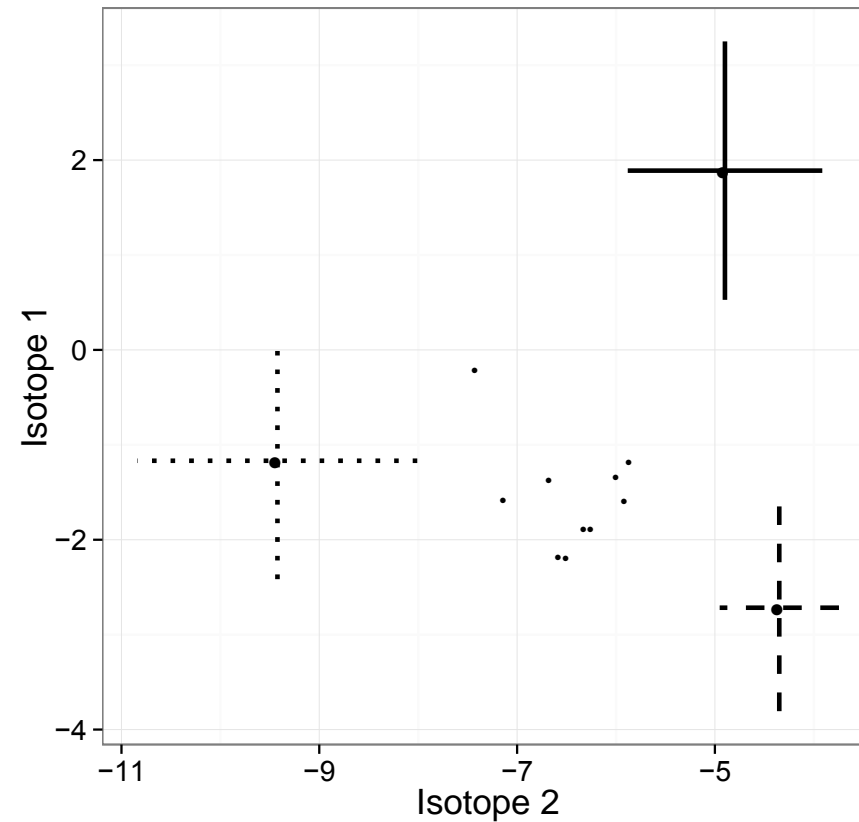


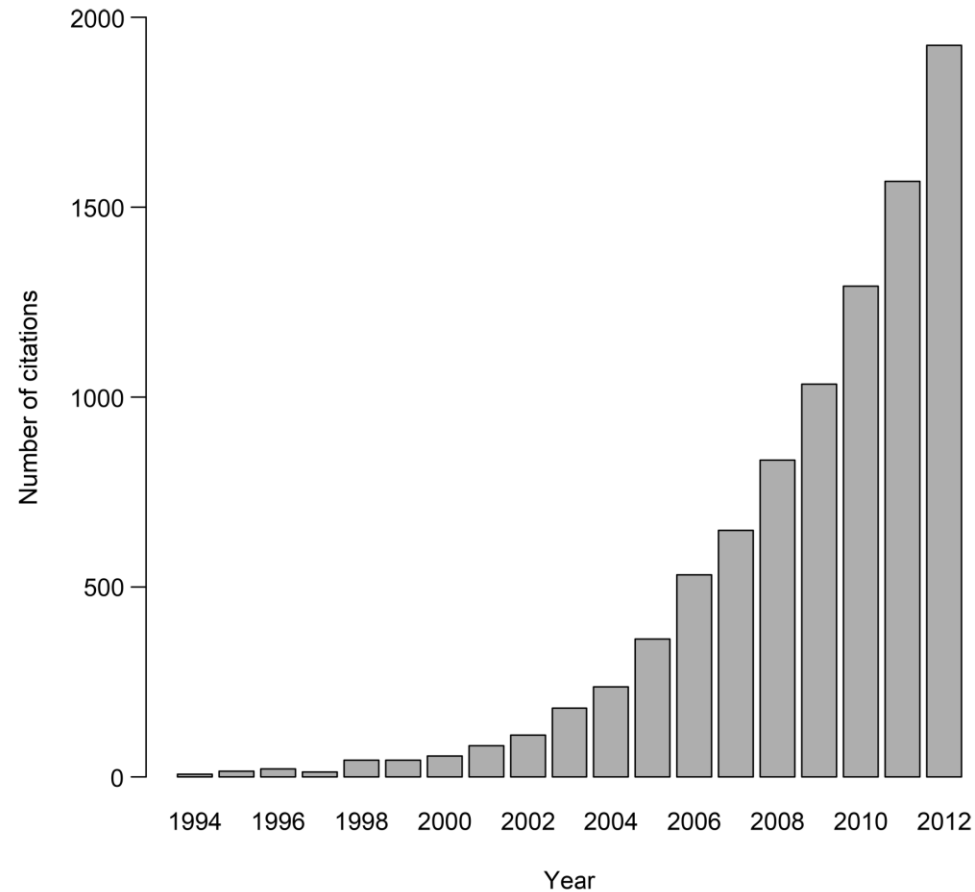
Use and Abuse of Mixing Models

BRIAN STOCK, BRICE SEMMENS, ERIC WARD, ANDREW PARNELL,
ANDREW JACKSON, DONALD PHILLIPS, STUART BEARHOP, RICHARD INGER

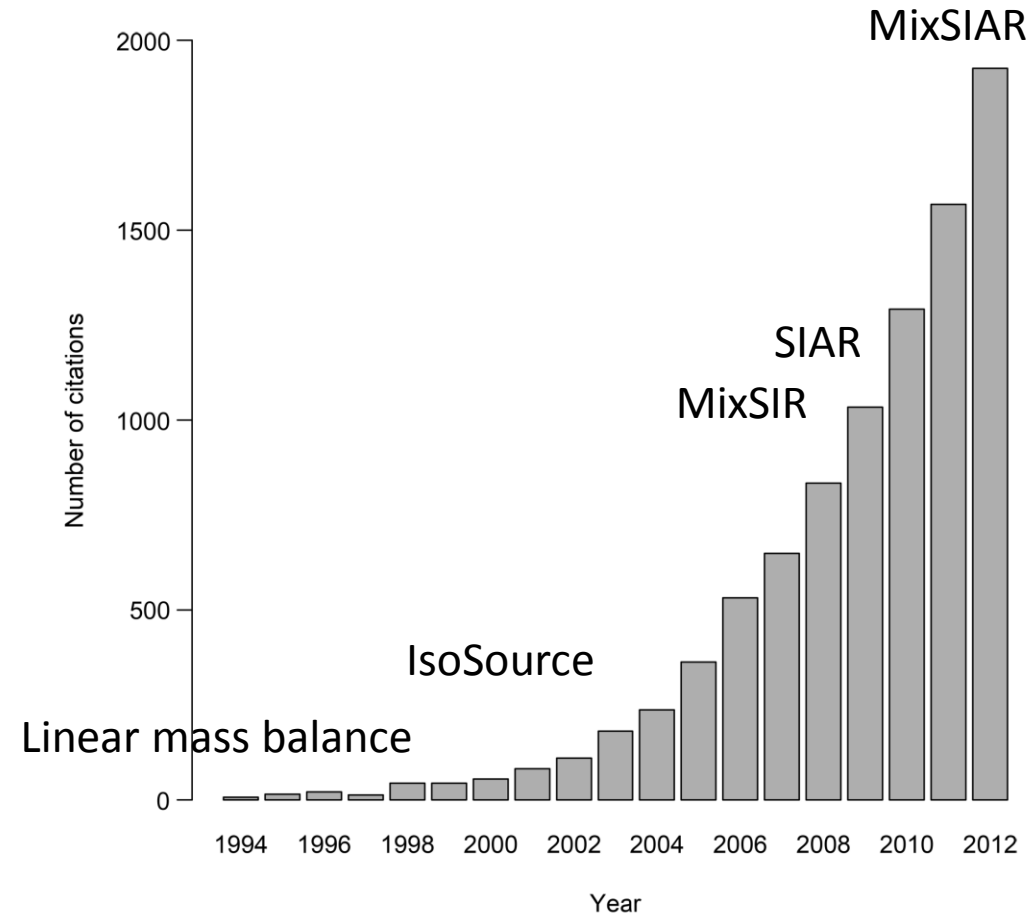
People use mixing models a lot



People use mixing models a lot



People use mixing models a lot



Pros of Bayesian mixing models

Firm statistical foundation

- True probability distributions
- Uncertainty in consumer, source, and TDF data

Biological complexity

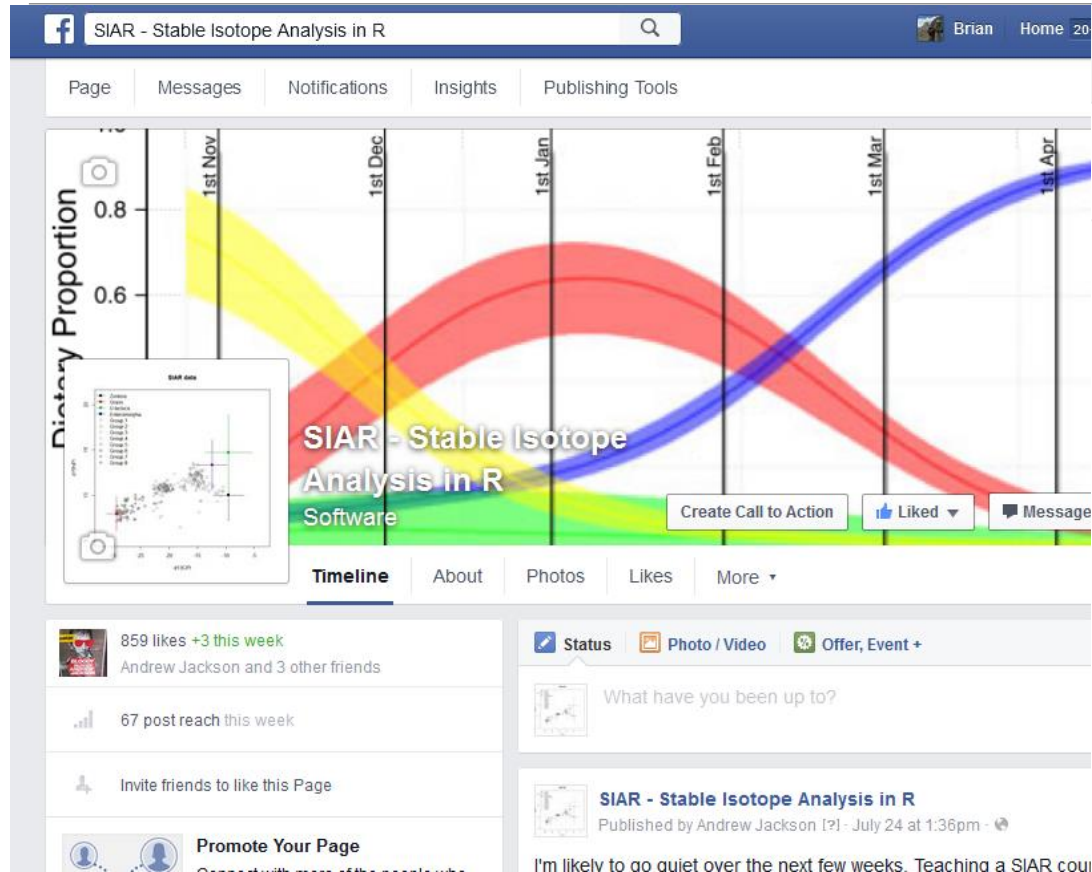
- Differences due to covariates (e.g. sex, region, size)
- Non-biotracer data as priors (e.g. stomach/fecal contents, prey abundance)

Cons of Bayesian mixing models

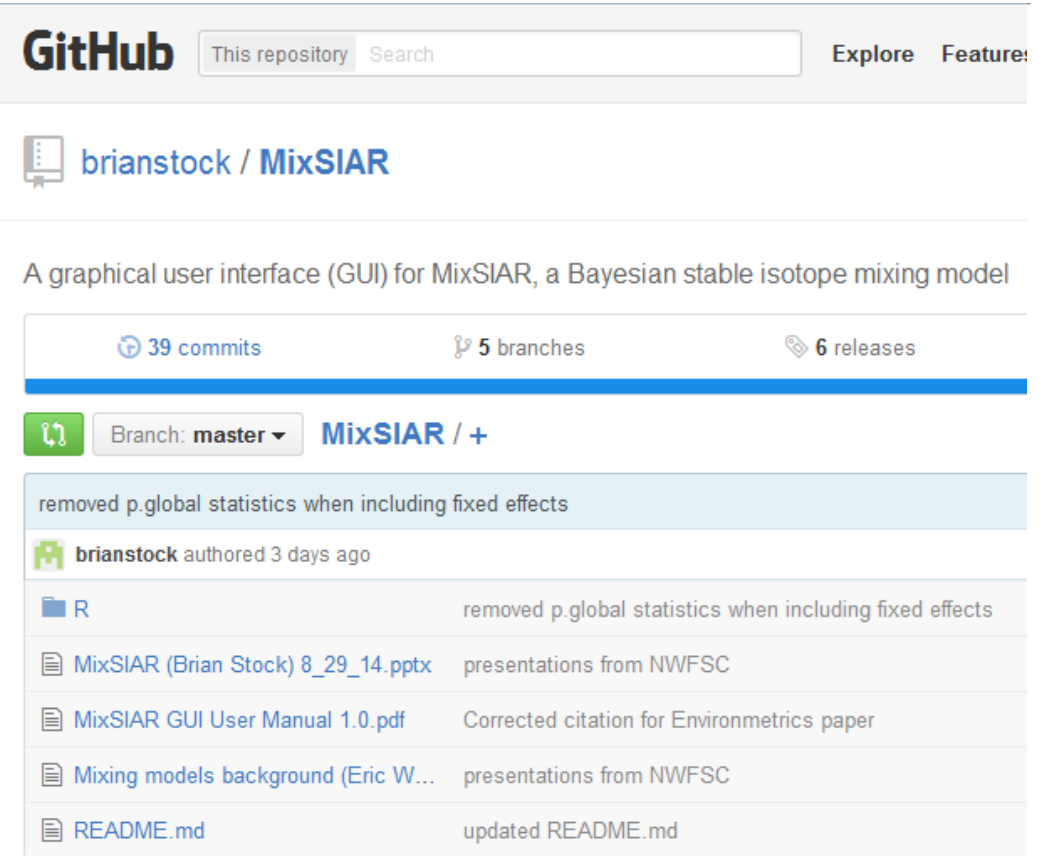
They're more complex and prone to abuse

Garbage in, garbage out (ex. many sources, 2 tracers)

Lots of questions



The image shows a Facebook page for "SIAR - Stable Isotope Analysis in R". The page features a large cover photo with a line graph showing "Dietary Proportion" on the y-axis (ranging from 0.6 to 0.8) and time on the x-axis (from 1st Nov to 1st Apr). The graph has three overlapping colored areas: yellow, red, and blue. A smaller inset graph is visible in the bottom left of the cover photo. The page has 859 likes and 67 post reach this week. A status update from Andrew Jackson is visible at the bottom, mentioning teaching a SIAR course.



The image shows the GitHub repository page for "brianstock / MixSIAR". The repository has 39 commits, 5 branches, and 6 releases. The current branch is "master". The commit history shows a recent commit by brianstock 3 days ago, titled "removed p.global statistics when including fixed effects". The commit message lists several files that were changed:

- R
- MixSIAR (Brian Stock) 8_29_14.pptx
- MixSIAR GUI User Manual 1.0.pdf
- Mixing models background (Eric W...)
- README.md

Pitfalls and misconceptions

1. Source geometry
2. MCMC convergence
3. Effect of priors
4. Error structures
5. Source lumping/splitting
6. How to include covariates
7. Application to biotracers other than stable isotopes

Pitfalls and misconceptions

1. Source geometry
2. MCMC convergence
3. **Effect of priors**
4. Error structures
5. Source lumping/splitting
6. How to include covariates
7. **Application to biotracers other than stable isotopes**

Effect of priors/ “Bayesian mixing models are biased”

REDUCE THE INFLUENCE OF THE GENERALIST PRIOR

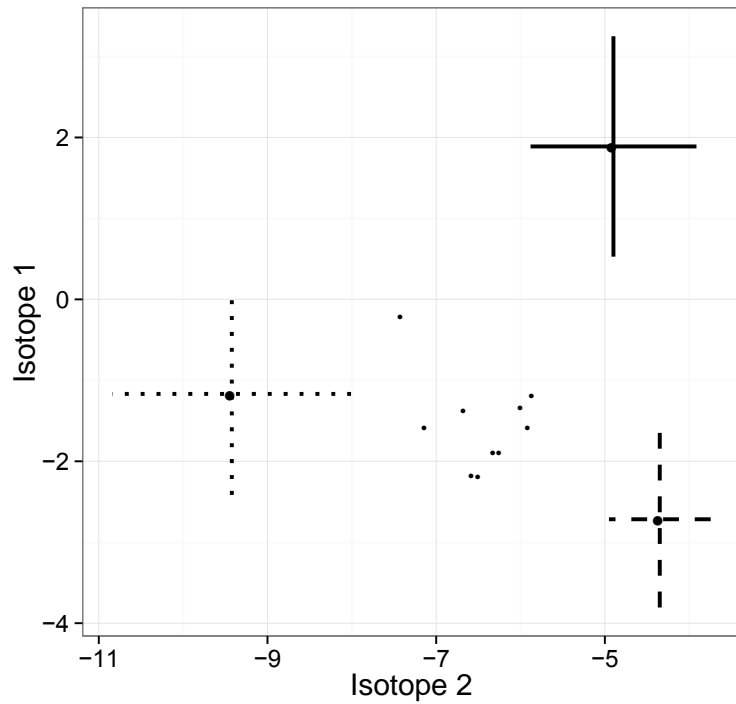
0. What is a prior?

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

Posterior Prior Likelihood

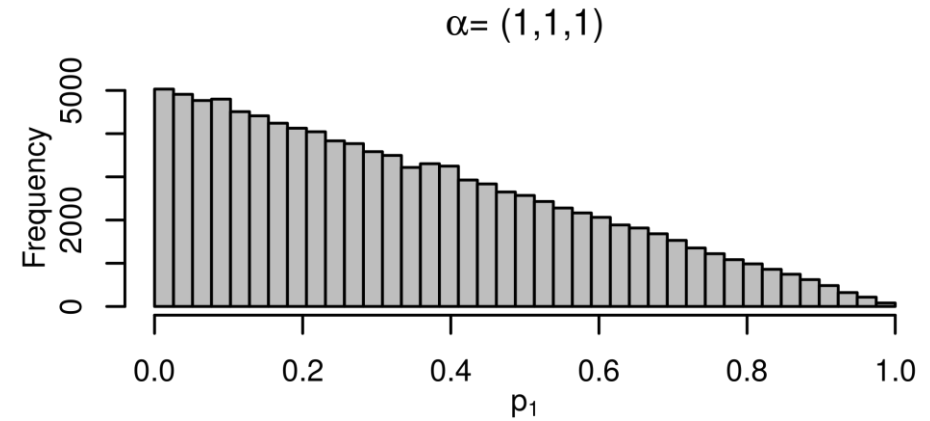
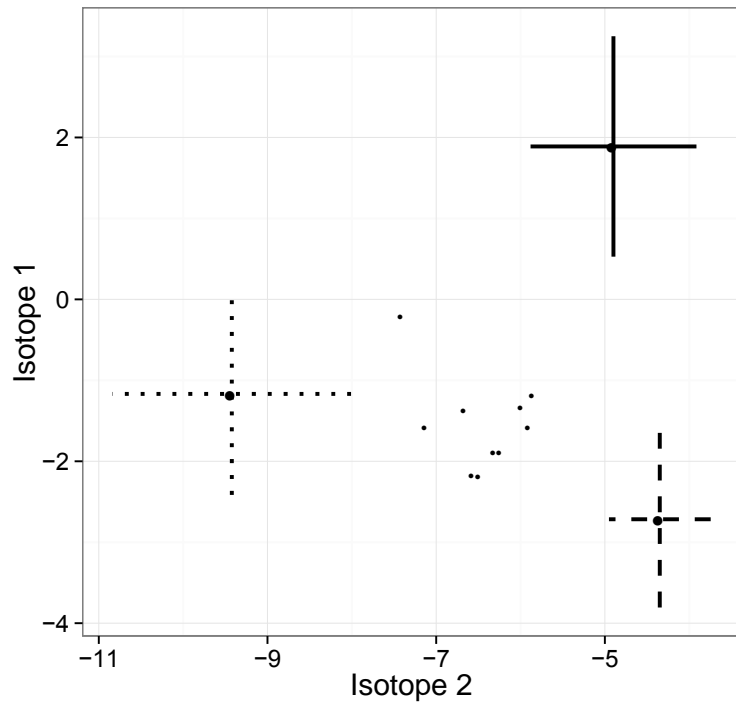
“From a Bayesian perspective, the principle of unbiasedness is reasonable in the limit of large samples, but otherwise it is potentially misleading.”

1. There is no “uninformative” prior



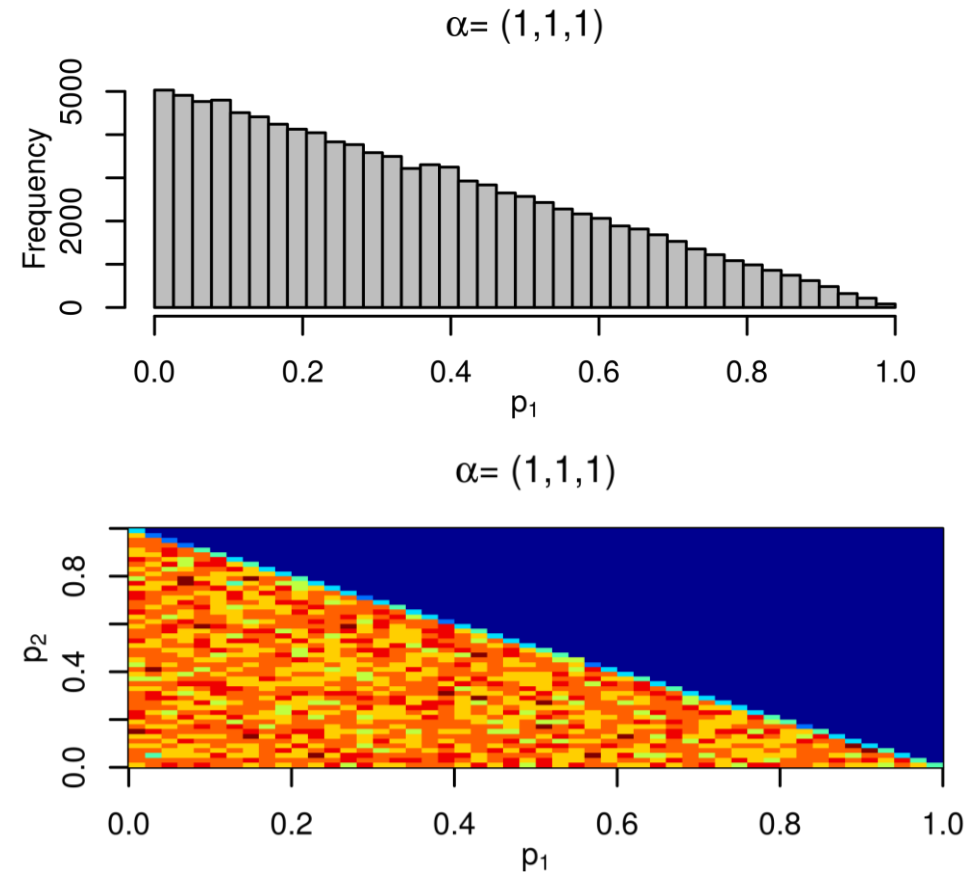
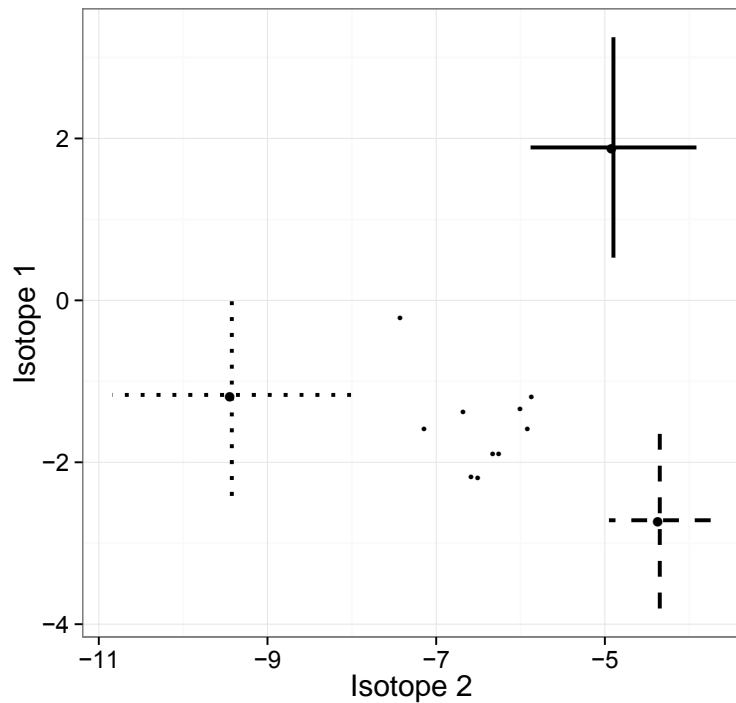
1. There is no “uninformative” prior

Problem: proportions are not independent!

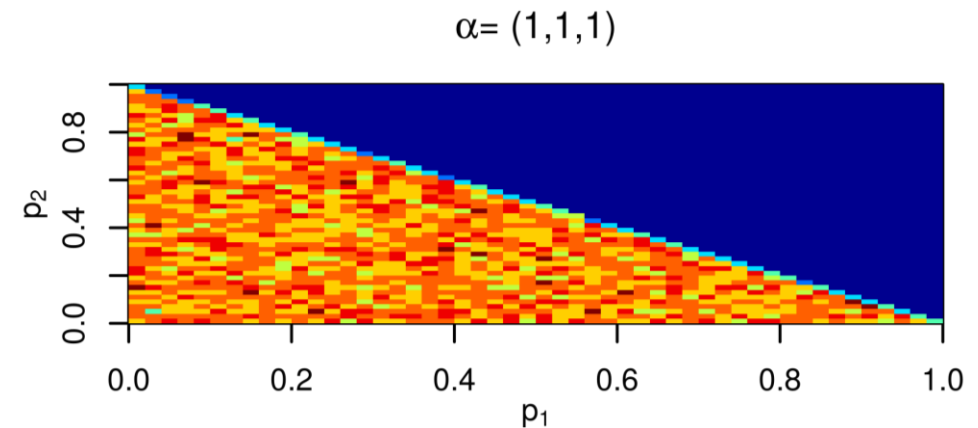
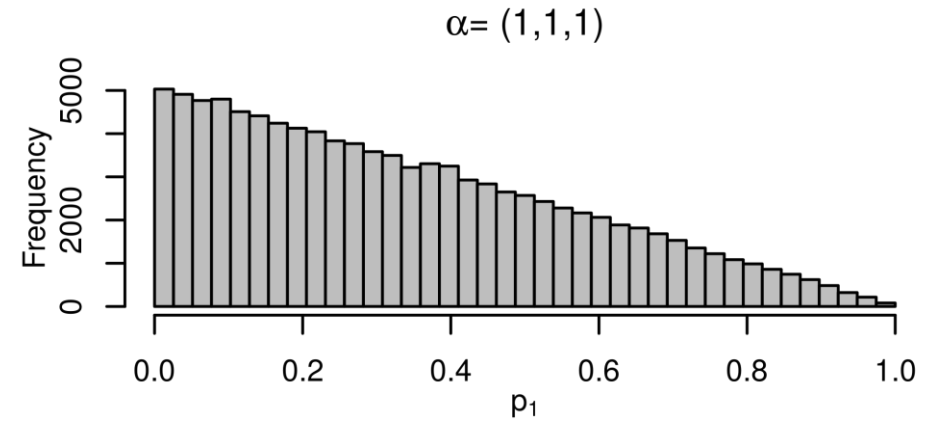
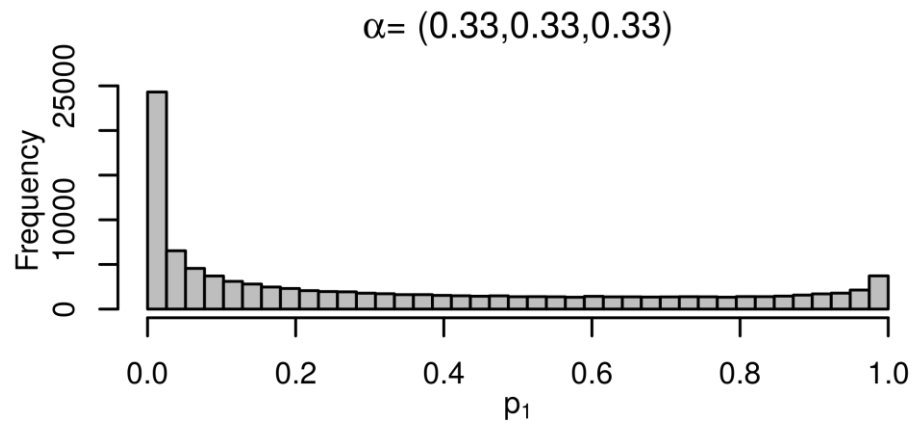


1. There is no “uninformative” prior

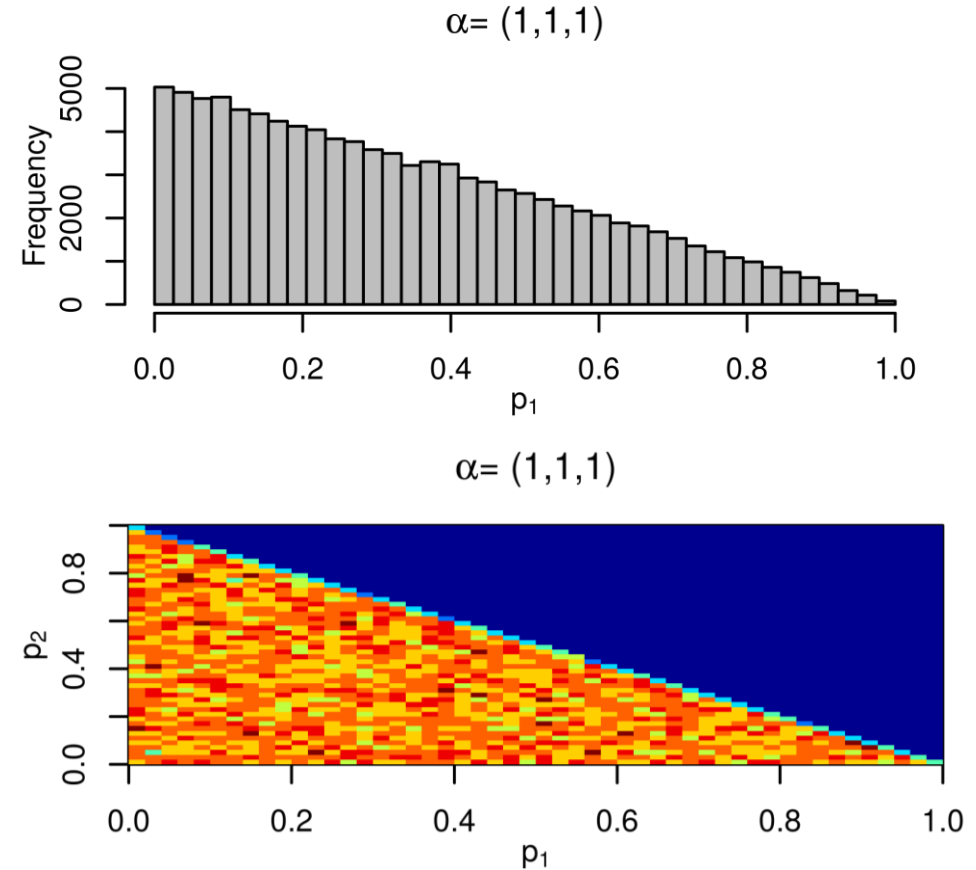
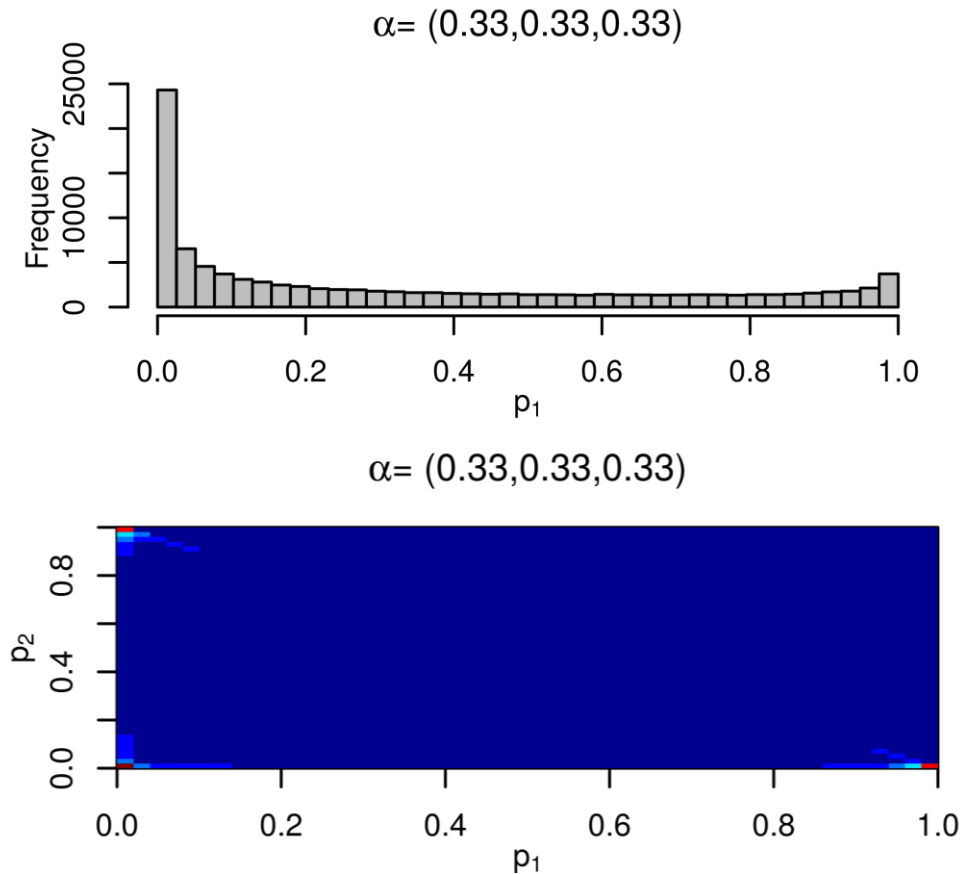
Problem: proportions are not independent!



1. There is no “uninformative” prior

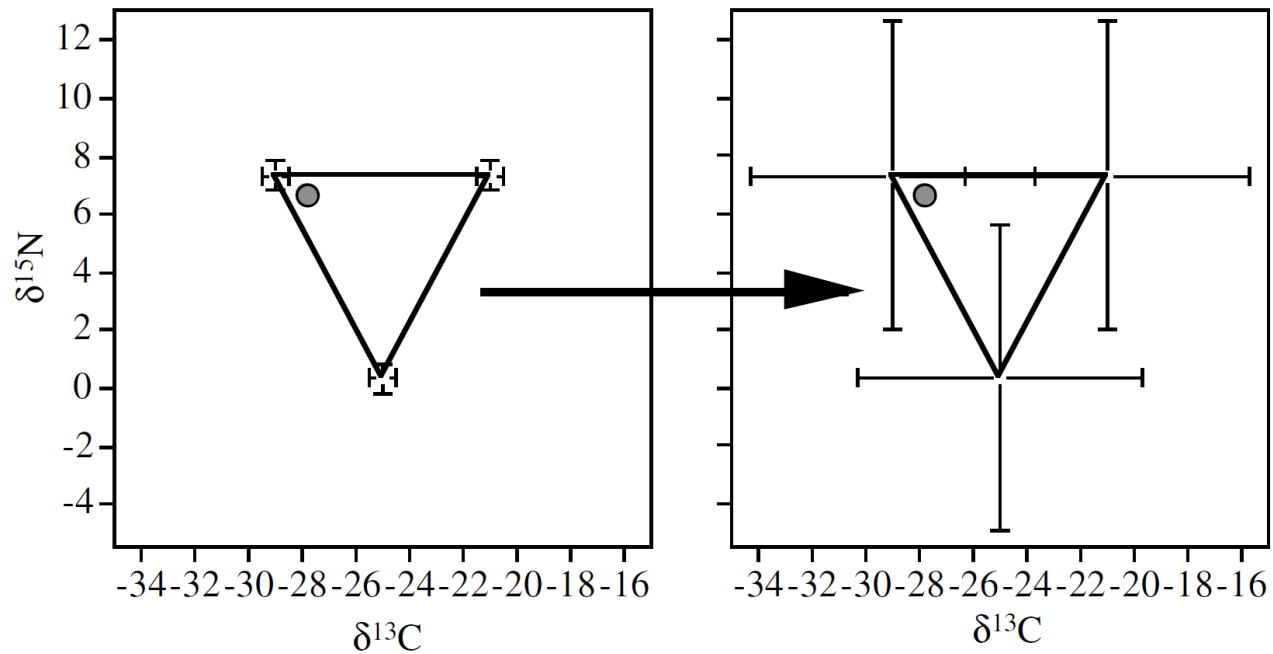


1. There is no “uninformative” prior



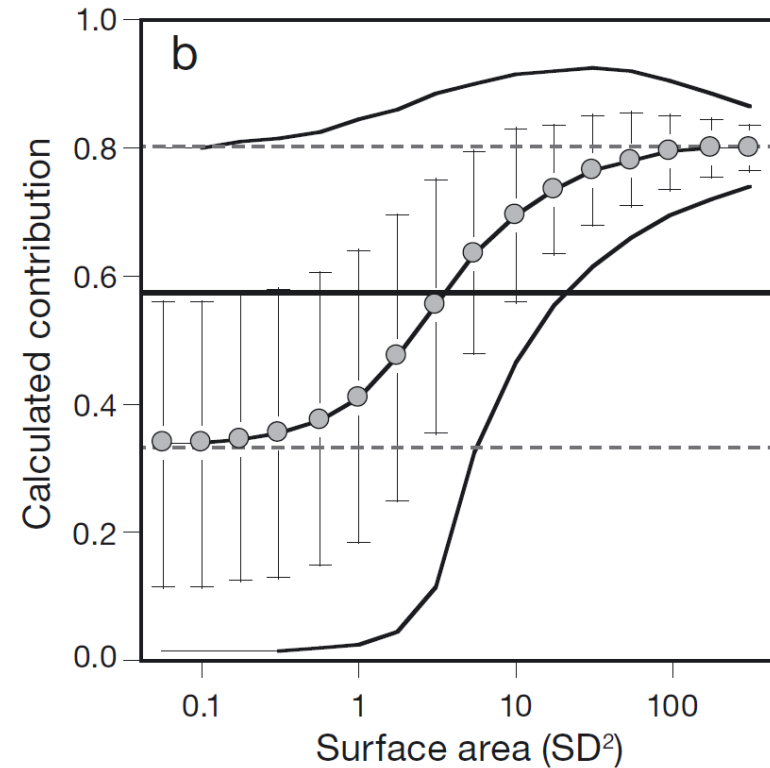
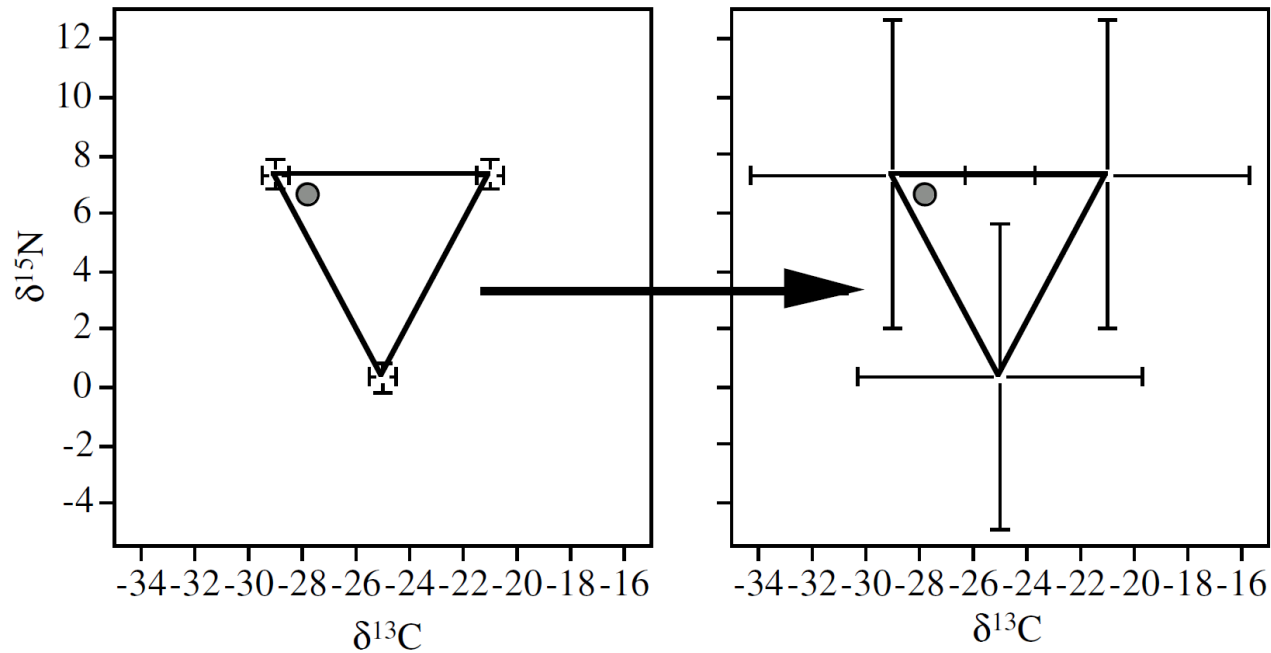
2. Effect of the “uninformative” prior

1. How good is your data?



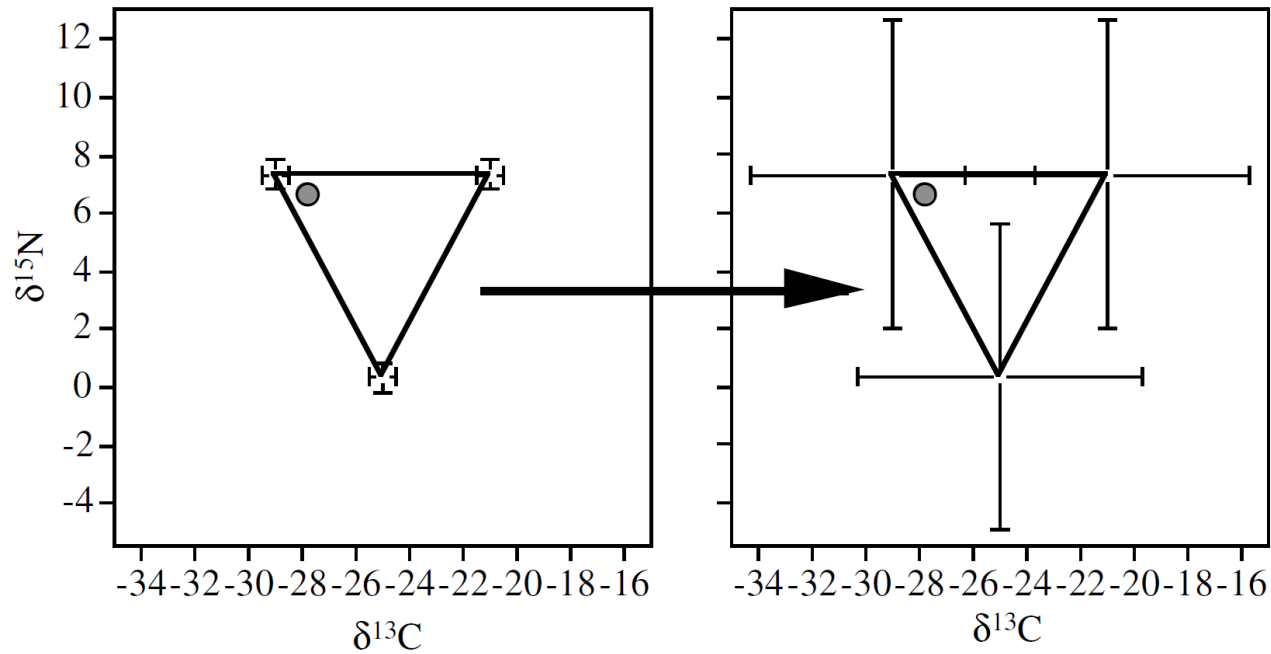
2. Effect of the “uninformative” prior

1. How good is your data?

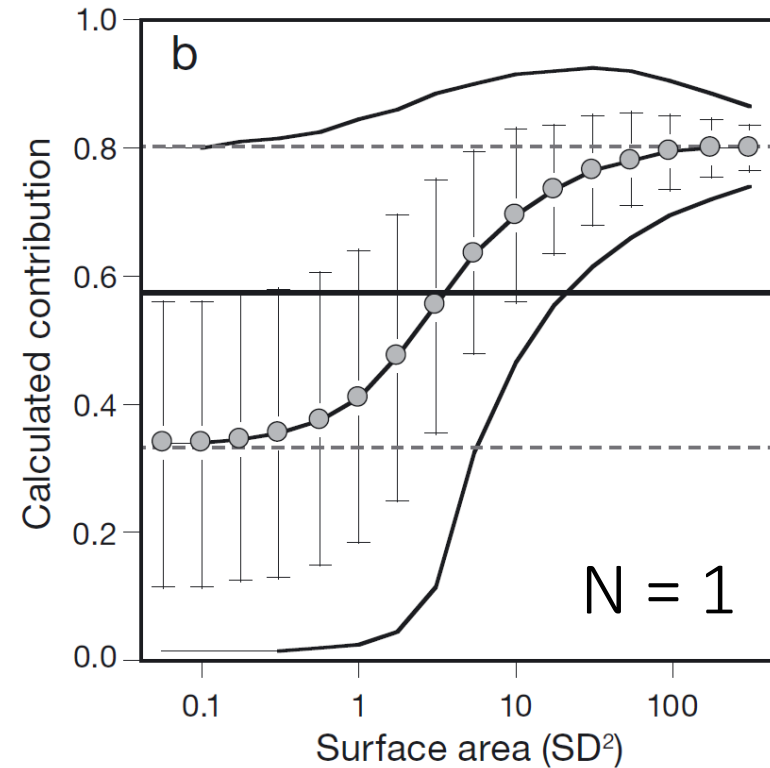


2. Effect of the “uninformative” prior

1. How good is your data?

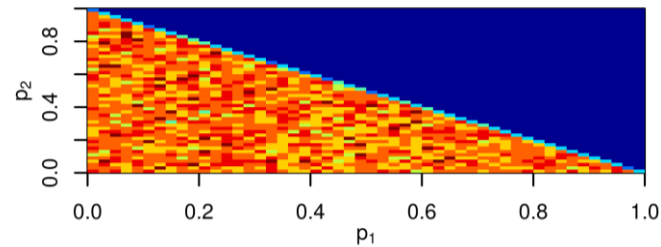
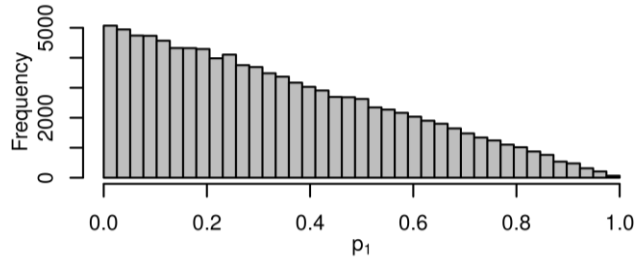


2. How much data do you have?



3. Constructing informative priors

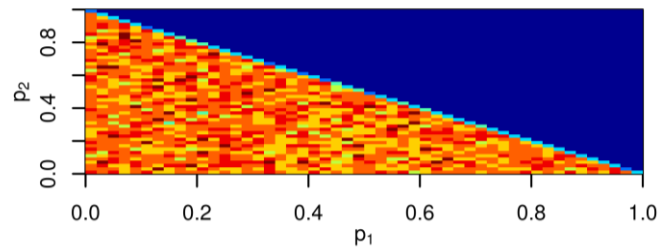
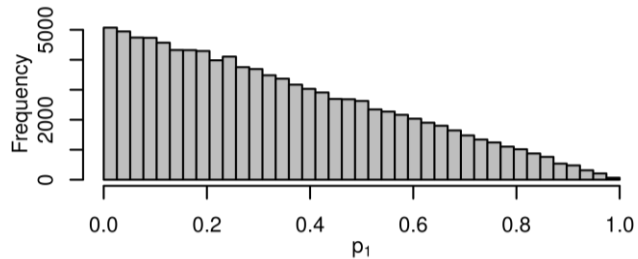
You control the mean proportions AND the variance (“informativeness”)



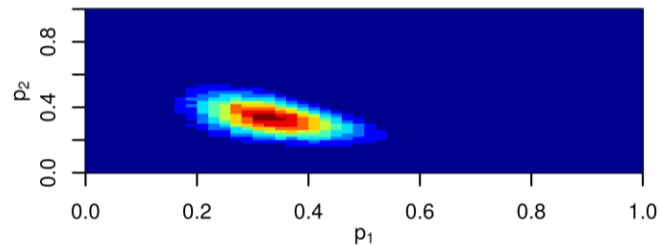
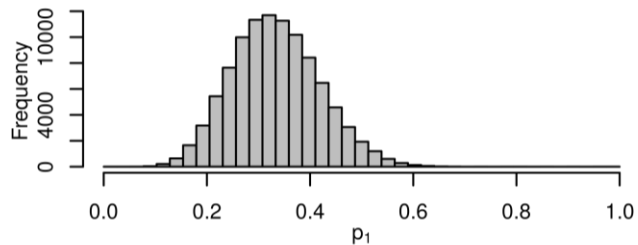
$$\alpha = (1, 1, 1)$$

3. Constructing informative priors

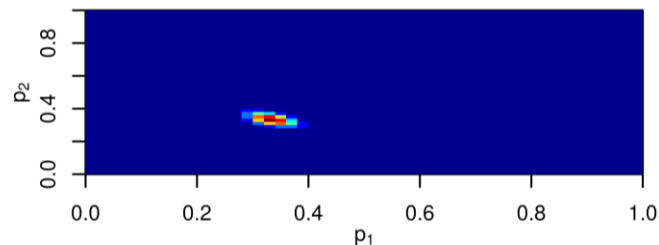
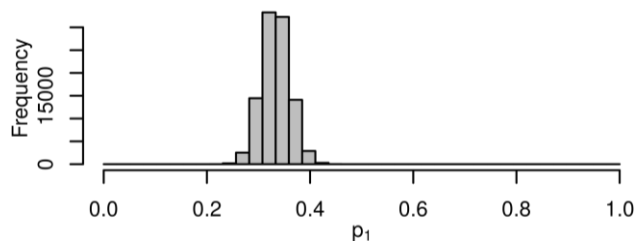
You control the mean proportions AND the variance (“informativeness”)



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



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



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

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



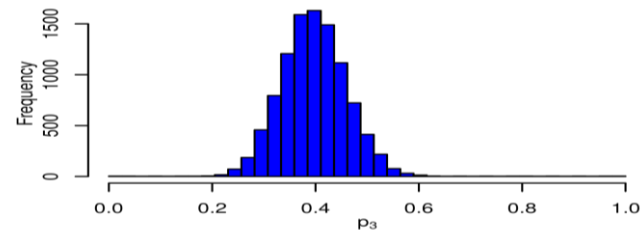
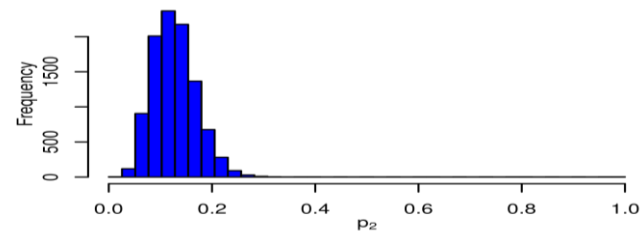
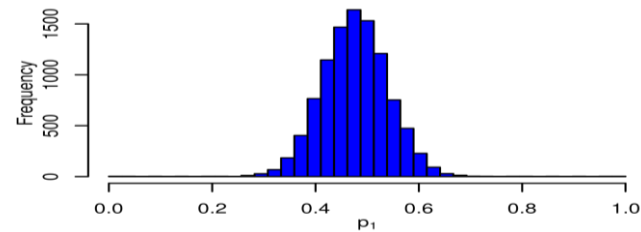
8



25



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



3. Constructing informative priors

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

30



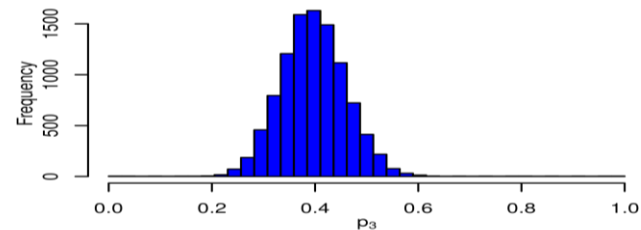
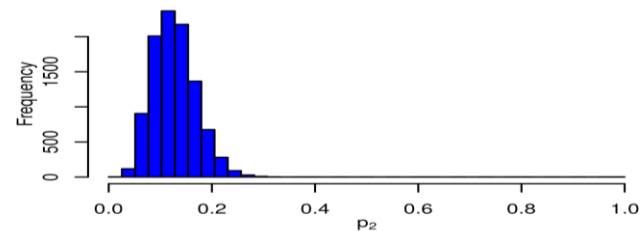
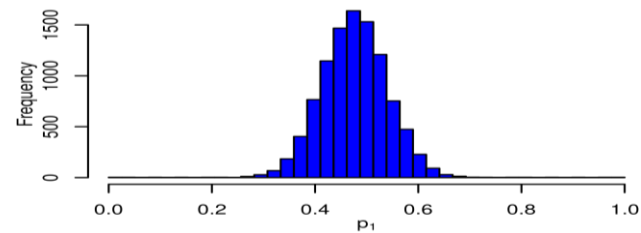
8



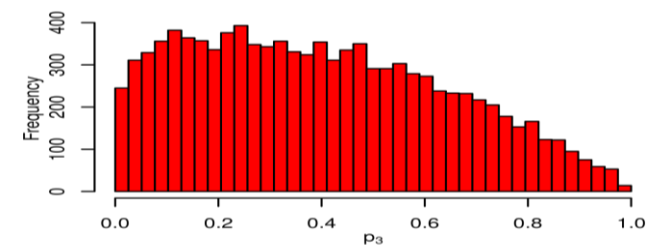
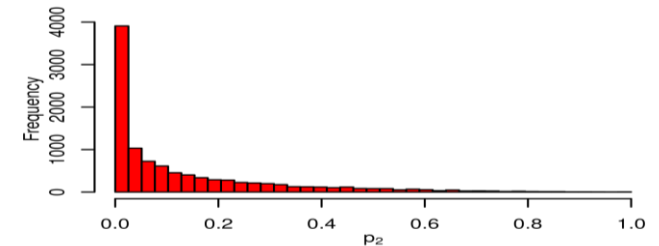
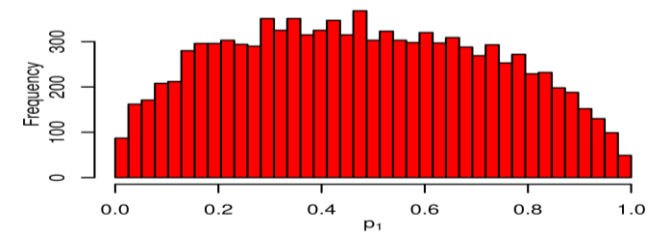
25



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



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



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

Application to other biotracers

“Stable isotope” mixing models

Application to other biotracers

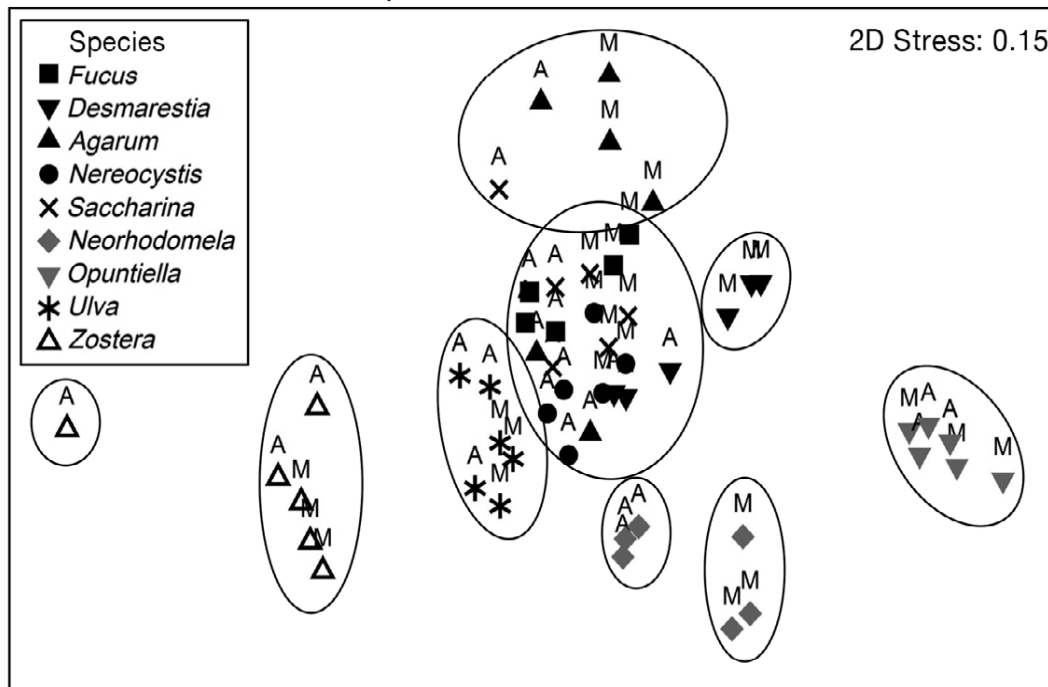
- Fatty acids
- Compound-specific stable isotopes
- Element concentrations
- Sediment color

Application to other biotracers

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

Great promise!

Application to other biotracers



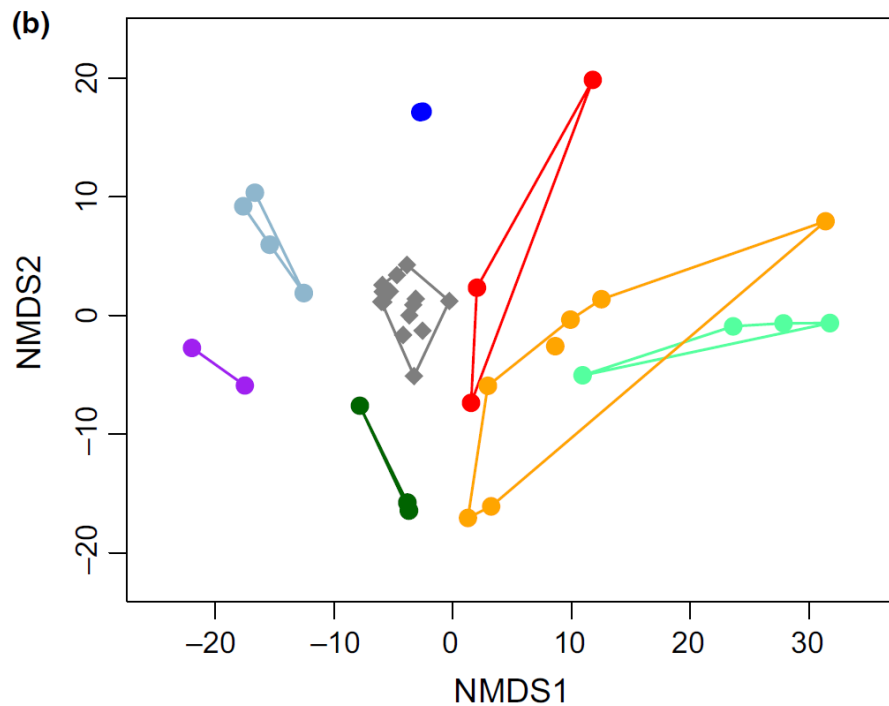
Theoretical consumer from source data

- 3 stable isotopes
- 6 essential fatty acids
- 19 non-essential fatty acids

SIAR

More biotracers = better performance

Application to other biotracers



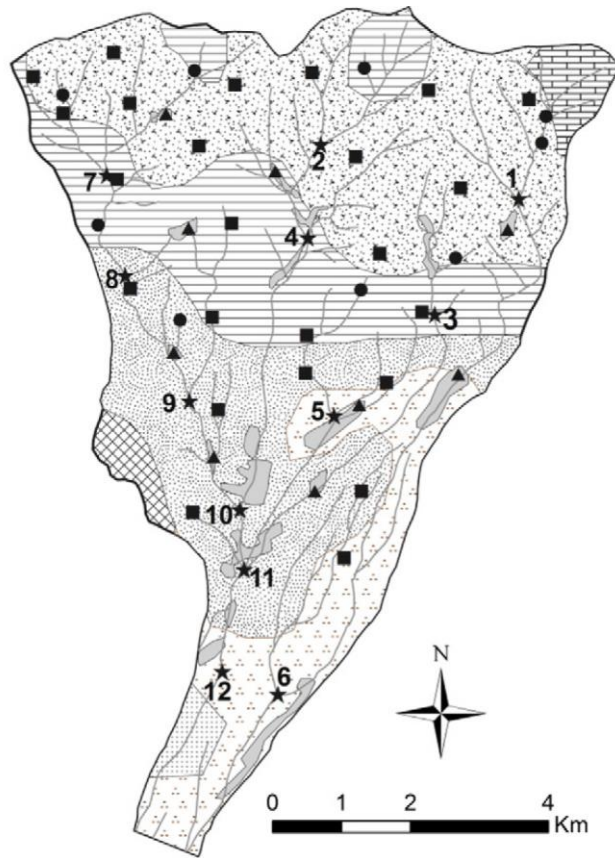
Source_{*i*} data are consumers fed source *i*

○ TDF = 0

22 fatty acids

MixSIR

Application to other biotracers



Mixtures are sediment samples

- TDF = 0

28 element concentrations

Other sediment datasets:

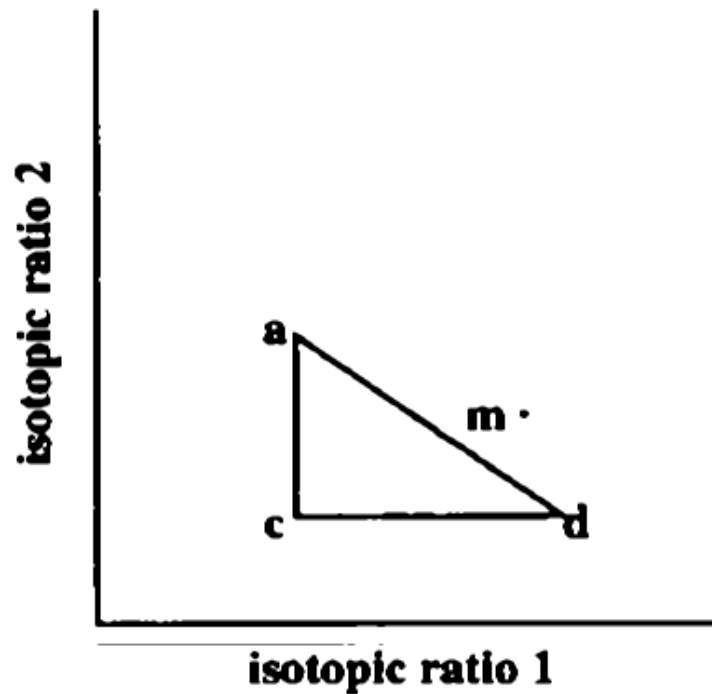
- element concentrations (n = 56)
- color variables (n = 15)
- CSSI (n = 20)

1. Testing mix/source geometry

Less obvious if mix data is inside source hypervolume

Standard in sediment fingerprinting:

- Check each dimension separately



2. Check for normality

Fatty acid profiles are *proportions*

$$t_j \sim N(\text{alr}(\tau_j), \Sigma_\tau)$$

$$\tau_j = C \left\{ \sum_s^n (\pi_{j,s} \Phi_s) (\kappa_s \otimes \phi_{j,s}) \right\}$$

3. Multiple data types

Fatty acid profiles (n = 25):

$$t_j \sim N(\text{clr}(\tau_j), \Sigma_\tau)$$

$$\tau_j = C \left\{ \sum_s^n (\pi_{j,s} \Phi_s) (\kappa_s \otimes \phi_{j,s}) \right\}$$

Stable isotopes (n = 3):

$$t_r^{SI} = \sum_s^n \pi_{r,s} (y_{q,r} + \gamma_s)$$

$$\text{clr}(\pi_r) \sim N(\Pi, \Sigma_\Pi)$$

$$\gamma_{s,SI} \sim N(\nu_{SI}, \sigma_{SI}).$$

Weight each data type equally?

Weight by number of tracers?

4. Selecting biotracers

Are more biotracers always better?

Discriminant function analysis (DFA) to choose “optimum subset”

Biotracer selection within mixing model?



Application to other biotracers “Stable isotope” mixing models

TEST MIX/SOURCE GEOMETRY

CHECK FOR NORMALITY

MULTIPLE DATA TYPES

SELECTING BIOTRACERS

Pitfalls and misconceptions

1. Source geometry
2. MCMC convergence
3. **Effect of priors**
4. Error structures
5. Source lumping/splitting
6. How to include covariates
7. **Application to biotracers other than stable isotopes**



Acknowledgements

MixSIAR team:

- Brice Semmens
- Eric Ward
- Andrew Parnell
- Andrew Jackson
- Donald Phillips
- Stuart Bearhop
- Richard Inger

Support:

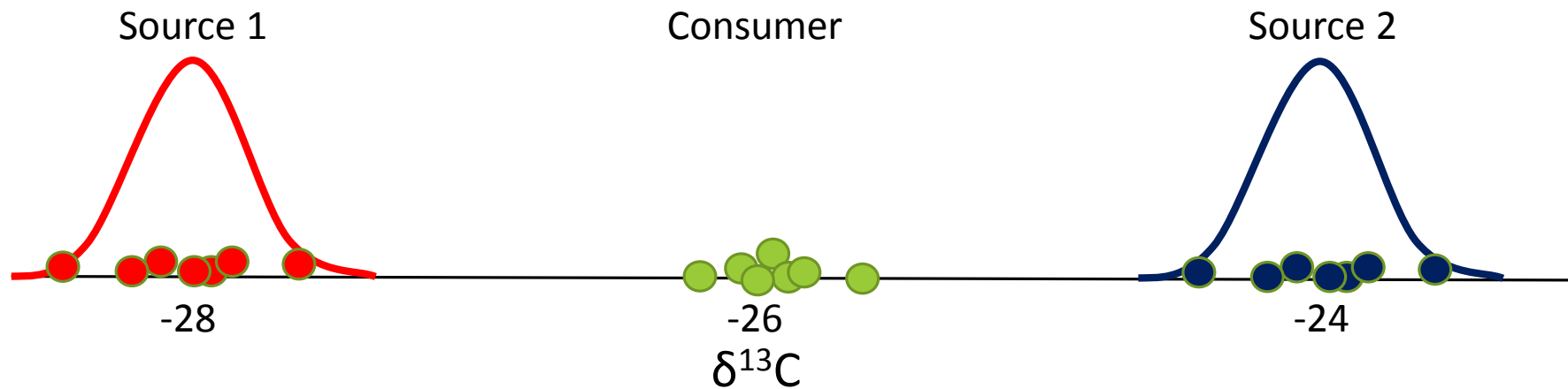


XSEDE

Extreme Science and Engineering
Discovery Environment

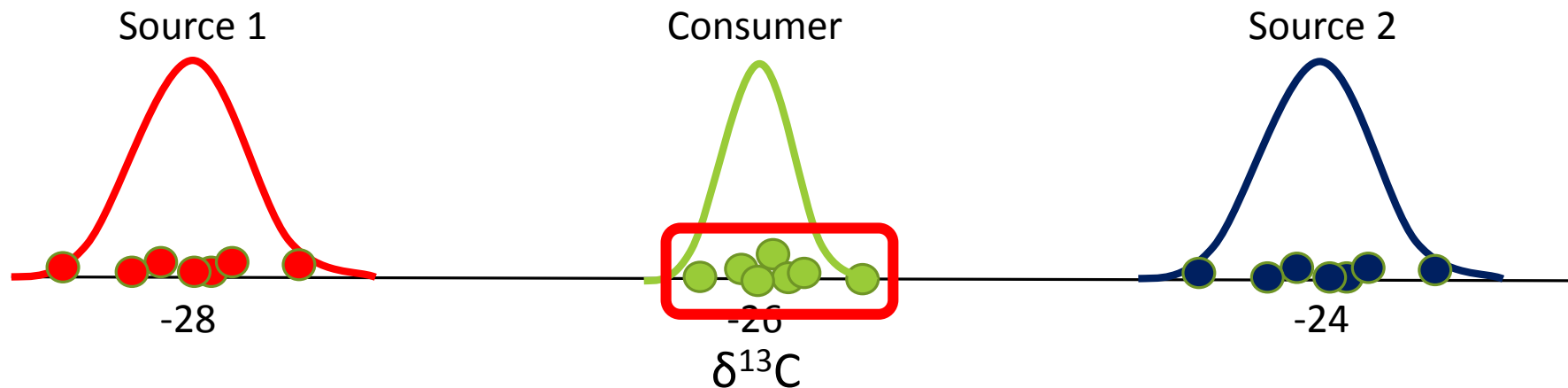
Error structures

Error structures



Error structures

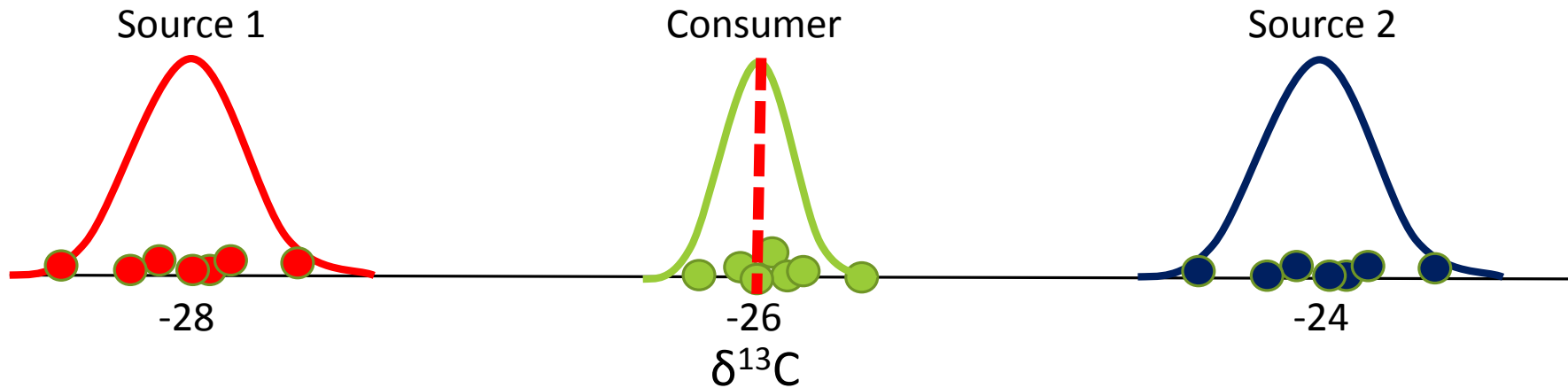
MixSIR $X_{ij} \sim N \left(\sum_{k=1}^K p_k (\mu_{jk} + \lambda_{jk}), \left[\sum_{k=1}^K p_k^2 (\omega_{jk}^2 + \tau_{jk}^2) \right] \right)$



Error structures

MixSIR

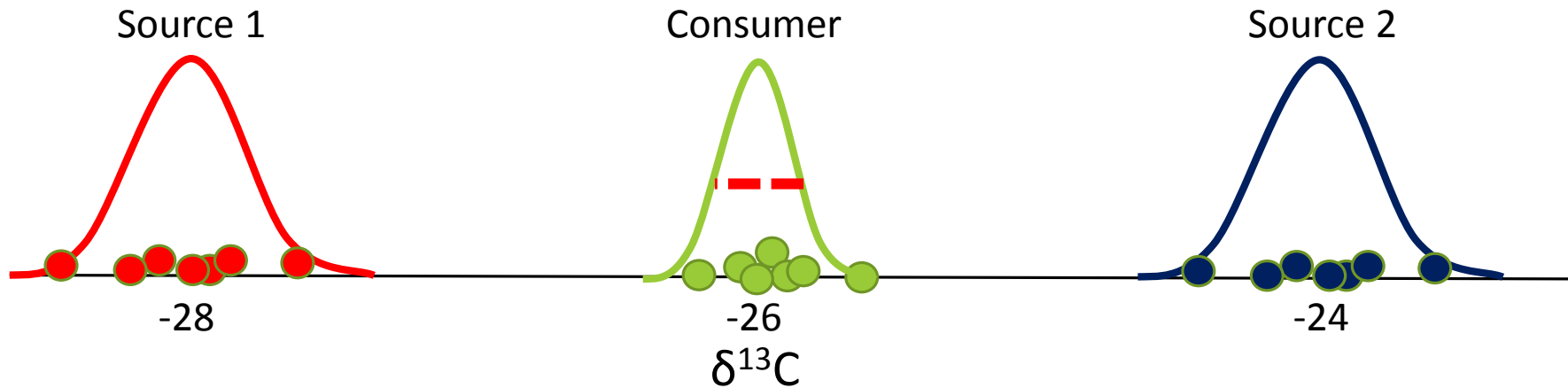
$$X_{ij} \sim N \left[\sum_{k=1}^K p_k (\mu_{jk} + \lambda_{jk}), \sum_{k=1}^K p_k^2 (\omega_{jk}^2 + \tau_{jk}^2) \right]$$



Error structures

MixSIR

$$X_{ij} \sim N \left(\sum_{k=1}^K p_k (\mu_{jk} + \lambda_{jk}), \sum_{k=1}^K p_k^2 (\omega_{jk}^2 + \tau_{jk}^2) \right)$$

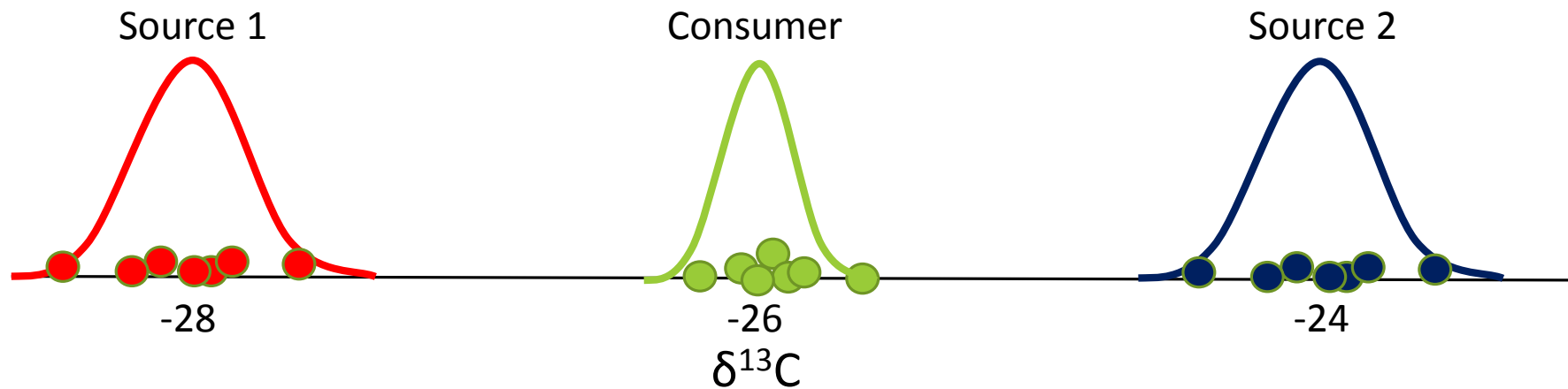


Error structures

MixSIR

$\sigma^2_{\text{process}}$

Medium variance

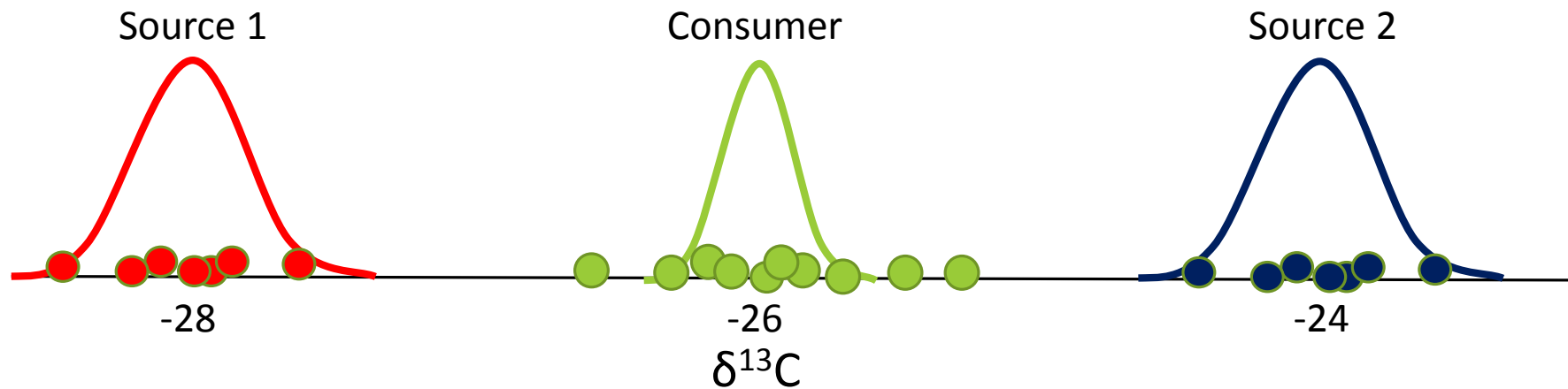


Error structures

MixSIR

$\sigma^2_{\text{process}}$

High variance



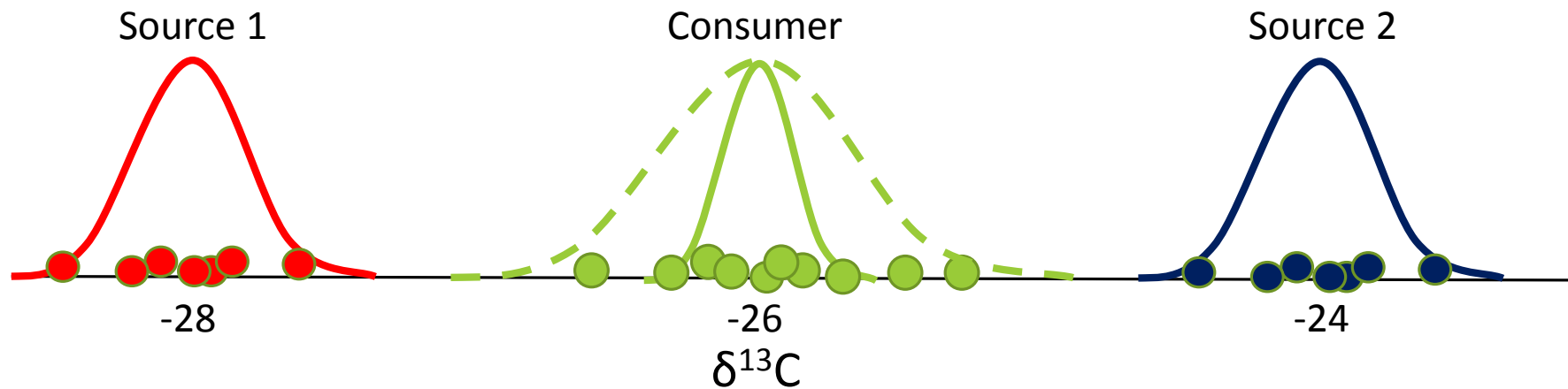
Error structures

SIAR

$$\sigma^2_{\text{process}} + \sigma^2_{\text{resid}}$$

High variance

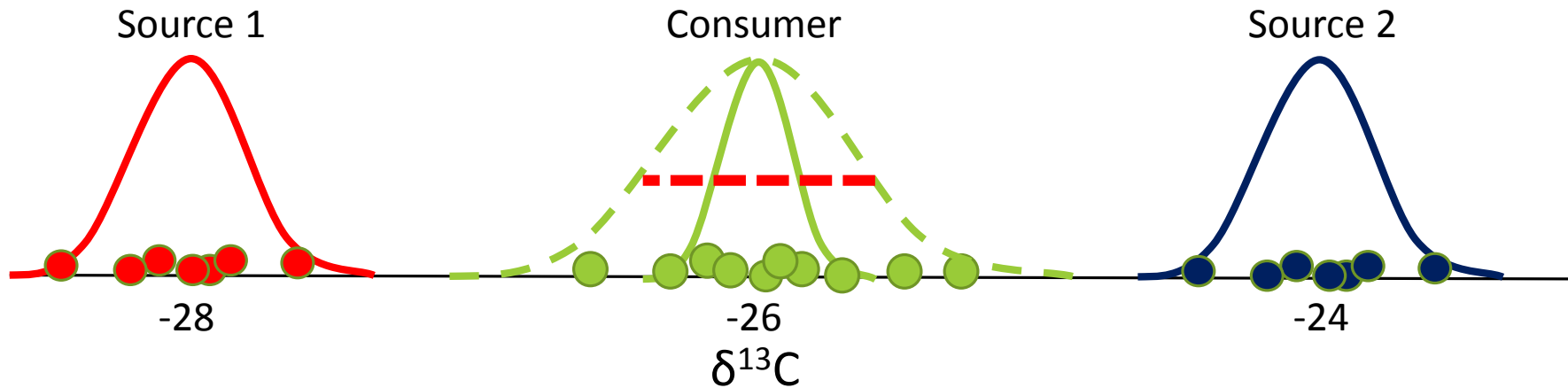
Note: cannot fit N = 1



Error structures

SIAR

$$X_{ij} \sim N \left(\sum_{k=1}^K p_k (\mu_{jk} + \lambda_{jk}), \left[\sum_{k=1}^K p_k^2 (\omega_{jk}^2 + \tau_{jk}^2) + \sigma_j^2 \right] \right)$$

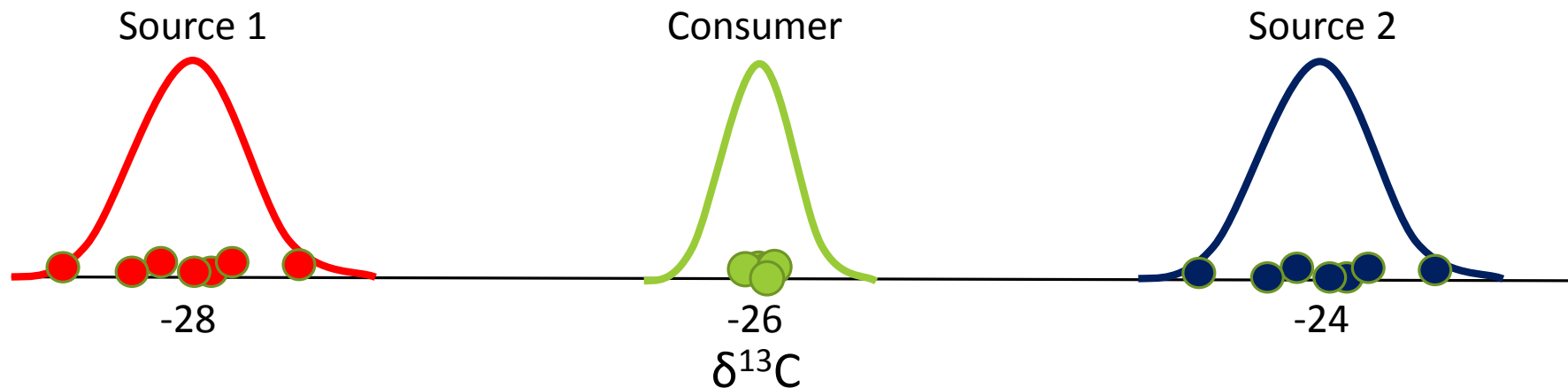


Error structures

SIAR

$$\sigma^2_{\text{process}} + \sigma^2_{\text{resid}}$$

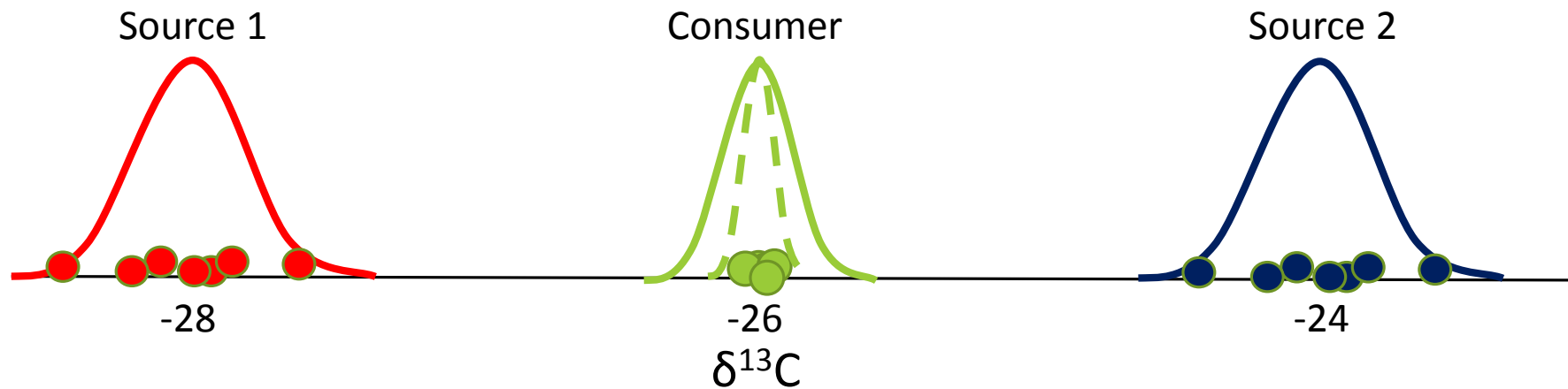
Low variance



Error structures

$$\sigma^2_{\text{process}} * \epsilon_{\text{resid}}$$

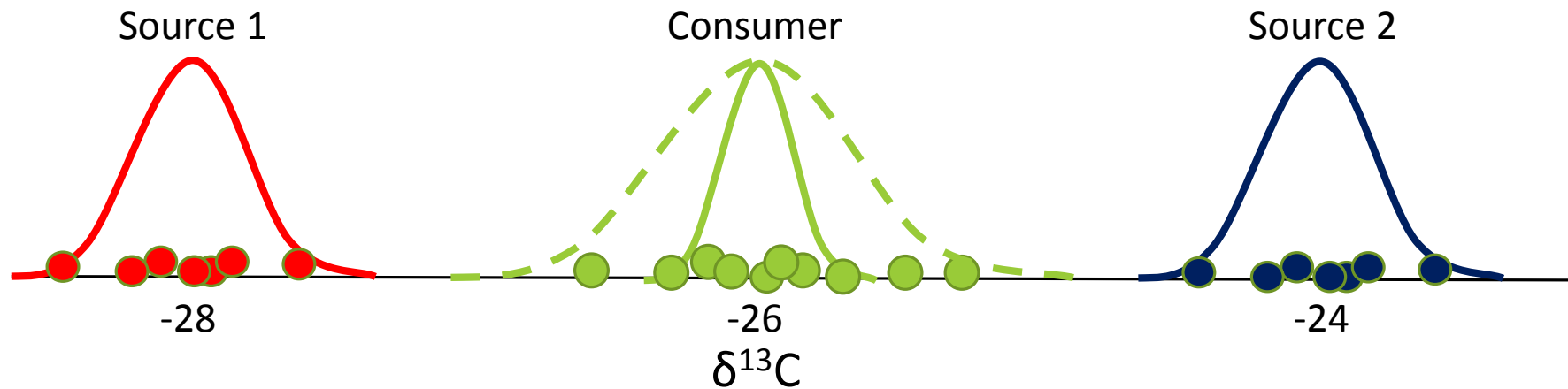
Low variance
 $\epsilon < 1$



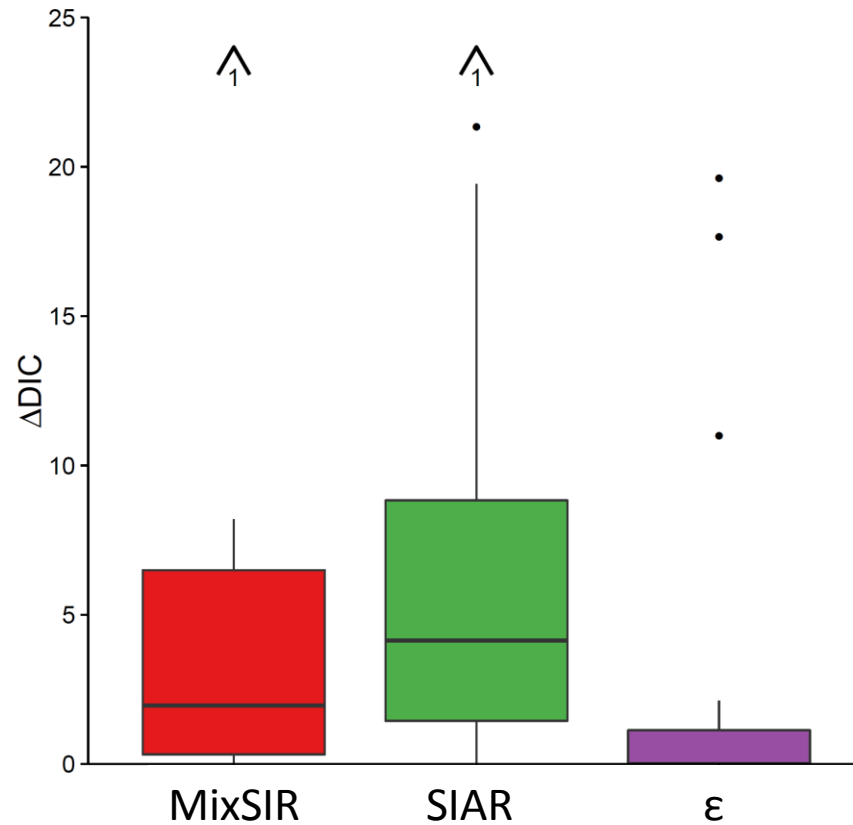
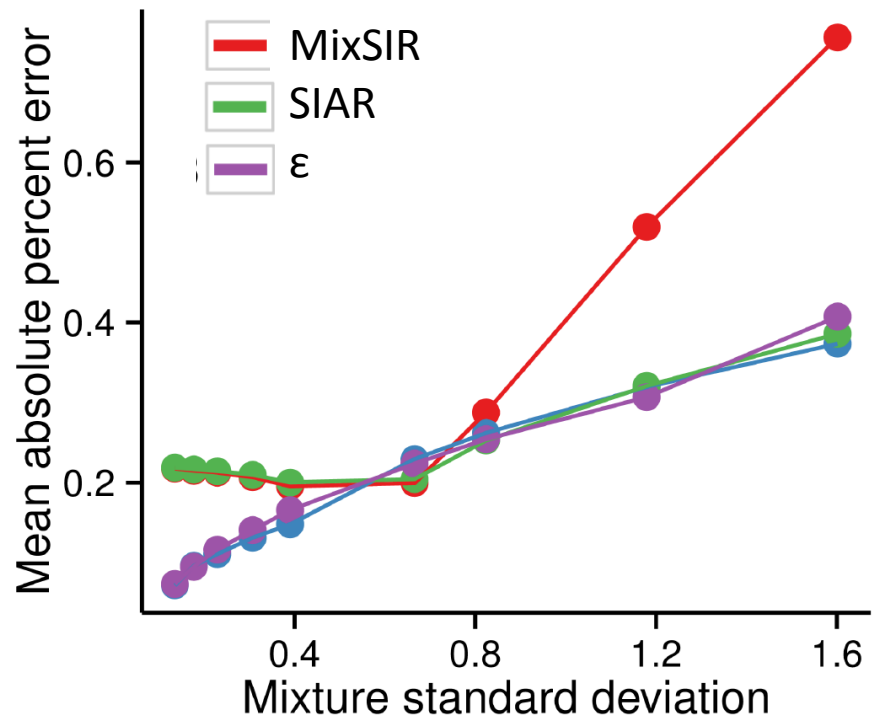
Error structures

$$\sigma^2_{\text{process}} * \epsilon_{\text{resid}}$$

High variance
 $\epsilon > 1$



Error structures



Error structures

MIXSIR ($N = 1$)

SIAR

MULTIPLICATIVE RESIDUAL ERROR