

→ Review workflow

Class tells me ↗

- 1) Model
2) Simdata ←
3) Prior PC
4) Real data
5) Retro PC
- Next: 2 reasons Step 2
(1) check code (R, Stan)
(2) understand your model given your data
- Also, it's a little toy model of your biological system. Yes. It should be that useful?

Ask Class: Examples where <sup>Reason 2 of 2</sup> would change how you approach your model or inference: (or, where you might make/see big changes between how you simulate for Reason 1 vs. 2)

$\sigma_y$  } atket design, inference

$n$

un-evenness in data

confounded grouping factors (study ID, spp.)

You may see these also at step 4 (when your model fails) but a) you mod sim. data to diagnose this b) you will get better at seeing these @ Step 2 w/ practice.

Retrodictive checks are the last way in our workflow to diagnose & fix model problems (mis-specification)

We looked at a hint of a retrodictive check last time: Group parameter posteriors by other factors not (yet?) in your model.

Now we'll do some 'proper' retrodictive (PPC) checks ← But nothing is spelled out in how you do Bayesian? 'proper'

Recall from Step 2: I set parameters:

$$\hat{y}_i = \alpha + \beta ; y_i \sim \text{normal}(\hat{y}_i, \sigma_y)$$

↑
3

↑
0.5

↑
0.2

MODEL OUTPUT sets your values

For Step 5, you DRAW THESE FROM POSTERiors (or could take pt. estimates but why do that?)



Draw a sample of all parameters from one iteration.

& then, everything else your simulated data.

CAN be the same from

⇒ Exercise: Make one new  $y_i$  from your model. \*

in hierarchical ⇒ retrocheck start. R

[After this exercise] could discuss LATER

When might you change from your simulated data?

- more  $n$
- forecasting

for retrodictive checks we stick w/ data structure similar to ours in model But we can do these things w/ our model output (Lynch et al. 2024)

LATER

[Could ask: Is me draw enough? What else could we do?]

But me draw from your posterior is NOT a good representation of a posterior. You need to draw from your posterior samples (grab multiple iterations).

Once you do this you can't just look at your me new  $\hat{y}$  rep

You need summaries usually. Shiny Stan gives

- $\hat{y}_{mean}$
- $\hat{y}_{max}$
- $\hat{y}_{min}$

Which ones are relevant?

Useful?  
Relevant?  
Depends on question.

Ask Class!

Other options  $\Rightarrow$

Returning to workflow: Things you often see may be wrong in retrodictive checks:

- Wrong error (ordinal or such instead of Gaussian)

$$y_i \sim \text{normal}(\hat{y}, \sigma_y)$$

- Missing grouping factors

Side Note: You won't see when study & sp. hier. struct. is wrong w/out specific retrodictive checks to look at.

$\rightarrow$  Or just compare data to estimates from no pool models.

(at end of retrochecks)

Now, return to LATER at top of page  $\uparrow$