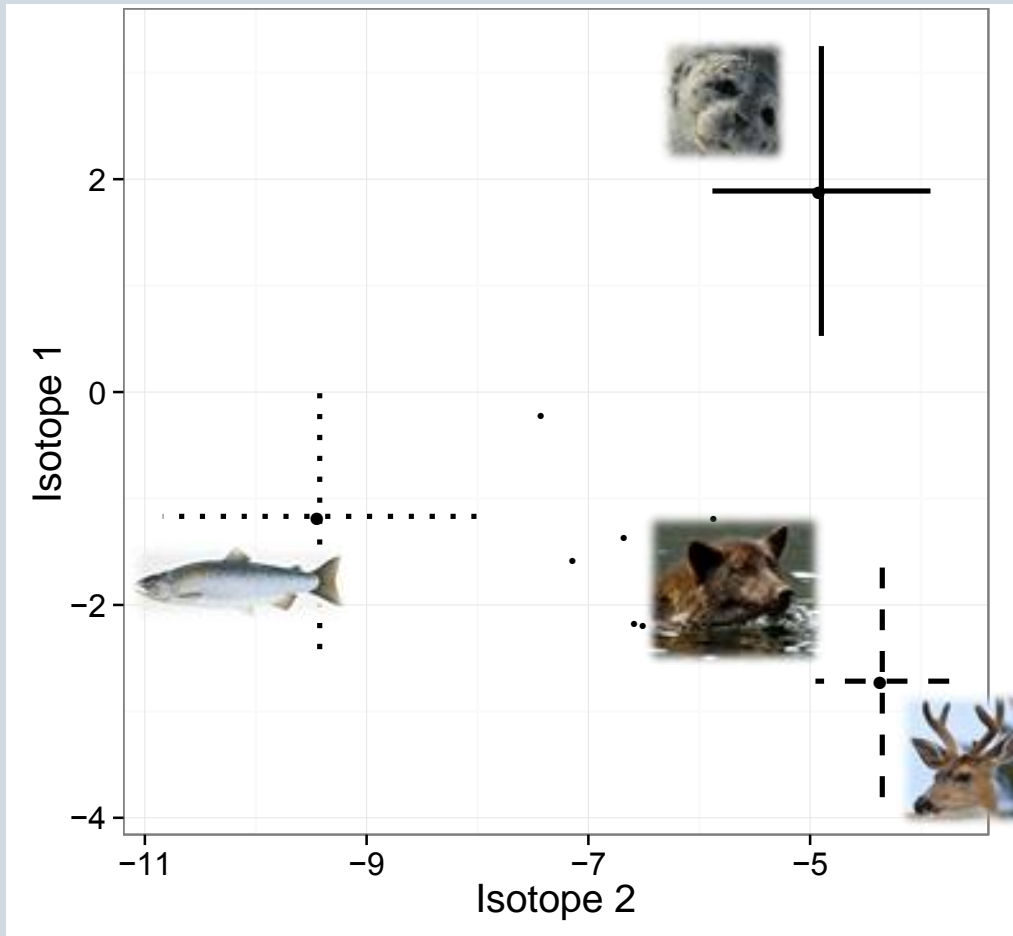
Marine mammals



Using stable isotope data



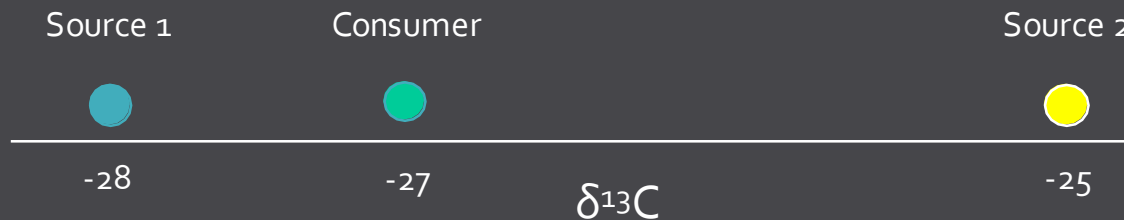
Using stable isotope data



How mixing models work

Linear mixing model:

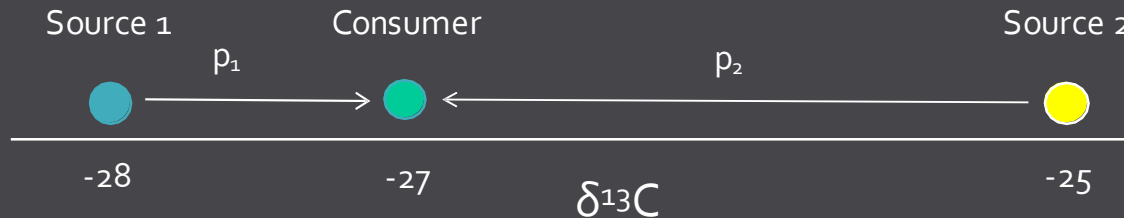
Diet = ?



How mixing models work

Linear mixing model:

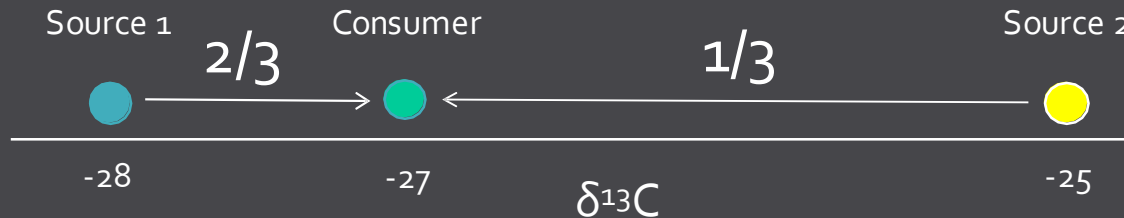
$$\text{Consumer} = p_1 * s_1 + p_2 * s_2 \quad (p_1 + p_2 = 1)$$



How mixing models work

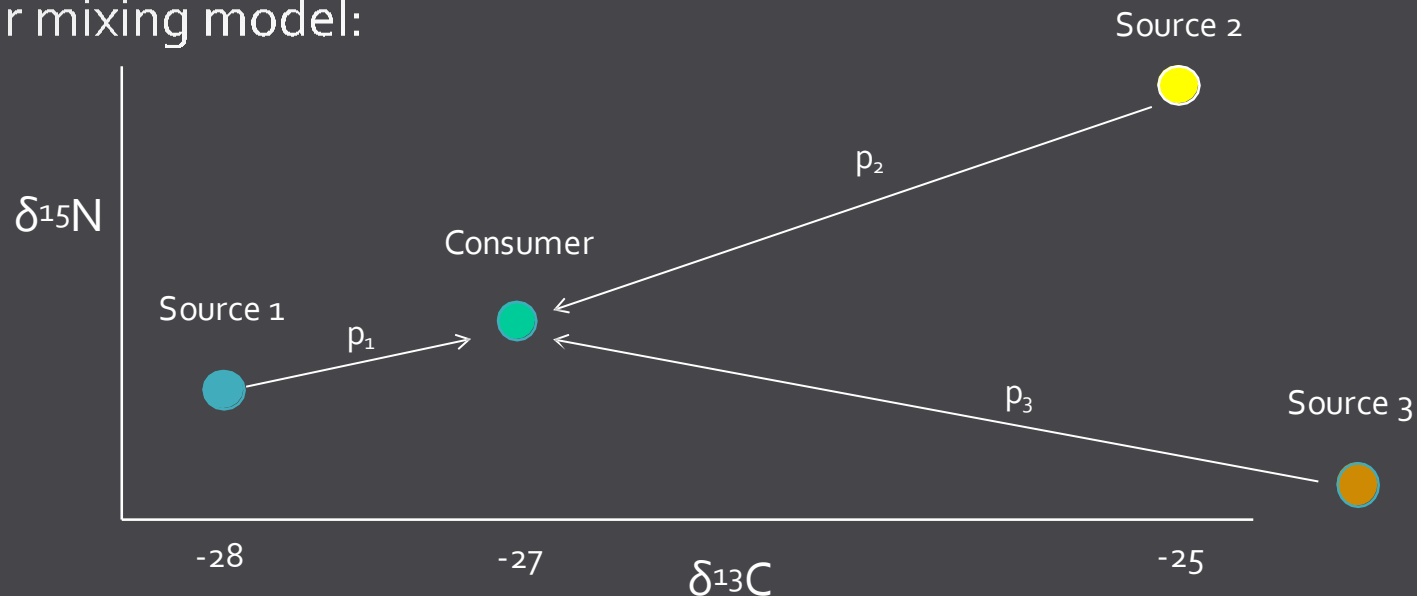
Linear mixing model:

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



How mixing models work

Linear mixing model:



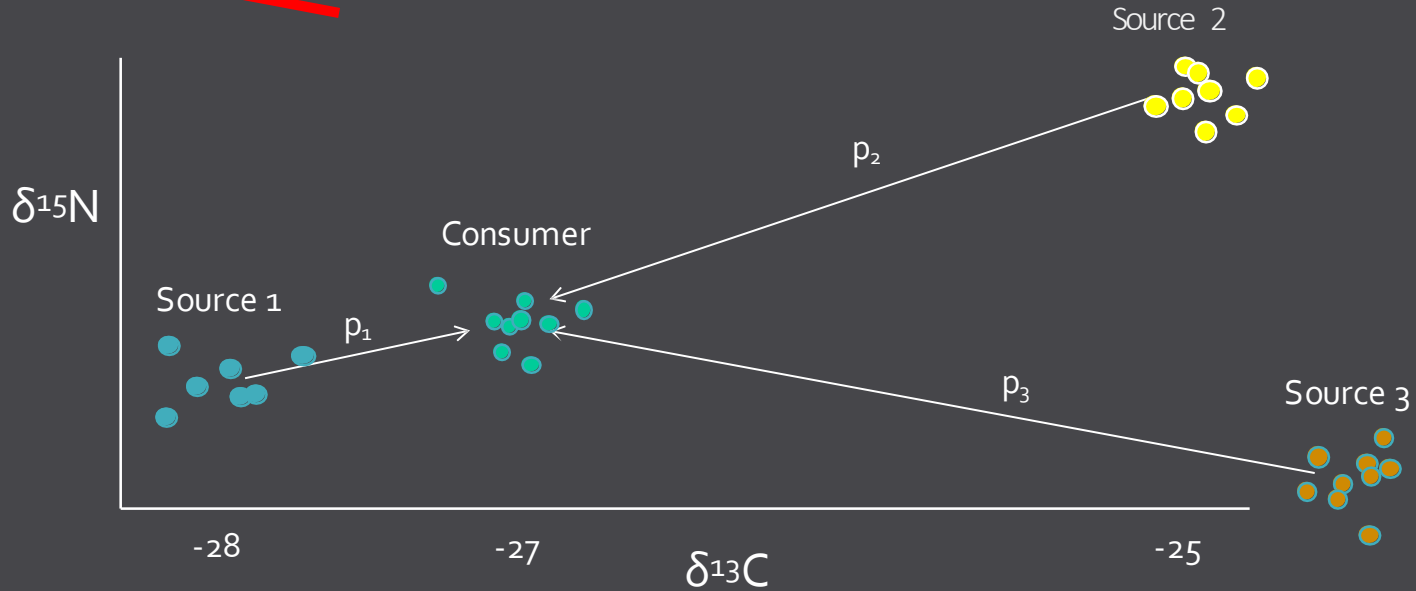
$$\text{Consumer}_C = p_1 s_{1C} + p_2 s_{2C} + p_3 s_{3C}$$

$$\text{Consumer}_N = p_1 s_{1N} + p_2 s_{2N} + p_3 s_{3N}$$

$$p_1 + p_2 + p_3 = 1$$

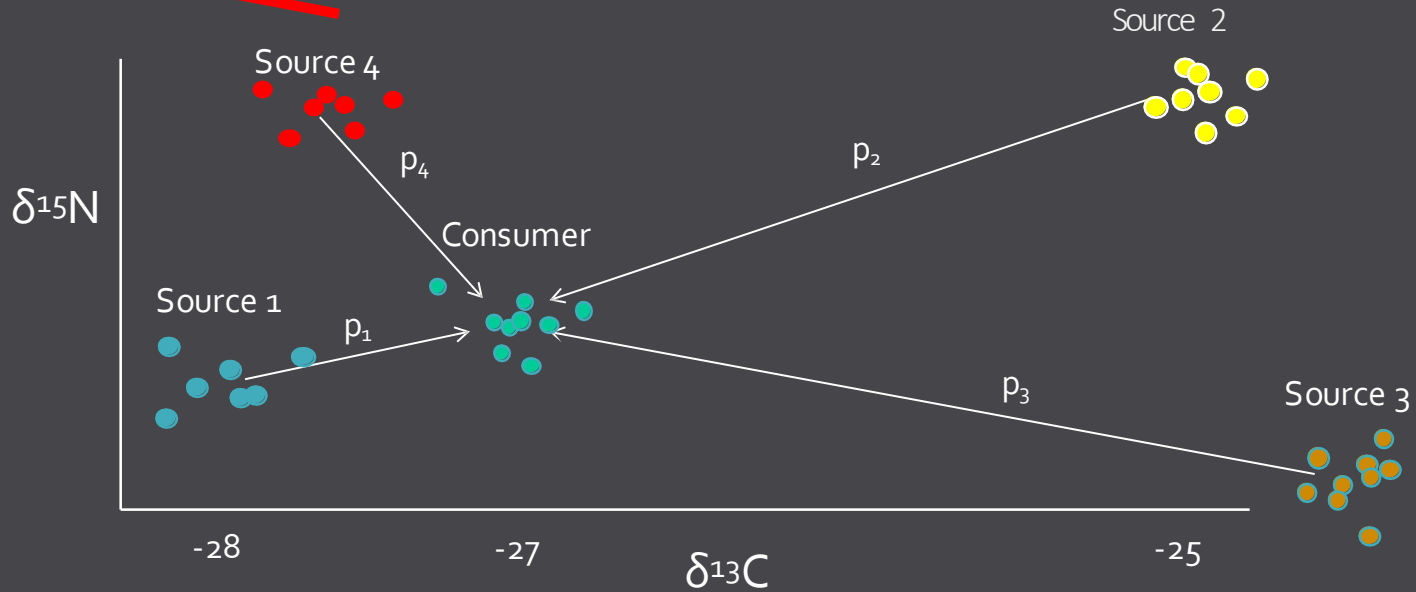
How mixing models work

~~Linear mixing model:~~



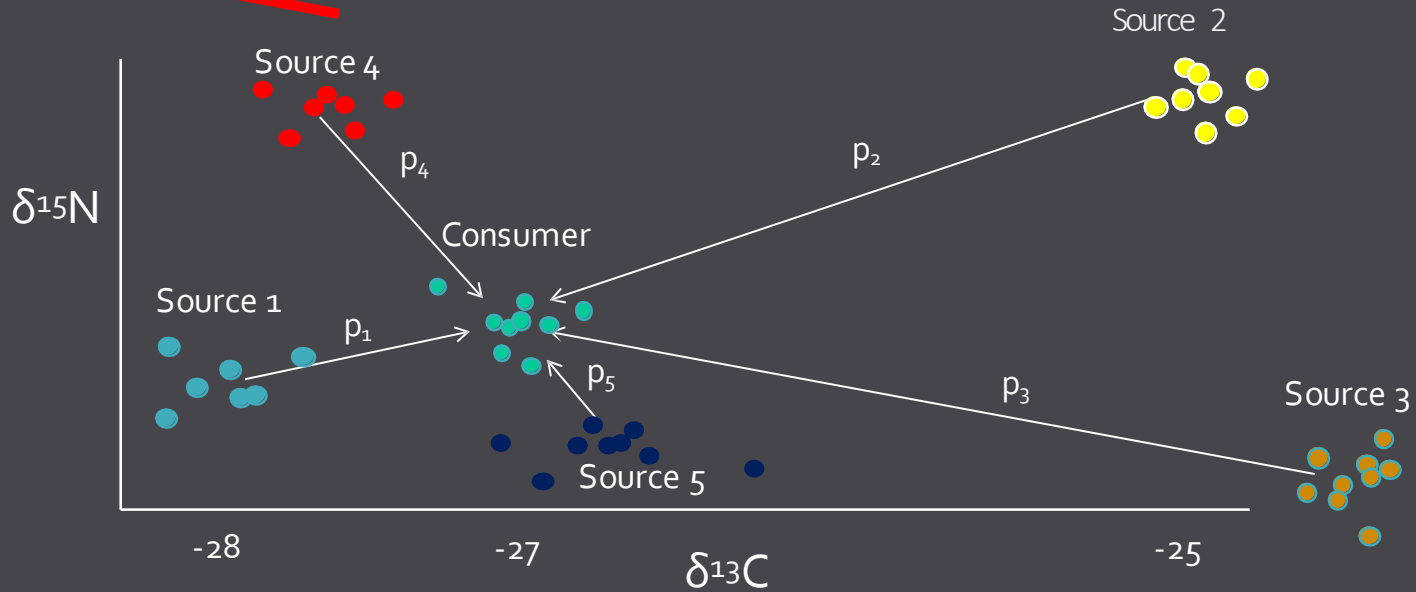
How mixing models work

~~Linear mixing model:~~



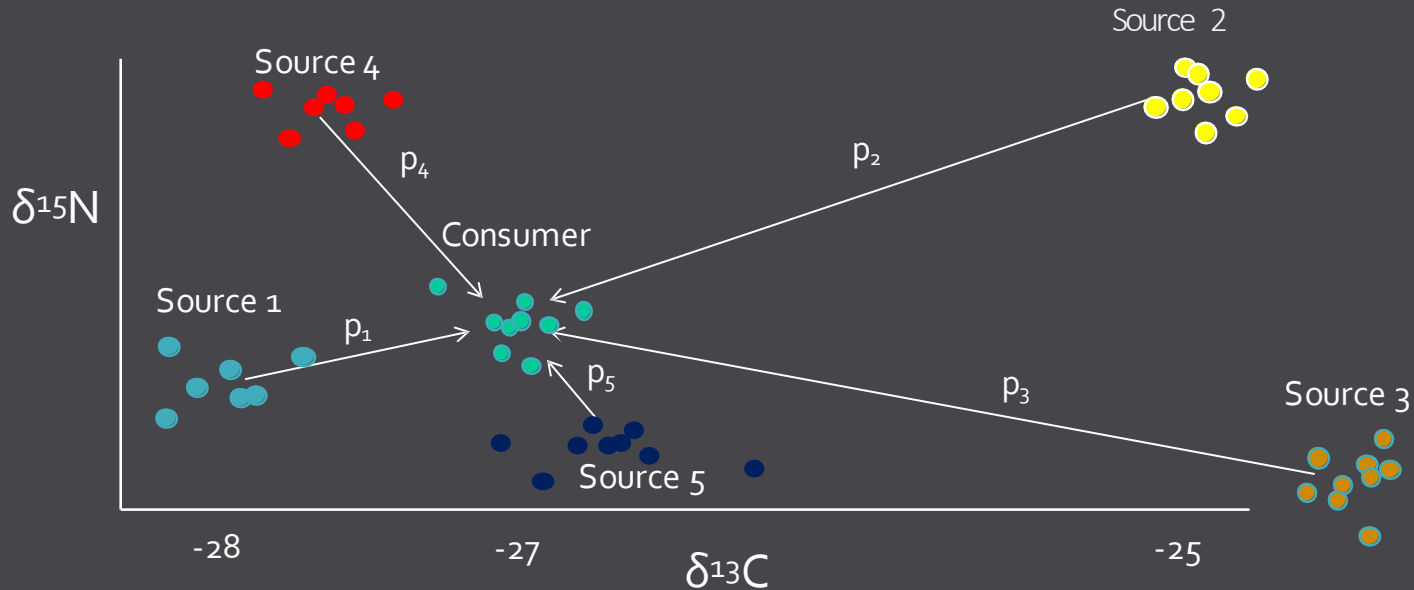
How mixing models work

~~Linear mixing model:~~



How mixing models work

Bayesian mixing model:



$$\mathbf{p} \sim \text{Dir}(\boldsymbol{\alpha})$$

$$Y_{ij} \sim \text{MVN} \left(\sum_k p_k \mu_{jk}^s, \Sigma \right)$$

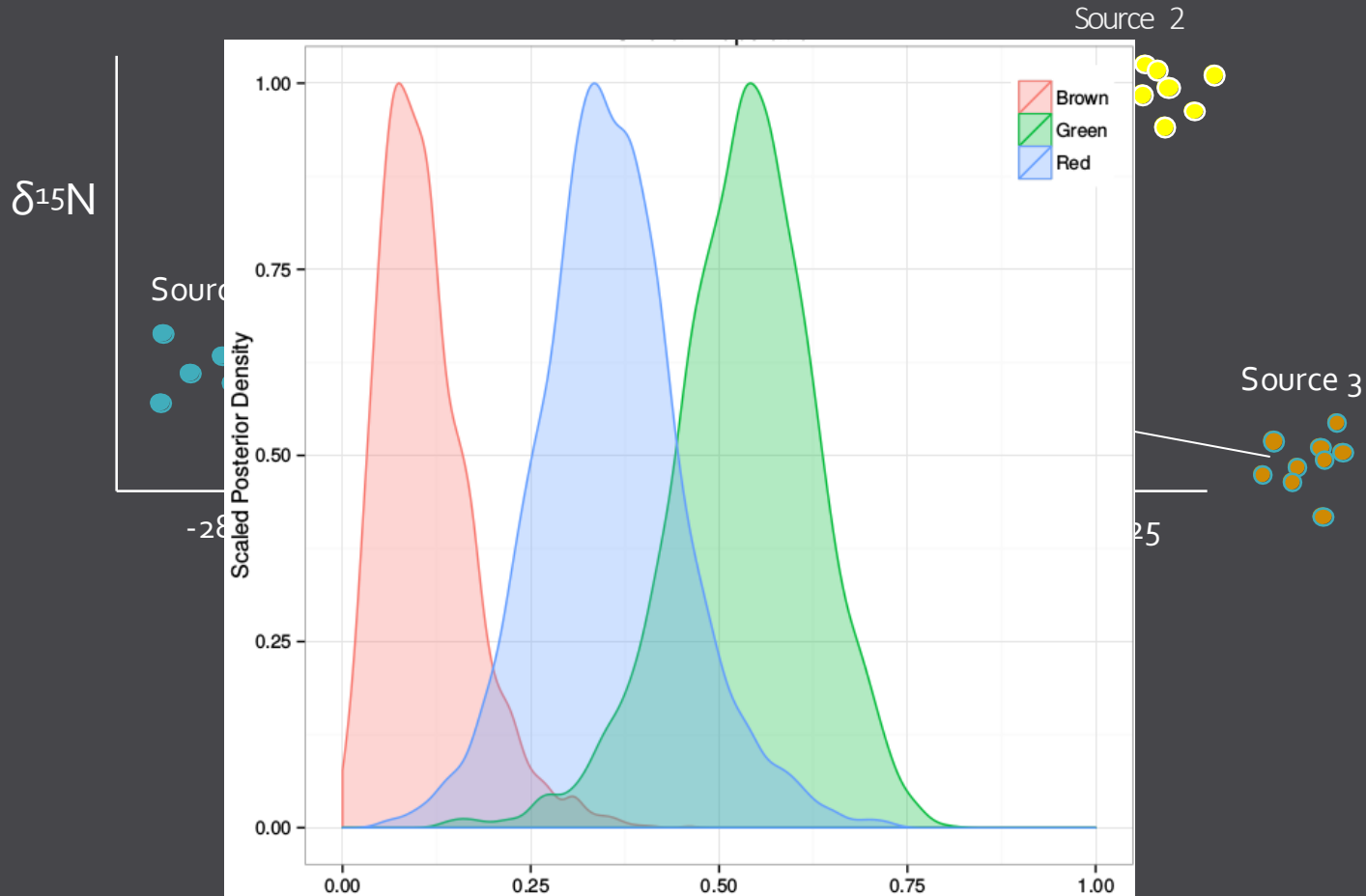
$$Y_{jk}^s \sim \text{MVN} (\mu_{jk}^s, \Sigma_k^s)$$

$$\mu_{jk}^s \sim \mathcal{N}(0, .001)$$

$$\tau_{jk} \sim \text{gamma}(.001, .001)$$

How mixing models work

Bayesian mixing model:



Bayesian models are better

1. Account for uncertainty in data (mix, source, TDF)
2. Solid statistical basis (likelihood)
3. Include additional info as priors
 - stomach/fecal contents
 - prey abundance

Bayesian models are better

1. Account for uncertainty in data (mix, source, TDF)
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LETTER

Incorporating uncertainty and prior information into stable isotope mixing models

MixSIR 2008

Source Partitioning Using Stable Isotopes: Coping with Too Much Variation

Andrew C. Parnell¹, Richard Inger², Stuart Bearhop², Andrew L. Jackson^{3*}

SIAR 2010

MixSIAR adds further improvements

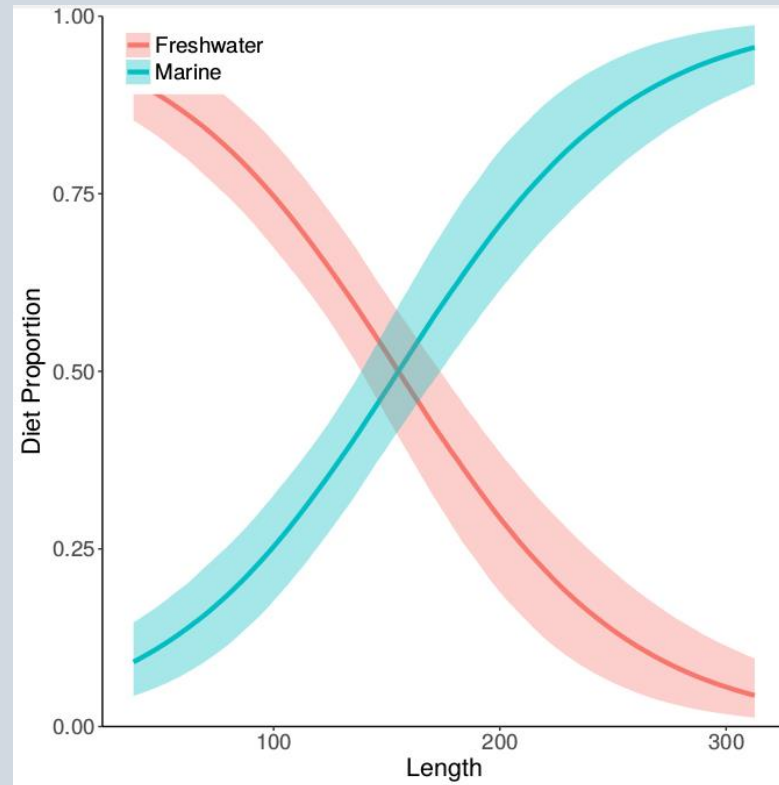
1. Graphical User Interface (GUI)

The screenshot displays the MixSIAR GUI with the following settings:

- Read in data:** (highlighted), ,
- 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
- Plot options:**
 - Save plot as: pdf png
 - Save plot as: pdf png
- Output options:**
 - Summary Statistics Save summary statistics to file:
 - Posterior Density Plot Save plot as: pdf png
 - Pairs Plot Save plot as: pdf png
 - XY Plot Save plot as: pdf png
- Diagnostics:** Gelman-Rubin (must have > 1 chain) Geweke
 Save diagnostics to file:
- Note:** diagnostics will print in the R command line if you do not choose to save to file
- Buttons:**

MixSIAR adds further improvements

1. Graphical User Interface (GUI)
2. Covariate effects



MixSIAR adds further improvements

1. Graphical User Interface (GUI)
2. Covariate effects
3. Fit source data within model

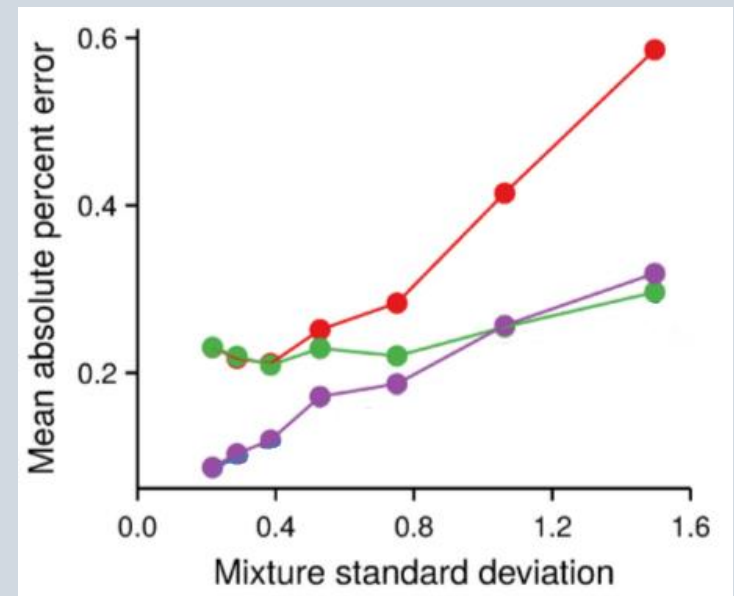
$$Y_{jk}^s \sim MVN(\mu_{jk}^s, \Sigma_k^s)$$

$$\mu_{jk}^s \sim \mathcal{N}(0, .001)$$

$$\tau_{jk} \sim \text{gamma}(.001, .001)$$

MixSIAR adds further improvements

1. Graphical User Interface (GUI)
2. Covariate effects
3. Fit source data within model
4. Better error structure(s)



MixSIAR adds further improvements

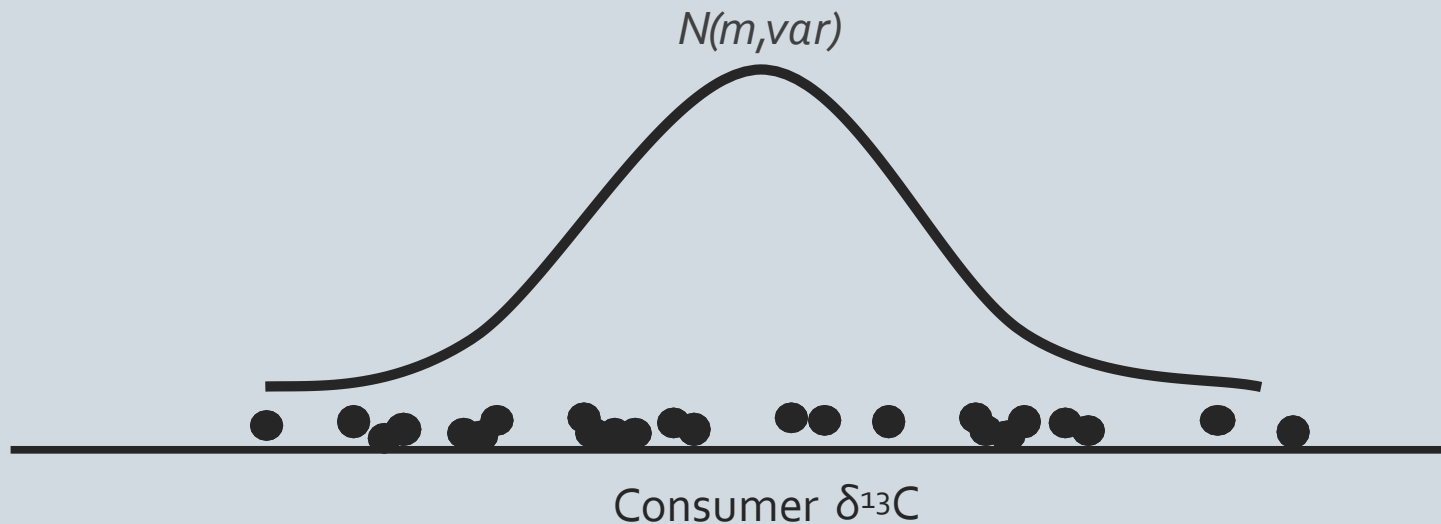
1. Graphical User Interface (GUI)
2. Covariate effects
3. Fit source data within model
4. Better error structure(s)
5. Plot/modify your prior

Covariate effects in MixSIAR

No covariate effects...

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

Assumes that all consumers have the *same diet*



1. Covariate effects

Covariate effects in MixSIAR

Transform \mathbf{p} 's

Linear regression in ILR-space

$$\mathbf{p} \sim \text{Dir}(\boldsymbol{\alpha})$$

$$p_{ik} = \text{inverseILR}(\text{ilr.global}_k + \text{ilr.fac1}_{mk} + \text{ilr.cont1}_k \text{Cont1}_i)$$

Covariate effects in MixSIAR

Transform \mathbf{p} 's

Linear regression in ILR-space

$$\mathbf{p} \sim Dir(\boldsymbol{\alpha})$$

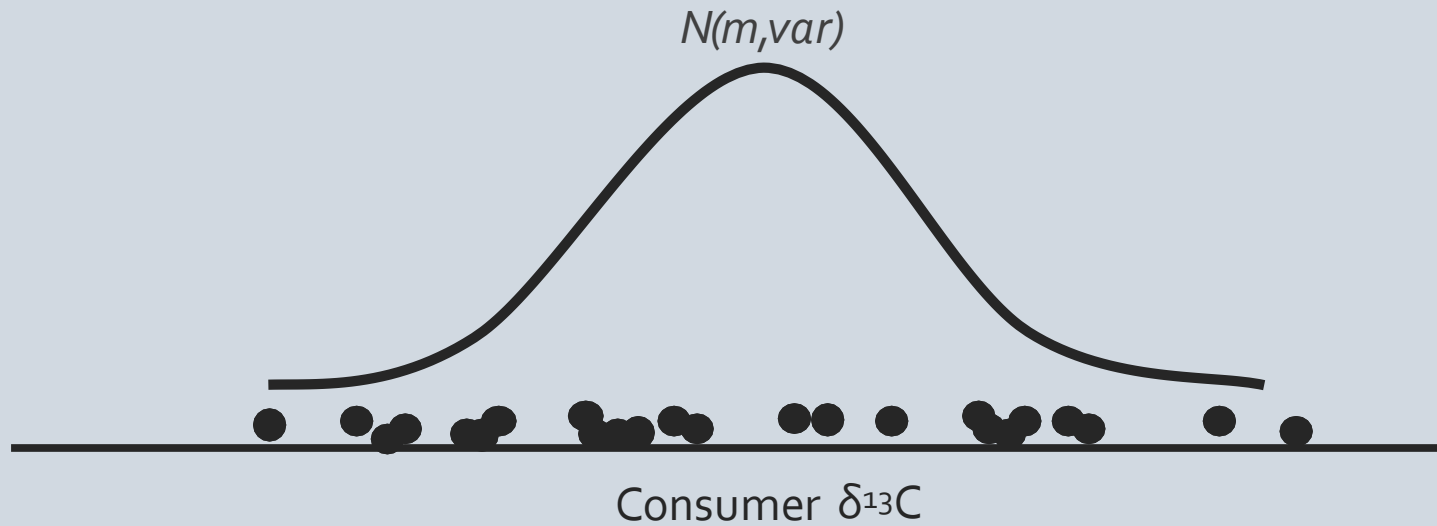
$$p_{ik} = \text{inverseILR}(ilr.global_k + ilr.fac1_{mk} + ilr.cont1_k Cont1_i)$$

↑
Intercept/mean

↑
Fixed/random effect

↑
Continuous effect
("slope")

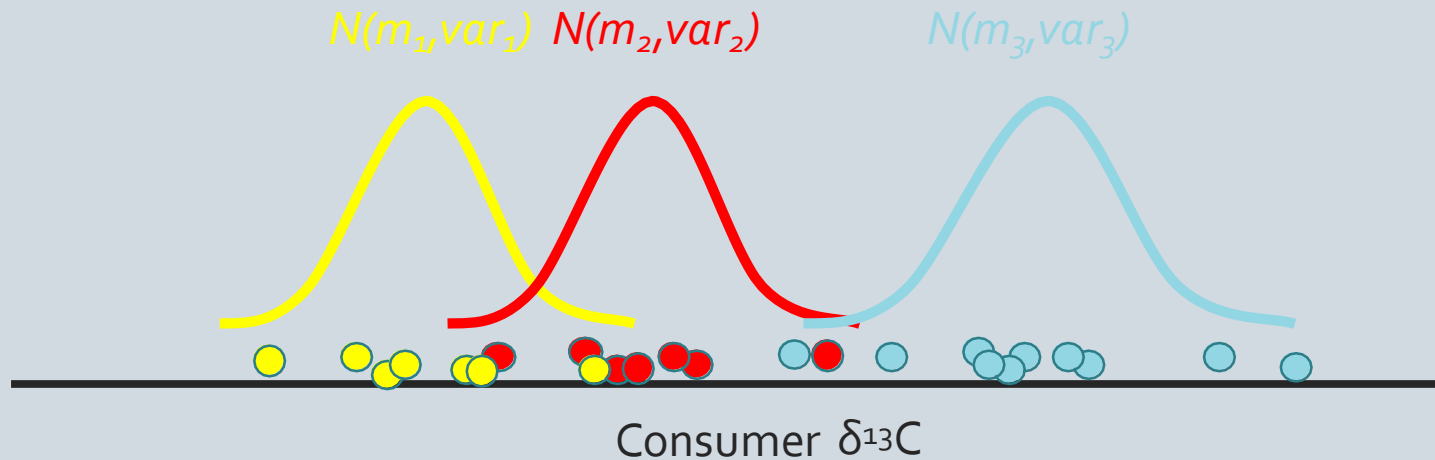
Fixed effects



1. Covariate effects

Fixed effects

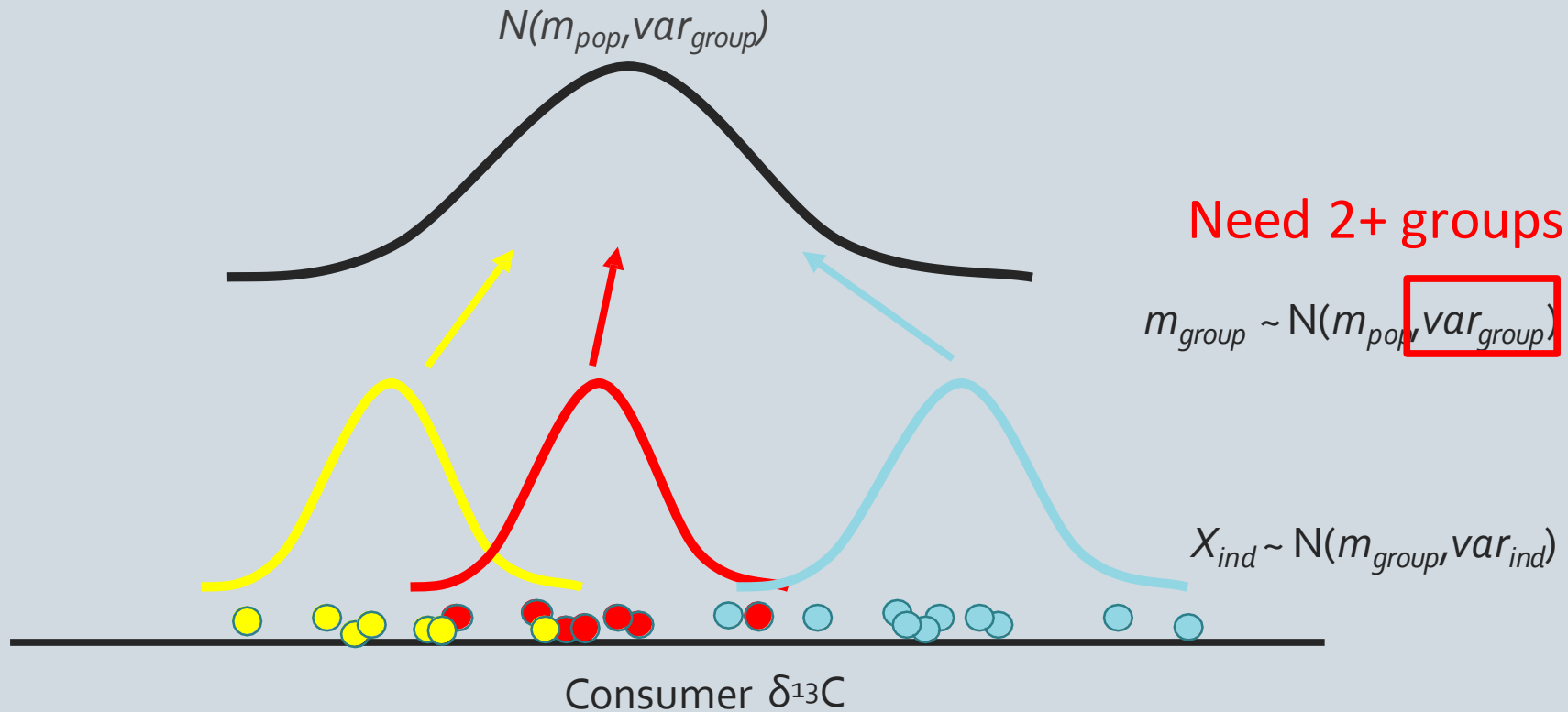
Simplest = estimate mean for different groups independently



1. Covariate effects

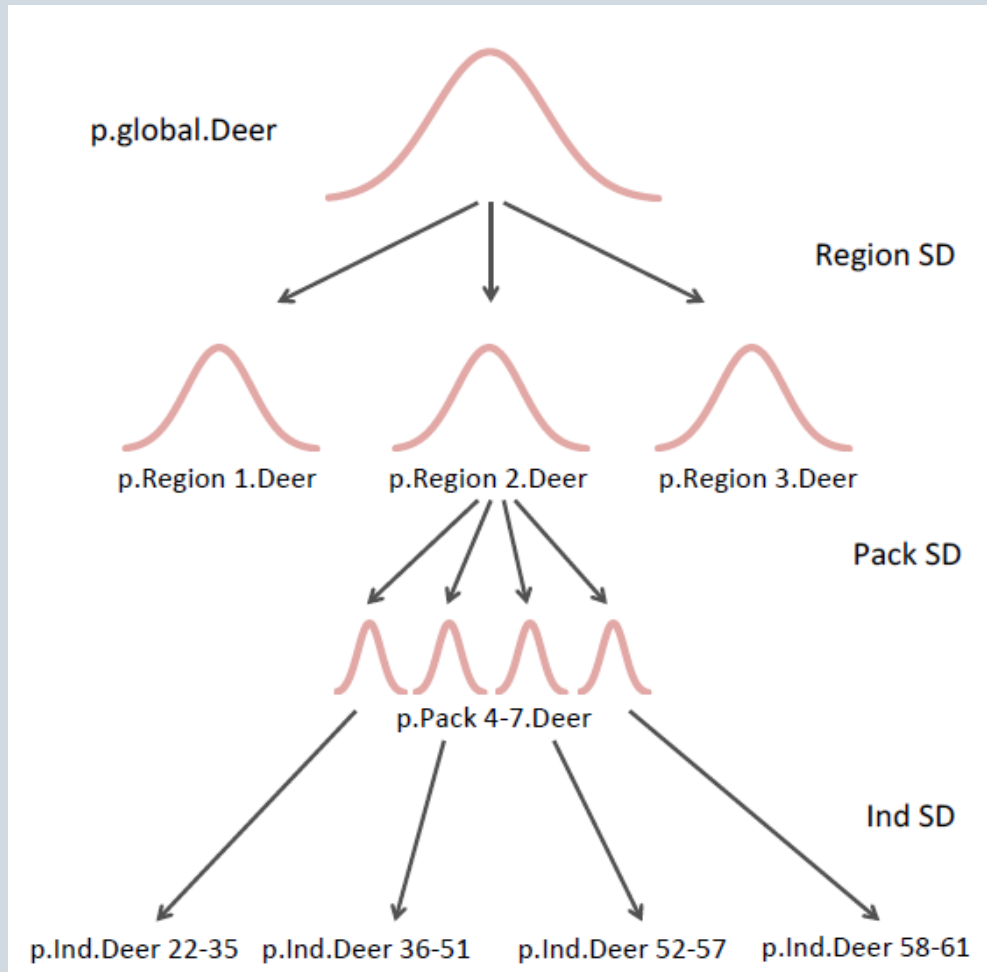
Random effects

More complex



1. Covariate effects

(Nested) Random effects: Wolves Ex



3 Regions

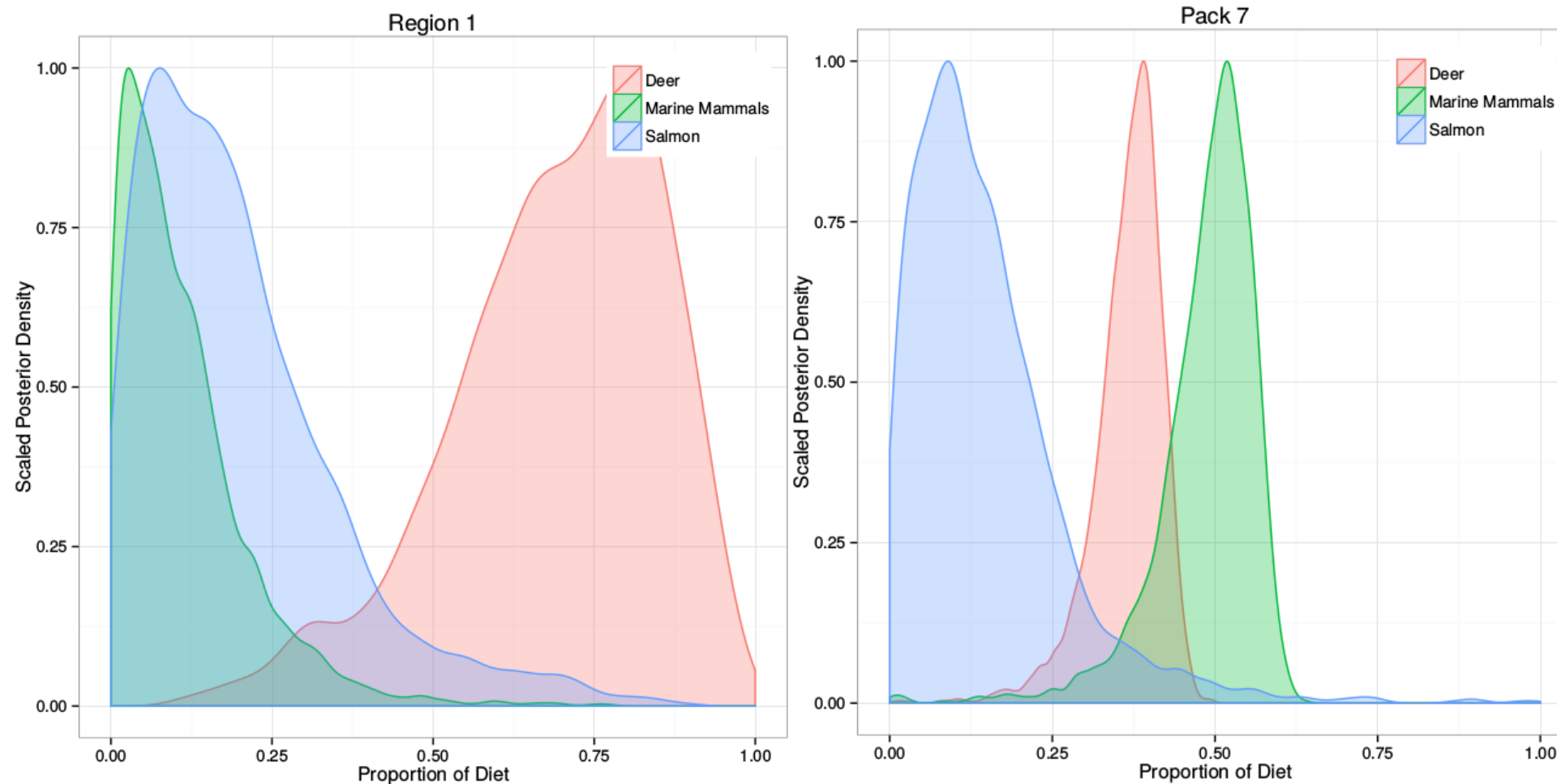
8 Packs

64 Wolves

1. Covariate effects

Semmens et al. (2009)

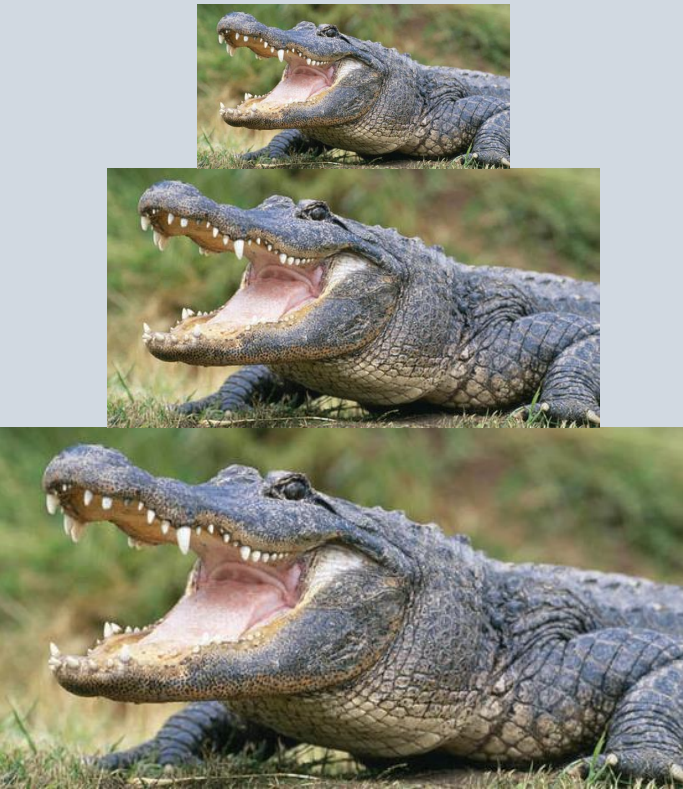
(Nested) Random effects: Wolves Ex



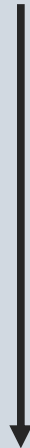
1. Covariate effects

Semmens et al. (2009)

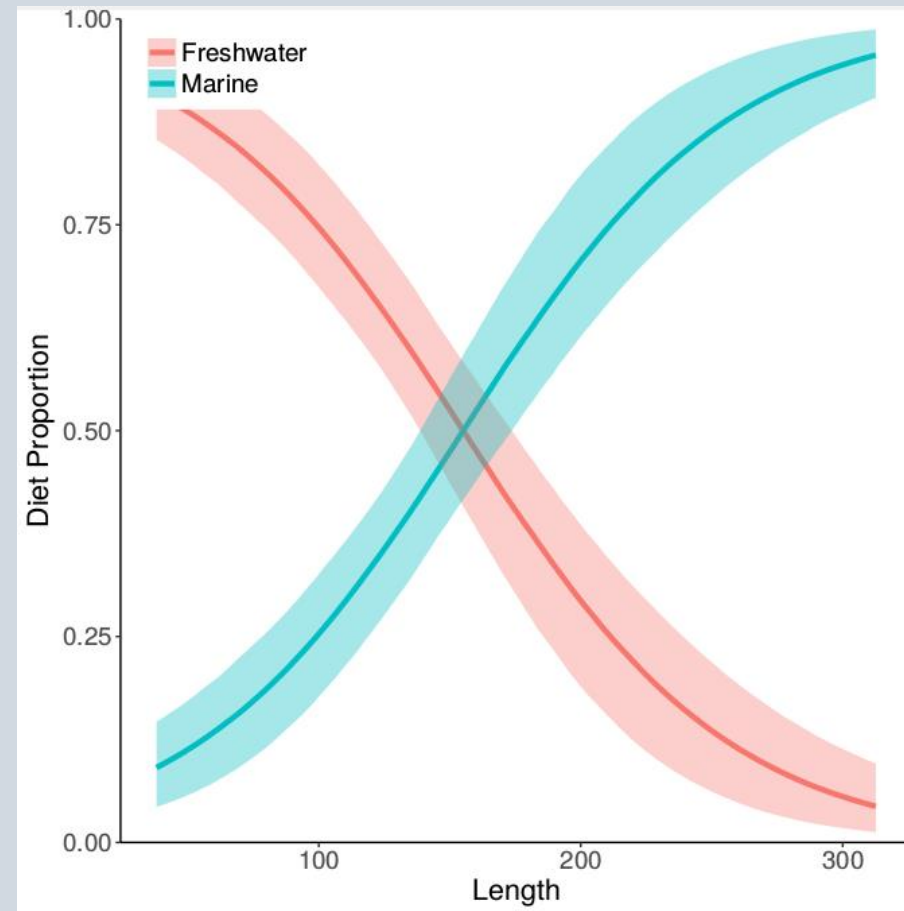
Continuous effect: Alligator length



Freshwater



Marine



Fit source data within model

Ask me later (>1 way to do this)

Boring to talk about...

but reduces error

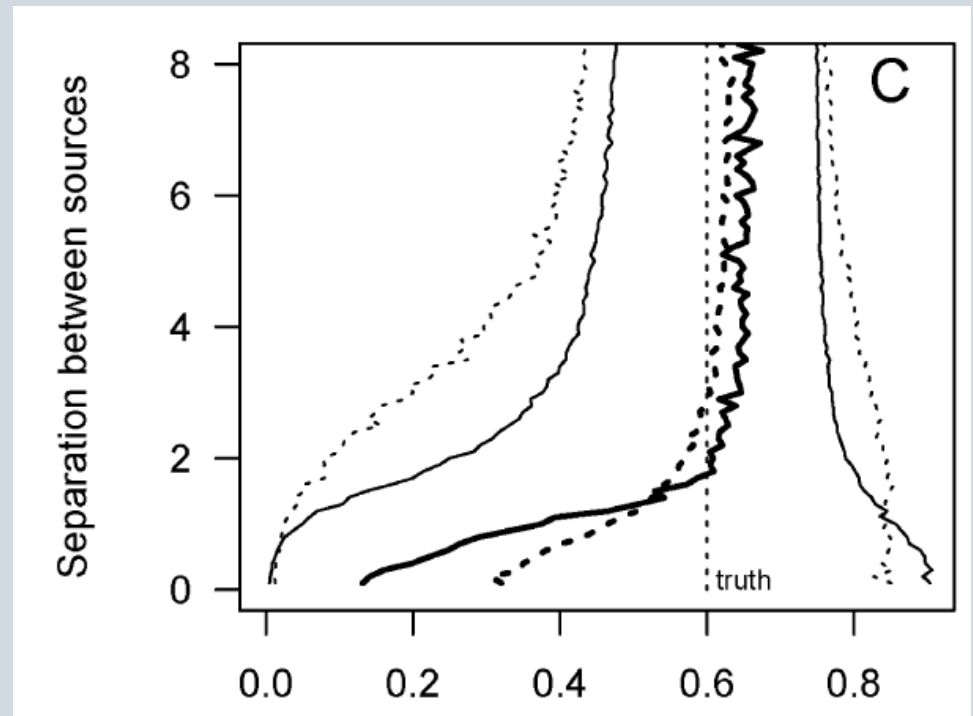
$$Y_{jk}^s \sim MVN(\mu_{jk}^s, \Sigma_k^s)$$

$$\mu_{jk} \sim \mathcal{N}(m_{jk}, n_k/s_{jk}^2),$$

$$tmp.X_{jk} \sim \chi^2(n_k),$$

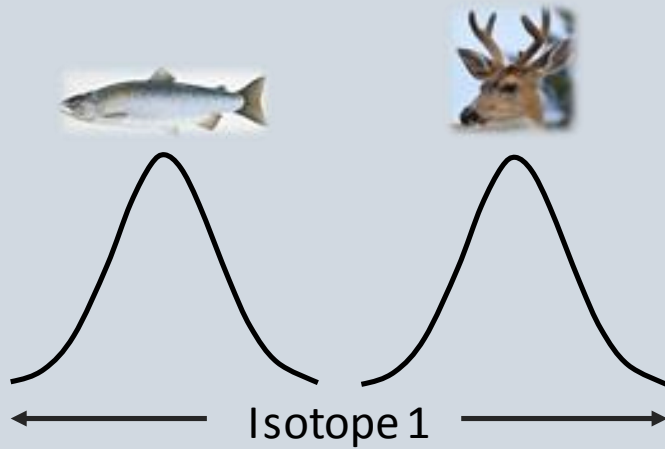
$$\tau_{jk} = \frac{tmp.X_{jk}}{s_{jk}^2 (n_k - 1)},$$

$$\Sigma_k^s = \text{diag}\left(\frac{1}{\tau_{jk}}\right),$$

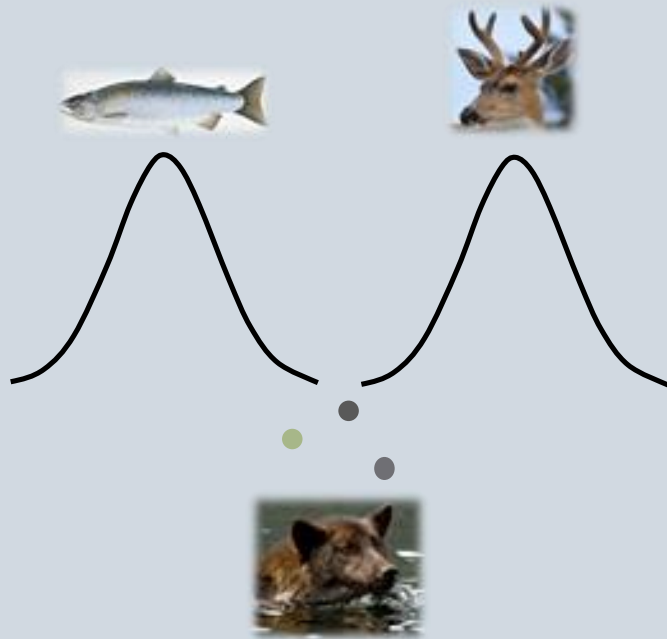


2. Fit source data within model

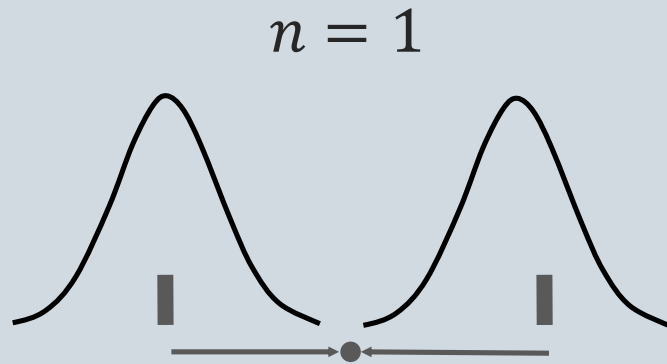
Previous models unrealistic



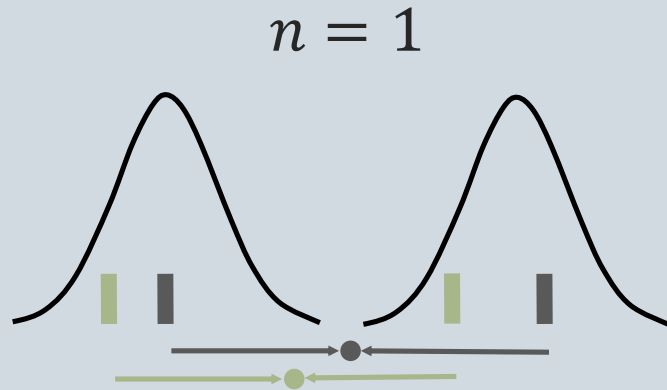
Previous models unrealistic



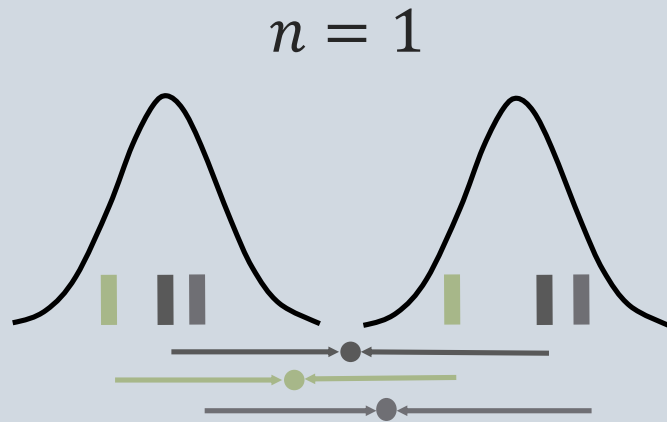
Previous models unrealistic



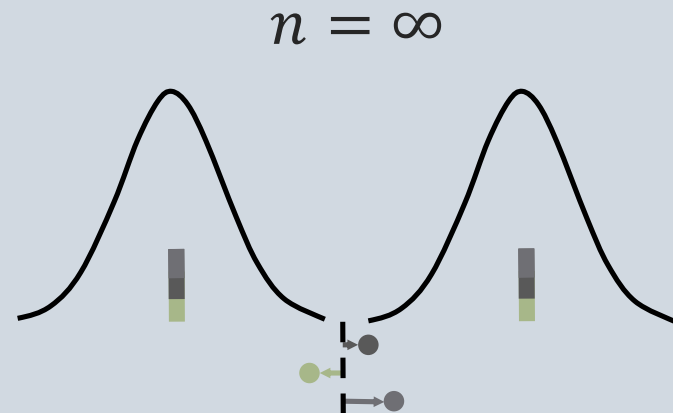
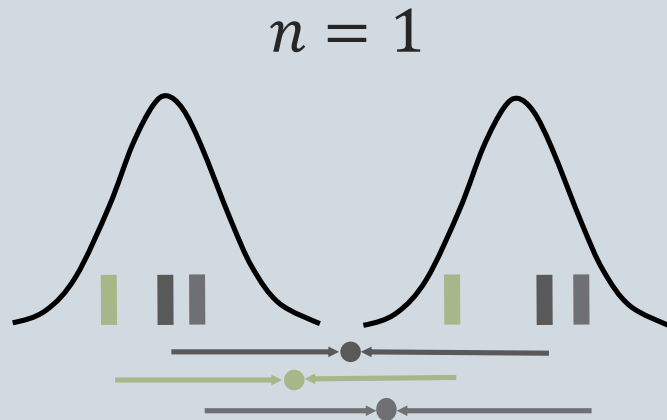
Previous models unrealistic



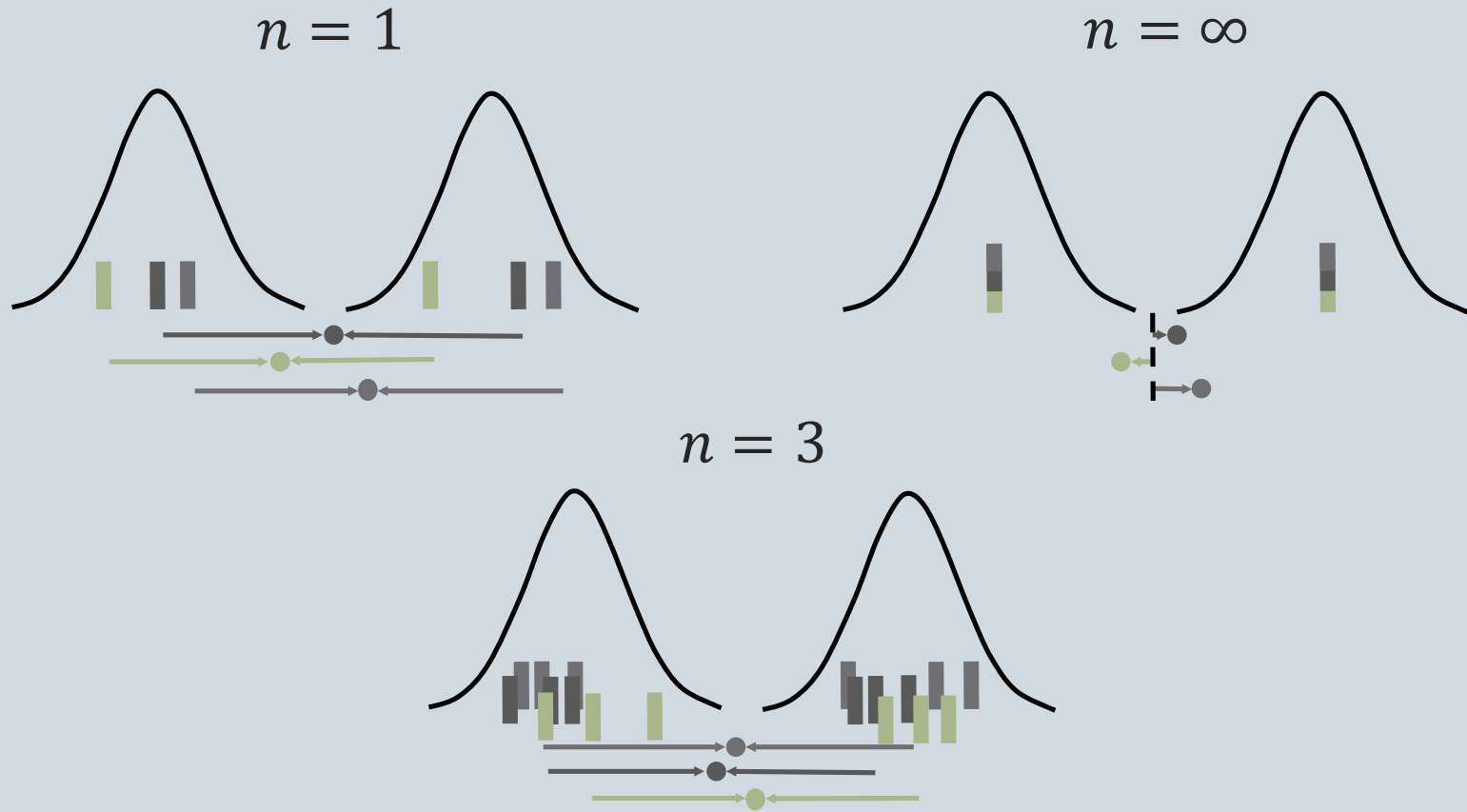
Previous models unrealistic



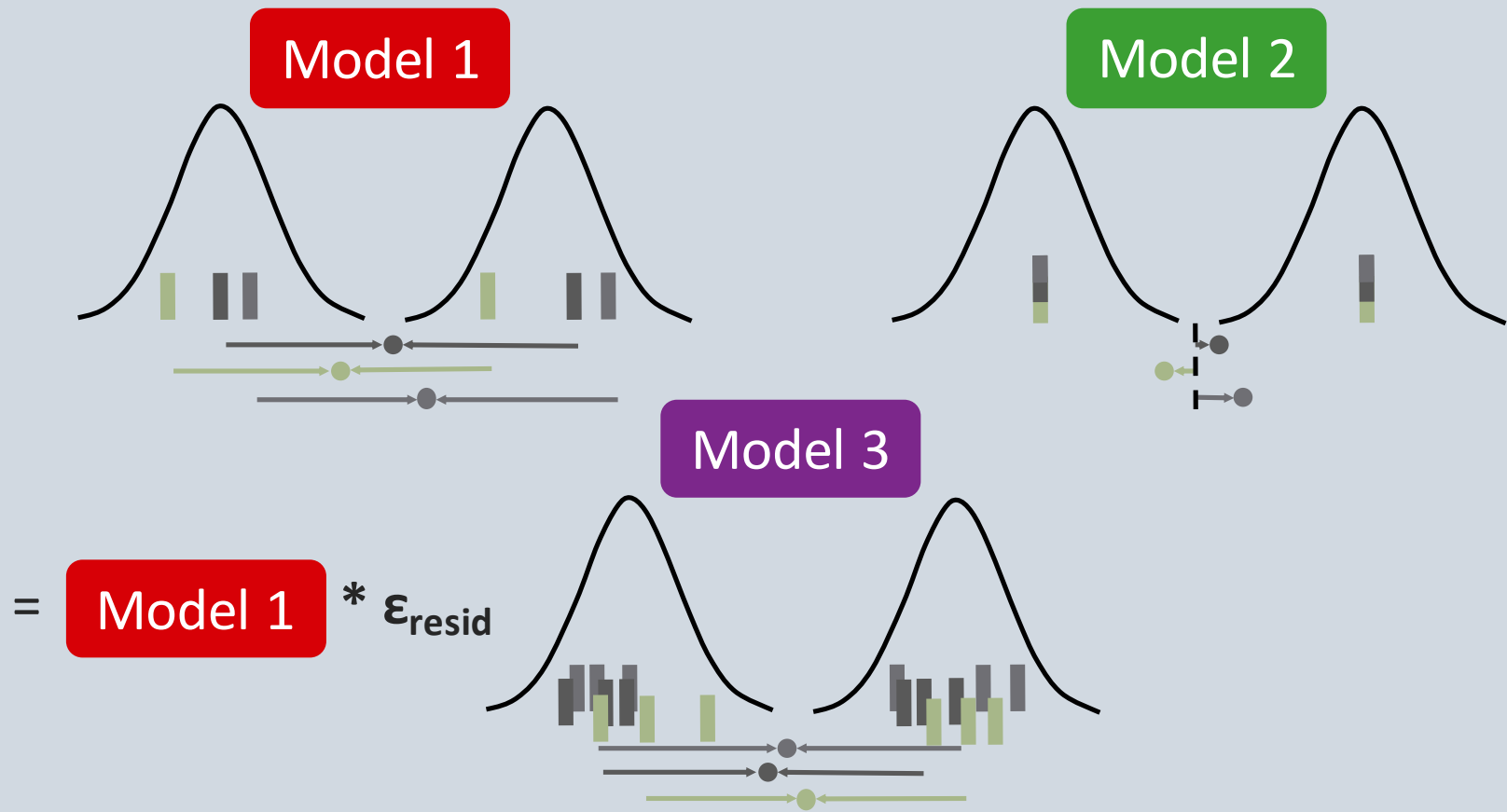
Previous models unrealistic



Previous models unrealistic



Previous models unrealistic

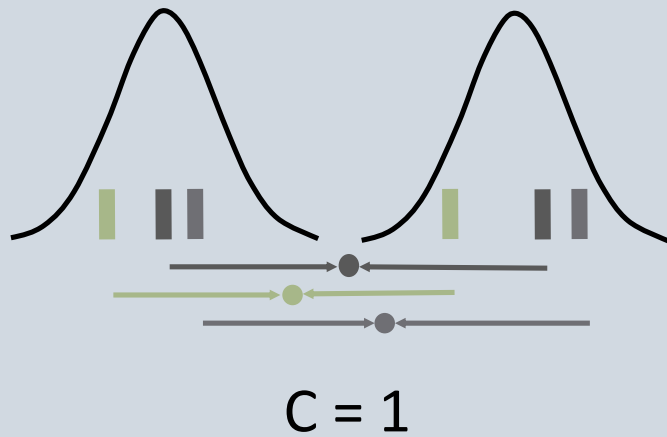


Ecologically meaningful

$$\frac{1}{\epsilon_{\text{resid}}} \propto \text{consumption}$$

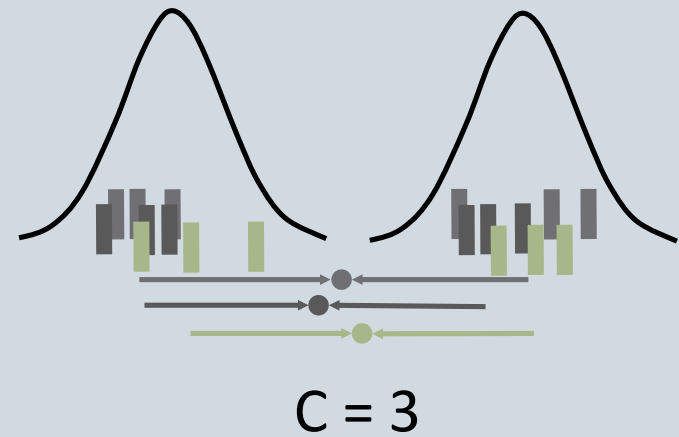
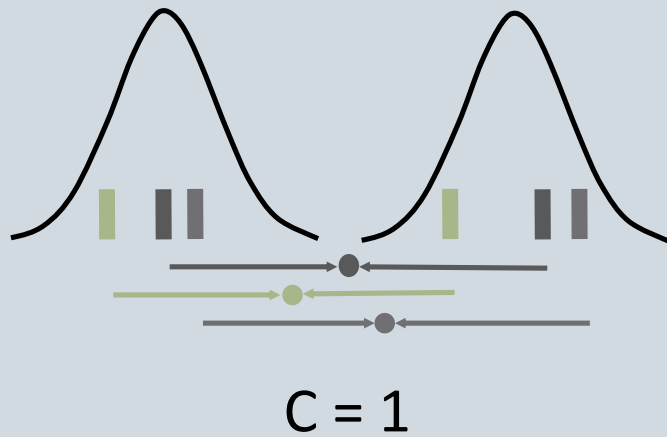
Ecologically meaningful

$$\frac{1}{\epsilon_{\text{resid}}} \propto \text{consumption}$$



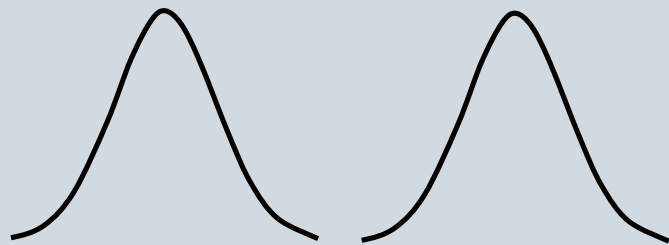
Ecologically meaningful

$$\frac{1}{\epsilon_{\text{resid}}} \propto \text{consumption}$$

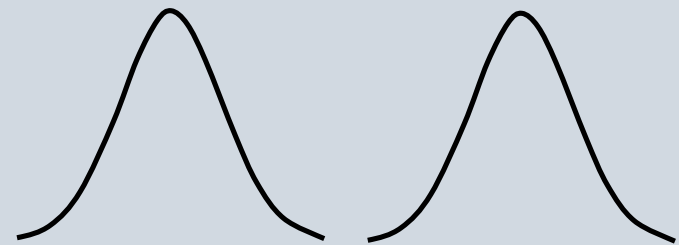


Ecologically meaningful

$$\frac{1}{\epsilon_{\text{resid}}} \propto \text{consumption}$$



C = 1



C = 3

Ecologically meaningful

$$\frac{1}{\epsilon_{\text{resid}}} \propto \text{consumption}$$



Oyster

Tissue

ϵ_{avg}

Muscle

0.23



Human

Bone

1.78

Confounding of $\varepsilon_{\text{resid}}$

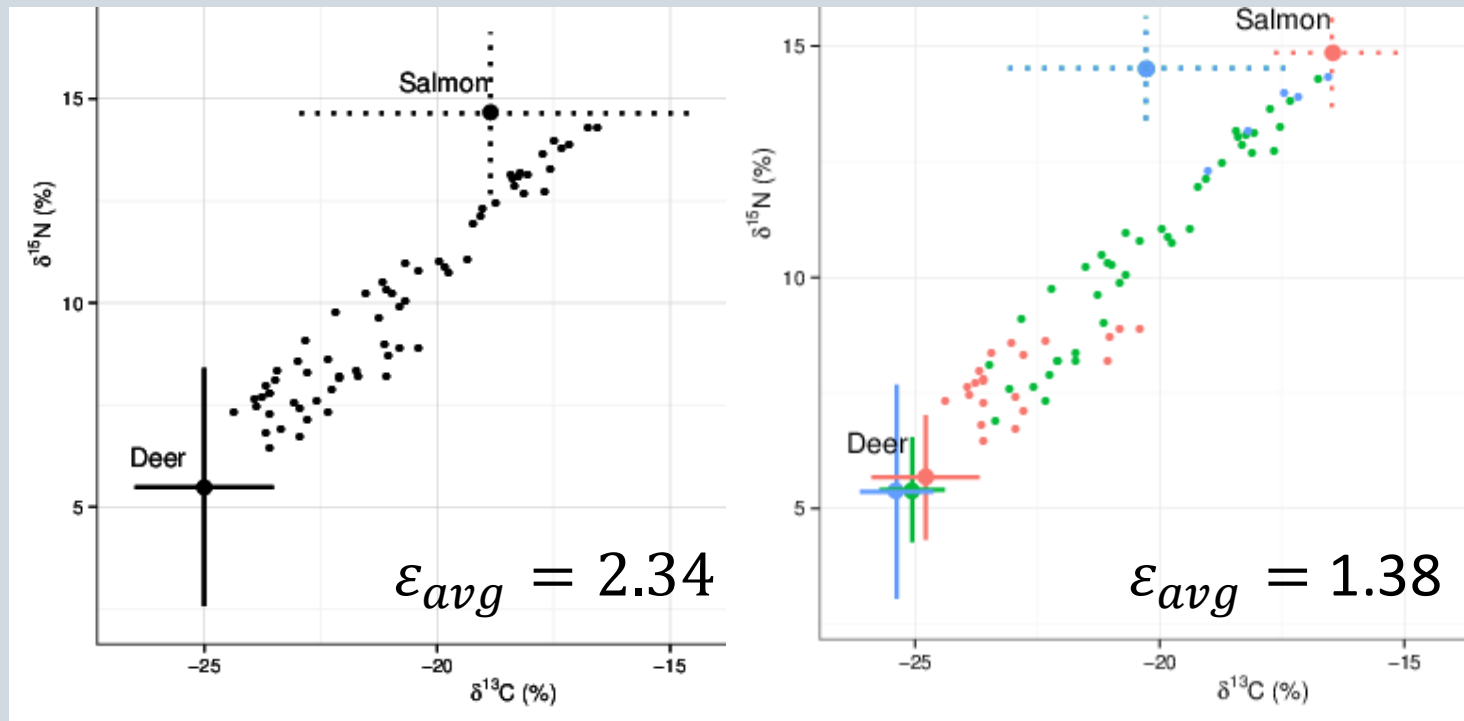
Depends on:

- Inclusion of covariates that explain variability
- TDF variance (rarely known)

Confounding of ϵ_{resid}

Depends on:

- Inclusion of covariates that explain consumer variability
- TDF variance (rarely known)

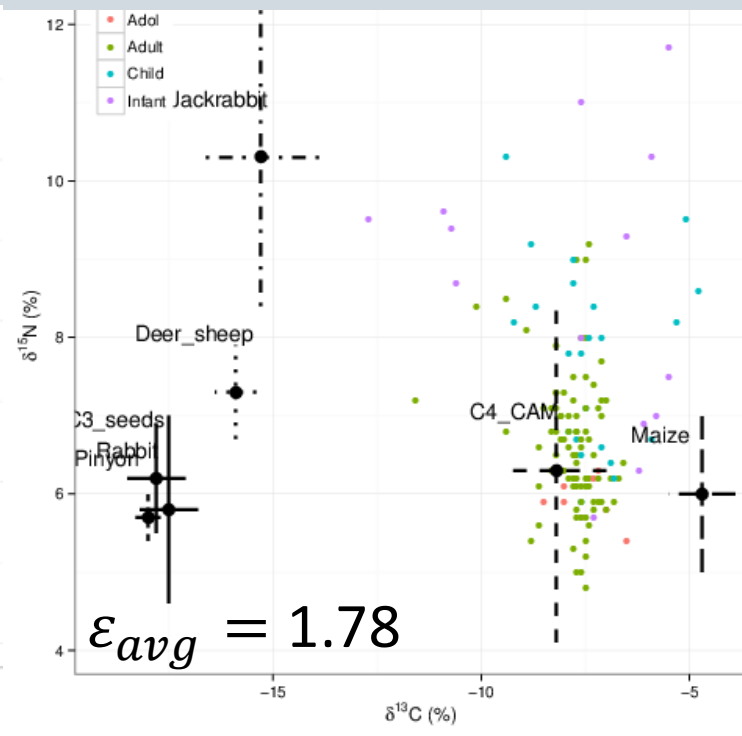
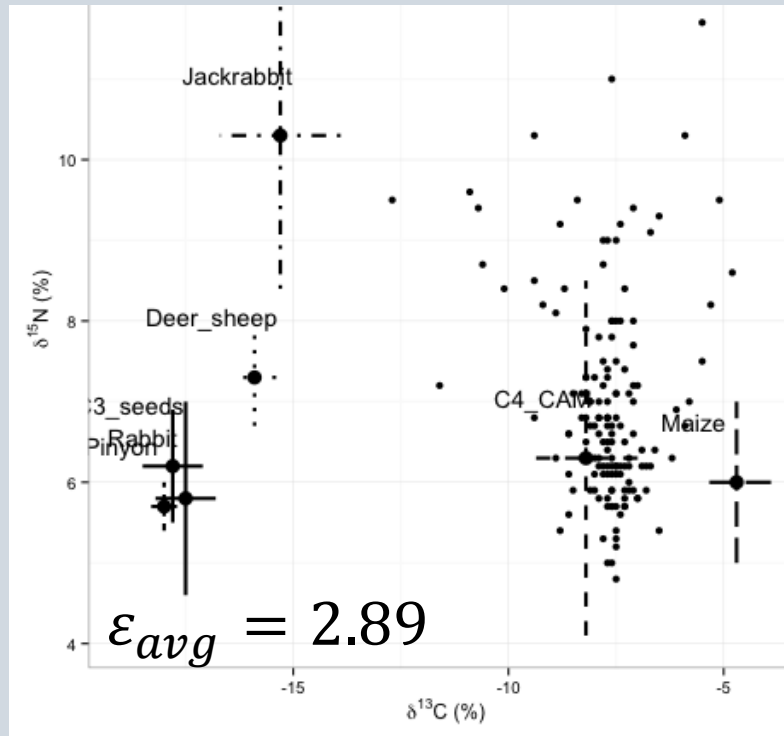


3. Better error structures

Confounding of ϵ_{resid}

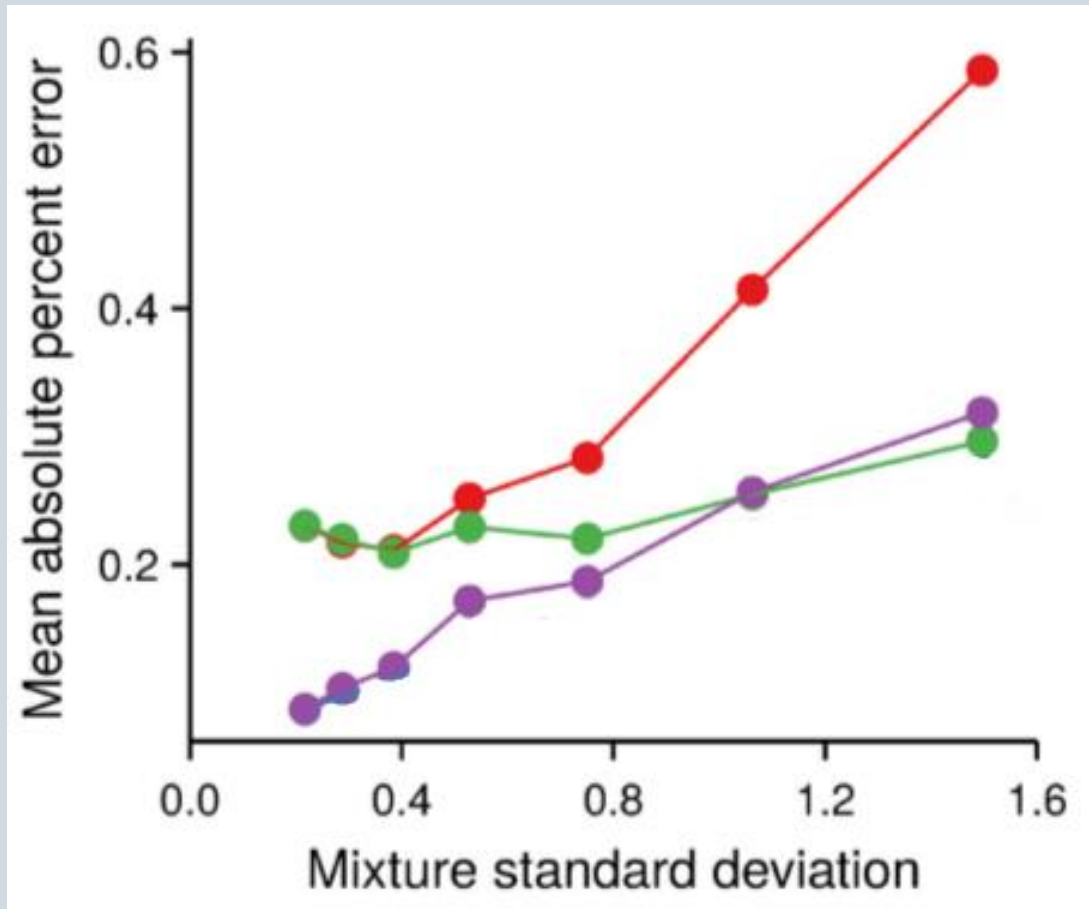
Depends on:

- Inclusion of covariates that explain consumer variability
- TDF variance (rarely known)



3. Better error structures

More accurate



MixSIR

SIAR

MixSIAR



4. Effect of priors/
“Bayesian mixing models are biased”

0. What is a *prior*?

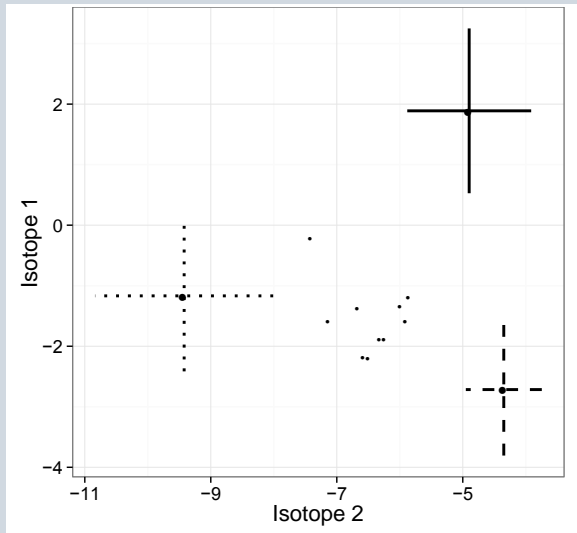
$$\text{Pr}(\theta|\text{data}) \propto \text{Pr}(\theta) * \text{Pr}(\text{data}|\theta)$$

Posterior **Prior** Likelihood

“From a Bayesian perspective, the principle of unbiasedness is reasonable in the limit of large samples, but otherwise it is potentially misleading.”

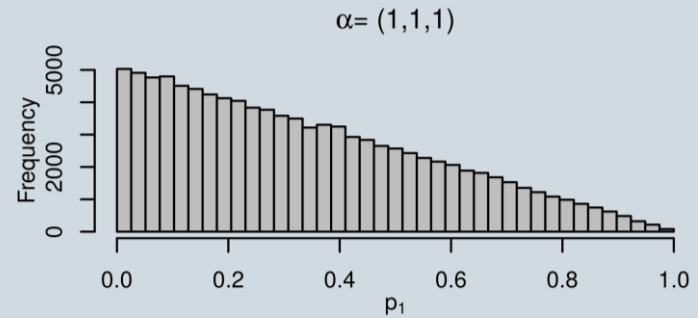
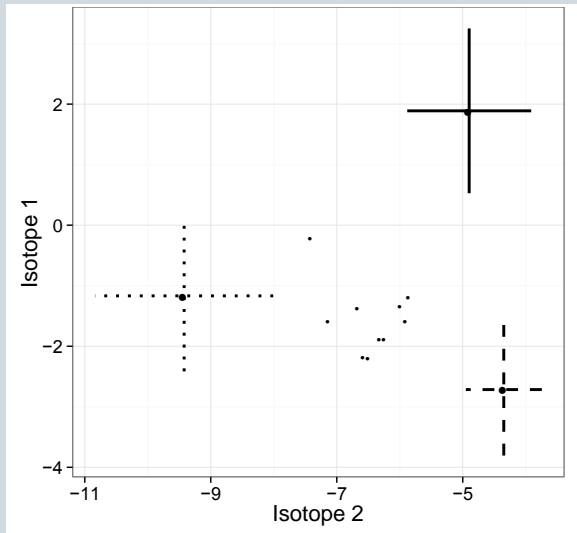
Gelman et al. (1995)

1. There is no “uninformative” prior



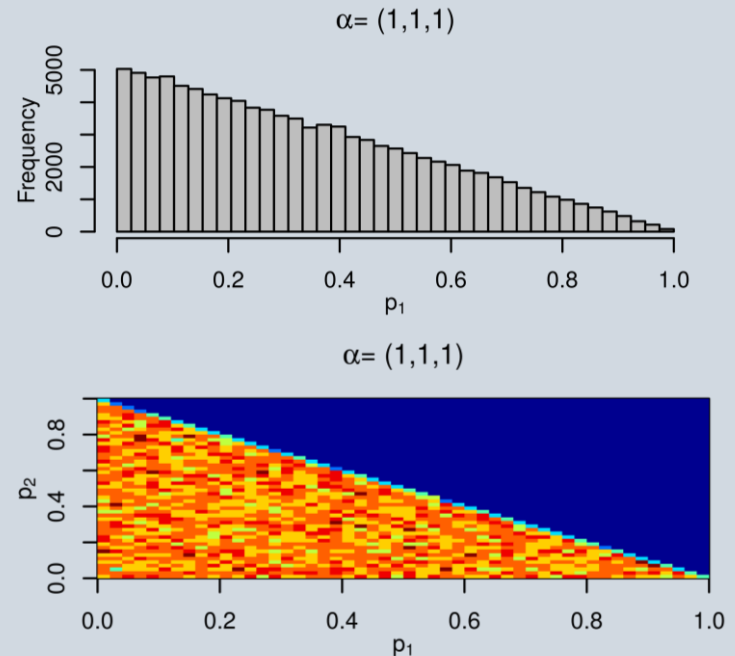
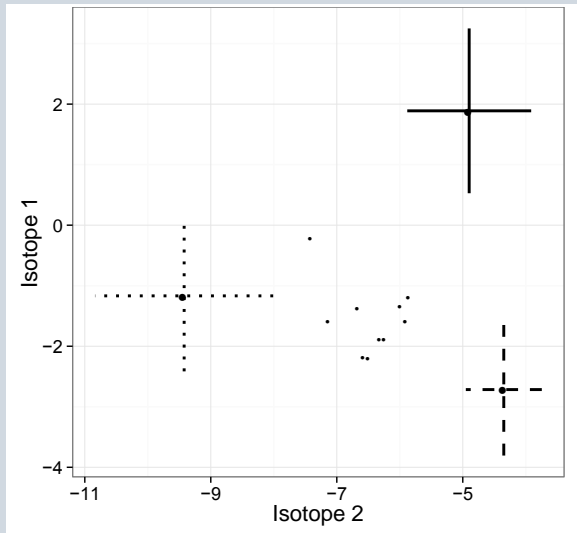
1. There is no “uninformative” prior

Problem: proportions are not independent!

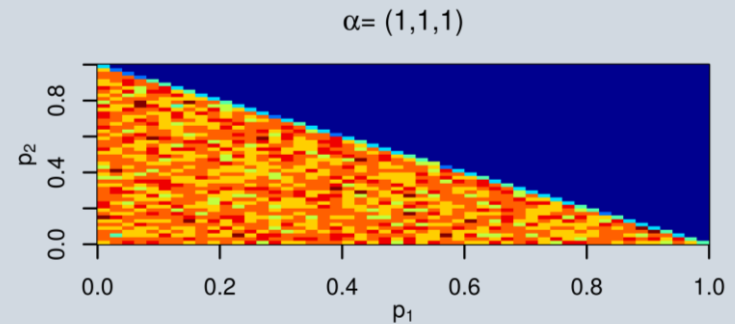
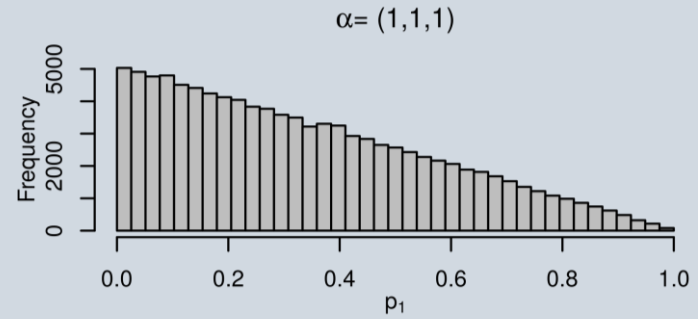
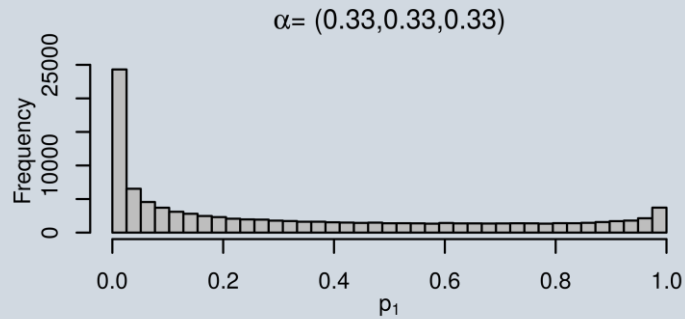


1. There is no “uninformative” prior

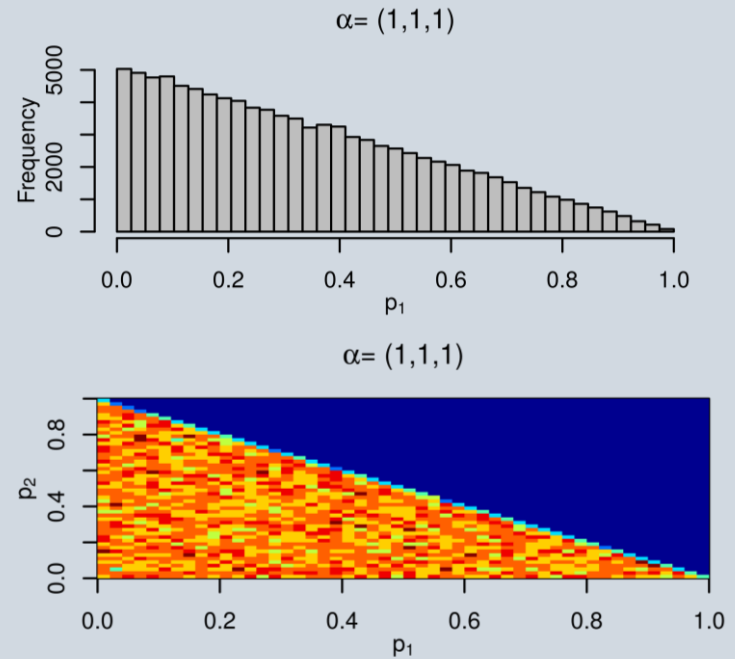
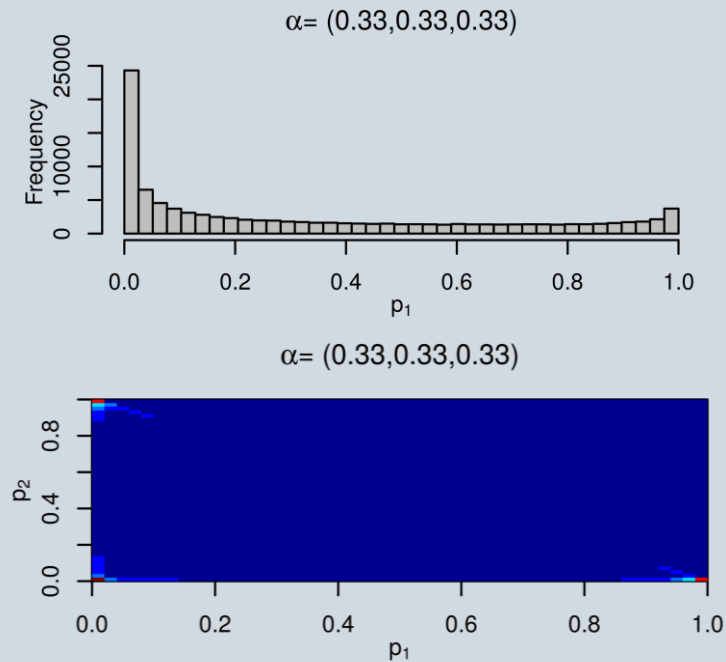
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1. There is no “uninformative” prior

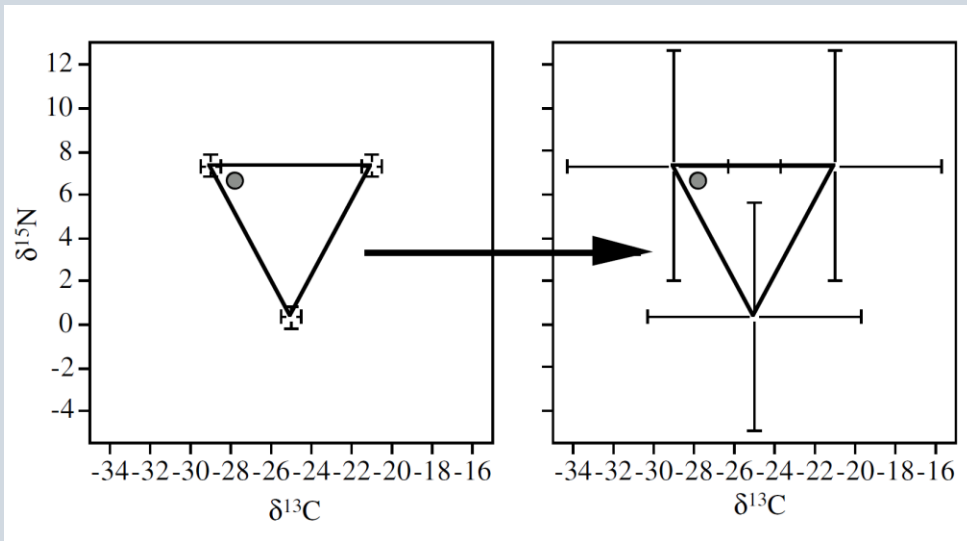


1. There is no “uninformative” prior



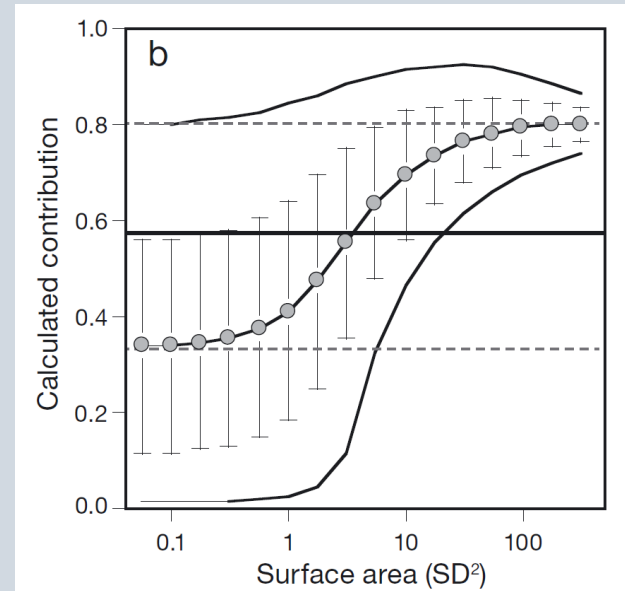
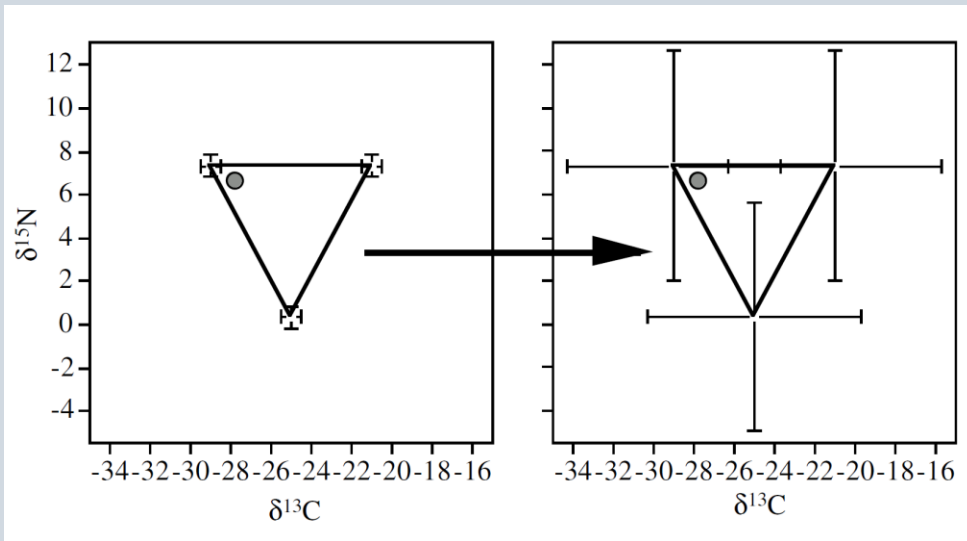
2. Effect of the “uninformative” prior

1. How good is your data?



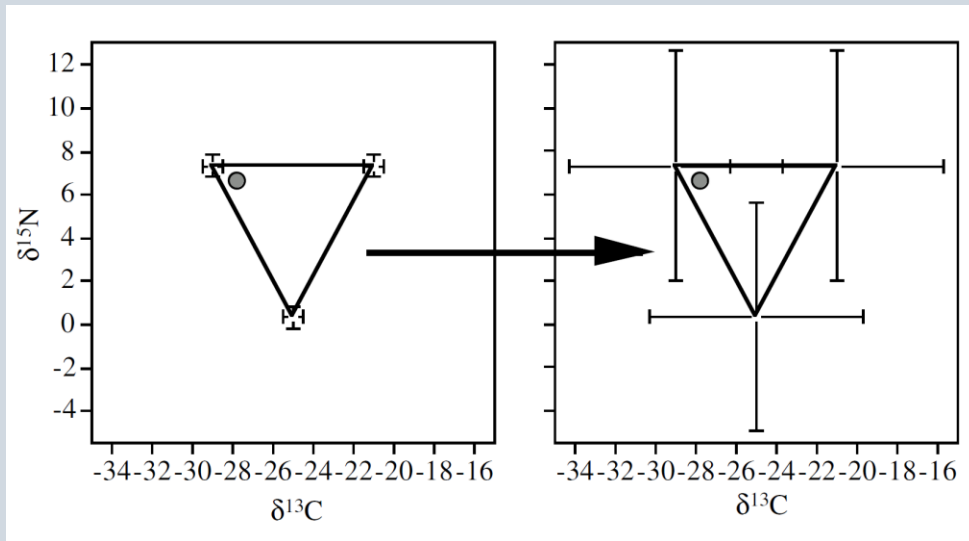
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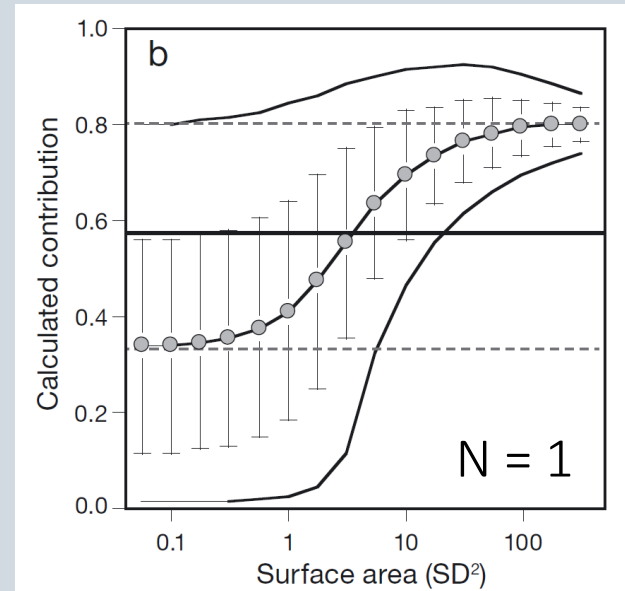


2. Effect of the “uninformative” prior

1. How good is your data?

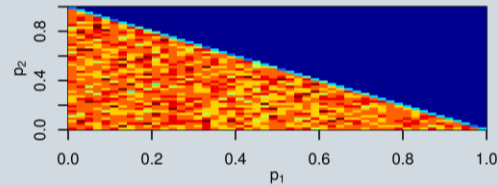
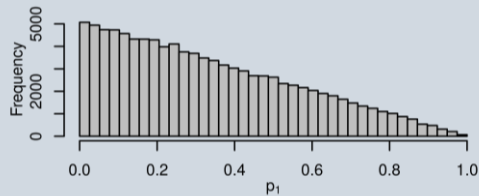


2. How much data do you have?



3. Constructing informative priors

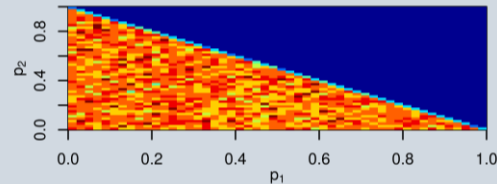
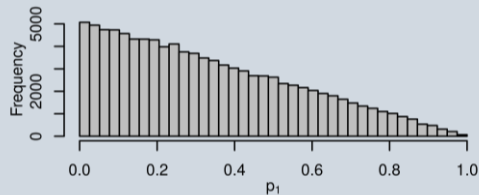
You control the mean proportions AND the variance (“informativeness”)



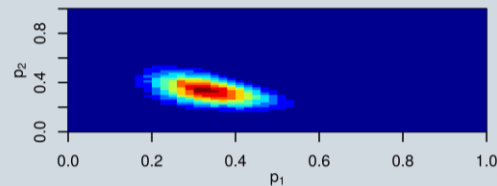
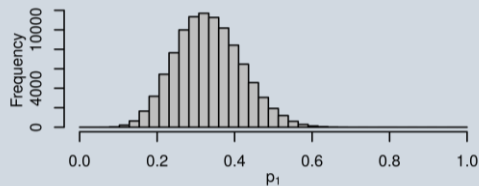
$$\alpha = (1, 1, 1)$$

3. Constructing informative priors

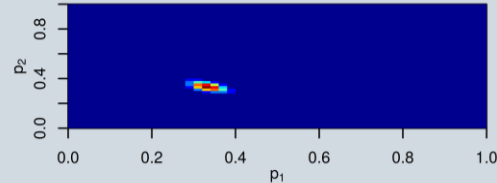
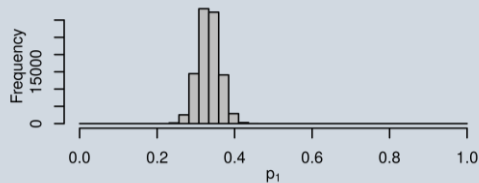
You control the mean proportions AND the variance (“informativeness”)



$$\alpha = (1, 1, 1)$$



$$\alpha = (10, 10, 10)$$



$$\alpha = (100, 100, 100)$$

3. Constructing informative priors

You control the mean proportions AND the variance (“informativeness”)

30



8



25



3. Constructing informative priors

You control the mean proportions AND the variance (“informativeness”)

30



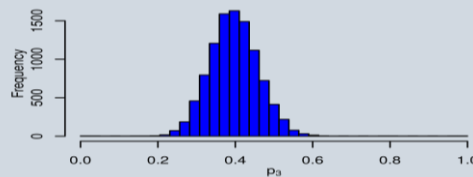
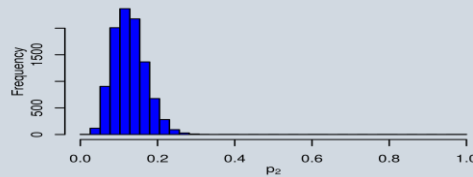
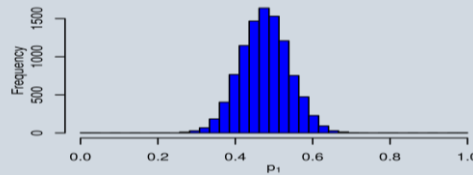
8



25



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



3. Constructing informative priors

You control the mean proportions AND the variance (“informativeness”)

30



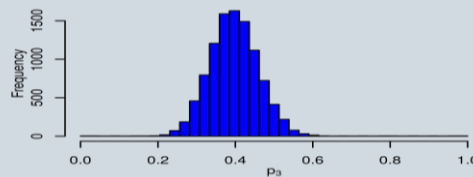
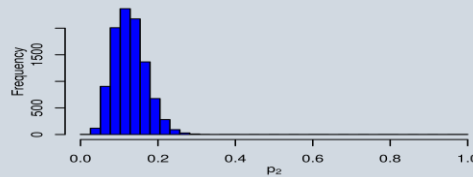
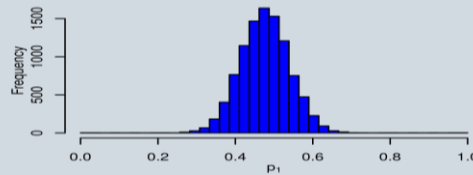
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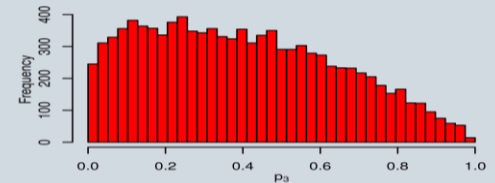
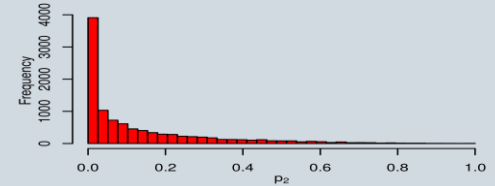
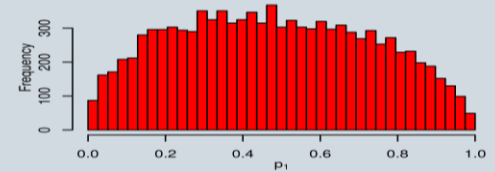
25



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



$$\alpha = \frac{3 * (30, 8, 25)}{63}$$



4. Effect of priors/ “Bayesian mixing models are biased”

REDUCE THE INFLUENCE OF THE GENERALIST PRIOR:

1. COLLECT MORE DATA (SOURCE AND CONSUMER)
2. SPECIFY A NON-GENERALIST PRIOR

Great! Where do I get MixSIAR?

CRAN (few months ago)

1. Download and install/update **R**
2. Download and install **JAGS**
3. Open R and run:

```
install.packages("MixSIAR")  
library(MixSIAR)
```

GitHub (latest)

1. Download and install/update **R**
2. Download and install **JAGS**
3. Open R and run:

```
library(devtools)  
install_github("brianstock/MixSIAR")
```

Great! Where do I get MixSIAR?

The screenshot shows the GitHub repository page for **brianstock / MixSIAR**. The repository is described as "A graphical user interface (GUI) for MixSIAR, creating Bayesian mixing models in R". It has 136 commits, 7 branches, and 16 releases. The current branch is **master**. A recent commit by **brianstock** is shown, with two files changed: **Manual** (updated citations in CITATION, manual, and README) and **R** (fixes issue #101 bug with 2FE or 1FE + 1RE).

brianstock / MixSIAR Unwatch 25

[Code](#) [Issues 20](#) [Pull requests 0](#) [Projects 0](#) [Wiki](#) [Pulse](#) [Graphs](#) [Settings](#)

A graphical user interface (GUI) for MixSIAR, creating Bayesian mixing models in R

[Add topics](#)

136 commits **7** branches **16** releases

Branch: **master** [New pull request](#) [Create new file](#) [Upload files](#)

brianstock added latest changes to NEWS.md

Manual	updated citations in CITATION, manual, and README
R	fixes issue #101 bug with 2FE or 1FE + 1RE

Great! Where do I get MixSIAR?

The screenshot shows a GitHub issue thread. At the top, a user named 'brianstock' has added a 'bug' label 19 days ago. Below that, 'brianstock' added a commit that referenced this issue 18 days ago. The commit message is 'fixes issue #101 bug with 2FE or 1FE + 1RE' with a commit hash of '91cf880'. The issue title is 'Accessing posterior chains with attach.jags function #80' and it is marked as 'Closed'. A comment from 'brianstock' 18 days ago states 'Fixed now.' and provides a link to 'Data files and script: #100'. The comment explains that with 1 fixed + 1 random effect, the proper proportions to use are created by combining the global intercept, the factor1 offset, and the factor2 offset. A code snippet is provided:

```
1. ilr.both[, f1, f2, src] = ilr.global[, src] + ilr.fac1[, f1, src] + ilr.fac2[, f2, src]
```