Hypothesis testing and analysis with R

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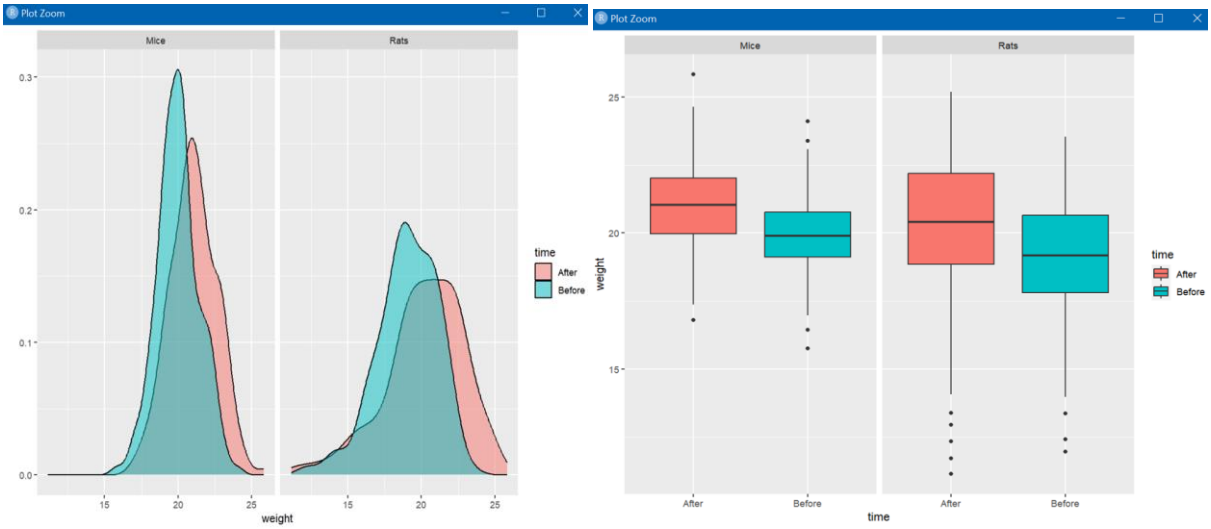
Introduction

Hypothesis testing in the R programming language is usually described as the process of testing a researcher's theory or validating their hypothesis through the open-source analysis tool. This means that to be able to compare the results of our research scientifically and produce plausible theories, we would need to be able to test the data hypothetically. Now hypothesis testing is important as with the results, researchers can accept or reject the hypothesis made from observing the sample, or in our case the effect of the treatments on the rats and mice before and after it was used. The main purpose of this report is comparing the effect of the nutritional supplements treatment before and after it was used on 200 rats and 200 mice. This report aims to show the effects of the treatments before and after they were used on these rats and mice through hypothesis testing and producing the most suitable underlying theories as well as assumptions. In this report we will be covering the discussion of the experiments in the following order: Section I: Data generation, Section II: Appropriateness for t-testing, Section III: Parametric and non-parametric tests, Section IV: Fitting distributions.

Section I: Data Generation

After the creation of the data using rnorm, we compared the datasets we created for both the rats and the mice before and after the treatment and this is what we produced:

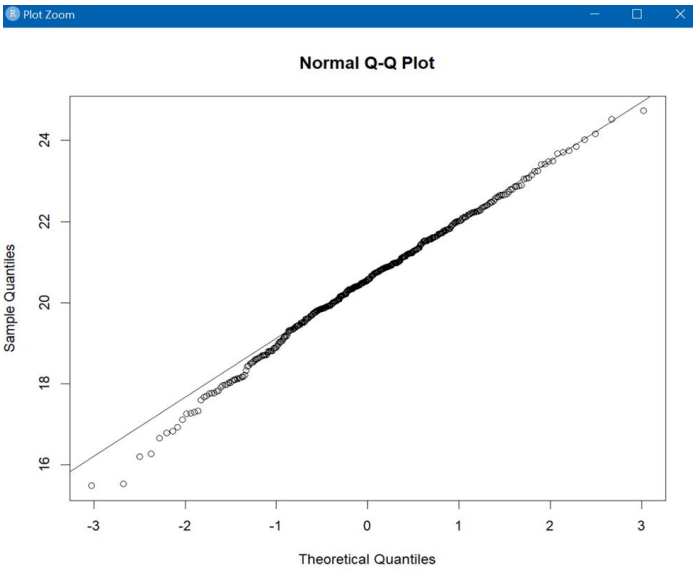


The density plot of figure 1 displays the weight for both the mice and rats before and after treatment. The weight distribution's shape and spread are revealed through this graph. We can see that the plots for the rat and mice are bell-shaped, meaning they are normally distributed, but there are some key differences in their spread and skewness. For the weights of the mice, we have the result of the density plots to be both positively skewed. The second plot, the box plot, shows the distribution of weights for mice and rats split into before and after treatment. It revealed the details about the central tendency and variability of the

data. In our experiment, we can see that for both before and after treatment, the median weight of mice is higher than the median weight of rats. Moreover, we may observe that rat weight variability is lower than mouse weight variability. Furthermore, after treatment, there are a few outliers for both mice and rats, which might be a sign of some extreme weight values. The box plot offers a helpful summary of the weight distribution, showing the central tendency and variability and any potential outliers.

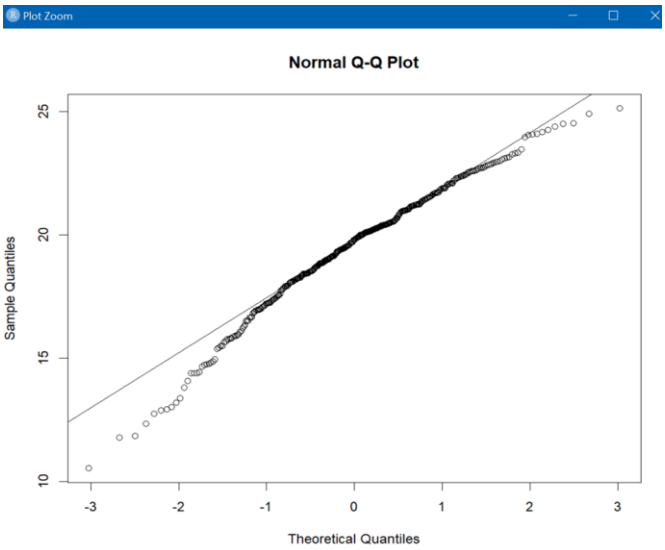
Section II: Appropriateness for t-testing

For the next section we tested the appropriateness for the hypothesis t-testing. We did this by examining the QQ plots and qualitatively using the Shapiro –wilk test. A Shapiro wilk test is a test of normality in which the null hypothesis is that the data is normally distributed, and the alternative hypothesis is that the data is not normally distributed. And this was the graphical result of this analysis:




```
> shapiro.test(mice)

        Shapiro-Wilk normality test

data:  mice
W = 0.99415, p-value = 0.1288
```

This is the QQ plot and the Shapiro wilk test for the mice. This QQ plot reveals that there are some deviations from normality since the data points vary significantly from a straight line. However, our normality assumption is not severely violated as the deviations are not too extreme. So, we would have to accept the null hypothesis and reject the alternative hypothesis. Our Shapiro wilk test gives a resulting p-value of 0.1288 which is greater than the usual level of significance which is 5%.




```
> shapiro.test(rats)

        Shapiro-Wilk normality test

data:  rats
W = 0.98779, p-value = 0.001965
```

For the rats' Shapiro-Wilk test and QQ plot, there is a larger deviation from the straight line by the data points, indicating that they depart from normality. This gives us premise to assume that we accept our alternative hypothesis and reject the null hypothesis. The P value from the Shapiro-wilk test on the rats is 0.001965 and which is less than the significance level 5%. The data is not normally distributed and thus does not pass the normality test.

Section III: Parametric and non-parametric tests

So, to be able to perform the parametric paired t-test, we had to split the data into two groups as before and after. We also happen to calculate the difference between the weights before and after the treatment. And the result of this analysis of the mice can be seen below:

```
> t.test(mice_after,mice_bfore,paired=TRUE)

        Paired t-test

data:  mice_after and mice_bfore
t = 8.2069, df = 199, p-value = 2.8e-14
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 0.8740504 1.4269315
sample estimates:
mean difference
       1.150491
```

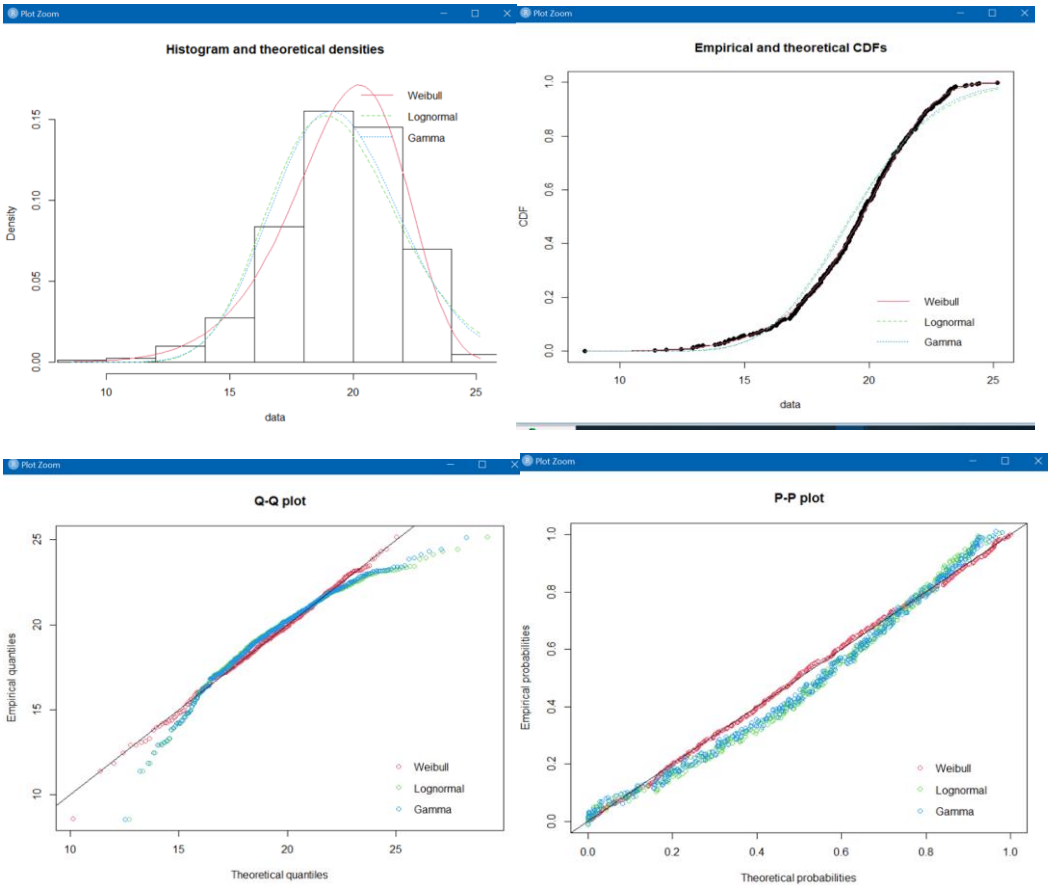
Through the analysis we were able to conclude that the mice had a degree of freedom of 199, a t- test statistic of 8.2069, p value of which is equal to 2.8e-14 which means that there is extraordinarily convincing evidence against the null hypothesis therefore we reject it. We also have a 95% confidence interval of 0.8740504, 1.4269315, and a sample estimate which is a mean difference of 1.150491. Meaning that the treatment is effective in increasing the weight of mice as the sample estimate falls within the confidence interval. For the rats dataset, we performed a non-parametric t-test: the Wilcoxon signed rank test. This is what we got for the result:

```
> wilcox.test(rats_after, rats_bfore, paired=TRUE)

        Wilcoxon signed rank test with continuity correction

data:  rats_after and rats_bfore
V = 13501, p-value = 2.551e-05
alternative hypothesis: true location shift is not equal to 0
```

This result shows us that the p value is 2.551e-05, which is smaller than the significance level 5%, meaning that we reject the null hypothesis. The result also shows that true location shift is not equal to 0, which reaffirms the statement of rejecting the null hypothesis and accept the alternative hypothesis as there is evidence to suggest that weight "before and after" have different central tendencies. Therefore, we can say that the treatment was also effective in increasing the weight of the rats.

Section IV: Fitting distributions

In this last section, we are going to examine the best-fit distribution for the rats' data



We have a density comparison for the first plot, and this clearly displays the x-axis of the density plot comparison representing the weight of the rats, and the y-axis the probability density. And it compares the probability density function for each distribution. The density curves of the Gamma and Lognormal overlap at the topmost part of the histogram of the observed data more closely than the Weibull curves. Therefore, the lognormal and gamma fit better than the Weibull. For the CDF plot comparison, the Weibull fit gives the best fit to the data than the lognormal and gamma curves which are a bit further away. The comparison of the QQ plot displays a scatter plot, the Weibull distribution is closer fitted to the solid straight line than the Gamma and Lognormal plots. And finally, when observing the PP comparison, we find that the Weibull distribution is closely fitted to the straight line, this giving the best fit to the data than the Gamma and lognormal distribution

Conclusion

In conclusion, the report has explored in length, the change in weight of the mice and rats before and after the treatment with using a combination of various statistical methods and tests.