# Week 2 Workshop

### Multiple Linear Regression Pt 1 Quantitative predictors

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This week we have started to learn about multiple linear regression. Multiple linear regression can be used to model numerical response variables using 2 or more explanatory variables. The explanatory variables can include numerical or categorical predictors and polynomial or interaction terms. This week we will focus on fitting main effects models using quantitative predictors. Next week, we will extend these concepts with interaction terms and qualitative predictors and in week 4 we will introduce polynomial terms.

The objective of this week's workshop is to:

- Learn how to fit a Multiple linear regression in R using lm().
- Interpret relevant output from a Multiple Linear Regression using anova(), summary(), and confint().
- Check conditions of a Multiple Linear Regression using resid\_panel().
- Introduce you to the GGally package as a method of exploratory analysis.

## 1 Example: Perch

The Weight (g), Length (cm) and Width (cm) of a sample of 56 perch were recorded. Also contained in the data set are the length class ( L ) and weight class ( Wd ) of the perch as well as the observation number ( Obs ). For this example today, we are just going to use Length , Width and Weight . Your task today is to find a multiple linear regression model for Weight based on the measurements of Length and Width .

Source: STAT2: Building Models for a World of Data, A. R. Cannon (2013), W. H. Freeman [Ed.].

# 1.1 Initial settings and importing data

Make sure you have your STAT210 or STAT410 project open and start a new R script. Name your new script something useful. EG Workshop 2 MLR. Use the options() command from last week to set the number of significant figures and hide the significance stars in outputs. Finally, load the Perch.csv data file.

### **▶ CHECK**

You can view your data set by clicking on the name of the data frame (per.df), which appears under Data in the top right hand window of RStudio. Note the names and order of the variables. The first variable is simply the observation number and is not included in the analysis. The second variable is the response, Weight.

## 1.2 Exploratory Analysis

This week we will introduce you to a new command, ggpairs() in the GGally package. A pairs plot generates a matrix of scatter plots for every combination of 2 variables, which is especially useful when looking at multiple predictors as we do for Multiple Linear Regression. The ggpairs() command also provides some extra information such as correlation coefficients (r) between predictors and a density plot for each predictor.

Produce a pairs plot using the ggpairs() command which is contained within the GGally package.

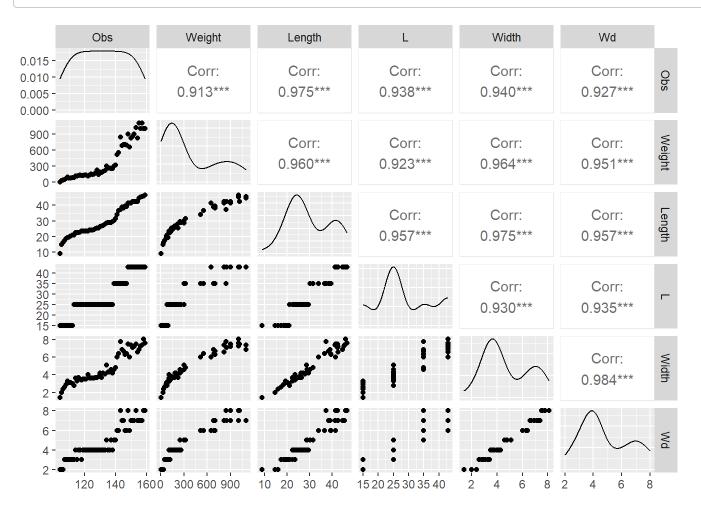
NOTE: You will need to install and load the GGally package in order to use ggpairs.

#### ► HINT

ggpairs(per.df)

## Warning: package 'ggplot2' was built under R version 4.3.3

## Warning in geom\_point(): All aesthetics have length 1, but the data has 36 rows.
## 
 Please consider using `annotate()` or provide this layer with data containing
## a single row.

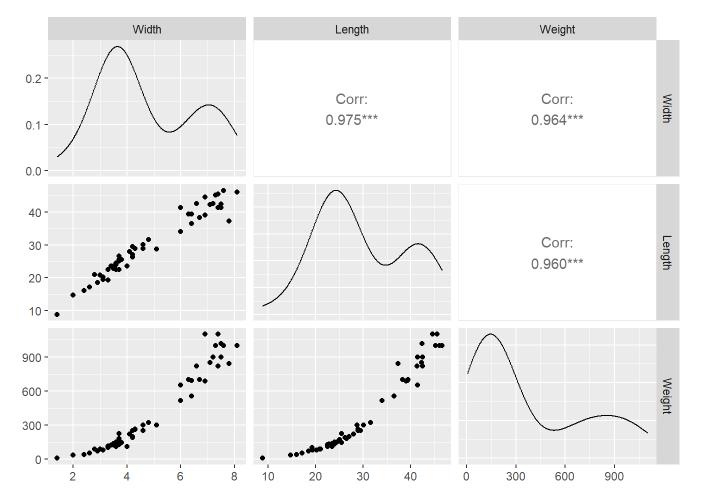


Just including the data name in the command will generate a pairs plot for all variables (columns) in your data frame. Sometimes data will contain variables that we are not interested in, as is the case here. For our example, we only want to include Width, Length and Weight. We can just include the variables we are interested in by specifying them with:

```
ggpairs(per.df, columns = c("Width", "Length", "Weight"))
```

**OR** we can use the column number in the data set instead. Here width is the 5th column, so we use 5; Length is the 3rd column, so we use 3; and Weight is the 2nd column, so we use 2.

ggpairs(per.df, columns = 
$$c(5, 3, 2)$$
)



The order that you state the variables in the code does not need to match the order they are in the data frame. Whichever order you place the variable names, is the order that they will appear in the plot matrix. I like to place my response variable at the very end as it makes reading the relationships between the predictors and the response variable easier. You could place it anywhere in the order though.

Now that we have our exploratory plot, we should discuss the relationships between each of our predictors and the response variable and also any relationships between our predictors. Take a moment to **write down the relationships between the response and the predictors and between the two predictors.** 

#### ► CHECK

**NOTE:** A pairs plot is often a good starting place for looking at relationships, but keep in mind that a single well designed scatter plot (or some other type of plot like a boxplot if dealing with qualitative predictors as well) might be a better choice for publication or understanding interactions (we will talk about interactions in more detail in week 3 & 4).

## Practice using ggplot()

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**Produce a plot looking at the relationship between Weight and Length** using ggplot(). You will need to load ggplot2 using the same library() command as you did for GGally.

NOTE: You should have installed ggplot2 in last weeks workshop. If you haven't, you will need to do this first.

► HINT

## 1.3 Fit a main effects MLR model and look at output

Now create a main effects model for Weight (call it mod1) with Length and Width as the predictors. The code is similar to what we used in SLR last week, but now we need to add an extra variable to the code like so:

```
mod1<-lm(Weight~Width+Length, data=per.df)
```

**NOTE:** Weight as our response variable is still placed to the left of the  $\sim$  and our two predictors are placed on the right, separated with a + (like you would separate them in the equation).

To look at the output from our model, we can produce an ANOVA table with anova(), look at the summary() table of the regression coefficients and generate confidence intervals of the coefficients using confint().

The p-values in the anova() table provide p-values when comparing increasingly complex models through the addition of an extra predictor. So these p-values indicate if the model with an additional predictor is useful when all predictors above in the sequence have been fitted first. This means that order of fit for the predictors is important when looking at this output. In our example we have fitted width first and Length second. If we were to reverse the order of our predictors (EG Weight~Length+Width), the p-values in the anova table will change.

```
anova(mod1)
```

Looking at the ANOVA table, we are comparing 3 models:

1. An intercept only model. This is always the default starting model in an ANOVA and is essentially just fitting a single mean for all values of Weight. EG Weight does not change in response to predictors.

$$\hat{Weight} = b_0$$

2. A model with only Width fitted (EG a Simple linear regression). EG Weight changes in response to Width only.

$$\hat{Weight} = b_0 + b_1(Width)$$

3. A model with width and Length fitted (A Multiple linear regression). EG Weight changes in response to Width and Length.

$$\hat{y} = b_0 + b_1(Weight) + b_2(Length)$$

The p-value for width in the ANOVA table is comparing the intercept only model to the model with only width fitted. So here we are asking "Does adding width to the model explain more variation in our response than an intercept only model?" Since the p-value is <0.05, we can say yes it does *OR* that a model with width is a better model to explain the variation in Weight than an intercept (mean) only model.

The same concept can be applied to Length in the ANOVA output, only here we are comparing the model with only Width fitted to a model with Width and Length fitted. Since the p-value is less than 0.05, we can say that the more complex model;

$$\hat{Weight} = b_0 + b_1(Width) + b_2(Length)$$

explains significantly more variation in Weight than the simpler model;

$$\hat{Weight} = b_0 + b_1(Width)$$

The p-values in the <code>summary()</code> table indicate if the predictor is important when all other predictors are included in the model we fitted. Here we are looking at the individual components of the model we fitted, rather than comparing increasingly complex models as we were with the ANOVA table. This means that when interpreting the p-values from the summary output, order of fit is not important and changing the order of the predictors in our model will not change the p-values.

```
summary(mod1)
```

```
##
## Call:
  lm(formula = Weight ~ Width + Length, data = per.df)
##
## Residuals:
       Min
##
                1Q
                   Median
                                3Q
                                      Max
## -113.86 -59.02 -23.29
                             30.93
                                   299.85
##
## Coefficients:
##
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -578.758
                           43.667 -13.254 < 2e-16 ***
## Width
               113.500
                           30.265
                                    3.750 0.000439 ***
## Length
                14.307
                            5.659
                                    2.528 0.014475 *
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 88.68 on 53 degrees of freedom
## Multiple R-squared: 0.9373, Adjusted R-squared: 0.9349
## F-statistic: 396.1 on 2 and 53 DF, p-value: < 2.2e-16
```

Lets have a look at the output in the summary table a little more closely.

We can use the table of coefficients from the summary() output to write the fitted model equation. A fitted MLR model is defined as:

$$\hat{y} = b_0 + b_1 x_1 + b_2 x_2 + \ldots + b_k x_k$$

Where;  $b_0$  is the intercept,  $b_1$  is the coefficient for the first predictor  $x_1$  ( Width ) and  $b_2$  is the coefficient for the second predictor  $x_2$  ( Length ). We can have parameters in our model up to the kth parameter. However, since we only have the two for this model, we will stop at  $x_2$  for our equation. Therefore the equation for Weight using our fitted model is defined as:

$$\hat{Weight} = -578.76 + 113.50 (Width) + 14.31 (Length)$$

Finally, we can look at the the confidence intervals for each of the components of the model. Remember that the interpretation of the confidence interval for each predictor is made while assuming that the other predictors in the model are not changing.

```
confint(mod1)
```

```
## 2.5 % 97.5 %

## (Intercept) -666.343179 -491.17237

## Width 52.796272 174.20304

## Length 2.957273 25.65749
```

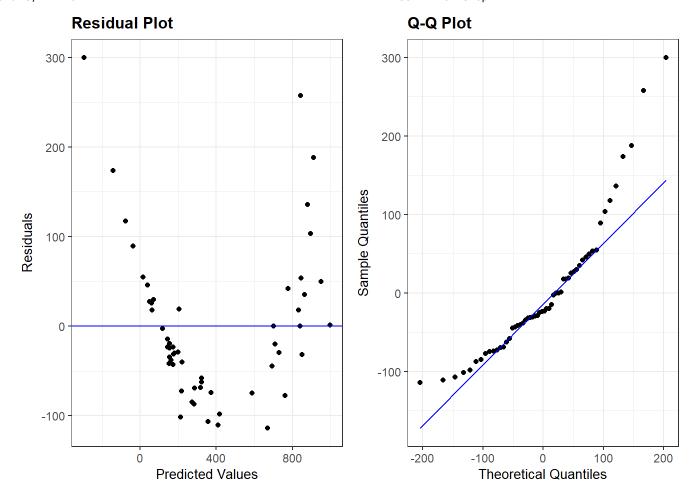
## 1.4 Check the Assumptions of the main effects model

We should check the assumptions of our model to make sure that an MLR is the appropriate model choice. To do this we will use the <code>resid\_panel()</code> function from last week.

```
library(ggResidpanel)
```

```
## Warning: package 'ggResidpanel' was built under R version 4.3.3
```

```
resid_panel(mod1, plots=c("resid","qq"))
```



The 4 conditions that we check for an MLR are the same as what we checked for an SLR. That is the residuals are independent and  $\epsilon \sim N(0, \sigma^2)$ .

Use the diagnostic plots to check that the conditions for this model have been satisfied.

#### **▶ CHECK**

Ordinarily at this point, you would try to fit a different model that doesn't have these violations in the assumptions of the residuals. Perhaps a model with an interaction (next week) or a polynomial (week 4) model would account for the non-normal residuals and the obvious bend in the residual scatter.

In general, we can say that Length and Width does influence perch Weight , since the trends are so strong between these variables. However, the estimates of the coefficients of Length and Width are probably not as reliable, since we were fitting straight lines to a relationship that was curvy. We wouldn't want to be making specific numerical inference using those  $\beta$  estimates from the model or using the model for prediction.

For now, let us put this problem aside and use this model to practice interpretations and predictions from a main effects multiple linear regression model. We will revisit some ways to deal with this issue in the coming weeks.

# 1.5 Use the Multiple Linear Regression model to make predictions.

We can use the same <code>predict()</code> command as last week to make predictions with our model. However, because we have multiple predictors in our model, we need to make sure that our <code>predict()</code> code includes a value for all predictors in the model.

```
predict(mod1, new=data.frame(Width=5, Length=30), interval="confidence")
```

```
## fit lwr upr
## 1 417.962 391.7151 444.2089
```

With 95% confidence, when width of perch is 5 cm and Length is 30 cm, mean weight will be between 391.72 and 444.21 g.

```
predict(mod1, new=data.frame(Width=5, Length=30), interval="prediction")
```

```
## fit lwr upr
## 1 417.962 238.1743 597.7497
```

With 95% confidence, when Width of one perch is 5 cm and Length is 30 cm, weight of the fish will be between 238.17 and 597.75 g.

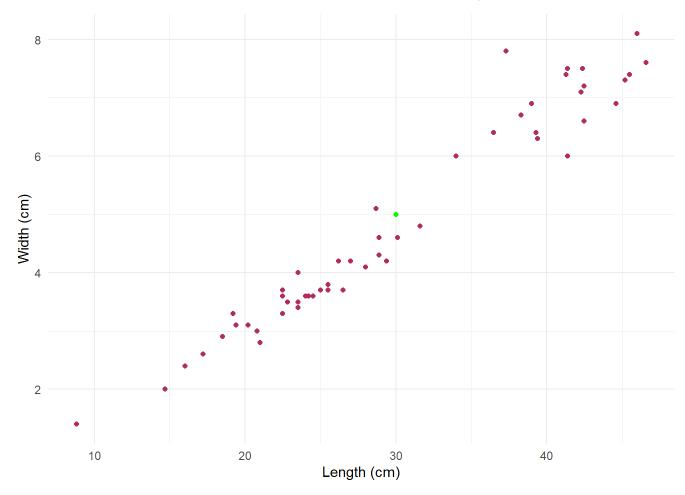
When making these predictions, the reliability can be influenced by three points:

- 1. The  $r^2$  value: Larger  $r^2$  values indicate that your model explains more the variation in your response. Low  $r^2$  values won't impact the reliability of your intervals (you will end up with wider intervals generally though), but may impact the reliability of the fitted value for your predictions.
- 2. **The conditions of the residuals:** If conditions of the residuals are not met, then your predictions are going to be more unreliable.
- 3. **If you are extrapolating:** Predictions using extrapolation are often less reliable as you only have an idea of the true relationship through the data you have collected. Making predictions inside your range of observations (interpolation) is more reliable than those made outside of the observations (extrapolation).

You should check whether your predicted value is going to be made within your range of observations. One way to do this is to create a scatter plot of your 2 explanatory variables and see where the new point will fall in relation to your observations. Here we have added an extra point using <code>geom\_point</code> and the x and y coordinates from the new point we want to predict.

**NOTE:** Here x=30 is used in the last line because Length=30 in our prediction and we have placed Length on the x axis in our plot. If we were to place Length on the y axis instead, then we would need to say y=30 in the last line.

```
#add predicted point to predictor exploratory plot
ggplot(data=per.df, aes(x=Length, y=Width))+
  geom_point(col="maroon", pch=16)+
  labs(y="Width (cm)", x="Length (cm)")+
  theme_minimal()+
  geom_point(x=30, y=5, colour="green")
```



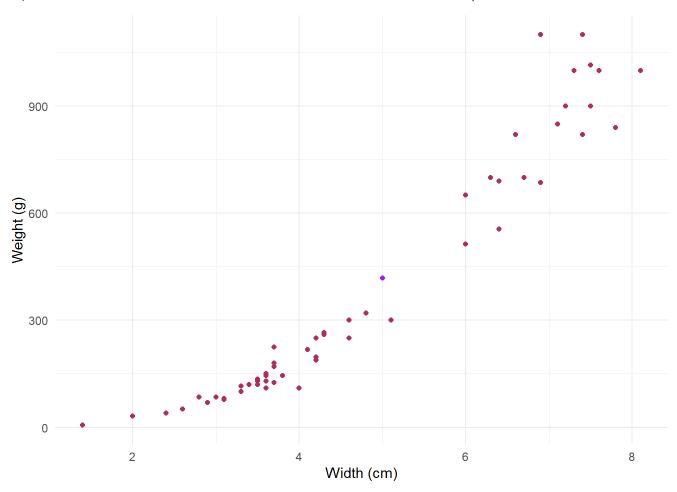
With this example, the point falls close to the scatter and is within the boundary of our observations, so this prediction is not extrapolation. However, the prediction is still unreliable as the assumed conditions for the residuals were not met for this model.

Make a plot to check whether a prediction for perch weight when length is 40cm and width is 4cm is extrapolation.

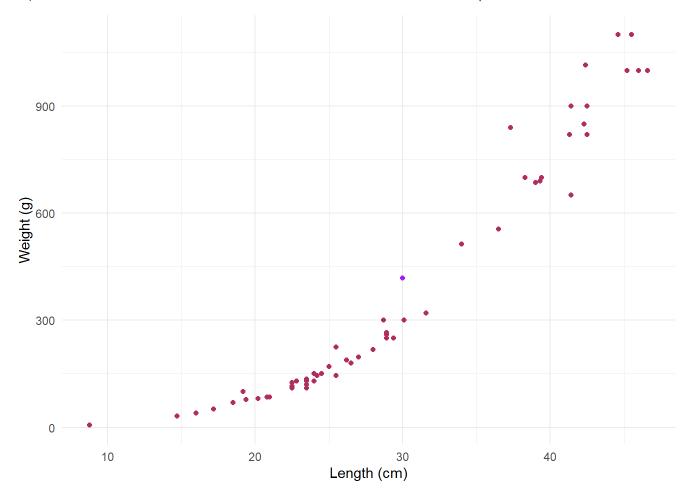
#### ► CHECK

We mentioned earlier that the fitted values for our predictions are probably not reliable due to the violations in the conditions of the residuals. Lets see where our predicted point falls in relation to the scatter of our observations. To look at this, we will create a plot looking at the relationship between weight and the predictors and add our predicted point.

```
#add predicted point to exploratory plot
ggplot(data=per.df, aes(x=Width, y=Weight))+
  geom_point(col="maroon", pch=16)+
  labs(y="Weight (g)", x="Width (cm)")+
  theme_minimal()+
  geom_point(x=5, y=417.96, colour="purple")
```



```
#add predicted point to exploratory plot
ggplot(data=per.df, aes(x=Length, y=Weight))+
  geom_point(col="maroon", pch=16)+
  labs(y="Weight (g)", x="Length (cm)")+
  theme_minimal()+
  geom_point(x=30, y=417.96, colour="purple")
```



We can see that our predicted point is in the ball park, but doesn't quite follow the observed trend. This is the main problem with fitting straight lines to relationships that are curved.

## 1.6 Write an informative conclusion

Finally, we should write a conclusion detailing our main findings from our output.

So far we have only looked at the coefficients from our model to define our model equation. Remember for an MLR we should also look at:

- The global utility p-value to assess the overall usefulness of the model.
- ullet The p-value for each of our predictors;  $b_1$  and  $b_2$  to see if Width and Length are significant predictors of Weight .
- ullet The  $r^2$  to see how much of the variability in Weight is explained using a model with Width and Length as the predictors and,
- The confidence intervals for  $b_1$  and  $b_2$  to give us a range of where the true value of  $\beta_1$  and  $\beta_2$  might lie.

From the output we generated earlier:

```
##
## Call:
## lm(formula = Weight ~ Width + Length, data = per.df)
##
## Residuals:
      Min
##
               10 Median
                               3Q
                                      Max
## -113.86 -59.02 -23.29
                            30.93 299.85
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) -578.758
                           43.667 -13.254 < 2e-16 ***
             113.500
## Width
                           30.265
                                    3.750 0.000439 ***
## Length
               14.307
                            5.659 2.528 0.014475 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 88.68 on 53 degrees of freedom
## Multiple R-squared: 0.9373, Adjusted R-squared: 0.9349
## F-statistic: 396.1 on 2 and 53 DF, p-value: < 2.2e-16
```

```
## 2.5 % 97.5 %

## (Intercept) -666.343179 -491.17237

## Width 52.796272 174.20304

## Length 2.957273 25.65749
```

The global p-value for the model ( $p < 2X10^{-16}$ ) is much less than 0.05, so a model containing Length and Width is a useful predictor of Weight in perch.

The p-value (p=0.0004) for Width is much less than 0.05, so Width is a useful predictor of perch Weight when Length is also in the model.

The p-value (p=0.01) for Length is less than 0.05, so Length is a useful predictor of perch Weight when Width is also in the model.

The adjusted  $r^2$  value is 0.9349, indicating that 93.5% of the variability in perch weight is explained by a model including Length and Width.

With 95% confidence, when Length of perch increase by 1 cm, the weight of perch increases between 2.96 and 25.66 g on average, when Width is kept constant.

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With 95% confidence, when Width of perch increase by 1 cm, the weight of perch increases between 52.80 and 174.20 g on average, when Length is kept constant.

These conclusions should be made with caution as not all conditions of a linear regression where met for this model.

# 2 Practice Example: Timber Volume of Black Cherry Trees

Let's revisit the trees data set from last week.

The trees dataset in R contains measurements of the diameter (Girth in inches), Height (ft) and timber Volume (cubic ft) of timber in 31 felled black cherry trees.

Source: Forest Mensuration. H. A. Meyer (1953). Penns Valley Publishers, Inc.

Last week you were asked to model Volume using Girth or Height. This week your task is to fit a multiple linear regression to predict the timber Volume of cherry trees using Girth and Height as explanatory variables.

As part of fitting your model:

- Do some exploratory analysis using ggpairs().
- Fit an MLR using the lm() command and write the model equation.
- Check assumptions of your model using the resid\_panel() command.
- Write a meaningful conclusion using the output from the anova(), summary() and confint() commands.
- Predict mean timber Volume when Height of the cherry trees are 70 ft and when Girth of the cherry trees are 14 inches.
- Predict individual timber Volume of a tree when Height is 65 ft and Girth is 18 inces.

#### **▶ CHECK**

## 3 You're Finished!

