

The guts of MixSIAR

Brian Stock

NWFSC

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R Console

```

Natural language support bu
R is a collaborative project
Type 'contributors()' for mor
'citation()' on how to cite R
Type 'demo()' for some demos,
'help.start()' for an HTML br
Type 'q()' to quit R.

[Previously saved workspace r
> source("mixsiar_gui.r")
> mixsiar_gui()
Loading required package: ggp
Loading required package: gWi
Loading required package: RGt
Loading required package: gWi
Loading required package: R2j
Loading required package: rja
Loading required package: cod
Loading require package: lat
Linked to JAGS 3.4.0
Loaded modules: basemod,bugs
Attaching package: 'R2jags'
The following object is maske
traceplot
Loading required package: MAS
Loading required package: RCo
Loading required package: res
> |

```

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)

Output options

Summary Statistics Save summary statistics to file:

Posterior Density Plot Suppress plot output
Save plot as: pdf png

Pairs Plot Suppress plot output
Save plot as: pdf png

XY Plot Suppress plot output
Save plot as: pdf png

Diagnostics

- Gelman-Rubin (must have > 1 chain) Heidelberg-Welch Geweke
- Save diagnostics to file:

Note: diagnostics will print in the R command line if you do not choose to save to file

RUN MODEL **Process output**

Mix data

1. Random effects
2. Fixed effects
3. Continuous effect
4. Individuals as RE
5. Hierarchy / nested

Source data

6. Source by factor
7. Concentration dependence
8. "Raw" or "means"
9. MCMC parameters
10. Error structure

Inside the black box

User options

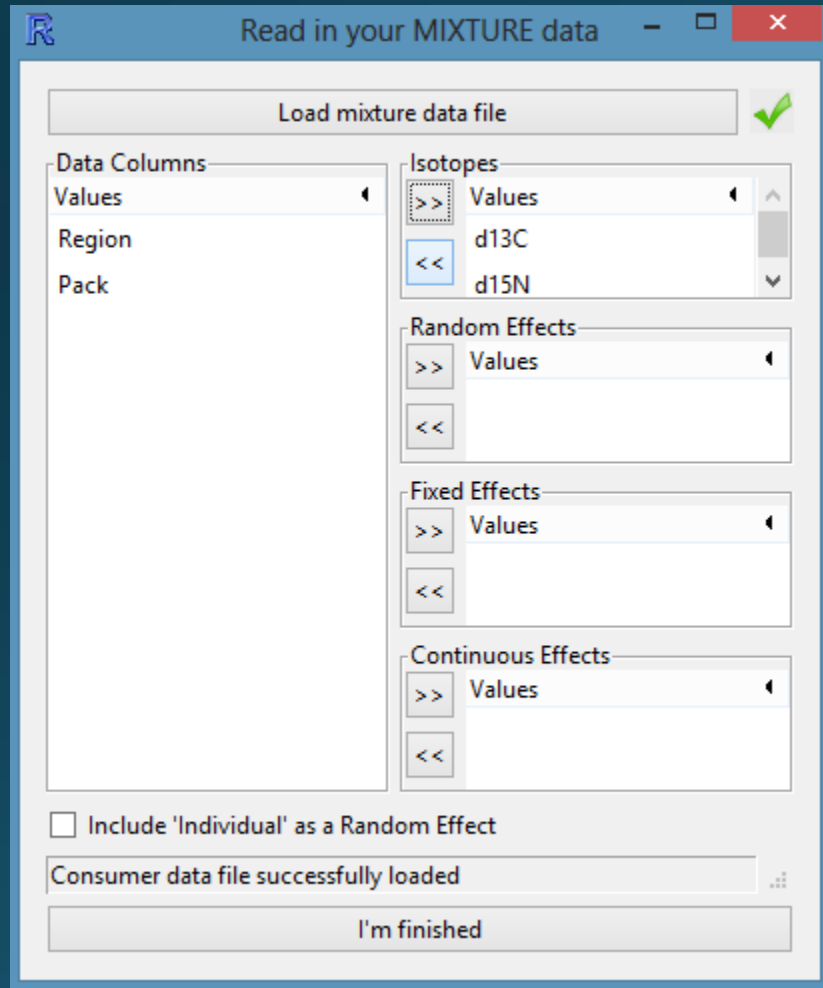
```
if(mix$n.re > 0){ # at least 1 random effect
cat("
  fac1.sig ~ dunif(0,20);
  fac1.invSig2 <- 1/(fac1.sig*fac1.sig);
  # draw the fac1 (region) specific ILR terms (random effect)
  for(f1 in 1:factor1_levels) {
    for(src in 1:(n.sources-1)) {
      ilr.fac1[f1,src] ~ dnorm(0,fac1.invSig2);
    }
  }
", file=filename, append=T)}
```

```
if(resid_err){
cat("
  # Additive residual error (SIAR)
  for(iso in 1:n.iso){
    resid.prcsn[iso] ~ dgamma(.001,.001);
    resid.var[iso] <- 1/resid.prcsn[iso];
  }
", file=filename, append=T)}
```

write_JAGS_model.r

JAGS → R

Mix data options



1. Random effects
2. Fixed effects
3. Continuous effect
4. Individuals as RE
5. Hierarchy / nested

1) random and 2) fixed effects

Previously (w/o random or fixed effects):

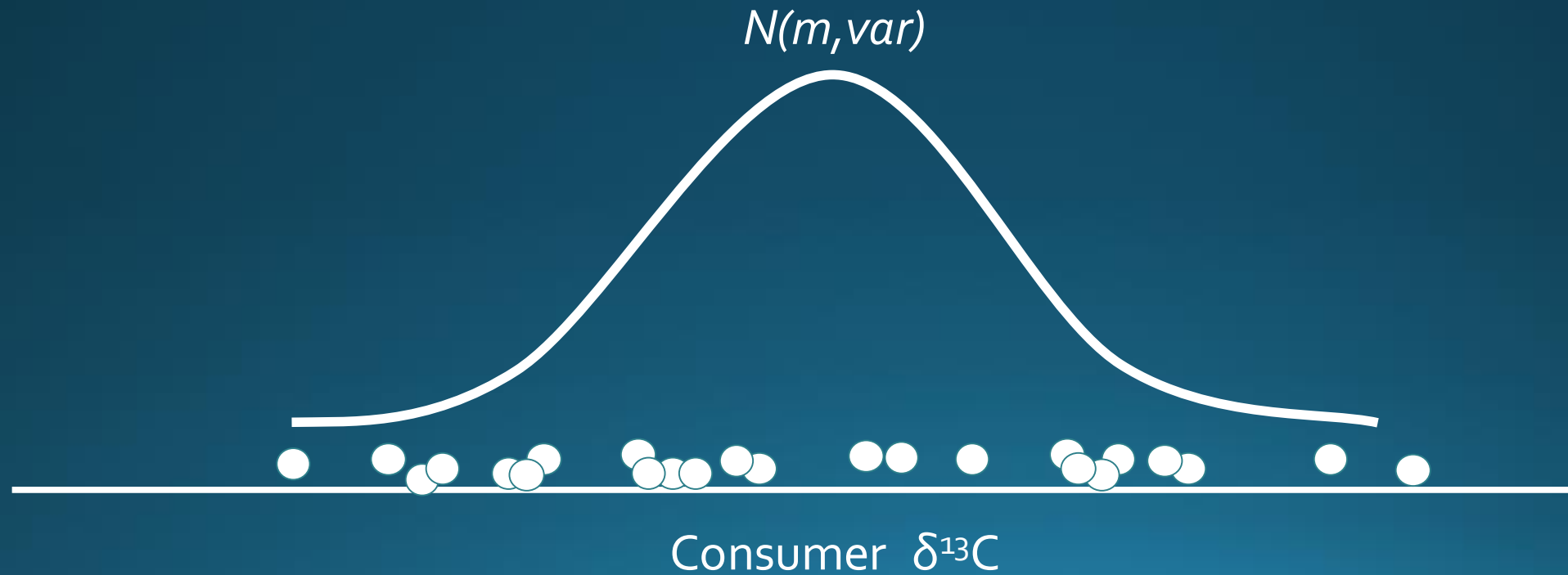
$$p = [20\%, 50\%, 20\% 10\%]$$

Assumes that all consumers have the *same diet*

1) random and 2) fixed effects



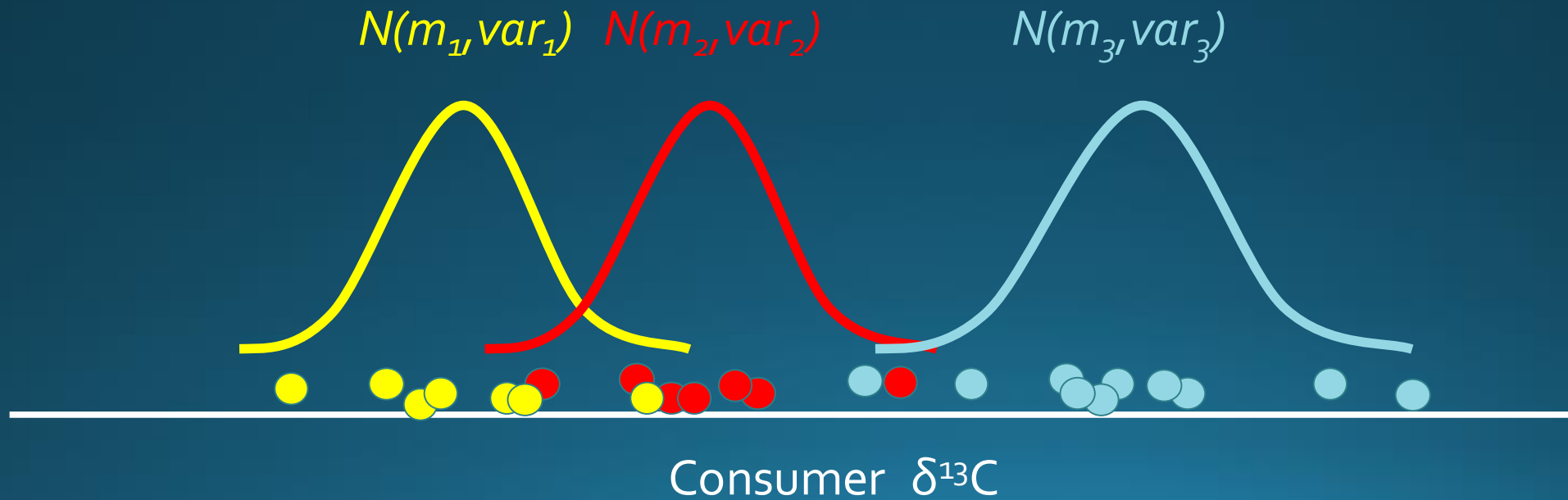
1) random and 2) fixed effects



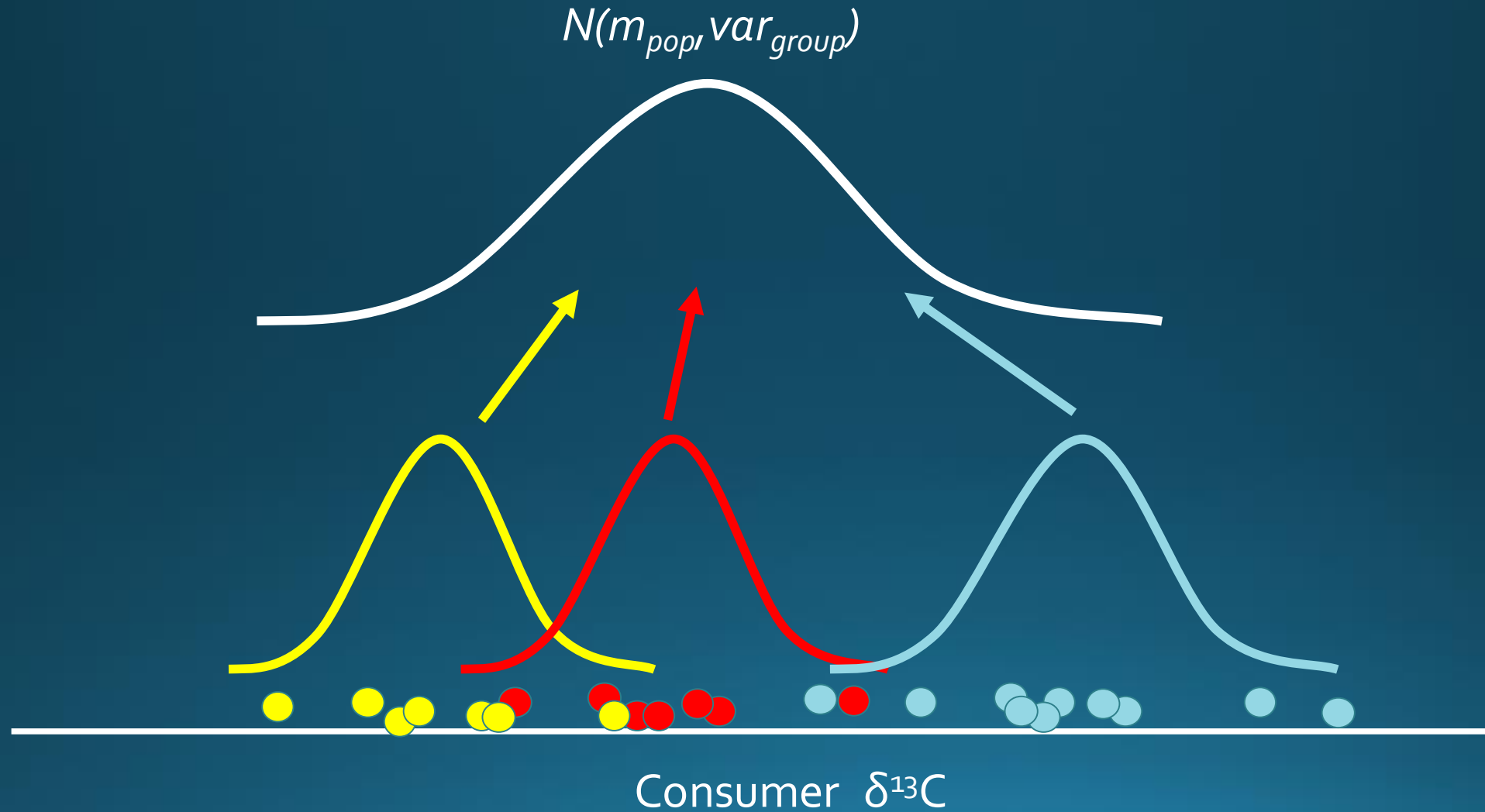
1) random and 2) fixed effects



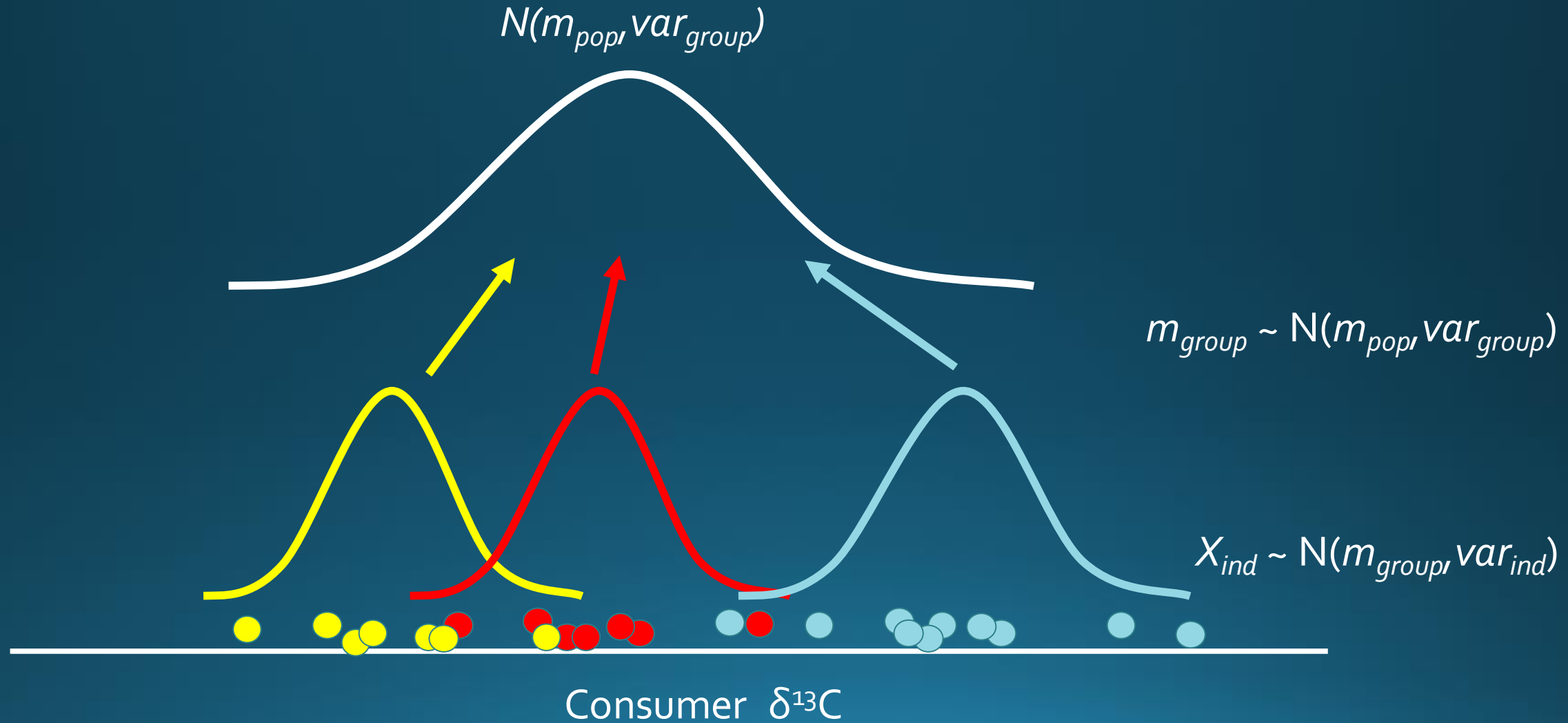
1) random and 2) fixed effects



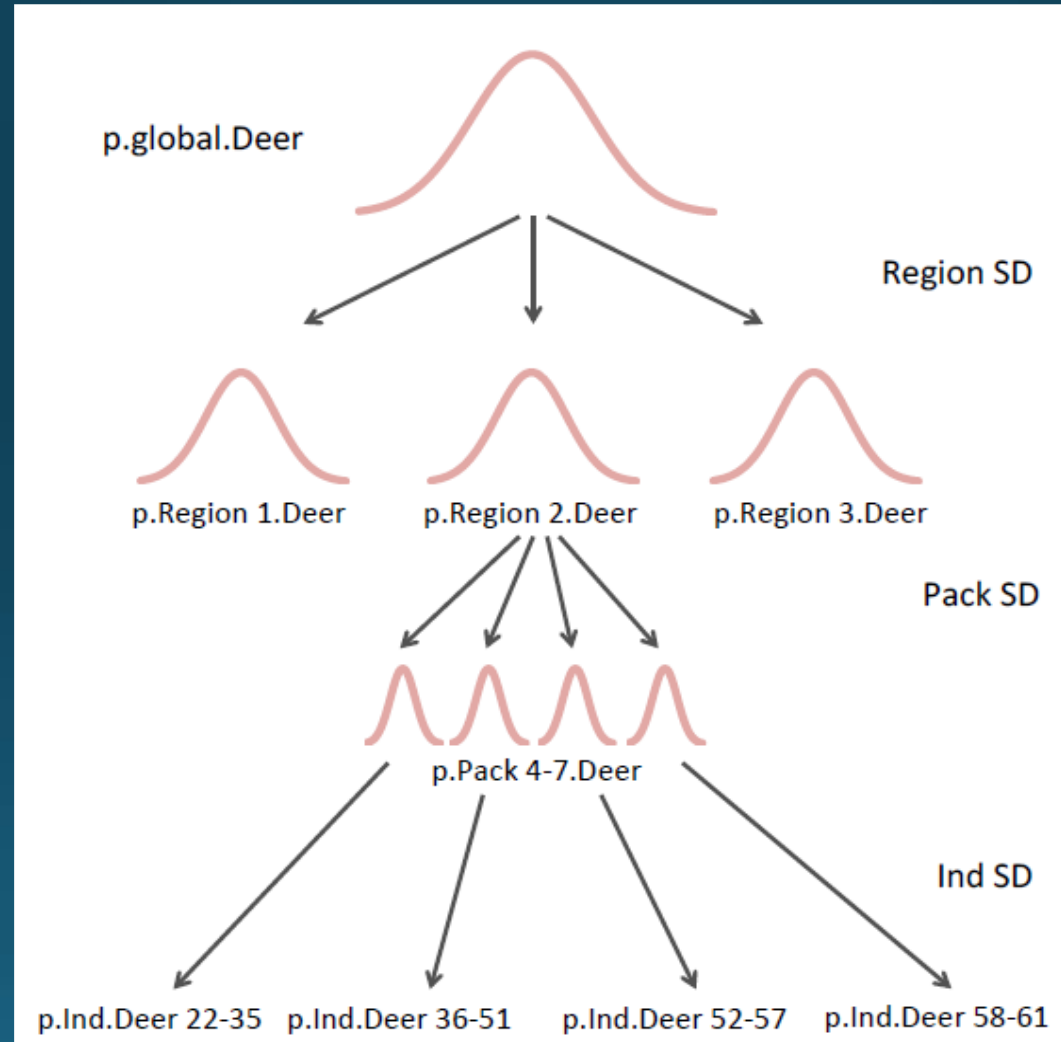
1) random and 2) fixed effects



1) random and 2) fixed effects



1) random and 2) fixed effects



1) random and 2) fixed effects

Random effects:

- Suspect levels come from global/overall distribution
- Interested in global/overall as well as specific levels
 - With multiple RE, can get info on relative importance of each
- At least 3 levels (ideally more)

Fixed effects:

- Suspect levels are unrelated
- Interested in specific levels only, not a broader distribution
- Only 2 (or 3) levels

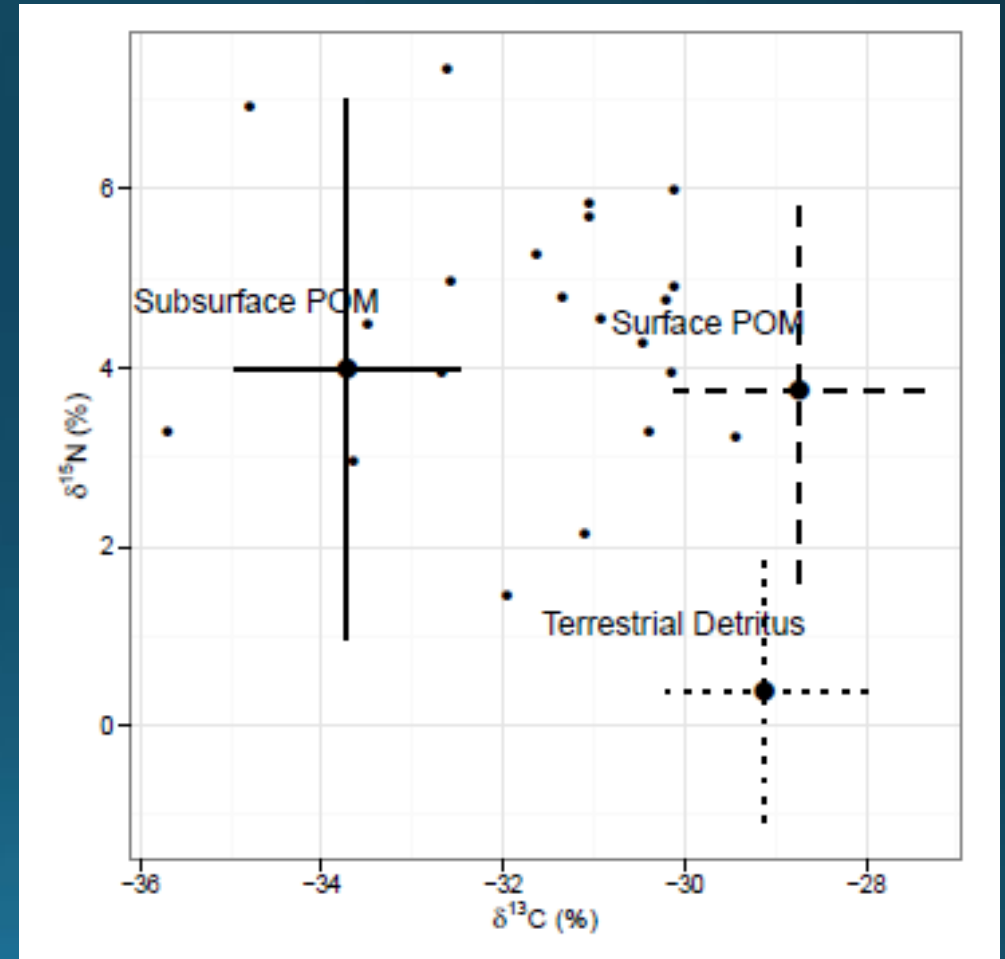
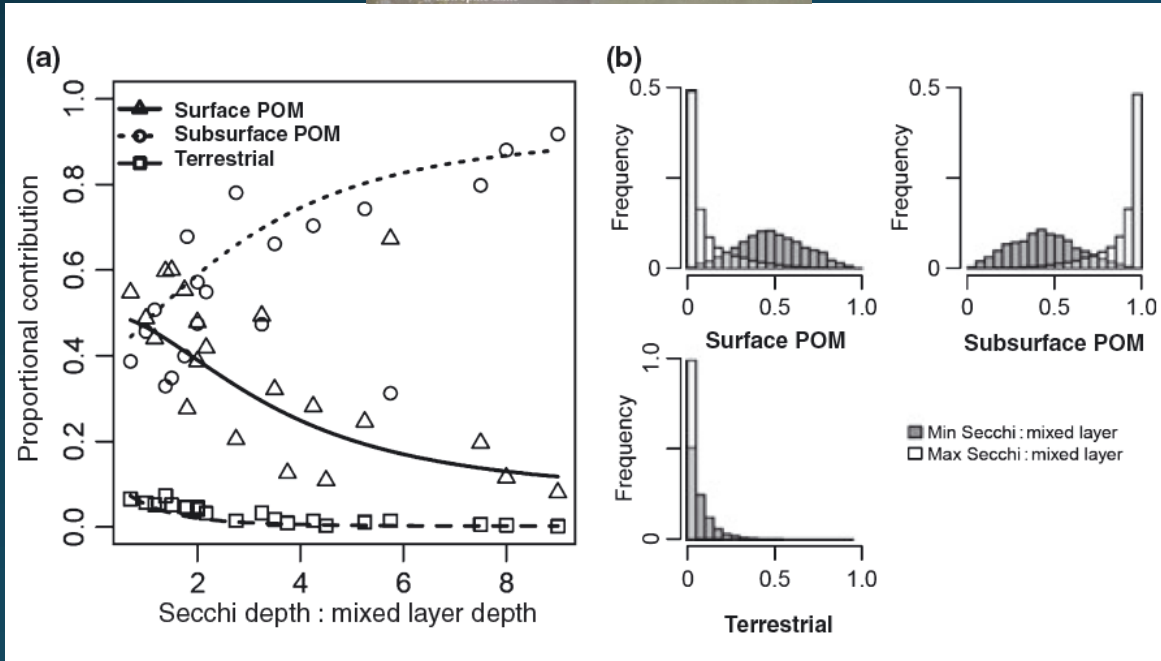
Note: SIAR can run one fixed effect (“group”)

3) continuous effect

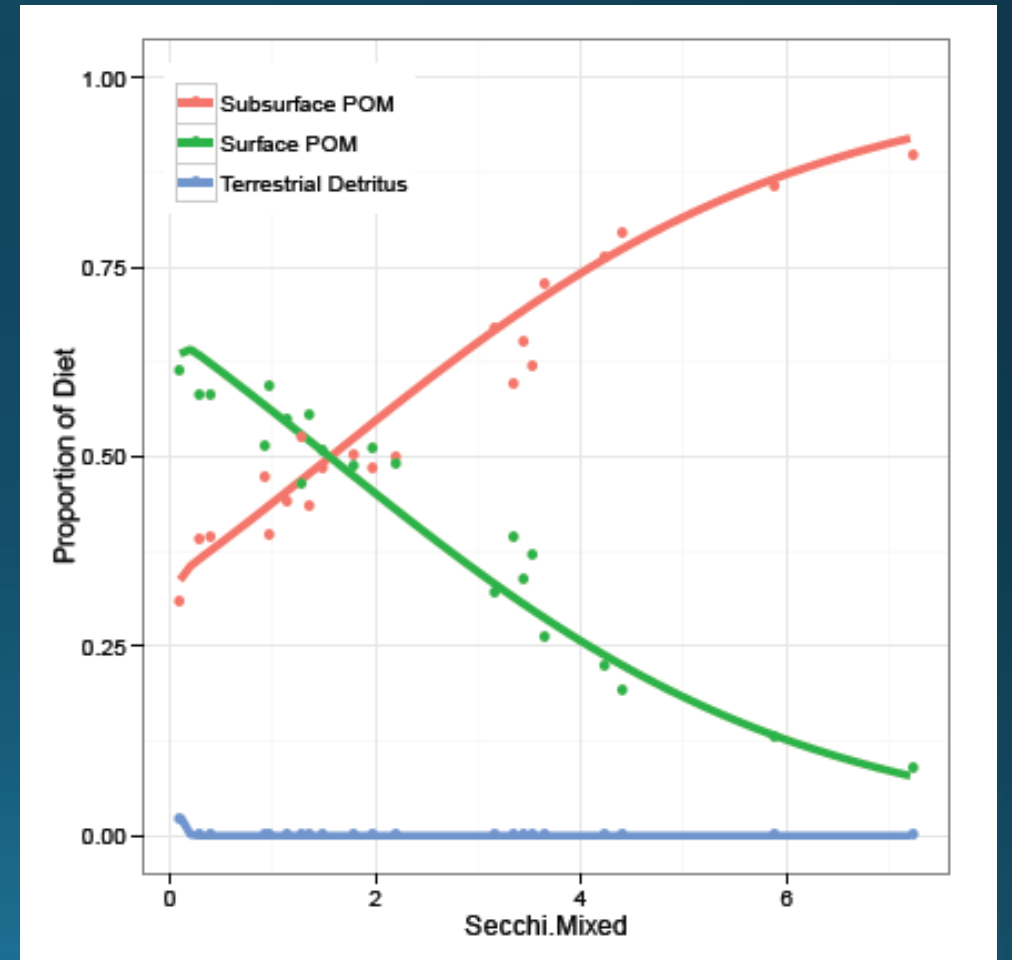
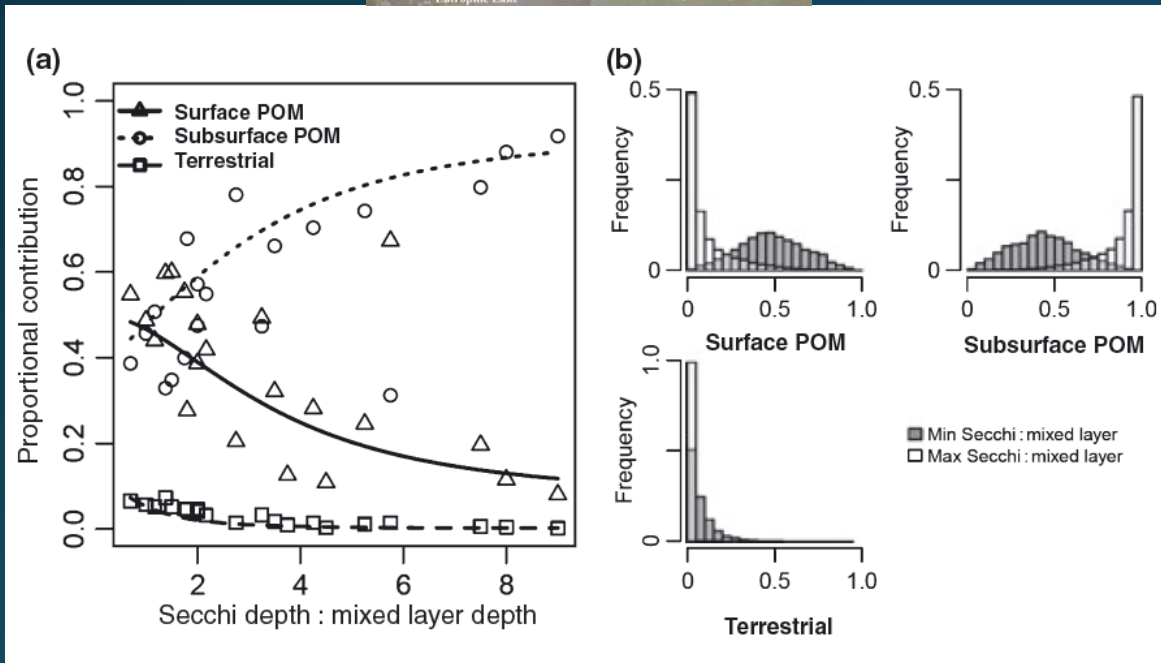


$$\delta_c = p_1 s_1 + p_2 s_2 + \dots + p_i s_i$$
$$p_1 = B_0 + B_1 * \text{Predictor}_c$$

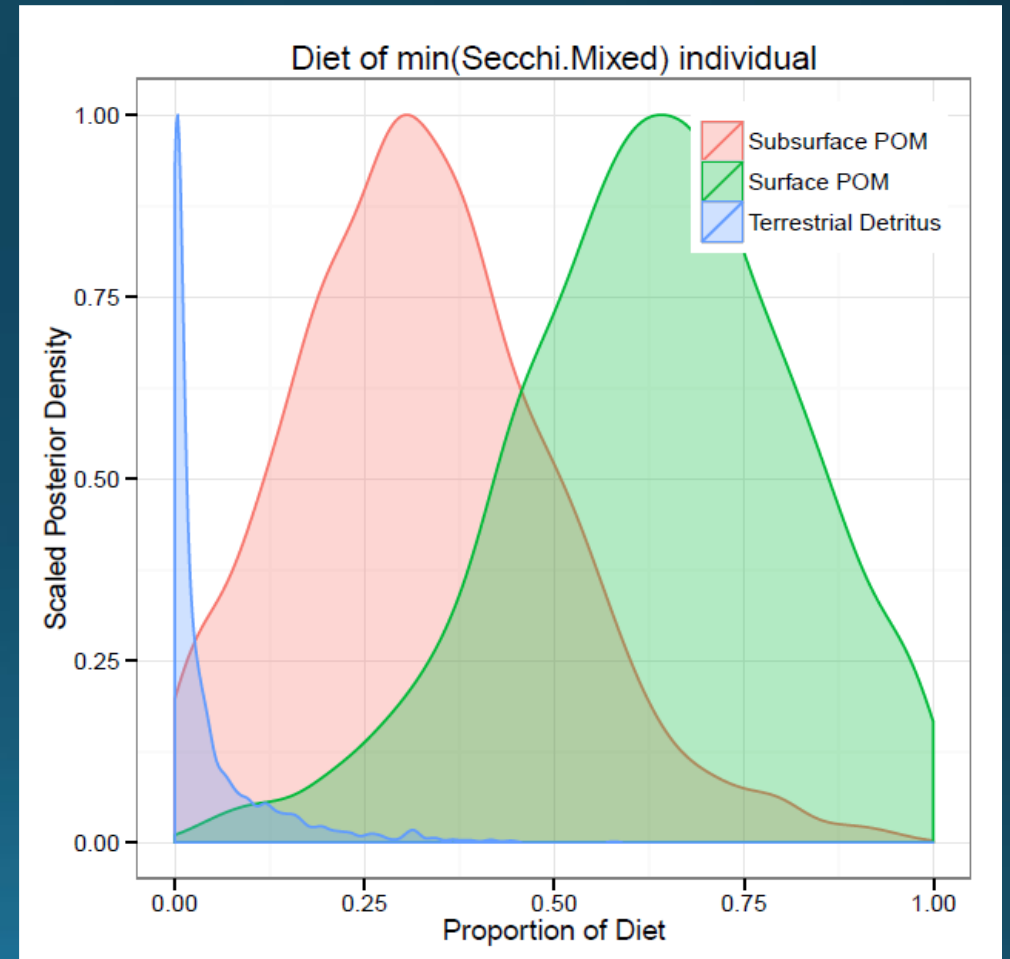
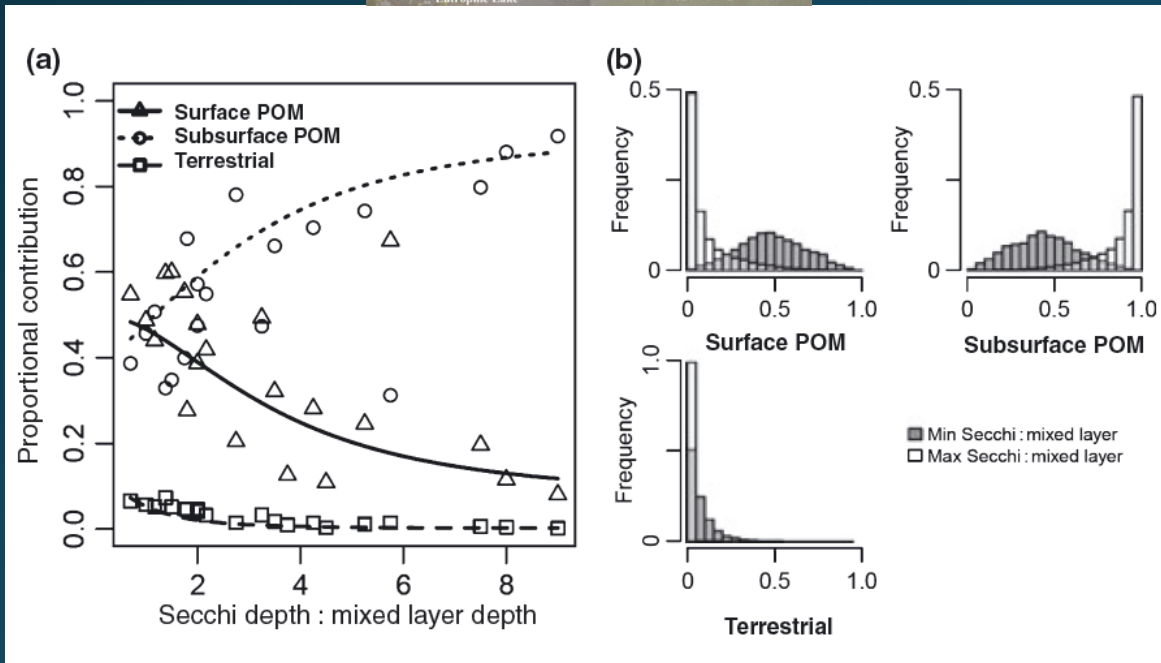
3) continuous effect



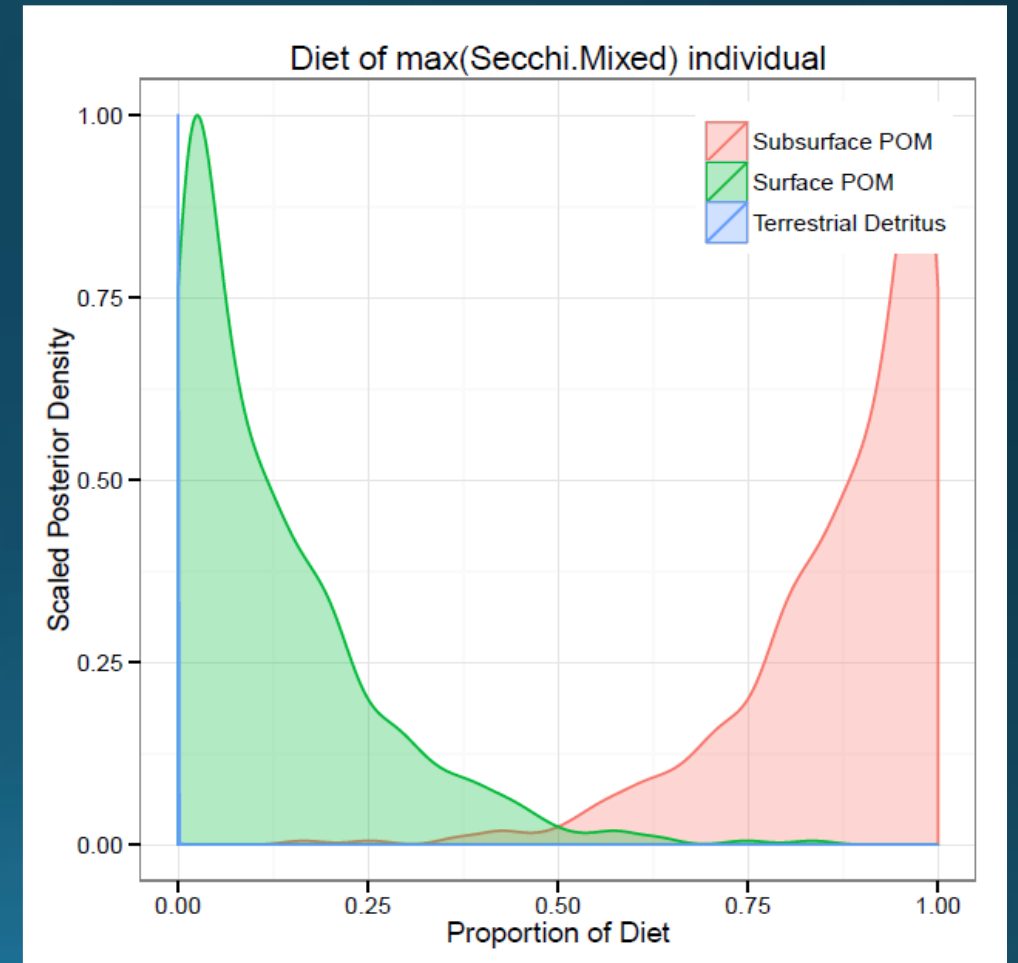
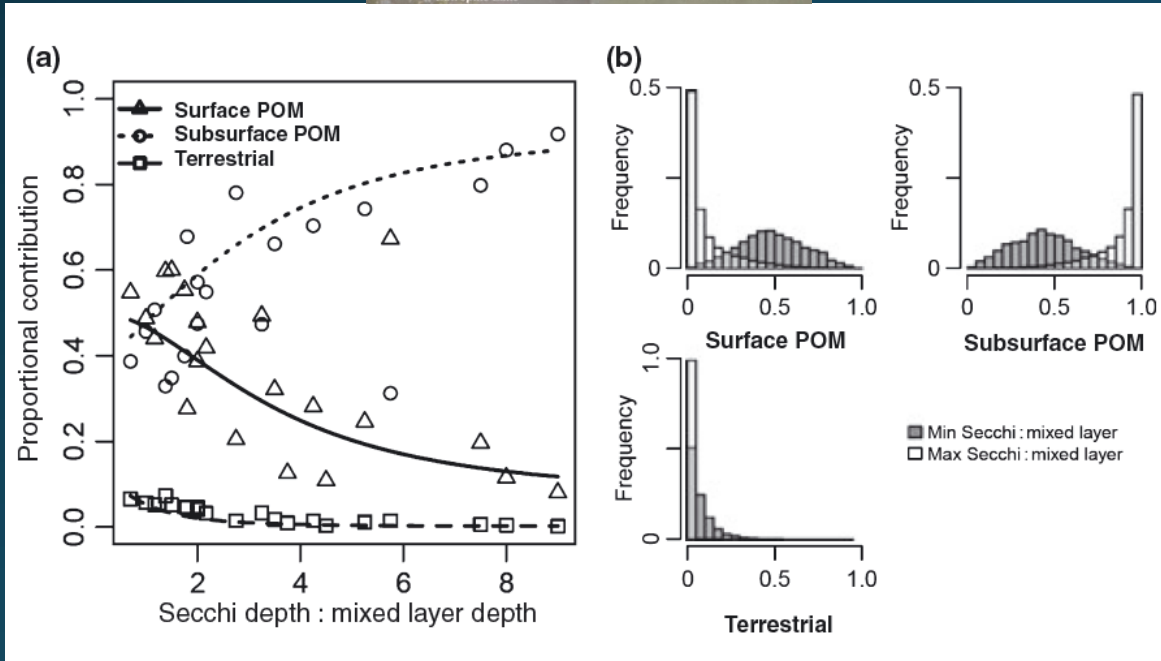
3) continuous effect



3) continuous effect



3) continuous effect

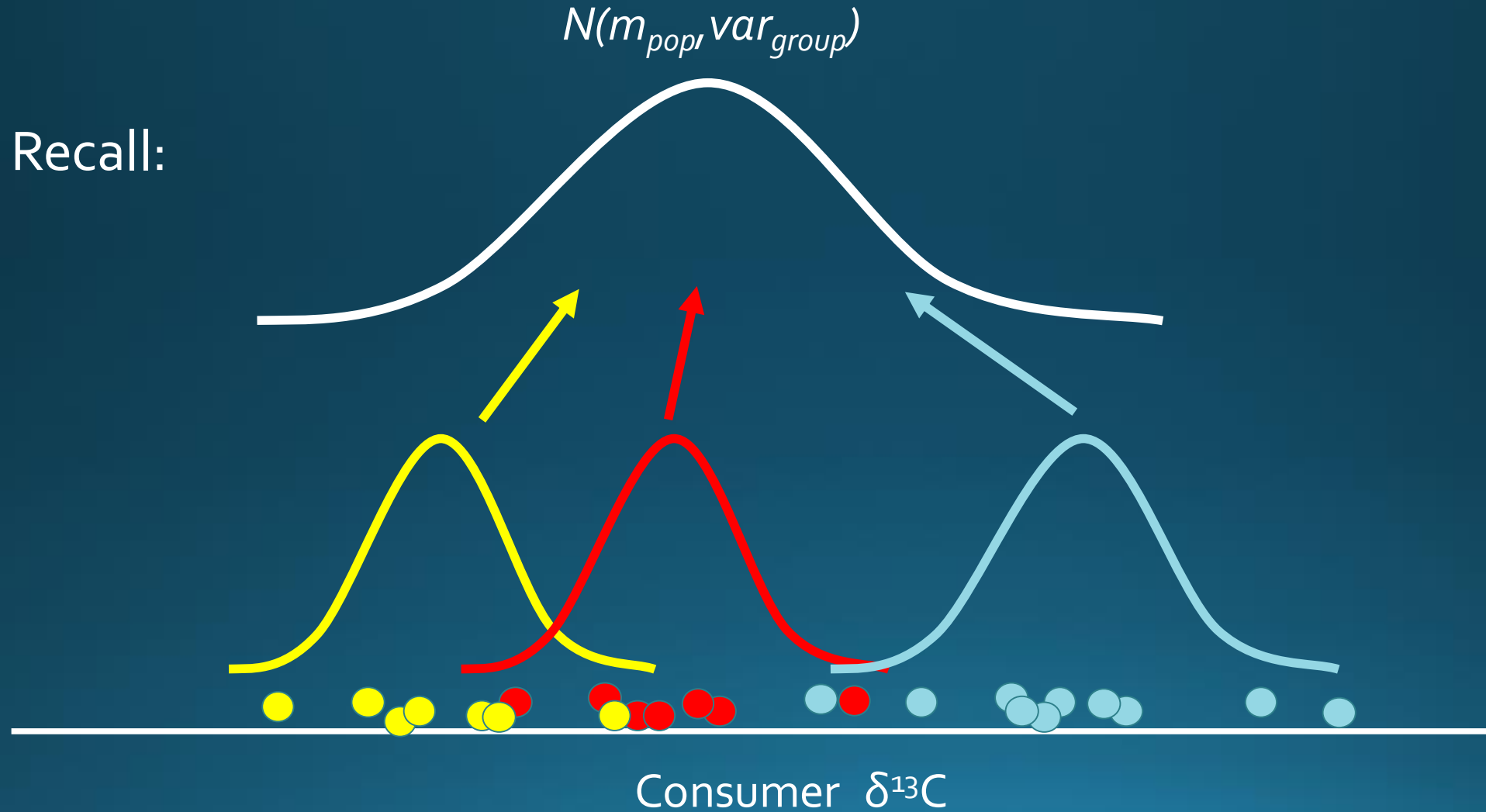


3) continuous effect

Issues

- Must select “Individuals as random effect”
- Covariate should be standardized first
- Can be finicky

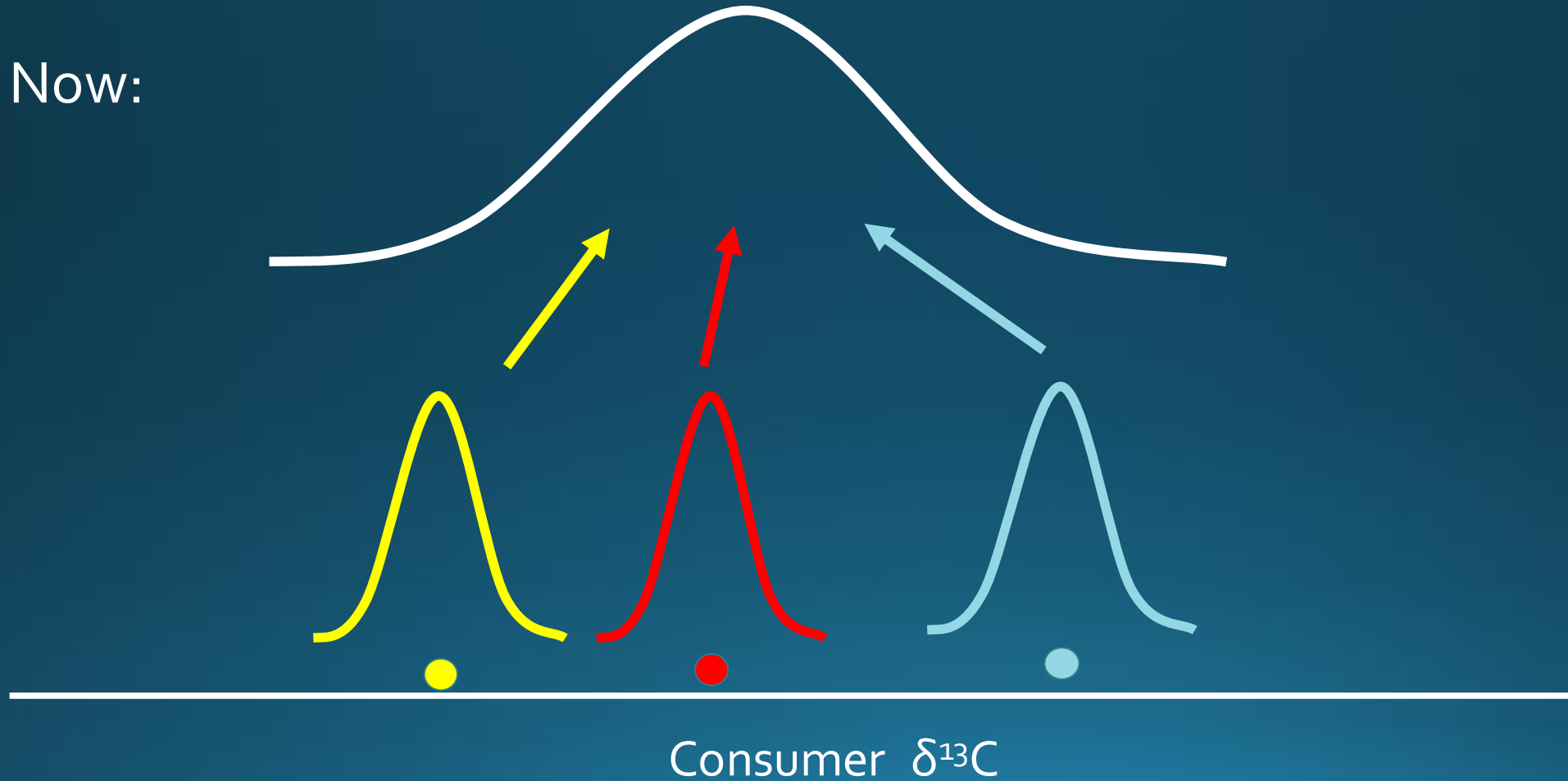
4) Individuals as random effects



4) Individuals as random effects

$$N(m_{pop}, var_{ind})$$

Now:

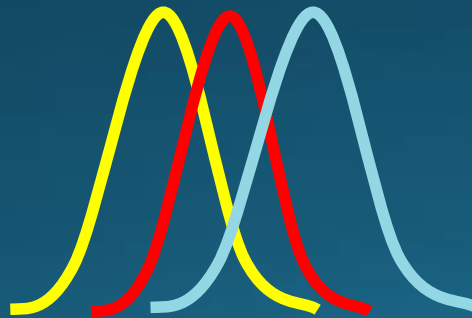


4) Individuals as random effects

$$N(m_{pop}, var_{ind})$$



Caution:
extreme shrinkage!



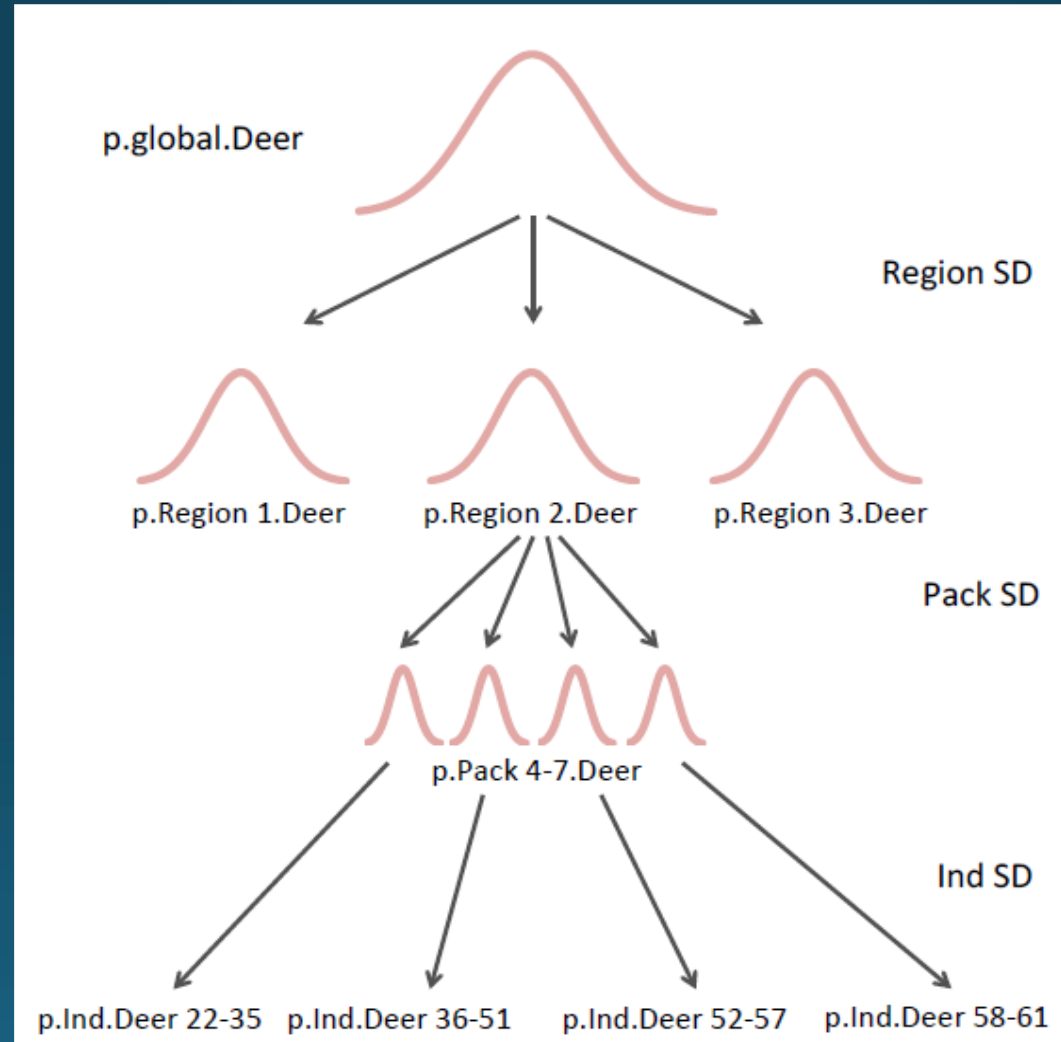
Consumer $\delta^{13}\text{C}$

4) Individuals as random effects

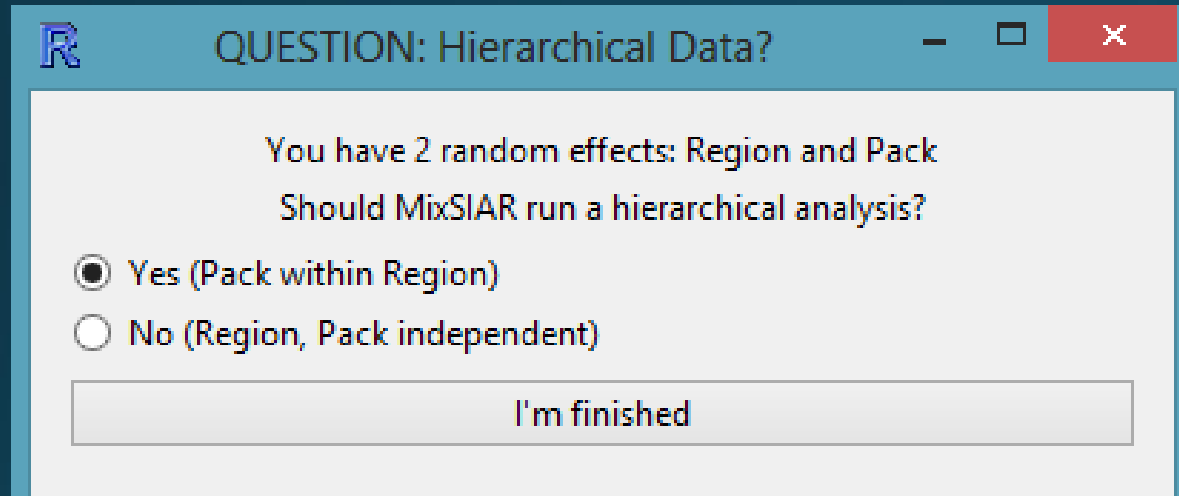
Issues

- Can't really estimate individual diets with $n=1$
- Confounding with residual error term (choose one or the other)
- Greatly increases number of parameters
- Default = FALSE

5) hierarchy / nested



5) hierarchy / nested



Yes `ilr.fac2.tot[f2,src] <- ilr.global[src] + ilr.fac1[factor1_lookup[f2],src] + ilr.fac2[f2,src];`

No `ilr.fac2.tot[f2,src] <- ilr.global[src] + ilr.fac2[f2,src];`

5) hierarchy / nested

- Look at results when Region, Pack nested vs. not

Source data options

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 Concentration Dependence data? Yes No

Do you have raw source data, or source means and SDs?

OR

6. Source by factor / effect
7. Concentration dependence
8. "Raw" or "means + SD" (+ n)

6) Source by factor

R Read in your SOURCE data

Does your source data vary by Region? Yes No

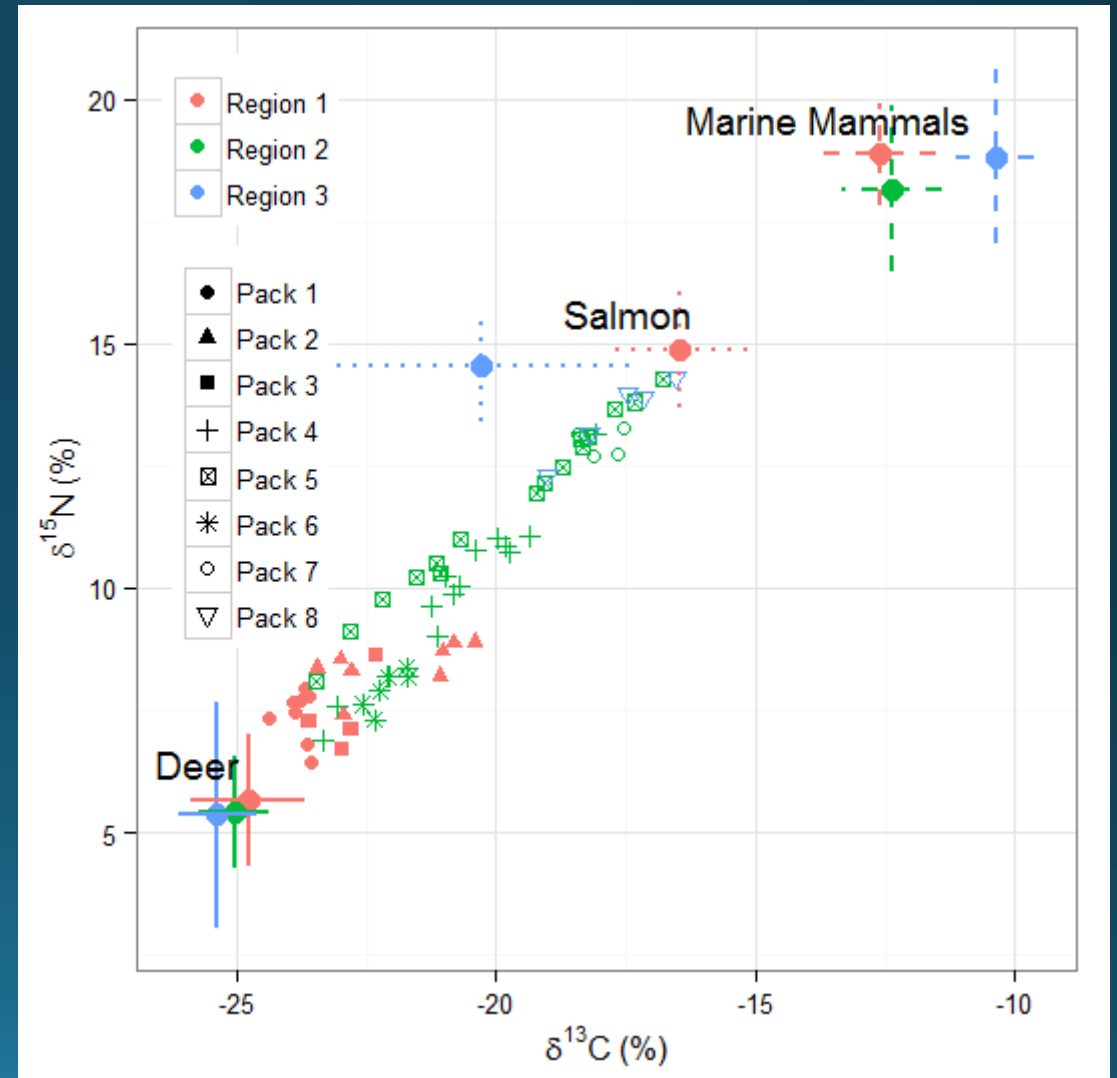
Does your source data vary by Pack? Yes No

Do you have Concentration Dependence data? 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



6) Source by factor

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 Concentration Dependence data? Yes No

Do you have raw source data, or source means and SDs?

OR

Yes `src_mu[,iso,Factor.1[i]],p.ind[i,])`

No `src_mu[,iso],p.ind[i,])`

7) Concentration dependence

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 Concentration Dependence data? 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

Yes

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

No

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

See Geese example

8) "Raw" or "means + SD"

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 Concentration Dependence data? Yes No

Do you have raw source data, or source means and SDs?

OR

"raw"

	d13C	d15N
Reef	-15.084	15.47462
Reef	-15.026	14.95905
Reef	-11.0315	13.70018
Reef	-15.171	15.18441
Reef	-15.2272	15.33783
Reef	-15.3472	15.67877
Reef	-15.9438	15.3765
Reef	-15.9573	15.21001
Reef	-14.9398	15.2757

⋮

See Palmyra example

8) "Raw" or "means + SD"

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 Concentration Dependence data? 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

"raw"

```
# uninformed priors on source means and precisions
for(src in 1:n.sources){
  for(iso in 1:n.iso){
    src_mu[src,iso] ~ dnorm(0,.001)
    src_tau[src,iso] ~ dgamma(.001,.001)
  }
}
```

See Palmyra example

8) "Raw" or "means + SD"

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 Concentration Dependence data? 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

"means + SD" (+ n)

	Region	Meand13(SDd13C	Meand15(SDd15N	n
Deer	1	-26.88 1.1	3.07 1.35	24
Deer	2	-27.15 0.67	2.8 1.14	37
Deer	3	-27.47 0.75	2.76 2.32	9
Salmon	1	-18.58 1.34	12.26 1.18	6
Salmon	2	-22.38 2.85	11.92 1.12	5
Salmon	3	-22.38 2.85	11.92 1.12	5
Marine M	1	-14.7 1.08	16.26 1.06	7
Marine M	2	-14.47 0.95	15.55 1.69	6
Marine M	3	-12.48 0.75	16.21 1.78	6

See Wolves example

8) "Raw" or "means + SD"

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 Concentration Dependence data? Yes No

Do you have raw source data, or source means and SDs?

Load raw source data OR Load source means and SDs

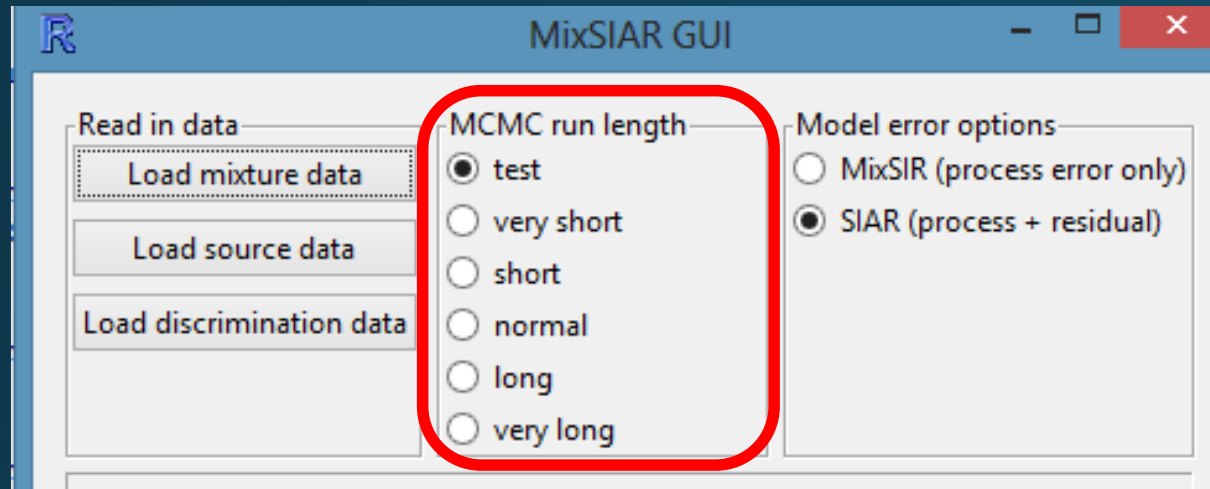
I'm finished

"means + SD" (+ n)

```
for(src in 1:n.sources){
  for(iso in 1:n.iso){
    src_mu[src,iso] ~ dnorm(MU_array[src,iso], n_array[src]/SIG2_array[src,iso]);
    tmp.X[src,iso] ~ dchisqr(n_array[src]);
    src_tau[src,iso] <- tmp.X[src,iso]/(SIG2_array[src,iso]*(n_array[src] - 1));
  }
}
```

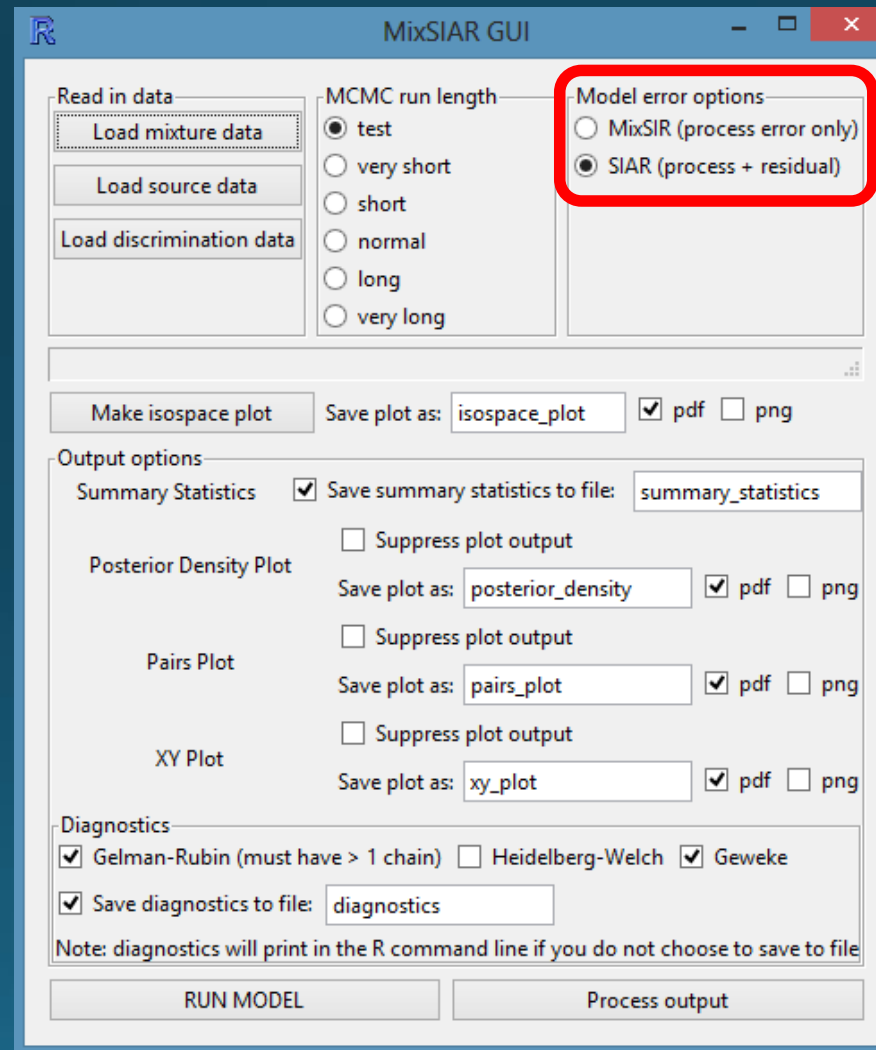
See Wolves example

9) MCMC parameters



```
run=="test") mcmc <- list(chainLength=1000, burn=500, thin=1, chains=3, calcDIC=TRUE)
run=="very short") mcmc <- list(chainLength=10000, burn=5000, thin=5, chains=3, calcDIC=TRUE)
run=="short") mcmc <- list(chainLength=50000, burn=25000, thin=25, chains=3, calcDIC=TRUE)
run=="normal") mcmc <- list(chainLength=100000, burn=50000, thin=50, chains=3, calcDIC=TRUE)
run=="long") mcmc <- list(chainLength=300000, burn=200000, thin=100, chains=3, calcDIC=TRUE)
run=="very long") mcmc <- list(chainLength=1000000, burn=700000, thin=300, chains=3, calcDIC=TRUE)
run=="extreme") mcmc <- list(chainLength=3000000, burn=2700000, thin=300, chains=3, calcDIC=TRUE)
!exists("mcmc")) mcmc <- run # if the user has entered custom mcmc parameters, use them
```

10) error structure



MixSIR
SIAR

10) error structure

LETTER

Incorporating uncertainty and prior information into stable isotope mixing models

Moore and Semmens (2008)

MixSIR

TECHNICAL COMMENT

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

Jackson et al. (2009)

TECHNICAL COMMENT

Improving Bayesian isotope mixing models: a response to Jackson *et al.* (2009)

Semmens et al. (2009)

SIAR

OPEN ACCESS Freely available online

 PLOS one

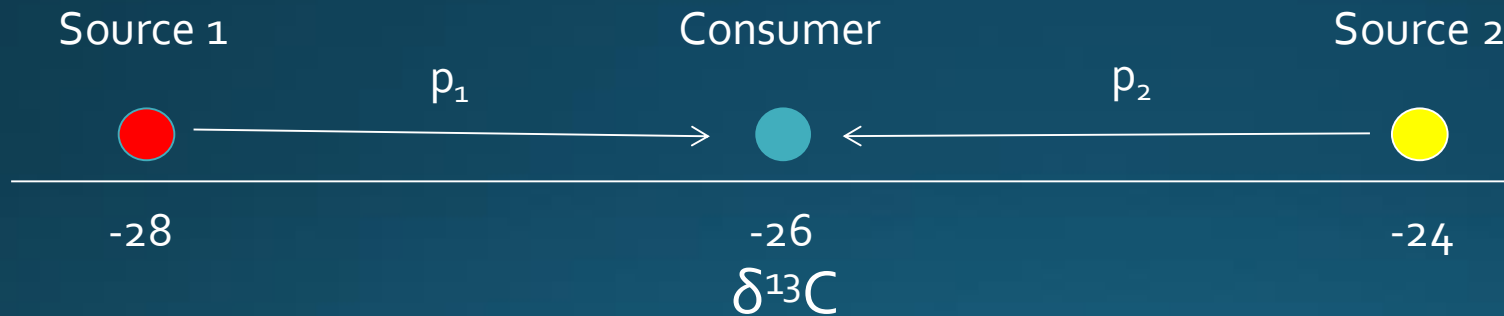
Source Partitioning Using Stable Isotopes: Coping with Too Much Variation

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

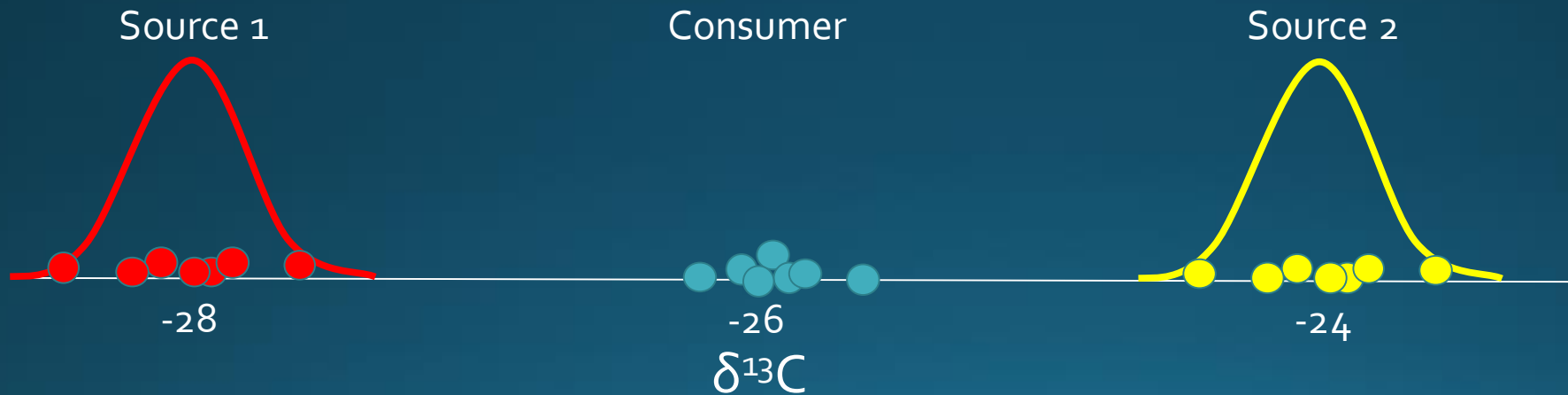
Parnell et al. (2010)

10) error structure

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



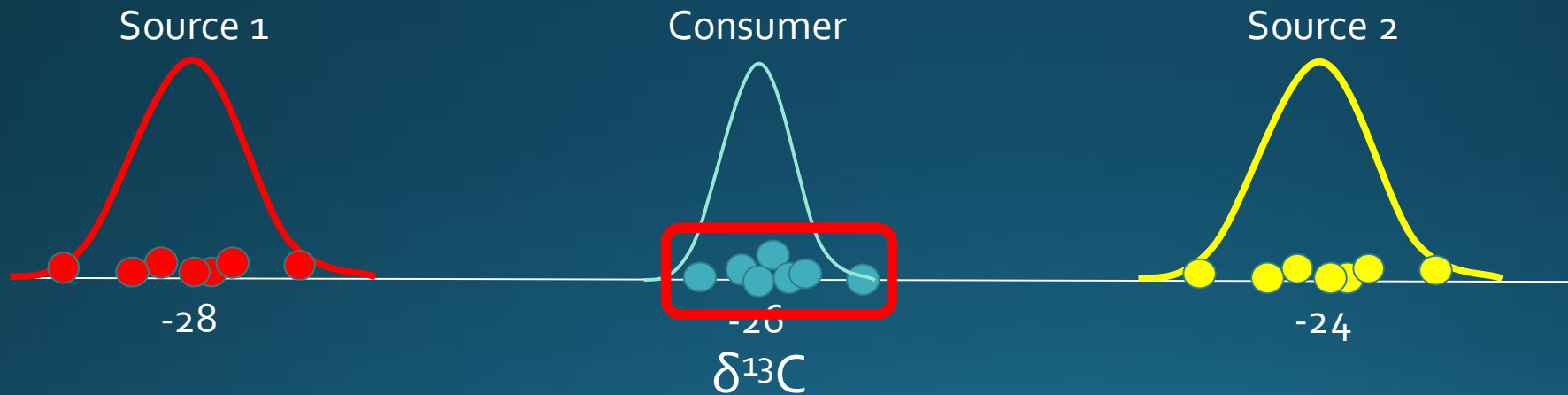
10) error structure



10) error structure

MixSIR

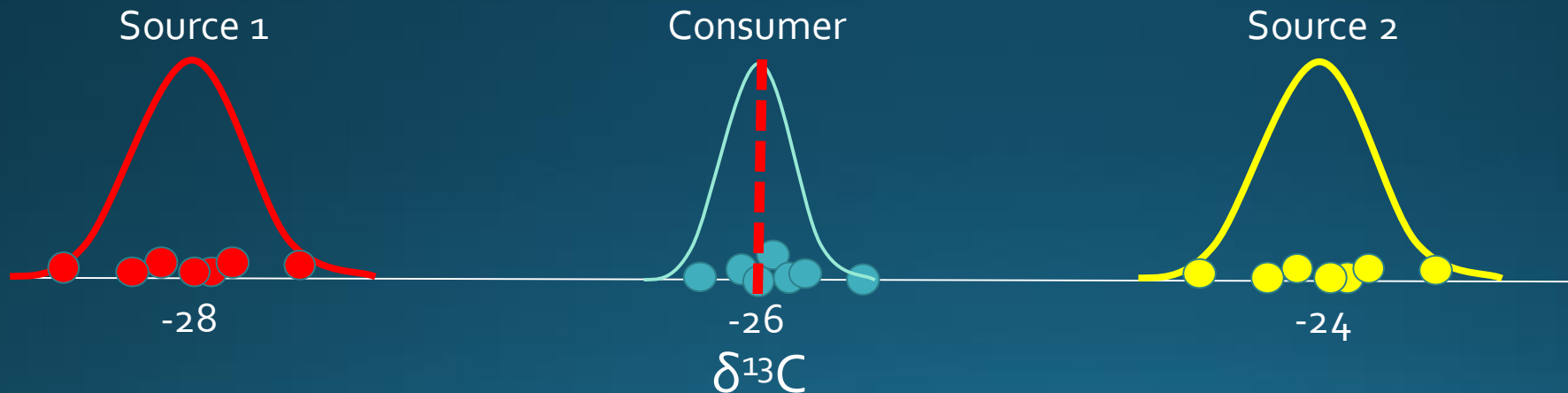
$$X_{ij} \sim N \left(\sum_{k=1}^K p_k (\mu_{jk} + \lambda_{jk}), \left[\sum_{k=1}^K p_k^2 (\omega_{jk}^2 + \tau_{jk}^2) \right] \right)$$



10) error structure

MixSIR

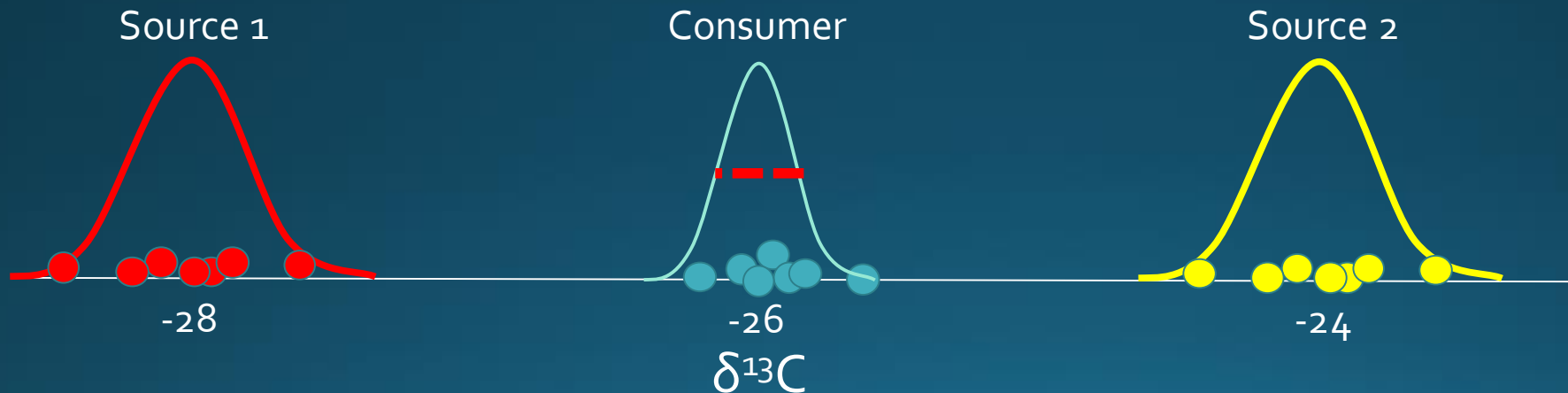
$$X_{ij} \sim N \left(\sum_{k=1}^K p_k (\mu_{jk} + \lambda_{jk}), \left[\sum_{k=1}^K p_k^2 (\omega_{jk}^2 + \tau_{jk}^2) \right] \right)$$



10) error structure

MixSIR

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

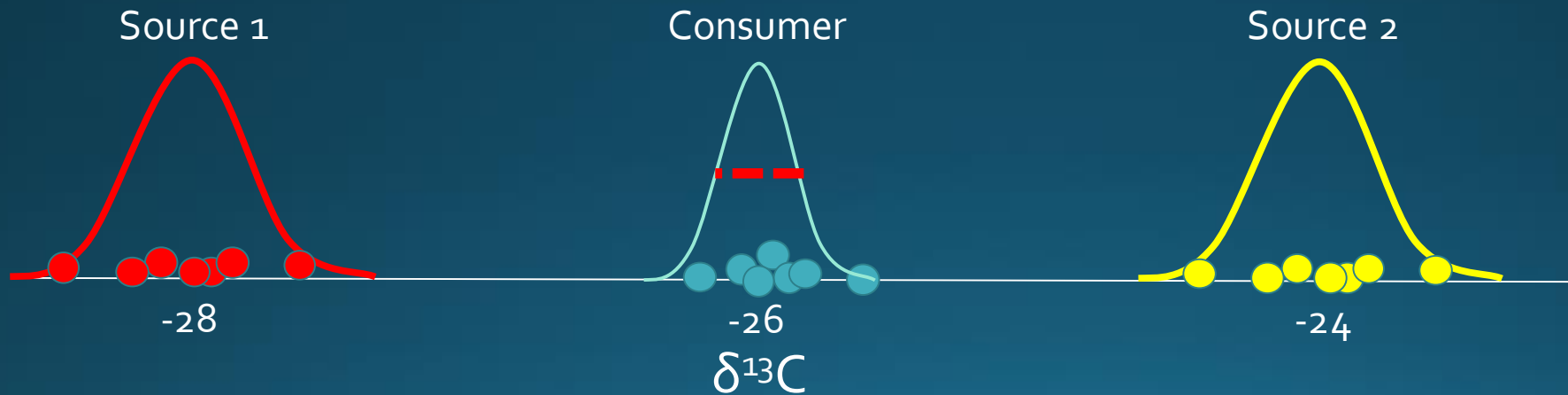


10) error structure

MixSIR

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

Medium variance

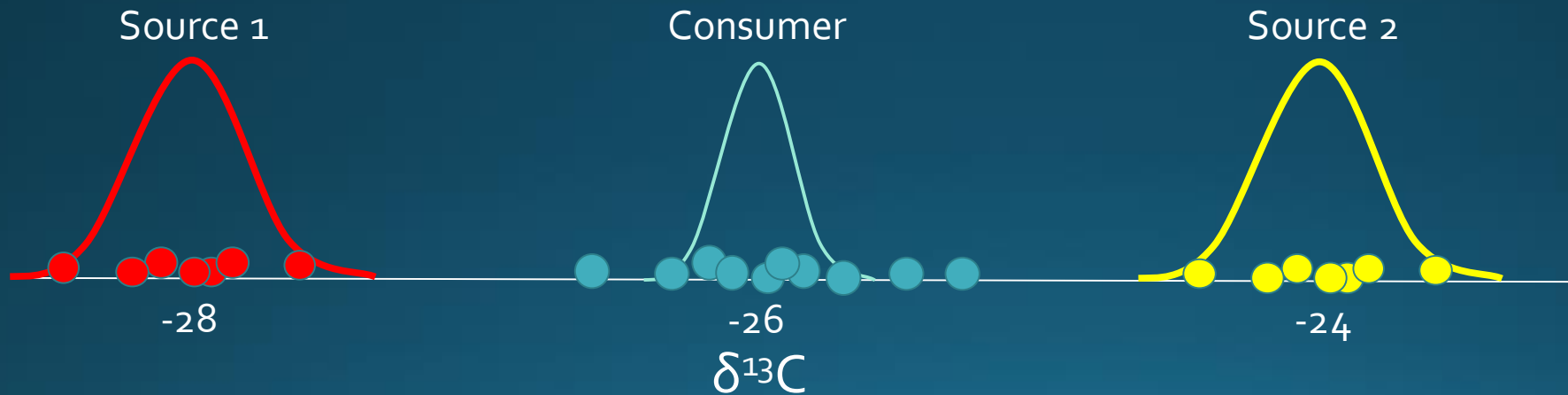


10) error structure

MixSIR

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

High variance

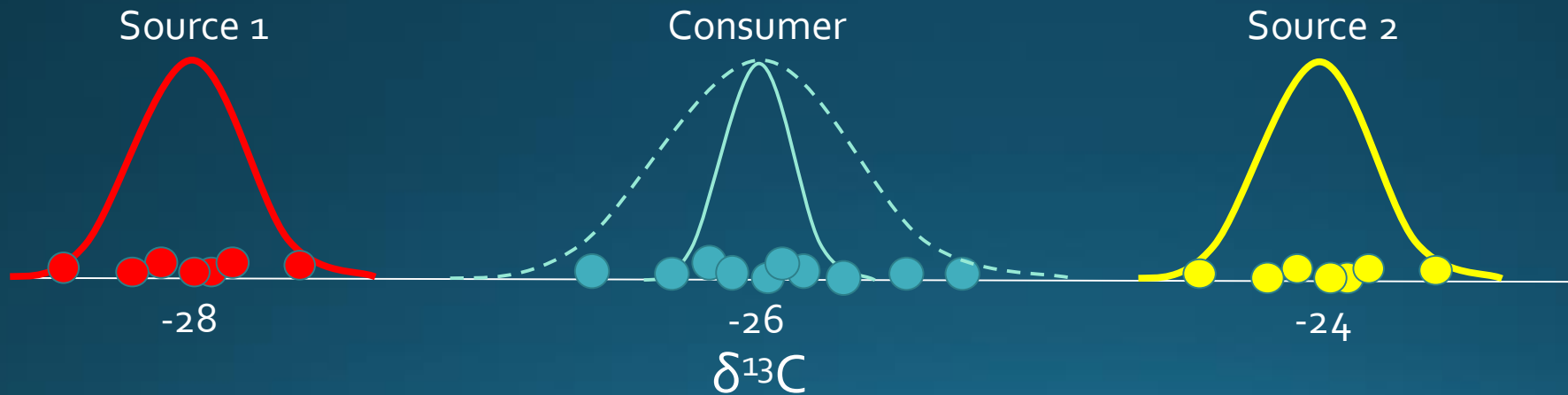


10) error structure

SIAR

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

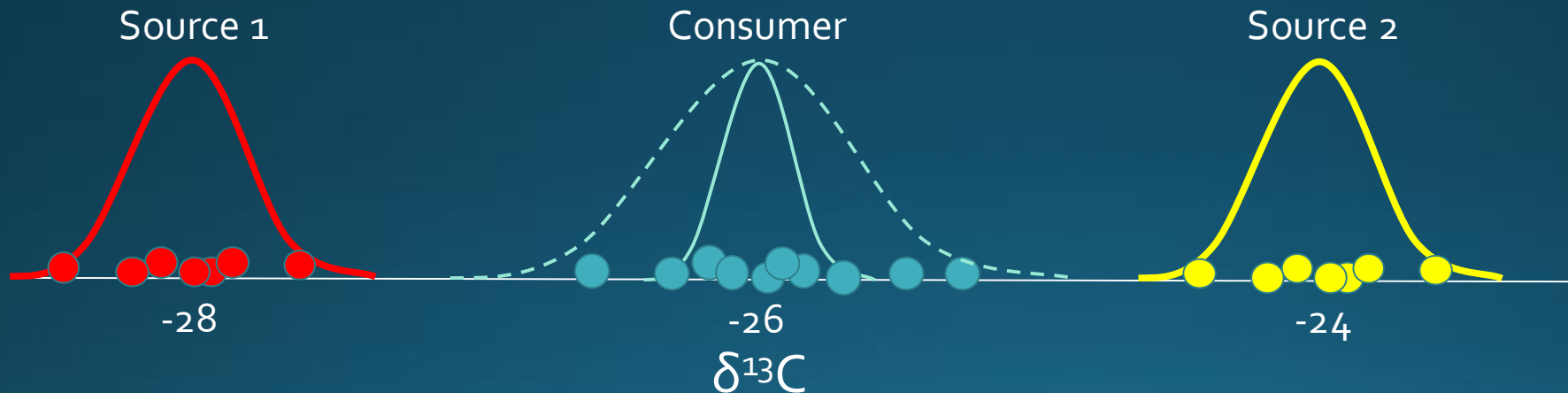
High variance



10) error structure

SIAR

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

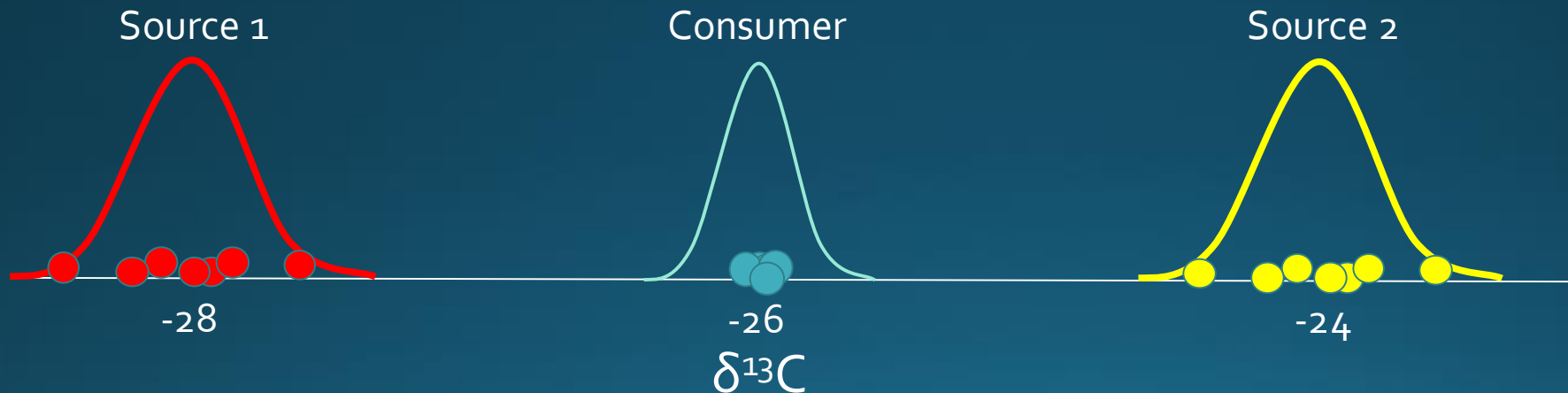


10) error structure

SIAR

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

Low variance



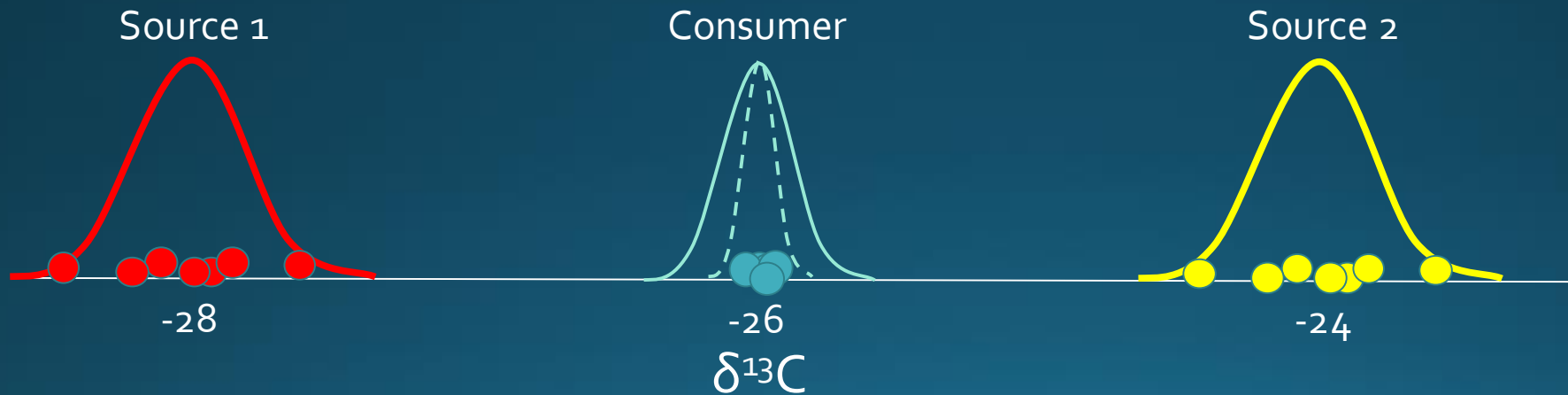
10) error structure

MixSIAR

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

Low variance

$$\epsilon < 1$$



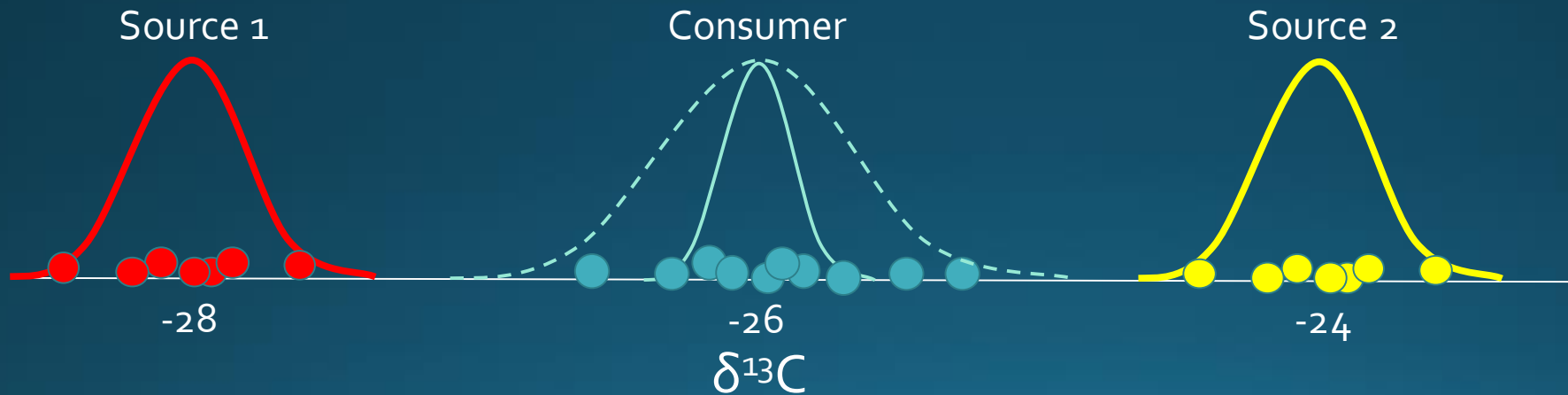
10) error structure

MixSIAR

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

High variance

$$\epsilon > 1$$



10) error structure

MixSIR	$\sigma^2_{\text{process}}$	
SIAR	$\sigma^2_{\text{process}} + \sigma^2_{\text{resid}}$	
MixSIAR	$\sigma^2_{\text{process}} * \epsilon$	(not yet)

Issues:

- Default = SIAR (+ residual)
- Do not include both SIAR error and "Indiv as RE"
 - *NOTE: must include "Indiv as RE" for continuous effect*
- MixSIR error may be slightly better than SIAR for small variance

Happy mixing!

b1stock@ucsd.edu