

# Market Forecasting Assignment: Multiple Linear Regression

Teacher: Dr. Stefan Groesser, Dr. Christoph Imboden

Autors: Benedech Rodolpho, Buehler Pascal, Geeler Ken 04.12.2021

## Short Theory Recap Multiple Linear Regression (MLR)

The model equation for MLR has the form  $y = X\Theta + \epsilon$ , with  $y$  being the target vector,  $X$  the explanatory Matrix,  $\Theta$  the parameter vector and the residuals with the assumption that they are normally distributed  $\epsilon \sim N(0, \sigma^2)$ . The estimation of  $\Theta$  is done with the Maximum likelihood  $L(\theta) = P(X|\theta) = \frac{1}{\sqrt{(2\pi)\sigma}} * e^{-\frac{1}{2\sigma^2} * ||y - \theta X||^2}$  by solving the equation  $\Theta = (X^T X)^{-1} X^T y$ .

## Dataset

The data from 7 common fish species for fishmarket is provided from Kaggle.

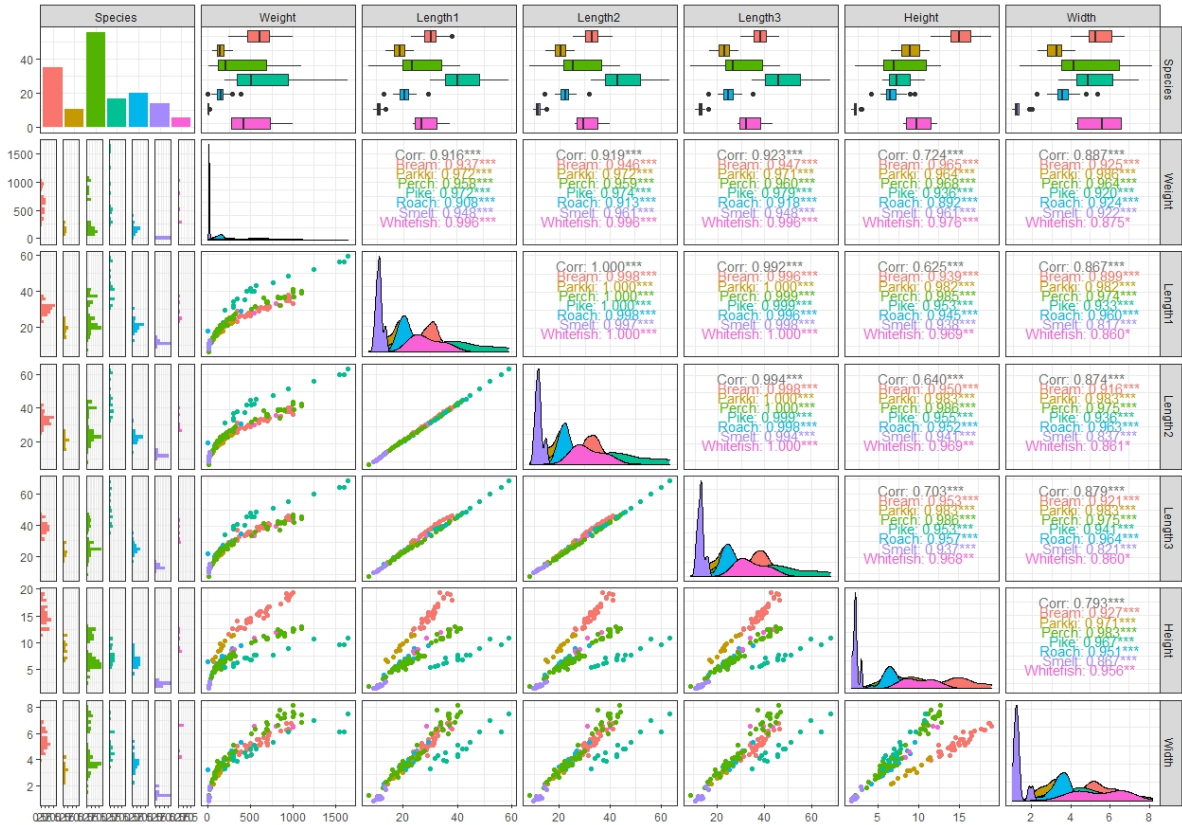


Figure 1: pairwise plot of the fish dataset

## Data exploration

Information of the Dataset is gained with the following commands.

```
fish_dat=readr::read_csv("Fish.csv")           # reading as tibble
GGally::ggpairs(fish_dat,aes(color = Species)) + theme_bw() # pairwise plot
summary(fish_dat);str(fish_dat);View(fish_dat)    # statistics and structure
```

The pairwise plot Figure 1 provides a visual overview of the dataset. It consists of 159 observations measured for 6 numerical variables which measure properties of the fish and one categorical variable to describe the Species. The coloring in the pairwise plot allows a distinction of the Species, one can immediately observe that the species Perch has the most observations.

From the pairwise scatterplots a nonlinear relation between weight and the other numerical variables is observed, therefore the correlation *cannot* be correctly interpreted with these variablepairs. Further the other numerical variables are linearly correlated (the correlation statistic can be interpreted), interestingly the 3 length measurements have a very strong correlation to each other. The length of the fish is measured in different ways, which is why there are three different Length1 (vertical length), Length2 (diagonal length) and Length3 (cross length).

The density plots helps see how the variables themselves are distributed. For example the width of Smelt tends to have a bimodal distribution, although this has to be taken with a grain of salt due to the sparse data, see on the inverted histograms on the left. Also the pairwise boxplots gives a good overview for comparison between the different variables. For example it can be seen that the variance of the species vary amongst the levels.

The distribution of the target variables is actually very important since MLR assumes multivariate normality of the data, for other distributions we might choose another model such as a Generalized-Linear-Model to improve the model validity, but for this analysis we stick to MLR.

## Building a Model

To evaluate the accuracy of the model created in this chapter, the data is split into a train and test set, using Simple Random Sampling without Replacement (SRSWR). 80% of the data is used for training and the remaining 20% is for testing prediction accuracy. The corresponding R code is given below.

```
set.seed(42);samp= sample(1:56,size = 11,replace = F)           # Seed & sample size 80%
Perch_train=Perch_dat[-samp,];Perch_test=Perch_dat[samp,]      # train / test sample
```

The dataset provides many different options to do linear regression, nevertheless for MLR there is a problem with multicollinearity since a lot of the variables are strongly correlated, meaning that if multiple independent variables would be in the model it wouldn't be clear which one explains the effect the best for the target variable.

Therefore the first thing we do is fitting a simple linear regression model. We use the weight of a fish as a response variable. The explanatory variable width is used, since this is intuitively a good indicator for the weight of a fish from "fishing experience". In a next step, we will also check whether a MLR model can represent the data even better.

Finally, the models are compared quantitatively with the residual sum of squares (RSS), R-squared and the Akaike information criterion (AIC). Subsequently, the models will be used with the test set for predictions, whose performance will be measured with the Mean Absolute Deviation(MAD). The reason why we don't use Mean Squared Error(MSE) is because of the small test set, one far point could massively influence the statistic due to the square.

## Simple Linear Regression

For a first approach we could just focus on the species Perch (in swiss-german it's called Egli) since we have the most data there. Since the weight hasn't got a linear relation to the other variables, we'll have to transform it properly.

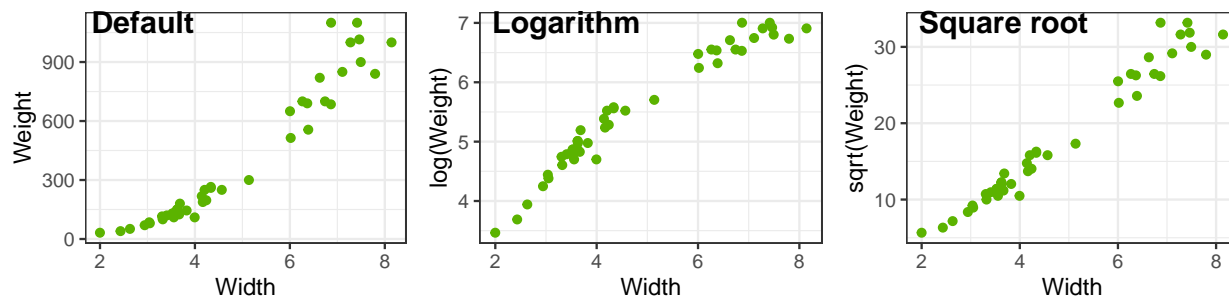


Figure 2: transformations of weight for Perch

If we transform the weight with the logarithm it looks a bit better but still isn't linear see Figure 2. The squareroot transformation looks better, the data seems much more linearly dependent. One can observe that the variance towards the right side of the model increases even with after the transformations.

```
Perch_fit=lm(sqrt(Weight)~Width,data = Perch_train) # Simple linear regression model
```

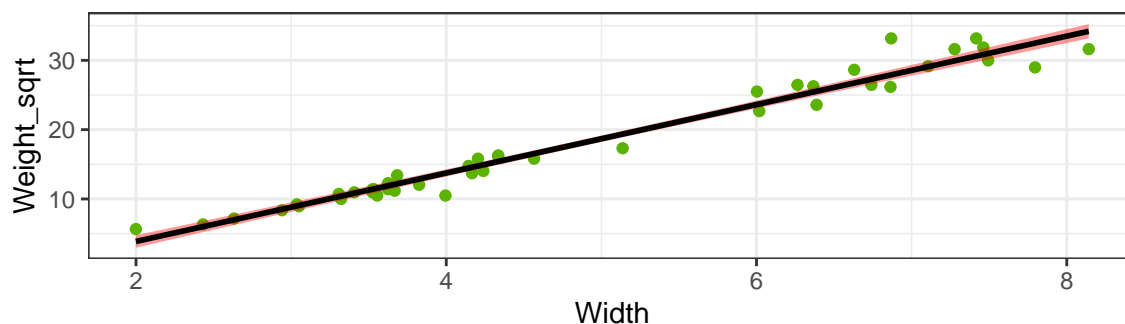


Figure 3: Simple linear regression model for Species Perch weight vs width

From the summary output we get the following model  $Weight_i = (-6.000 + 4.9368 * Width_i)^2$ . The explained Variance measurement  $R^2$  is with 0.9683 very high. the  $AIC$  for this model is 171.6. The p-values for the both parameters hypothesis tests are also significant. By inspecting the residuals in Figure 4 we can check the model assumptions. The residuals seem to follow a normal distribution, have constant mean and there are no points which are crucial to shift the model. Nevertheless the variance is not constant and increases towards the right side.

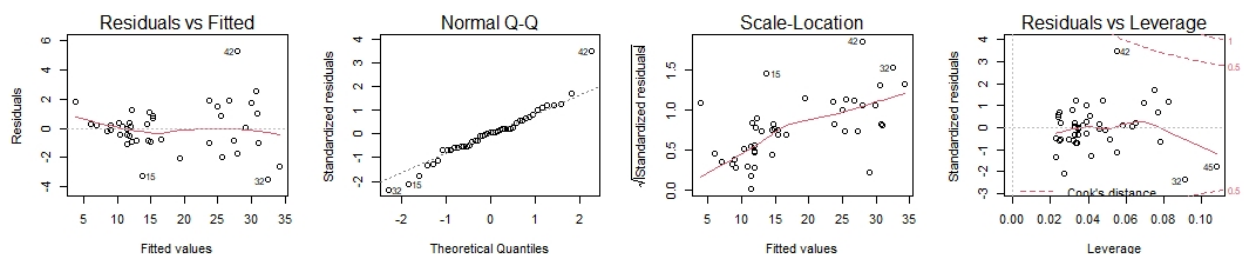


Figure 4: Residual analysis for the SLR

## Multiple Linear Regression and the Problem of Multicollinearity

Lets make now a full model and test if it is more beneficial.

```
Perch_fit_full=lm(sqrt(Weight)~.,data = Perch_dat[,-1]) # MLR
car::vif(Perch_fit_full);drop1(Perch_fit_full);summary(Perch_fit_full) # VIF, drop1, output
```

VIF	Length1	Length2	Length3	Height	Width
	1780.07795	4626.41486	2376.77263	54.03761	30.85782

MLR	Estimate	Std. Error	t value	Pr(> t )	Df	Sum of Sq	RSS	AIC
(Intercept)	-7.0051	0.6527	-10.733	1.41e-14 ***			43.916	-1.6126
Length1	0.4430	0.6227	0.711	0.480156	1	0.4445	44.360	-3.0487
Length2	-0.5321	0.9527	-0.558	0.579014	1	0.2739	44.190	-3.2644
Length3	0.4118	0.6465	0.637	0.527082	1	0.3563	44.272	-3.1601
Height	1.1788	0.3228	3.652	0.000622 ***	1	11.7162	55.632	9.6306
Width	1.3754	0.3956	3.477	0.001059 **	1	10.6182	54.534	8.5143

Figure 5: VIF, MLR Output and Drop1 Global F-test

The VIF helps us to identify multicollinearity and indicates that the variables have a very high collinearity as expected. Especially the three variables of the lengths result in massively higher VIF values than for the other variables.

The problem is also visible as the summary output in Figure 5 is examined. The variables Length1 Length2 and Length3 aren't even significant although they are highly correlated with the target. This is because the collinearity inflates the standarderror which leads to insignificant t-statistics [1].

According to that research paper we can't reliably interpret these statistics. Further if there would be a full correlation between 2 variables meaning that  $X_1$  would be a linear combination of  $X_2$ , the Covariance  $\frac{1}{n}X^T X$  wouldn't have an inverse and (1) cannot be solved. With PCA we could check which of the variables explain the most variance and then remove the "unimportant" ones.

Due to the task limitation we just keep this consideration in mind and simply remove the Length variables and fit a model with two explanatory variables for a final comparison.

```
Perch_fit_full=lm(sqrt(Weight)~Width+Height,data = Perch_dat[,-1])
summary(Perch_fit_full) # MLR
```

##

```
## Call:
## lm(formula = sqrt(Weight) ~ Width + Height, data = Perch_dat[,
##      -1])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.37662 -0.71608 -0.02496  0.60473  2.22412
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -6.1166     0.4053  -15.093  < 2e-16 ***
## Width         1.6714     0.4273   3.912 0.000262 ***
## Height        1.9983     0.2634   7.586 5.16e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.034 on 53 degrees of freedom
## Multiple R-squared:  0.9865, Adjusted R-squared:  0.986
## F-statistic: 1939 on 2 and 53 DF,  p-value: < 2.2e-16
```

## Comparison of the two models

```
## [1] 0.4237973
```

```
## [1] 0.4694862
```

```
## [1] 1.184863
```

```
## [1] 1.539654
```

```
###Conclusion
```

## Appendix

*This work is generated in R-Studio 2021.09.0 with R-4.1 with Rmarkdown, Full Code and Project can be found on [https://github.com/buehlpa/TSM\\_MarkFor](https://github.com/buehlpa/TSM_MarkFor)*

## Literature

*[1] Multicollinearity and Regression Analysis, December 2017, Journal of Physics Conference Series 949(1):012009, Jamal Daoud*