Introduction to hierarchical (mixed-effects) models

FW 891

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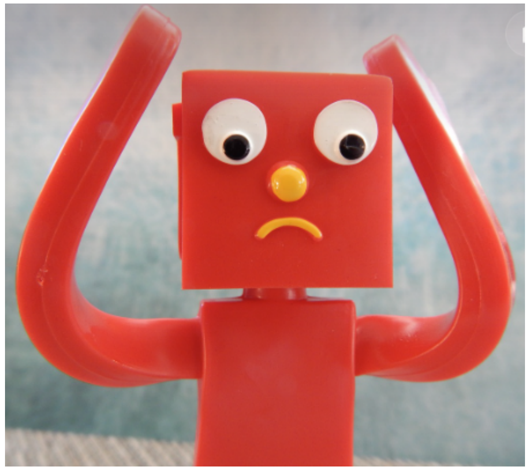
Purpose

- Introduce an important extention of all previous models
  - Will have several lectures on mixed effects models
- An example
  - both frequentist and Bayesian
  - Explain in words and algebra what mixed effects models are
- Pros and cons of mixed effects modeling
- Why these models likely deserve to be the default approach to many problems

The polyonomous model (misery)

- These models are known by many names:
  - Mixed effects models (fixed effects + random effects)
  - Multilevel models
  - Hierarchical models
  - Partial-pooling models
- Our example model might also be called:
  - Random-intercepts model



Kery and Schaub 2012; McElreath 2023

An example to get things started

image credit

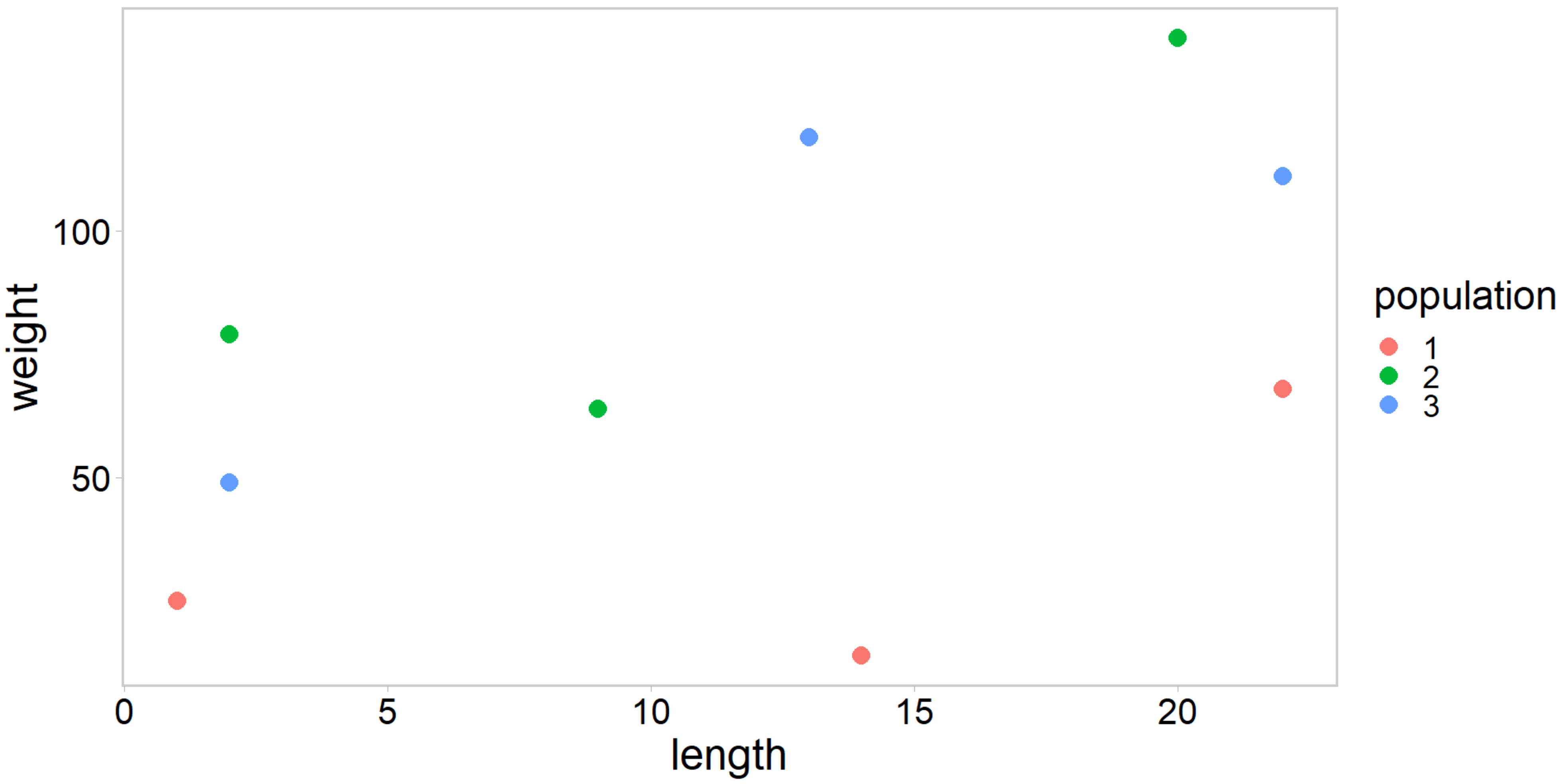
An example to get things started

- Revisiting the ANCOVA example, but let’s change the variable names
  - Plot the weight of emperor scorpions as a function of length

```r
library(tidyverse)
library(ggqfc)
weight <- c(25, 14, 68, 79, 64, 139, 49, 119, 111) # obs
population <- factor(c(1, 1, 1, 2, 2, 2, 3, 3, 3)) # group
length <- c(1, 14, 22, 2, 9, 20, 2, 13, 22)        # covariate
my_df <- data.frame(weight, population, length)

my_df %>%
  ggplot(aes(length, weight, color = population)) +
  geom_point(pch = 16, size = 3.5) + theme_qfc()
```

An example to get things started



- What does this plot suggest?

An example to get things started

- Linear relationship between weight and length
    - Perhaps with a different intercept for each population?
    - Regression model should account for population differences
- The simplest way to account for population differences:

$$\text{weight}_i = \alpha_{j(i)} + \beta \cdot \text{ length }_i + \varepsilon_i$$
$$\varepsilon_i \sim \text{Normal}\left(0, \sigma^2\right)$$

- Weight of scorpion *i* depends on length in a linear way, where each population *j* has a different intercept, and residuals come from a zero-mean normal distribution

Motivating random effects

- Independent intercepts for each population represents one assumption that we might make about the data
- **Assumption 1: No Pooling**: these are the only three populations we are interested in (no pooling; estimate each α_j separately)

see Gelman and Hill 2007; Kery and Schaub 2012

Motivating random effects

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- **Assumption 1: No Pooling**: these are the only three populations we are interested in (no pooling; estimate each α_j separately)
- **Assumption 2: Complete Pooling**: we think these actually represent one population (complete pooling; estimate one α across all three populations)

see Gelman and Hill 2007; Kery and Schaub 2012

Motivating random effects

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- **Assumption 2: Complete Pooling**: we think these actually represent one population (complete pooling; estimate one α across all three populations)
- **Assumption 3: Partial Pooling**: these populations merely represent a sample from a larger number of scorpion populations that we could have studied and we want our conclusions to generalize to this larger universe of statistical populations (hierarchical, partial pooling; model parameters are viewed as a sample from a population distribution)

see Gelman and Hill 2007; Kery and Schaub 2012

Translating assumption 1 to math

- No pooling:

$$
\begin{aligned}
&\text{weight}_i = \alpha_{j(i)} + \beta \cdot \text{ length }_i + \varepsilon_i \\
&\varepsilon_i \sim \text{Normal}\left(0, \sigma^2\right)
\end{aligned}
$$

Translating assumption 2 to math

- Complete pooling:

$$\text{weight}_i = \alpha + \beta \cdot \text{length}_i + \varepsilon_i$$
$$\varepsilon_i \sim \text{Normal}(0, \sigma^2)$$

- This is literally just a linear regression with one intercept and one slope

Translating assumption 3 to math

- Hierarchical, partial pooling:

$$\text{weight}_i = \alpha_{j(i)} + \beta \cdot \text{ length }_i + \varepsilon_i$$
$$\varepsilon_i \sim \text{Normal}\left(0, \sigma^2\right)$$
$$\alpha_j \sim \text{Normal}\left(\mu_\alpha, \sigma_\alpha^2\right). \qquad \text{This line makes } \alpha_j \text{ random!}$$

- Third equation is the *only* difference between a model that treats α_j as a fixed effect (assumption 1) and one where α_j is a random effect (assumption 3)

Kery and Schaub 2012

Translating assumptions 1-3 to R code (Frequentist)

```r
# ass. 1 - no pooling
fit_no <- lm(my_df$weight ~ my_df$population - 1 + my_df$length)

# ass. 2 - complete pooling:
fit_complete <- lm(my_df$weight ~ 1 + my_df$length)

# ass. 3 - partial pooling:
library(lme4)
fit_partial <- lmer(my_df$weight ~ 1 + my_df$length + (1|my_df$population))
```

- Don't worry about the computational details underlying how `lmer()` is estimating the random effects

Compare the models (Frequentist)

```r
AIC(fit_no)
```

```
[1] 88.22643
```

```r
AIC(fit_complete)
```

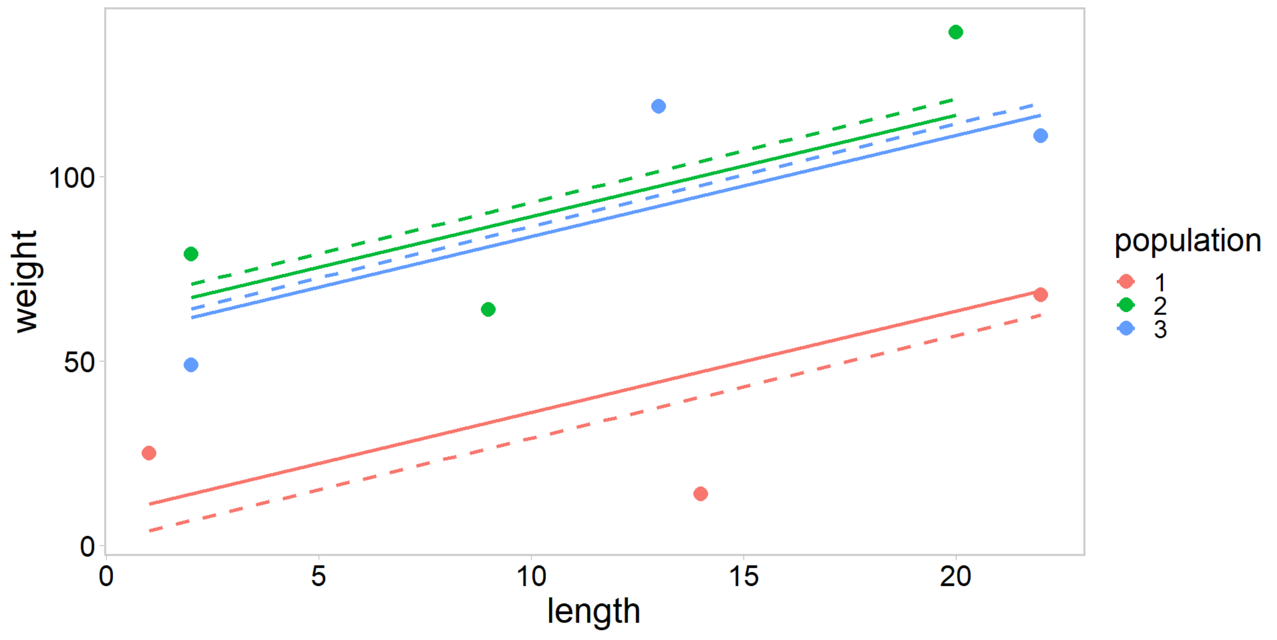
```
[1] 95.11368
```

```r
AIC(fit_partial)
```

```
[1] 85.08788
```

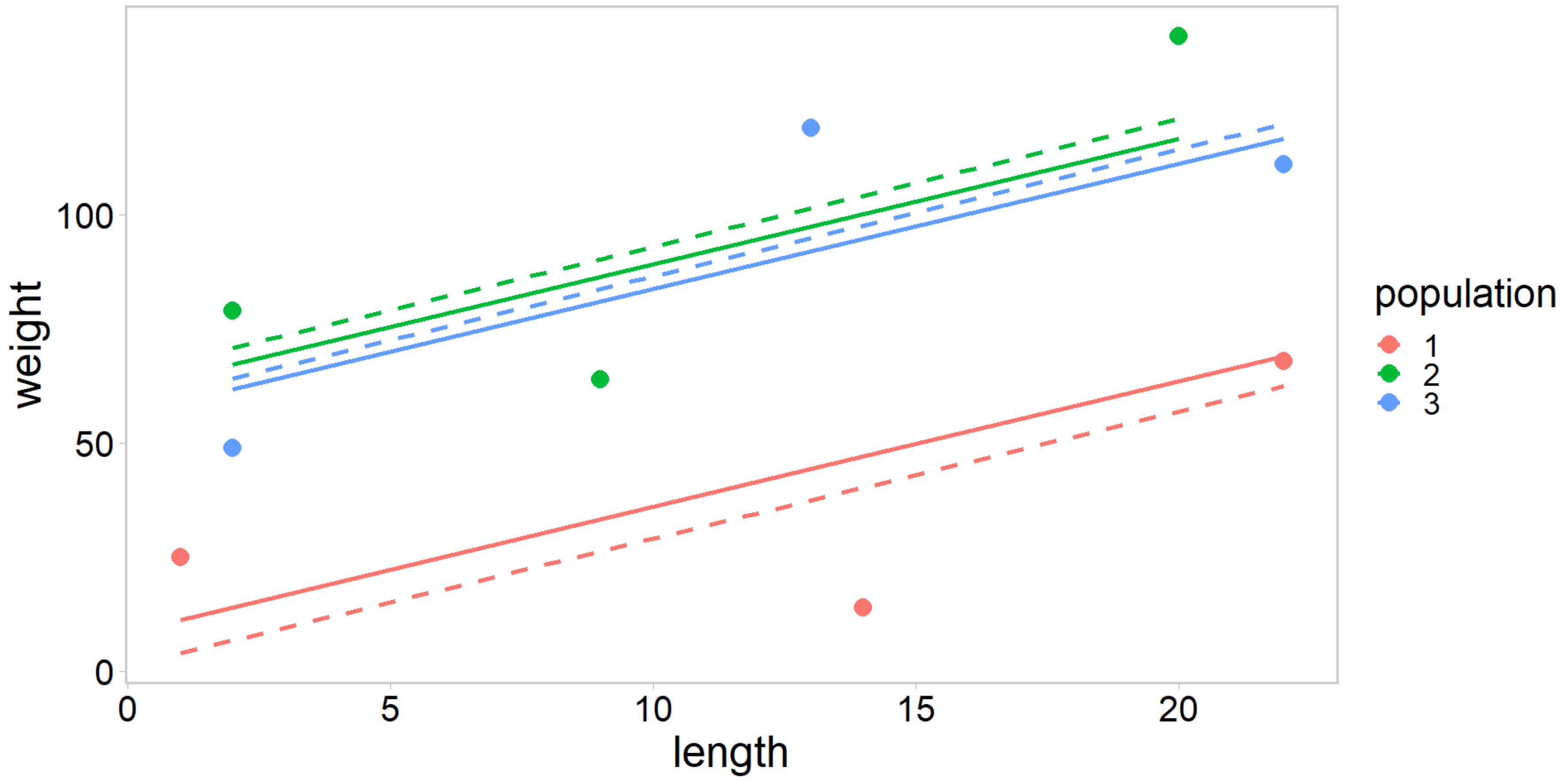
Plot no pooling vs. partial pooling

```r
my_df$pred_no <- predict(fit_no, newdata = my_df)
my_df$pred_partial <-  predict(fit_partial, newdata = my_df, level = 0)
my_df %>%
  ggplot(aes(length, weight, color = population)) +
  geom_point(pch = 16, size = 3.5) +
  geom_line(data = my_df, aes(y = pred_no), size = 1, lty = 2) +
  geom_line(data = my_df, aes(y = pred_partial), size = 1) +
  theme_qfc()
```



What is going on here?

- Solid lines are from mixed-effects model with partial pooling, dashed lines are from ANCOVA with no pooling



Another example of shrinkage

- county-level radon levels

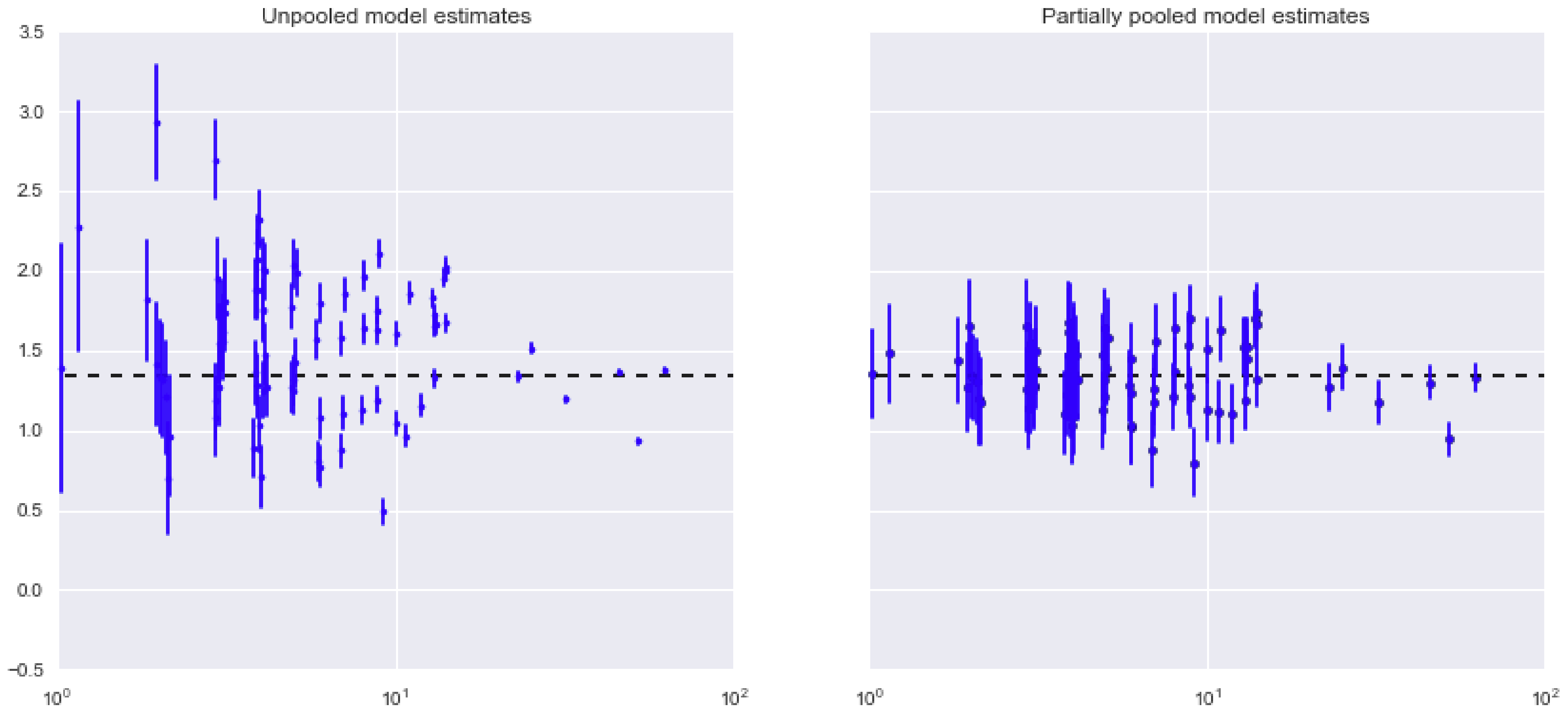
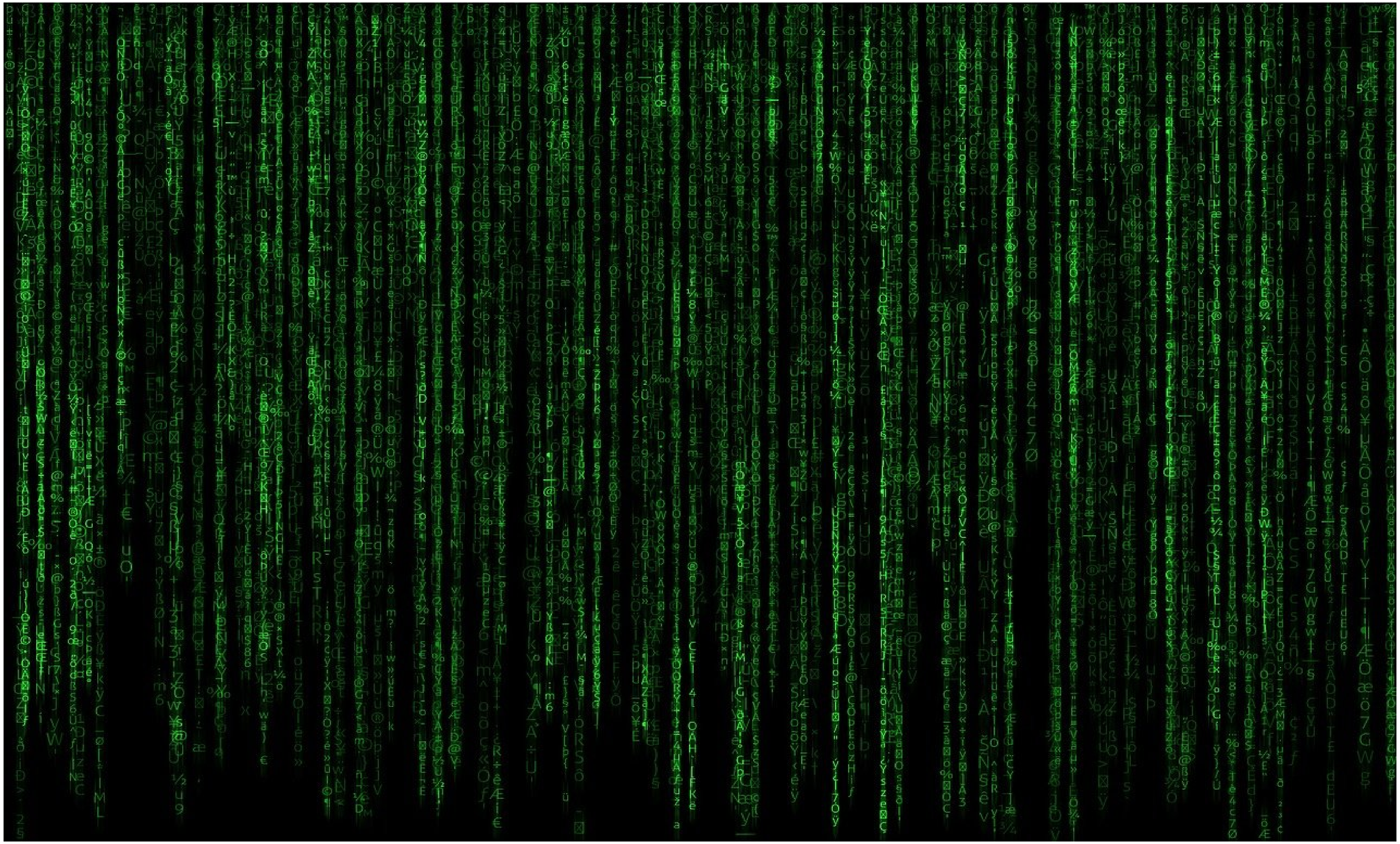


image credit

Let's build the scorpion model in Stan



Math for the random intercepts model

- Hierarchical, partial pooling:

$$\text{weight}_i = \alpha_{j(i)} + \beta \cdot \text{ length }_i + \varepsilon_i$$
$$\varepsilon_i \sim \text{Normal}\left(0, \sigma^2\right)$$
$$\alpha_j \sim \text{Normal}\left(\mu_\alpha, \sigma_\alpha^2\right). \qquad \text{This line makes } \alpha_j \text{ random!}$$

- Third equation is the *only* difference between a model that treats α_j as a fixed effect (assumption 1) and one where α_j is a random effect (assumption 3)

Kery and Schaub 2012

Stan code for the random intercepts model

```stan
data {
  int<lower=0> n;
  vector[n] weights;
  array[n] int population;
  vector[n] lengths;
}
parameters {
  real mu_alpha;
  vector[3] alpha_j;
  real<lower=0> sd_alpha;
  real b1;
  real<lower=0> sd_obs;
}
// more code below
```

Stan code for the random intercepts model

```
//... see code on previous slide
model {
  vector[n] w_preds;
  mu_alpha ~ normal(50, 15);                // hyper prior
  sd_alpha ~ normal(0, 100);                // hyper prior
  alpha_j ~ normal(mu_alpha, sd_alpha);     // hyper distribution
  b1 ~ normal(0, 10);                       // slope
  sd_obs ~ normal(0, 25);                   // likelihood error term
  for(i in 1:n){
    w_preds[i] = alpha_j[population[i]] + b1*lengths[i];
  }
  weights ~ normal(w_preds, sd_obs);        // likelihood
}
```

Compiling the Stan model

```r
library(cmdstanr)
mod <- cmdstan_model("src/random_ints.stan")
stan_data <- list(
  n = length(weight),
  weights = weight,
  population = population,
  lengths = length
)

inits <- function() {
  list(
    mu_alpha = 50,
    sd_alpha = 30,
    alpha_j = rep(0, 3),
    b1 = 10,
    sd_obs = 10
  )
}
```

Running that hawg 🐷 🐖 🐽

```r
fit <- mod$sample(
  data = stan_data,
  init = inits,
  seed = 1,
  chains = 4,
  iter_warmup = 1000,
  iter_sampling = 1000,
  parallel_chains = 4,
  refresh = 0,
  adapt_delta = 0.9999, # look here
  step_size = 1e-3      # look here
)
```

```
Running MCMC with 4 parallel chains...

Chain 1 finished in 0.6 seconds.
Chain 2 finished in 0.7 seconds.
Chain 3 finished in 0.7 seconds.
Chain 4 finished in 0.7 seconds.

All 4 chains finished successfully.
Mean chain execution time: 0.7 seconds.
Total execution time: 0.9 seconds.
```

Check the diagnostics (quick and dirty)

```
fit$cmdstan_diagnose()
```

```
Processing csv files: C:/Users/Chris/AppData/Local/Temp/RtmpigUBGr/random_ints-202310291723-1-
5a4d0e.csv, C:/Users/Chris/AppData/Local/Temp/RtmpigUBGr/random_ints-202310291723-2-5a4d0e.csv,
C:/Users/Chris/AppData/Local/Temp/RtmpigUBGr/random_ints-202310291723-3-5a4d0e.csv,
C:/Users/Chris/AppData/Local/Temp/RtmpigUBGr/random_ints-202310291723-4-5a4d0e.csv

Checking sampler transitions treedepth.
Treedepth satisfactory for all transitions.

Checking sampler transitions for divergences.
5 of 4000 (0.12%) transitions ended with a divergence.
These divergent transitions indicate that HMC is not fully able to explore the posterior
distribution.
Try increasing adapt delta closer to 1.
If this doesn't remove all divergences, try to reparameterize the model.

Checking E-BFMI - sampler transitions HMC potential energy.
E-BFMI satisfactory.

Effective sample size satisfactory.
```

Pluck out the posterior summaries and compare to `lmer()`

```
fit$summary("alpha_j")                           # Bayesian
```

```
# A tibble: 3 × 10
  variable     mean median    sd   mad    q5   q95  rhat ess_bulk ess_tail
  <chr>       <num>  <num> <num> <num> <num> <num> <num>    <num>    <num>
1 alpha_j[1]   7.66   7.41  22.0  20.1 -27.5  44.7  1.00    1355.    1353.
2 alpha_j[2]  59.8   60.5   19.9  18.4  26.9  91.2  1.00    1435.    1595.
3 alpha_j[3]  54.9   55.1   20.3  18.4  20.7  85.8  1.00    1069.    1432.
```

```
coef(fit_partial)$`my_df$population`[,1]     # frequentist
```

```
[1]  8.650009 61.667157 56.276072
```

- Pretty similar estimates (small sample size)
- You have now fitted a Bayesian hierarchical model

Pluck out the posterior summaries and compare to `lmer()`

```r
fit$summary("b1")            # Bayesian
```

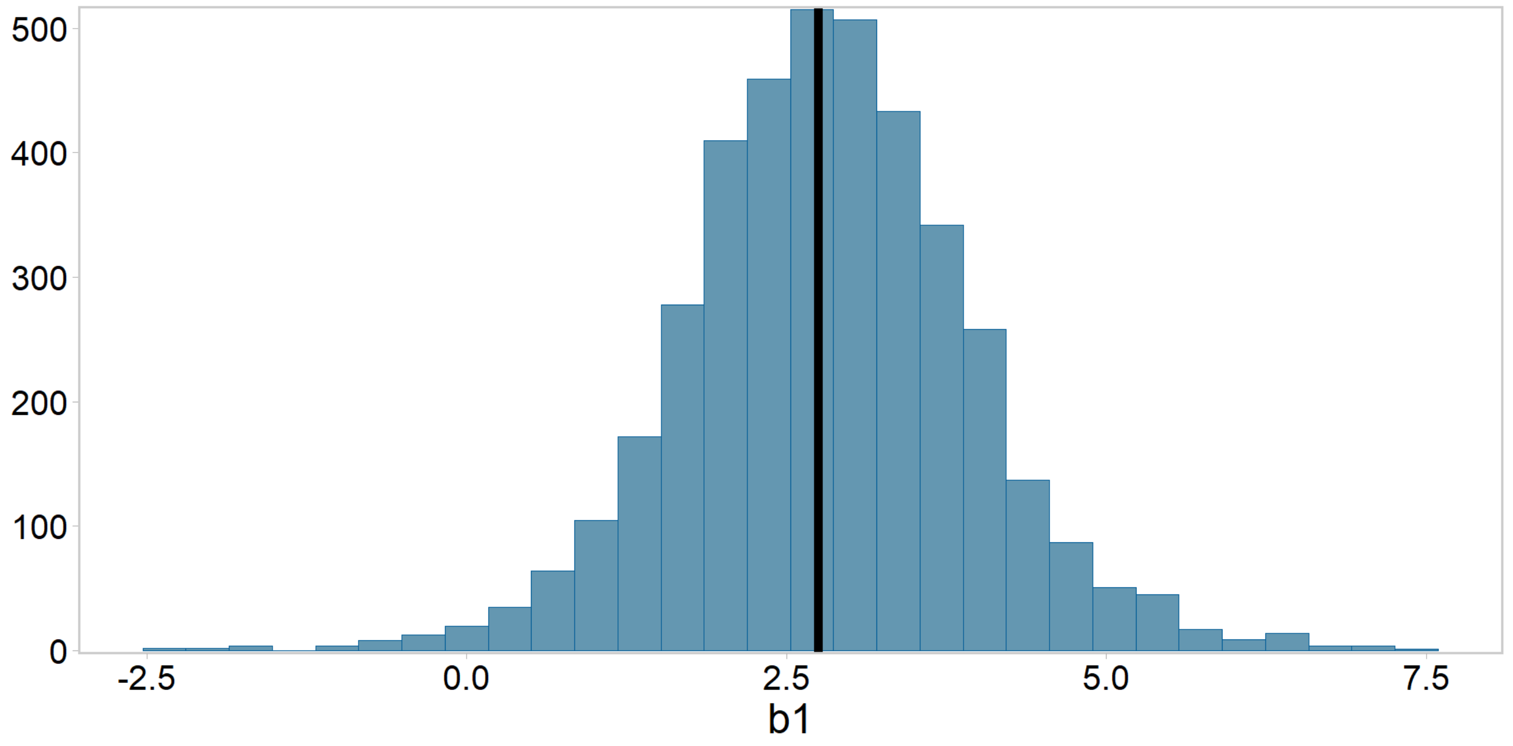
```
# A tibble: 1 × 10
  variable  mean median    sd   mad    q5   q95  rhat ess_bulk ess_tail
  <chr>    <num>  <num> <num> <num> <num> <num> <num>    <num>    <num>
1 b1        2.82   2.80  1.13  1.04  1.01  4.67  1.00    1132.    1588.
```

```r
fixef(fit_partial)[2]     # frequentist
```

```
my_df$length
    2.744955
```

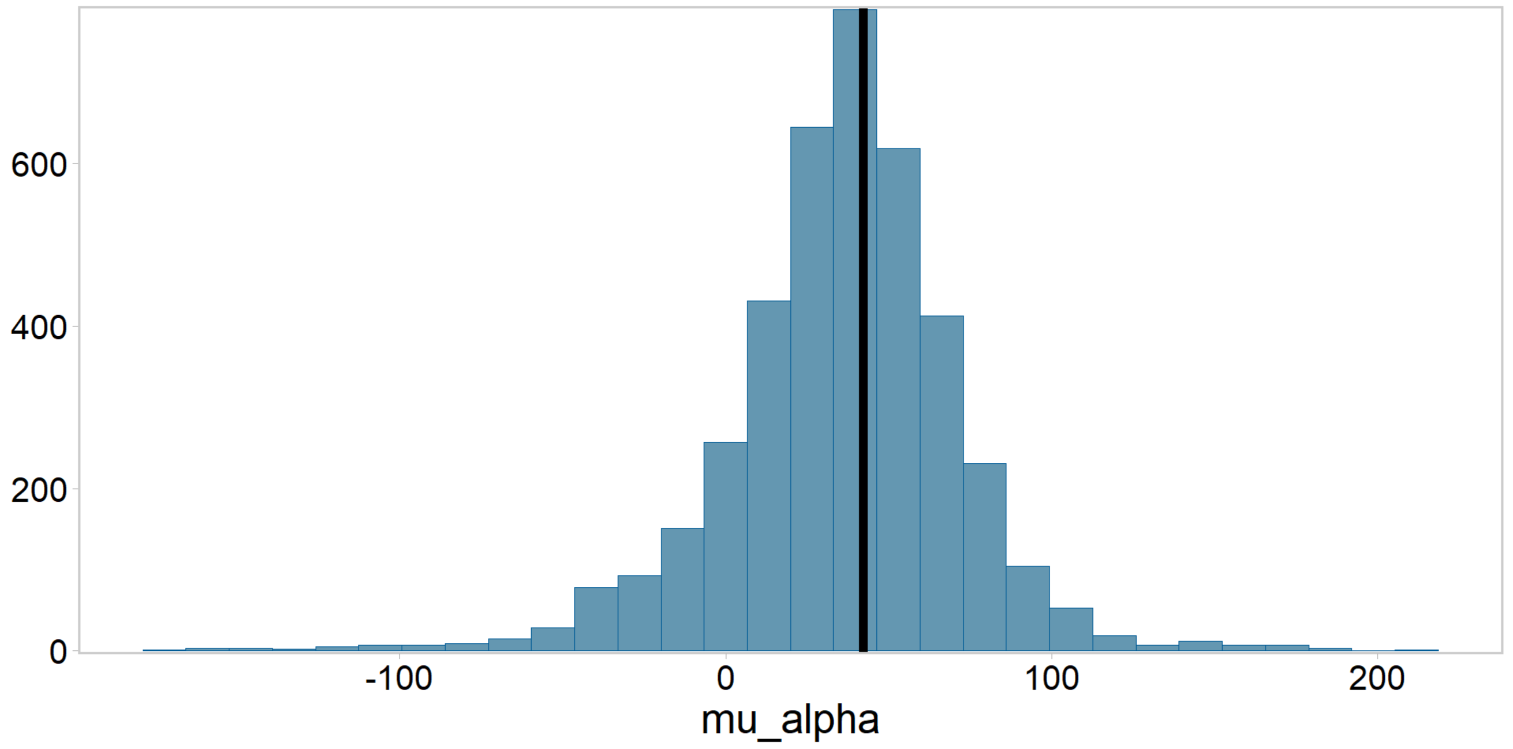
Posterior for β_1 vs. frequentist estimate

```r
library(bayesplot)
posterior <- fit$draws(format = "df")
color_scheme_set("blue")
p <- mcmc_hist(posterior, par = "b1")
p + geom_vline(xintercept = fixef(fit_partial)[2], lwd = 2) + theme_qfc()
```



Posterior for μ_α vs. frequentist estimate

```r
library(bayesplot)
posterior <- fit$draws(format = "df")
color_scheme_set("blue")
p <- mcmc_hist(posterior, par = "mu_alpha")
p + geom_vline(xintercept = fixef(fit_partial)[1], lwd = 2) + theme_qfc()
```



This was meant to be an ‘easy’ example for a reason

- Probably too few groups (usually want 5-10)
    - Obviously we can do it, but likely means our priors are more influential
- I had to fiddle with this a bit to get it to behave
    - Also low sample size within groups
- This likely explains at least some of the discrepancy among methods

What is a random effect (words)

- Two or more effects or parameters that “belong together” in some way
  - e.g., originating from some common distribution
  - sometimes called “latent variables,” may not be observable
- Bayesians put prior probabilities on all unknown quantities, MCMC
- Frequentists remove random effects from the model via numerical integration
- Exchangeability as a key assumption
  - Ordering of the random effects doesn’t matter

Royle and Dorazio 2008; Kery and Schaub 2012

The distribution of random effects

- Called the hyperdistribution
- The parameters of the random effects distribution are called hyperparameters
  - The priors of the hypperparameters are called hyperpriors
- No rule against more than one level (i.e., we could have hyper-hyperparameters etc.)
- Key point is to note the hierarchy of effects
- Typically random effects are continuous in ecology
  - however see occupancy models or binomial mixture models

Royle and Dorazio 2008; Kery and Schaub 2012

Benefits of hierarchical modeling

- Sounds dope, also scares a lot of people
- *de facto* standard for modern ecological analyses
- Helps you draw (statistical) universe-level inferences if you have a good experimental design
- Borrowing information via a hyperprior
  - Robin-Hooding (see Punt et al. 2011)
- Helps safeguard against overfitting

Some reasons we might use mixed effects models

- To adjust for repeat sampling
- To adjust estimates for imbalanced sampling
- To study variation among groups
- To partition variation among groups
- Borrow information

Royle and Dorazio 2008; Kery and Schaub 2012; McElreath 2023

Some reasons we might use mixed effects models

- Avoiding pseudoreplication
- Improving scope of inference
- To avoid averaging
- Improve understanding
  - Many common classes of models can be reformulated as hierarchical models
- McElreath (2023) argues mixed effects methods should be the default for many modeling problems

Royle and Dorazio 2008; Kery and Schaub 2012; McElreath 2023

Drawbacks of hierarchical modeling?

Why treat any parameter as fixed?

- Treating a factor with very few levels as random results in very imprecise estimates of the hyperparameter
    - Rarely treat factors with fewer than 5-10 levels as random (however see Gelman 2005)
- Assumption of exchangeability may not hold, particularly if groups differ in some systematic way

Hierarchical modeling as a philosophical middle ground

- Berliner (1966) offered a definition of hierarchical models based on sub-models and inference from a joint probability distribution:

$$[data|process, parameters][process|parameters][parameters]$$

- observation model component
- process model component
- assumptions about parameters
- A key point:

Berliner 1996; Royle and Dorazio 2008

Hierarchical modeling as a philosophical middle ground

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  - Hierarchical models admit observation error, conditioned on some (underlying) ecological process of interest and your prior assumptions

Berliner 1996; Royle and Dorazio 2008

Hierarchical modeling as a philosophical middle ground

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$$[data|process, parameters][process|parameters][parameters]$$

- observation model component
- process model component
- assumptions about parameters
- A key point:
  - Hierarchical models admit observation error, conditioned on some (underlying) ecological process of interest and your prior assumptions
- Whenever possible, prefer a hiearchical model based on an explicit ecological process

Berliner 1996; Royle and Dorazio 2008

Summary and outlook

- Many names for the same general type of model
- Shrinkage as a key concept, which is related to the phrase “partial pooling”
- The difference between fixed effects and random effects, at least for this simple example
- A powerful framework for decomposing complex problems into manageable subcomponents/models
- Many important extentions to this simple model

References

- Berliner, L. M. 1996, Hierarchical Bayesian time series models”, Maximum Entropy and Bayesian Methods, 15-22.
- Gelman and Hill 2007. Data analysis using regression and multilevel models
- Royle and Dorazio 2008. Hierarchical modeling and inference in ecology.
- Kery and Schaub. 2012. Bayesian Population Analysis using WinBUGS. Chapter 3
- McElreath 2023. Statistical Rethinking. Second Edition, Chapters 2 and 9.
- Punt et al. 2011. Among-stock comparisons for improving stock assessments of data-poor stocks: the “Robin Hood” approach. ICES Journal of Marine Sci.

Exercises (optional)

1. **Prior sensitivity test and model evaluation**

It is always good to think critically about model fit. Check the sensitivity of your estimates to the priors used in the sripts, and conduct standard model evaluations. Report your findings.

2. **Derived parameters**

A biologist wants to know whether scorpions in populations 2 and 3 are “different” in some way. Kick out the difference between α_{pop_2} and α_{pop_3} as a derived variable. Calculate the $\Pr(\alpha_{pop_2} > \alpha_{pop_3})$ and report this information back to your biologist friend.

3. **Hyperdistributions**

The hyperdistribution contains information on the among-group variability in scorpion weight-length relationship intercept terms. Generate a posterior predictive hyperdistribution for α_{pop} and plot it to examine the uncertainty we might expect if we were to measure scorpions from an entirely new population (but was otherwise similar to our original three populations)