

Chapter 3

Chapter Precap

- Introduce the concept of a regression model and explain what makes a regression model ‘Bayesian’.
- We discuss posterior and prior probabilities.
- Introduce `brms`, an R package that can be used to fit Bayesian regression models using the Stan programming language.
- We fit an ‘intercept-only’ Bayesian regression model and present topics related to model fitting such as thinning, chains, and iterations
- We outline the interpretation of the `brm` model print statement and introduce the concepts of errors and residuals.

Regression Models

- Very vague and general concept.
- General definition: Models that help you predict the value some parameter (e.g., μ) for a probability distribution using a combination of predictor variables.
- Often, the predictors are linearly combined but don't have to be.

Normal Regression Models

- Here's a general summary of the concepts underlying a regression that assumes normally distributed errors:
 - You have a variable you are interested in, y .
 - You assume that the random variation around the mean (μ) is normally distributed.
 - You assume the random variation (the error) has a mean of 0 and a standard deviation of σ .

$$y[i] \sim N(\mu, \sigma) \qquad y[i] = \mu + N(0, \sigma)$$

Predicting Variation in μ

- The mean of this distribution may vary systematically.
- Variation in the mean can be understood using some predictor variables.
- Regression is a tool for modeling these relations.

$$\mu = x_1 + x_2 + x_3$$

$$\mu_{[i]} = x_{1[i]} + x_{2[i]} + x_{3[i]}$$

$$\mu_{[i]} = \alpha_1 \cdot x_{1[i]} + \alpha_2 \cdot x_{2[i]} + \alpha_3 \cdot x_{3[i]}$$

Regression Models

$$y[i] = \mu + \mathbf{N}(0, \sigma)$$



$$\mu[i] = \alpha_1 \cdot x_1[i] + \alpha_2 \cdot x_2[i] + \alpha_3 \cdot x_3[i]$$


$$y[i] = \left(\alpha_1 \cdot x_1[i] + \alpha_2 \cdot x_2[i] + \alpha_3 \cdot x_3[i] \right) + \mathbf{N}(0, \sigma)$$



$$y[i] = \alpha_1 \cdot x_1[i] + \alpha_2 \cdot x_2[i] + \alpha_3 \cdot x_3[i] + \epsilon[i]$$

Regression Models

- 'Fitting' a regression model means estimating these quantities.

$$y[i] = \alpha_1 \cdot x_1[i] + \alpha_2 \cdot x_2[i] + \alpha_3 \cdot x_3[i] + \epsilon[i]$$


- These are our model 'parameters'.

Regression Models

Our observations are expected to be randomly distributed around the mean value according to a normal distribution with a standard deviation equal to sigma (σ), and a mean of mu (μ). We expect the mean of our variable to vary from trial to trial based on three predictors. The combination of these predictors is based on model-specific coefficients ($\alpha_1, \alpha_2, \alpha_3$) that are static across trials.

$$y[i] \sim \mathcal{N}(\mu, \sigma)$$

$$\mu[i] = \alpha_1 \cdot x_1[i] + \alpha_2 \cdot x_2[i] + \alpha_3 \cdot x_3[i]$$

Errors and Residuals

- Errors are the variation around expected values.
- Errors are what we model probabilistically (variation in μ is deterministic).

$$y[i] = \mu[i] + \varepsilon[i] \quad \varepsilon[i] = y[i] - \mu[i]$$

$$\varepsilon[i] \sim \mathbf{N}(0, \sigma)$$

Errors and Residuals

- We don't know the real μ and can only estimate it ($\hat{\mu}$).
- Residuals are variation around our predicted values, they are estimated errors ($\hat{\epsilon}$).

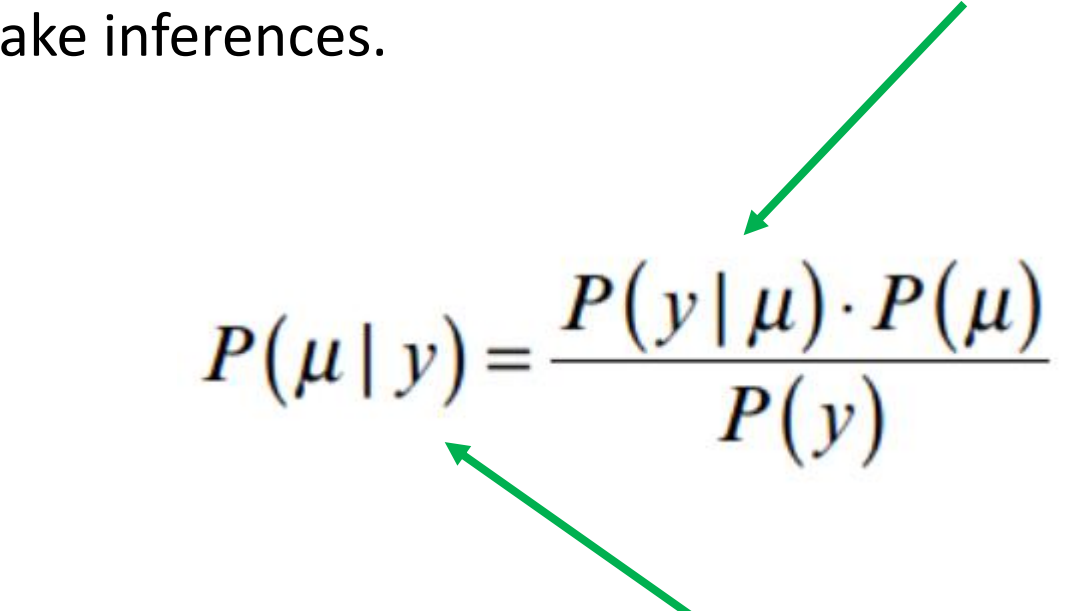
$$\epsilon_{[i]} = y_{[i]} - \mu_{[i]}$$

$$\hat{\epsilon}_{[i]} = y_{[i]} - \hat{\mu}_{[i]}$$

$$\hat{\epsilon}_{[i]} \sim N(0, \sigma)$$

What's 'Bayesian' about our Models?

- 'Traditional' (frequentist) models focus mostly on the likelihoods of parameters to make inferences.



A diagram consisting of two green arrows. One arrow originates from the word 'likelihoods' in the first bullet point and points diagonally down and to the right towards the term $P(y | \mu)$ in the numerator of the Bayesian formula. The second arrow originates from the phrase 'posterior probability' in the second bullet point and points diagonally up and to the left towards the term $P(\mu | y)$ in the denominator of the same formula.

$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$

- Bayesian models make inferences using the posterior probability of parameters.

Bayes Theorem

$$P(A \& B) = P(B \& A)$$

$$P(A | B) \cdot P(B) = P(B | A) \cdot P(A)$$

$$P(\mu | y) \cdot P(y) = P(y | \mu) \cdot P(\mu)$$


$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$

Bayes Theorem

$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$


Prior Probabilities

- The probability of different values of your parameter prior to collecting data.
- This a priori expectation can come from world knowledge, previous experiments, common sense, or some combination thereof.

$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$



Likelihoods

- The product of the probability density values corresponding to the data points for a given value of μ .
- Reflects the probability that the data, y , would be observed or generated for particular values of μ .


$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$


Marginal/Total Probability

- Necessary to scale the numerator so that the posterior density has a total area under the curve equal to one.
- Since the marginal probability does not vary as a function of μ , it does not affect the relative posterior probability of values of μ .
- For this reason, you don't typically need to worry about it.

$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$


Posterior Probability

- The posterior probability (*a posteriori*, after observation) of values of μ given your data y , and the structure of your model.
- The posterior is a combination of the prior distribution and the likelihood, a combination of old and new information.


$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$

Bayes Theorem

$$P(\mu|y) = \frac{P(y|\mu) \cdot P(\mu)}{P(y)} = \frac{P(y|\mu)}{P(y)} \cdot P(\mu)$$

$$\log(P(\mu|y)) = \\ (\log(P(y|\mu)) - \log(P(y))) + \log(P(\mu))$$

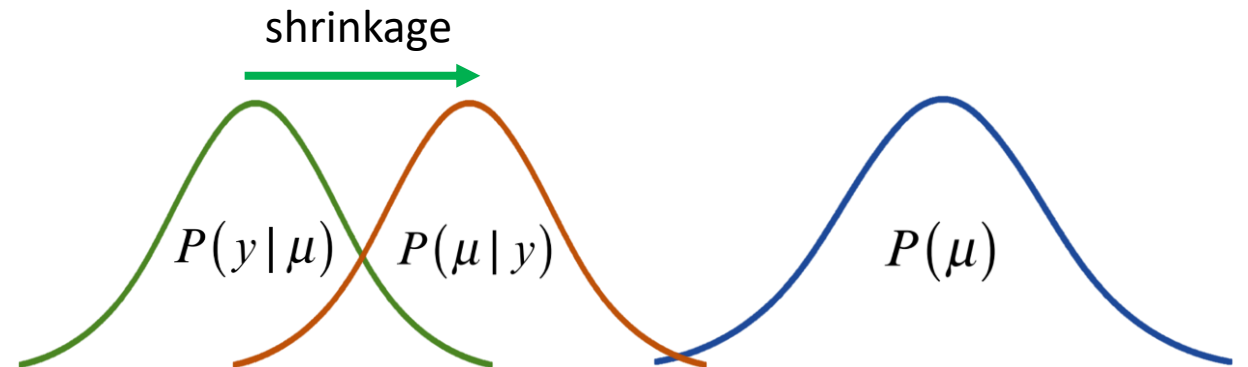
Posterior Distributions and Shrinkage

- Posterior probabilities can be pulled away from the most likely parameter values, towards the prior.

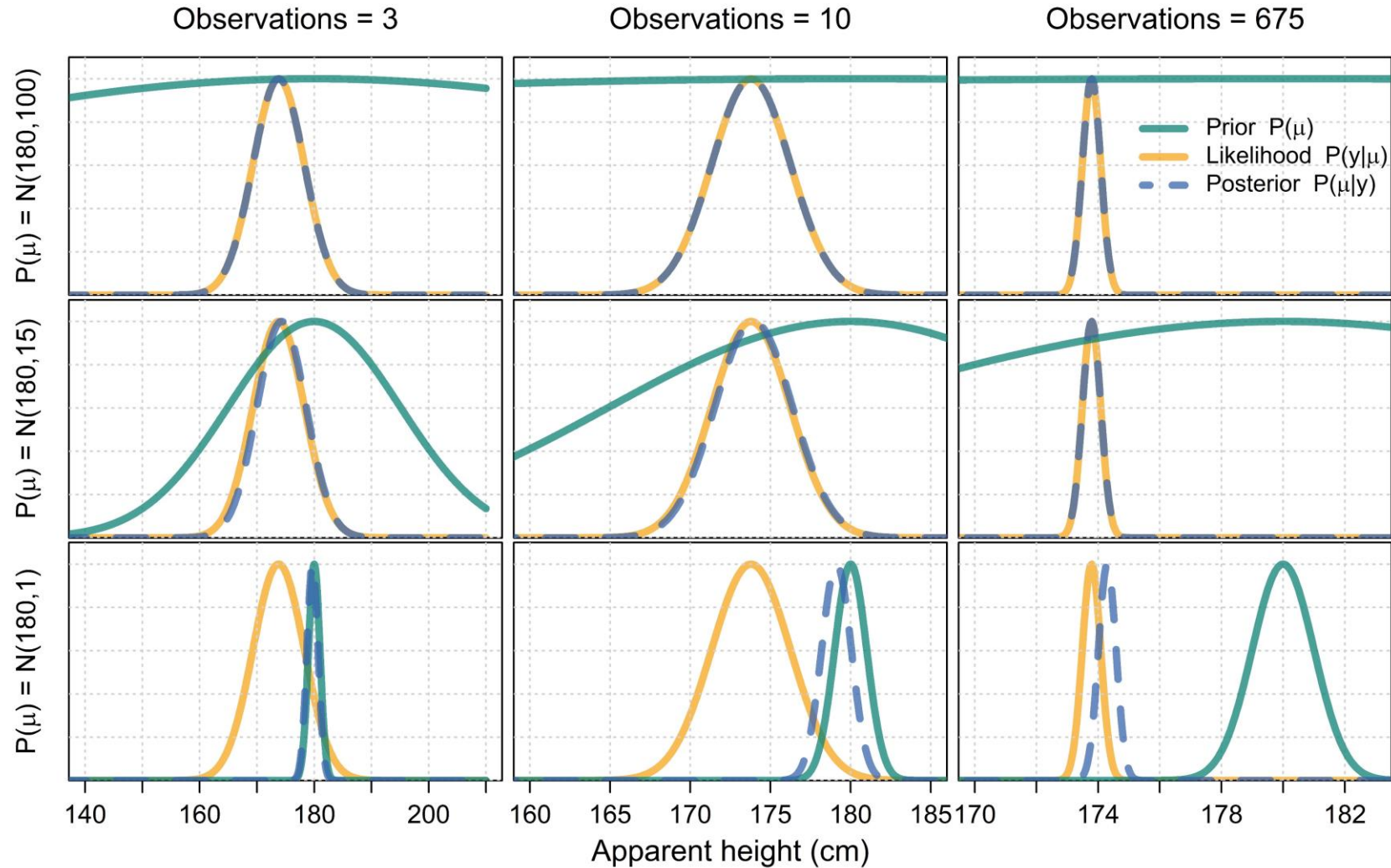
$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$

The equation is annotated with three arrows: an orange arrow pointing down to μ in the numerator, a green arrow pointing down to y in the numerator, and a blue arrow pointing down to μ in the denominator.

- This 'pull' is called *shrinkage*, values get *shrunk* towards the prior.




Posterior Distributions and Shrinkage



$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$

Sampling from Posterior Distributions

- Many complex models can't be analyzed analytically.
- The characteristics of posterior probabilities is investigated using numerical methods.
- Modern Bayesian models require sophisticated sampling software.


$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$

Stan and brms

- Stan – “Stan is a state-of-the-art platform for statistical modeling and high-performance statistical computation.”
- brms – An interface for the easy use of Stan in R.

Data and Research Questions

```
# load book package and brms
library (bmmb)
library (brms)

# load and subset experimental data
data (exp_data)
men = exp_data[exp_data$C_v=='m',]
mens_height = men$height
```

Data and Research Questions

Goal: Use the data in our experiment to answer these questions:

- (Q1) How tall does the average adult male 'sound'?
- (Q2) Can we set limits on credible average apparent heights based on the data we collected?

Description of the Model

- The apparent height for a given observation i is normally distributed according to some trial-specific expected value and some unknown (but fixed) standard deviation.
- The expected value for any given trial ($\mu_{[i]}$) is equal to the intercept of the model for all trials (i.e. it's fixed, we have the same expected value for all observations).

$$y_{[i]} \sim \text{N}(\mu_{[i]}, \sigma)$$

$$\mu_{[i]} = \alpha_1 \cdot 1$$

$$\text{height}_{[i]} \sim \text{N}(\mu_{[i]}, \sigma)$$

$$\mu_{[i]} = \text{Intercept}$$

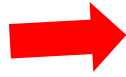
The Model Formula

- The dependent variable goes on the left of the \sim , predictors go on the right.

```
y ~ predictors
```

```
height ~ 1
```

Fitting a Model



```
model = brms::brm (height ~ 1, data = men, chains = 1, cores = 1)
## Compiling Stan program...
## Start sampling
##
## SAMPLING FOR MODEL '03859e54349182b6cd9cd51aa7ca25d3' NOW
## (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 0 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per
## transition would take 0 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:      1 / 2000 [  0%] (Warmup)
## Chain 1: Iteration:    200 / 2000 [ 10%] (Warmup)
## Chain 1: Iteration:    400 / 2000 [ 20%] (Warmup)
## Chain 1: Iteration:    600 / 2000 [ 30%] (Warmup)
## Chain 1: Iteration:    800 / 2000 [ 40%] (Warmup)
## Chain 1: Iteration:   1000 / 2000 [ 50%] (Warmup)
## Chain 1: Iteration:   1001 / 2000 [ 50%] (Sampling)
## Chain 1: Iteration:   1200 / 2000 [ 60%] (Sampling)
## Chain 1: Iteration:   1400 / 2000 [ 70%] (Sampling)
## Chain 1: Iteration:   1600 / 2000 [ 80%] (Sampling)
## Chain 1: Iteration:   1800 / 2000 [ 90%] (Sampling)
## Chain 1: Iteration:   2000 / 2000 [100%] (Sampling)
## Chain 1:
## Chain 1: Elapsed Time: 0.103 seconds (Warm-up)
## Chain 1:                0.057 seconds (Sampling)
## Chain 1:                0.16 seconds (Total)
```

The Model Print Statement

- Evaluating the name of your model in the console shows you the model print statement.

```
# inspect model  
model
```

```
Family: gaussian  
Links: mu = identity; sigma = identity  
Formula: height ~ 1  
Data: men (Number of observations: 675)  
Draws: 1 chains, each with iter = 2000; warmup = 1000; thin = 1;  
       total post-warmup draws = 1000  
  
Population-Level Effects:  
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS  
Intercept  173.78      0.30  173.16  174.33 1.00    1055     714  
  
Family Specific Parameters:  
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS  
sigma      7.77      0.22   7.37   8.21 1.00    1139     741  
  
Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS  
and Tail_ESS are effective sample size measures, and Rhat is the potential  
scale reduction factor on split chains (at convergence, Rhat = 1).
```

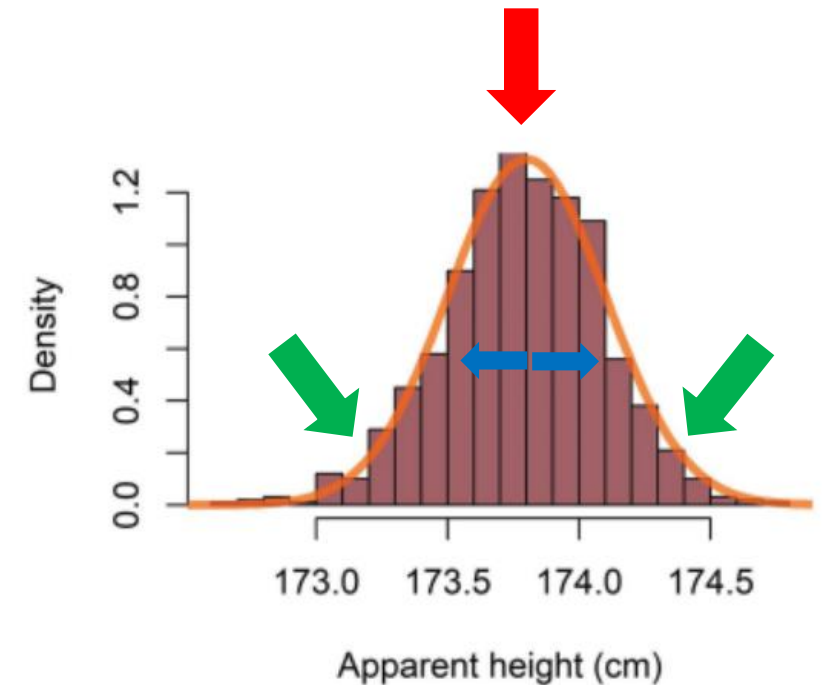
Fit and Model Information

- Information about the model you fit, and the sampling carried out.

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: height ~ 1
Data: men (Number of observations: 675)
Draws: 1 chains, each with iter = 2000; warmup = 1000; thin = 1;
       total post-warmup draws = 1000
```

Population-Level Effects

- Population-level effects are shared by all observations, or at least all observations in a given group.
- Your model will give you information about the posterior distribution: **the mean**, **the standard error**, **and the 95% credible interval**.



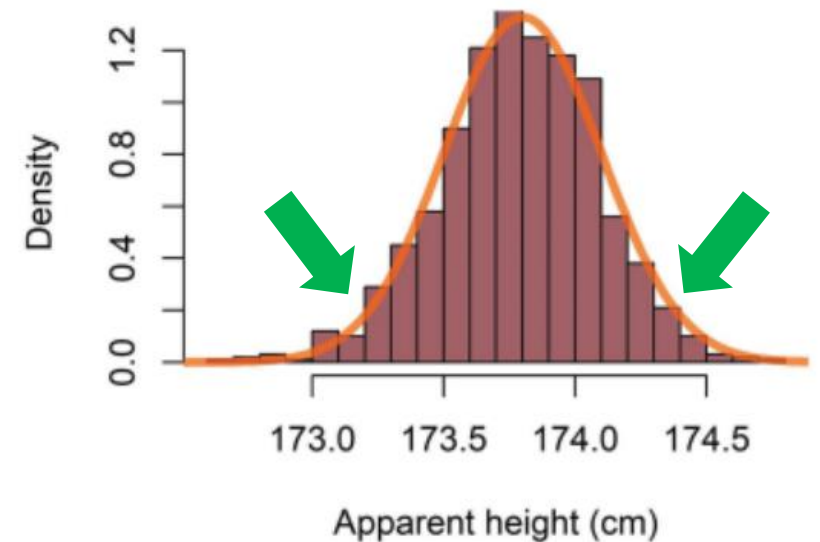
Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	173.78	0.30	173.16	174.33	1.00	1055	714



Credible Intervals

- Credible intervals tell you what values are credible for your parameters given your data and model structure.
- They are based on the quantiles of your posterior distribution.
- 95% intervals are common but not special in any way.




Population-Level Effects:


	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	173.78	0.30	173.16	174.33	1.00	1055	714

Family Specific Parameters

- Most distributions have at least a location parameter (like μ).
- Some distributions have other parameters (e.g., σ). These go here.


$$\text{height}_{[i]} \sim N(\mu_{[i]}, \sigma)$$
$$\mu_{[i]} = \text{Intercept}$$

Family Specific Parameters:



	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	7.77	0.22	7.37	8.21	1.00	1139	741

Boilerplate Text

- Related to the sampling process, pretty much the same always.

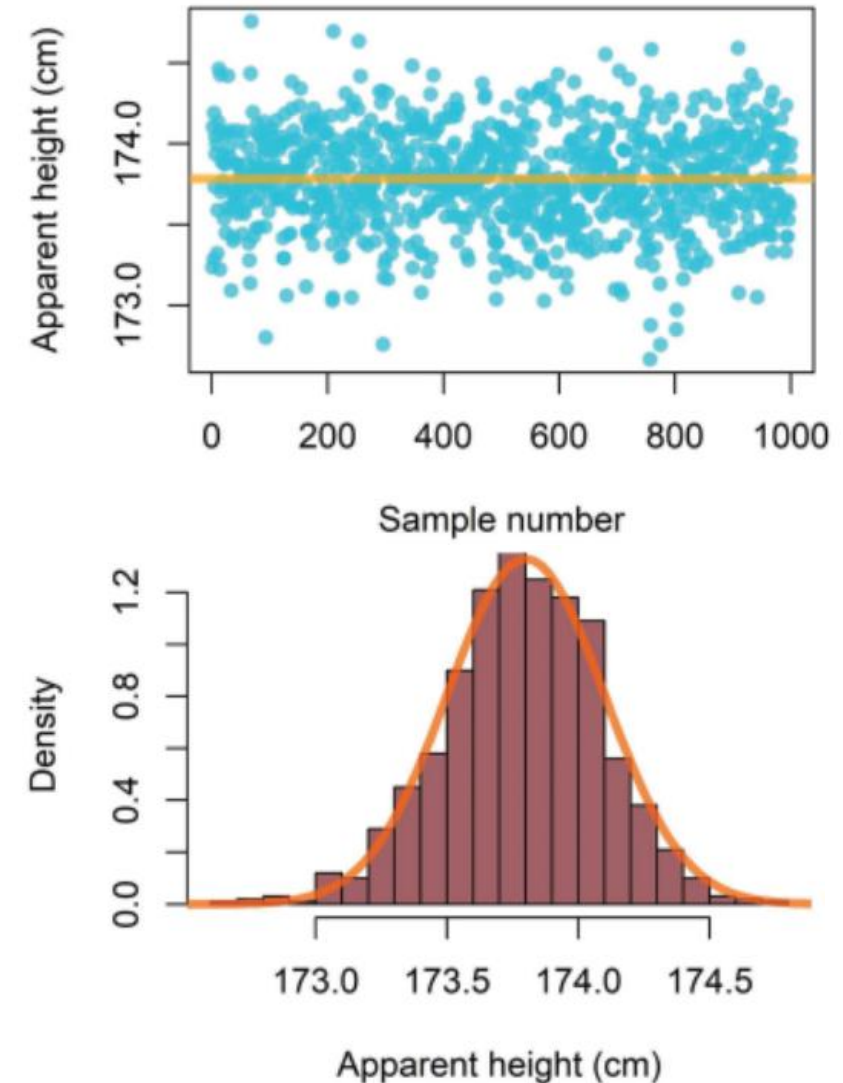
```
Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS  
and Tail_ESS are effective sample size measures, and Rhat is the potential  
scale reduction factor on split chains (at convergence, Rhat = 1).
```

Seeing the Samples

```
# get posterior samples from model
samples = bmmb::get_samples (model)

# check number of samples
nrow (samples)
## [1] 1000

# see first six samples
head (samples)
##      b_Intercept sigma lprior  lp__
## 1      173.2  7.518  -5.885  -2347
## 2      174.1  7.613  -5.880  -2345
## 3      173.3  7.940  -5.945  -2346
## 4      174.2  7.564  -5.872  -2346
## 5      173.7  7.879  -5.924  -2345
## 6      174.0  7.859  -5.916  -2345
```



Getting the Residuals

```
model_residuals = residuals (model, )  
head (model_residuals)
```

```
##           Estimate Est.Error      Q2.5      Q97.5  
## [1,]    -3.8844      0.2988    -4.4347    -3.2638  
## [2,]    -0.2844      0.2988    -0.8347     0.3362  
## [3,]    -1.7844      0.2988    -2.3347    -1.1638  
## [4,]   -16.0844      0.2988   -16.6347   -15.4638  
## [5,]   -20.3844      0.2988   -20.9347   -19.7638  
## [6,]     0.4156      0.2988    -0.1347     1.0362
```

```
model_residuals = residuals (model, summary=FALSE)  
dim (model_residuals)  
## [1] 1000  675
```

Getting the Residuals

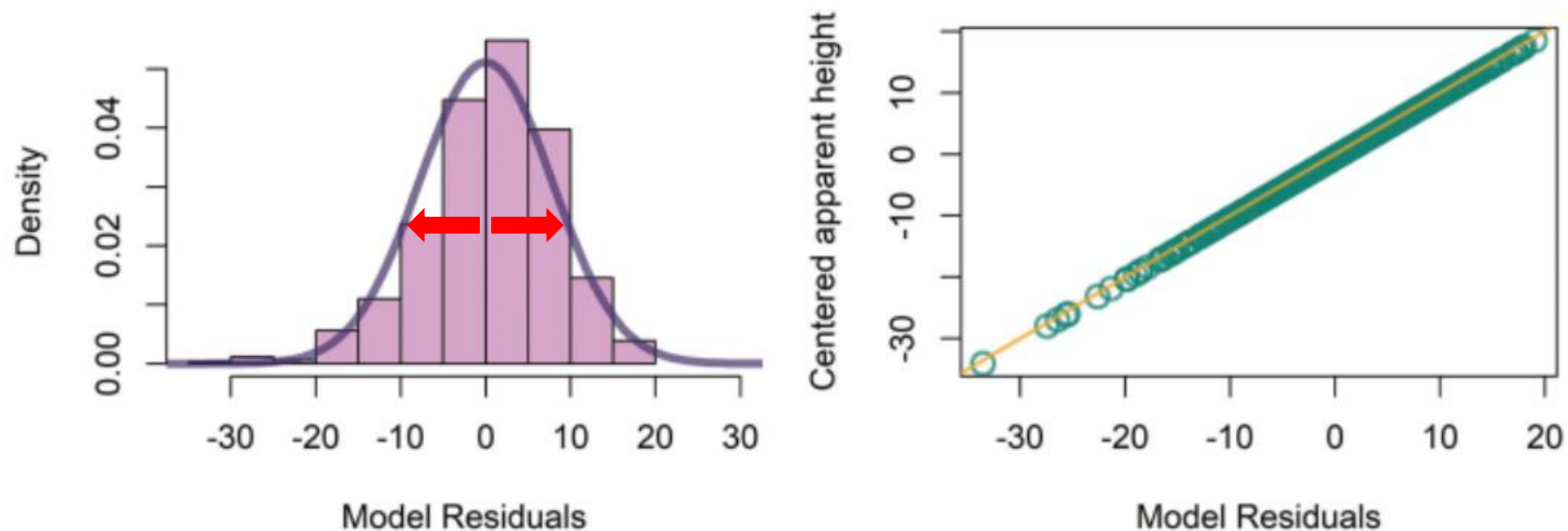


Figure 3.3 (left) Histogram of the residuals for `model`. (right) A comparison of our residuals and centered height judgments shows that these are nearly equal.

Family Specific Parameters:


	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	7.77	0.22	7.37	8.21	1.00	1139	741

Model Convergence

```
## Warning messages:  
## 1: Bulk Effective Samples Size (ESS) is too low,  
indicating posterior means and  
## medians may be unreliable. Running the chains for more  
iterations may help. See:  
## http://mc-stan.org/misc/warnings.html#bulk-ess  
## 2: Tail Effective Samples Size (ESS) is too low,  
indicating posterior variances  
## and tail quantiles may be unreliable.  
## Running the chains for more iterations may help. See  
## http://mc-stan.org/misc/warnings.html#tail-ess
```

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	173.78	0.30	173.16	174.33	1.00	1055	714



Model Convergence: Cores and Chains

- Each sequence of samples is called a chain.
- You can estimate several chains simultaneously across several cores.
- This can speed up computation time quite a bit.

```
parallel::detectCores()
```

```
# Fit the model yourself
```

```
model_multicore =
```

```
  brms::brm (height ~ 1, data = men, chains = 4, cores = 4)
```



Model Convergence: Iterations and Warmup

- Stan uses the warmup to tune the sampler and find good parameter values.
- Only samples past the warmup are kept: **iter** — **warmup**.

```
# Fit the model yourself
model_thinned =
  brms::brm (height ~ 1, data = men, chains = 4, cores = 4,
            warmup = 1000, iter = 3000, thin = 2)

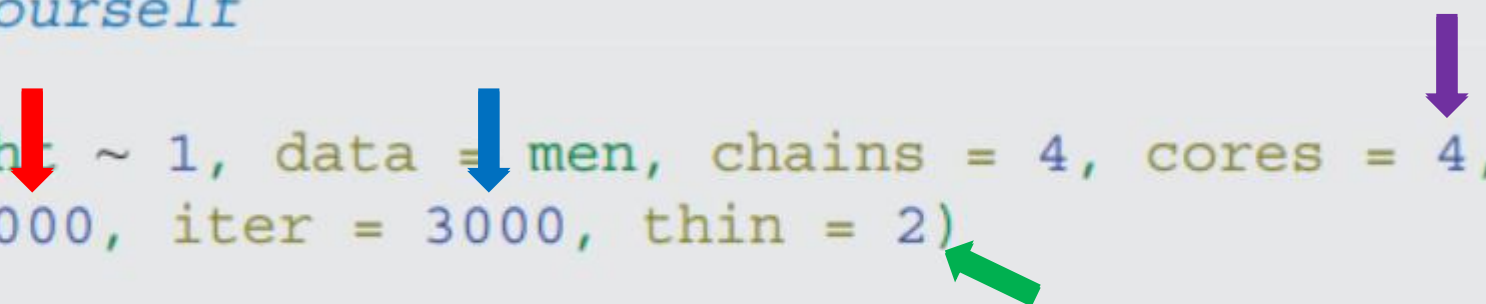
# Or download it from the GitHub page:
model_thinned = bmmmb::get_model ('3_model_thinned.RDS')
```

Model Convergence: Thinning

- Thinning keeps only every n^{th} sample: $(\text{iter} - \text{warmup}) / \text{thin}$.
- So, if you are sampling from k chains you will end up with:
 $(\text{iter} - \text{warmup}) / \text{thin} \cdot \text{cores}$ total samples.

```
# Fit the model yourself
model_thinned =
  brms::brm (height ~ 1, data = men, chains = 4, cores = 4,
            warmup = 1000, iter = 3000, thin = 2)

# Or download it from the GitHub page:
model_thinned = bmmmb::get_model ('3_model_thinned.RDS')
```



Divergent Transitions

- Divergent transitions should not be ignored.
- They tell you something is wrong with your model.

```
## There were n divergent transitions after warmup.  
Increasing adapt_delta  
## above 0.8 may help. See  
## http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup`
```

- You can (maybe) fix this by changing adapt_delta as shown below.

```
brms::brm (height ~ 1, data = men, chains = 4, cores = 4, warmup = 1000,  
          iter = 3000, thin = 2, control = list(adapt_delta = 0.9))
```

Specifying Priors

- The `get_prior` function can be used to see what priors your model needs you to specify.
- You can specify priors for classes of parameters. So far these are:
 - Intercept: A unique class, only for intercepts.
 - sigma: This is for the standard deviation of our error parameters, sigma (σ).

```
brms::get_prior (height ~ 1, data = men) [, -c(7:9)]  
##               prior      class coef group resp dpar  source  
## student_t(3, 174.5, 7.1) Intercept                        default  
## student_t(3, 0, 7.1)      sigma                          default
```

Specifying Priors

- You can set priors using the `set_prior` function.
- You can do this for whole classes or for individual parameters (more on this later).
- Below we specify priors for our two model parameters.

```
prior = c(brms::set_prior("normal(176, 15)", class = "Intercept"),  
          brms::set_prior("normal(0, 15)", class = "sigma"))
```

An Updated Model Description

$$\text{height}_{[i]} \sim \text{N}(\mu_{[i]}, \sigma)$$

$$\mu_{[i]} = \text{Intercept}$$

Priors:

$$\text{Intercept} \sim \text{N}(176, 15)$$

$$\sigma \sim \text{N}(0, 15)$$

```
# Fit the model yourself, or
model_priors =
  brms::brm (height ~ 1, data = men, chains = 4, cores = 4,
    warmup = 1000, iter = 3500, thin = 2,
    prior = c(brms::set_prior("normal(176, 15)", class = "Intercept"),
      brms::set_prior("normal(0, 15)", class = "sigma")))
```

An Updated Model Description

$\text{height}_{[i]} \sim N(\mu_{[i]}, \sigma)$

$\mu_{[i]} = \text{Intercept}$

Priors:

$\text{Intercept} \sim N(176, 15)$

$\sigma \sim N(0, 15)$

```
bmmb::short_summary (model_thinned)
## Formula: height ~ 1
## Population-Level Effects:
##           Estimate Est.Error 1-95% CI u-95% CI
## Intercept    173.8         0.3   173.2   174.4
##
## Family Specific Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI
## sigma         7.77         0.21   7.38    8.2
```

```
# Fit the model yourself, or
model_priors =
  brms::brm (height ~ 1, data = men, chains = 4, cores = 4,
    warmup = 1000, iter = 3500, thin = 2,
    prior = c(brms::set_prior("normal(176, 15)", class = "Intercept"),
      brms::set_prior("normal(0, 15)", class = "sigma")))
```


Comparison of Slightly Different Priors

```
bmmb::short_summary (model_thinned)
## Formula: height ~ 1
## Population-Level Effects:
##           Estimate Est.Error 1-95% CI u-95% CI
## Intercept      173.8         0.3   173.2   174.4
##
## Family Specific Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI
## sigma          7.77         0.21   7.38    8.2
```

```
bmmb::short_summary (model_priors)
## Formula: height ~ 1
## Population-Level Effects:
##           Estimate Est.Error 1-95% CI u-95% CI
## Intercept      173.8         0.31   173.2   174.4
##
## Family Specific Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI
## sigma          7.77         0.21   7.37    8.19
```

The Log Prior and Log Posterior Densities


- This part will be important when we talk about model comparison.
- You don't really need to worry about it for now.
- What are the log posterior (lp) and log prior (lprior)?

```
# get posterior samples from model
samples = bmb::get_samples (model)

# check number of samples
nrow (samples)
## [1] 1000

# see first six samples
head (samples)
```

	b_Intercept	sigma	lprior	lp__
## 1	173.2	7.518	-5.885	-2347
## 2	174.1	7.613	-5.880	-2345
## 3	173.3	7.940	-5.945	-2346
## 4	174.2	7.564	-5.872	-2346
## 5	173.7	7.879	-5.924	-2345
## 6	174.0	7.859	-5.916	-2345



The Log Prior and Log Posterior Densities

$$P(\mu | y) = \frac{P(y | \mu) \cdot P(\mu)}{P(y)}$$

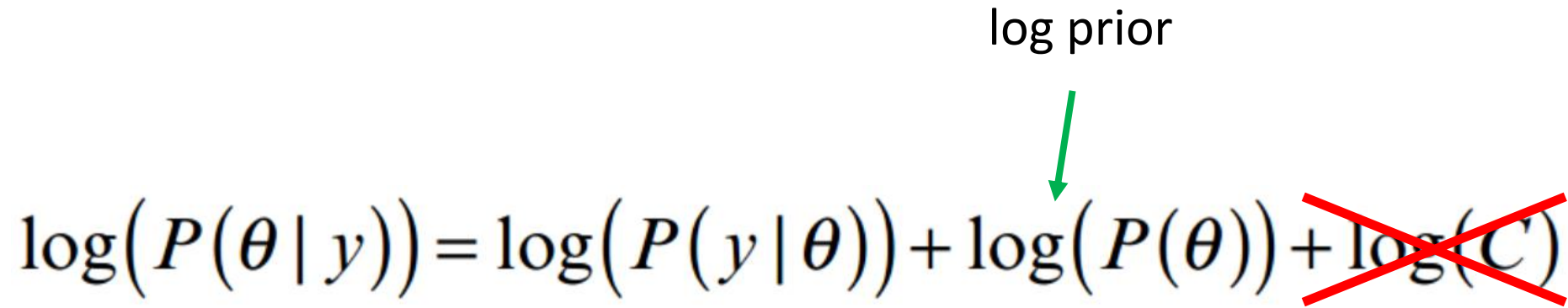
$$P(\theta | y) = [P(y | \theta) \cdot P(\theta)] \cdot C$$

$$\log(P(\theta | y)) = \log(P(y | \theta)) + \log(P(\theta)) + \log(C)$$

The Log Prior and Log Posterior Densities

$$\log(P(\theta | y)) = \log(P(y | \theta)) + \log(P(\theta)) + \log(C)$$

log prior



unnormalized log posterior

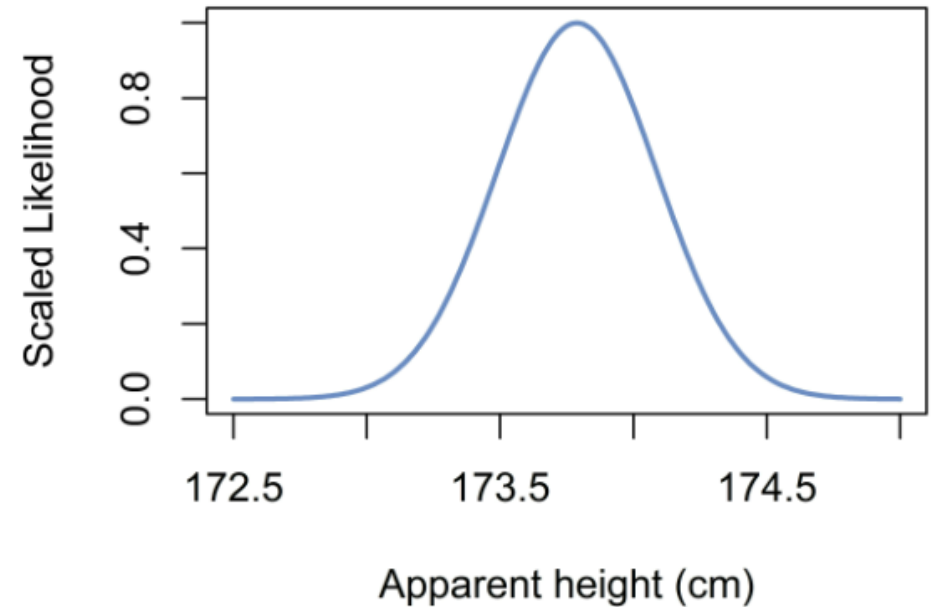
Answering our Research Questions: Last Week

(Q1) How tall does the average adult male ‘sound’?

A1: About 173.8 cm tall.

(Q2) Can we set limits on credible average apparent heights based on the data we collected?

A2: Yes, between 173 and 174.5 cm.

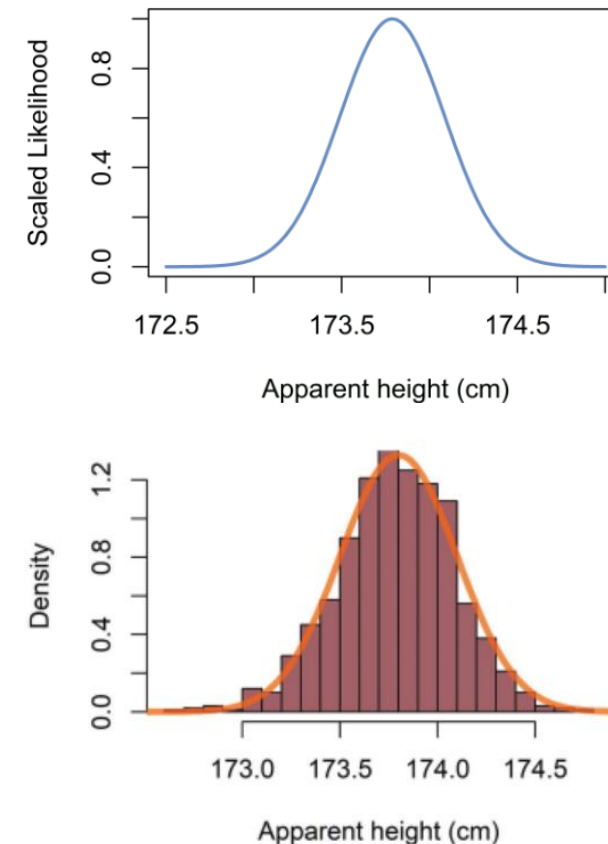


Answering our Research Questions: This Week

(Q1) How tall does the average adult male 'sound'?

(Q2) Can we set limits on credible average apparent heights based on the data we collected?

Based on our model, the average apparent height for adult males is likely to be 173.8 cm, and there is a 95% probability that the population mean is between 173.2 and 174.4 given our data and model structure.



```
## Population-Level Effects:
```

```
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept   173.78      0.30   173.16   174.33 1.00    1055      714
```

Answering our Research Questions




- In a paper we might report this like: “The mean apparent height is 174 cm (s.d. = 0.3, 95% CI = [173.2, 174.4])”.

```
## Population-Level Effects:  
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS  
## Intercept    173.78      0.30   173.16   174.33 1.00     1055      714
```




- It's necessary to report intervals in addition to point estimates!

Traditionalist's Corner: One-Sample t-test

```
t.test (mens_height)
##
##  One Sample t-test
##
## data:  mens_height
## t = 582, df = 674, p-value <2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 173.2 174.4
## sample estimates:
## mean of x
## 173.8
```

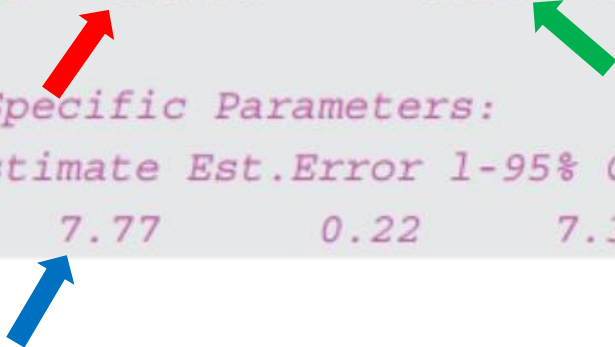


```
## Population-Level Effects:
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept  173.78      0.30   173.16   174.33 1.00    1055      714
```

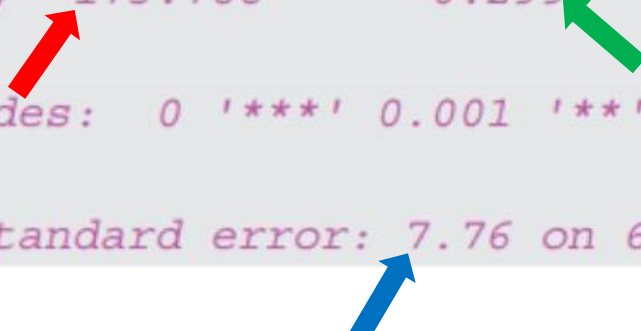


Traditionalist's Corner: OLS Regression

```
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rh
## Intercept   173.78      0.30   173.16   174.33 1
##
## Family Specific Parameters:
##           Estimate Est.Error l-95% CI u-95% CI Rhat
## sigma       7.77      0.22    7.37    8.21 1.00
```



```
ols_model = lm (mens_height ~ 1)
summary (ols_model)
##
## Call:
## lm(formula = mens_height ~ 1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -34.09  -4.59   0.71   5.31  18.51
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   173.788     0.299    581.2  <0.001
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.76 on 674
```



Exercises

Use the data in 'exp_ex' to do one of the following. You may also use your own data to answer a related question. In any case, describe the model, present and explain the results, and include at least two figures.

1. **Easy**: Analyze the (pre-fit) model that's exactly like model_priors, except using the data in exp_ex (bmmb::get_model("3_model_priors_ex.RDS")).
2. **Medium**: Fit a model just like model_priors, but for the data from some other group, for either the original or big resonance levels.
3. **Hard**: Fit two models like model_priors for two arbitrary groups, and compare results across models.

BE CAREFUL: Data must be normally distributed, not skewed, not distributed near its bounds...