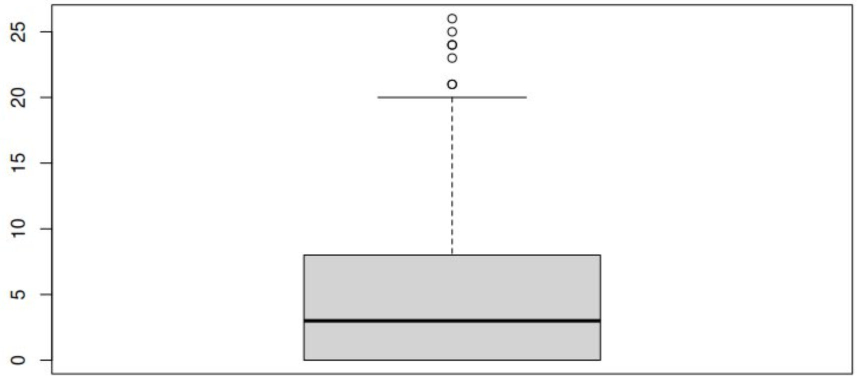
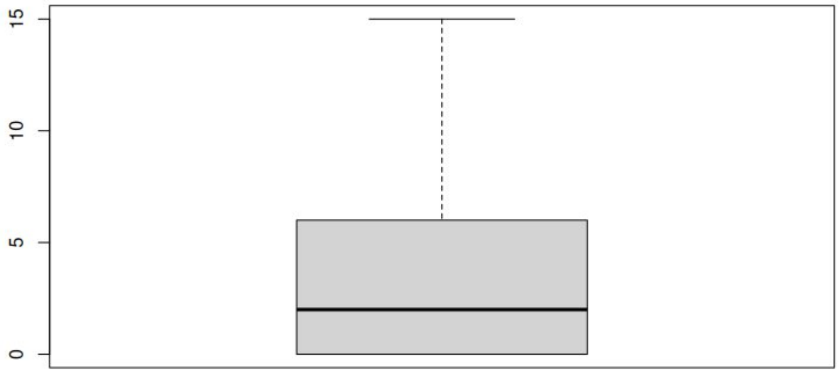
Some analyses on the COVID-19 database for the city of São Paulo:

Discrepancies, outliers, and new deaths.

First, after thorough data cleaning, we analyze the new deaths in São Paulo using a boxplot to identify significant discrepancies in this variable. This approach helps us begin to understand the concepts of outliers, mean, median, and quartiles in a more visual way.

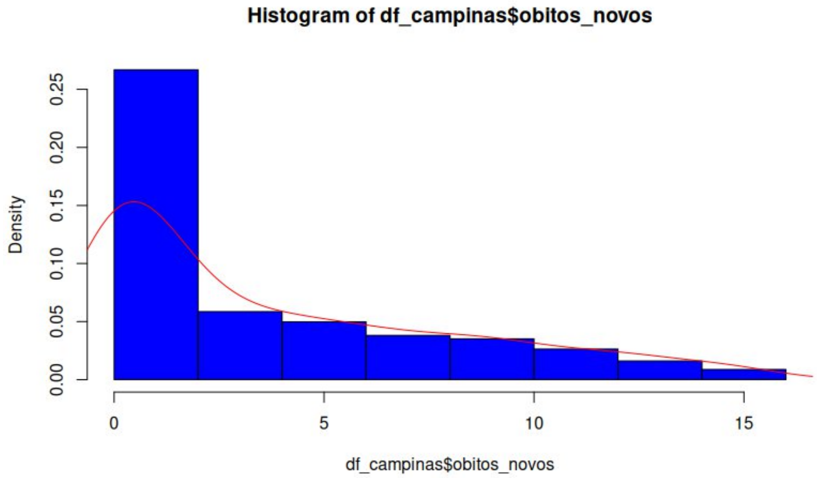


After that, I cleaned the outliers by removing all data below the lower limit and above the upper limit, resulting in the following representation:

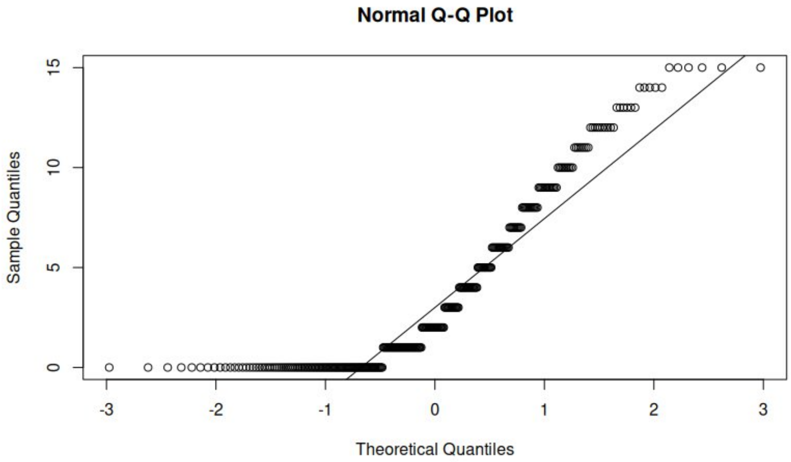


Normality Tests

By analyzing the variable for new deaths, we aim to determine whether it is a normally distributed symmetric variable, a crucial criterion for many other functions.

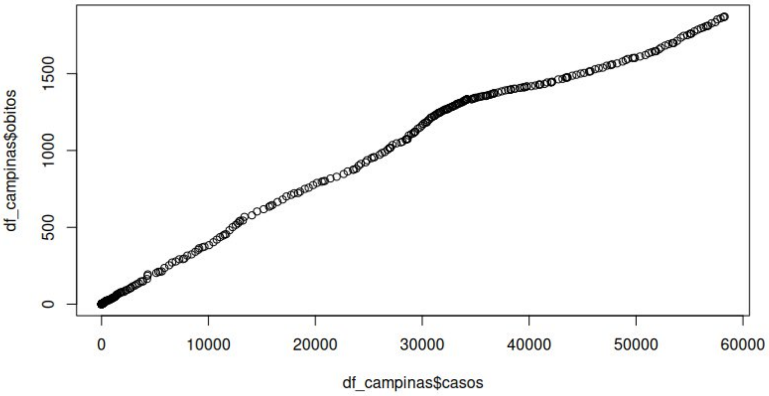


By examining the histogram, it is clear that the data does not follow a normal distribution. It does not adhere to the rules of standard deviation or median, nor does the curve form a bell shape. Additionally, I used qqnorm and qqline to assess normality, ensuring to check if the points align with the reference line.



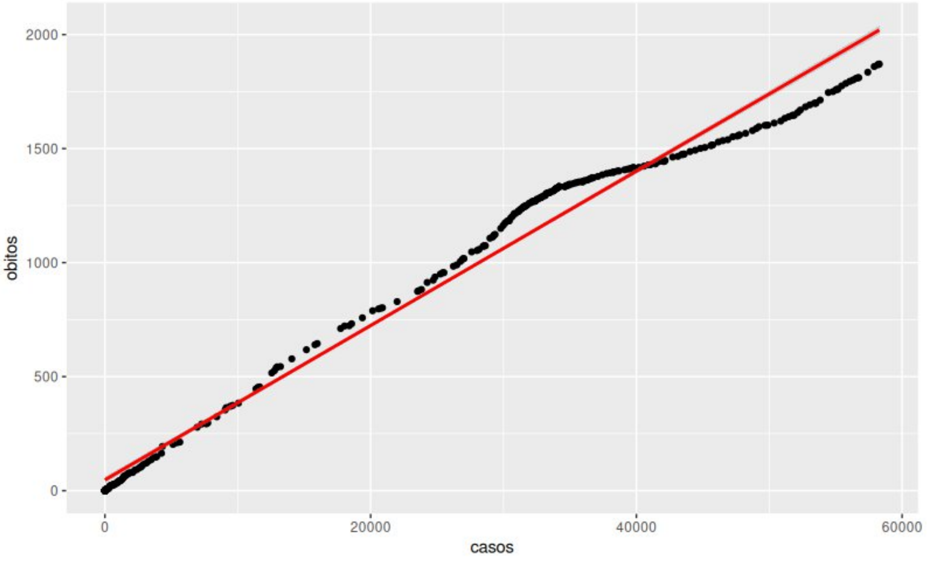
Correlation and Linear Regression

After several analyses, I aimed to develop a linear regression model to explore the relationship between cases and deaths. I checked the normality of both variables and plotted the line graph for this relationship. While the data does not exhibit normality, linearity is evident.



Thus, I used the Spearman correlation method, suitable for a large set of non-parametric data, resulting in a case-death correlation of 99.967%, which is nearly perfect.

From there, I used the lm function in R to calculate the regression coefficients. Using these coefficients, I constructed the regression function, achieving an R² (or accuracy) of 98% for the regression. Afterward, I employed ggplot to visualize the regression line (in red) and the case-death points (as dots), confirming the accuracy of the performed regression.



Afterward, I created a function to calculate, for each city, the number of deaths expected for a given number of cases using the linear regression model. The implementation is shown in the code below.

```
death_regression_function_city <- function(city, cases) {
        regression_df <- df %>% filter(municipality == city)
        regression <- lm(formula = deaths ~ cases, data = regression_df)
        coefficients <- regression$coefficients

        calculation <- coefficients[2] * cases + coefficients[1]
        r_squared <- summary(regression)$r.squared
        return(sprintf("%.2f deaths with an accuracy of %.4f%%", calculation, (r_squared * 100)))
}
death_regression_function_city("Campinas", 60000)
```