Series 3 - solutions

The fruitflies dataset

This dataset contains observations on five groups of male fruitflies – 25 fruitflies in each group – from an experiment designed to test if increased reproduction reduces longevity for male fruitflies. The five groups are: males forced to live alone, males assigned to live with one or eight interested females, and males assigned to live with one or eight non-receptive females.

```
#detach(data)
```

```
url <- "https://ww2.amstat.org/publications/jse/datasets/fruitfly.dat.txt"
data <- read.table(url)
data <- data[,c(-1,-6)] # remove id and sleep
names(data) <- c("partners","type","longevity","thorax")
attach(data)
```

```
head(data)
```

```
##   partners type longevity thorax
## 1        8    0        35   0.64
## 2        8    0        37   0.68
## 3        8    0        49   0.68
## 4        8    0        46   0.72
## 5        8    0        63   0.72
## 6        8    0        39   0.76
```

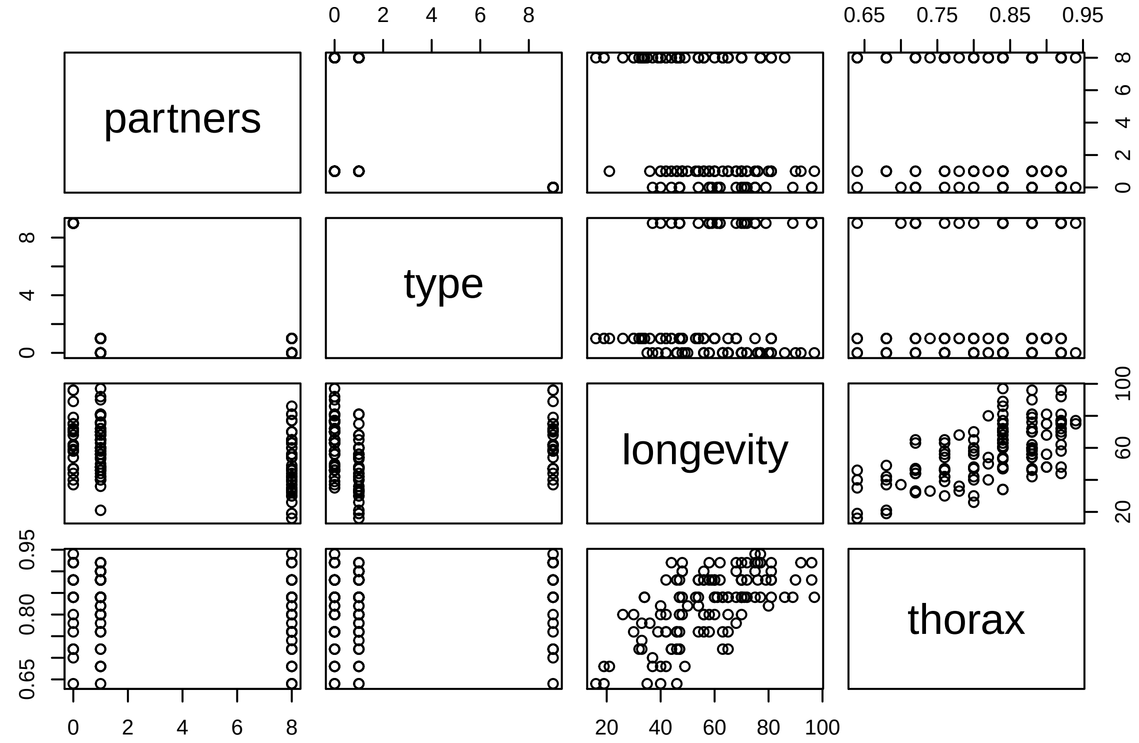
```
summary(data)
```

```
##     partners         type       longevity         thorax
##  Min.   :0.0   Min.   :0.0   Min.   :16.00   Min.   :0.640
##  1st Qu.:1.0   1st Qu.:0.0   1st Qu.:46.00   1st Qu.:0.760
##  Median :1.0   Median :1.0   Median :58.00   Median :0.840
##  Mean   :3.6   Mean   :2.2   Mean   :57.44   Mean   :0.821
##  3rd Qu.:8.0   3rd Qu.:1.0   3rd Qu.:70.00   3rd Qu.:0.880
##  Max.   :8.0   Max.   :9.0   Max.   :97.00   Max.   :0.940
```

```
dim(data)
```

```
## [1] 125   4
```

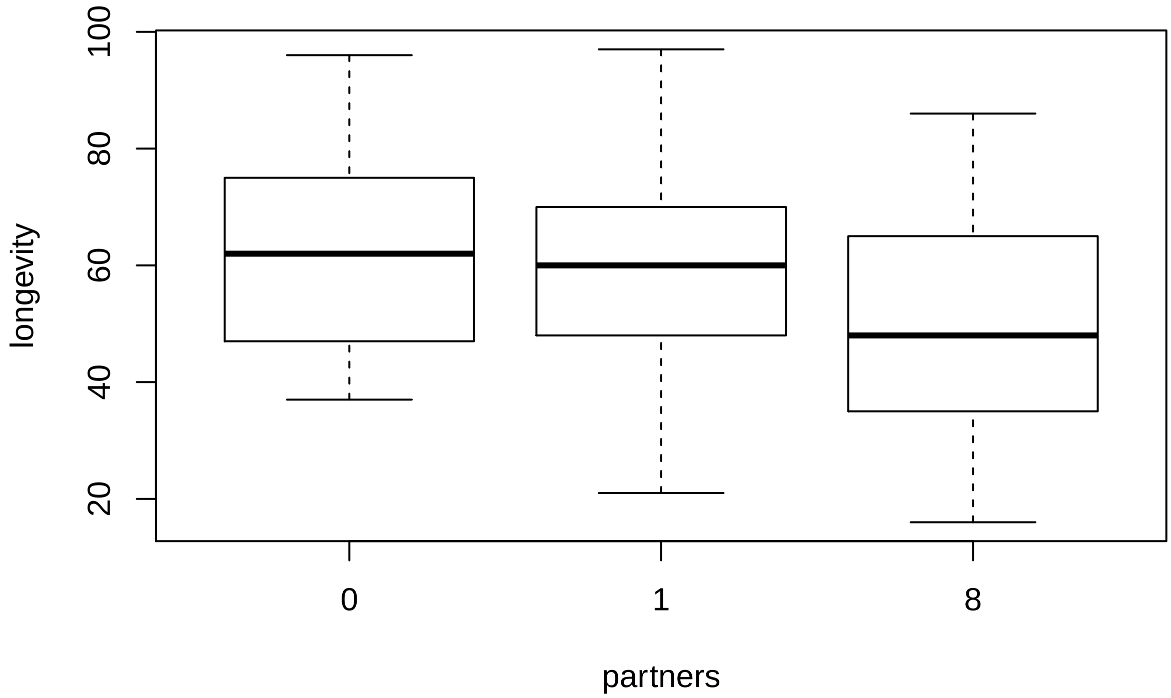
```
# let's get a visual understanding of this data
pairs(data)
```



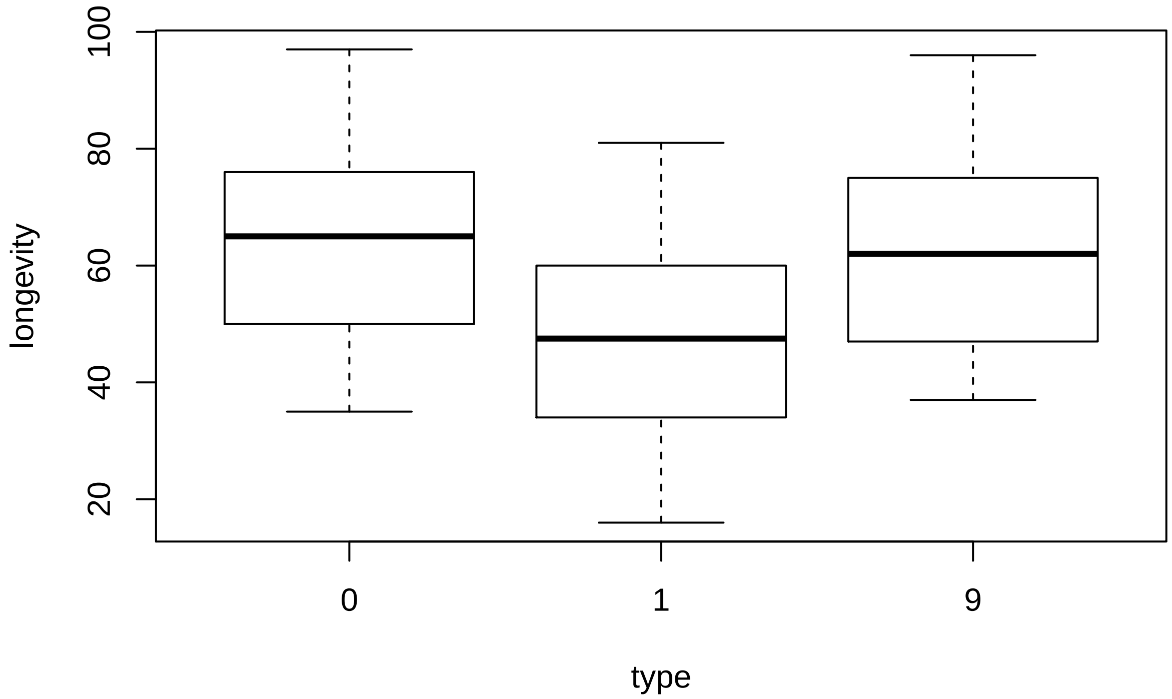
```r
cor(data)
```

```
##             partners        type  longevity      thorax
## partners   1.0000000 -0.49420708 -0.3030521 -0.19332920
## type      -0.4942071  1.00000000  0.1189528  0.09906777
## longevity -0.3030521  0.11895277  1.0000000  0.63648353
## thorax    -0.1933292  0.09906777  0.6364835  1.00000000
```

```r
boxplot(longevity~partners)
```



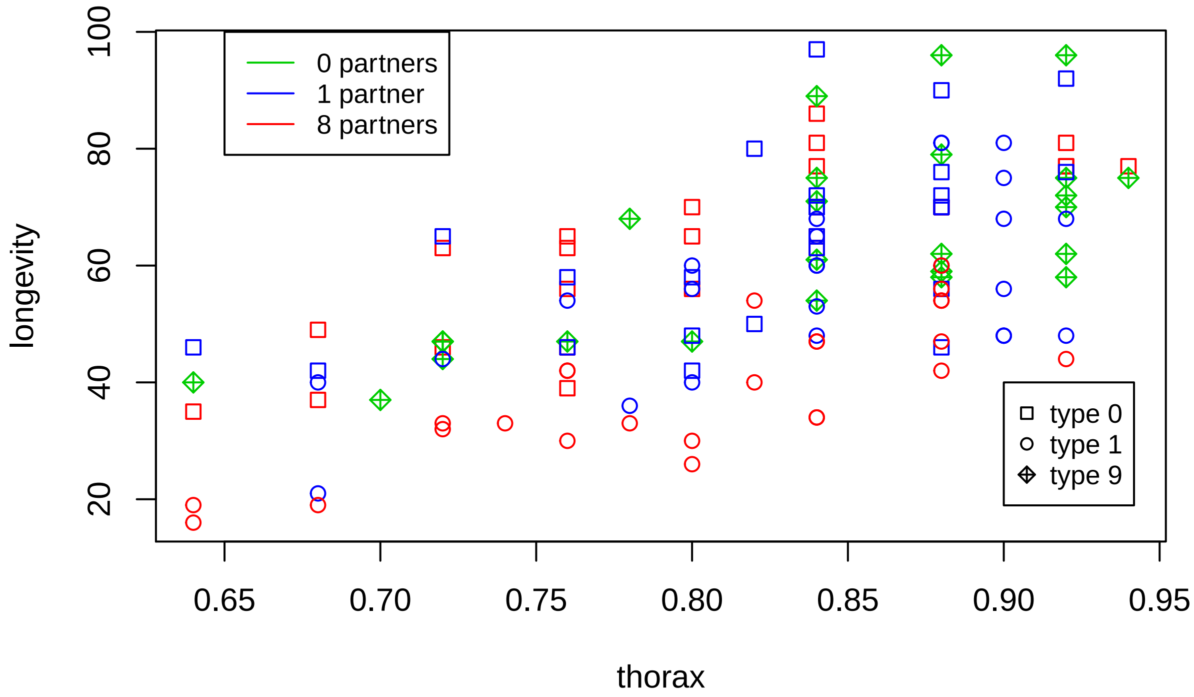
```
boxplot(longevity~type)
```



```
# preparing colors for the scatter plot
cols <- partners
cols[cols==0] <- 3
cols[cols==8] <- 2
cols[cols==1] <- 4
cols
```

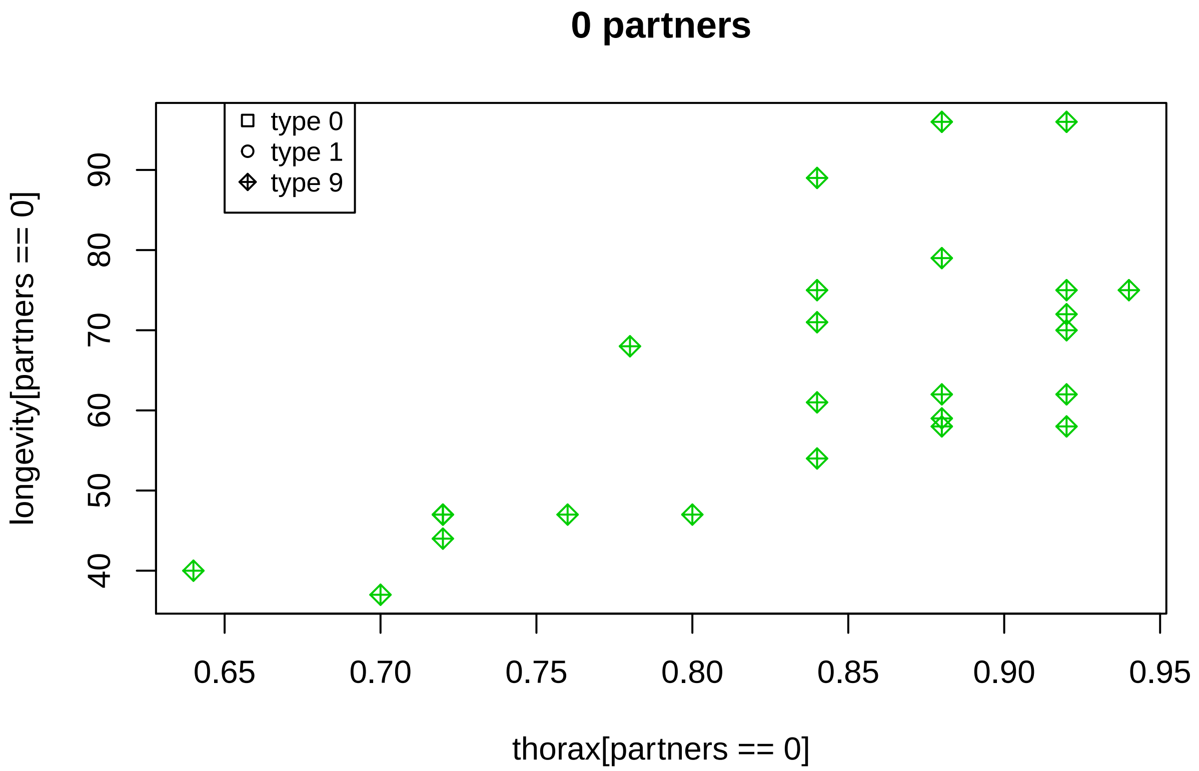
```
##   [1] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3
##  [38] 3 3 3 3 3 3 3 3 3 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
##  [75] 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 2 2 2 2 2 2 2 2 2 2 2
## [112] 2 2 2 2 2 2 2 2 2 2 2 2 2 2
```

```
plot(thorax, longevity, col=cols, pch=type)
legend(0.65, 100,
       legend=c("0 partners", "1 partner", "8 partners"),
       col=c("3","4","2"),
       cex=.8,
       lty=1)
legend(0.9, 40,
       legend=c("type 0", "type 1", "type 9"),
       col=1,
       cex=.8,
       pch=c(0,1,9))
```

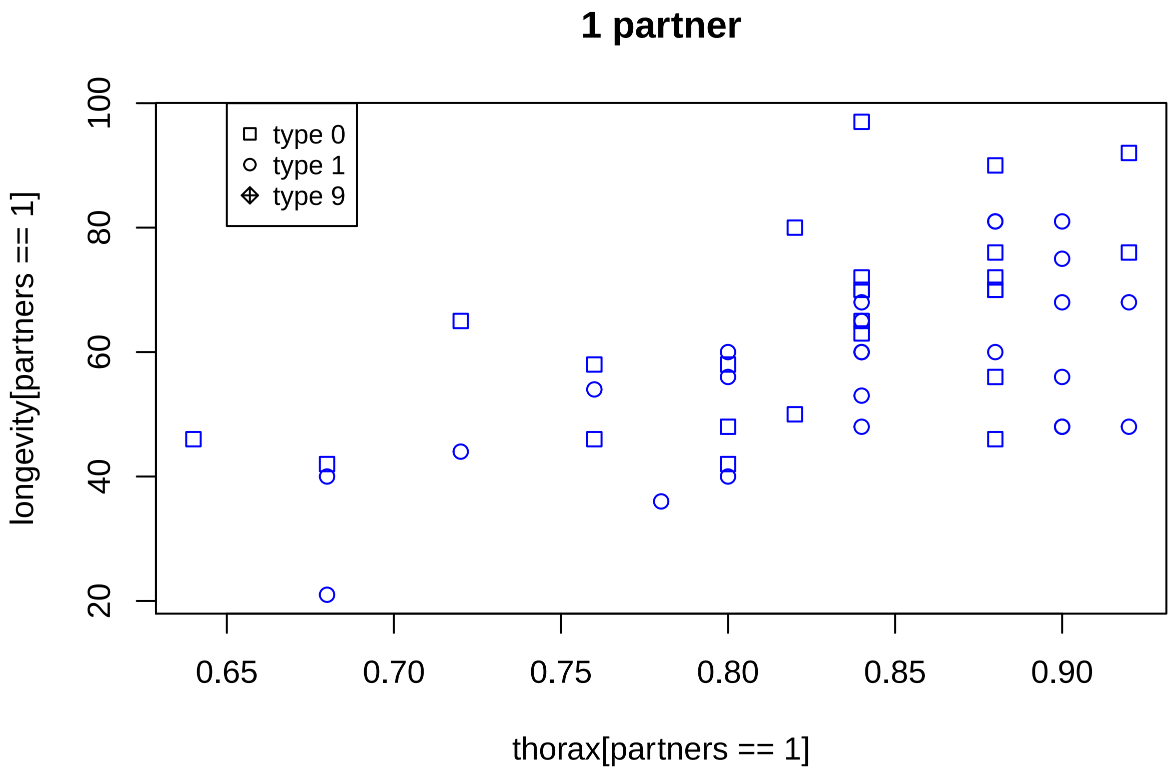


Let’s separate the points based on the number of partners available.

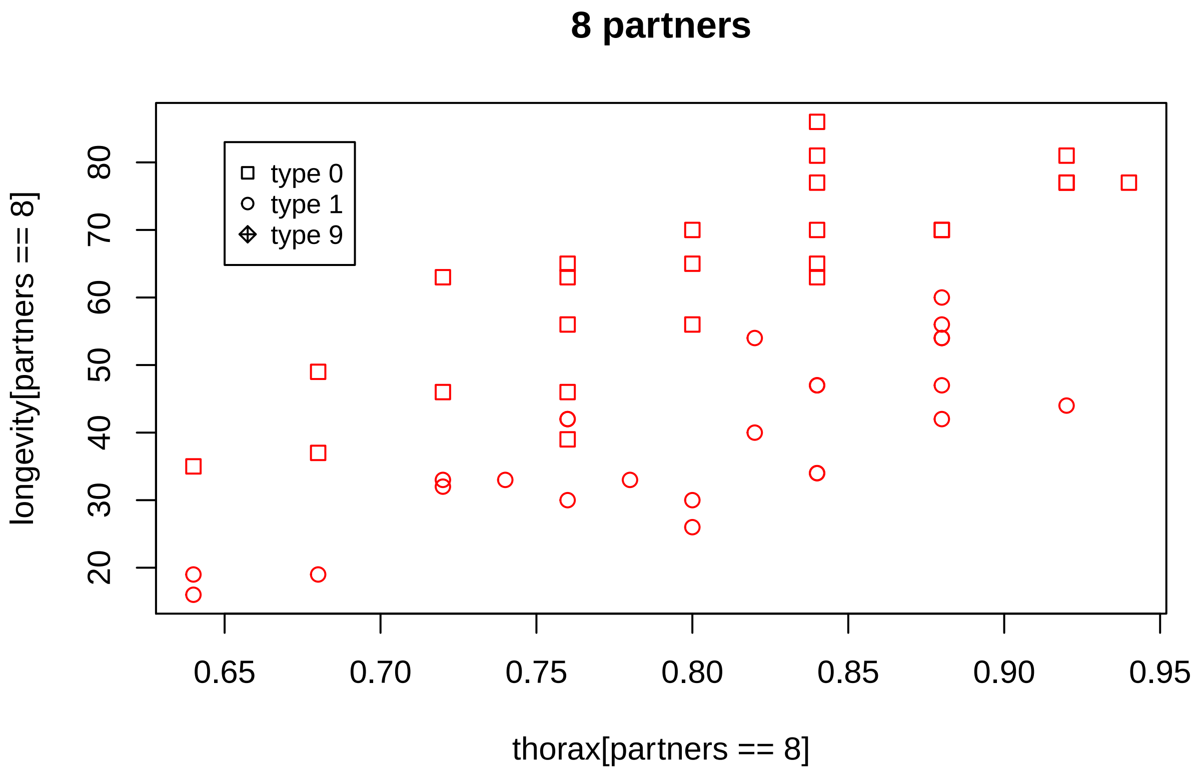
```
plot(thorax[partners==0], longevity[partners==0], col=3, pch=type[partners==0], main = "0 partners")
legend(0.65, 100,
       legend=c("type 0", "type 1", "type 9"),
       col=1,
       cex=.8,
       pch=c(0,1,9))
```



```
plot(thorax[partners==1], longevity[partners==1], col=4, pch=type[partners==1], main = "1 partner")
legend(0.65, 100,
       legend=c("type 0", "type 1", "type 9"),
       col=1,
       cex=.8,
       pch=c(0,1,9))
```



```
plot(thorax[partners==8], longevity[partners==8], col=2, pch=type[partners==8], main = "8 partners")
legend(0.65, 83,
       legend=c("type 0", "type 1", "type 9"),
       col=1,
       cex=.8,
       pch=c(0,1,9))
```

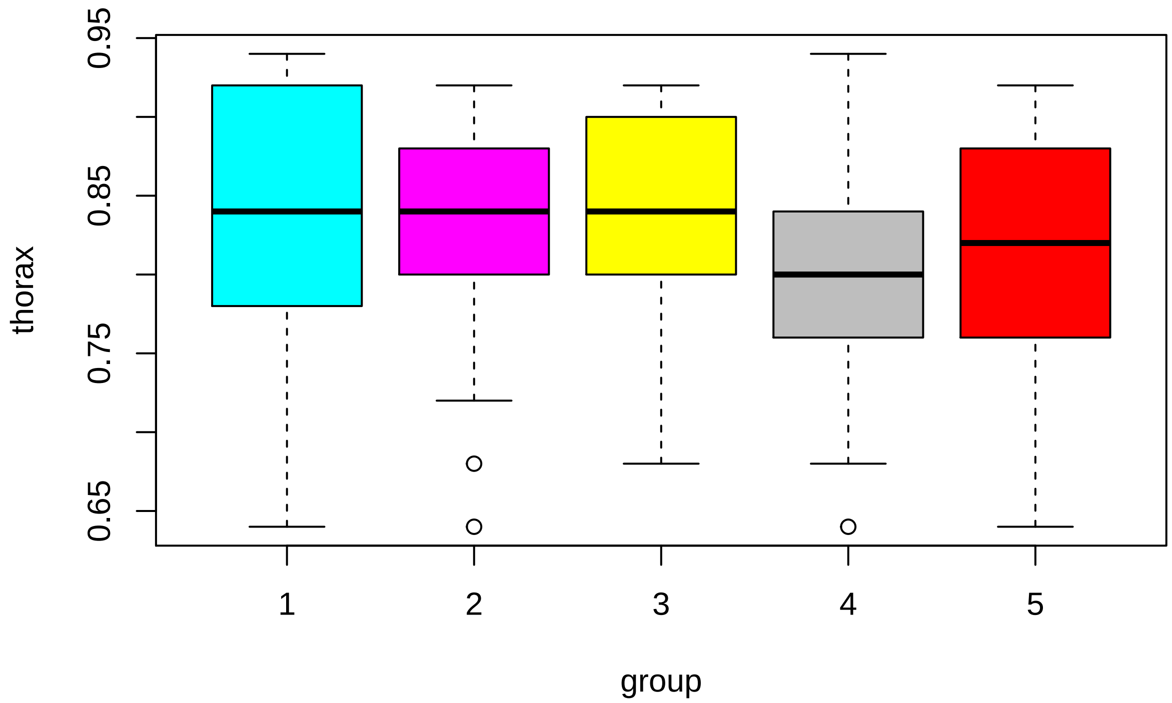


Looking at the second and third plot it emerges an interaction between the number of partners and the type of female (interested , . . .) on longevity. We now want to encode these 5 different study groups with dummy variables.

```
group1 <- (partners==0) * 1
group2 <- (partners==1 & type==0) *2
group3 <- (partners==1 & type==1) *3
group4 <- (partners==8 & type==0) *4
group5 <- (partners==8 & type==1) *5
group <- group1 + group2 + group3 + group4 + group5
```

Let’s look at the thorax length among these 5 different groups.

```
boxplot(thorax~group, col=c(5,6,7,8,2))
```



Is there a statistically significant different in the thorax length among the groups? Let's use an ANOVA to test it.

```
fit1 <- lm(thorax~1)
fit2 <- lm(thorax~group)
anova(fit1, fit2)
```

```
## Analysis of Variance Table
##
## Model 1: thorax ~ 1
## Model 2: thorax ~ group
##   Res.Df     RSS Df Sum of Sq      F  Pr(>F)
## 1    124 0.74388
## 2    123 0.72272  1   0.02116 3.6012 0.06008 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

By looking at the above table we can conclude that there's no statistically significant difference in terms of thorax length between the 5 groups. This was to be expected since the assignments to the groups were random, hence the distribution of thorax should be similar among the different groups.

But can we omit thorax from the model then? Probably not, because thorax length could be an fundamental indicator of the health of the animal, which is in the end positively correlated with longevity. But let's test it!

```
model1 <- lm(longevity~factor(group))
model2 <- lm(longevity~factor(group)+thorax)
anova(model1,model2)
```

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

```
##
## Model 1: longevity ~ factor(group)
## Model 2: longevity ~ factor(group) + thorax
##   Res.Df   RSS Df Sum of Sq      F    Pr(>F)
## 1    120 26314
## 2    119 13145  1     13169 119.22 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Let's test now the effect of the presence of thorax over a specific test group.

```
model1 <- lm(longevity[partners==1]~factor(group[partners==1]))
model2 <- lm(longevity[partners==1]~factor(group[partners==1])+thorax[partners==1])
anova(model1,model2)
```

```
## Analysis of Variance Table
##
## Model 1: longevity[partners == 1] ~ factor(group[partners == 1])
## Model 2: longevity[partners == 1] ~ factor(group[partners == 1]) + thorax[partners ==
##     1]
##   Res.Df     RSS Df Sum of Sq      F    Pr(>F)
## 1     48 11228.6
## 2     47  6962.9  1    4265.7 28.793 2.417e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Again, the presence of the variable thorax drastically reduces the RSS. Let's look at the difference in terms of coefficients.

```
summary(model1)
```

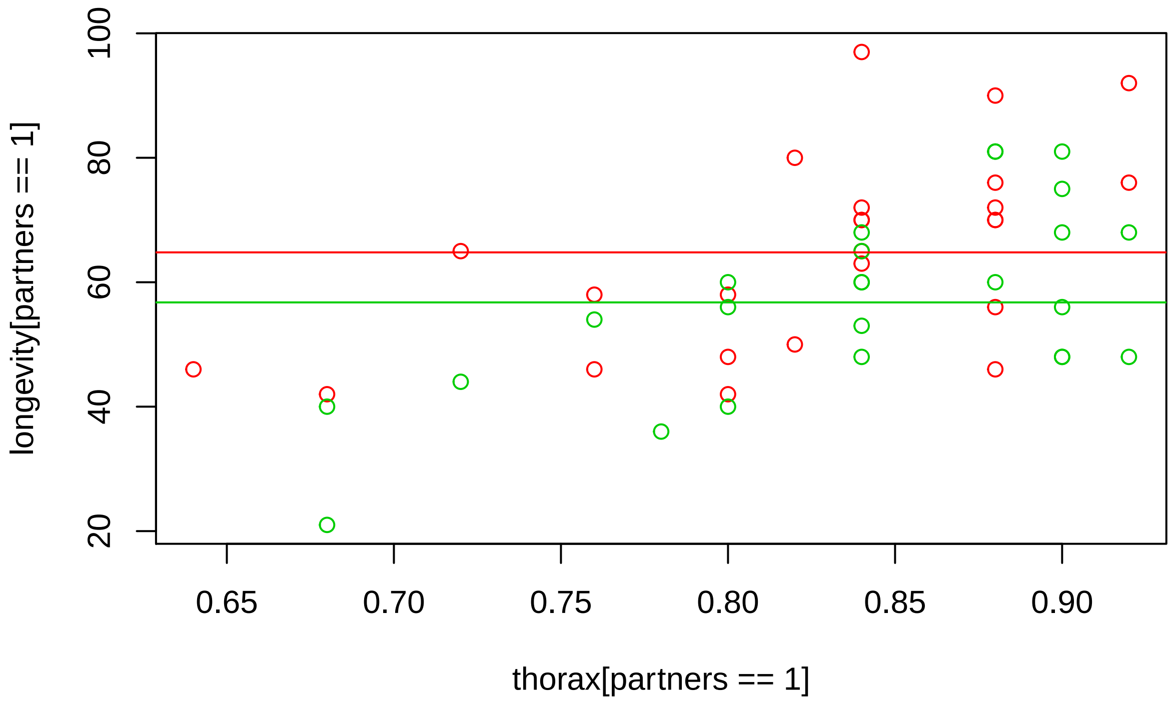
```
##
## Call:
## lm(formula = longevity[partners == 1] ~ factor(group[partners ==
##     1]))
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -35.76  -8.79   0.20  10.46  32.20
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     64.800      3.059  21.184   <2e-16 ***
## factor(group[partners == 1])3   -8.040      4.326  -1.859   0.0692 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.29 on 48 degrees of freedom
## Multiple R-squared:  0.06713,    Adjusted R-squared:  0.0477
## F-statistic: 3.454 on 1 and 48 DF,  p-value: 0.06923
```

```
summary(model2)
```

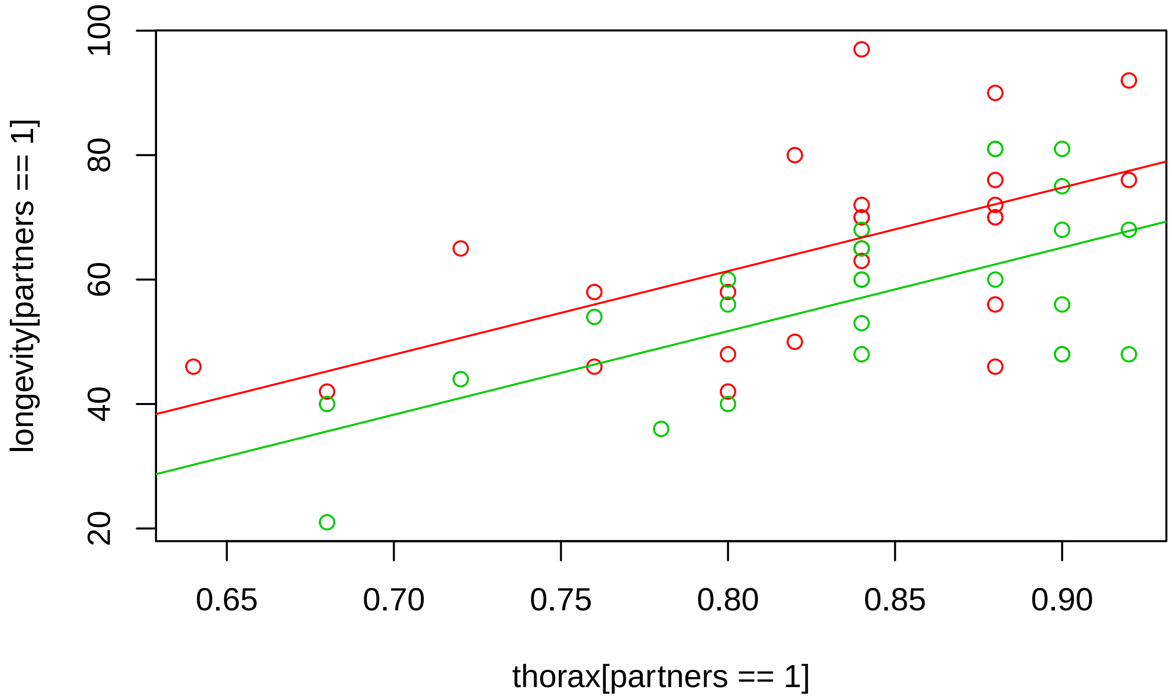
```
##
## Call:
## lm(formula = longevity[partners == 1] ~ factor(group[partners ==
##     1]) + thorax[partners == 1])
```

```
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -26.103  -9.123   1.092   7.273  30.267
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                    -46.038     20.799  -2.214  0.03175 *
## factor(group[partners == 1])3   -9.651      3.456  -2.793  0.00753 **
## thorax[partners == 1]          134.252     25.019   5.366 2.42e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12.17 on 47 degrees of freedom
## Multiple R-squared:  0.4215, Adjusted R-squared:  0.3969
## F-statistic: 17.12 on 2 and 47 DF,  p-value: 2.593e-06
```

```r
plot(thorax[partners==1], longevity[partners==1], col=group[partners==1])
abline(a=model1$coefficients[1],b=0,col=2)
abline(a=model1$coefficients[1]+model1$coefficients[2],b=0,col=3)
```



```r
plot(thorax[partners==1], longevity[partners==1], col=group[partners==1])
abline(a=model2$coefficients[1],b=model2$coefficients[3],col=2)
abline(a=model2$coefficients[1]+model2$coefficients[2],b=model2$coefficients[3],col=3)
```



Now ee want to test for interaction between type of female and number of females.

```
wrong.model <- lm(longevity~thorax+as.factor(type)*as.factor(partners))
summary(wrong.model)
```

```
##
## Call:
## lm(formula = longevity ~ thorax + as.factor(type) * as.factor(partners))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -26.189  -6.599  -0.989   6.408  30.244
##
## Coefficients: (4 not defined because of singularities)
##                                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)                           -46.055     10.239  -4.498 1.61e-05 ***
## thorax                                135.819     12.439  10.919  < 2e-16 ***
## as.factor(type)1                      -23.879      2.973  -8.031 7.83e-13 ***
## as.factor(type)9                       -3.929      2.997  -1.311 0.192347
## as.factor(partners)1                   -1.276      2.983  -0.428 0.669517
## as.factor(partners)8                       NA         NA      NA       NA
## as.factor(type)1:as.factor(partners)1  14.210      4.210   3.375 0.000996 ***
## as.factor(type)9:as.factor(partners)1      NA         NA      NA       NA
## as.factor(type)1:as.factor(partners)8      NA         NA      NA       NA
## as.factor(type)9:as.factor(partners)8      NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 10.51 on 119 degrees of freedom
## Multiple R-squared:  0.6564, Adjusted R-squared:  0.6419
## F-statistic: 45.46 on 5 and 119 DF,  p-value: < 2.2e-16
```

Note: the above model doesn't make sense since we should only account for 5 of the possible combination of dummy variables. Now let's create a better one.

```
better.model <- lm(longevity~thorax+as.factor(group2)+as.factor(group3)+as.factor(group4)+as.factor(grou
summary(better.model)
```

```
##
## Call:
## lm(formula = longevity ~ thorax + as.factor(group2) + as.factor(group3) +
##     as.factor(group4) + as.factor(group5))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -26.189  -6.599  -0.989   6.408  30.244
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         -49.984     10.609  -4.711 6.73e-06 ***
## thorax              135.819     12.439  10.919  < 2e-16 ***
## as.factor(group2)2    2.653      2.975   0.891   0.3745
## as.factor(group3)3   -7.017      2.973  -2.361   0.0199 *
## as.factor(group4)4    3.929      2.997   1.311   0.1923
## as.factor(group5)5  -19.951      3.006  -6.636 1.00e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.51 on 119 degrees of freedom
## Multiple R-squared:  0.6564, Adjusted R-squared:  0.6419
## F-statistic: 45.46 on 5 and 119 DF,  p-value: < 2.2e-16
```

Is the interaction between type and partners statistically significant? Let's test it with an ANOVA.

```
group1 <- (partners==0) * 1
group2 <- (partners==1 & type==0) *1
group3 <- (partners==1 & type==1) *1
group4 <- (partners==8 & type==0) *1
group5 <- (partners==8 & type==1) *1
reduced.model <- lm(longevity~thorax+(I(group2+group3))+(I(group2+group4))+(I(group5-group2)))
summary(reduced.model)
```

```
##
## Call:
## lm(formula = longevity ~ thorax + (I(group2 + group3)) + (I(group2 +
##     group4)) + (I(group5 - group2)))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -29.8501  -6.7025  -0.5518   6.6970  26.6700
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        -51.8097    11.0449  -4.691 7.27e-06 ***
## thorax             138.0021    12.9490  10.657  < 2e-16 ***
## I(group2 + group3) -10.5636     2.8988  -3.644 0.000398 ***
## I(group2 + group4)   0.4525     2.9334   0.154 0.877674
## I(group5 - group2) -16.3291     2.9273  -5.578 1.53e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.96 on 120 degrees of freedom
## Multiple R-squared:  0.6235, Adjusted R-squared:  0.6109
## F-statistic: 49.68 on 4 and 120 DF,  p-value: < 2.2e-16
```

```
anova(reduced.model, better.model)
```

```
## Analysis of Variance Table
##
## Model 1: longevity ~ thorax + (I(group2 + group3)) + (I(group2 + group4)) +
##     (I(group5 - group2))
## Model 2: longevity ~ thorax + as.factor(group2) + as.factor(group3) +
##     as.factor(group4) + as.factor(group5)
##   Res.Df   RSS Df Sum of Sq      F    Pr(>F)
## 1    120 14403
## 2    119 13145  1    1258.5 11.394 0.0009957 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From the anova we can conclude there's statistically significant interaction between the variables.

```
group <- as.factor(group)
full.model <- lm(longevity~thorax+group+thorax*group)
summary(full.model)
```

```
##
## Call:
## lm(formula = longevity ~ thorax + group + thorax * group)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -25.9509  -6.5324  -0.7693   6.3792  30.3071
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -50.2420    21.7221  -2.313   0.0225 *
## thorax        136.1268    25.8576   5.264 6.61e-07 ***
## group2          6.5172    33.7479   0.193   0.8472
## group3         -7.7501    33.8457  -0.229   0.8193
## group4         -5.4574    30.6537  -0.178   0.8590
## group5        -11.0380    31.1731  -0.354   0.7239
## thorax:group2  -4.6771    40.5042  -0.115   0.9083
## thorax:group3   0.8743    40.2786   0.022   0.9827
## thorax:group4  11.6629    37.1806   0.314   0.7543
## thorax:group5 -11.1268    37.9816  -0.293   0.7701
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.67 on 115 degrees of freedom
## Multiple R-squared:  0.6575, Adjusted R-squared:  0.6307
## F-statistic: 24.53 on 9 and 115 DF,  p-value: < 2.2e-16
```

```r
anova(better.model, full.model)
```

```
## Analysis of Variance Table
##
## Model 1: longevity ~ thorax + as.factor(group2) + as.factor(group3) +
##     as.factor(group4) + as.factor(group5)
## Model 2: longevity ~ thorax + group + thorax * group
##   Res.Df   RSS Df Sum of Sq      F Pr(>F)
## 1    119 13145
## 2    115 13102  4    42.523 0.0933 0.9844
```

The life expectancy dataset

```r
url <- "https://raw.githubusercontent.com/jawj/coffeestats/master/lifeexp.dat"
data <- read.table(url, sep="\t", header=T, row.names=1)
data <- data[,c("LifeExp","People.per.TV","People.per.Dr")]
```

```r
detach(data)
attach(data)
head(data)
```

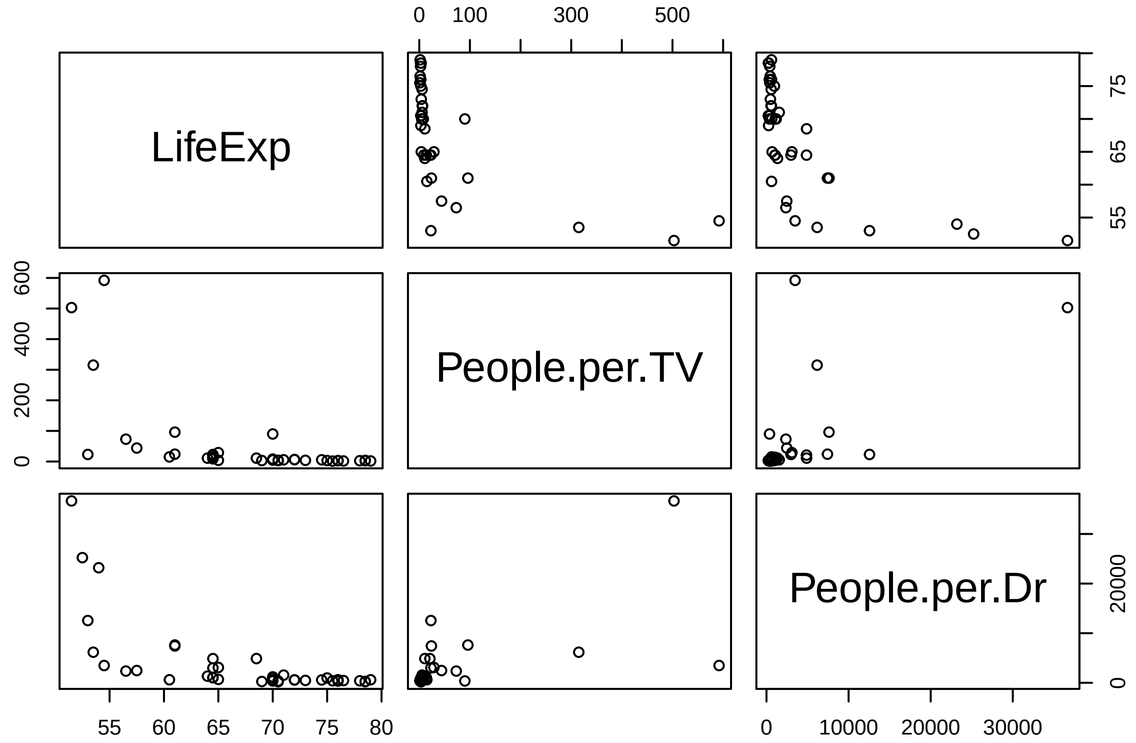
```
##            LifeExp People.per.TV People.per.Dr
## Argentina     70.5           4.0           370
## Bangladesh    53.5         315.0          6166
## Brazil        65.0           4.0           684
## Canada        76.5           1.7           449
## China         70.0           8.0           643
## Colombia      71.0           5.6          1551
```

```r
dim(data)
```

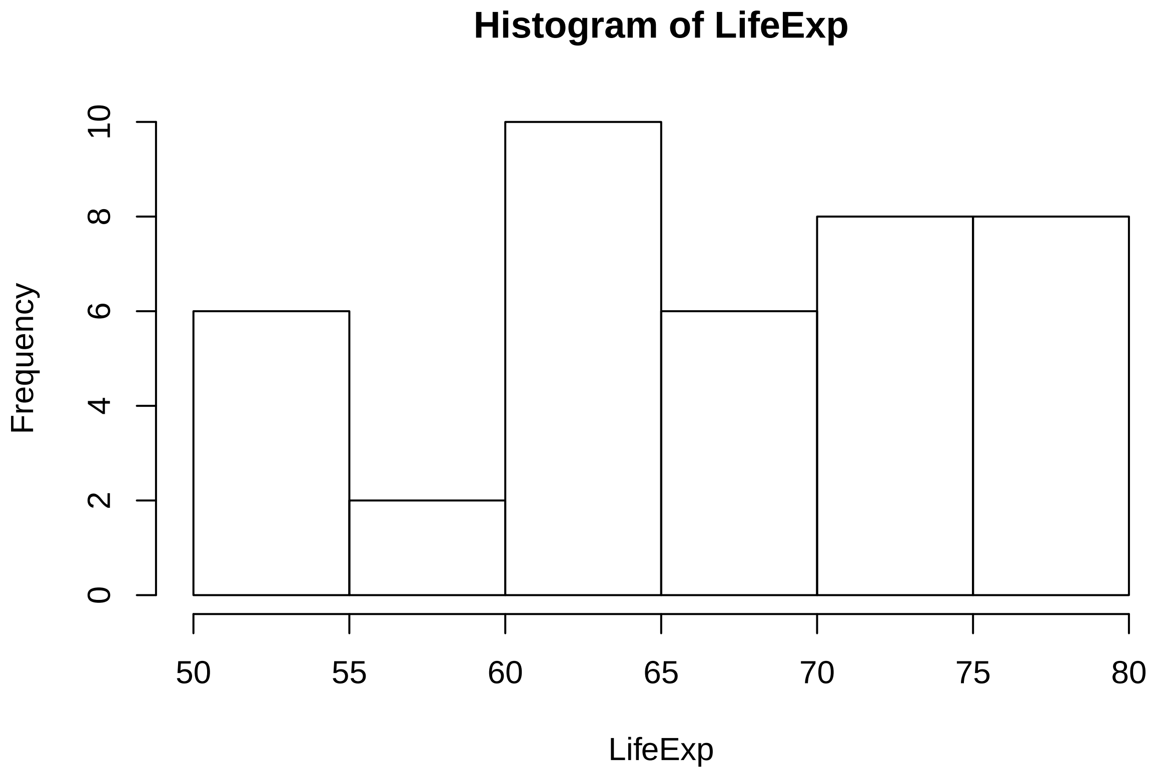
```
## [1] 40  3
```

Let's have a look at the data!

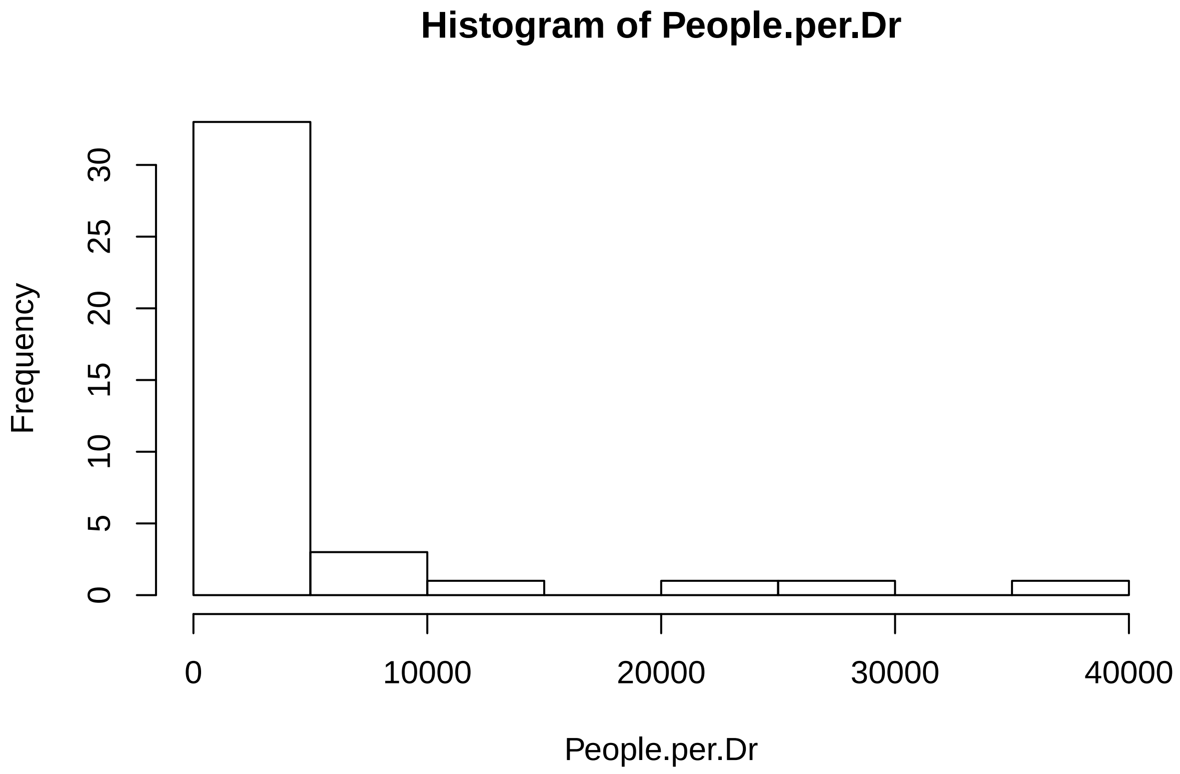
```r
pairs(data)
```



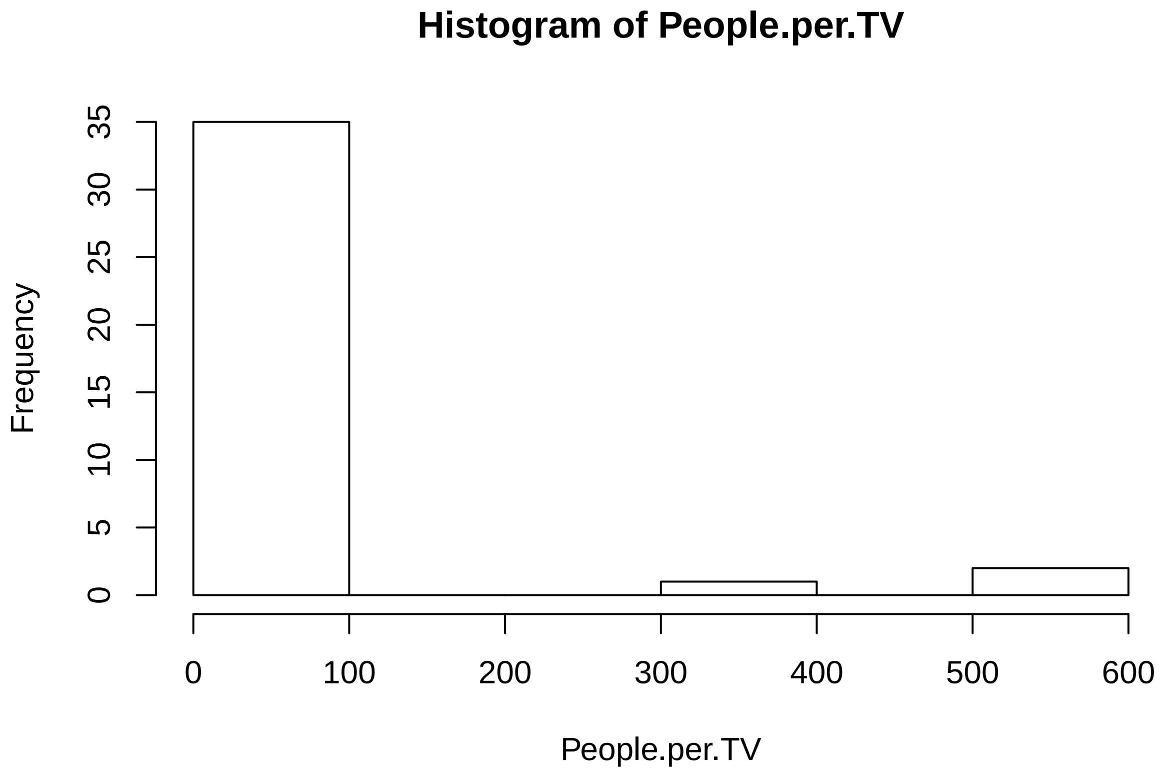
```r
hist(LifeExp)
```



```
hist(People.per.Dr)
```



```r
hist(People.per.TV)
```



```
# States with highest life expectancy
data[order(LifeExp, decreasing = TRUE),]
```

```
##              LifeExp People.per.TV People.per.Dr
## Japan           79.0           1.8           609
## Italy           78.5           3.8           233
## Spain           78.5           2.6           275
## France          78.0           2.6           403
## Canada          76.5           1.7           449
## Germany         76.0           2.6           346
## UK              76.0           3.0           611
## USA             75.5           1.3           404
## Taiwan          75.0           3.2           965
## Venezuela       74.5           5.6           576
## Poland          73.0           3.9           480
## Mexico          72.0           6.6           600
## Romania         72.0           6.0           559
## Colombia        71.0           5.6          1551
## Argentina       70.5           4.0           370
## Ukraine         70.5           3.0           226
## China           70.0           8.0           643
## Korea.North     70.0          90.0           370
## Korea.South     70.0           4.9          1066
## Turkey          70.0           5.0          1189
## Russia          69.0           3.2           259
## Thailand        68.5          11.0          4883
## Brazil          65.0           4.0           684
## Vietnam         65.0          29.0          3096
## Iran            64.5          23.0          2992
## Morocco         64.5          21.0          4873
## Peru            64.5          14.0          1016
## Philippines     64.5           8.8          1062
## South.Africa    64.0          11.0          1340
## Indonesia       61.0          24.0          7427
## Kenya           61.0          96.0          7615
## Egypt           60.5          15.0           616
## India           57.5          44.0          2471
## Pakistan        56.5          73.0          2364
## Burma           54.5         592.0          3485
## Zaire           54.0            NA         23193
## Bangladesh      53.5         315.0          6166
## Sudan           53.0          23.0         12550
## Tanzania        52.5            NA         25229
## Ethiopia        51.5         503.0         36660
```

```
# States with highest PeoplexTV
data[order(People.per.TV, decreasing = TRUE),]
```

```
##              LifeExp People.per.TV People.per.Dr
## Burma           54.5         592.0          3485
## Ethiopia        51.5         503.0         36660
## Bangladesh      53.5         315.0          6166
## Kenya           61.0          96.0          7615
## Korea.North     70.0          90.0           370
## Pakistan        56.5          73.0          2364
## India           57.5          44.0          2471
## Vietnam         65.0          29.0          3096
## Indonesia       61.0          24.0          7427
## Iran            64.5          23.0          2992
## Sudan           53.0          23.0         12550
## Morocco         64.5          21.0          4873
## Egypt           60.5          15.0           616
## Peru            64.5          14.0          1016
## South.Africa    64.0          11.0          1340
## Thailand        68.5          11.0          4883
## Philippines     64.5           8.8          1062
## China           70.0           8.0           643
## Mexico          72.0           6.6           600
## Romania         72.0           6.0           559
## Colombia        71.0           5.6          1551
## Venezuela       74.5           5.6           576
## Turkey          70.0           5.0          1189
## Korea.South     70.0           4.9          1066
## Argentina       70.5           4.0           370
## Brazil          65.0           4.0           684
## Poland          73.0           3.9           480
## Italy           78.5           3.8           233
## Russia          69.0           3.2           259
## Taiwan          75.0           3.2           965
## Ukraine         70.5           3.0           226
## UK              76.0           3.0           611
## France          78.0           2.6          403
## Germany         76.0           2.6          346
## Spain           78.5           2.6          275
## Japan           79.0           1.8          609
## Canada          76.5           1.7          449
## USA             75.5           1.3          404
## Tanzania        52.5            NA        25229
## Zaire           54.0            NA        23193
```

```
# States with highest PeoplexDr
data[order(People.per.Dr, decreasing = TRUE),]
```

```
##                LifeExp People.per.TV People.per.Dr
## Ethiopia          51.5         503.0         36660
## Tanzania          52.5            NA         25229
## Zaire             54.0            NA         23193
## Sudan             53.0          23.0         12550
## Kenya             61.0          96.0          7615
## Indonesia         61.0          24.0          7427
## Bangladesh        53.5         315.0          6166
## Thailand          68.5          11.0          4883
## Morocco           64.5          21.0          4873
## Burma             54.5         592.0          3485
## Vietnam           65.0          29.0          3096
## Iran              64.5          23.0          2992
## India             57.5          44.0          2471
## Pakistan          56.5          73.0          2364
## Colombia          71.0           5.6          1551
## South.Africa      64.0          11.0          1340
## Turkey            70.0           5.0          1189
## Korea.South       70.0           4.9          1066
## Philippines       64.5           8.8          1062
## Peru              64.5          14.0          1016
## Taiwan            75.0           3.2           965
## Brazil            65.0           4.0           684
## China             70.0           8.0           643
## Egypt             60.5          15.0           616
## UK                76.0           3.0           611
## Japan             79.0           1.8           609
## Mexico            72.0           6.6           600
## Venezuela         74.5           5.6           576
## Romania           72.0           6.0           559
## Poland            73.0           3.9           480
## Canada            76.5           1.7           449
## USA               75.5           1.3           404
## France            78.0           2.6           403
## Argentina         70.5           4.0           370
## Korea.North       70.0          90.0           370
## Germany           76.0           2.6           346
## Spain             78.5           2.6           275
## Russia            69.0           3.2           259
## Italy             78.5           3.8           233
## Ukraine           70.5           3.0           226
```

Now we’ll get rid of the missing values by simply deleting the corresponsing entries in the dataframe.

```r
data <- na.omit(data)
dim(data)
```

```
## [1] 38  3
```

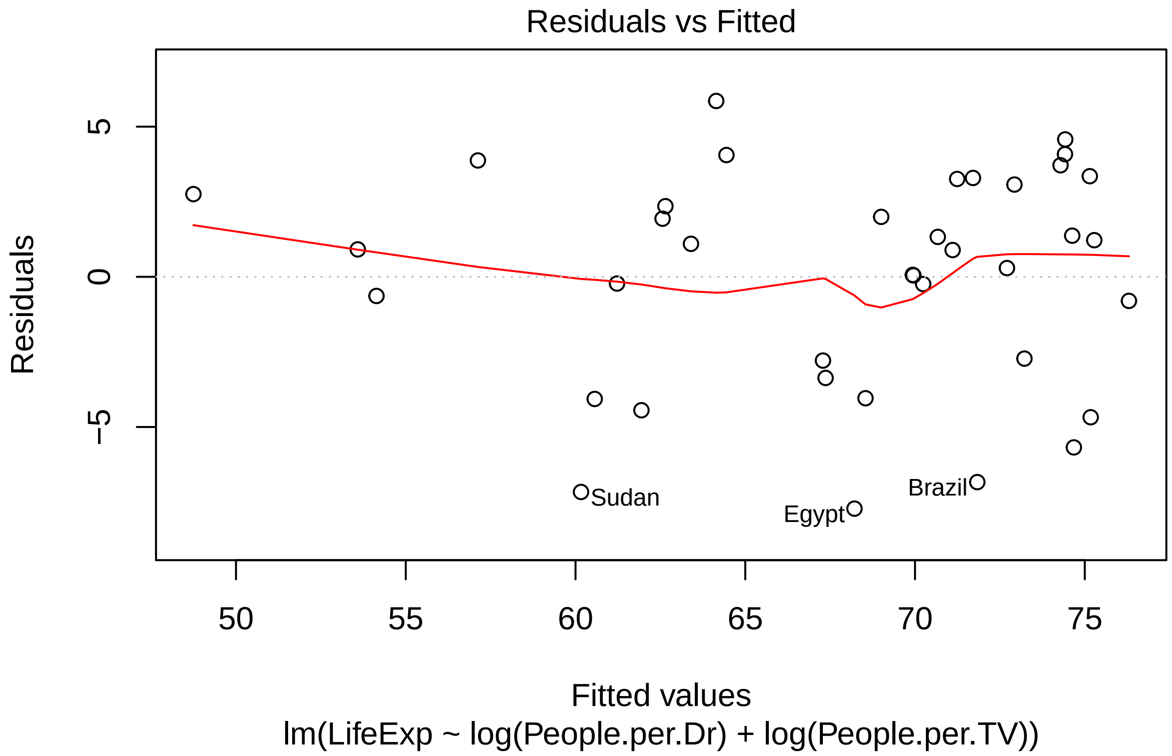
Let's fit a linear model on the logged transformed variables.

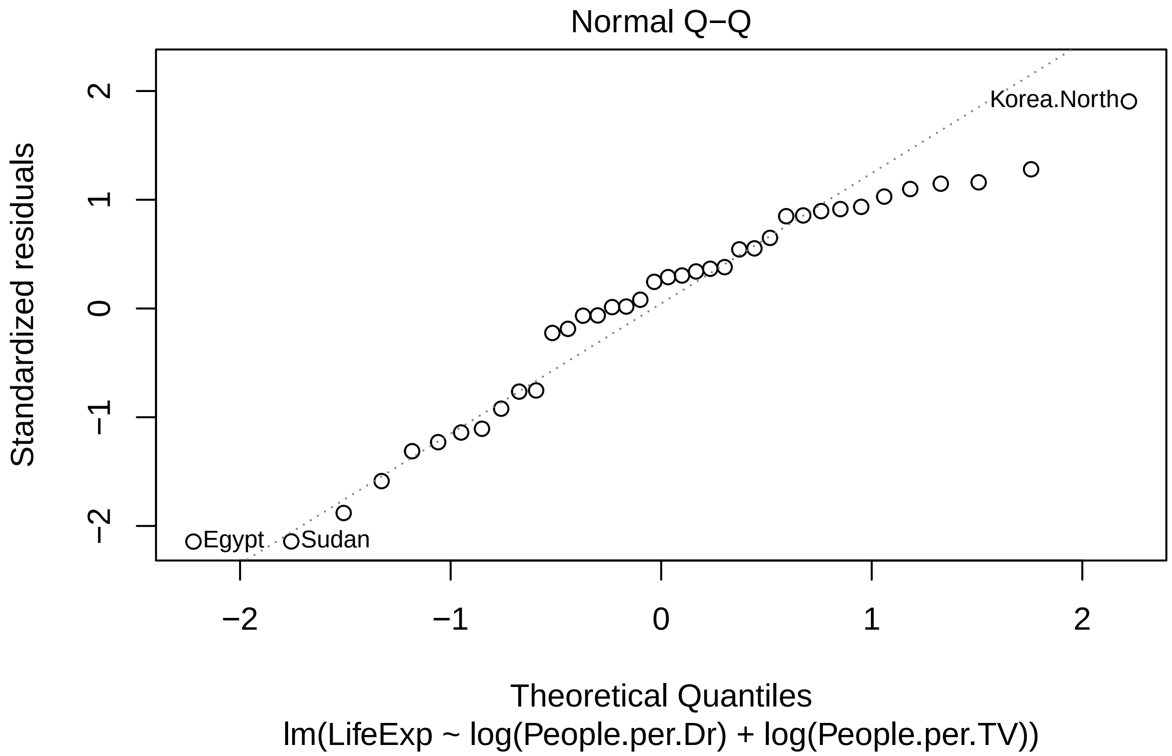
```r
model <- lm(LifeExp~log(People.per.Dr)+log(People.per.TV), data=data)
summary(model)
```

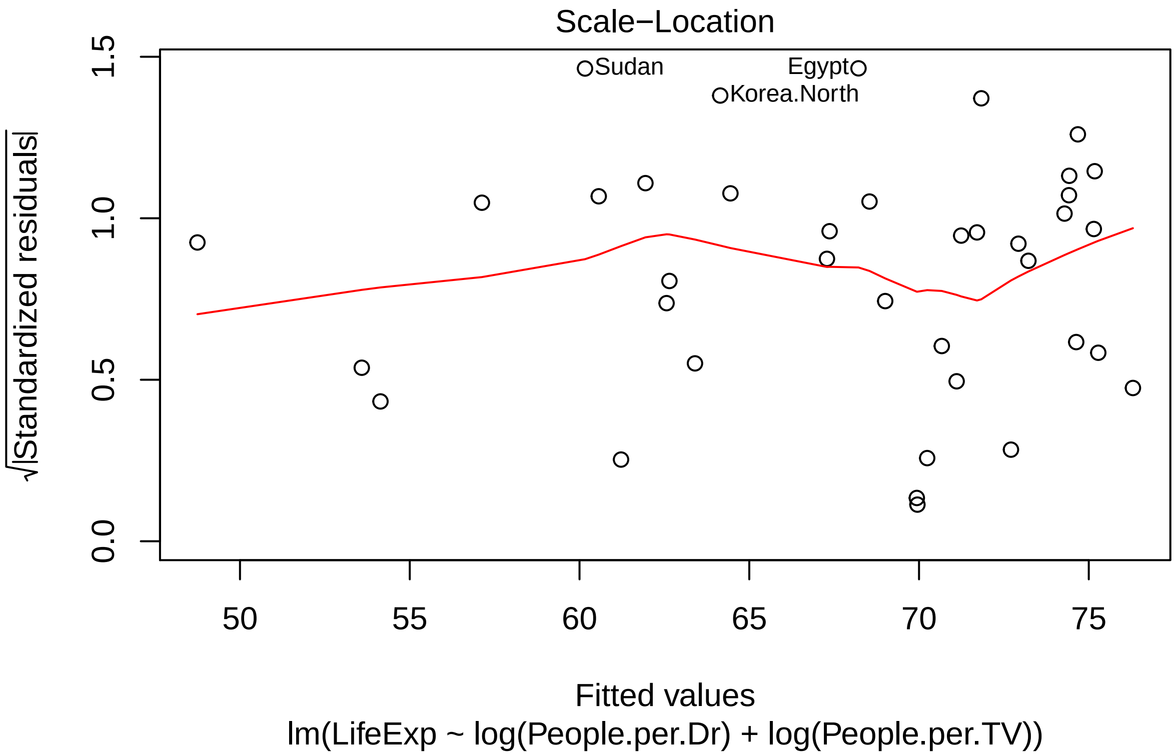
```
##
## Call:
## lm(formula = LifeExp ~ log(People.per.Dr) + log(People.per.TV),
##     data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7.7173 -2.7718  0.9026  2.9923  5.8553
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         90.6222     4.3557  20.806  < 2e-16 ***
## log(People.per.Dr)  -2.2589     0.7474  -3.022  0.00467 **
## log(People.per.TV)  -2.9156     0.5907  -4.936 1.95e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.704 on 35 degrees of freedom
## Multiple R-squared:  0.7868, Adjusted R-squared:  0.7747
## F-statistic:  64.6 on 2 and 35 DF,  p-value: 1.788e-12
```

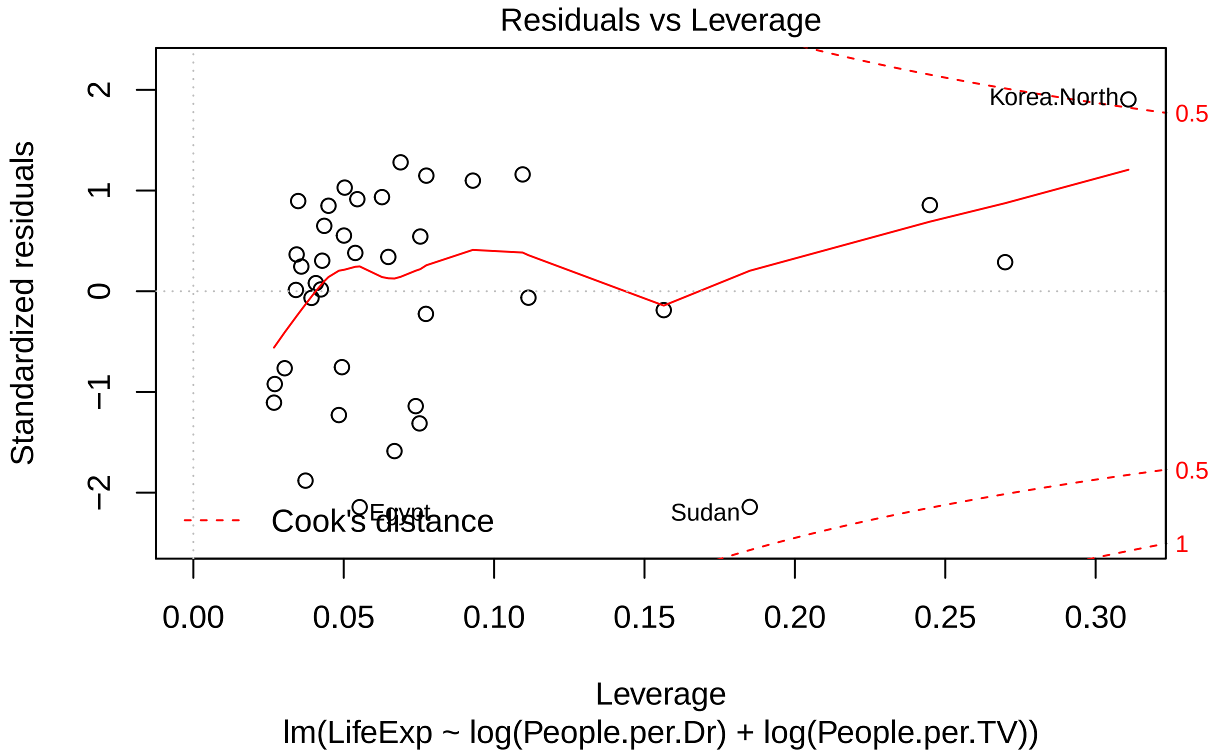
Beware: the coefficients refer to the log-transformed variables, hence the right interpretation , for instance of the second coefficient, would be: by increasing the number of people per Dr. by a factor of (e), while keeping the other variable fixed, the life expectancy would, on average, decrease by -2.25**.

```r
plot(model)
```


Residuals vs Fitted
Residuals
5
0
−5
50
55
60
65
70
75
Fitted values
lm(LifeExp ~ log(People.per.Dr) + log(People.per.TV))
Sudan
Egypt
Brazil


Normal Q−Q
Standardized residuals
−2
−1
0
1
2
Egypt
Sudan
Korea.North
−2
−1
0
1
2
Theoretical Quantiles
lm(LifeExp ~ log(People.per.Dr) + log(People.per.TV))


Scale−Location
Sudan
Egypt
Korea.North
√|Standardized residuals|
0.0
0.5
1.0
1.5
50
55
60
65
70
75
Fitted values
lm(LifeExp ~ log(People.per.Dr) + log(People.per.TV))



Can we conclude that more TVs imply a higher life expectancy? No, because we're not analysing the data with a causal model. However, we can use the estimated coefficient to predict the LifeExp for a new point.

Looking at the Cook distance we can clearly pinpoint at least two outliers in the dataset: 17 and 30.

```
data[c(17,30),]
```

```
##             LifeExp People.per.TV People.per.Dr
## Korea.North      70            90           370
## Sudan            53            23         12550
```

Let's remove the two outliers and refit the model.

```
data.no.out <- data[c(-17,-30),]
dim(data.no.out)
```

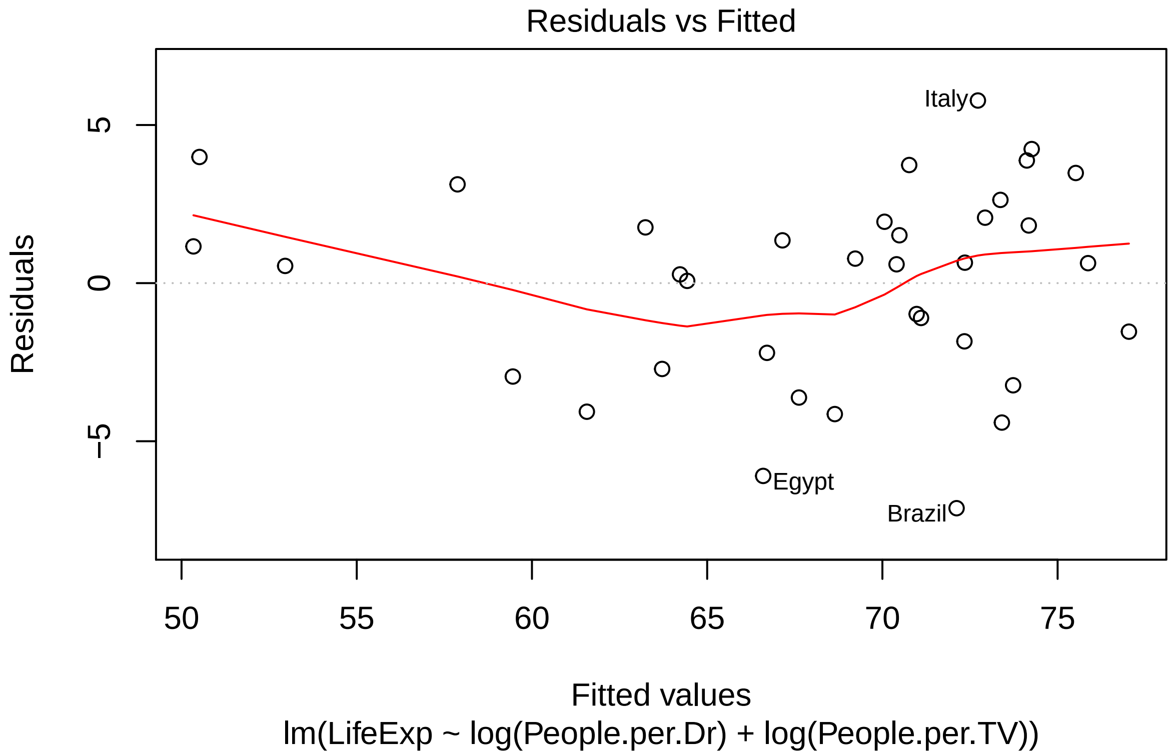
```
## [1] 36  3
```

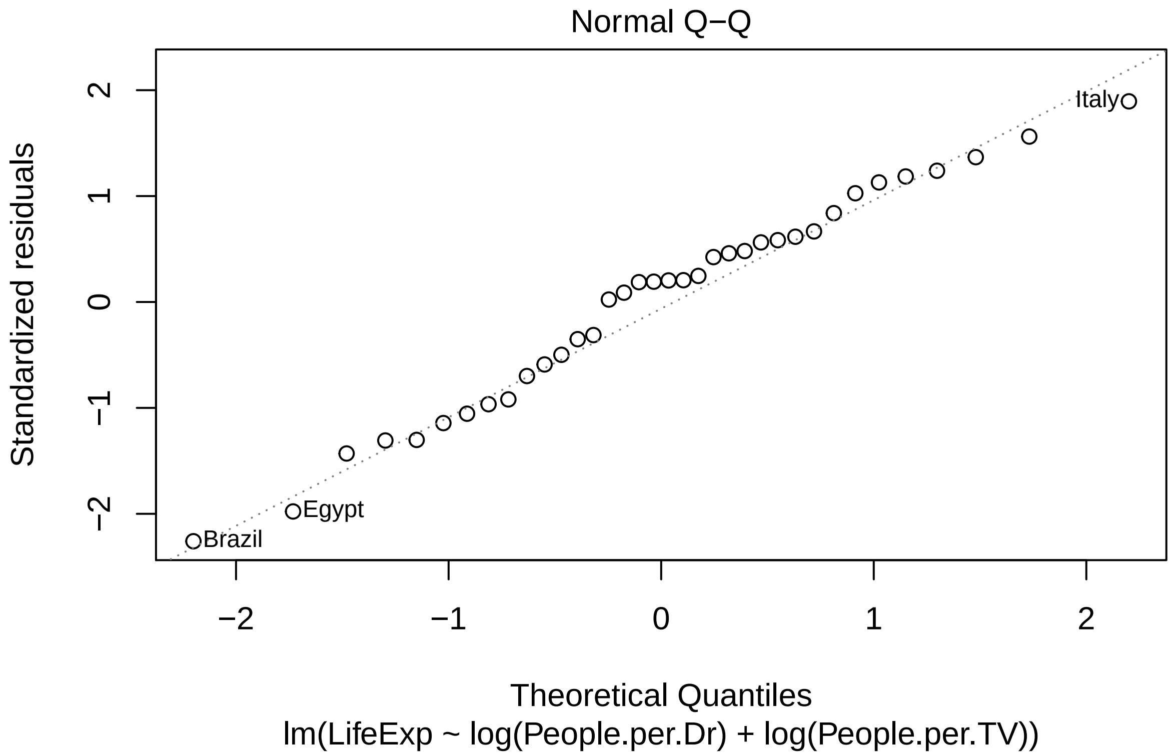
```
model <- lm(LifeExp~log(People.per.Dr)+log(People.per.TV), data=data.no.out)
summary(model)
```

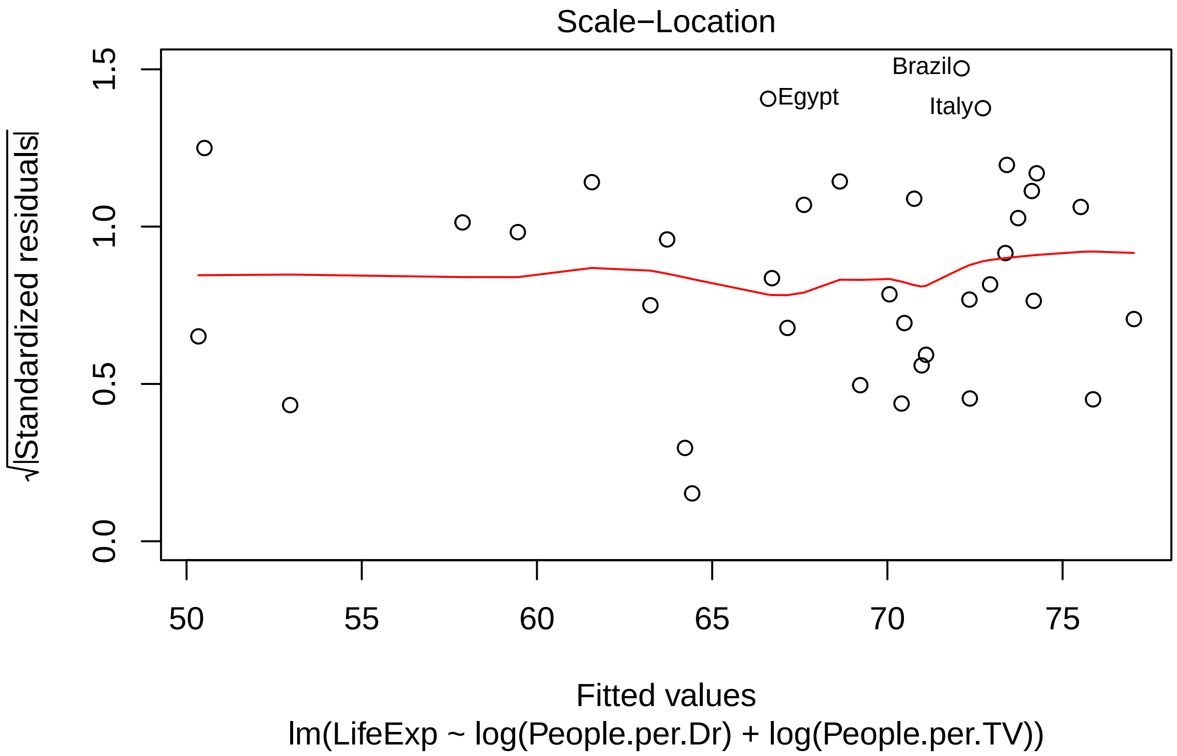
```
##
## Call:
## lm(formula = LifeExp ~ log(People.per.Dr) + log(People.per.TV),
##     data = data.no.out)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7.1175 -2.3328  0.6134  1.9728  5.7746
##
```

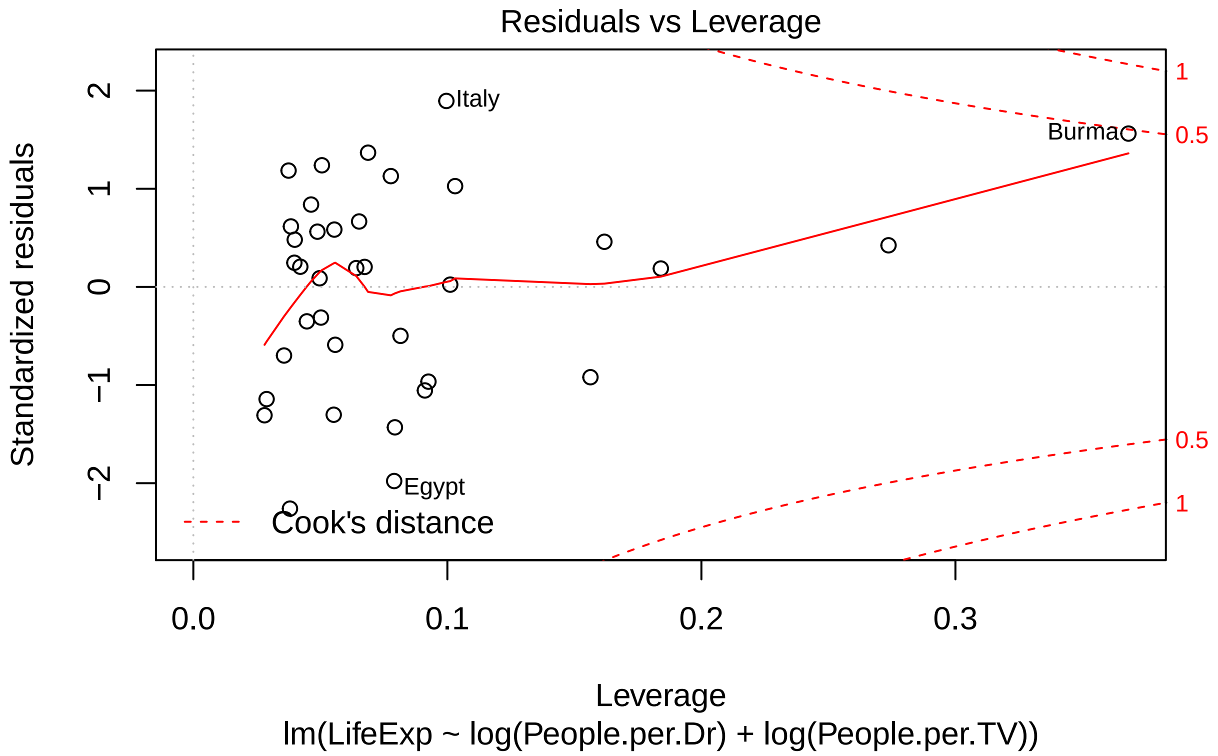
```
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)           80.3245     4.7221  17.010  < 2e-16 ***
## log(People.per.Dr)    -0.3642     0.8327  -0.437    0.665
## log(People.per.TV)    -4.2050     0.6348  -6.624 1.56e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.212 on 33 degrees of freedom
## Multiple R-squared:  0.8319, Adjusted R-squared:  0.8217
## F-statistic: 81.63 on 2 and 33 DF,  p-value: 1.675e-13
```

```
plot(model)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(LifeExp ~ log(People.per.Dr) + log(People.per.TV))
−2
−1
0
1
2
−2
−1
0
1
2
Italy
Egypt
Brazil


Scale−Location
1.5
1.0
0.5
0.0
√|Standardized residuals|
50
55
60
65
70
75
Fitted values
lm(LifeExp ~ log(People.per.Dr) + log(People.per.TV))
Brazil
Egypt
Italy



Notice that the R-squared has significantly improved, while the coefficient estimates have changed markedly. Now let's use the summary data to compute some confidence intervals.

```
new.point <- data.frame(People.per.Dr=3000,People.per.TV=50)
#95% confidence interval for the
predict(model, new.point, interval = "confidence")
```

```
##        fit      lwr      upr
## 1 60.95844 59.37872 62.53816
```

```
predict(model, new.point, interval = "prediction")
```

```
##        fit      lwr      upr
## 1 60.95844 54.23489 67.68199
```

Where did these 2 interval come out from?

```
n <- dim(data.no.out)[1]
p <- dim(data.no.out)[2]
n
```

```
## [1] 36
```

```
p
```

```
## [1] 3
```

```
beta.hat <- model$coefficients
x0 <- matrix(c(1,log(3000),log(50)))
point.estimate <- t(x0)%*%beta.hat
point.estimate
```

```
##           [,1]
## [1,] 60.95844
```

```
X <- as.matrix(cbind(1,data.no.out[,2:3]))
se.hat <- summary(model)$sigma
xtx.inv <- solve(t(X)%*%X)
confidence.average <- sqrt(t(x0)%*%xtx.inv%*%x0)*se.hat*qt(0.975, df=n-p)
c(point.estimate-confidence.average, point.estimate+confidence.average)
```

```
## [1] 59.76292 62.15395
```

```
confidence.actual <- sqrt(1 + t(x0)%*%xtx.inv%*%x0)*se.hat*qt(0.975, df=n-p)
c(point.estimate-confidence.actual, point.estimate+confidence.actual)
```

```
## [1] 54.31465 67.60223
```

The bias variance tradeoff