Multiple Regression & Model Selection

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1 Multiple Regression and Model Selection

1.1 Load packages

```
library(tidyverse)
library(broom)
library(palmerpenguins)
library(data.table)
library(performance)
```

```r
library(patchwork)
library(car) #to check collinearity
```

My favorite mixed models selection tutorial: Our Coding Club

1.2 Get our penguin data ready!

```r
penguins <- palmerpenguins::penguins

head(penguins)
```

```
# A tibble: 6 x 8
  species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
  <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
1 Adelie  Torgersen           39.1          18.7               181        3750
2 Adelie  Torgersen           39.5          17.4               186        3800
3 Adelie  Torgersen           40.3          18                 195        3250
4 Adelie  Torgersen           NA            NA                  NA          NA
5 Adelie  Torgersen           36.7          19.3               193        3450
6 Adelie  Torgersen           39.3          20.6               190        3650
# i 2 more variables: sex <fct>, year <int>
```

```r
penguins<-drop_na(penguins)

penguins$year=as.factor(penguins$year) #we are interested in year as a grouping/categorica
```

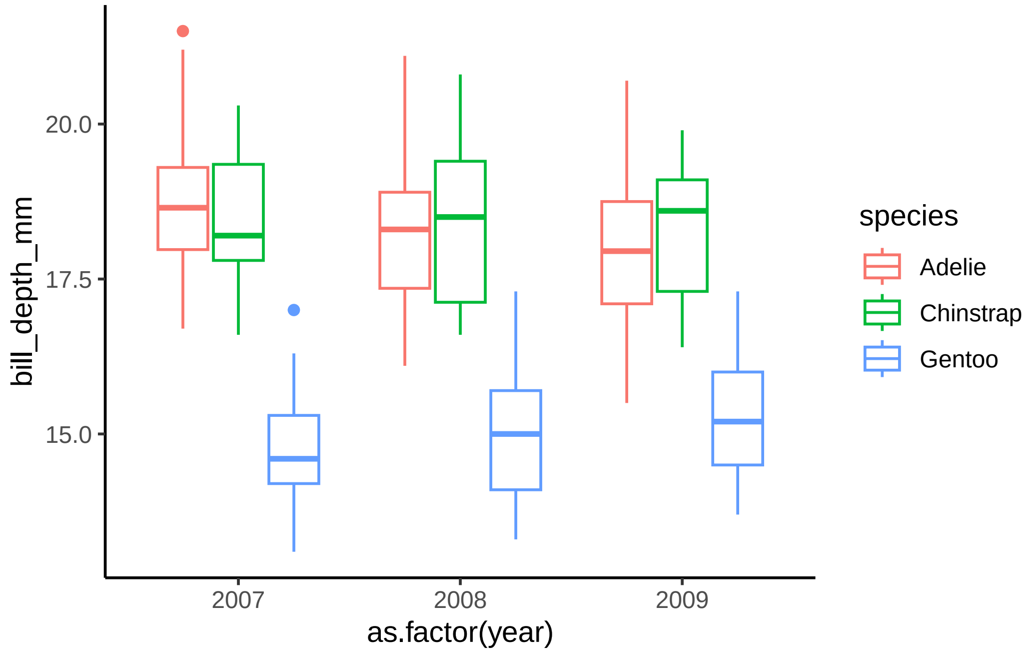
1.3 What is the effect of year on bill depth by species?

1.3.1 1.) Make a graph to visualize!

We will start with a boxplot for a quick check. We would eventually want to calculate means and error bars for the final visualization though! Note that the graph below is a good way to view the interaction of our explanatory variables, which is not what we modeled… We only consider the additive effects (each variable on its own)

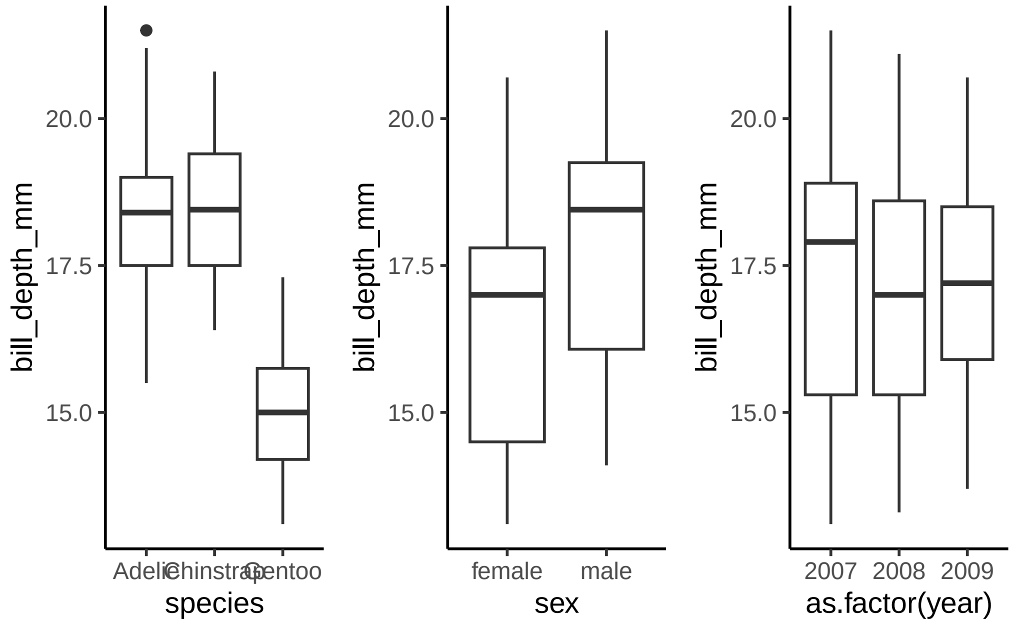
```r
# effect of year on bill depth by species
ggplot(data=penguins, aes(x=as.factor(year), y=bill_depth_mm, color=species))+
  geom_boxplot()+
```

```
  theme_classic()
```



Visualization of each variable on its own:

```
speciesgraph<-ggplot(data=penguins, aes(x=species, y=bill_depth_mm))+
  geom_boxplot()+
  theme_classic()

sexgraph<-ggplot(data=penguins, aes(x=sex, y=bill_depth_mm))+
  geom_boxplot()+
  theme_classic()

yeargraph<-ggplot(data=penguins, aes(x=as.factor(year), y=bill_depth_mm))+
  geom_boxplot()+
  theme_classic()

speciesgraph+sexgraph+yeargraph
```



1.3.2 2.) Build the model

```
#build the model
lm1<- lm(bill_depth_mm ~ species+sex+year, data=penguins)
```

1.3.3 3.) view tabular results

```
summary(lm1) #check R2 and p-value! How well does the model fit?
```

```
Call:
lm(formula = bill_depth_mm ~ species + sex + year, data = penguins)

Residuals:
     Min       1Q   Median       3Q      Max 
-2.07890 -0.56431 -0.00782  0.48485  3.12581 

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)    
(Intercept)      17.71835    0.10760 164.672   <2e-16 ***
```

```
speciesChinstrap  0.05649    0.12232   0.462   0.6445
speciesGentoo    -3.36375    0.10268 -32.760   <2e-16 ***
sexmale           1.50471    0.09107  16.523   <2e-16 ***
year2008         -0.21053    0.11374  -1.851   0.0651 .
year2009         -0.14416    0.11239  -1.283   0.2005
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8308 on 327 degrees of freedom
Multiple R-squared:  0.8247,	Adjusted R-squared:  0.822
F-statistic: 307.6 on 5 and 327 DF,  p-value: < 2.2e-16
```

```
summary(lm1)$coefficient #just the coef table from the summary!
```

```
                    Estimate Std. Error     t value      Pr(>|t|)
(Intercept)      17.71835149 0.10759801 164.6717403 1.229960e-316
speciesChinstrap  0.05649237 0.12231501   0.4618597  6.444891e-01
speciesGentoo    -3.36375169 0.10267709 -32.7604888 2.664705e-105
sexmale           1.50470770 0.09106922  16.5226813  5.184519e-45
year2008         -0.21053181 0.11373677  -1.8510443  6.506474e-02
year2009         -0.14416134 0.11238907  -1.2826989  2.005060e-01
```

```
anova(lm1) # an ANOVA table of our lm
```

```
Analysis of Variance Table

Response: bill_depth_mm
           Df Sum Sq Mean Sq  F value Pr(>F)    
species     2 870.79  435.39 630.7435 <2e-16 ***
sex         1 188.50  188.50 273.0716 <2e-16 ***
year        2   2.45    1.23   1.7771 0.1708    
Residuals 327 225.72    0.69                    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
confint(lm1) #CIs for our model predictors!
```

```
                       2.5 %      97.5 %
(Intercept)       17.5066798 17.93002315
speciesChinstrap -0.1841312  0.29711599
speciesGentoo    -3.5657427 -3.16176068
sexmale           1.3255522  1.68386318
year2008         -0.4342799  0.01321630
year2009         -0.3652582  0.07693551
```

-t / pvalue tells us whether there is a sig association between the predictor and the outcome variable…

-in stats terms, this tells us whether the beta coef of predictor is significantly different form zero

-coefficient can be interpreted as average effect on y of a one unit increase in predictor, holding all other predictors fixed

Here, we have an additive model and we see from the anova table and the lm summary that there are significant effects of species and sex on bill depth but that there is not effect on year. Next, let's look at the data again to confirm!

1.3.4 4.) Model fit assessment

Here, we want to know how well the model represent the data. We need: 1. The R2 value of the model (closer to 1 is best) 2. The p-value of the model (<0.05 is required for there to be a relationship) 3. We can calculate residual standard error. Lower = more accurate!

The R2 and p are in the summary! Below is the formula for RMSE

```r
summary(lm1)
```

```
Call:
lm(formula = bill_depth_mm ~ species + sex + year, data = penguins)

Residuals:
     Min       1Q   Median       3Q      Max 
-2.07890 -0.56431 -0.00782  0.48485  3.12581 

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)    
(Intercept)      17.71835    0.10760 164.672   <2e-16 ***
speciesChinstrap  0.05649    0.12232   0.462   0.6445    
speciesGentoo    -3.36375    0.10268 -32.760   <2e-16 ***
```

```
sexmale           1.50471    0.09107  16.523   <2e-16 ***
year2008         -0.21053    0.11374  -1.851   0.0651 .
year2009         -0.14416    0.11239  -1.283   0.2005
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8308 on 327 degrees of freedom
Multiple R-squared:  0.8247,    Adjusted R-squared:  0.822
F-statistic: 307.6 on 5 and 327 DF,  p-value: < 2.2e-16
```

```r
#RSE: <- LOWER RSE= more accurate the model!
sigma(lm1)
```

```
[1] 0.8308337
```

```r
mean(penguins$bill_depth_mm)
```

```
[1] 17.16486
```

```r
sigma(lm1)/mean(penguins$bill_depth_mm)
```

```
[1] 0.04840316
```

```r
#0.048, or 4.8% error rate
```

We can also get this information from the performance package using model_performance. This function tells us many things, including R2 and RMSE. We will discuss the rest of this later

```r
model_performance(lm1)
```

```
# Indices of model performance

AIC     |    AICc |     BIC |    R2 | R2 (adj.) |  RMSE | Sigma
---------------------------------------------------------------
829.532 | 829.876 | 856.189 | 0.825 |     0.822 | 0.823 | 0.831
```

1.3.5 5.) A 95% CI plot of model coefficients

combine data! Use tidy() from the broom package to get nice neat dataframes from models

```
coefs<-tidy(lm1, quick=FALSE)
coefs
```

```
# A tibble: 6 x 5
  term              estimate std.error statistic   p.value
  <chr>                <dbl>     <dbl>     <dbl>     <dbl>
1 (Intercept)        17.7       0.108    165.    1.23e-316
2 speciesChinstrap    0.0565    0.122      0.462 6.44e-  1
3 speciesGentoo      -3.36      0.103    -32.8   2.66e-105
4 sexmale             1.50      0.0911    16.5   5.18e- 45
5 year2008           -0.211     0.114     -1.85  6.51e-  2
6 year2009           -0.144     0.112     -1.28  2.01e-  1
```

```
ci<-data.table(confint(lm1), keep.rownames='term')
ci
```

```
               term      2.5 %      97.5 %
1:      (Intercept) 17.5066798 17.93002315
2: speciesChinstrap -0.1841312  0.29711599
3:    speciesGentoo -3.5657427 -3.16176068
4:          sexmale  1.3255522  1.68386318
5:         year2008 -0.4342799  0.01321630
6:         year2009 -0.3652582  0.07693551
```

```
cidf<-cbind(coefs,ci)
cidf
```

```
              term    estimate  std.error   statistic       p.value
1      (Intercept) 17.71835149 0.10759801 164.6717403 1.229960e-316
2 speciesChinstrap  0.05649237 0.12231501   0.4618597  6.444891e-01
3    speciesGentoo -3.36375169 0.10267709 -32.7604888 2.664705e-105
4          sexmale  1.50470770 0.09106922  16.5226813  5.184519e-45
5         year2008 -0.21053181 0.11373677  -1.8510443  6.506474e-02
6         year2009 -0.14416134 0.11238907  -1.2826989  2.005060e-01
              term      2.5 %      97.5 %
```

```
1      (Intercept) 17.5066798 17.93002315
2 speciesChinstrap -0.1841312  0.29711599
3    speciesGentoo -3.5657427 -3.16176068
4          sexmale  1.3255522  1.68386318
5         year2008 -0.4342799  0.01321630
6         year2009 -0.3652582  0.07693551
```

```
colnames(cidf)
```

```
[1] "term"      "estimate"  "std.error" "statistic" "p.value"   "term"
[7] "2.5 %"     "97.5 %"
```

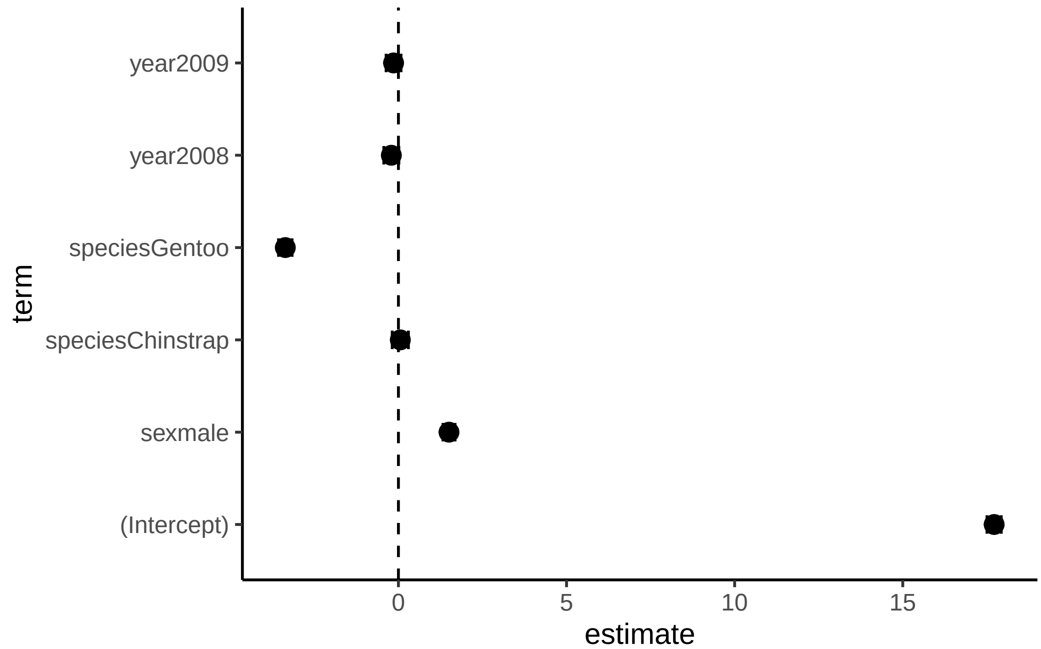
```
cidf<-cidf[,-6]

cidf<- cidf %>%
  rename("lower"="2.5 %",
         "upper"="97.5 %")

cidf
```

```
              term    estimate  std.error   statistic       p.value      lower
1      (Intercept) 17.71835149 0.10759801 164.6717403 1.229960e-316 17.5066798
2 speciesChinstrap  0.05649237 0.12231501   0.4618597  6.444891e-01 -0.1841312
3    speciesGentoo -3.36375169 0.10267709 -32.7604888 2.664705e-105 -3.5657427
4          sexmale  1.50470770 0.09106922  16.5226813  5.184519e-45  1.3255522
5         year2008 -0.21053181 0.11373677  -1.8510443  6.506474e-02 -0.4342799
6         year2009 -0.14416134 0.11238907  -1.2826989  2.005060e-01 -0.3652582
        upper
1 17.93002315
2  0.29711599
3 -3.16176068
4  1.68386318
5  0.01321630
6  0.07693551
```

```
cidf$term=as.factor(cidf$term)
```

Now make a plot!

```r
ggplot(data=cidf, aes(x=estimate, y=term))+
  geom_vline(xintercept = 0, linetype=2)+
  geom_point(size=3)+
  geom_errorbarh(aes(xmax=lower, xmin=upper),height=0.2)+
  theme_classic()
```



Note that there are many ways to build a dataframe and plot for these. This is just one example. Here we can visualize that the effects of each variable individually are not very large.

1.4 An example with numerical vars

1.4.1 1.) Run an additive model and an interactive model. View summaries

```r
lm2<-lm(bill_depth_mm ~ bill_length_mm + species, data=penguins)
lm3<-lm(bill_depth_mm ~ bill_length_mm * species, data=penguins)

#look at summary
summary(lm2)
```

```
Call:
lm(formula = bill_depth_mm ~ bill_length_mm + species, data = penguins)

Residuals:
    Min      1Q  Median      3Q     Max 
-2.4579 -0.6814 -0.0431  0.5441  3.5994 

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)    
(Intercept)      10.56526    0.69093  15.291  < 2e-16 ***
bill_length_mm    0.20044    0.01768  11.337  < 2e-16 ***
speciesChinstrap -1.93308    0.22572  -8.564 4.26e-16 ***
speciesGentoo    -5.10332    0.19440 -26.252  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9543 on 329 degrees of freedom
Multiple R-squared:  0.7673,	Adjusted R-squared:  0.7652 
F-statistic: 361.6 on 3 and 329 DF,  p-value: < 2.2e-16
```

```r
summary(lm3)
```

```
Call:
lm(formula = bill_depth_mm ~ bill_length_mm * species, data = penguins)

Residuals:
    Min      1Q  Median      3Q     Max 
-2.6574 -0.6559 -0.0483  0.5203  3.4990 

Coefficients:
                                Estimate Std. Error t value Pr(>|t|)    
(Intercept)                     11.48771    1.15987   9.904  < 2e-16 ***
bill_length_mm                   0.17668    0.02981   5.928 7.79e-09 ***
speciesChinstrap                -3.91857    2.06731  -1.895   0.0589 .  
speciesGentoo                   -6.36675    1.77990  -3.577   0.0004 ***
bill_length_mm:speciesChinstrap  0.04553    0.04594   0.991   0.3224    
bill_length_mm:speciesGentoo     0.03093    0.04112   0.752   0.4525    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9556 on 327 degrees of freedom
```

```
Multiple R-squared:  0.7681,	Adjusted R-squared:  0.7645
F-statistic: 216.6 on 5 and 327 DF,  p-value: < 2.2e-16
```

1.4.2 2.) make the coef data neat and look at model fits

```r
tidy(lm2)
```

```
# A tibble: 4 x 5
  term              estimate std.error statistic  p.value
  <chr>                <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)         10.6      0.691      15.3  2.98e-40
2 bill_length_mm       0.200    0.0177     11.3  2.26e-25
3 speciesChinstrap    -1.93     0.226      -8.56 4.26e-16
4 speciesGentoo       -5.10     0.194     -26.3  1.04e-82
```

```r
tidy(lm3)
```

```
# A tibble: 6 x 5
  term                            estimate std.error statistic  p.value
  <chr>                              <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)                      11.5       1.16       9.90  2.14e-20
2 bill_length_mm                    0.177     0.0298     5.93  7.79e- 9
3 speciesChinstrap                 -3.92      2.07      -1.90  5.89e- 2
4 speciesGentoo                    -6.37      1.78      -3.58  4.00e- 4
5 bill_length_mm:speciesChinstrap   0.0455    0.0459     0.991 3.22e- 1
6 bill_length_mm:speciesGentoo      0.0309    0.0411     0.752 4.52e- 1
```

```r
#have a look at model fit
glance(lm2) #R2 is really good-> 76.5!
```

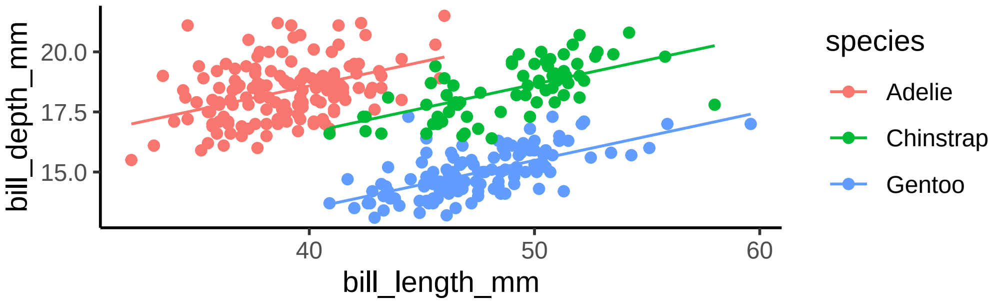
```
# A tibble: 1 x 12
  r.squared adj.r.squared sigma statistic   p.value    df logLik   AIC   BIC
      <dbl>         <dbl> <dbl>     <dbl>     <dbl> <dbl>  <dbl> <dbl> <dbl>
1     0.767         0.765 0.954      362. 8.88e-104     3  -455.  920.  939.
# i 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

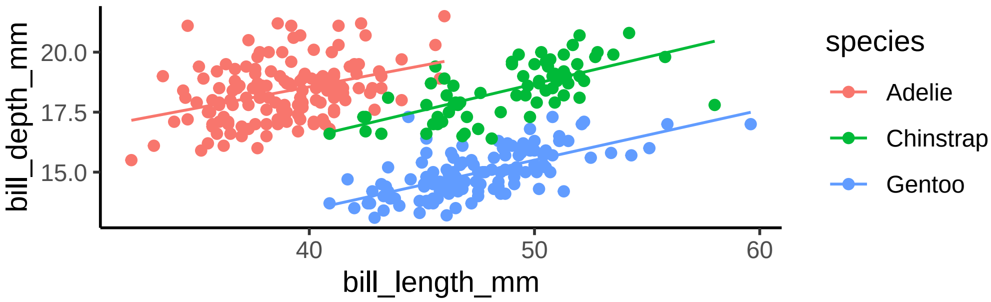
```r
glance(lm3) #r2 is 0.768!
```

```
# A tibble: 1 x 12
  r.squared adj.r.squared sigma statistic   p.value    df logLik   AIC   BIC
      <dbl>         <dbl> <dbl>     <dbl>     <dbl> <dbl>  <dbl> <dbl> <dbl>
1     0.768         0.765 0.956      217. 1.87e-101     5  -454.  923.  949.
# i 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

1.4.3 3.) make a pretty graph!

```
lm2g<-lm2 %>%
  augment() %>%
  ggplot(aes(x=bill_length_mm, y=bill_depth_mm, color=species))+
  geom_point()+
  geom_line(aes(y=.fitted))+
  theme_classic()

lm3g<-lm3 %>%
  augment() %>%
  ggplot(aes(x=bill_length_mm, y=bill_depth_mm, color=species))+
  geom_point()+
  geom_line(aes(y=.fitted))+
  theme_classic()

lm2g/lm3g #lm2 has same y int for all! lm3 does not (because of the interaction term!!!)
```





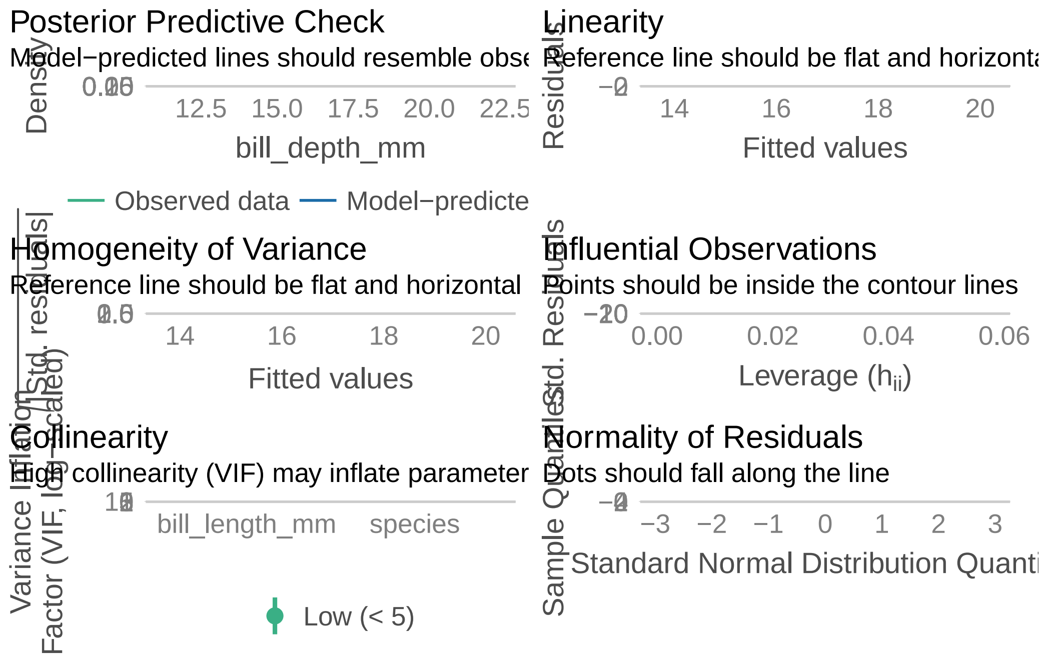
1.5 Model Selection

1.5.1 1.) test assumptions (use performance!)

```
model_performance(lm2)
```

```
# Indices of model performance

AIC     |     AICc |      BIC |    R2 | R2 (adj.) |  RMSE | Sigma
---------------------------------------------------------------
919.835 | 920.018 | 938.875 | 0.767 |     0.765 | 0.949 | 0.954
```

```
check_model(lm2)#things look good, including low collinearity (VIF)
```




```r
vif(lm2)
```

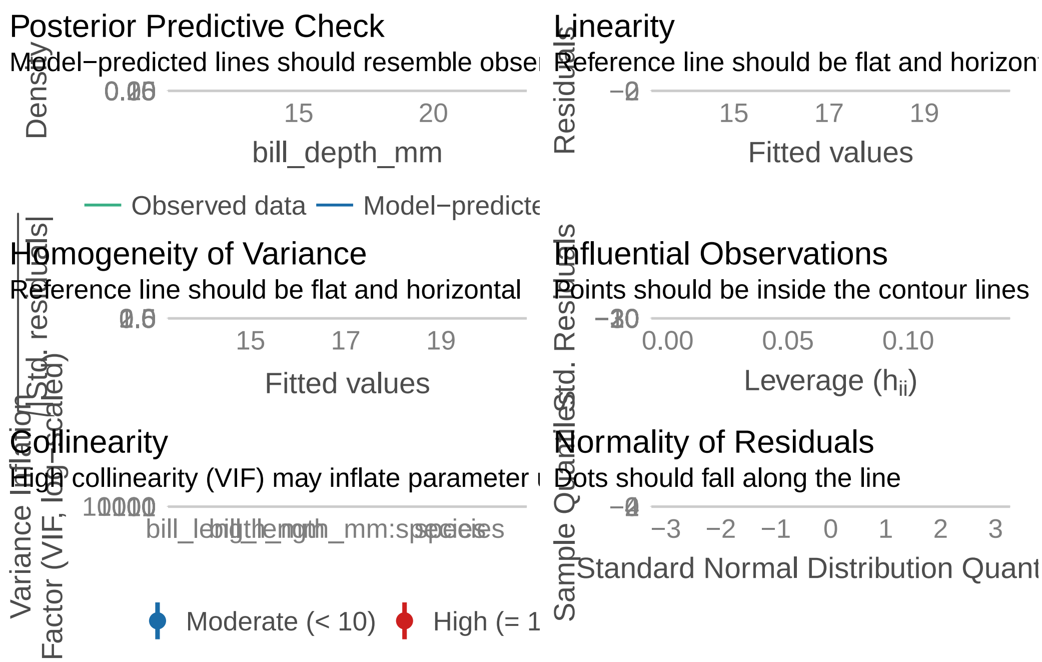
```
                    GVIF Df GVIF^(1/(2*Df))
bill_length_mm 3.407875  1        1.846043
species        3.407875  2        1.358692
```

```r
model_performance(lm3)
```

```
# Indices of model performance

AIC     |    AICc |     BIC |    R2 | R2 (adj.) |  RMSE | Sigma
---------------------------------------------------------------
922.729 | 923.074 | 949.386 | 0.768 |     0.765 | 0.947 | 0.956
```

```r
check_model(lm3) #things look good, but we have super high VIF
```

```
Model has interaction terms. VIFs might be inflated.
  You may check multicollinearity among predictors of a model without
  interaction terms.
```




```
check_collinearity(lm3) #a table of collinearity results - we would need to remove stuff f
```

```
Model has interaction terms. VIFs might be inflated.
  You may check multicollinearity among predictors of a model without
  interaction terms.


# Check for Multicollinearity

Moderate Correlation

           Term  VIF           VIF 95% CI Increased SE Tolerance
 bill_length_mm 9.66 [    7.94,    11.81]         3.11      0.10
 Tolerance 95% CI
     [0.08, 0.13]

High Correlation

                   Term      VIF           VIF 95% CI Increased SE Tolerance
                species 49899.43 [40473.88, 61520.04]       223.38  2.00e-05
 bill_length_mm:species 64717.85 [52493.21, 79789.42]       254.40  1.55e-05
 Tolerance 95% CI
```

```
[0.00, 0.00]
[0.00, 0.00]
```

```
vif(lm3) #gives us a more useful table- tells us that species and species*bill length are
```

```
there are higher-order terms (interactions) in this model
consider setting type = 'predictor'; see ?vif
```

```
                              GVIF Df GVIF^(1/(2*Df))
bill_length_mm            9.658784  1        3.107858
species               49899.425896  2       14.945962
bill_length_mm:species 64717.849261  2       15.949829
```

What do we do? We remove interaction terms one by one, thereby simplifying the model, until the VIF are low enough to be meaningful (all below 5 is a good rule of thumb)

since the model without the * is just lm2, we are all set.

1.5.2 2.) check the model performances and choose the best fit

```
compare_performance(lm2,lm3,rank=TRUE)
```

```
# Comparison of Model Performance Indices

Name | Model |    R2 | R2 (adj.) |  RMSE | Sigma | AIC weights | AICc weights | BIC weights
------------------------------------------------------------------------------------------
lm2  |    lm | 0.767 |     0.765 | 0.949 | 0.954 |       0.810 |        0.822 |       0.995
lm3  |    lm | 0.768 |     0.765 | 0.947 | 0.956 |       0.190 |        0.178 |       0.005
```

-This is a comprehensive model check that uses many vars to assess the best model.

-Here, lm2 wins easily! R2 are about the same, RMSE (residual mean square error) is about the same.

-AICweights tell us thje relative likelihood of a model– closer to 1 is best. ***when you look at AIC scores (slightly different from AIC weights, the lower the value, the better)

1.5.3 3.) MORE COMPLEX EXAMPLE :)

```
lm4<-lm(bill_depth_mm ~ bill_length_mm * species * sex, data=penguins)

#look at summary
summary(lm4)
```

```
Call:
lm(formula = bill_depth_mm ~ bill_length_mm * species * sex,
    data = penguins)

Residuals:
     Min       1Q   Median       3Q      Max 
-2.06730 -0.52452 -0.06471  0.45593  2.90319 

Coefficients:
                                        Estimate Std. Error t value Pr(>|t|)
(Intercept)                             14.84023    1.77185   8.376 1.73e-15
bill_length_mm                           0.07466    0.04749   1.572   0.1169
speciesChinstrap                        -0.25160    2.77579  -0.091   0.9278
speciesGentoo                           -5.76780    2.98938  -1.929   0.0546
sexmale                                  4.92359    2.46355   1.999   0.0465
bill_length_mm:speciesChinstrap         -0.01026    0.06596  -0.155   0.8765
bill_length_mm:speciesGentoo             0.03871    0.07101   0.545   0.5860
bill_length_mm:sexmale                  -0.09177    0.06360  -1.443   0.1500
speciesChinstrap:sexmale               -11.35403    5.67926  -1.999   0.0464
speciesGentoo:sexmale                   -2.41202    3.94469  -0.611   0.5413
bill_length_mm:speciesChinstrap:sexmale  0.24451    0.12006   2.037   0.0425
bill_length_mm:speciesGentoo:sexmale     0.06197    0.09131   0.679   0.4978
                                           
(Intercept)                             ***
bill_length_mm                             
speciesChinstrap                           
speciesGentoo                           .  
sexmale                                 *  
bill_length_mm:speciesChinstrap            
bill_length_mm:speciesGentoo               
bill_length_mm:sexmale                     
speciesChinstrap:sexmale                *  
speciesGentoo:sexmale                      
bill_length_mm:speciesChinstrap:sexmale *  
```

```
bill_length_mm:speciesGentoo:sexmale
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8175 on 321 degrees of freedom
Multiple R-squared:  0.8334,    Adjusted R-squared:  0.8277
F-statistic: 145.9 on 11 and 321 DF,  p-value: < 2.2e-16
```

```
#make that pretty
tidy(lm4)
```

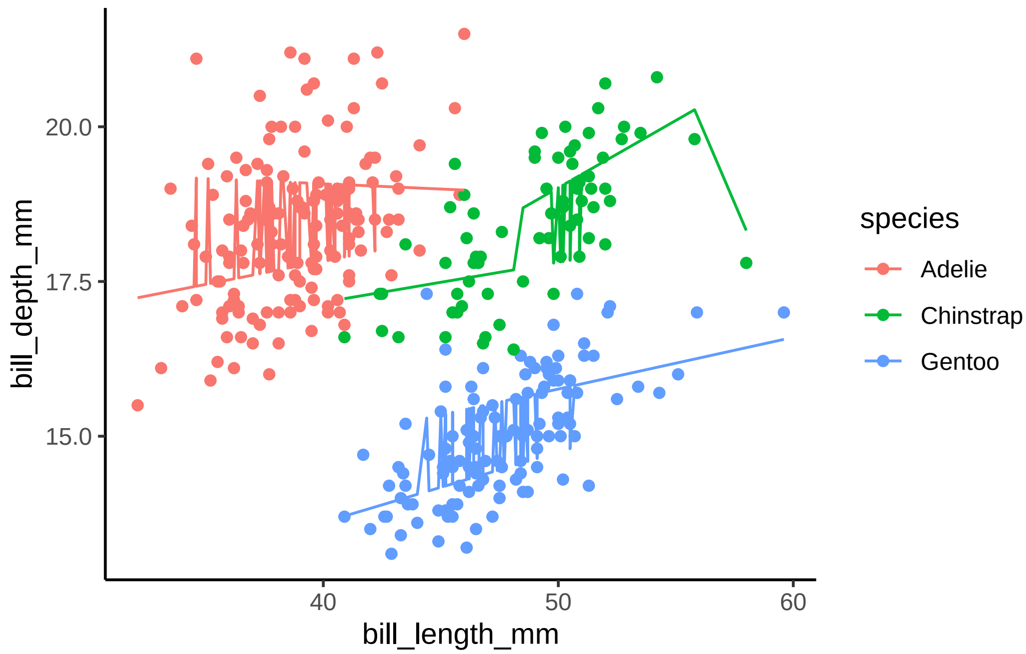
```
# A tibble: 12 x 5
   term                                  estimate std.error statistic  p.value
   <chr>                                    <dbl>     <dbl>     <dbl>    <dbl>
 1 (Intercept)                            14.8       1.77      8.38   1.73e-15
 2 bill_length_mm                          0.0747    0.0475    1.57   1.17e- 1
 3 speciesChinstrap                       -0.252     2.78     -0.0906 9.28e- 1
 4 speciesGentoo                          -5.77      2.99     -1.93   5.46e- 2
 5 sexmale                                 4.92      2.46      2.00   4.65e- 2
 6 bill_length_mm:speciesChinstrap        -0.0103    0.0660   -0.155  8.77e- 1
 7 bill_length_mm:speciesGentoo            0.0387    0.0710    0.545  5.86e- 1
 8 bill_length_mm:sexmale                 -0.0918    0.0636   -1.44   1.50e- 1
 9 speciesChinstrap:sexmale              -11.4       5.68     -2.00   4.64e- 2
10 speciesGentoo:sexmale                  -2.41      3.94     -0.611  5.41e- 1
11 bill_length_mm:speciesChinstrap:sexmale  0.245    0.120     2.04   4.25e- 2
12 bill_length_mm:speciesGentoo:sexmale    0.0620    0.0913    0.679  4.98e- 1
```

```
#look at fit
glance(lm4) #nice r2!
```

```
# A tibble: 1 x 12
  r.squared adj.r.squared sigma statistic   p.value    df logLik   AIC   BIC
      <dbl>         <dbl> <dbl>     <dbl>     <dbl> <dbl>  <dbl> <dbl> <dbl>
1     0.833         0.828 0.818      146. 9.55e-118    11  -399.  825.  874.
# i 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

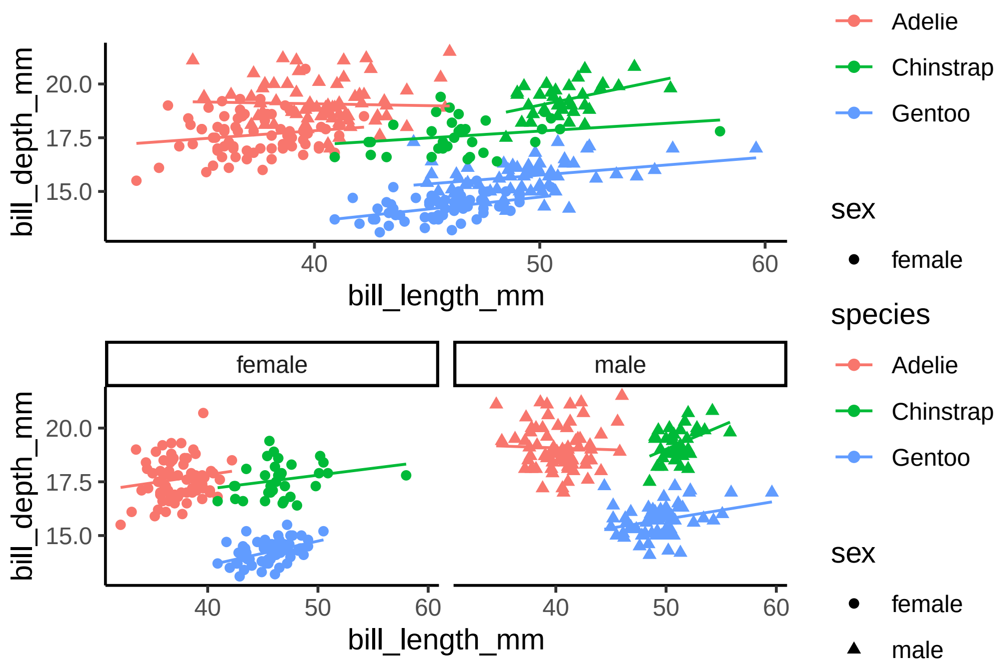
```
# make a pretty graph!
lm4 %>%
  augment() %>%
```

```
ggplot(aes(x=bill_length_mm, y=bill_depth_mm,color=species))+
  geom_point()+
  geom_line(aes(y=.fitted))+
  theme_classic()
```




```
#oops, that isn't quite right. What are we missing?
lm4g2<-lm4 %>%
  augment() %>%
  ggplot(aes(x=bill_length_mm, y=bill_depth_mm,color=species, shape=sex))+
  geom_point()+
  geom_line(aes(y=.fitted))+
  theme_classic()

#OR

lm4g3<-lm4 %>%
  augment() %>%
  ggplot(aes(x=bill_length_mm, y=bill_depth_mm,color=species, shape=sex))+
  geom_point()+
  geom_line(aes(y=.fitted))+
  theme_classic()+
```

```
  facet_wrap(~sex)

#compare graphs!
lm4g2/lm4g3
```



1.5.3.1 CIs and a graph for this one!

```
coefs<-tidy(lm4)
coefs
```

```
# A tibble: 12 x 5
   term                             estimate std.error statistic  p.value
   <chr>                               <dbl>     <dbl>     <dbl>    <dbl>
 1 (Intercept)                       14.8        1.77     8.38   1.73e-15
 2 bill_length_mm                     0.0747     0.0475   1.57   1.17e- 1
 3 speciesChinstrap                  -0.252      2.78    -0.0906 9.28e- 1
 4 speciesGentoo                     -5.77       2.99    -1.93   5.46e- 2
 5 sexmale                            4.92       2.46     2.00   4.65e- 2
 6 bill_length_mm:speciesChinstrap   -0.0103     0.0660  -0.155  8.77e- 1
 7 bill_length_mm:speciesGentoo       0.0387     0.0710   0.545  5.86e- 1
 8 bill_length_mm:sexmale            -0.0918     0.0636  -1.44   1.50e- 1
```

```
 9 speciesChinstrap:sexmale                 -11.4       5.68      -2.00   4.64e- 2
10 speciesGentoo:sexmale                     -2.41      3.94      -0.611  5.41e- 1
11 bill_length_mm:speciesChinstrap:sexmale    0.245     0.120      2.04   4.25e- 2
12 bill_length_mm:speciesGentoo:sexmale       0.0620    0.0913     0.679  4.98e- 1
```

```
cis<-data.table(confint(lm4), keep.rownames = 'term')
cis
```

```
                                       term         2.5 %      97.5 %
 1:                             (Intercept)  11.354321139 18.32613470
 2:                          bill_length_mm  -0.018764802  0.16808708
 3:                        speciesChinstrap  -5.712636771  5.20943941
 4:                           speciesGentoo -11.649049135  0.11344307
 5:                                 sexmale   0.076849623  9.77033563
 6:         bill_length_mm:speciesChinstrap  -0.140025236  0.11951459
 7:            bill_length_mm:speciesGentoo  -0.100987370  0.17840241
 8:                  bill_length_mm:sexmale  -0.216904270  0.03335517
 9:                speciesChinstrap:sexmale -22.527308826 -0.18075321
10:                   speciesGentoo:sexmale -10.172726533  5.34869591
11: bill_length_mm:speciesChinstrap:sexmale   0.008304843  0.48071943
12:    bill_length_mm:speciesGentoo:sexmale  -0.117669226  0.24160110
```

```
CI<-merge(coefs,cis)
CI
```

```
                                      term     estimate  std.error   statistic
1                              (Intercept)  14.84022792 1.77185076  8.37555183
2                           bill_length_mm   0.07466114 0.04748745  1.57222883
3                   bill_length_mm:sexmale  -0.09177455 0.06360216 -1.44294716
4          bill_length_mm:speciesChinstrap  -0.01025532 0.06596072 -0.15547623
5  bill_length_mm:speciesChinstrap:sexmale   0.24451214 0.12006175  2.03655314
6             bill_length_mm:speciesGentoo   0.03870752 0.07100548  0.54513425
7     bill_length_mm:speciesGentoo:sexmale   0.06196594 0.09130672  0.67865695
8                                  sexmale   4.92359263 2.46354990  1.99857638
9                         speciesChinstrap  -0.25159868 2.77578981 -0.09064039
10                speciesChinstrap:sexmale -11.35403102 5.67926283 -1.99920859
11                           speciesGentoo  -5.76780303 2.98937724 -1.92943298
12                   speciesGentoo:sexmale  -2.41201531 3.94469014 -0.61145875
        p.value         2.5 %      97.5 %
1  1.731943e-15  11.354321139 18.32613470
```

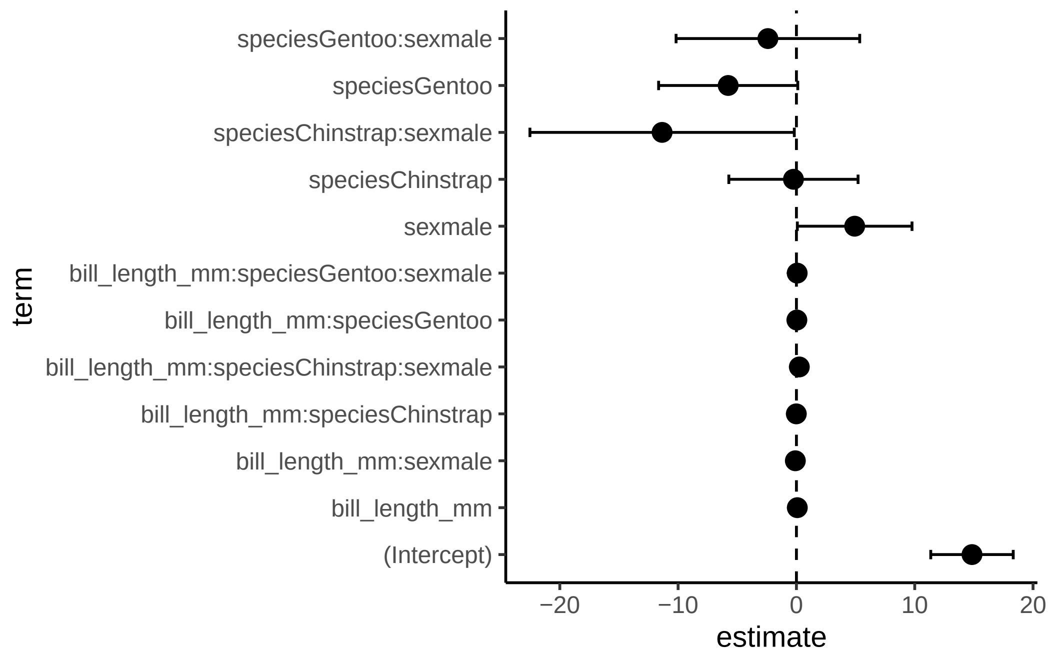
```
2  1.168826e-01  -0.018764802  0.16808708
3  1.500104e-01  -0.216904270  0.03335517
4  8.765436e-01  -0.140025236  0.11951459
5  4.251519e-02   0.008304843  0.48071943
6  5.860397e-01  -0.100987370  0.17840241
7  4.978442e-01  -0.117669226  0.24160110
8  4.649725e-02   0.076849623  9.77033563
9  9.278349e-01  -5.712636771  5.20943941
10 4.642846e-02 -22.527308826 -0.18075321
11 5.455827e-02 -11.649049135  0.11344307
12 5.413287e-01 -10.172726533  5.34869591
```

```r
CI<- CI %>%
  rename("lower"="2.5 %",
         "upper"="97.5 %")
CI
```

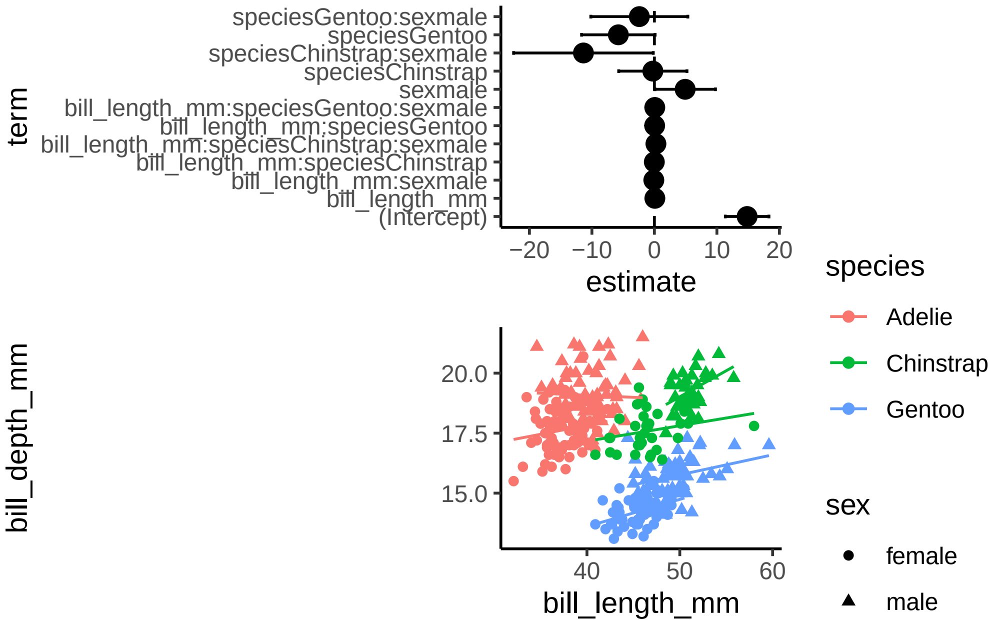
```
                                      term     estimate  std.error   statistic
1                              (Intercept)  14.84022792 1.77185076  8.37555183
2                           bill_length_mm   0.07466114 0.04748745  1.57222883
3                   bill_length_mm:sexmale  -0.09177455 0.06360216 -1.44294716
4          bill_length_mm:speciesChinstrap  -0.01025532 0.06596072 -0.15547623
5  bill_length_mm:speciesChinstrap:sexmale   0.24451214 0.12006175  2.03655314
6             bill_length_mm:speciesGentoo   0.03870752 0.07100548  0.54513425
7     bill_length_mm:speciesGentoo:sexmale   0.06196594 0.09130672  0.67865695
8                                  sexmale   4.92359263 2.46354990  1.99857638
9                         speciesChinstrap  -0.25159868 2.77578981 -0.09064039
10                speciesChinstrap:sexmale -11.35403102 5.67926283 -1.99920859
11                           speciesGentoo  -5.76780303 2.98937724 -1.92943298
12                   speciesGentoo:sexmale  -2.41201531 3.94469014 -0.61145875
        p.value         lower       upper
1  1.731943e-15  11.354321139 18.32613470
2  1.168826e-01  -0.018764802  0.16808708
3  1.500104e-01  -0.216904270  0.03335517
4  8.765436e-01  -0.140025236  0.11951459
5  4.251519e-02   0.008304843  0.48071943
6  5.860397e-01  -0.100987370  0.17840241
7  4.978442e-01  -0.117669226  0.24160110
8  4.649725e-02   0.076849623  9.77033563
9  9.278349e-01  -5.712636771  5.20943941
10 4.642846e-02 -22.527308826 -0.18075321
11 5.455827e-02 -11.649049135  0.11344307
```

```
12 5.413287e-01 -10.172726533  5.34869591
```

```
ciplot<-ggplot(data=CI, aes(x=estimate, y=term))+
  geom_vline(xintercept = 0, linetype=2)+
  geom_point(size=3)+
  geom_errorbarh(aes(xmin=lower, xmax=upper), height=0.2)+
  theme_classic()

ciplot
```




```
#a graph of the good stuff
ciplot/lm4g2
```


speciesGentoo:sexmale
speciesGentoo
speciesChinstrap:sexmale
speciesChinstrap
sexmale
bill_length_mm:speciesGentoo:sexmale
bill_length_mm:speciesGentoo
bill_length_mm:speciesChinstrap:sexmale
bill_length_mm:speciesChinstrap
bill_length_mm:sexmale
bill_length_mm
(Intercept)
term
−20
−10
0
10
20
estimate
species
Adelie
Chinstrap
Gentoo
20.0
17.5
15.0
bill_depth_mm
40
50
60
bill_length_mm
sex
female
male