Lab-05

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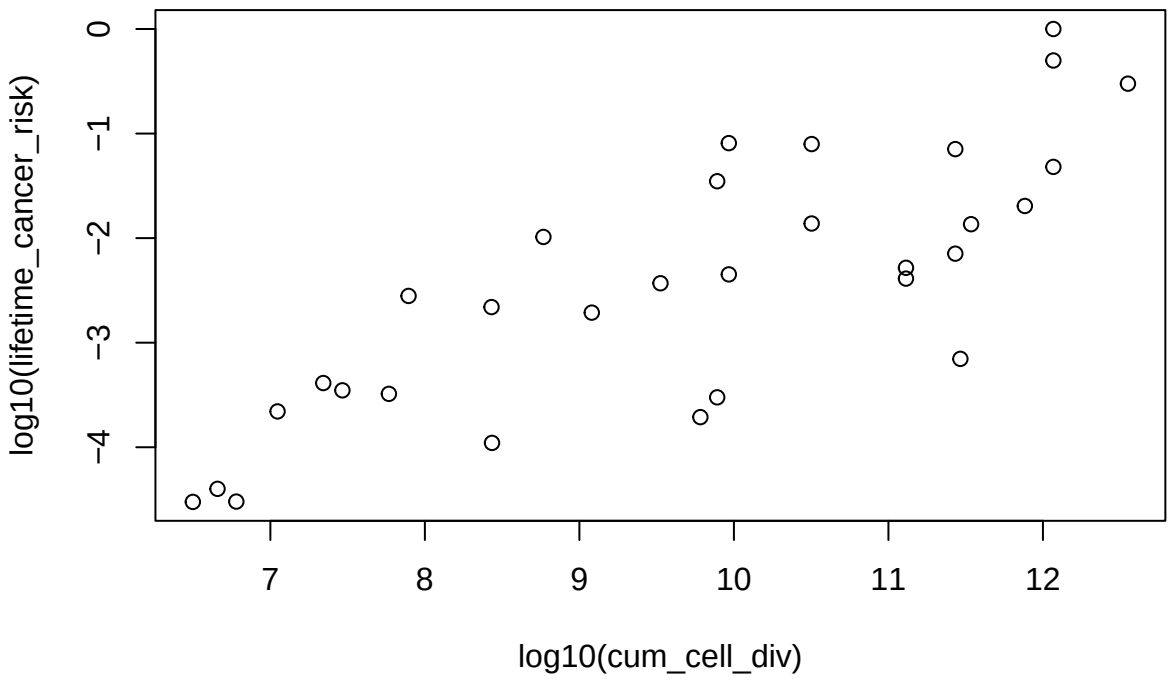
Problem-1A:

On a log10-log10 scale graph Lifetime_cancer_risk (on the y-axis) vs. CumulativeCellDivisions (on the x-axis)

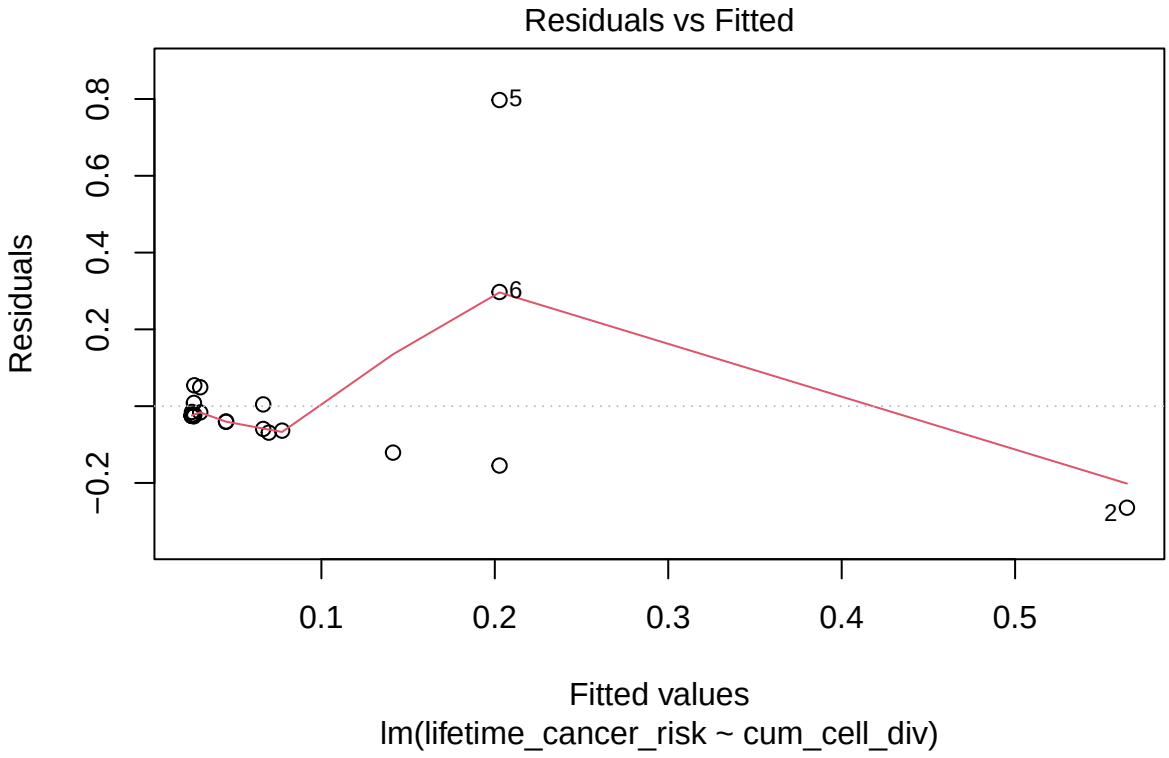
```
myT = read.table('data/cancerRisk.txt', header = TRUE, sep='\t')

lifetime_cancer_risk = myT[ , c('Lifetime_cancer_risk')]
cum_cell_div = myT[ , c('CumulativeCellDivisions')]

plot(log10(cum_cell_div), log10(lifetime_cancer_risk))
```

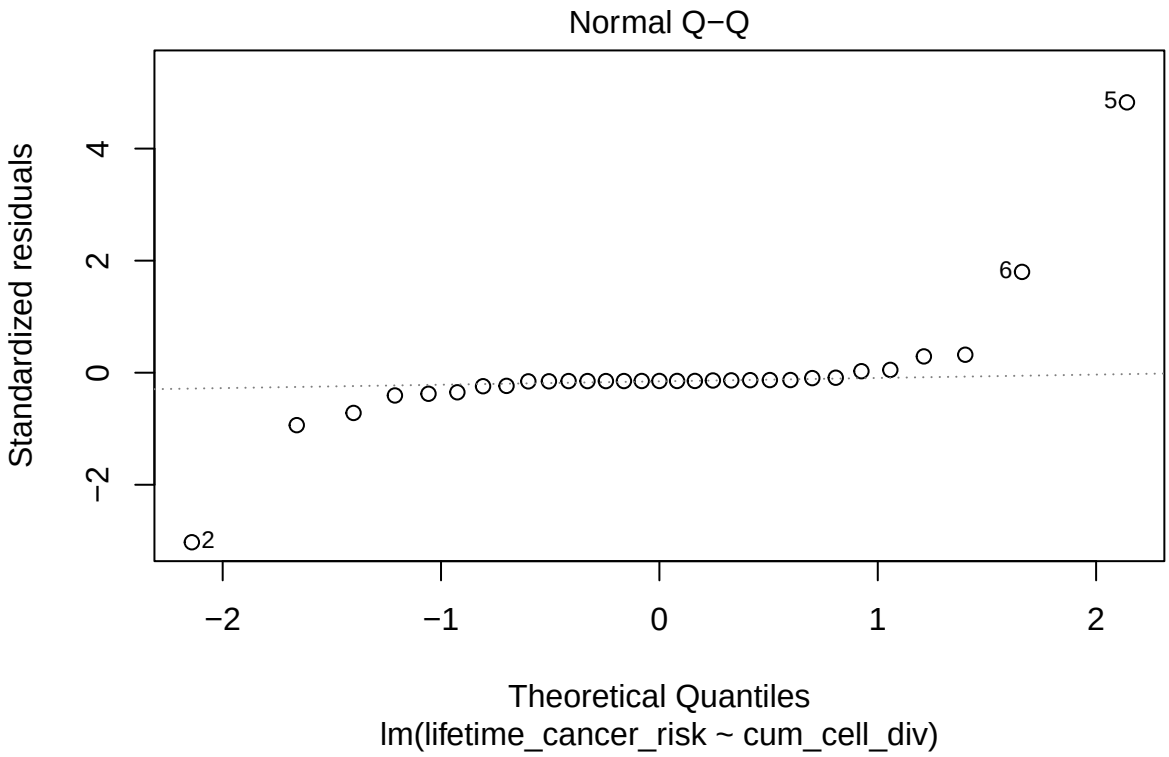


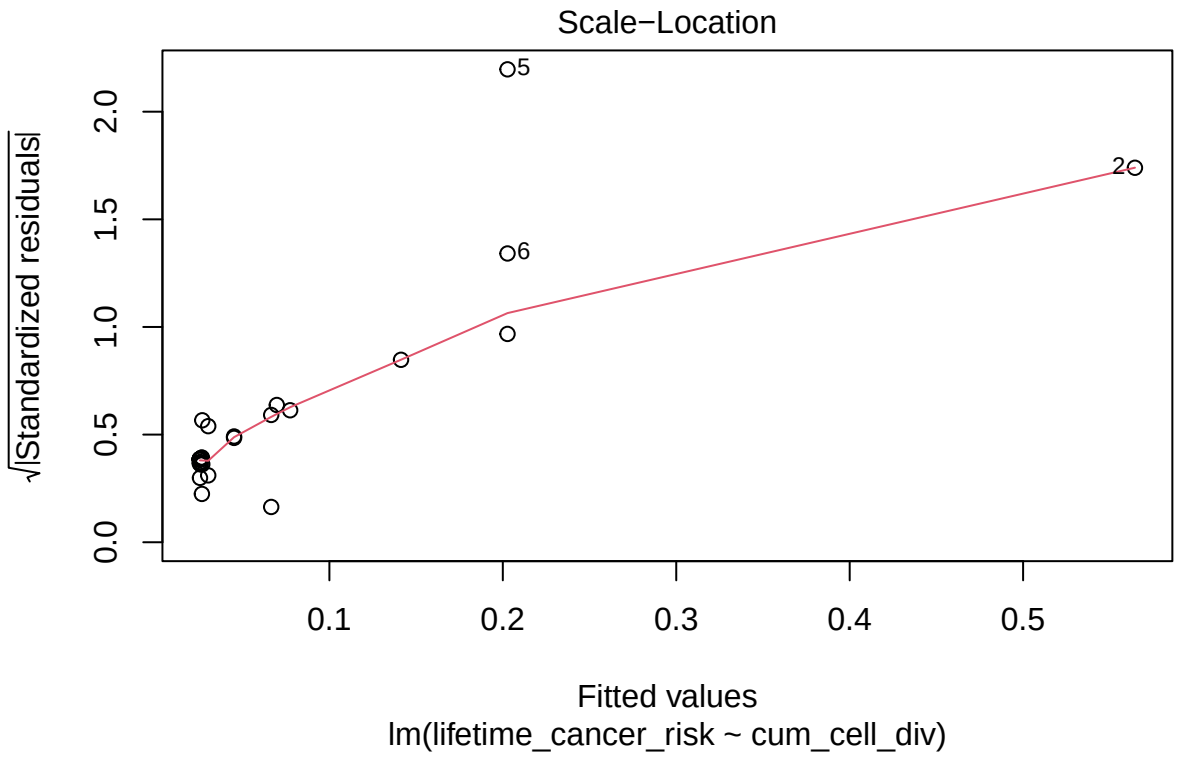
Problem-1B:

Using the lm function, fit a linear model with Lifetime_cancer_risk as the Y variable and CumulativeCell-Divisions as the x-data. Add the regression line to the plot using the function abline(myLm)

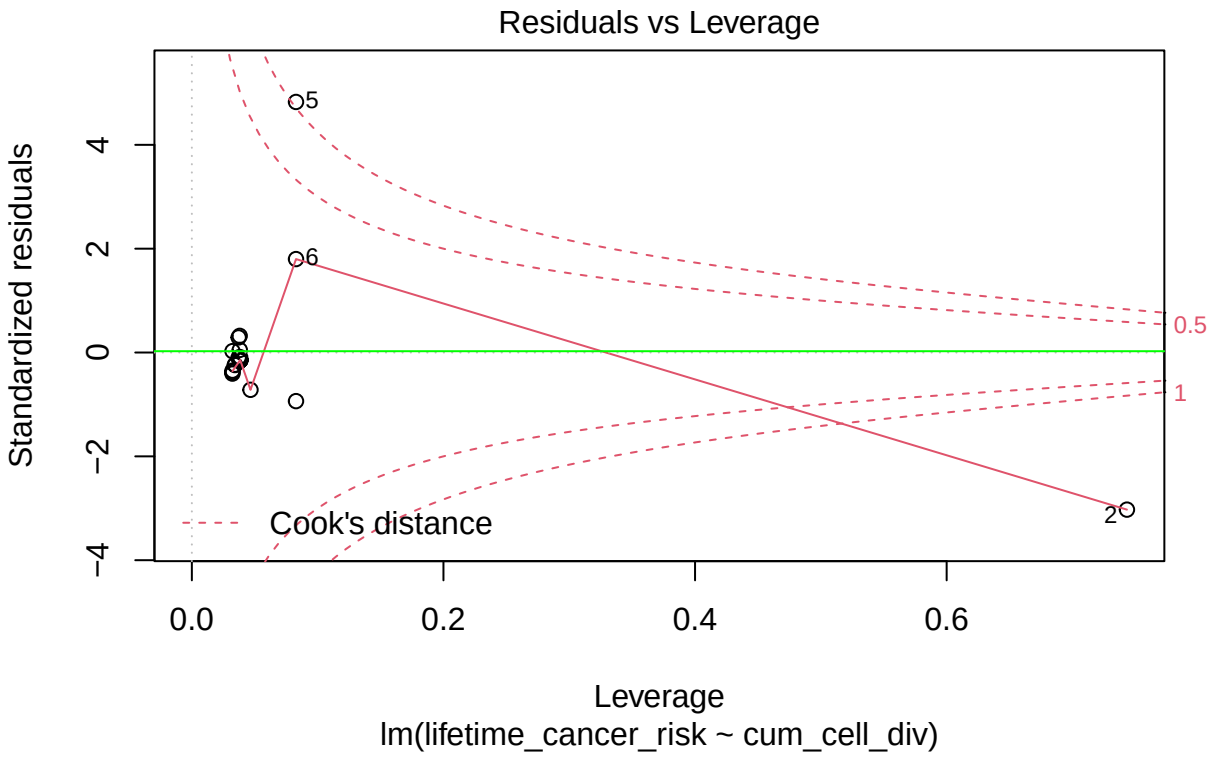
```
myLm = lm(lifetime_cancer_risk~cum_cell_div)

plot(myLm)
```




Normal Q−Q
Standardized residuals
−2
0
2
4
5
6
2
−2
−1
0
1
2
Theoretical Quantiles
lm(lifetime_cancer_risk ~ cum_cell_div)




```
abline(myLm, col='green')
```



Problem-1C:

What is the p-value for the null hypothesis that the slope of the regression between these two variables is zero? What is the r-squared value of the model?

```
sumT = summary(myLm)

anova( myLm)$"Pr(>F)"[1]
```

```
## [1] 0.002027674
```

```
cor(lifetime_cancer_risk, cum_cell_div) * cor(lifetime_cancer_risk, cum_cell_div)
```

```
## [1] 0.2839264
```

```
paste('p-value: ', sumT$coefficients[2,4])
```

```
## [1] "p-value:  0.00202767415572347"
```

```
paste('r-squared value: ',sumT$r.squared)
```

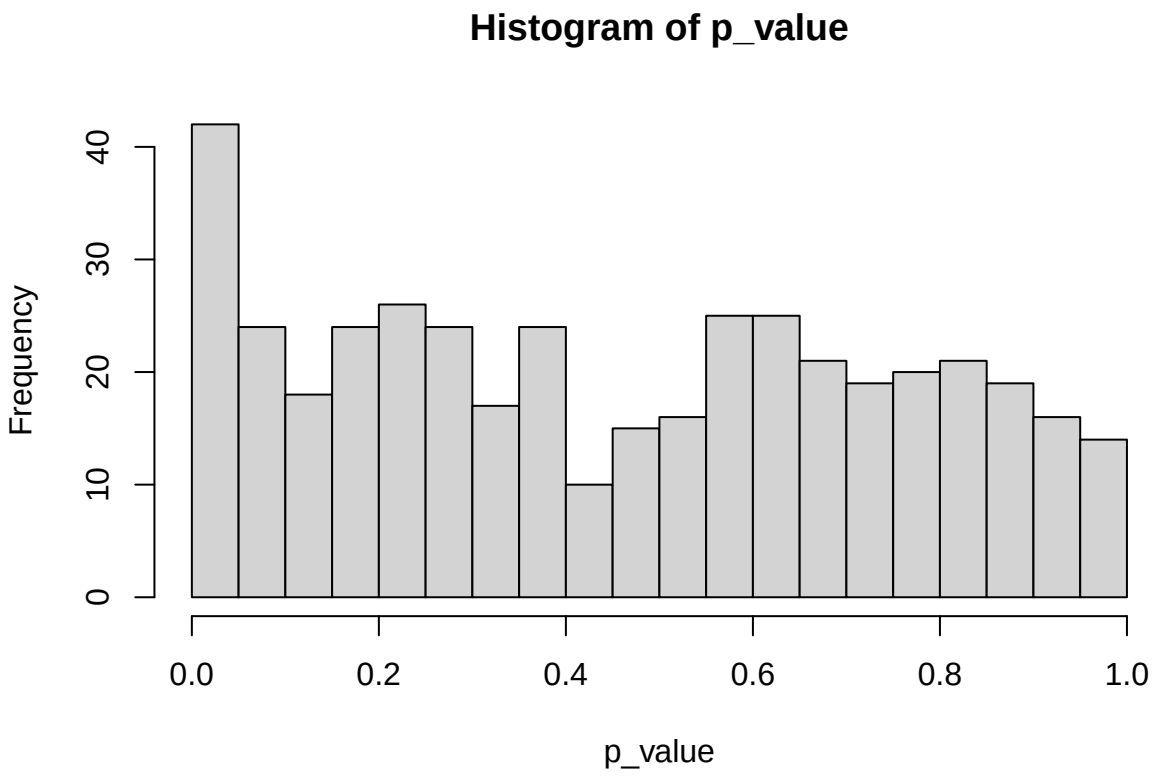
```
## [1] "r-squared value:  0.283926428052786"
```

Problem-1D:

From the independence and normality assumptions of linear regression, we assume that the data has constant variance and they are normally distributed. For **Problem-1** Data. if we look at the Q-Q plot we see that almost all the points reside in the regression line which tells us that the data has very small differences in their variance (this is of of the cleanest biological data that has constant variance).

Problem-2:

```
myTcaseCont = read.table('data/caseControlData.txt', header = TRUE, sep='\t')

myTbmi = read.table('data/BMI_Data.txt', header = TRUE, sep='\t')


casecont_sample = myTcaseCont[ , c("sample")]
casecont_col = colnames(myTcaseCont)
casecont_col = casecont_col[! casecont_col %in% c('sample')]

bmi_val = myTbmi[, c("bmi")]
bmi_id = myTbmi[, c("studyid")]

case_id = vector()
for (i in 1:length(casecont_sample)) {
  subStr = substring(casecont_sample[i],1,10)
  case_id[i] = subStr
}

new_bmi_id = vector()
new_bmi_val = vector()
index = 1
for (i in 1:length(bmi_id)) {
  id = bmi_id[i]
  val = bmi_val[i]
  if (id %in% case_id == TRUE){
    new_bmi_id[index] = id
    new_bmi_val[index] = val
    index = index + 1
  }
}

new_bmi_val[29] = mean(new_bmi_val, na.rm = TRUE)

p_value = vector()

for (i in 1:length(casecont_col)) {
  col_name = casecont_col[i]
  otu = myTcaseCont[ , c(col_name)]
  myLmBMI = lm(new_bmi_val~otu)
  pVal = anova( myLmBMI)$"Pr(>F)"[1]
  p_value[i]=pVal
}

hist(p_value, breaks = 25)
```




```
pValue_adj = p.adjust(p_value, method = 'BH')

sum(pValue_adj <= 0.1)
```

```
## [1] 0
```

The p_values before applying p.adjust() do not seem to be entirely uniformly distributed since we can see a peak at pvalue = 0.0 but other then these few samples they look uniform.

Since most of the samples are uniformly distributed, we can say that other then some specific samples the microbial community does not have influence to the body weight.