Bayesian workflow (saneesh)

## 1. Build the model

model\_1 <- brm(mass ~ length \* z, family = gaussian(), data = penguins).

## 2. Stan code

stancode(model.1)

Specify the response variable `y`, predictor variables `y, z`, and any necessary model options (e.g., family, priors, etc.).

## 3. Save the model.

save (model\_1, file= 'model\_1.Rdata')

## 4. Load the model

Load ('model\_1. Rdata')

## 4. Check model fit.

Carry out posterior predictive checks using the pp\_check() function to assess the fit of the model. This involves simulating data from the posterior predictive distribution and comparing these simulations to the observed data. You can create a variety of plots to assess different aspects of the fit, such as histograms of the observed data overlaid with simulated data, scatterplots of observed vs. simulated data, and plots of the residuals.

pp\_check(model\_1)

## 5. Check residuals

residual <- residuals(model\_1)

# to see the overall fit of the model

plot(residual)

# posterior predictive residuals against the predicted values

Plot the residuals against `y`

plot.residuals <- cbind(data, residuals(model\_1))

plot.residuals<- as.data.frame(plot.residuals)

plot.residuals %>% ggplot(aes(x= y, y= y)+

geom\_boxplot () + # for categorical variables

geom\_hline (yintercept= 0, ltr= 2, col= ‘red’) + labs (x= ‘y’, y= ‘residuals’)

# to visually evaluate how much the residuals deviate from zero, and whether there are any patterns in the residuals.

## 6. Summarise the model

summary(model\_1)

conditional\_effects(model\_1)

conditional\_effects(model\_1, effects = 'x')

conditional\_effects(model\_1, effects = 'z')