Model Selection

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04 June 2021

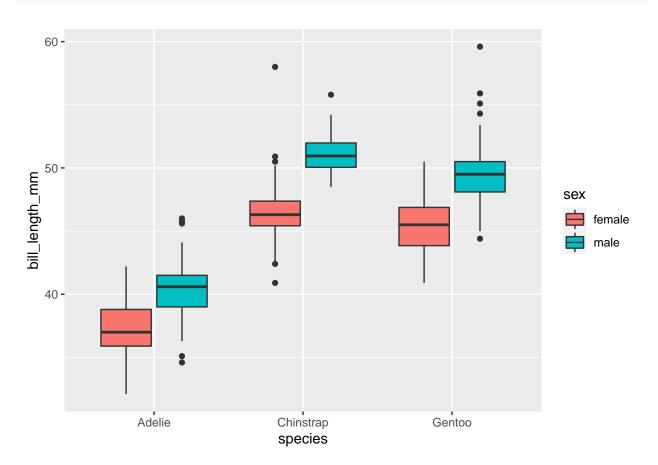
hypothesis testing

1. Import the palmerpenguin data

```
penguins_df <- penguins %>%
  drop_na()
```

2. Test the hypothesis that bill length differs between species.

```
penguins_df %>%
  ggplot(aes(x = species, y = bill_length_mm, fill = sex)) +
  geom_boxplot()
```



```
lm_df <- lm(bill_length_mm~species, data = penguins_df)
anova(lm_df)</pre>
```

3. Test the hypothesis that bill length differs by sex in addition to species.

```
lm_df2 <- lm(bill_length_mm~species + sex, data = penguins_df)
anova(lm_df,lm_df2)</pre>
```

```
## Analysis of Variance Table
##
## Model 1: bill_length_mm ~ species
## Model 2: bill_length_mm ~ species + sex
## Res.Df RSS Df Sum of Sq F Pr(>F)
## 1 330 2913.5
## 2 329 1777.8 1 1135.7 210.17 < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1</pre>
```

4. How should the p-values be interpreted.

Exploratory model building

Normally you would be doing this on a separate data set

- 5. Use forward selection to find the best model to explain bill length.
- 6. Build a set of candidate models to explain bill depth using one or two predictors.
- 7. Extract the AIC from each models (hint use function AIC). Which is the better model?
- 8. Calculate the deltaAIC for each model.
- 9. Calculate the AIC weights for each model. Interpret these weights.

Collinearity

- 12. Make a model predicting bill_length from all other variables. Find the VIF of each predictor. Are there any problem variables? olsrr::ols_vif_tol
- 13. Use GGally::ggpairs() to plot the data to try to identify the cause of any high vif.
- 14. Use MASS::mvrnorm() to simulate 100 observation of two predictor variables (x and z) with a given correlation. Simulate a response variable y = b0 + b1x + b2z. Test how the uncertainty in the coefficients changes with the correlation (and hence vif) of the predictor variables.