Assignment 1

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Exercise 1. Post-operative nausea.

The file contains data about post-operative nausea after medication against nausea. Two different medicines were administered to patients that complained about post-operative nausea. One of the medicines, Pentobarbital, was administered in two different doses.

```
nausea_df <- read.table("data/nauseatable.txt", header=TRUE)
nausea_df
```

```
##                       Incidence.of.no.nausea Incidence.of.Nausea
## Chlorpromazine                           100                  52
## Pentobarbital(100mg)                      32                  35
## Pentobarbital(150mg)                      48                  37
```

a) Discuss whether a contingency table test is appropriate here. If yes, perform this test in order to test whether the different medicines work equally well against nausea. Where are the main inconsistencies?

There are two factors: presence of nausea and the medication. For each combination of factors, the number of cases are registered. Contingency table test is applicable in terms of the task to find the dependency between the factors. For that a specific condition has to be met.

```
z=chisq.test(nausea_df)
z
```

```
##
##  Pearson's Chi-squared test
##
## data:  nausea_df
## X-squared = 6.6248, df = 2, p-value = 0.03643
```

There are no contraindications for the chi-square test. The test concludes that there is a dependence between row and column variables. Let's check what is that difference.

```
library(corrplot)
```

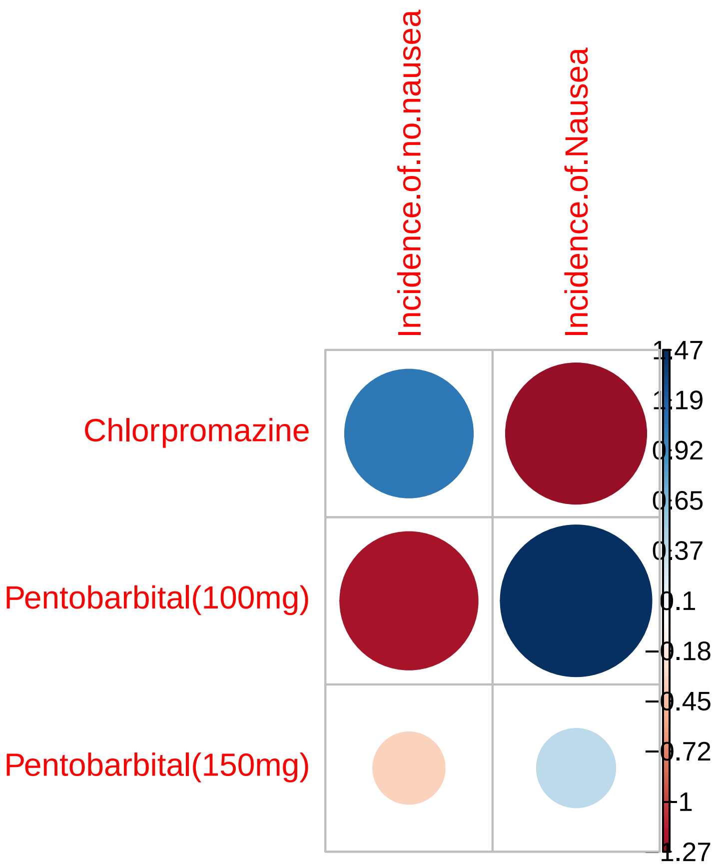
```
## corrplot 0.92 loaded
```

```
z$residuals
```

```
##                       Incidence.of.no.nausea Incidence.of.Nausea
```

```
## Chlorpromazine                     1.0540926          -1.270001
## Pentobarbital(100mg)              -1.2179181           1.467383
## Pentobarbital(150mg)              -0.3282848           0.395527
```

```
corrplot(z$residuals, is.cor = FALSE)
```



Chlorpromazine is relatevily more helpful in terms of fighting against nausea in comparison to both dosages of Pentobarbital. Also, 100mg of Pentobarbital has more nausea cases.

b) Perform a permutation test in order to test whether the different medicines work equally well against nausea. Permute the medicine labels for this purpose. Use as test statistic the chisquare test statistic for contingency tables, which can be extracted from the output of the command chisq.test. (Hint: make a data frame in R consisting of two columns. One column should contain an indicator whether or not the patient in that row suffered from nausea, and the other column should indicate the medicine.)

```
indicator_col <- c()
label_col <- c()
for(i in 1:3){
  indicator_col <- append(indicator_col, rep(0, nausea_df[i, 1]))
  indicator_col <- append(indicator_col, rep(1, nausea_df[i, 2]))
  label_col <- append(label_col, rep(rownames(nausea_df)[i], rowSums(nausea_df[i, ])))
}
```

```r
nausea_two_col_df <- data.frame(indicator_col, label_col)
head(nausea_two_col_df)
```

```
##   indicator_col      label_col
## 1             0 Chlorpromazine
## 2             0 Chlorpromazine
## 3             0 Chlorpromazine
## 4             0 Chlorpromazine
## 5             0 Chlorpromazine
## 6             0 Chlorpromazine
```

```r
mystat <- function(x) chisq.test(x)$statistic
B <- 1000
tstar <- numeric(B)
for(i in 1:B){
  perm_label <- sample(nausea_two_col_df$label_col) ## permuting the labels
  tstar[i] <- mystat(table(data.frame(nausea_two_col_df$indicator_col, perm_label)))
}
myt <- mystat(table(data.frame(nausea_two_col_df$indicator_col, nausea_two_col_df$label_col)))

pl <- sum(tstar<myt)/B
pr <- sum(tstar>myt)/B
p_perm <- min(pl, pr)
p_perm
```

```
## [1] 0.048
```

The permutation test rejects the null hypethesis that different medicines work equally well against nausea.

c) Compare the p-value found by the permutation test with the p-value found from the chisquare test for contingency tables. Explain the difference/equality of the two p-values.

Relaunch of the permutation test retrieves the p-value of about 0.03-0.04 while the p-value from the chi-square test is 0.036. The permutation test is completely suitable for such kind of tasks. It also reveals the same conclusion and similar p-value as the chi-square test.

Exercise 2. Airpollution.

The data were obtained to determine predictors related to air pollution. We want to investigate which explanatory variables need to be included into a linear regression model with oxidant as the response variable.

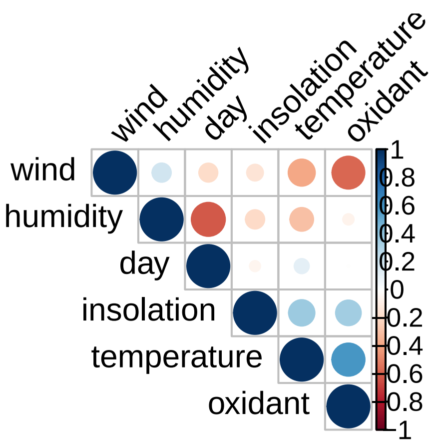
```r
pollution_df <- read.table("data/airpollution.txt", header=TRUE)
head(pollution_df)
```

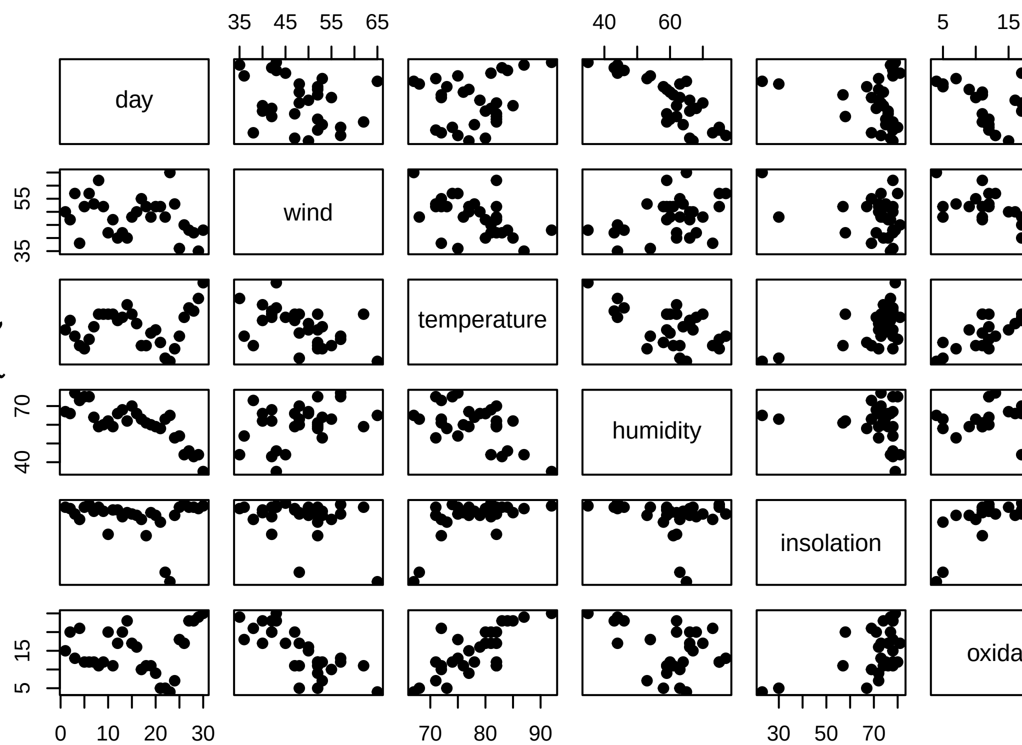
```
##   day wind temperature humidity insolation oxidant
## 1   1   50          77       67         78      15
## 2   2   47          80       66         77      20
```

```
## 3    3    57           75          77           73         13
## 4    4    38           72          73           69         21
## 5    5    52           71          75           78         12
## 6    6    57           74          75           80         12
```

a) Make some graphical summaries of the data. Investigate the problem of potential and influence points, and the problem of collinearity.

```r
# cor(pollution_df, method = c("spearman"))
if (!require("corrplot")) install.packages("corrplot")
library(corrplot)
par(mfrow=c(2, 1))
res <- cor(pollution_df, method='kendall')
corrplot(res, type = "upper", order = "hclust",
         tl.col = "black", tl.srt = 45)
pairs(pollution_df, pch = 19)
```






```r
cor(pollution_df, method='kendall')
```

```
##                      day       wind temperature    humidity  insolation
## day          1.000000000 -0.1863835   0.1150492 -0.61937558 -0.05912545
## wind        -0.186383489  1.0000000  -0.3879563  0.19117541 -0.14320431
## temperature  0.115049153 -0.3879563   1.0000000 -0.29489725  0.36715940
## humidity    -0.619375582  0.1911754  -0.2948973  1.00000000 -0.19163999
## insolation  -0.059125451 -0.1432043   0.3671594 -0.19163999  1.00000000
## oxidant     -0.002359285 -0.5786925   0.5879586 -0.06213201  0.34708840
##                  oxidant
```

```
## day         -0.002359285
## wind        -0.578692494
## temperature  0.587958635
## humidity    -0.062132009
## insolation   0.347088401
## oxidant      1.000000000
```

The command order(abs(residuals(model))) gives the indices of the ordered absolute values of residuals from smallest to largest.

```
pollution_lm = lm(oxidant~insolation+humidity+wind+temperature+day, data=pollution_df)
order(abs(residuals(pollution_lm)))
```

```
##  [1] 25  8 10 13 29 26 14  1 15 24 16  7  5 17 18  6 30  3  2 19 12 20 22  9 23
## [26] 27  4 28 21 11
```

The mean shift outlier model can be applied to test whether the k-th point significantly deviates from the other points in a linear regression setting.

```
u_out=rep(0, nrow(pollution_df)); u_out[21]=1
pollution_lm_outlier=lm(oxidant~insolation+humidity+wind + u_out, data=pollution_df); summary(p
```

```
##
## Call:
## lm(formula = oxidant ~ insolation + humidity + wind + u_out,
##     data = pollution_df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.1135 -1.7707  0.3907  2.7188  5.0021
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 33.79741    7.16856   4.715 7.81e-05 ***
## insolation   0.12672    0.05119   2.476   0.0204 *
## humidity    -0.04665    0.06837  -0.682   0.5013
## wind        -0.51577    0.09917  -5.201 2.22e-05 ***
## u_out       -7.76237    3.54111  -2.192   0.0379 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.449 on 25 degrees of freedom
## Multiple R-squared:  0.7181, Adjusted R-squared:  0.673
## F-statistic: 15.92 on 4 and 25 DF,  p-value: 1.335e-06
```

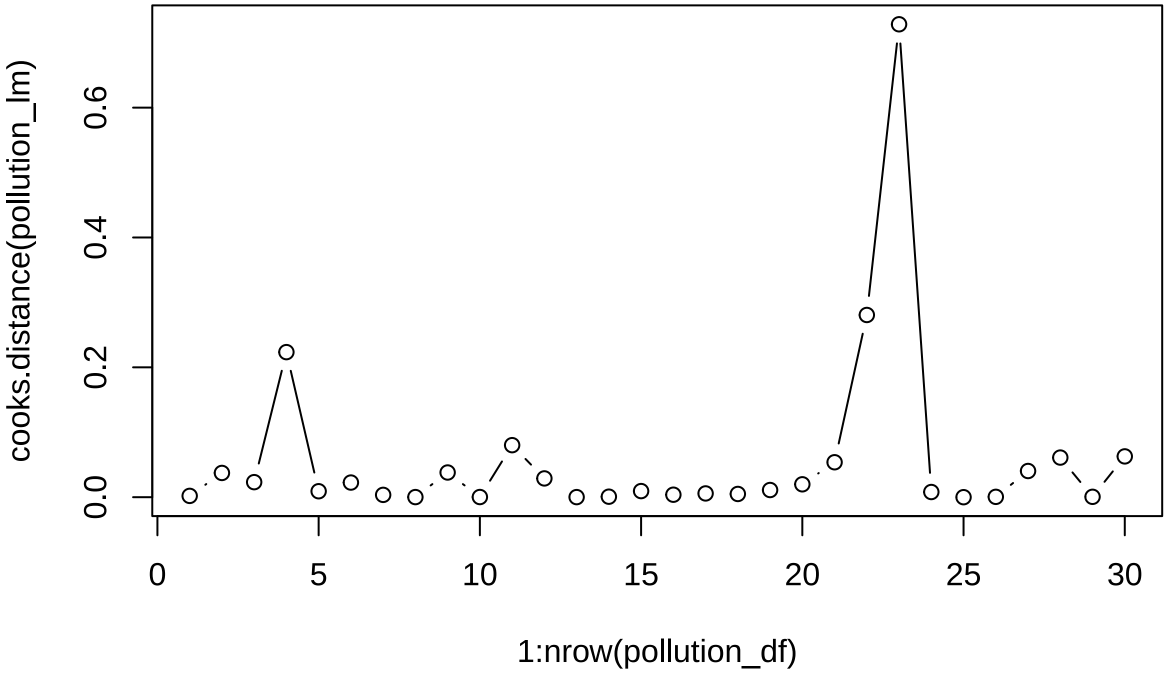
Only the 21 outlier is significant.

The Cook's distance Di quantifies the influence of observation i on the predictions: $D_i = \frac{1}{(p+1)\hat{\sigma}^2} \sum_{j=1}^{n} \left(\hat{Y}_{(i),j} - \hat{Y}_j\right)^2$

```r
max(cooks.distance(pollution_lm))
```

```
## [1] 0.7283678
```

```r
plot(1:nrow(pollution_df), cooks.distance(pollution_lm), type="b")
```

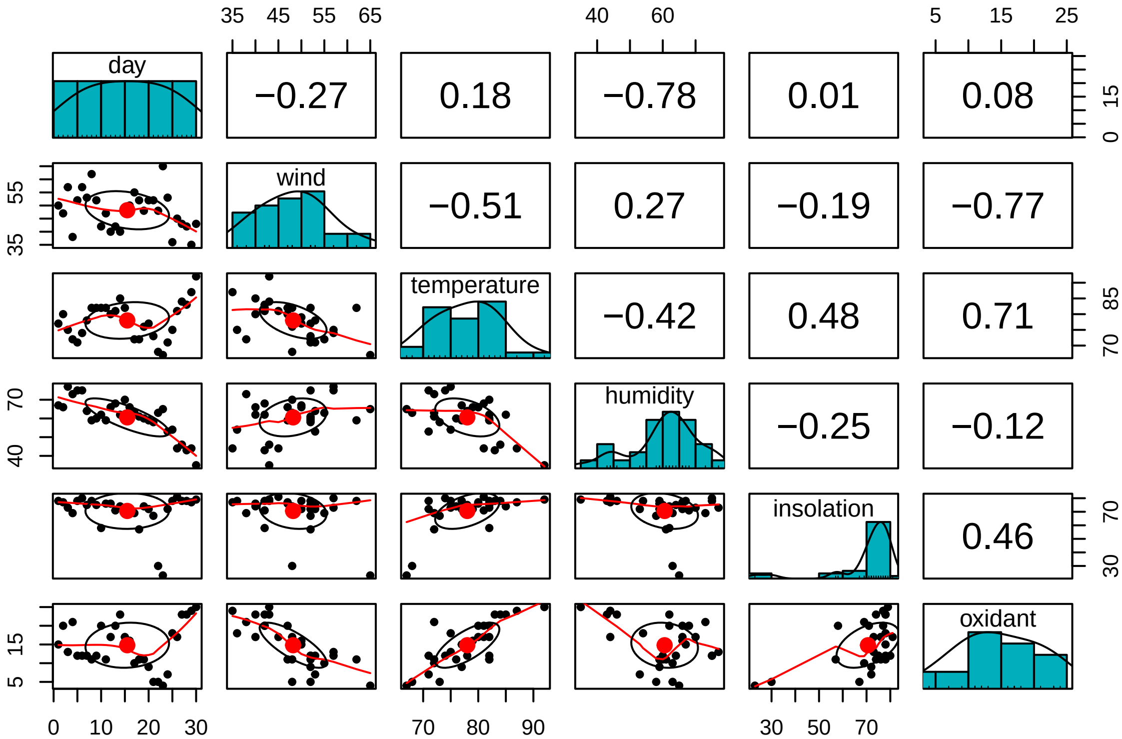


Rule of thumb: if the Cook's distance for some data point is close to or larger than 1, it is considered to be an influence point. So the point 23 is an influence here.

```r
if (!require("psych")) install.packages("psych")
```

```
## Loading required package: psych
```

```r
library(psych)
pairs.panels(pollution_df,
             method = "spearman", # correlation method
             hist.col = "#00AFBB",
             density = TRUE,  # show density plots
             ellipses = TRUE # show correlation ellipses
             )
```

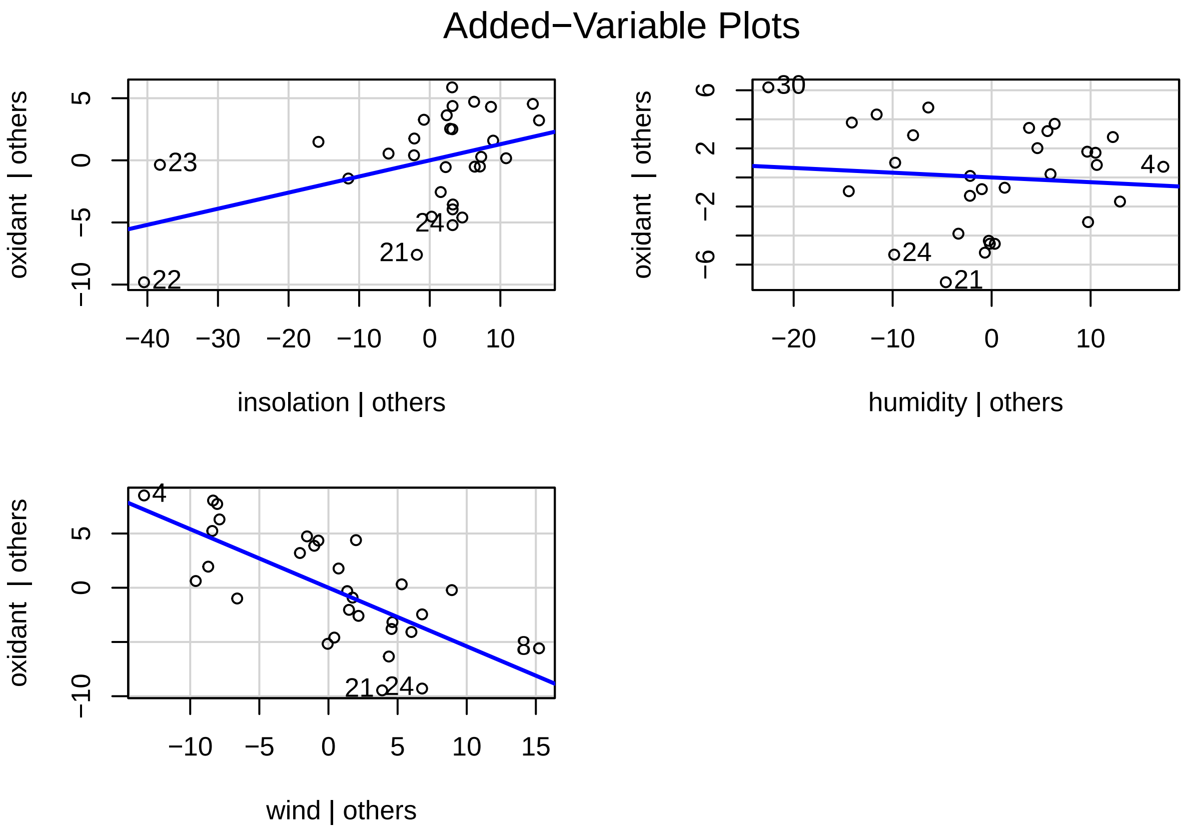


b) Use the added variable plot to depict the relationship between response oxidant and predictor wind. What is the meaning of the slope of fitted regression for this scatter plot?

```
if (!require("car")) install.packages("car")
```

```
## Loading required package: car

## Loading required package: carData

##
## Attaching package: 'car'

## The following object is masked from 'package:psych':
##
##     logit
```

```
library(car)

attach(pollution_df)
mod = lm(oxidant~insolation+humidity+wind)
par(mfrow=c(2, 1))
avPlots(mod)
```

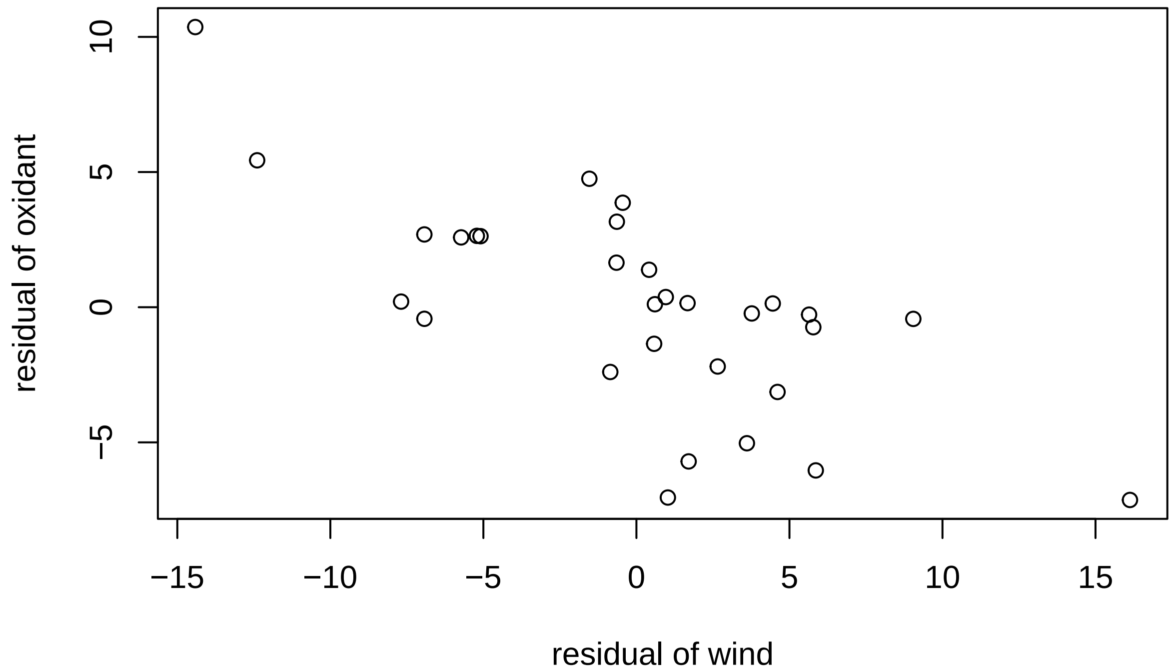



```
summary(mod)
```

```
##
## Call:
## lm(formula = oxidant ~ insolation + humidity + wind)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7.3630 -2.4212  0.5585  3.0466  5.4644
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 33.65768    7.67492   4.385  0.00017 ***
## insolation   0.12984    0.05479   2.370  0.02550 *
## humidity    -0.03266    0.07288  -0.448  0.65775
## wind        -0.54037    0.10550  -5.122 2.44e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.693 on 26 degrees of freedom
## Multiple R-squared:  0.6639, Adjusted R-squared:  0.6251
## F-statistic: 17.12 on 3 and 26 DF,  p-value: 2.423e-06
```

The slopes on the plots reflect the regression coefficients from the original multiple regression model mod.

```
y = residuals(lm(pollution_df$oxidant~pollution_df$temperature+pollution_df$insolation+pollutio
x = residuals(lm(pollution_df$wind~pollution_df$temperature+pollution_df$insolation+pollution_d
plot(x, y, xlab='residual of wind', ylab='residual of oxidant')
```



c) Fit a linear regression model to the data. Use both the step-up and step-down methods to find the best model. If step-up and step-down yield two different models, choose one and motivate your choice.

```
for(i in names(pollution_df)){
  if(i == 'oxidant'){next}
  # summary(lm(oxidant~i))
  print(summary(lm(paste('pollution_df$oxidant',  '~pollution_df$', i))))
}
```

Step-up

```
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$",
##     i))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.3373  -3.8537   0.1298   5.5403   9.1613
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        13.68966    2.28580   5.989 1.89e-06 ***
```

```
## pollution_df$day  0.07164    0.12876   0.556    0.582
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.104 on 28 degrees of freedom
## Multiple R-squared:  0.01093,    Adjusted R-squared:  -0.02439
## F-statistic: 0.3095 on 1 and 28 DF,  p-value: 0.5824
##
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$",
##     i))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.9266 -2.5923  0.2065  2.6636  6.9077
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        45.3171     4.8976   9.253 5.19e-10 ***
## pollution_df$wind  -0.6331     0.1005  -6.300 8.20e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.948 on 28 degrees of freedom
## Multiple R-squared:  0.5863, Adjusted R-squared:  0.5715
## F-statistic: 39.68 on 1 and 28 DF,  p-value: 8.205e-07
##
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$",
##     i))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.9400 -2.2138  0.3775  2.5550 10.9099
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              -46.4292     9.9542  -4.664 6.94e-05 ***
## pollution_df$temperature   0.7850     0.1273   6.168 1.17e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.997 on 28 degrees of freedom
## Multiple R-squared:  0.576,  Adjusted R-squared:  0.5609
## F-statistic: 38.04 on 1 and 28 DF,  p-value: 1.167e-06
##
```

```
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$",
##     i))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.3358  -4.0749   0.8782   4.7800   8.7957
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)            27.4446     6.4368   4.264 0.000206 ***
## pollution_df$humidity  -0.2088     0.1049  -1.991 0.056317 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.745 on 28 degrees of freedom
## Multiple R-squared:  0.124,  Adjusted R-squared:  0.09273
## F-statistic: 3.964 on 1 and 28 DF,  p-value: 0.05632
##
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$",
##     i))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.9723 -4.4841 -0.3281  4.7631  8.2686
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -1.43279    5.32967  -0.269  0.79003
## pollution_df$insolation  0.22993    0.07424   3.097  0.00441 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.297 on 28 degrees of freedom
## Multiple R-squared:  0.2552, Adjusted R-squared:  0.2286
## F-statistic: 9.592 on 1 and 28 DF,  p-value: 0.004411
```

Wind variable gives maximum increase in the R^2. The variable is significant. Therefore, we can continue.

```
for(i in names(pollution_df)){
  if(i %in% c('oxidant', 'wind')){next}
  print(summary(lm(paste('pollution_df$oxidant',  '~pollution_df$wind+pollution_df$', i))))
}
```

```
##
```

```
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$wind+pollution_df$",
##     i))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.4129 -2.5621  0.4498  2.3827  7.9267
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       47.84224    5.62785   8.501 4.10e-09 ***
## pollution_df$wind -0.65984    0.10489  -6.291 9.87e-07 ***
## pollution_df$day  -0.07986    0.08691  -0.919    0.366
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.959 on 27 degrees of freedom
## Multiple R-squared:  0.5989, Adjusted R-squared:  0.5691
## F-statistic: 20.15 on 2 and 27 DF,  p-value: 4.411e-06
##
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$wind+pollution_df$",
##     i))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.3939 -1.8608  0.5826  1.9461  4.9661
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              -5.20334   11.11810  -0.468    0.644
## pollution_df$wind        -0.42706    0.08645  -4.940 3.58e-05 ***
## pollution_df$temperature  0.52035    0.10813   4.812 5.05e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.95 on 27 degrees of freedom
## Multiple R-squared:  0.7773, Adjusted R-squared:  0.7608
## F-statistic: 47.12 on 2 and 27 DF,  p-value: 1.563e-09
##
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$wind+pollution_df$",
##     i))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -9.8120 -2.2808  0.3433  3.0476  5.8757
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)           46.91570    5.68573   8.251 7.38e-09 ***
## pollution_df$wind     -0.60955    0.10971  -5.556 6.86e-06 ***
## pollution_df$humidity -0.04516    0.07866  -0.574    0.571
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.996 on 27 degrees of freedom
## Multiple R-squared:  0.5913, Adjusted R-squared:  0.561
## F-statistic: 19.53 on 2 and 27 DF,  p-value: 5.674e-06
##
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$wind+pollution_df$",
##     i))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7.2119 -2.7198  0.4815  2.8733  6.2012
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             32.32615    6.97098   4.637 8.07e-05 ***
## pollution_df$wind       -0.55639    0.09778  -5.690 4.81e-06 ***
## pollution_df$insolation  0.13161    0.05383   2.445   0.0213 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.638 on 27 degrees of freedom
## Multiple R-squared:  0.6613, Adjusted R-squared:  0.6362
## F-statistic: 26.36 on 2 and 27 DF,  p-value: 4.491e-07
```

Temperature variable works in the same way as the previous choice. Continue.

```r
for(i in names(pollution_df)){
  if(i %in% c('oxidant', 'wind', 'temperature')){next}
  print(summary(lm(paste('pollution_df$oxidant',
                         '~pollution_df$wind',
                         '+pollution_df$temperature',
                         '+pollution_df$',
                         i))))
}
```

```
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$wind",
```

```
##     "+pollution_df$temperature", "+pollution_df$", i))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.9010 -1.3477  0.1596  1.7766  3.9405
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              -2.98987   10.94466  -0.273    0.787
## pollution_df$wind        -0.45604    0.08644  -5.276 1.63e-05 ***
## pollution_df$temperature  0.52918    0.10568   5.008 3.29e-05 ***
## pollution_df$day         -0.09711    0.06328  -1.535    0.137
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.878 on 26 degrees of freedom
## Multiple R-squared:  0.7958, Adjusted R-squared:  0.7722
## F-statistic: 33.78 on 3 and 26 DF,  p-value: 4.042e-09
##
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$wind",
##     "+pollution_df$temperature", "+pollution_df$", i))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.5887 -1.1686  0.1978  1.9004  4.1544
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)              -16.60697   13.07154  -1.270    0.215
## pollution_df$wind         -0.44620    0.08513  -5.241 1.78e-05 ***
## pollution_df$temperature   0.60190    0.11764   5.117 2.47e-05 ***
## pollution_df$humidity      0.09850    0.06316   1.559    0.131
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.874 on 26 degrees of freedom
## Multiple R-squared:  0.7964, Adjusted R-squared:  0.7729
## F-statistic: 33.89 on 3 and 26 DF,  p-value: 3.904e-09
##
##
## Call:
## lm(formula = paste("pollution_df$oxidant", "~pollution_df$wind",
##     "+pollution_df$temperature", "+pollution_df$", i))
##
## Residuals:
##    Min     1Q Median     3Q    Max
```

```
## -6.407 -2.056  1.012  1.760  4.792
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -4.45496   11.26714  -0.395 0.695778
## pollution_df$wind       -0.42353    0.08737  -4.848 5.02e-05 ***
## pollution_df$temperature  0.47558    0.12564   3.785 0.000816 ***
## pollution_df$insolation   0.03646    0.05071   0.719 0.478636
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.976 on 26 degrees of freedom
## Multiple R-squared:  0.7816, Adjusted R-squared:  0.7565
## F-statistic: 31.02 on 3 and 26 DF,  p-value: 9.583e-09
```

Humidity has the highest R-squared increase but the variable is not significant. Therefore, we don't add it to the model. Resulting model is:

```
print(summary(lm(pollution_df$oxidant~pollution_df$wind+pollution_df$temperature)))
```

```
##
## Call:
## lm(formula = pollution_df$oxidant ~ pollution_df$wind + pollution_df$temperature)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.3939 -1.8608  0.5826  1.9461  4.9661
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -5.20334   11.11810  -0.468    0.644
## pollution_df$wind       -0.42706    0.08645  -4.940 3.58e-05 ***
## pollution_df$temperature  0.52035    0.10813   4.812 5.05e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.95 on 27 degrees of freedom
## Multiple R-squared:  0.7773, Adjusted R-squared:  0.7608
## F-statistic: 47.12 on 2 and 27 DF,  p-value: 1.563e-09
```

oxidant = -5.2 - 0.4*wind + 0.5*temperature + error, with R-squared = 0.8.

```
summary(lm(pollution_df$oxidant~ pollution_df$wind + pollution_df$temperature + pollution_df$da
```

Step-down

```
##
## Call:
## lm(formula = pollution_df$oxidant ~ pollution_df$wind + pollution_df$temperature +
```

```
##     pollution_df$day + pollution_df$humidity + pollution_df$insolation)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.6920 -1.1675  0.2582  1.8289  4.0773
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)              -12.04010   21.20961  -0.568  0.57553
## pollution_df$wind         -0.44749    0.09103  -4.916 5.14e-05 ***
## pollution_df$temperature   0.55714    0.15347   3.630  0.00133 **
## pollution_df$day          -0.02997    0.13995  -0.214  0.83227
## pollution_df$humidity      0.06818    0.13336   0.511  0.61384
## pollution_df$insolation    0.01822    0.05583   0.326  0.74694
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.977 on 24 degrees of freedom
## Multiple R-squared:  0.7984, Adjusted R-squared:  0.7564
## F-statistic: 19.01 on 5 and 24 DF,  p-value: 1.203e-07
```

Day has the largest p-value and the value is larger than 0.05. Removing it.

```
summary(lm(pollution_df$oxidant ~ pollution_df$wind + pollution_df$temperature + pollution_df$h
```

```
##
## Call:
## lm(formula = pollution_df$oxidant ~ pollution_df$wind + pollution_df$temperature +
##     pollution_df$humidity + pollution_df$insolation)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.5861 -1.0961  0.3512  1.7570  4.0712
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)              -15.49370   13.50647  -1.147  0.26219
## pollution_df$wind         -0.44291    0.08678  -5.104 2.85e-05 ***
## pollution_df$temperature   0.56933    0.13977   4.073  0.00041 ***
## pollution_df$humidity      0.09292    0.06535   1.422  0.16743
## pollution_df$insolation    0.02275    0.05067   0.449  0.65728
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.92 on 25 degrees of freedom
## Multiple R-squared:  0.798,  Adjusted R-squared:  0.7657
## F-statistic: 24.69 on 4 and 25 DF,  p-value: 2.279e-08
```

Insolation is the largers from the insignificant. Removing it.

```r
summary(lm(pollution_df$oxidant~ pollution_df$wind + pollution_df$temperature + pollution_df$hu
```

```
##
## Call:
## lm(formula = pollution_df$oxidant ~ pollution_df$wind + pollution_df$temperature +
##     pollution_df$humidity)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.5887 -1.1686  0.1978  1.9004  4.1544
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -16.60697   13.07154  -1.270    0.215
## pollution_df$wind        -0.44620    0.08513  -5.241 1.78e-05 ***
## pollution_df$temperature   0.60190    0.11764   5.117 2.47e-05 ***
## pollution_df$humidity      0.09850    0.06316   1.559    0.131
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.874 on 26 degrees of freedom
## Multiple R-squared:  0.7964, Adjusted R-squared:  0.7729
## F-statistic: 33.89 on 3 and 26 DF,  p-value: 3.904e-09
```

Humidity is the only insignificant. Removing.

```r
summary(lm(pollution_df$oxidant~ pollution_df$wind + pollution_df$temperature))
```

```
##
## Call:
## lm(formula = pollution_df$oxidant ~ pollution_df$wind + pollution_df$temperature)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.3939 -1.8608  0.5826  1.9461  4.9661
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -5.20334   11.11810  -0.468    0.644
## pollution_df$wind       -0.42706    0.08645  -4.940 3.58e-05 ***
## pollution_df$temperature  0.52035    0.10813   4.812 5.05e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.95 on 27 degrees of freedom
## Multiple R-squared:  0.7773, Adjusted R-squared:  0.7608
## F-statistic: 47.12 on 2 and 27 DF,  p-value: 1.563e-09
```

All remaining variables are significant. Resulting model: oxidant = -5.2 - 0.4*wind + 0.5*temperature

+ error, with R-squared = 0.8. The model is the same as obtained with the step-up approach.

d) Determine 95% confidence and prediction intervals for oxidant using the model you preferred in c) for wind=33, temperature=54, humidity=77 and insolation=21.

```
x1 <- pollution_df$wind
x2 <- pollution_df$temperature

mod = lm(pollution_df$oxidant ~ x1 + x2)

newxdata = data.frame(x1=33, x2=54)

predict(mod, newxdata, interval='prediction', level=0.95)
```

```
##       fit        lwr      upr
## 1 8.80281 -0.5617877 18.16741
```

```
predict(mod, newxdata, interval='confidence', level=0.95)
```

```
##       fit      lwr      upr
## 1 8.80281 1.656548 15.94907
```

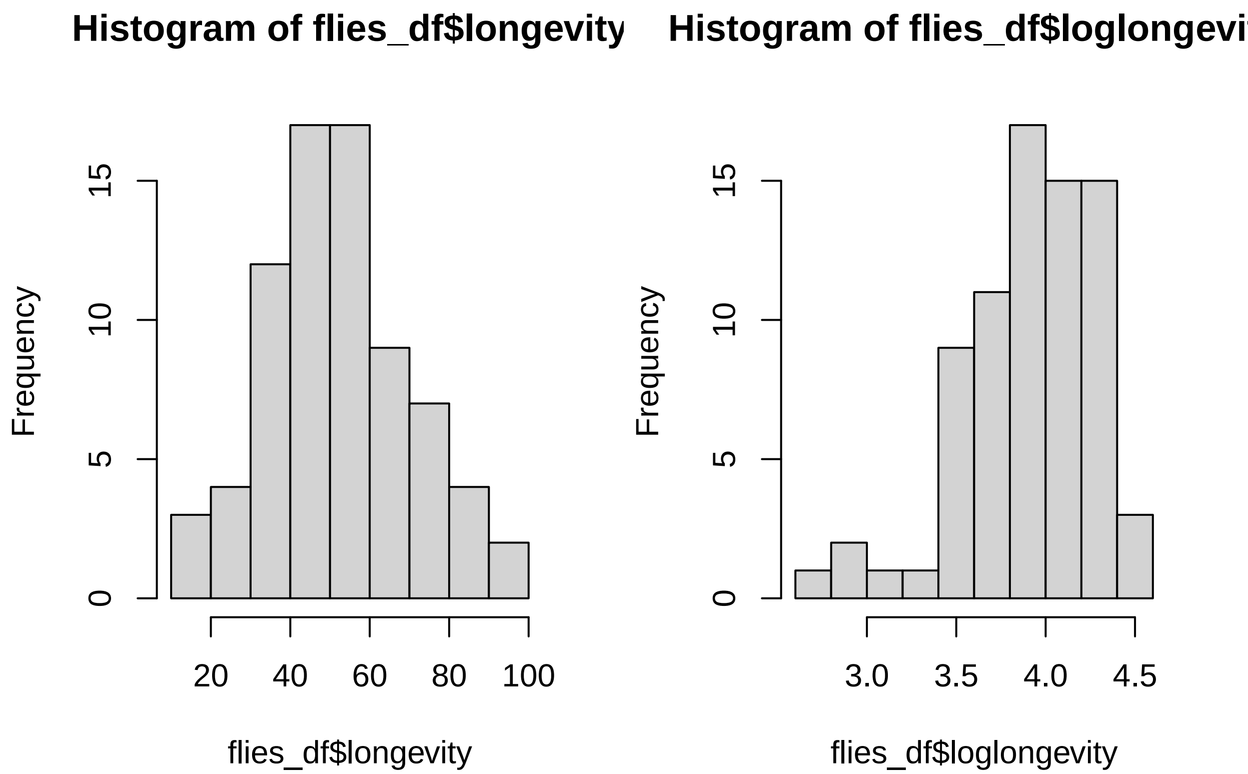
Exercise 3. Fruit flies.

To investigate the effect of sexual activity on longevity of fruit flies, 75 male fruit flies were divided randomly in three groups of 25. The fruit flies in the first group were kept solitary, those in the second were kept together with one virgin female fruit fly per day, and those in the third group were kept together with eight virgin female fruit flies a day. In the data-file three groups are labelled isolated, low and high. The number of days until death (longevity) was measured for all flies. Later, it was decided to measure also the length of their thorax. Add a column loglongevity to the data-frame, containing the logarithm of the number of days until death. *Use this as the response variable in the following.*

```
flies_df <- read.table("data/fruitflies.txt", header=TRUE)
flies_df$loglongevity=log(flies_df$longevity)
head(flies_df)
```

```
##   thorax longevity activity loglongevity
## 1   0.64        40 isolated     3.688879
## 2   0.70        37 isolated     3.610918
## 3   0.72        44 isolated     3.784190
## 4   0.72        47 isolated     3.850148
## 5   0.72        47 isolated     3.850148
## 6   0.76        47 isolated     3.850148
```

```
par(mfrow=c(1, 2))
hist(flies_df$longevity)
hist(flies_df$loglongevity)
```




```
shapiro.test(flies_df$longevity)
```

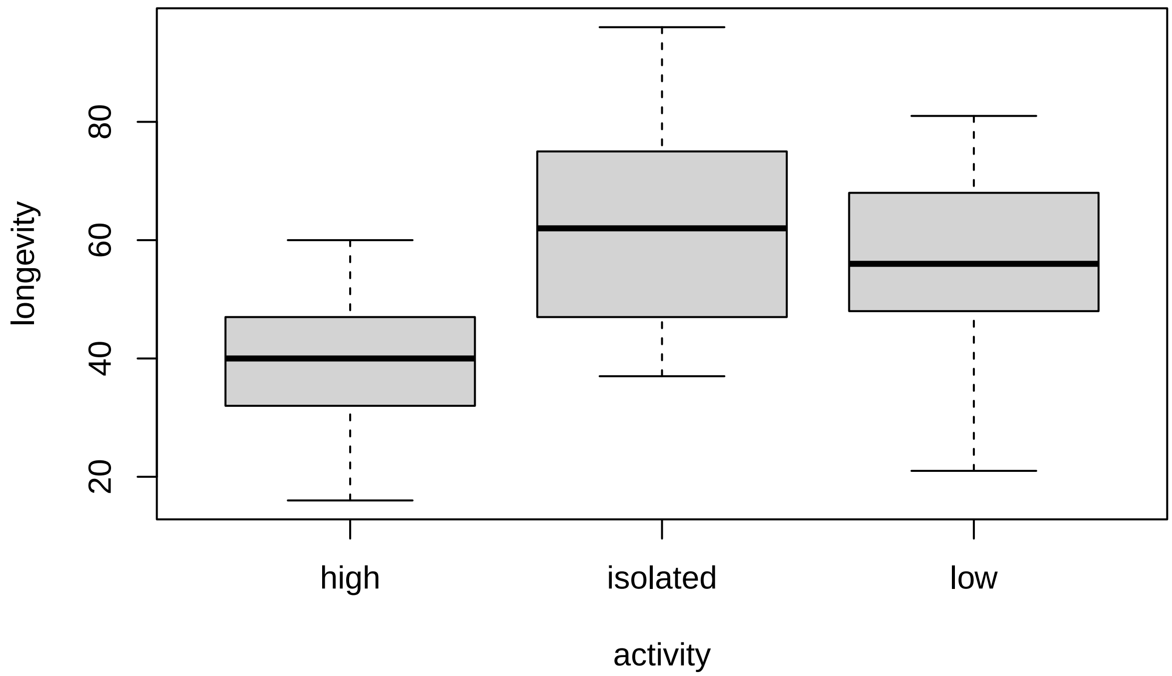
```
##
##  Shapiro-Wilk normality test
##
## data:  flies_df$longevity
## W = 0.98686, p-value = 0.6333
```

```
shapiro.test(flies_df$loglongevity)
```

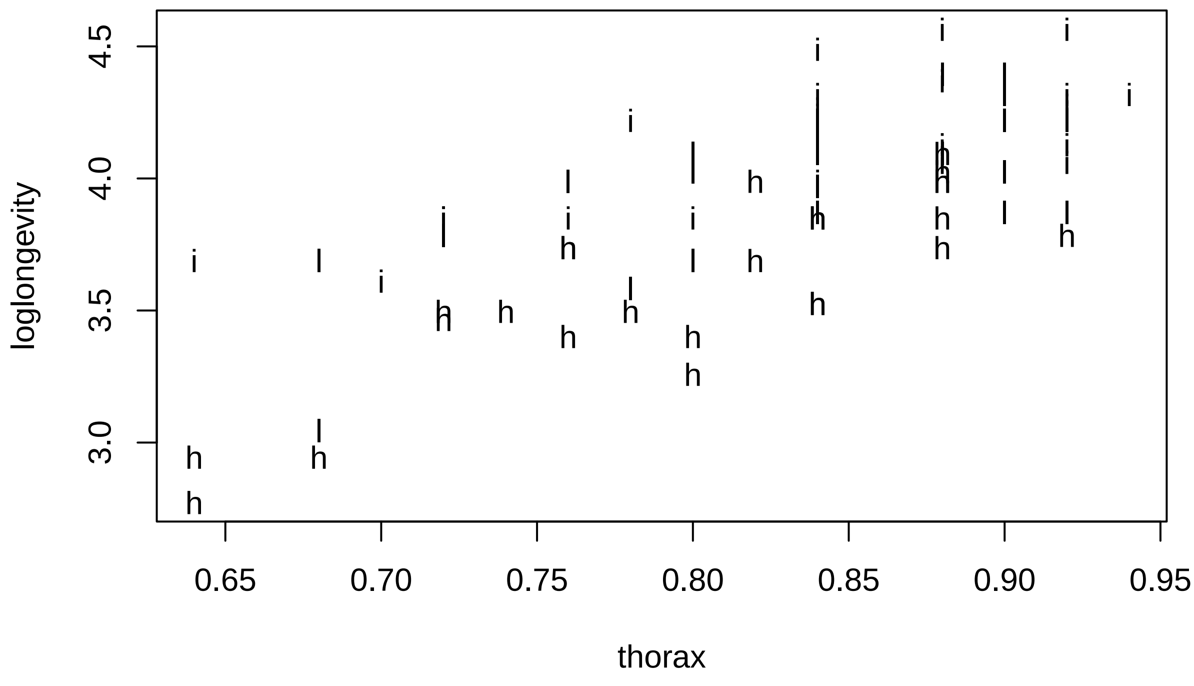
```
##
##  Shapiro-Wilk normality test
##
## data:  flies_df$loglongevity
## W = 0.95437, p-value = 0.008728
```

The original column is normal while the log of it is not.

```
boxplot(longevity~activity, data=flies_df)
```




```r
plot(loglongevity~thorax, pch=as.character(activity), data=flies_df)
```



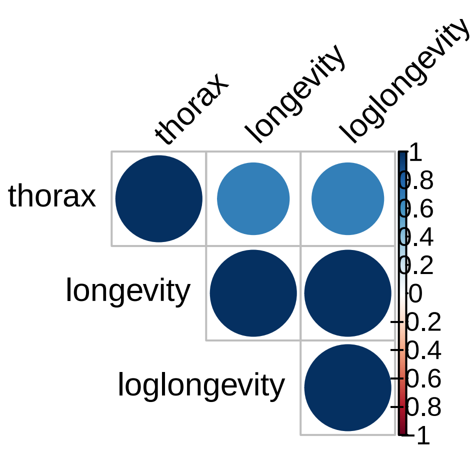
a) Make an informative plot of the data. Investigate whether sexual activity influences longevity by performing a statistical test, without taking the thorax length into account. What are the estimated longevities for the three conditions? Comment.

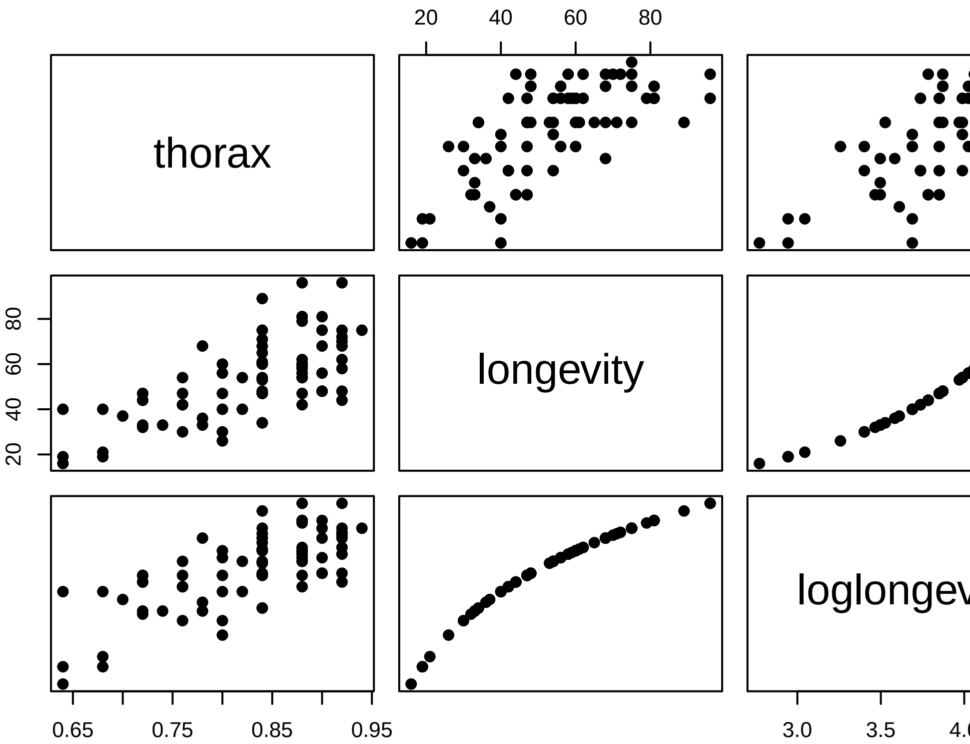
```r
if (!require("dplyr")) install.packages("dplyr")
```

```
## Loading required package: dplyr
```

```
##
## Attaching package: 'dplyr'

## The following object is masked from 'package:car':
##
##     recode

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(dplyr)

par(mfrow=c(2, 1))
res <- cor(select_if(flies_df, is.numeric), method='spearman')
corrplot(res, type = "upper", order = "hclust",
         tl.col = "black", tl.srt = 45)
pairs(select_if(flies_df, is.numeric), pch = 19)
```






```
flies_df$activity=as.factor(flies_df$activity)

flies_lm = lm(loglongevity ~ activity, data=flies_df)
anova(flies_lm)
```

```
## Analysis of Variance Table
```

```
##
## Response: loglongevity
##           Df Sum Sq Mean Sq F value    Pr(>F)
## activity   2 3.6665  1.8333  19.421 1.798e-07 ***
## Residuals 72 6.7966  0.0944
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

H0 is rejected. Sexual activity influences longevity.

```
summary(flies_lm)
```

```
##
## Call:
## lm(formula = loglongevity ~ activity, data = flies_df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.95531 -0.13338  0.02552  0.20891  0.49222
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       3.60212    0.06145  58.621  < 2e-16 ***
## activityisolated  0.51722    0.08690   5.952 8.82e-08 ***
## activitylow       0.39771    0.08690   4.577 1.93e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3072 on 72 degrees of freedom
## Multiple R-squared:  0.3504, Adjusted R-squared:  0.3324
## F-statistic: 19.42 on 2 and 72 DF,  p-value: 1.798e-07
```

estimated longevities for the three conditions:

```
high = 3.60212
isolated = high + 0.51722
low = high + 0.39711
high; isolated; low
```

```
## [1] 3.60212

## [1] 4.11934

## [1] 3.99923
```

b) Investigate whether sexual activity influences longevity by performing a statistical test, now including thorax length as an explanatory variable into the analysis. Does sexual activity increase or decrease longevity? What are the estimated longevities for the three groups, for flies with the minimal and maximal thorax lengths?

```
ancova_lm = lm(loglongevity ~ activity + thorax, data=flies_df) ## order matters but we use dro
drop1(ancova_lm, test="F")
```

```
## Single term deletions
##
## Model:
## loglongevity ~ activity + thorax
##          Df Sum of Sq    RSS     AIC F value    Pr(>F)
## <none>                2.9180 -235.50
## activity  2    2.1129 5.0309 -198.64  25.705 4.000e-09 ***
## thorax    1    3.8786 6.7966 -174.08  94.374 1.139e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(ancova_lm)
```

```
##
## Call:
## lm(formula = loglongevity ~ activity + thorax, data = flies_df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4858 -0.1612  0.0104  0.1510  0.3574
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       1.21893    0.24865   4.902 5.79e-06 ***
## activityisolated  0.40998    0.05839   7.021 1.07e-09 ***
## activitylow       0.28570    0.05849   4.885 6.18e-06 ***
## thorax            2.97899    0.30665   9.715 1.14e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2027 on 71 degrees of freedom
## Multiple R-squared:  0.7211, Adjusted R-squared:  0.7093
## F-statistic:  61.2 on 3 and 71 DF,  p-value: < 2.2e-16
```

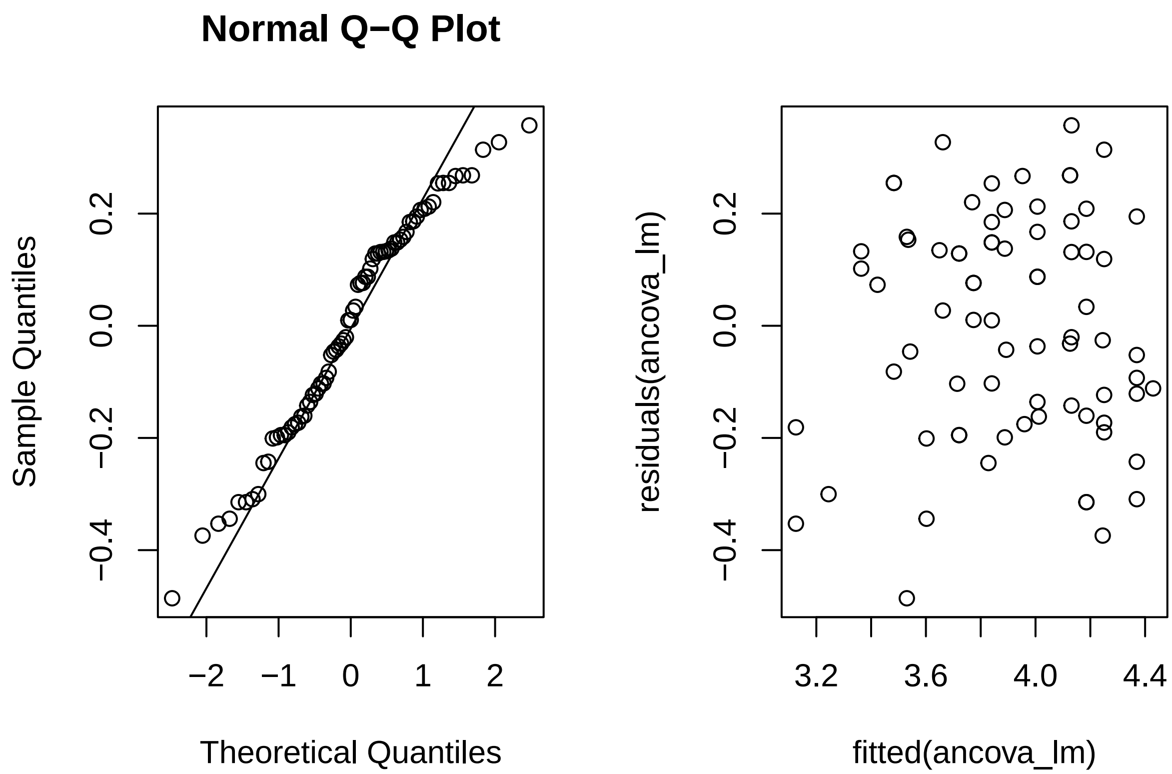
From the coefficients we can conclude that more sex - shorter life.

```
shapiro.test(residuals(ancova_lm))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(ancova_lm)
```

```
## W = 0.96838, p-value = 0.05748
```

```
par(mfrow=c(1, 2))
qqnorm(residuals(ancova_lm)); qqline(residuals(ancova_lm))
plot(fitted(ancova_lm), residuals(ancova_lm))
```




```
anova(lm(loglongevity ~ activity + thorax, data=flies_df))
```

```
## Analysis of Variance Table
##
## Response: loglongevity
##           Df Sum Sq Mean Sq F value    Pr(>F)
## activity   2 3.6665  1.8332  44.606 2.838e-13 ***
## thorax     1 3.8786  3.8786  94.374 1.139e-14 ***
## Residuals 71 2.9180  0.0411
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# anova(lm(loglongevity ~ thorax + activity, data=flies_df))
summary(lm(loglongevity ~ thorax + activity, data=flies_df))
```

```
##
## Call:
## lm(formula = loglongevity ~ thorax + activity, data = flies_df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.4858 -0.1612  0.0104  0.1510  0.3574
```

```
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        1.21893    0.24865   4.902 5.79e-06 ***
## thorax             2.97899    0.30665   9.715 1.14e-14 ***
## activityisolated  0.40998    0.05839   7.021 1.07e-09 ***
## activitylow        0.28570    0.05849   4.885 6.18e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2027 on 71 degrees of freedom
## Multiple R-squared:  0.7211, Adjusted R-squared:  0.7093
## F-statistic:  61.2 on 3 and 71 DF,  p-value: < 2.2e-16
```

```
ancova_lm_int = lm(loglongevity ~ activity * thorax, data=flies_df)
anova(ancova_lm_int)
```

```
## Analysis of Variance Table
##
## Response: loglongevity
##                  Df Sum Sq Mean Sq F value    Pr(>F)
## activity          2 3.6665  1.8332 45.7687 2.228e-13 ***
## thorax            1 3.8786  3.8786 96.8327 9.020e-15 ***
## activity:thorax  2 0.1542  0.0771  1.9251    0.1536
## Residuals        69 2.7638  0.0401
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

There is no significant interaction between factor activity and predictor thorax.

```
summary(ancova_lm_int)
```

```
##
## Call:
## lm(formula = loglongevity ~ activity * thorax, data = flies_df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.49803 -0.15920 -0.00031  0.14624  0.35984
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)                0.5978     0.4192   1.426   0.1584
## activityisolated           1.5465     0.5845   2.646   0.0101 *
## activitylow                0.9717     0.6423   1.513   0.1349
## thorax                     3.7554     0.5216   7.199 5.78e-10 ***
## activityisolated:thorax  -1.3929     0.7122  -1.956   0.0545 .
## activitylow:thorax       -0.8539     0.7794  -1.096   0.2771
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 0.2001 on 69 degrees of freedom
## Multiple R-squared:  0.7359, Adjusted R-squared:  0.7167
## F-statistic: 38.44 on 5 and 69 DF,  p-value: < 2.2e-16
```

The interaction term is not significant. So, no indication that the initial analysis (ancova_lm without interaction) is in trouble.

```
# predict(ancova_lm, flies_df[which.min(flies_df$thorax), c('thorax', 'activity')])
# predict(ancova_lm, flies_df[which.max(flies_df$thorax), c('thorax', 'activity')])

min_thorax = min(flies_df$thorax)
max_thorax = max(flies_df$thorax)

# min_high = predict(ancova_lm, data.frame(thorax = min_thorax, activity = "high"))
min_high = 1.21893 + 2.97899 * min_thorax
max_high = 1.21893 + 2.97899 * max_thorax

min_iso = 1.21893 + 0.40998 + 2.97899 * min_thorax
max_iso = 1.21893 + 0.40998 + 2.97899 * max_thorax

min_low = 1.21893 + 0.28570 + 2.97899 * min_thorax
max_low = 1.21893 + 0.28570 + 2.97899 * max_thorax

exp(min_high); max_high
```

```
## [1] 22.7709

## [1] 4.019181
```

```
min_iso; exp(max_iso)
```

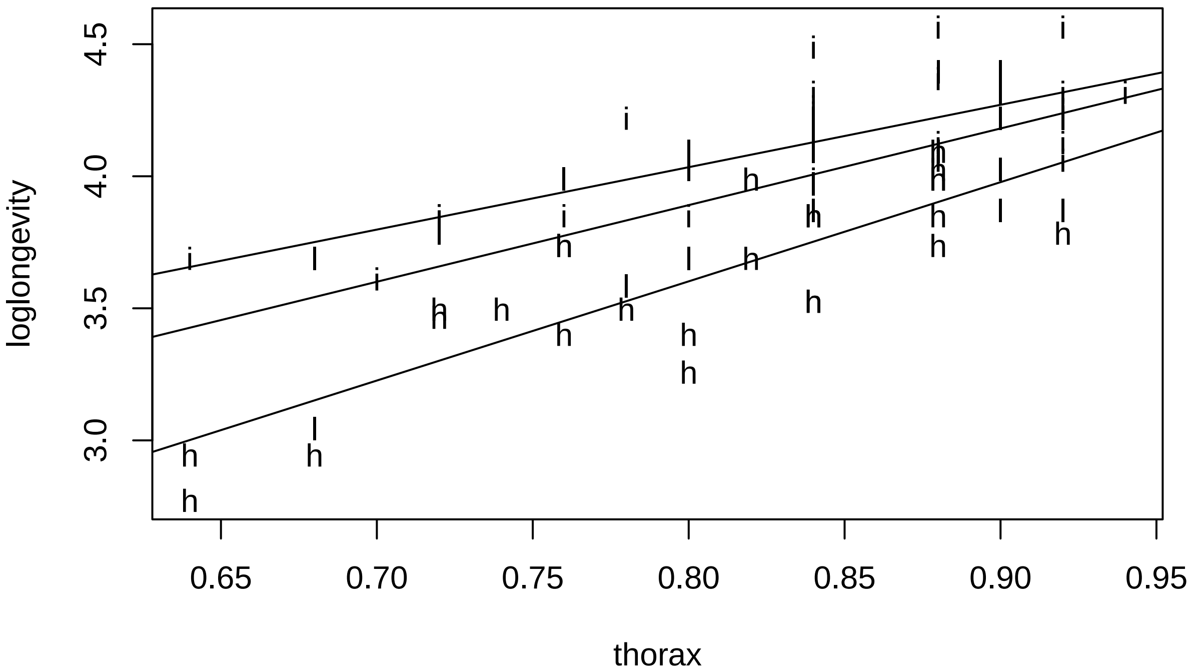
```
## [1] 3.535464

## [1] 83.86099
```

```
exp(min_low); exp(max_low)
```

```
## [1] 30.30109

## [1] 74.06037
```

c) How does thorax length influence longevity? Investigate graphically and by using an appropriate test whether this dependence is similar under all three conditions of sexual activity.

```
plot(loglongevity~thorax, pch=as.character(activity), data=flies_df)
for (i in unique(flies_df$activity)) abline(lm(loglongevity~thorax, data=flies_df[flies_df$acti
```




```
ancova_lm_int = lm(loglongevity ~ activity * thorax, data=flies_df)
anova(ancova_lm_int)
```

```
## Analysis of Variance Table
##
## Response: loglongevity
##                 Df Sum Sq Mean Sq F value    Pr(>F)
## activity         2 3.6665  1.8332 45.7687 2.228e-13 ***
## thorax           1 3.8786  3.8786 96.8327 9.020e-15 ***
## activity:thorax  2 0.1542  0.0771  1.9251    0.1536
## Residuals       69 2.7638  0.0401
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Only the last p-value is relevant which always concerns interaction for models with interaction. We conclude from it that $H_0 : \beta_1 = \beta_2$ is not rejected, i.e., there is no interaction between factor activity and predictor thorax.

d) Which of the two analyses, without or with thorax length, do you prefer? Is one of the analyses wrong?

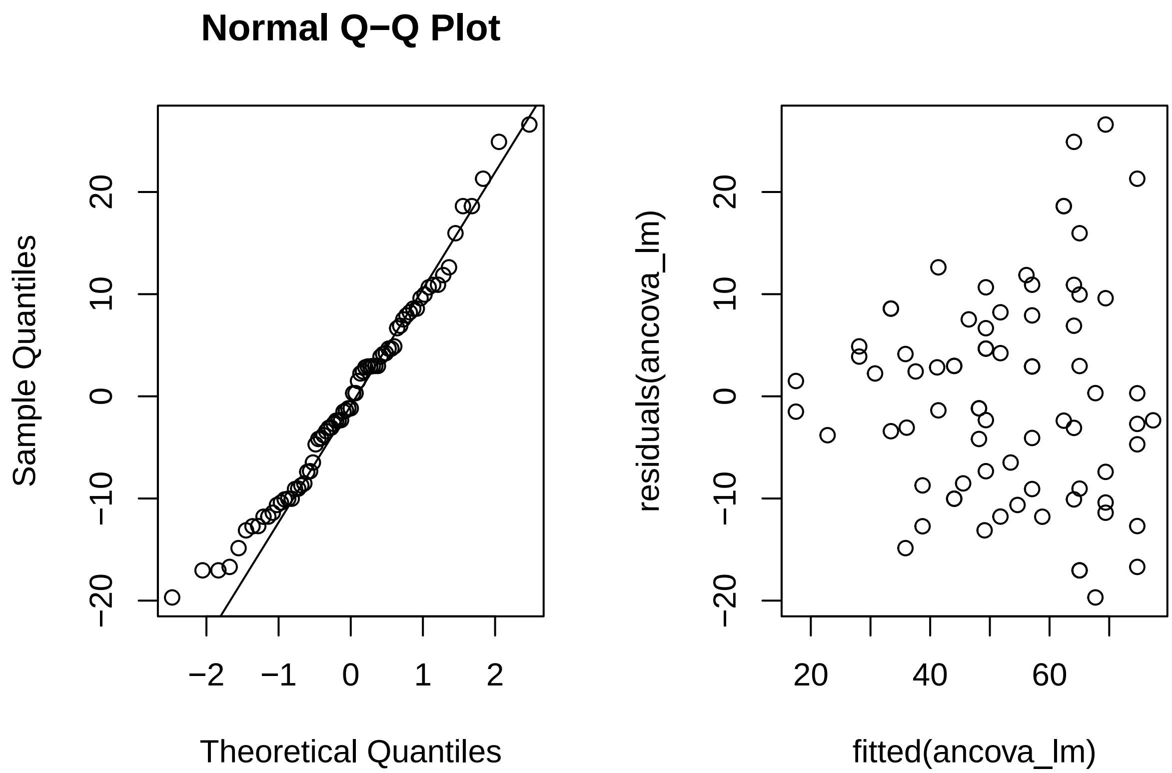
Both analyses came to the conclusion that sexual activity influences longevity, more sex - shorter life.

e) Perform the ancova analysis with the number of days as the response, rather than its logarithm. Was it wise to use the logarithm as response?

```
ancova_lm = lm(longevity ~ activity + thorax, data=flies_df) ## order matters but we use drop
drop1(ancova_lm, test="F")
```

```
## Single term deletions
##
## Model:
## longevity ~ activity + thorax
##          Df Sum of Sq   RSS    AIC F value    Pr(>F)
## <none>                 7673 355.10
## activity  2    4966.7 12640 388.53  22.979 2.016e-08 ***
## thorax    1    7686.8 15360 405.15  71.127 2.624e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
par(mfrow=c(1, 2))
qqnorm(residuals(ancova_lm)); qqline(residuals(ancova_lm))
plot(fitted(ancova_lm), residuals(ancova_lm))
```




```
shapiro.test(residuals(ancova_lm))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(ancova_lm)
## W = 0.98091, p-value = 0.3176
```

Residuals are normal.

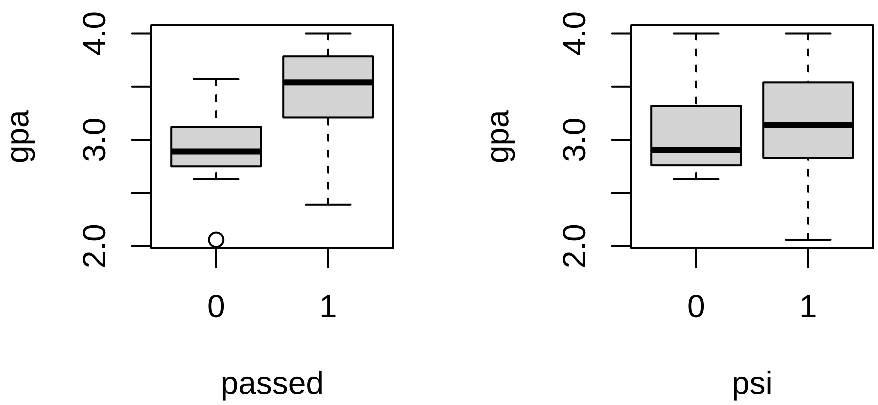
It's wise. For both columns the residuals are normal. If they were not, ANCOVA would not be relevant. For non-log model the residuals look non-homogenious.

##Exercise 4. Personalized system of instruction The data was collected to study the effect of a new teaching method called "personalized system of instruction" (psi), 32 students were randomized to either receive psi or to be taught using the existing method. At the end of the teaching period the success of the teaching method was assessed by giving the students a difficult assignment, which they could pass or not. The average grade of the students were also available for analysis: gpa on a scale of 0–4, with 4 being the best grade.

```
psi_df <- read.table("data/psi.txt", header=TRUE)
head(psi_df)
```

```
##   passed psi  gpa
## 1      0   0 2.66
## 2      0   0 2.89
## 3      0   0 3.28
## 4      0   0 2.92
## 5      1   0 4.00
## 6      0   0 2.86
```

```
par(mfrow=c(1, 2))
boxplot(gpa ~ passed, data=psi_df)
boxplot(gpa ~ psi, data=psi_df)
```




```
xtabs(~psi+passed, data=psi_df)
```

```
##    passed
## psi  0  1
##   0 15  3
##   1  6  8
```

```
is.numeric(psi_df$passed)
```

```
## [1] TRUE
```

```
is.numeric(psi_df$gpa)
```

```
## [1] TRUE
```

a) Fit a logistic regression model with both explanatory variables, perform relevant tests. Does psi work?

```
psi_glm = glm(passed ~ psi + gpa, data=psi_df, family=binomial)
summary(psi_glm)
```

```
##
## Call:
## glm(formula = passed ~ psi + gpa, family = binomial, data = psi_df)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8396  -0.6282  -0.3045   0.5629   2.0378
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -11.602      4.213  -2.754  0.00589 **
## psi            2.338      1.041   2.246  0.02470 *
## gpa            3.063      1.223   2.505  0.01224 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 41.183  on 31  degrees of freedom
## Residual deviance: 26.253  on 29  degrees of freedom
## AIC: 32.253
##
## Number of Fisher Scoring iterations: 5
```

The R-function glm (generalized linear model) is used instead of lm to create the glm object. The option family=binomial overrules the default normal model (which gives lm). The 2 explanatory variables are inserted here as numerical.

```
drop1(psi_glm, test="Chisq")
```

```
## Single term deletions
##
## Model:
## passed ~ psi + gpa
##        Df Deviance    AIC    LRT Pr(>Chi)
## <none>      26.253 32.253
## psi     1   32.418 36.418 6.1647 0.013033 *
## gpa     1   35.342 39.342 9.0885 0.002572 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
psi_df$psi = as.factor(psi_df$psi)
psi_glm2 = glm(passed ~ psi + gpa, data=psi_df, family=binomial)
```

```r
drop1(psi_glm2, test="Chisq")
```

```
## Single term deletions
##
## Model:
## passed ~ psi + gpa
##        Df Deviance    AIC    LRT Pr(>Chi)
## <none>      26.253 32.253
## psi     1   32.418 36.418 6.1647 0.013033 *
## gpa     1   35.342 39.342 9.0885 0.002572 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(psi_glm2)$coefficients
```

```
##                Estimate Std. Error   z value    Pr(>|z|)
## (Intercept) -11.601565   4.212977 -2.753769 0.005891336
## psi1          2.337776   1.040798  2.246138 0.024695156
## gpa           3.063367   1.222868  2.505067 0.012242815
```

psi really works

b) Estimate the probability that a student with a gpa equal to 3 who receives psi passes the assignment. Estimate the same probability for a student who does not receive psi. Comment.

```r
# Response gives you the numerical result while class gives you the label assigned to that val
# exp(-11 + 2.33*1 + 3.06*3)
predict(psi_glm2, data.frame(psi="1", gpa=3), type="response")
```

```
##         1
## 0.4815864
```

```r
predict(psi_glm2, data.frame(psi="0", gpa=3), type="response")
```

```
##          1
## 0.08230274
```

c) Estimate the relative change in odds of passing the assignment rendered by instructing students with psi rather than the standard method (for an arbitrary student). What is the interpretation of this number? Is it dependent on gpa?

With psi: 2.337776.

```r
exp(-11.601565+2.337776)
```

```
## [1] 9.479546e-05
```

```r
psi_glm3 = glm(passed ~ psi * gpa, data=psi_df, family=binomial)
drop1(psi_glm3, test="Chisq")
```

```
## Single term deletions
##
## Model:
## passed ~ psi * gpa
##         Df Deviance    AIC    LRT Pr(>Chi)
## <none>       24.381 32.381
## psi:gpa  1   26.253 32.253 1.8725   0.1712
```

There is no interaction between psi and gpa.

d) Propose and perform an alternative method of analysis based on contingency tables. Compare its results to the results of the first approach.

```
matrix = table(psi_df[, c('psi', 'passed')])

# assumption is not met -> bootstrap
z=chisq.test(matrix, simulate.p.value=TRUE)
z
```

```
##
##  Pearson's Chi-squared test with simulated p-value (based on 2000
##  replicates)
##
## data:  matrix
## X-squared = 5.7192, df = NA, p-value = 0.02349
```

There are no contraindications for the chi-square test. The test concludes that there is a dependence between row and column variables. Fisher is also applicable as the table is 2x2.

```
fisher.test(matrix)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  matrix
## p-value = 0.0265
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##   1.047057 49.595860
## sample estimates:
## odds ratio
##   6.227408
```

Same conclusion. psi and passed are dependent.

e) Given the way the experiment was conducted, is this second approach wrong? Name both an advantage and a disadvantage of the two approaches, relative to each other.

Assumption for chi-square is not met. In first we can include numeric variable.

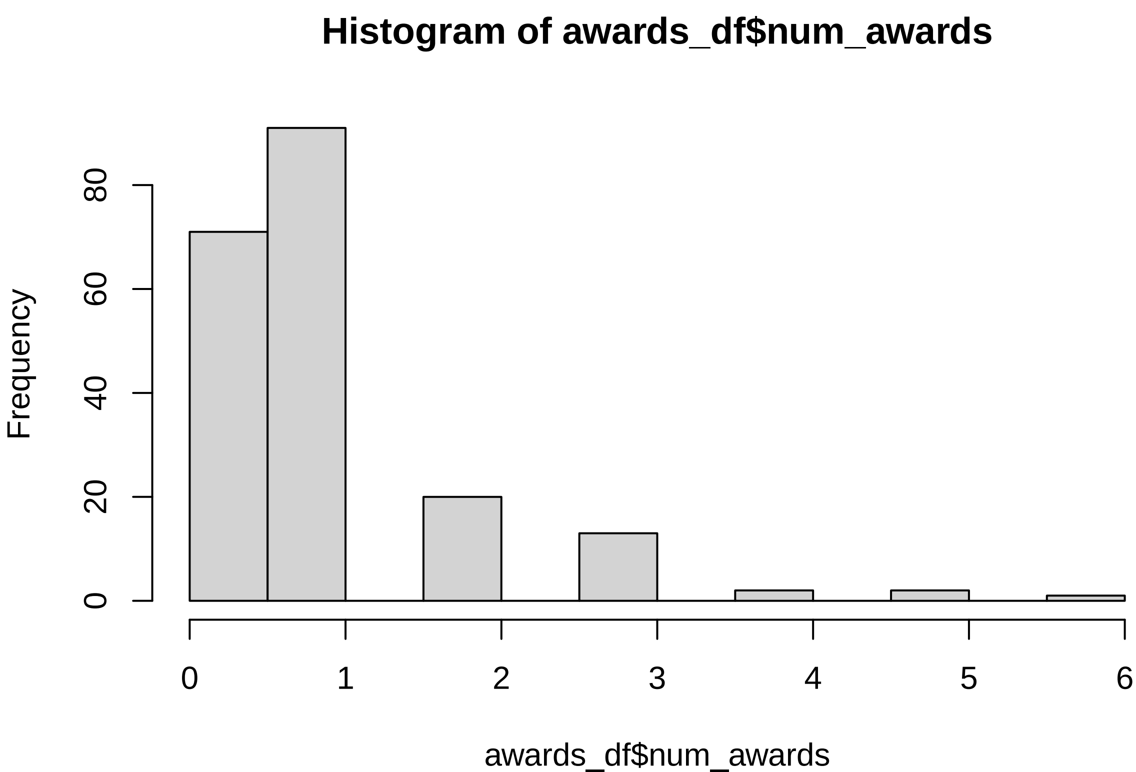
Exercise 5. School awards.

The file contains data on the numbers of awards earned by students at one high school. Predictors of the number of awards earned include the type of program (column prog) in which the student was enrolled (1=vocational, 2=general, 3=academic) and the score on their final exam in math (column math).

```
awards_df <- read.table("data/awards.txt", header=TRUE)
awards_df$prog = as.factor(awards_df$prog)
head(awards_df)
```

```
##   num_awards prog math
## 1          1    3   41
## 2          1    1   41
## 3          1    3   44
## 4          1    3   42
## 5          1    3   40
## 6          1    1   42
```

```
hist(awards_df$num_awards)
```




```
# awards_df$num_awards = as.factor(awards_df$num_awards)
```

a) Investigate whether the type of program influences the number of awards by performing a Poisson regression, without taking variable math into account. Estimate the numbers of awards for all the three types of program. Which program type is the best for the number of awards for this model?

```
awards_glm = glm(num_awards ~ prog, family=poisson, data=awards_df)
summary(awards_glm)
```

```
##
## Call:
## glm(formula = num_awards ~ prog, family = poisson, data = awards_df)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5306  -1.0750  -0.1625   0.5027   3.1536
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.5486     0.1961  -2.797  0.00515 **
## prog2         0.7068     0.2158   3.275  0.00106 **
## prog3         0.4432     0.2463   1.799  0.07199 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 228.83  on 199  degrees of freedom
## Residual deviance: 216.10  on 197  degrees of freedom
## AIC: 512.42
##
## Number of Fisher Scoring iterations: 5
```

The first two programs (vocational, general) influence the amount of awards while the academic one doesn't.

```
predict(awards_glm, data.frame(prog="1"), type="response")
```

```
##         1
## 0.5777778
```

```
predict(awards_glm, data.frame(prog="2"), type="response")
```

```
##        1
## 1.171429
```

```
predict(awards_glm, data.frame(prog="3"), type="response")
```

```
##   1
## 0.9
```

The general (2) one is the best in terms of awards.

b) For the situation in a), can the Kruskall-Wallis test also be used? If yes, apply the test and comment on the results; if no, explain why this test cannot be used.

Assumption about ni>5?

```
table(awards_df$prog)
```

```
##
##   1   2   3
##  45 105  50
```

```
table(awards_df$num_awards)
```

```
##
##  0  1  2  3  4  5  6
## 71 91 20 13  2  2  1
```

```
attach(awards_df)
kruskal.test(num_awards, prog)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  num_awards and prog
## Kruskal-Wallis chi-squared = 10.755, df = 2, p-value = 0.00462
```

c) Now include predictor math into analysis and investigate the influence of the explanatory variables prog and math (and their interaction) on the numbers of awards. Which program type is the best for the number of awards? Comments on your findings. Estimate the numbers of awards for the vocational program and math score 55.

```
awards_glm2=glm(num_awards~prog*math, family=poisson, data=awards_df)
summary(awards_glm2)
```

```
##
## Call:
## glm(formula = num_awards ~ prog * math, family = poisson, data = awards_df)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.11193  -1.11317   0.03167   0.37709   2.44301
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.578440   1.391426  -1.134    0.257
## prog2       -1.061226   1.534523  -0.692    0.489
## prog3        0.962144   1.635965   0.588    0.556
## math         0.020365   0.026950   0.756    0.450
## prog2:math   0.027437   0.028969   0.947    0.344
## prog3:math  -0.009441   0.032396  -0.291    0.771
##
```

```
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 228.83  on 199  degrees of freedom
## Residual deviance: 194.36  on 194  degrees of freedom
## AIC: 496.67
##
## Number of Fisher Scoring iterations: 5
```

```
drop1(awards_glm2, test='Chisq')
```

```
## Single term deletions
##
## Model:
## num_awards ~ prog * math
##           Df Deviance    AIC    LRT Pr(>Chi)
## <none>         194.35 496.67
## prog:math  2   198.05 496.36 3.6911   0.1579
```

```
mod2=glm(num_awards~math,family=poisson,data=awards_df); anova(mod2,awards_glm2, test="Chisq")
```

```
## Analysis of Deviance Table
##
## Model 1: num_awards ~ math
## Model 2: num_awards ~ prog * math
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       198     204.23
## 2       194     194.35  4   9.8748  0.04259 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interactions are insignificant.

```
awards_glm3 = glm(num_awards~prog+math, family=poisson, data=awards_df)
summary(awards_glm3)
```

```
##
## Call:
## glm(formula = num_awards ~ prog + math, family = poisson, data = awards_df)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.96335  -1.14818  -0.01392   0.35710   2.52541
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.372577   0.475525  -4.989 6.06e-07 ***
## prog2        0.452621   0.224746   2.014   0.0440 *
## prog3        0.561720   0.247482   2.270   0.0232 *
## math         0.035779   0.008344   4.288 1.80e-05 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 228.83  on 199  degrees of freedom
## Residual deviance: 198.05  on 196  degrees of freedom
## AIC: 496.36
##
## Number of Fisher Scoring iterations: 5
```

All programs now have a significant influence on the amount of awards. Math score is also significant.

```
predict(awards_glm3, data.frame(prog="1", math=mean(awards_df$math)), type="response")
```

```
##         1
## 0.6132557
```

```
predict(awards_glm3, data.frame(prog="2", math=mean(awards_df$math)), type="response")
```

```
##         1
## 0.9643005
```

```
predict(awards_glm3, data.frame(prog="3", math=mean(awards_df$math)), type="response")
```

```
##        1
## 1.075458
```

The academic group is now better for awards.

```
predict(awards_glm3, data.frame(prog="1", math=55), type="response")
```

```
##         1
## 0.6671683
```