Activity 14 - Stats Reasoning

Jocelyn Rojas & Seleona Hunter

Loading Packages

```
library(tidyverse) # For data wrangling
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.6
v forcats   1.0.1     v stringr   1.6.0
v ggplot2   4.0.1     v tibble    3.3.1
v lubridate 1.9.4     v tidyr     1.3.2
v purrr     1.2.1
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
```

```
library(brms) # For stats
```

```
Loading required package: Rcpp
Loading 'brms' package (version 2.23.0). Useful instructions
can be found by typing help('brms'). A more detailed introduction
to the package is available through vignette('brms_overview').

Attaching package: 'brms'

The following object is masked from 'package:stats':

    ar
```

```r
library(ggeffects) # for plotting model predictions
# Note: I needed to also install the `insight` and `see` packages to get `modelbased` to ins
# install.packages('modelbased') # if you need to install this package
library(modelbased) # for plotting model predictions. supports the link scale (ggeffects doe
```

```
Attaching package: 'modelbased'

The following objects are masked from 'package:ggeffects':

    collapse_by_group, pool_predictions, residualize_over_grid
```

```r
# install.packages('faraway') # if you need to install this package
library(faraway) # For data on galapagos species richess
```

```
Attaching package: 'faraway'

The following object is masked from 'package:brms':

    epilepsy
```

Q1.1a and Q1.1b

1. Counts of Clarkia flowers in a meadow

- Values of response variables: Positive real numbers (can't have a negative number of flowers), could include zeros (there may not be any flowers)
- Distribution: Normal distribution

2. Whether or not a female elephant seal gives birth

- Values of response variables: 0s and 1s (for yes: birth or no: did not give birth)
- Distribution: Poisson distribution

3. The percent cover of red algae in the intertidal

- Values of response variables: fractions, positive numbers
- Distribution: Binomial distribution

4. Growth of a tree from one year to the next

- Values of response variables: positive integers
- Distribution: Normal distribution

5. The spatial area of a forest in square meters

- Values of response variables: integers, fractions
- Distribution: Binomial distribution

Q1.2

1. Response variable for final project: rate of flock movement (through a forest)
2. Values of response variables: positive real numbers, integers
3. Distribution: Normal distribution

1.2 GLM with a log link

```r
# Read in the pre-stored data
data("gala")
# Check out the first 6 rows
head(gala)
```

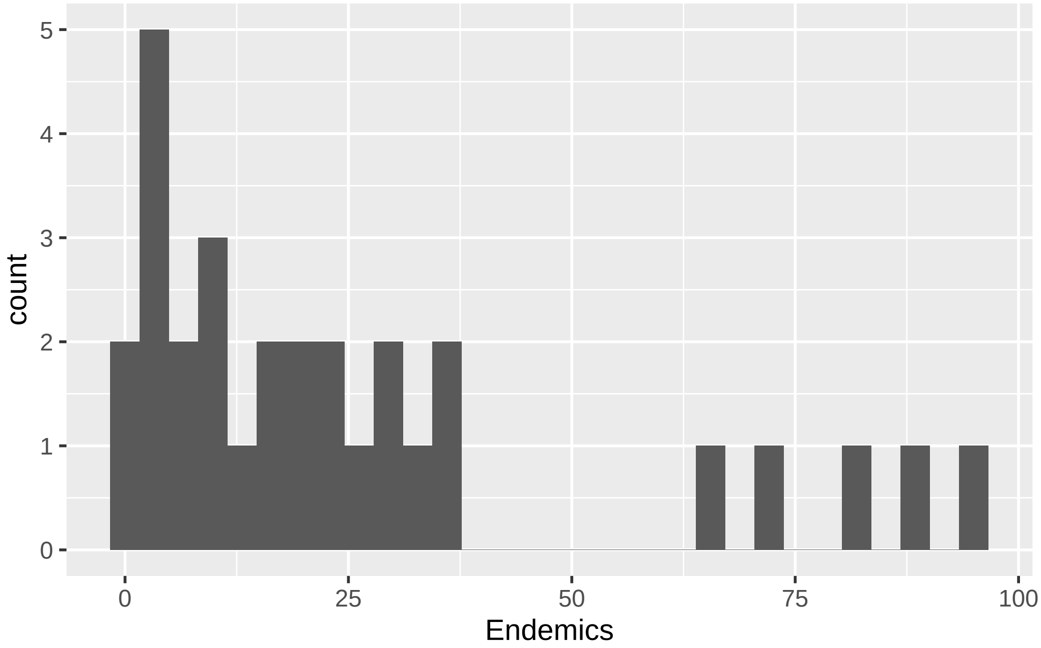
```
             Species Endemics  Area Elevation Nearest Scruz Adjacent
Baltra            58       23 25.09       346     0.6   0.6     1.84
Bartolome         31       21  1.24       109     0.6  26.3   572.33
Caldwell           3        3  0.21       114     2.8  58.7     0.78
Champion          25        9  0.10        46     1.9  47.4     0.18
Coamano            2        1  0.05        77     1.9   1.9   903.82
Daphne.Major      18       11  0.34       119     8.0   8.0     1.84
```

```r
# Look at the help page too!
?gala
```

Q1.3 Plot a histogram of the response variable Endemics

```r
ggplot(data = gala, aes(x=Endemics)) +
  geom_histogram()
```

```
`stat_bin()` using `bins = 30`. Pick better value `binwidth`.
```

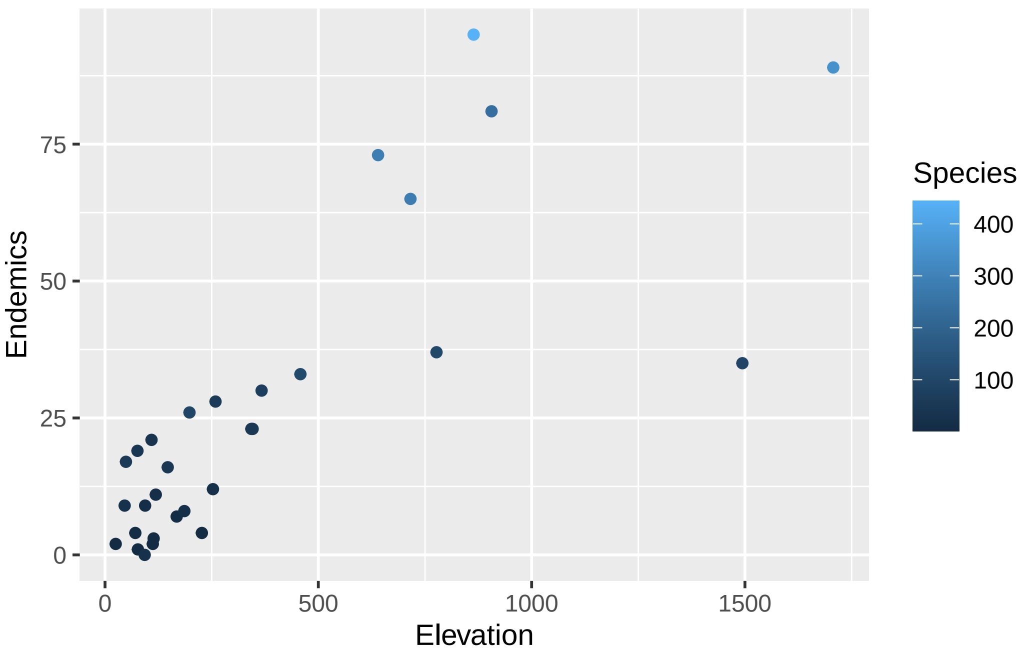


Q1.3 Answer

This data does not appear to be normally distributed. The data seems to be skewed to the left with outliers far to the right in the graph.

Q1.4 Plot Endemics ~ Elevation

```
ggplot(data = gala, aes(x = Elevation,y = Endemics, color = Species )) +
  geom_point()
```



```
  labs(
    x = "Elevation",
    y = "Endemics"
  )
```

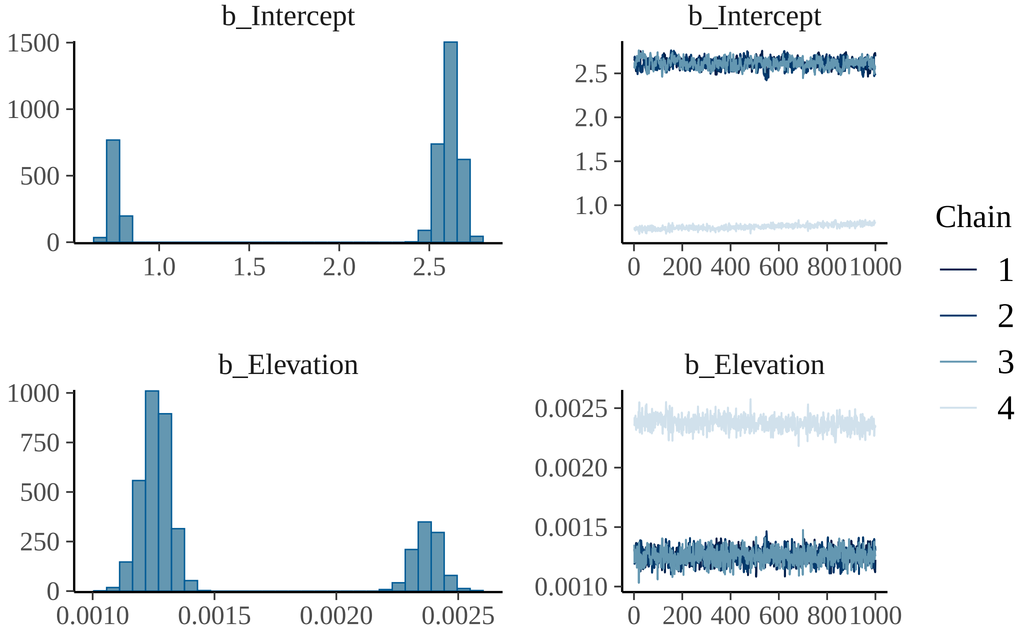
```
<ggplot2::labels> List of 2
 $ x: chr "Elevation"
 $ y: chr "Endemics"
```

Run the model

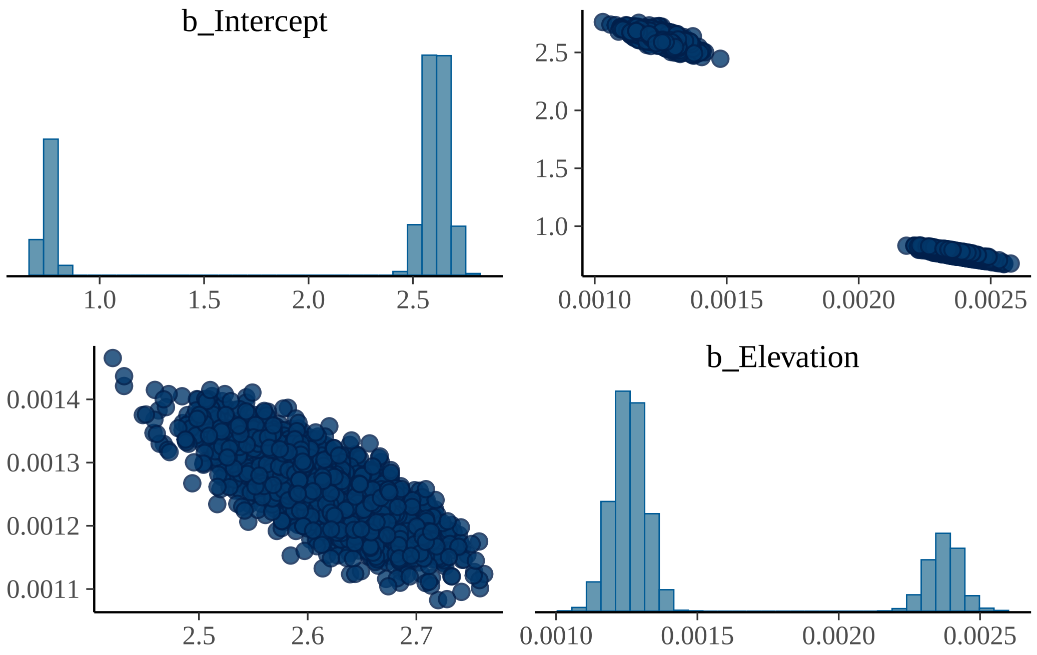
```
# Endemics ~ Elevation
m.elev <-
  brm(data = gala, # Give the model the penguins data
      # Choose a poisson distribution - THIS IS THE NEW PART!
      family = poisson(link = "log"),
      # Specify the model here.
      Endemics ~ 1 + Elevation,
      # Here's where you specify parameters for executing the Markov chains
      # We're using similar to the defaults, except we set cores to 4 so the analysis runs fa
      iter = 2000, warmup = 1000, chains = 4, cores = 4,
      # Save the fitted model object as output - helpful for reloading in the output later
      file = "output/m.elev")
```

model summary

```
plot(m.elev)
```



```
pairs(m.elev)
```



```r
summary(m.elev)
```

```
Warning: Parts of the model have not converged (some Rhats are > 1.05). Be
careful when analysing the results! We recommend running more iterations and/or
setting stronger priors.
```

```
 Family: poisson
  Links: mu = log
Formula: Endemics ~ 1 + Elevation
   Data: gala (Number of observations: 30)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Regression Coefficients:
          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept     2.15      0.81     0.72     2.71 1.57        7       13
Elevation     0.00      0.00     0.00     0.00 1.53        7       27

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).
```

Q1.5 Evaluate the output

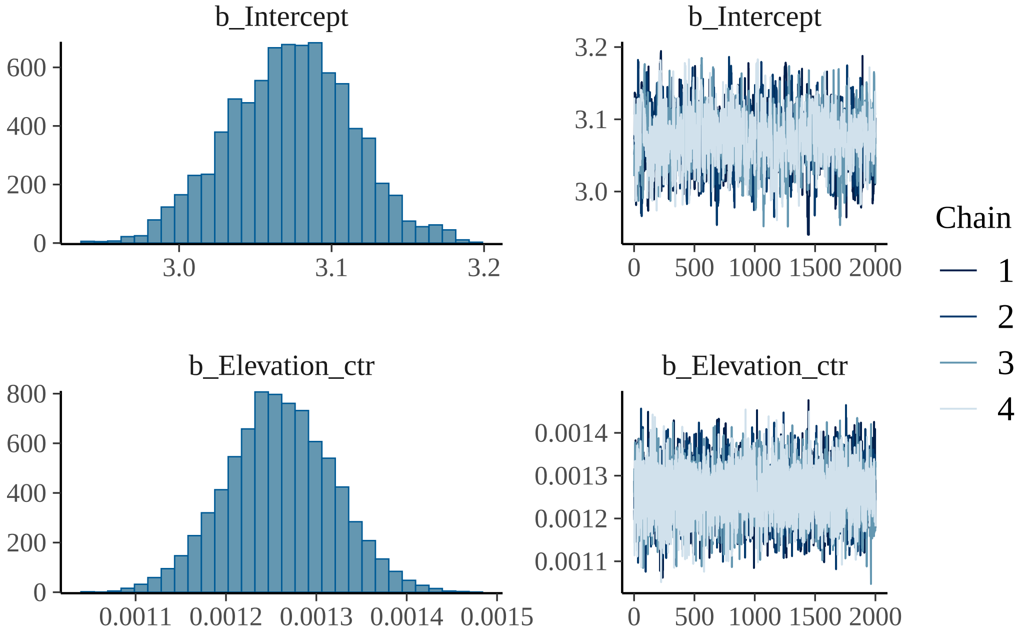
Based on the summary output, the model fitting algorithm did not converge. Our RHat value exceeds 1 and the chains do not align.

Q1.6 Center the predictors

```r
gala <- gala |>
  mutate(Elevation_ctr = Elevation - mean(Elevation))

# Endemics ~ Elevation
m.elev2 <-
  brm(data = gala, # Give the model the penguins data
      # Choose a poisson distribution - THIS IS THE NEW PART!
      family = poisson(link = "log"),
      # Specify the model here.
      Endemics ~ 1 + Elevation_ctr,
      # Here's where you specify parameters for executing the Markov chains
      # We're using similar to the defaults, except we set cores to 4 so the analysis runs fa
      iter = 6000, warmup = 4000, chains = 4, cores = 4,
      prior = prior(normal(0, 0.1), class = b),
      # Save the fitted model object as output - helpful for reloading in the output later
      file = "output/m.elev2")
```

checking the model

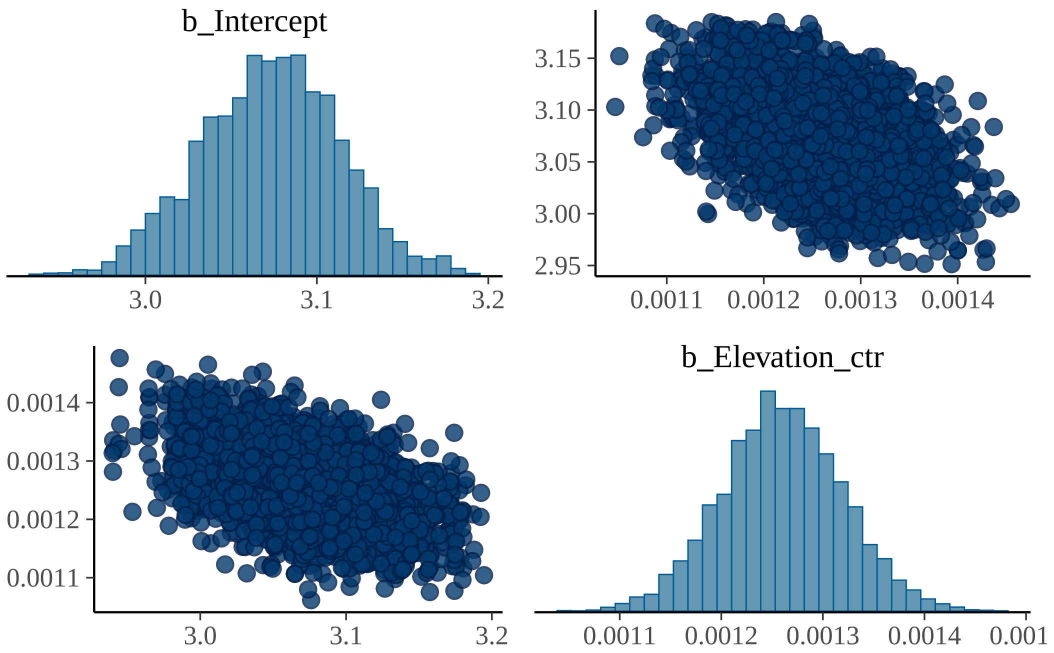
```r
plot(m.elev2)
```



```r
summary(m.elev2)
```

```
 Family: poisson
  Links: mu = log
Formula: Endemics ~ 1 + Elevation_ctr
   Data: gala (Number of observations: 30)
  Draws: 4 chains, each with iter = 6000; warmup = 4000; thin = 1;
         total post-warmup draws = 8000

Regression Coefficients:
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept         3.07      0.04     2.99     3.15 1.00     1137     1217
Elevation_ctr     0.00      0.00     0.00     0.00 1.00     3801     4656

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).
```

```r
pairs(m.elev2)
```

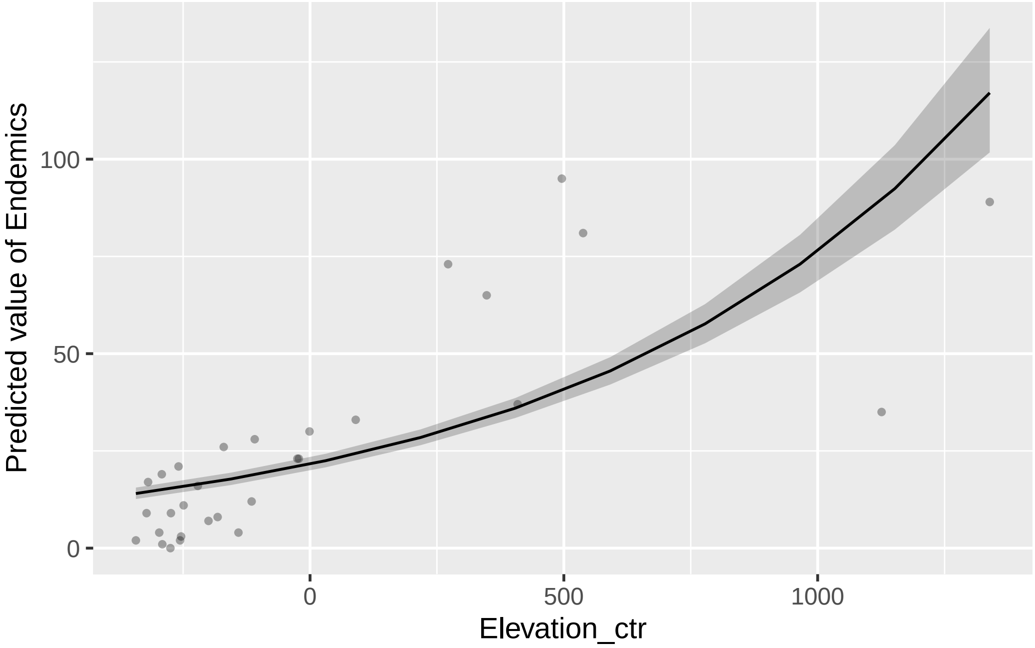


```
# summary(m.elev2)
print(m.elev2, digits = 4) #alternative summary with more decimals
```

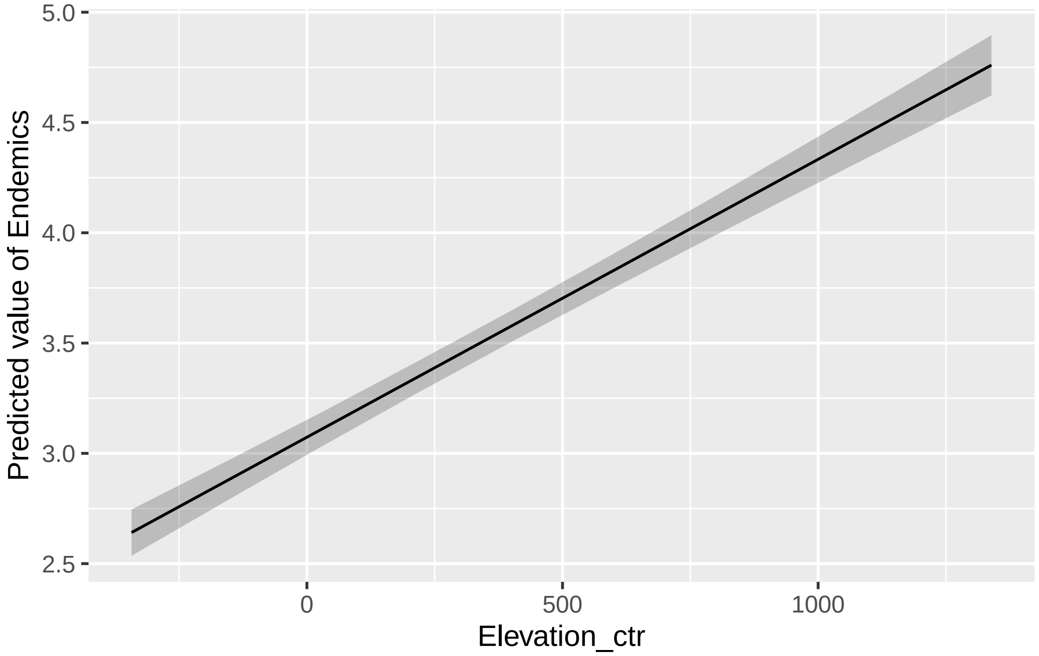
```
 Family: poisson
  Links: mu = log
Formula: Endemics ~ 1 + Elevation_ctr
   Data: gala (Number of observations: 30)
  Draws: 4 chains, each with iter = 6000; warmup = 4000; thin = 1;
         total post-warmup draws = 8000

Regression Coefficients:
              Estimate Est.Error l-95% CI u-95% CI   Rhat Bulk_ESS Tail_ESS
Intercept       3.0731    0.0404   2.9936   3.1513 1.0023     1137     1217
Elevation_ctr   0.0013    0.0001   0.0011   0.0014 1.0001     3801     4656

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).
```

Plot the posterior

```
#plotting posterior predictions
preds <- estimate_expectation(m.elev2, by = 'Elevation_ctr')
plot(preds, show_data = TRUE)
```



```
# visualizing linear model
predslog <- estimate_expectation(m.elev2, by = 'Elevation_ctr', predict = 'link')
plot(predslog)
```



##Interpreting Link scale coeffs

```
print(m.elev2, digits = 4)
```

```
 Family: poisson
  Links: mu = log
Formula: Endemics ~ 1 + Elevation_ctr
   Data: gala (Number of observations: 30)
  Draws: 4 chains, each with iter = 6000; warmup = 4000; thin = 1;
         total post-warmup draws = 8000

Regression Coefficients:
              Estimate Est.Error l-95% CI u-95% CI   Rhat Bulk_ESS Tail_ESS
Intercept       3.0731    0.0404   2.9936   3.1513 1.0023     1137     1217
Elevation_ctr   0.0013    0.0001   0.0011   0.0014 1.0001     3801     4656

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).
```

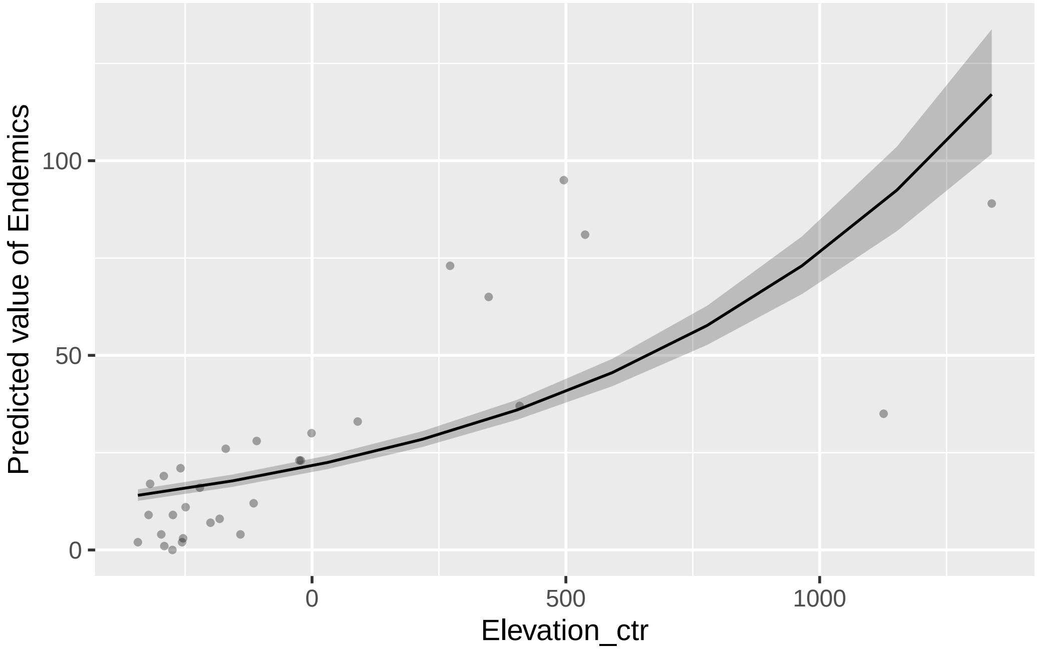
1. Backtransform

```
# backtransforming slope value
exp(0.0013)
```

```
[1] 1.001301
```

2. Interpret

```
plot(preds, show_data = TRUE)
```



```
# for every 1m of elevation, you get an increase in 1.0013 times as many species as the previ
```

##Q1.7 What is the percent change on the response scale?

1. Number of Clarkias blooming as a function of temperature in Celsius: 1.09

```
exp(1.09)
```

```
[1] 2.974274
```

```
(2.974274 - 1)*100
```

```
[1] 197.4274
```

```
# Back transformed: 197.4274% increase in number of Clarkias for every 1 degree increase in
```

2. Density of sea urchins per square meter in a quadrat as a function of number of sea otters: -2.5

```
(exp(-2.5) - 1)*100
```

```
[1] -91.7915
```

```
# Back transformed: 0.082085

# For every increase in 1 sea otter there is a 91.7915% decrease in density of sea urchins pe
```

3. Number of tomatoes per plant as a function of kg of fertilizer: 6.24

```
exp(6.24)
```

```
[1] 512.8585
```

```
(exp(6.24)-1)*100
```

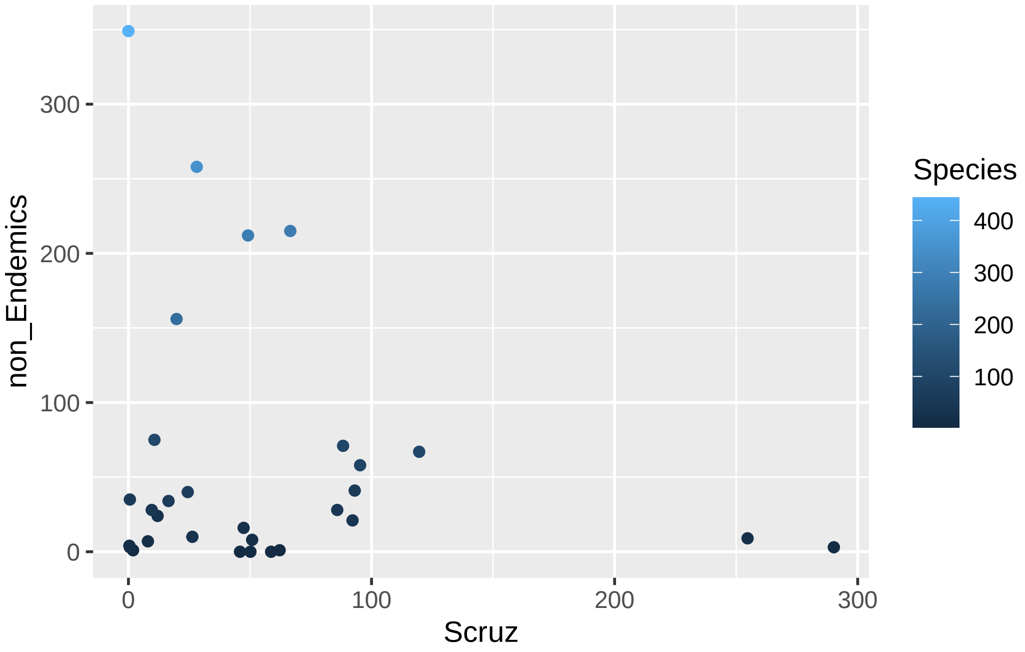
```
[1] 51185.85
```

```
# Back transformed: 512.8585 tomatoes per plant

# For every increase in 1kg of fertilizer, there will be a 51185.85% increase in tomatoes per
```

DIY: Run a model of non-endemic species ~ distance from Santa Cruz Island

Q1.8 Create a non-endemic column

```
gala2 <- gala %>%
  mutate(non_Endemics = Species - Endemics)

# making a plot with new tibble
ggplot(data = gala2, aes(x = Scruz,y = non_Endemics, color = Species )) +
  geom_point()
```



```
  labs(
    x = "Santa Cruz Island (km)",
    y = "Non Endemic Species"
  )
```

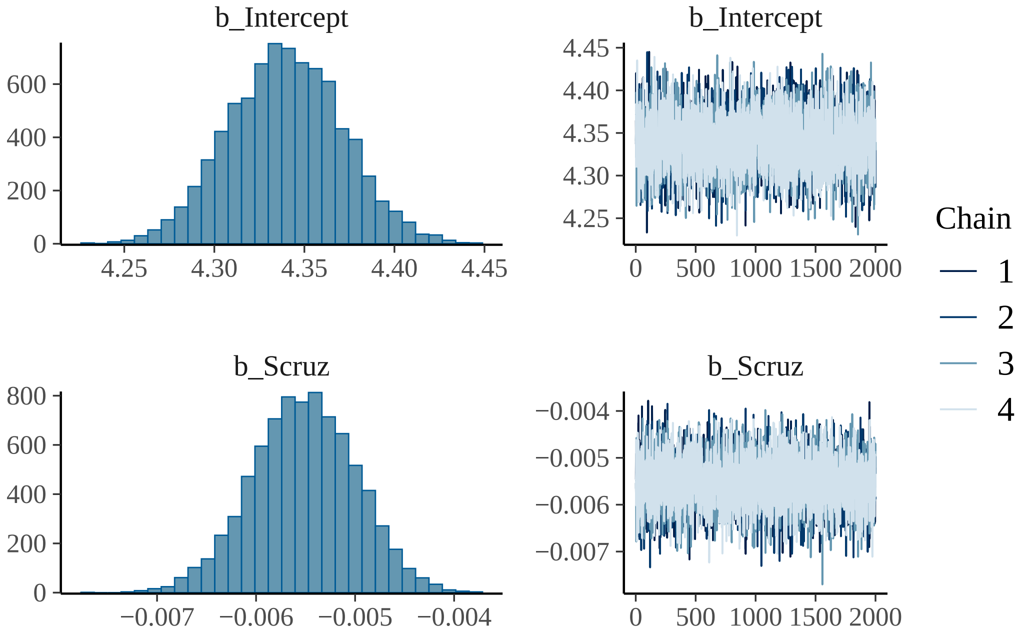
```
<ggplot2::labels> List of 2
 $ x: chr "Santa Cruz Island (km)"
 $ y: chr "Non Endemic Species"
```

Q1.9 Run a model of non Endemics ~ distance from Santa Cruz Island

```
#model for non edemics as function of distance from santa cruz islands
gala2model <-
  brm(data = gala2, # Give the model the penguins data
      # Choose a poisson distribution - THIS IS THE NEW PART!
      family = poisson(link = "log"),
      # Specify the model here.
      non_Endemics ~ 1 + Scruz,
      # Here's where you specify parameters for executing the Markov chains
      # We're using similar to the defaults, except we set cores to 4 so the analysis runs fa
      iter = 6000, warmup = 4000, chains = 4, cores = 4,
      prior = prior(normal(0, 0.1), class = b),
      # Save the fitted model object as output - helpful for reloading in the output later
      file = "output/gala2model")
```

Q1.10 Evaluate the output

```
plot(gala2model)
```



```r
print(gala2model, digits = 4)
```

```
 Family: poisson
  Links: mu = log
Formula: non_Endemics ~ 1 + Scruz
   Data: gala2 (Number of observations: 30)
  Draws: 4 chains, each with iter = 6000; warmup = 4000; thin = 1;
         total post-warmup draws = 8000

Regression Coefficients:
          Estimate Est.Error l-95% CI u-95% CI   Rhat Bulk_ESS Tail_ESS
Intercept   4.3396    0.0316   4.2785   4.4020 1.0001     5774     5636
Scruz      -0.0055    0.0005  -0.0066  -0.0045 1.0006     5365     5369

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).
```

Our model ran correctly. The Rhat is 1, the chains overlap, and the posteriors are normally distributed. Our confidence intervals do not contain zero.

Q1.11 Interpret the output

1. The number of non endemic species decreases as distance from Santa Cruz island increases.

a. Original output on log scale: 0.0055 log(non-endemic species)
b. Backtransformed:0.9945151

```r
exp(-0.0055)
```

```
[1] 0.9945151
```

c. % change: For every 1 km increase in the distance from Santa Cruz island, there is a 0.54% decrease in non endemic species.

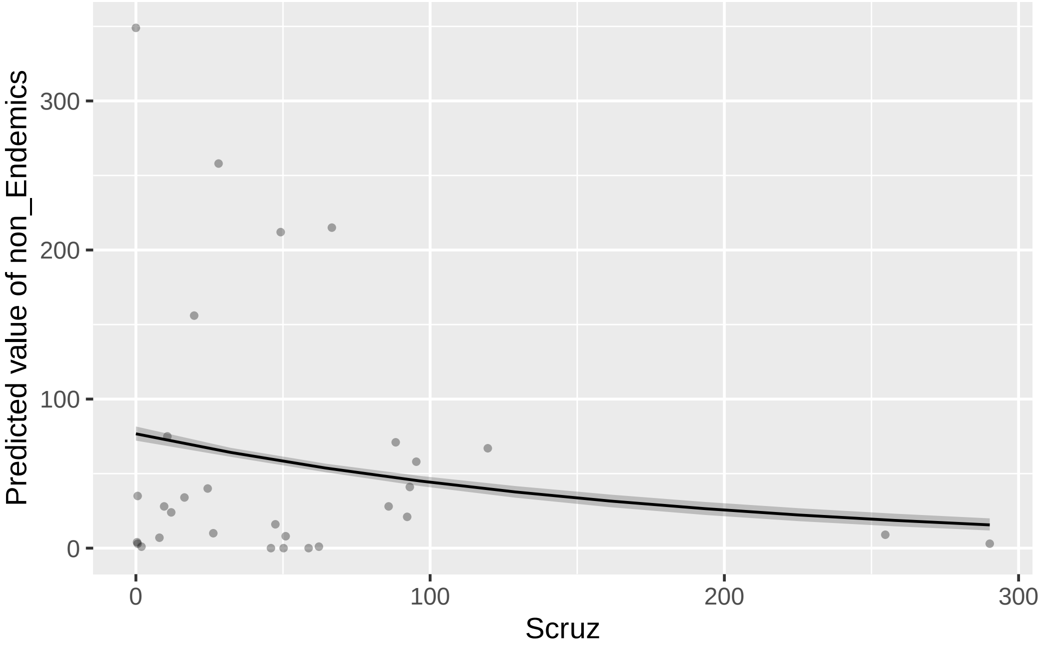
```r
(exp(-0.0055)-1)*100
```

```
[1] -0.5484903
```

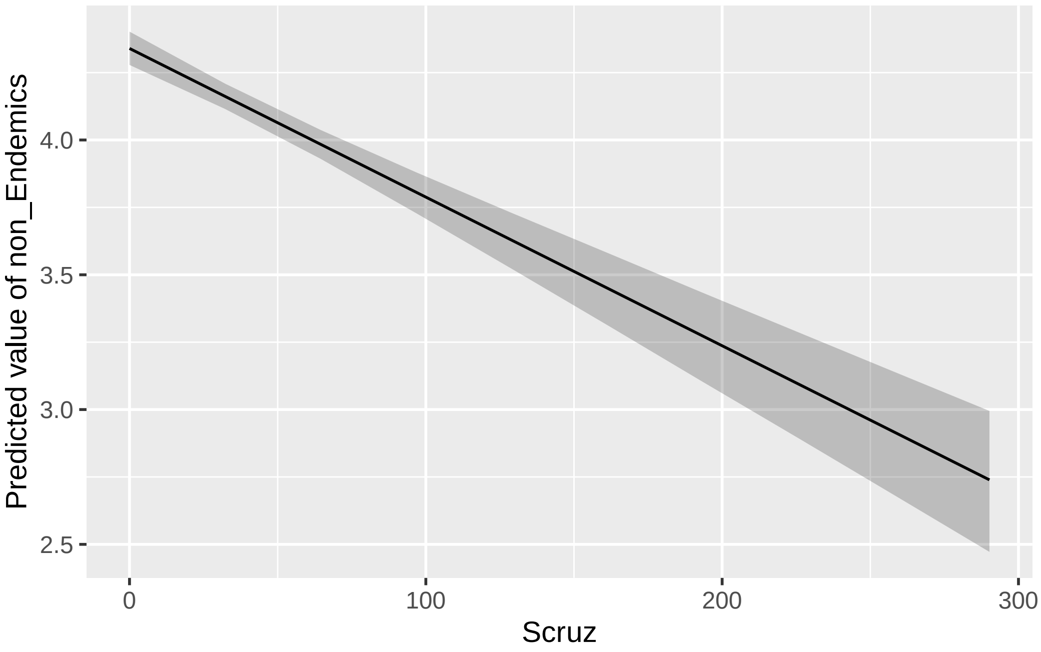
2. Yes it appears the slope estimate is different from zero because the confidence intervals do not contain zero.

Q1.12 Plot the posterior

```
# log link scale
preds <- estimate_expectation(gala2model, by = 'Scruz')
plot(preds, show_data = TRUE)
```

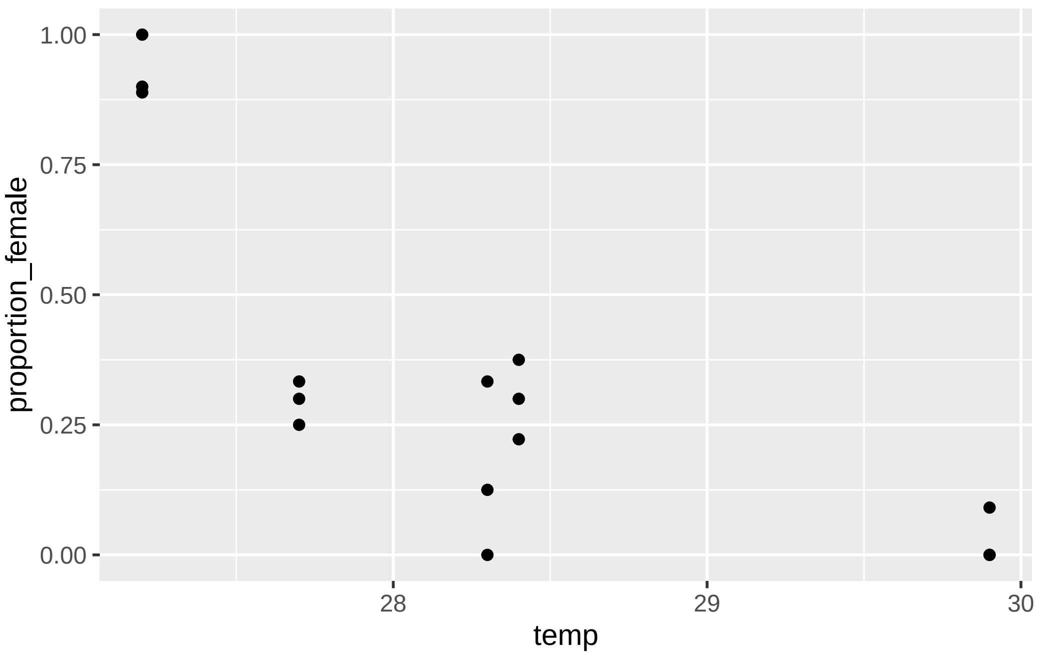


```
# visualizing linear model
predslog <- estimate_expectation(gala2model, by = 'Scruz', predict = 'link')
plot(predslog)
```



1.3 GLM with a logit link

```r
# loading data
turtle <- faraway::turtle %>%
  mutate(total_turtles = male + female,
         proportion_female = female/total_turtles)

# plotting data
turtle %>%
  ggplot(aes(x = temp, y = proportion_female)) +
  geom_point()
```



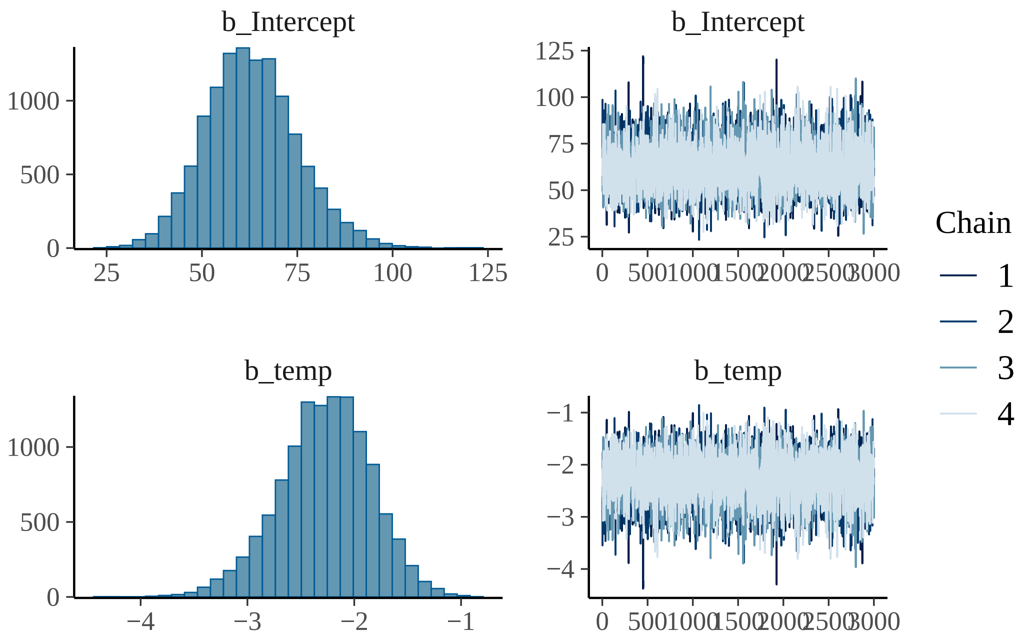
```
# running model

m.turt <-
  brm(data = turtle, # Give the model the data
      # Choose a binomial distribution - THIS IS THE NEW PART!
      family = binomial(link = "logit"),
      # Specify the model here.
      female | trials(total_turtles) ~ 1 + temp,
      # Here's where you specify parameters for executing the Markov chains
      # We're using similar to the defaults, except we set cores to 4 so the analysis runs fa
      iter = 4000, warmup = 1000, chains = 4, cores = 4,
      # Save the fitted model object as output - helpful for reloading in the output later
      file = "output/m.turt")
```

```
# model output
summary(m.turt)
```

```
 Family: binomial
  Links: mu = logit
Formula: female | trials(total_turtles) ~ 1 + temp
   Data: turtle (Number of observations: 15)
  Draws: 4 chains, each with iter = 4000; warmup = 1000; thin = 1;
```

```
         total post-warmup draws = 12000

Regression Coefficients:
          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept    63.00     12.08    40.68    88.62 1.00     4675     5550
temp         -2.27      0.43    -3.19    -1.47 1.00     4623     5557

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).
```

```r
plot(m.turt)
```

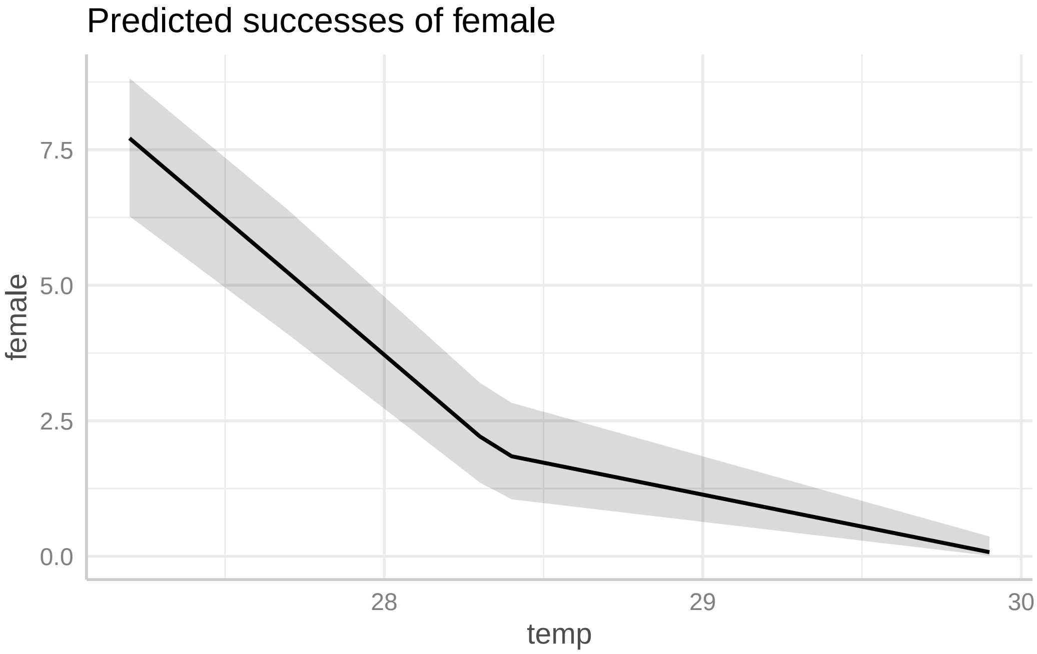


Model interpretations

Our model ran correctly. The Rhat is 1, posteriors are normally distributed, the chains overlap, and the confidence intervals do no include zero.

Interpreting plot predictions

```
pred <- predict_response(m.turt, condition = c(total_turtles = 10))

plot(pred)
```



2. Multilevel models

Q2.1 Fixed effects vs random effects

1. Student high school graduation rates as a function of: parental income, state of residence, and school district

- Fixed: state of residence, school district
- Random: parental income

2. Density of kelp as a function of: latitude, site, transect number, and density of sea urchins

- Fixed: latitude, transect number
- Random: density of sea urchins, site

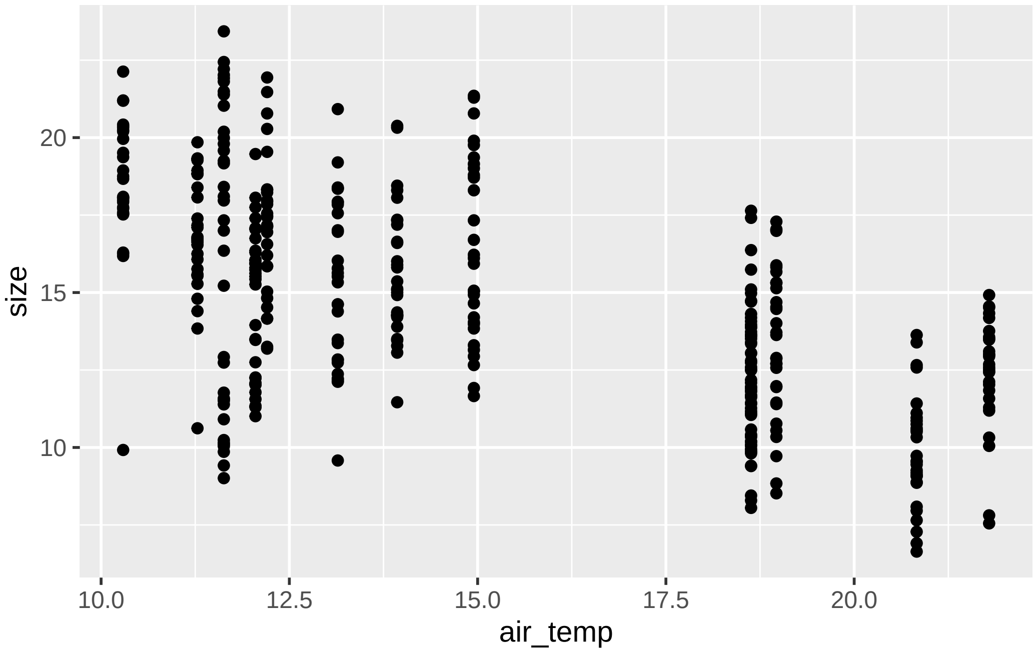
3. Probability of whale giving birth as a function of: age, annual temperature, year, individual ID

- Fixed: individual ID, year
- Random: age, annual temperature

Random Effects

```
# loading crab data

pie_crab <- lterdatasampler::pie_crab %>%
  mutate(site = as.factor(site))
```

```
pie_crab %>%
  ggplot(aes(x = air_temp, y = size)) +
  geom_point()
```



```
# running crab model
m.watertemp <-
  brm(data = pie_crab, # Give the model the penguins data
      # Use a gamma distribution
      family = Gamma(link = "log"),
      # Specify the model here.
      size ~ 1 + water_temp,
      # Here's where you specify parameters for executing the Markov chains
      # We're using similar to the defaults, except we set cores to 4 so the analysis runs fa
      iter = 2000, warmup = 1000, chains = 4, cores = 4,
      # Save the fitted model object as output - helpful for reloading in the output later
      file = "output/m.watertemp")

print(m.watertemp, digits = 3)
```

```
 Family: gamma
  Links: mu = log
Formula: size ~ 1 + water_temp
   Data: pie_crab (Number of observations: 392)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Regression Coefficients:
           Estimate Est.Error l-95% CI u-95% CI  Rhat Bulk_ESS Tail_ESS
Intercept     3.356     0.055    3.250    3.465 1.001     5308     3289
water_temp   -0.039     0.003   -0.044   -0.033 1.001     5255     3218

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI  Rhat Bulk_ESS Tail_ESS
shape   23.242     1.644   20.153   26.554 1.001     2572     2582

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).
```

```
#site as a random effect

m.watertemp.site <-
  brm(data = pie_crab, # Give the model the penguins data
      # Use a gamma distribution
      family = Gamma(link = "log"),
      # Specify the model here.
      size ~ 1 + water_temp + (1|site),
      # Here's where you specify parameters for executing the Markov chains
      # We're using similar to the defaults, except we set cores to 4 so the analysis runs fa
      iter = 2000, warmup = 1000, chains = 4, cores = 4,
      # Save the fitted model object as output - helpful for reloading in the output later
      file = "output/m.watertemp.site")

print(m.watertemp.site, digits = 3)
```

```
 Family: gamma
  Links: mu = log
Formula: size ~ 1 + water_temp + (1 | site)
   Data: pie_crab (Number of observations: 392)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Multilevel Hyperparameters:
~site (Number of levels: 13)
              Estimate Est.Error l-95% CI u-95% CI  Rhat Bulk_ESS Tail_ESS
sd(Intercept)    0.125     0.035    0.077    0.213 1.002      886     1198

Regression Coefficients:
           Estimate Est.Error l-95% CI u-95% CI  Rhat Bulk_ESS Tail_ESS
Intercept     3.372     0.203    2.970    3.778 1.003     1055     1133
water_temp   -0.040     0.011   -0.062   -0.017 1.003     1072     1220

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI  Rhat Bulk_ESS Tail_ESS
shape   30.115     2.168   26.002   34.555 1.000     3067     2243

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).
```

Q2.2 What is the effect of water_temp on crab size on the response scale?

1. What is the effect of water_temp on crab size?

a) original output on the log scale: -0.039

b) your backtransformed value

```r
exp(-0.039)
```

```
[1] 0.9617507
```

c) the percent change that this translates to. Describe the effect using the proper units.

For every 1 degree Celsius increase in water temperature, there crab size decrease by 3.82%.

```r
(exp(-0.039)-1)*100
```

```
[1] -3.824929
```

2. Does it seem like the slope estimate is different from zero? Why?

Yes, the confidence interval for slope does not include zero.

Q2.3 Compare WAIC and PSIS of the two models

The model including water temperature and site was better predictive power that the model that only included water temperature.

```r
loo(m.watertemp.site)
```

```


Computed from 4000 by 392 log-likelihood matrix.

         Estimate   SE
elpd_loo   -938.3 13.7
p_loo        12.1  0.8
looic      1876.6 27.4
------
MCSE of elpd_loo is 0.1.
MCSE and ESS estimates assume MCMC draws (r_eff in [0.6, 1.8]).

All Pareto k estimates are good (k < 0.7).
See help('pareto-k-diagnostic') for details.
```

```r
loo(m.watertemp)
```

```
Computed from 4000 by 392 log-likelihood matrix.

         Estimate   SE
elpd_loo   -984.7 12.1
p_loo         2.8  0.2
looic      1969.5 24.3
------
MCSE of elpd_loo is 0.0.
MCSE and ESS estimates assume MCMC draws (r_eff in [0.6, 1.1]).

All Pareto k estimates are good (k < 0.7).
See help('pareto-k-diagnostic') for details.
```

```
waic(m.watertemp.site)
```

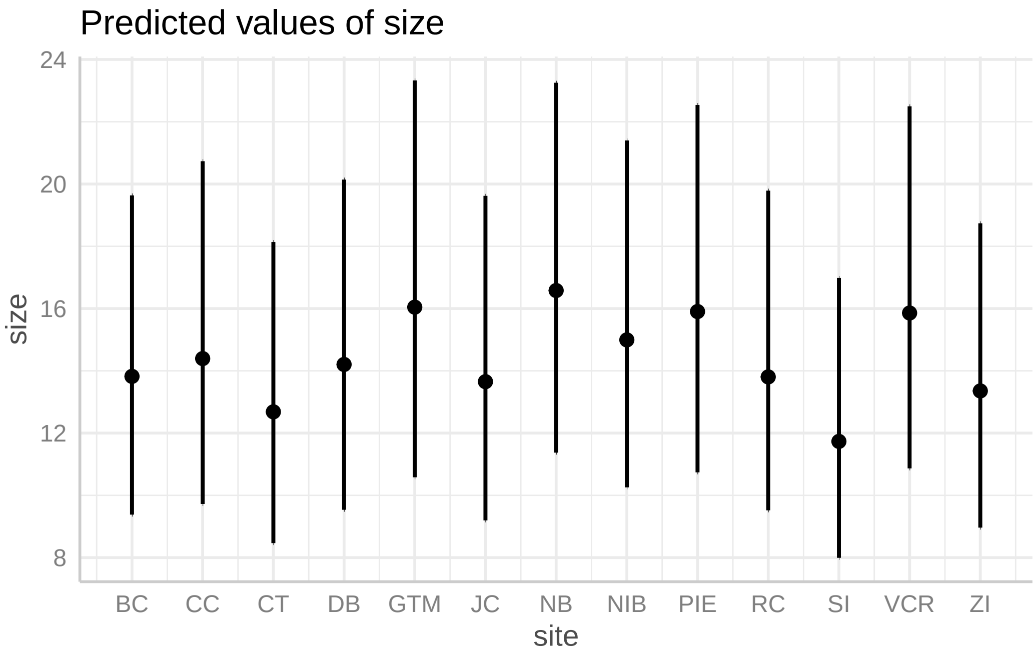
```
Computed from 4000 by 392 log-likelihood matrix.

          Estimate   SE
elpd_waic   -938.3 13.7
p_waic        12.0  0.8
waic        1876.6 27.4
```

```
waic(m.watertemp)
```

```
Computed from 4000 by 392 log-likelihood matrix.

          Estimate   SE
elpd_waic   -984.7 12.1
p_waic         2.8  0.2
waic        1969.5 24.3
```

Predict response of random effects

```
preds <- predict_response(m.watertemp.site,
                          interval = "prediction",
                                                    terms = "site",
                                                    type = "random")

plot(preds)
```


Predicted values of size
size
BC
CC
CT
DB
GTM
JC
NB
NIB
PIE
RC
SI
VCR
ZI
site