Machine Learning - Day 2

Data modelling

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Libraries

```
library(dplyr)
```

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

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

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

```
library(ggplot2)
library(here)
```

```
## here() starts at /home/chiara/dev/machineLearningClass
```

DATA IMPORT

```
dc <-  file.path(here(), "data", "dc-wikia-data.csv") %>%
  read.csv(na.strings = "")

max_year <- max(dc$YEAR, na.rm =T)

dc <- dc %>%
  mutate(active_years = max_year - YEAR)
```

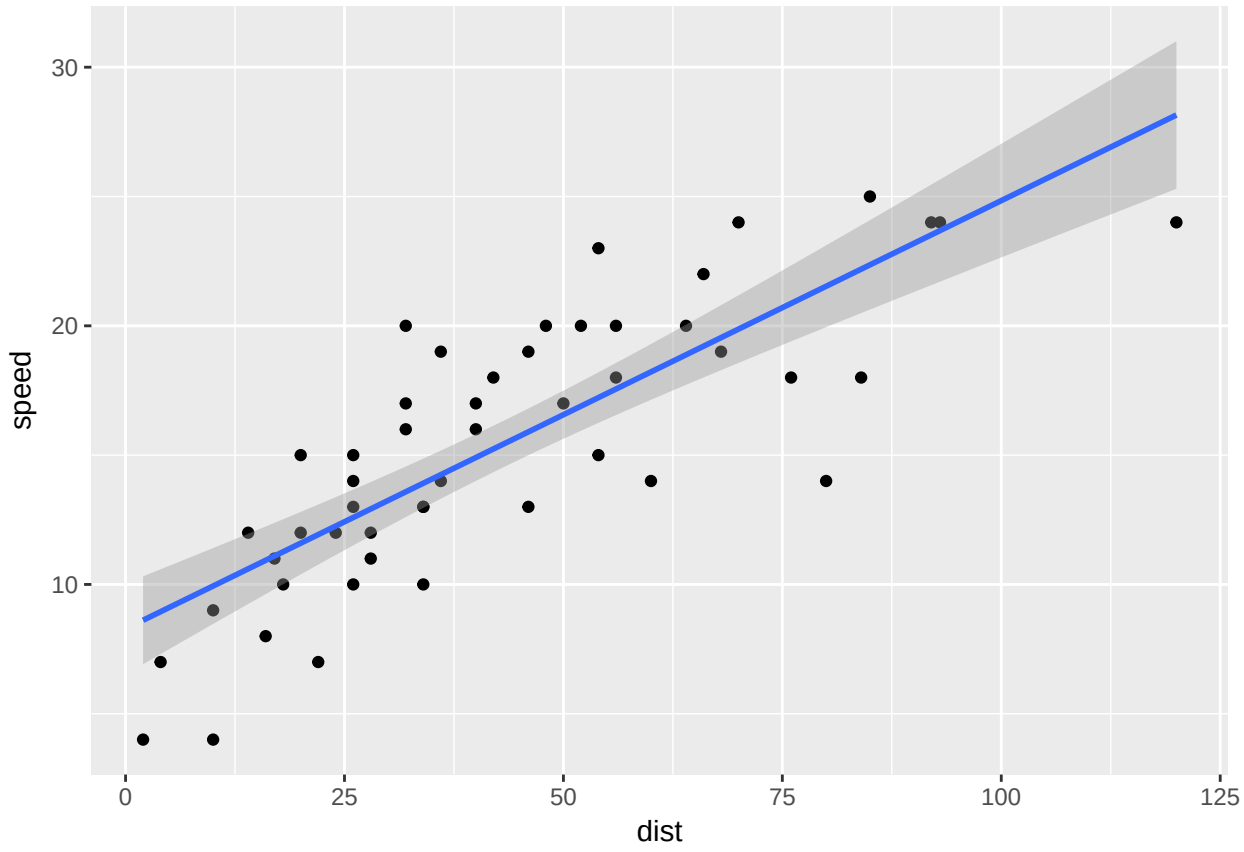
DATA MODELING

LINEAR REGRESSION

Simple linear regression

Easy ex

```
ggplot(data = cars, aes(x = dist, y = speed)) +
  geom_point() +
  geom_smooth(method='lm',formula=y~x)
```




```
m1 <- lm(data = cars, speed ~ dist)

summary(m1)
```

```
##
## Call:
## lm(formula = speed ~ dist, data = cars)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7.5293 -2.1550  0.3615  2.4377  6.4179
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  8.28391    0.87438   9.474 1.44e-12 ***
## dist         0.16557    0.01749   9.464 1.49e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.156 on 48 degrees of freedom
## Multiple R-squared:  0.6511, Adjusted R-squared:  0.6438
## F-statistic: 89.57 on 1 and 48 DF,  p-value: 1.49e-12
```

```
residuals(m1)
```

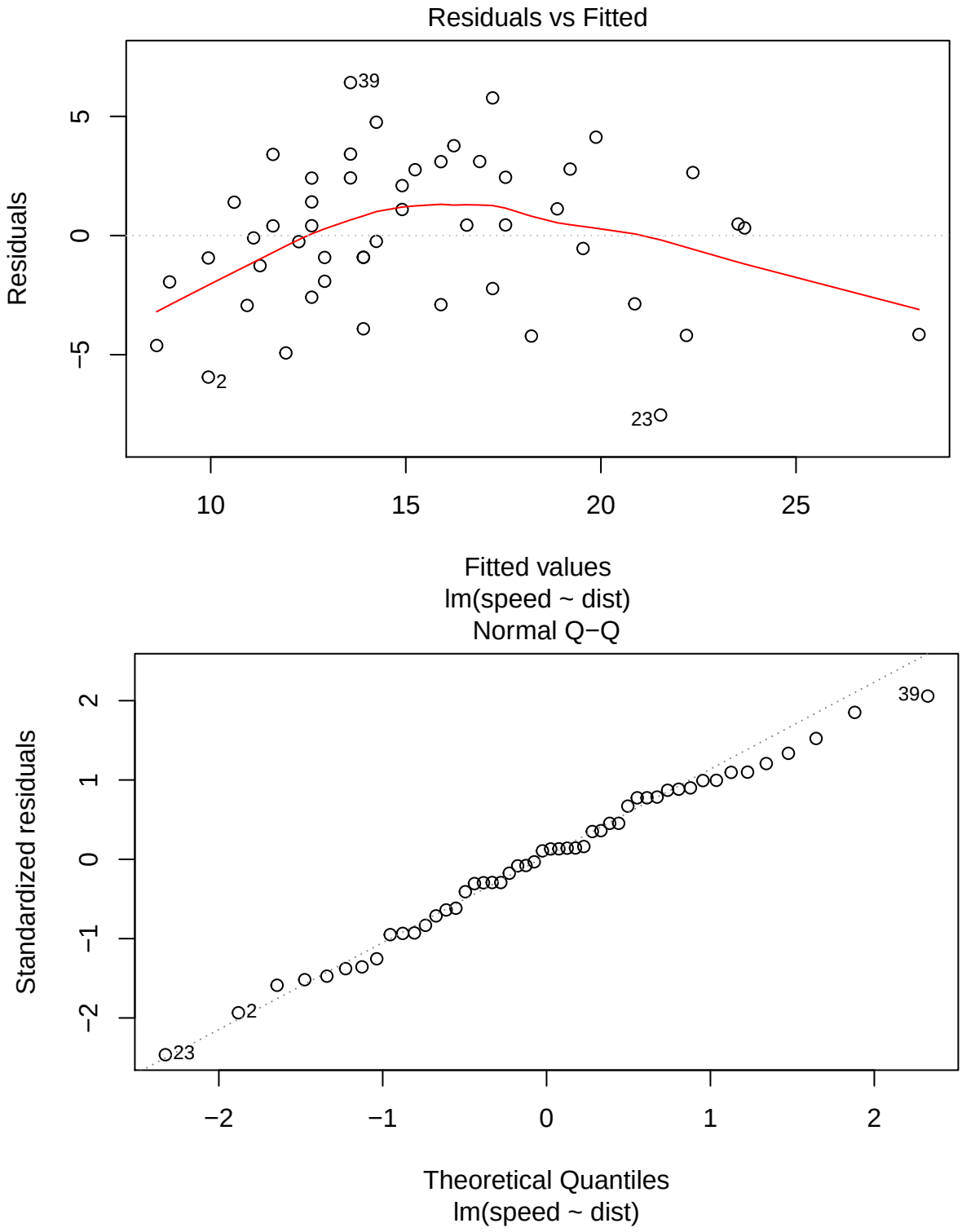
```
##           1           2           3           4           5           6
## -4.61504079 -5.93958139 -1.94617594 -4.92639228 -2.93298684 -0.93958139
##           7           8           9          10          11          12
```

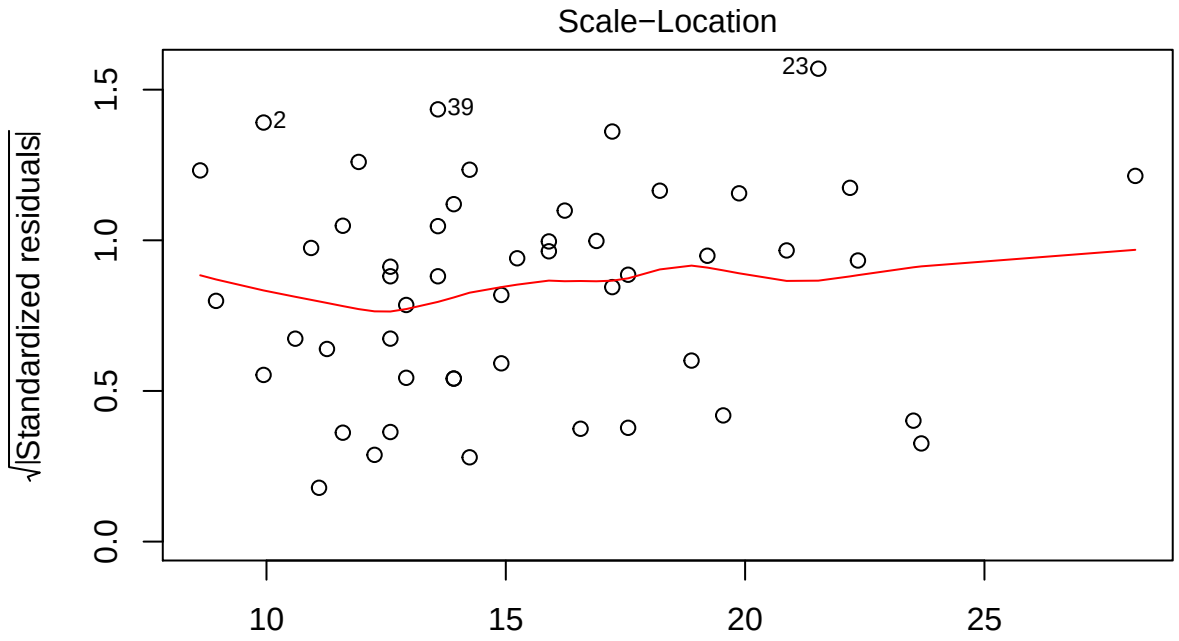
```
## -1.26412199 -2.58866258 -3.91320318 -0.09855441 -1.91979773  1.39814831
##          13          14          15          16          17          18
##  0.40474287 -0.25752743 -0.91979773  0.41133742 -0.91320318 -0.91320318
##          19          20          21          22          23          24
## -2.90001408  1.41133742 -0.24433833 -4.21796012 -7.52931161  3.40474287
##          25          26          27          28          29          30
##  2.41133742 -2.22455467  2.41793197  1.09339137  3.41793197  2.09339137
##          31          32          33          34          35          36
##  0.43771563  2.76225622  0.44431018 -2.86704131 -4.19158191  4.75566167
##          37          38          39          40          41          42
##  3.09998592 -0.54250072  6.41793197  3.76885078  3.10658048  2.44431018
##          43          44          45          46          47          48
##  1.11976958  2.78863443  5.77544533  4.12636413  0.48387749  0.31830992
##          49          50
## -4.15201460  2.64285051
```

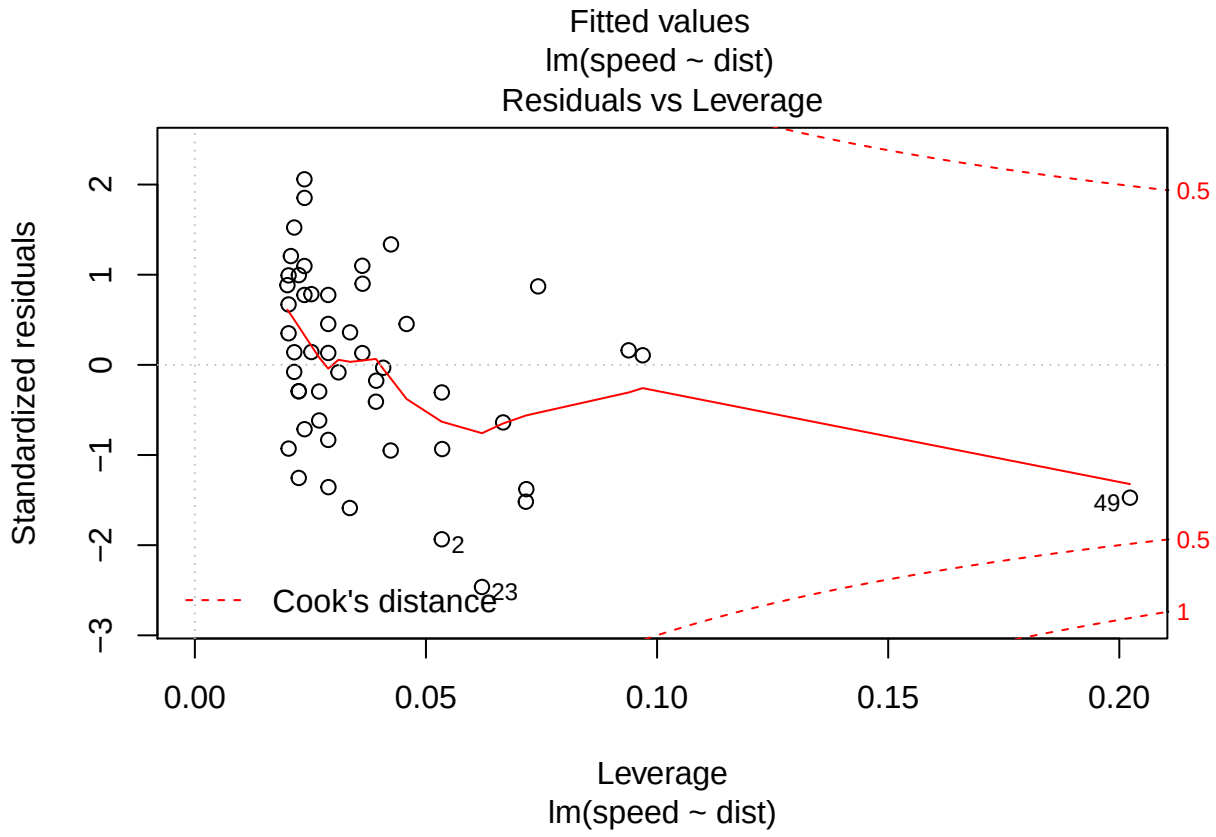
```
predict(m1)
```

```
##         1         2         3         4         5         6         7
##  8.615041  9.939581  8.946176 11.926392 10.932987  9.939581 11.264122
##         8         9        10        11        12        13        14
## 12.588663 13.913203 11.098554 12.919798 10.601852 11.595257 12.257527
##        15        16        17        18        19        20        21
## 12.919798 12.588663 13.913203 13.913203 15.900014 12.588663 14.244338
##        22        23        24        25        26        27        28
## 18.217960 21.529312 11.595257 12.588663 17.224555 13.582068 14.906609
##        29        30        31        32        33        34        35
## 13.582068 14.906609 16.562284 15.237744 17.555690 20.867041 22.191582
##        36        37        38        39        40        41        42
## 14.244338 15.900014 19.542501 13.582068 16.231149 16.893420 17.555690
##        43        44        45        46        47        48        49
## 18.880230 19.211366 17.224555 19.873636 23.516123 23.681690 28.152015
##        50
## 22.357149
```

```
plot(m1)
```


Residuals vs Fitted
Residuals
Fitted values
lm(speed ~ dist)
Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(speed ~ dist)



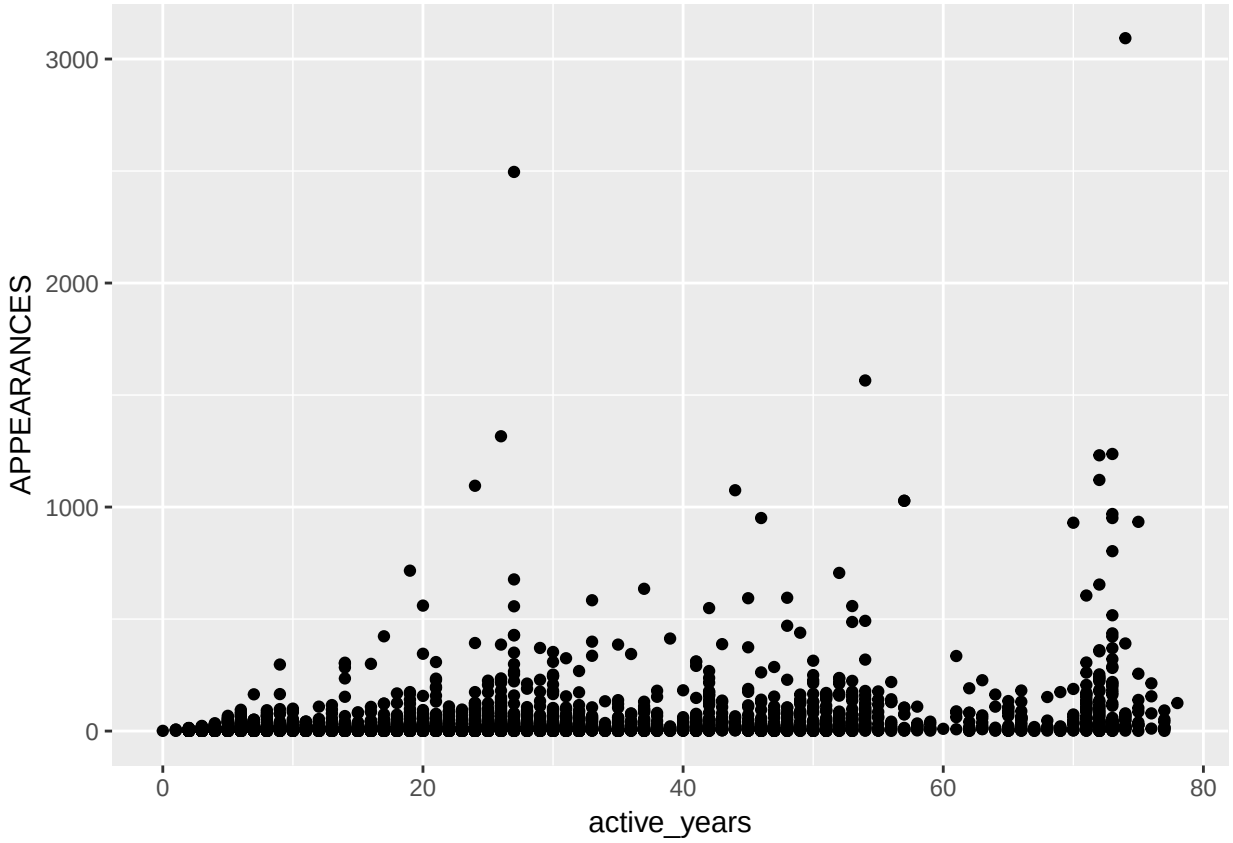


Comics example

```
dc_small <- dc %>%
  filter(APPEARANCES >20)
```

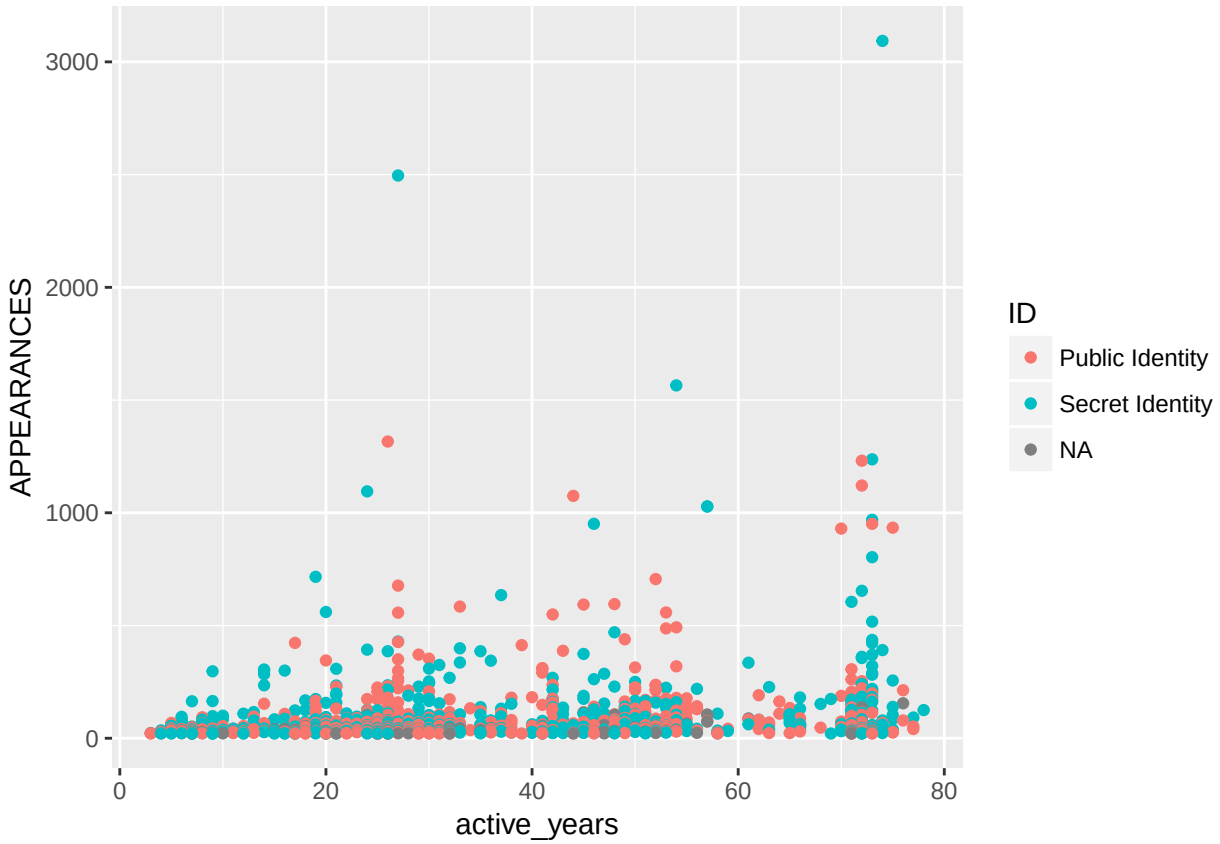
```
dc %>%
  ggplot(aes(x = active_years, y = APPEARANCES)) +
  geom_point()
```

```
## Warning: Removed 415 rows containing missing values (geom_point).
```




```
dc_small %>%
  ggplot(aes(x = active_years, y = APPEARANCES, col = ID)) +
  geom_point()
```

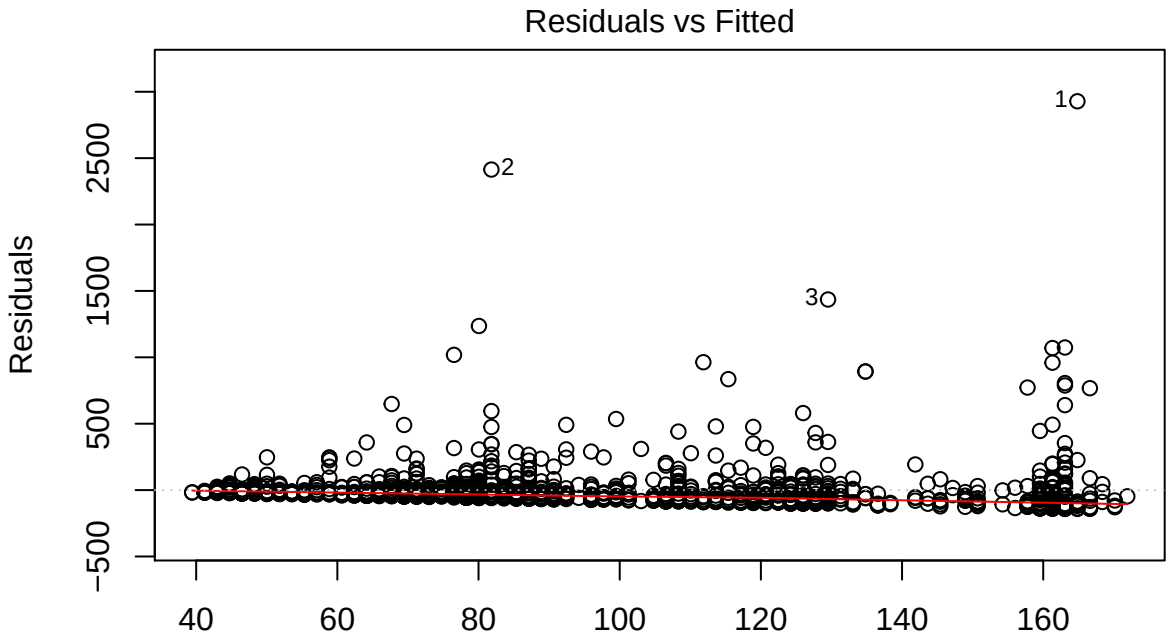
```
## Warning: Removed 1 rows containing missing values (geom_point).
```

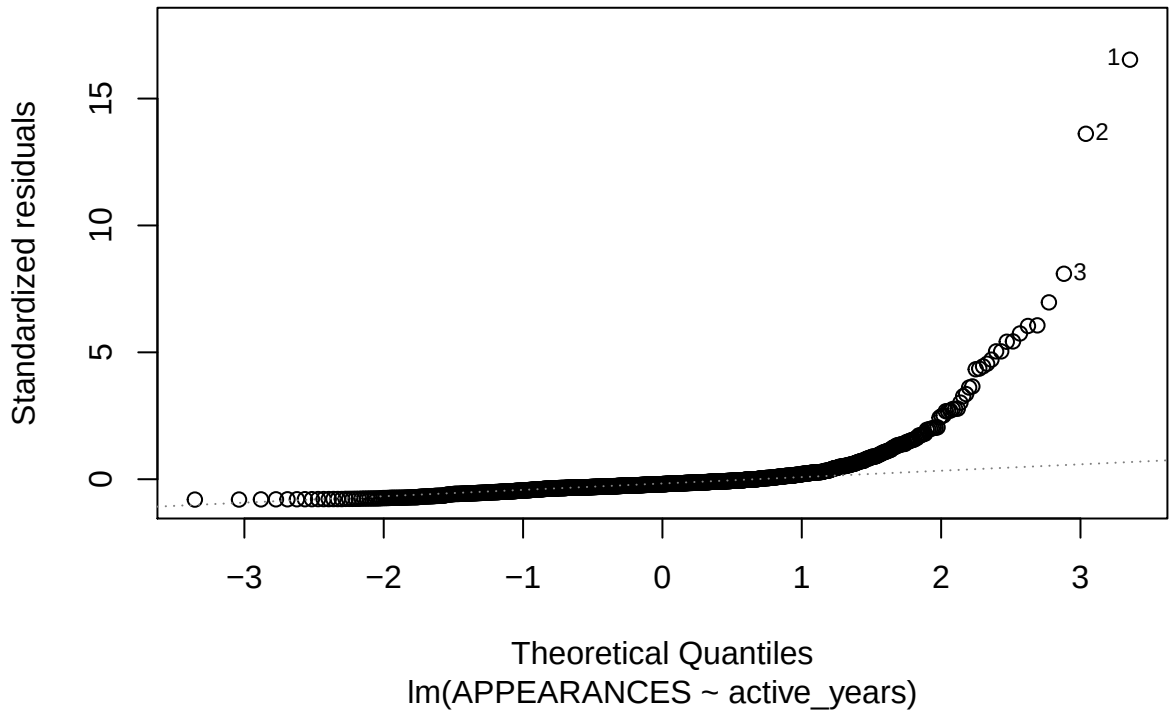


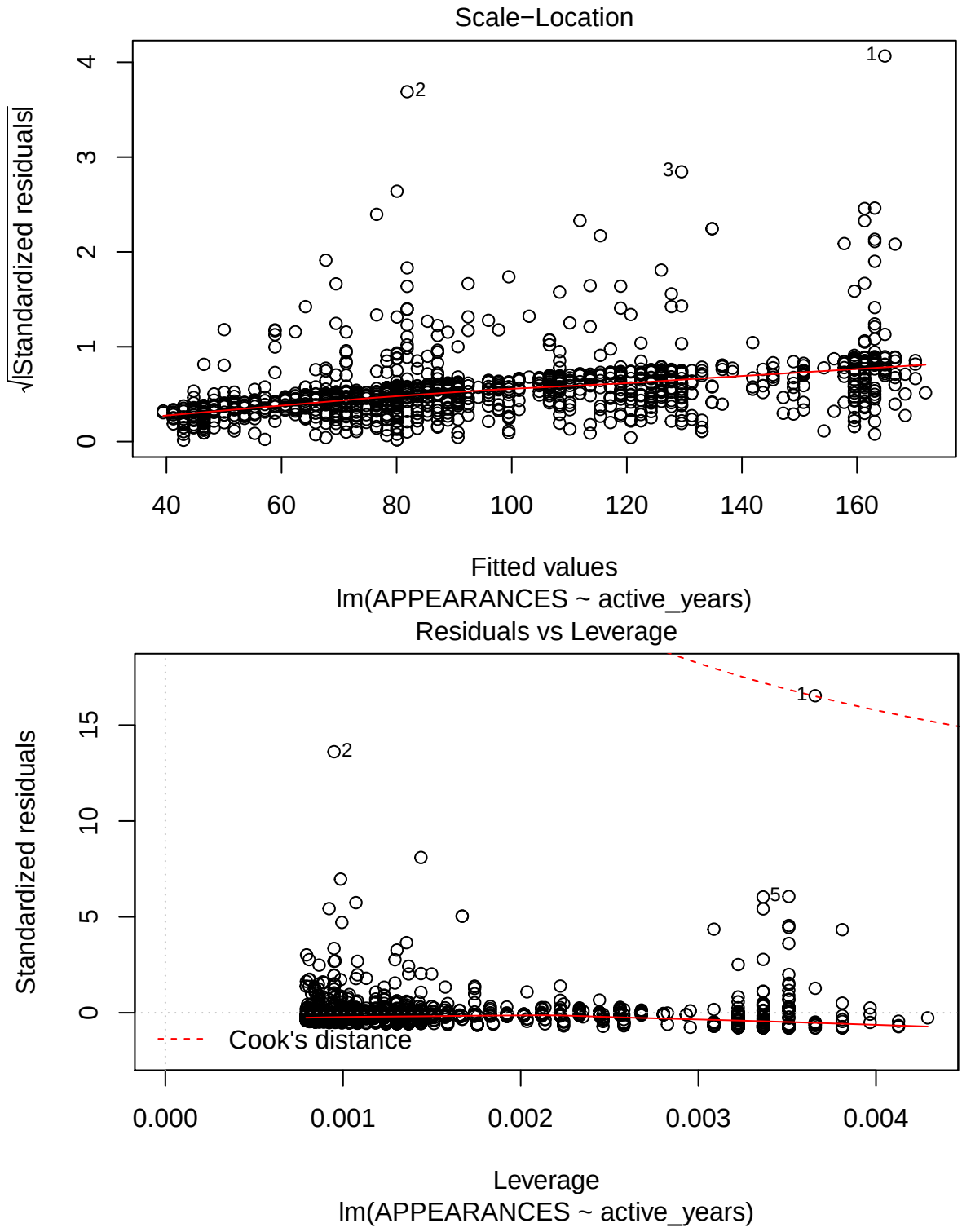

```
m1 <- lm(data=dc_small, APPEARANCES ~ active_years)

summary(m1)
```

```
##
## Call:
## lm(formula = APPEARANCES ~ active_years, data = dc_small)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -142.08  -59.87  -34.17    0.34 2928.16
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   34.1321    10.2537   3.329 0.000898 ***
## active_years   1.7664     0.2494   7.084 2.33e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 177.4 on 1260 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.0383, Adjusted R-squared:  0.03753
## F-statistic: 50.18 on 1 and 1260 DF,  p-value: 2.331e-12
```

```
plot(m1)
```


Residuals vs Fitted
Residuals
2500
1500
500
−500
1
2
3
40
60
80
100
120
140
160
Fitted values
lm(APPEARANCES ~ active_years)


Normal Q−Q
Standardized residuals
15
10
5
0
1
2
3
−3
−2
−1
0
1
2
3
Theoretical Quantiles
lm(APPEARANCES ~ active_years)



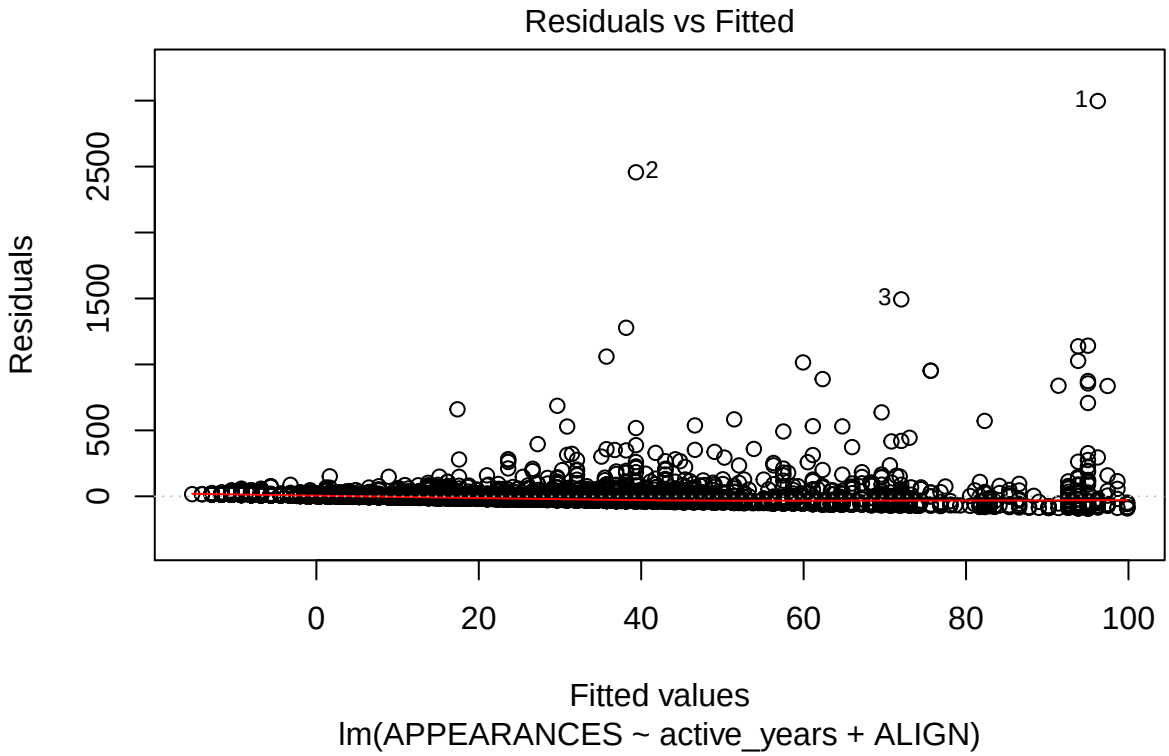
Multiple linear regression

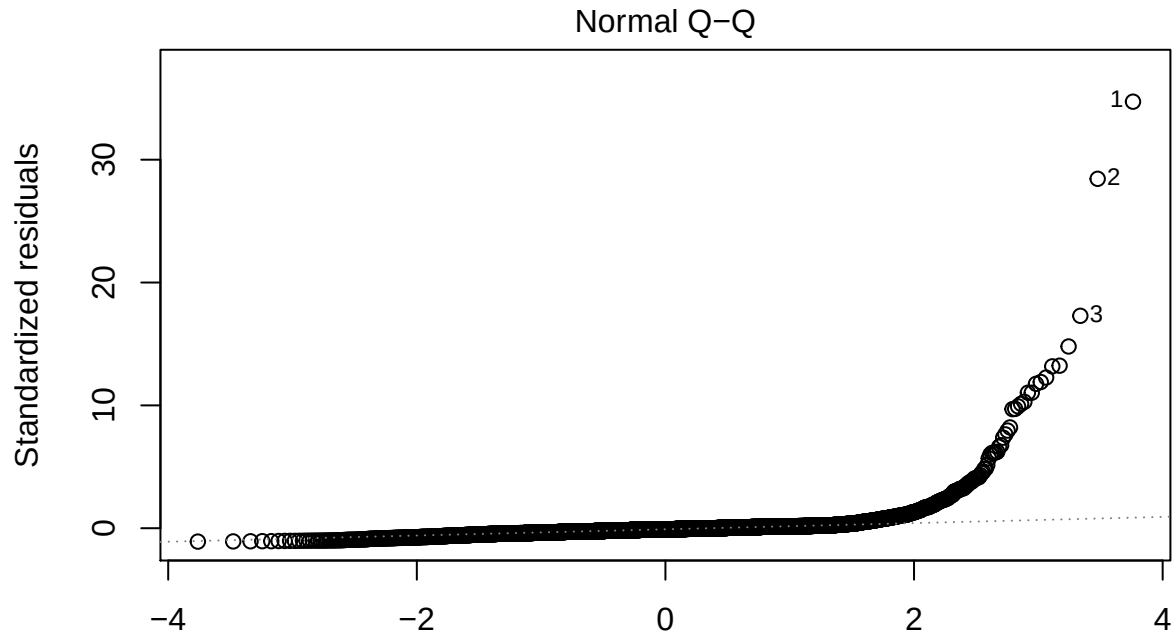
```
m3 <- lm(data=dc, APPEARANCES ~ active_years + ALIGN)
```

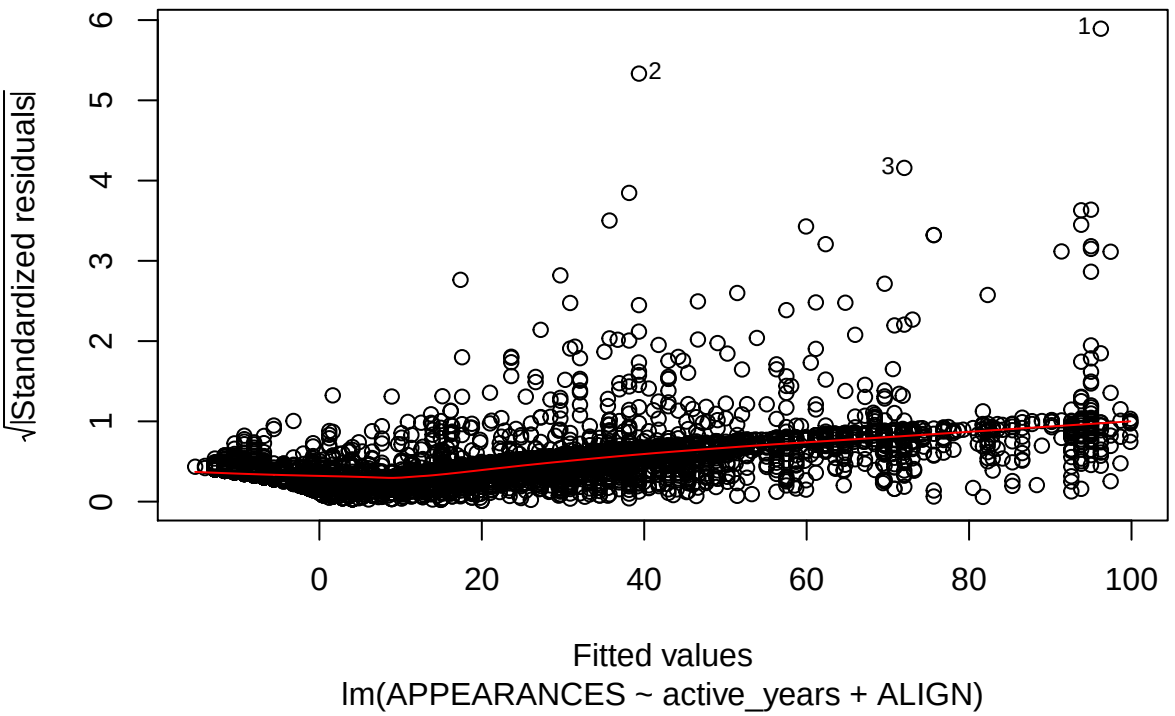
```r
summary(m3)
```

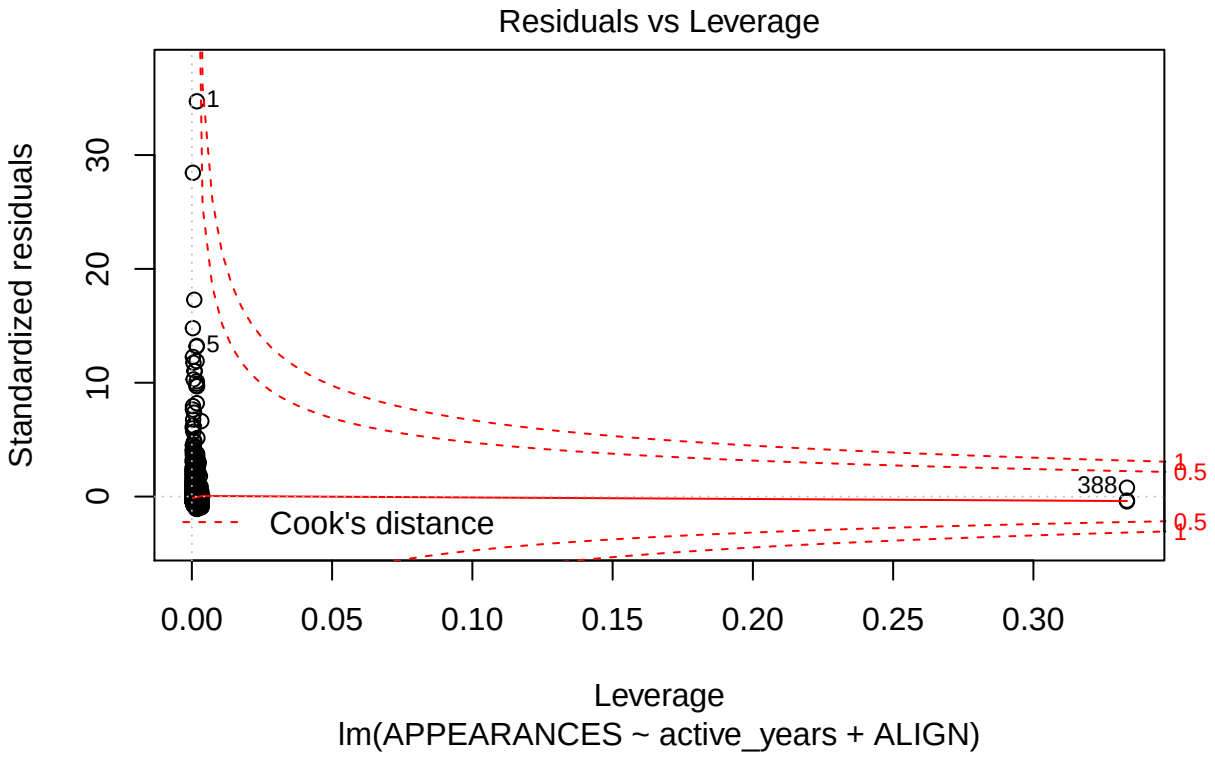
```
##
## Call:
## lm(formula = APPEARANCES ~ active_years + ALIGN, data = dc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
##  -94.01  -22.47   -8.10    6.98 2996.78
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)              -15.2929     2.2004  -6.950 4.05e-12 ***
## active_years               1.2101     0.0675  17.927  < 2e-16 ***
## ALIGNGood Characters      21.9737     2.3721   9.263  < 2e-16 ***
## ALIGNNeutral Characters   10.4623     4.0650   2.574   0.0101 *
## ALIGNReformed Criminals   27.2122    49.9045   0.545   0.5856
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 86.39 on 5918 degrees of freedom
##   (973 observations deleted due to missingness)
## Multiple R-squared:  0.07101,    Adjusted R-squared:  0.07039
## F-statistic: 113.1 on 4 and 5918 DF,  p-value: < 2.2e-16
```

```r
plot(m3)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(APPEARANCES ~ active_years + ALIGN)
1
2
3
−4
−2
0
2
4
0
10
20
30


Scale−Location
√|Standardized residuals|
Fitted values
lm(APPEARANCES ~ active_years + ALIGN)
1
2
3
0
20
40
60
80
100
0
1
2
3
4
5
6

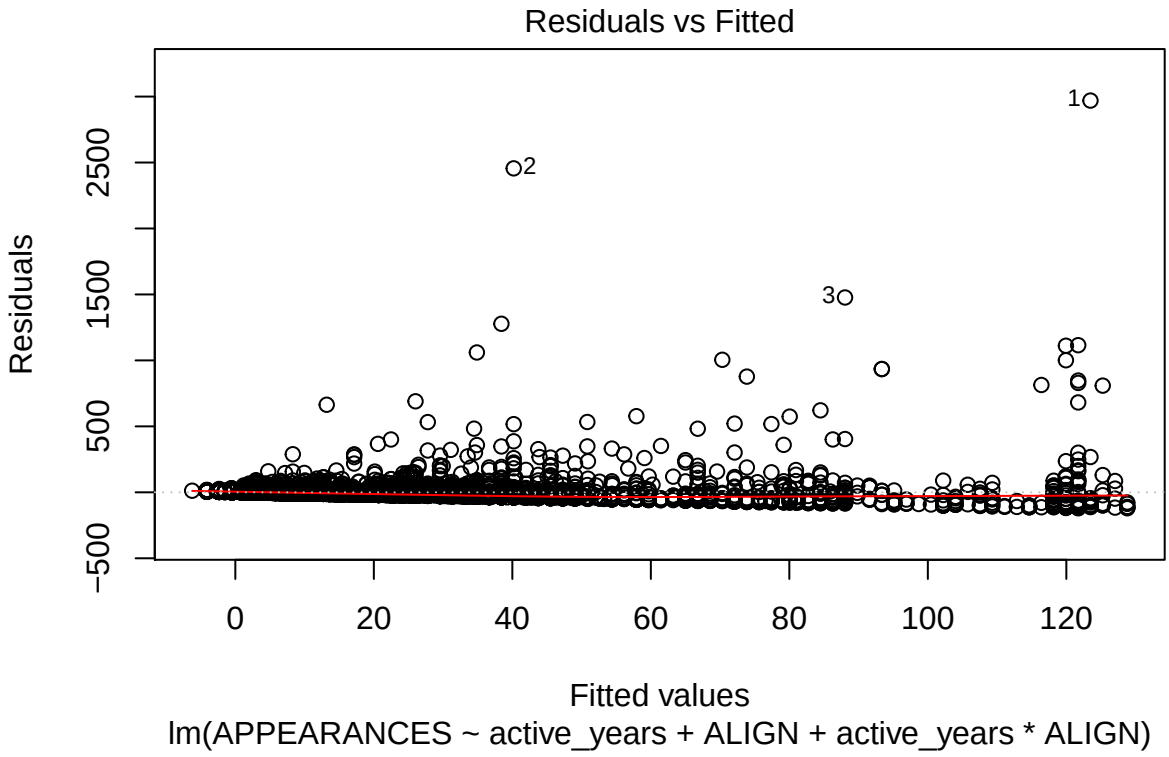


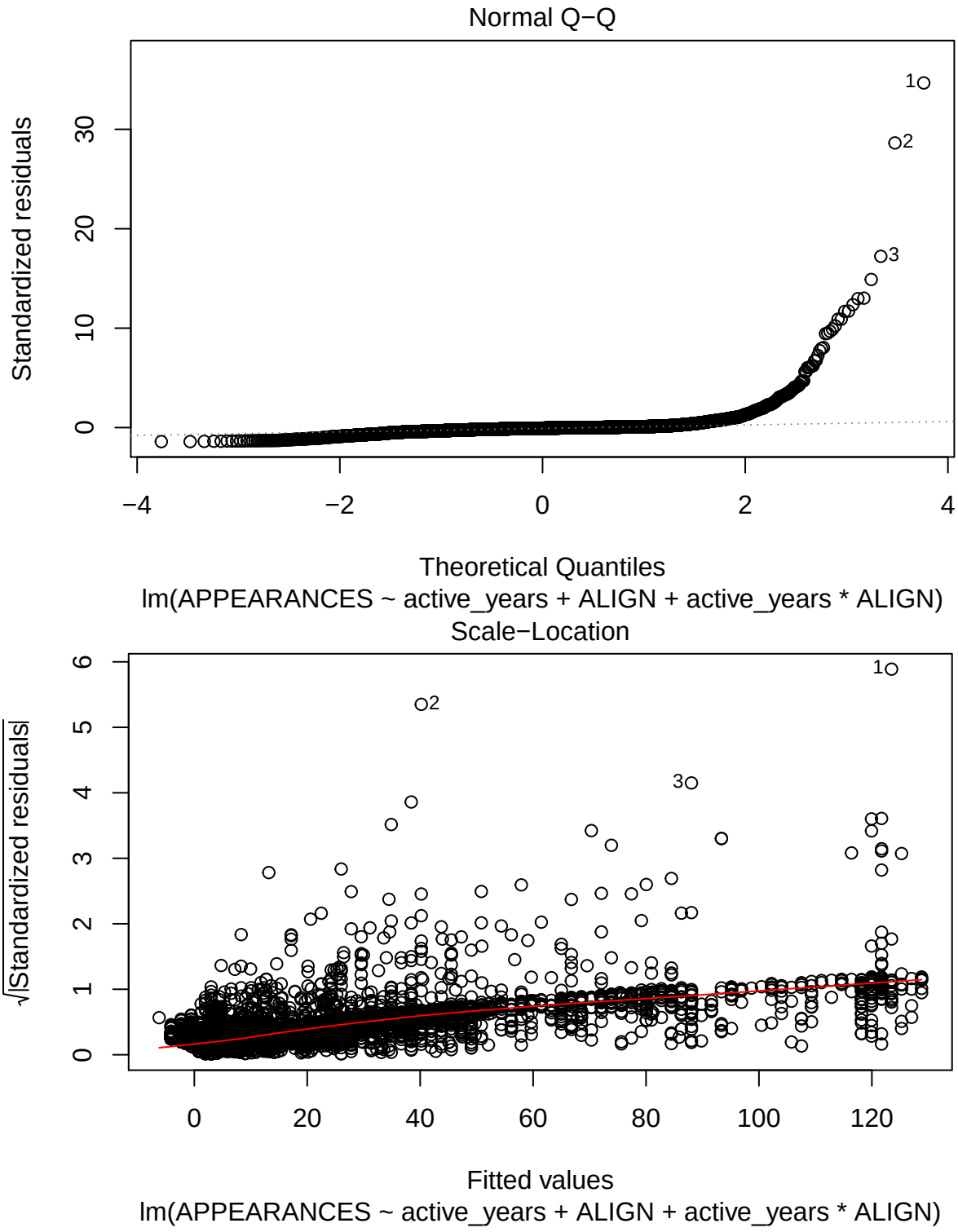

```
m4 <- lm(data=dc, APPEARANCES ~ active_years + ALIGN + active_years*ALIGN)

summary(m4)
```

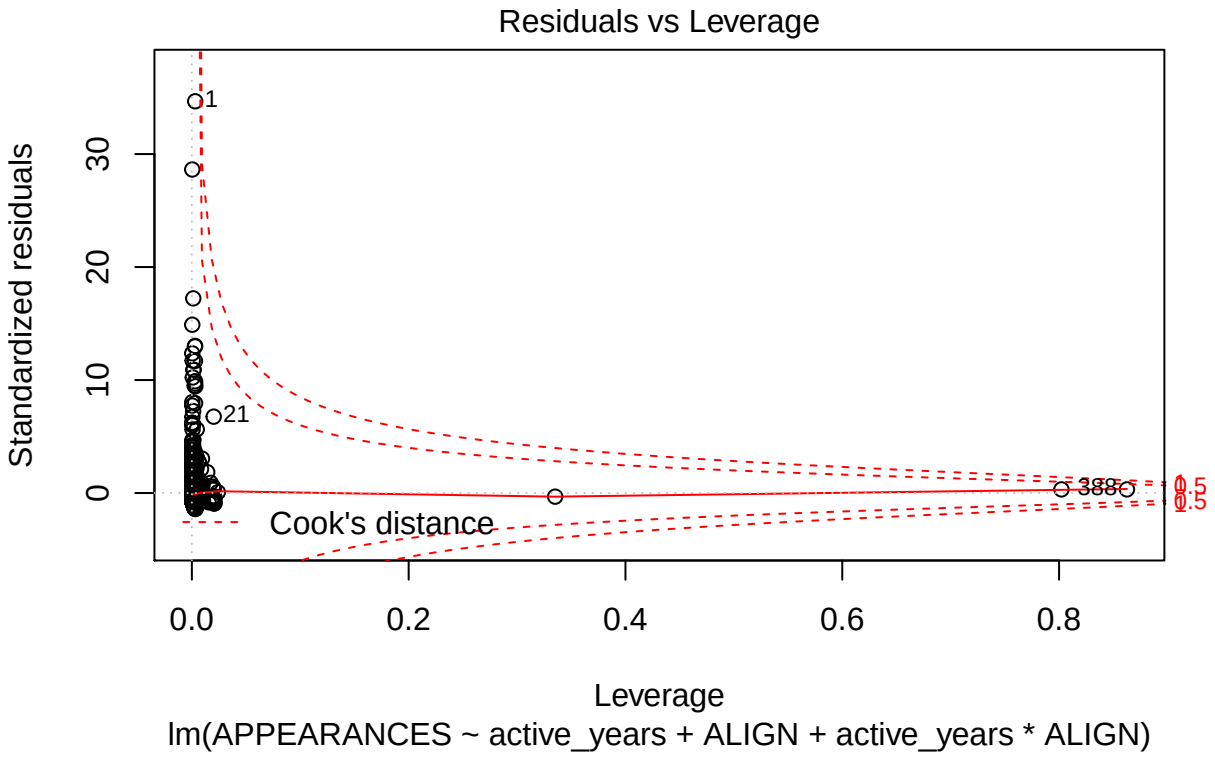
```
##
## Call:
## lm(formula = APPEARANCES ~ active_years + ALIGN + active_years *
##     ALIGN, data = dc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -120.80  -17.56   -5.56    2.56 2969.52
##
## Coefficients:
##                                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)                                0.7058     2.8269   0.250  0.80285
## active_years                               0.4626     0.1073   4.311 1.65e-05
## ALIGNGood Characters                      -8.3553     4.0374  -2.069  0.03855
## ALIGNNeutral Characters                   -4.5558     6.8834  -0.662  0.50809
## ALIGNReformed Criminals                  127.6788   168.9829   0.756  0.44994
## active_years:ALIGNGood Characters          1.3095     0.1416   9.247  < 2e-16
## active_years:ALIGNNeutral Characters       0.7027     0.2554   2.751  0.00596
## active_years:ALIGNReformed Criminals      -7.1934    11.0144  -0.653  0.51373
##
## (Intercept)
## active_years                             ***
## ALIGNGood Characters                     *
## ALIGNNeutral Characters
## ALIGNReformed Criminals
## active_years:ALIGNGood Characters        ***
```

```
## active_years:ALIGNNeutral Characters **
## active_years:ALIGNReformed Criminals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 85.79 on 5915 degrees of freedom
##   (973 observations deleted due to missingness)
## Multiple R-squared:  0.08434,    Adjusted R-squared:  0.08325
## F-statistic: 77.83 on 7 and 5915 DF,  p-value: < 2.2e-16
```

```
plot(m4)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(APPEARANCES ~ active_years + ALIGN + active_years * ALIGN)
Scale−Location
√|Standardized residuals|
Fitted values
lm(APPEARANCES ~ active_years + ALIGN + active_years * ALIGN)

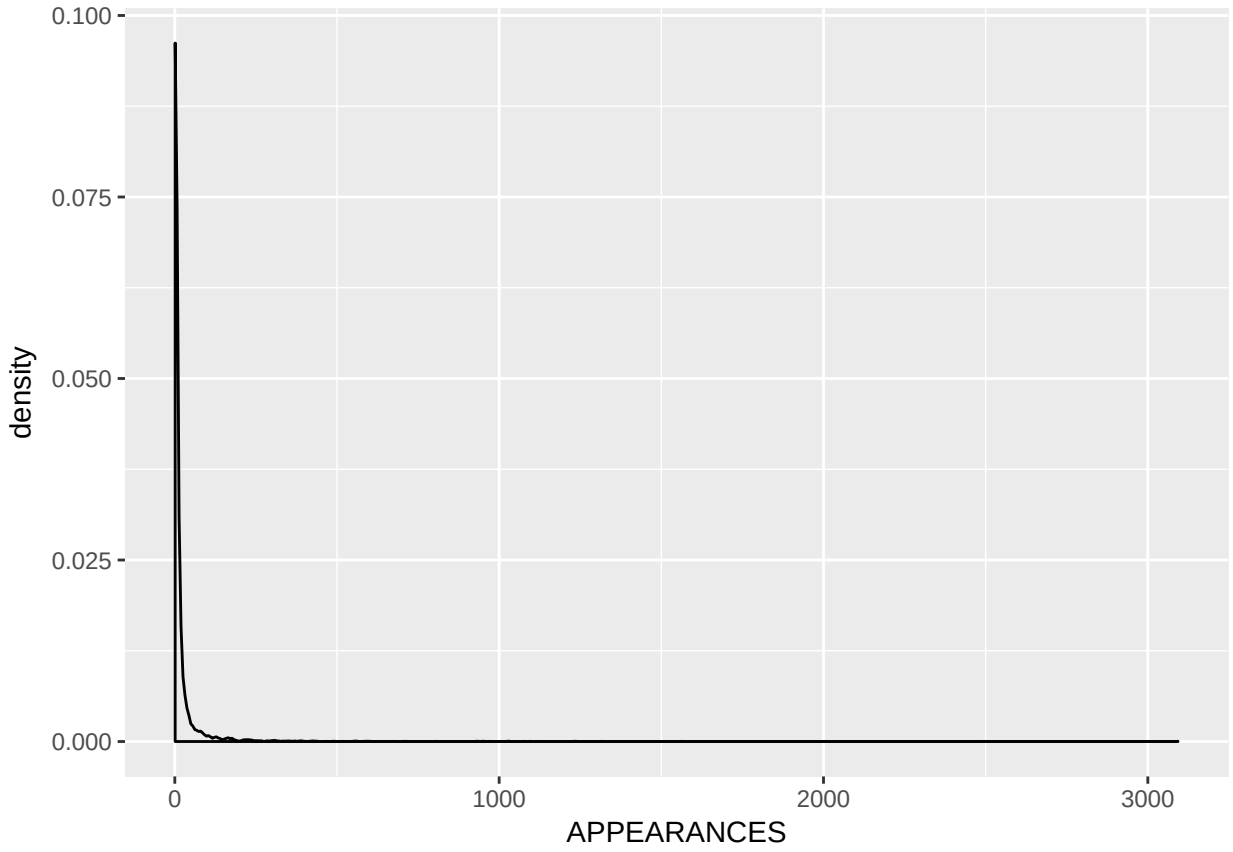


Log-level regression

http://www.cazaar.com/ta/econ113/interpreting-beta

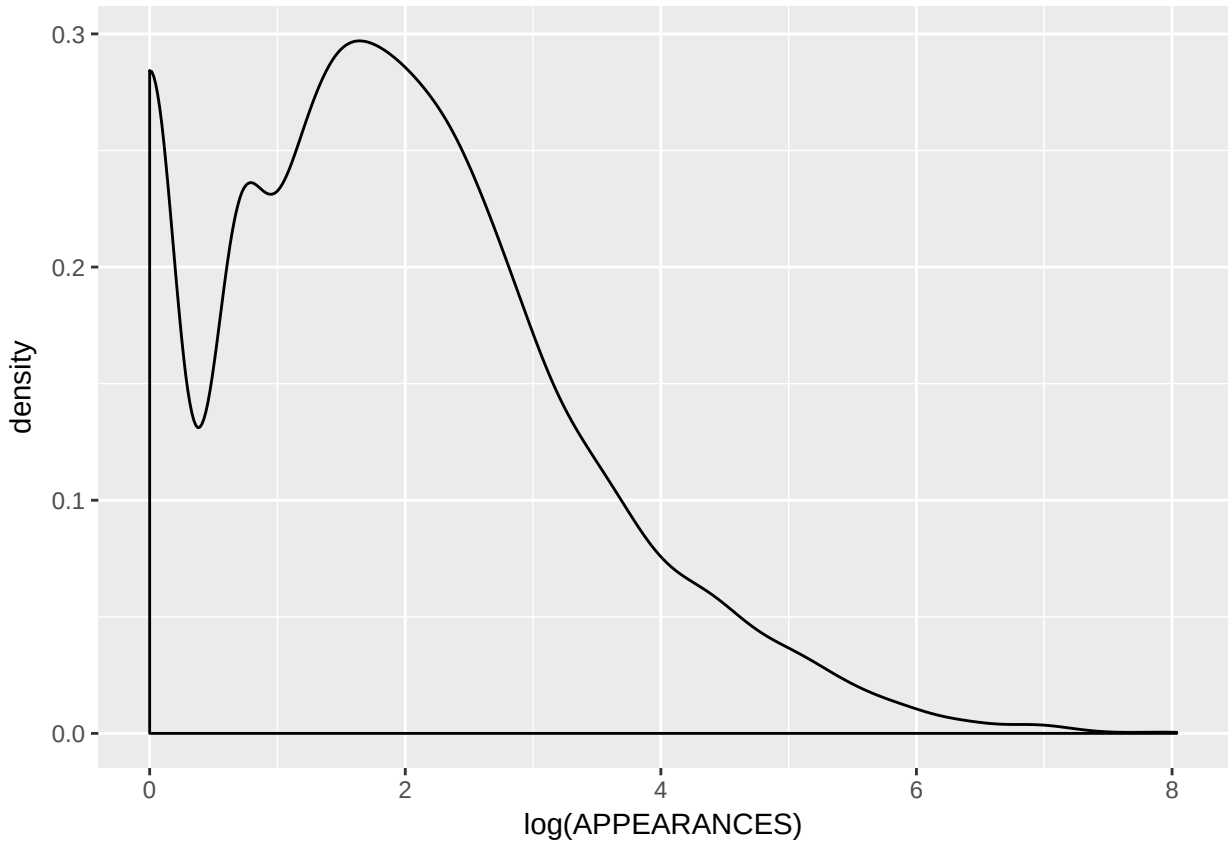
```
dc %>%
  ggplot(aes(x = APPEARANCES)) +
  geom_density()
```

```
## Warning: Removed 355 rows containing non-finite values (stat_density).
```



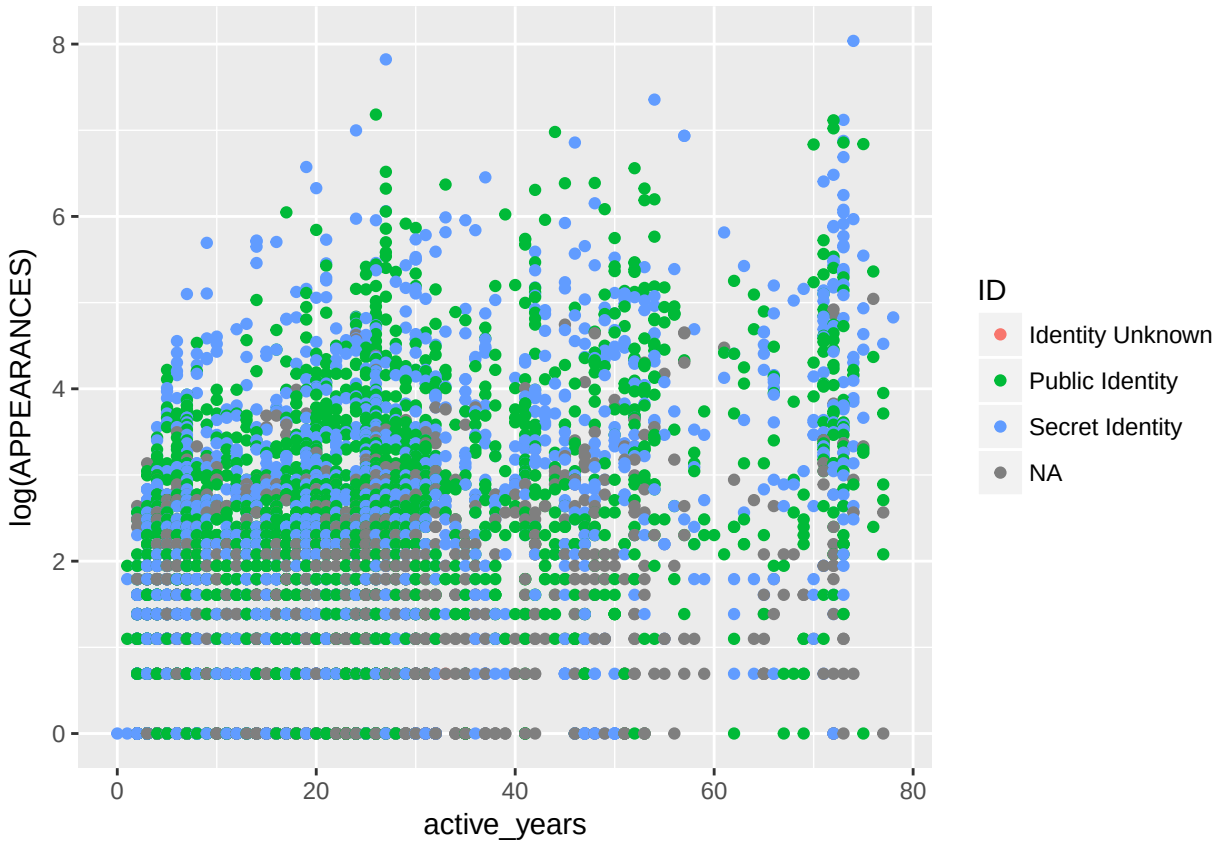

```
dc %>%
  ggplot(aes(x = log(APPEARANCES))) +
  geom_density()
```

```
## Warning: Removed 355 rows containing non-finite values (stat_density).
```




```
dc %>%
  ggplot(aes(x = active_years, y = log(APPEARANCES), col = ID)) +
  geom_point()
```

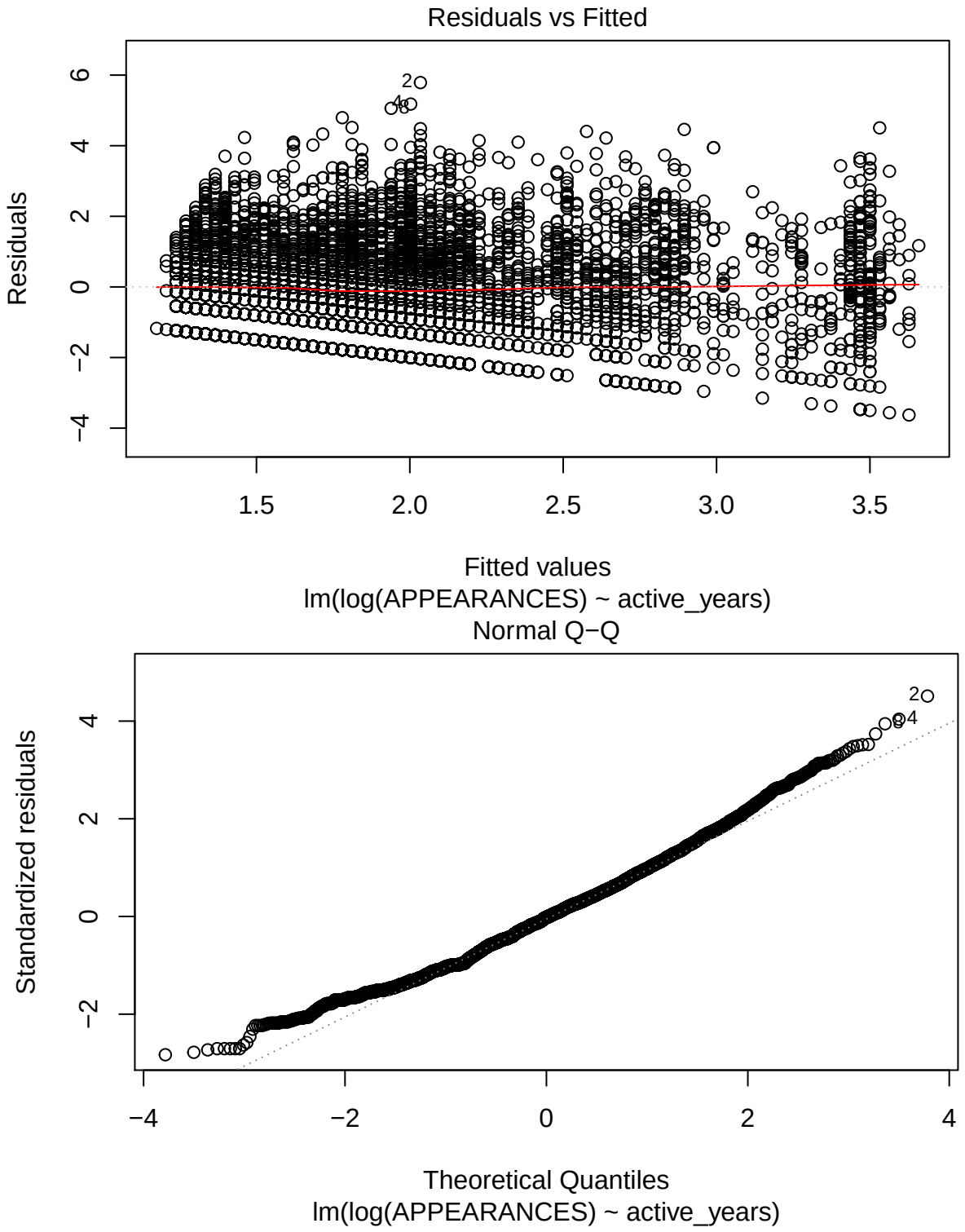
```
## Warning: Removed 415 rows containing missing values (geom_point).
```

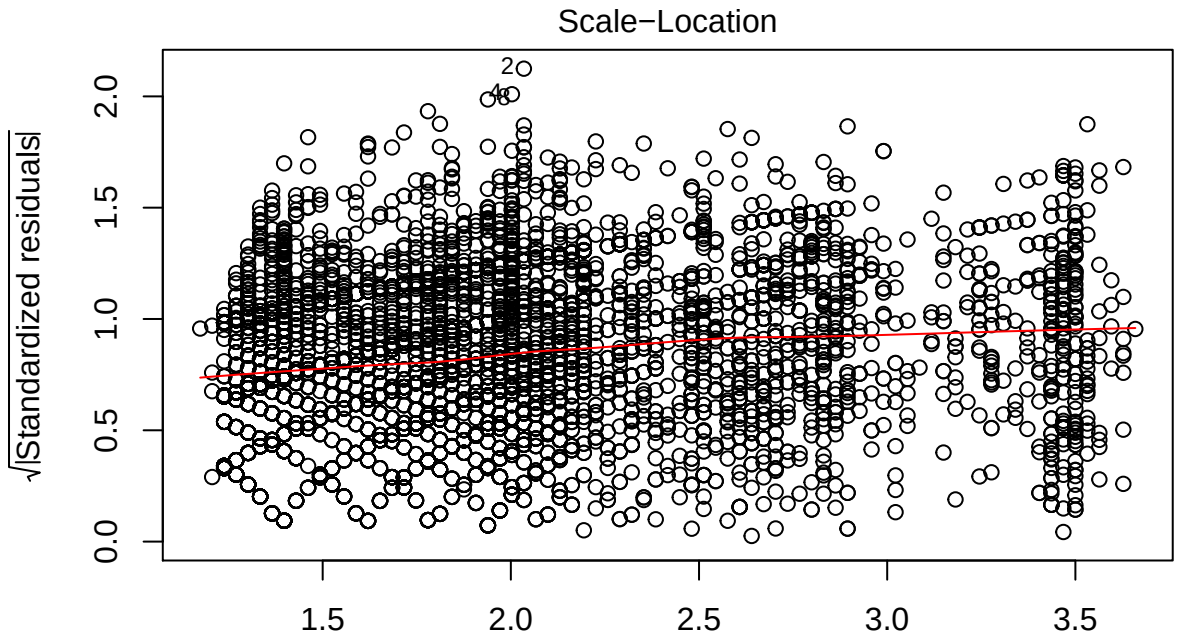


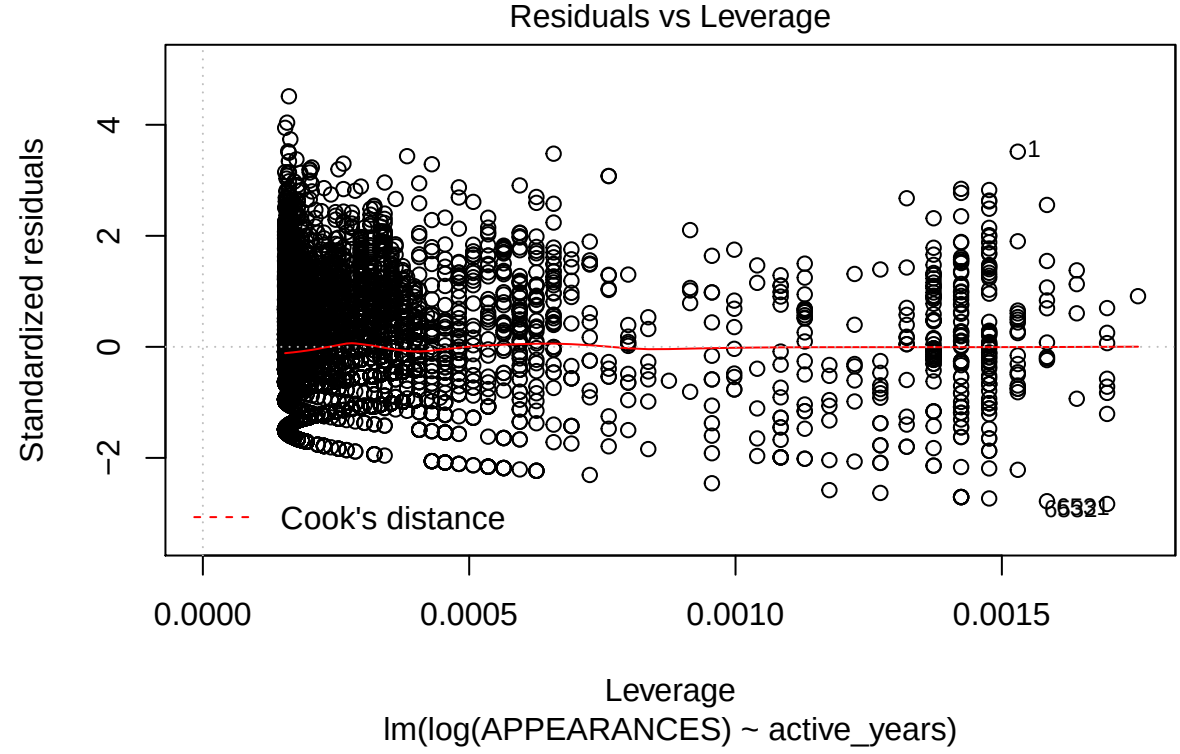

```
m2_l <- lm(data=dc, log(APPEARANCES) ~ active_years)

summary(m2_l)
```

```
##
## Call:
## lm(formula = log(APPEARANCES) ~ active_years, data = dc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.6274 -0.9350 -0.0199  0.7997  5.7878
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.1745566  0.0270642   43.40   <2e-16 ***
## active_years 0.0318549  0.0009385   33.94   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.283 on 6479 degrees of freedom
##   (415 observations deleted due to missingness)
## Multiple R-squared:  0.151,  Adjusted R-squared:  0.1508
## F-statistic:  1152 on 1 and 6479 DF,  p-value: < 2.2e-16
```

```
plot(m2_l)
```


Residuals vs Fitted
Residuals
Fitted values
lm(log(APPEARANCES) ~ active_years)
Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(log(APPEARANCES) ~ active_years)





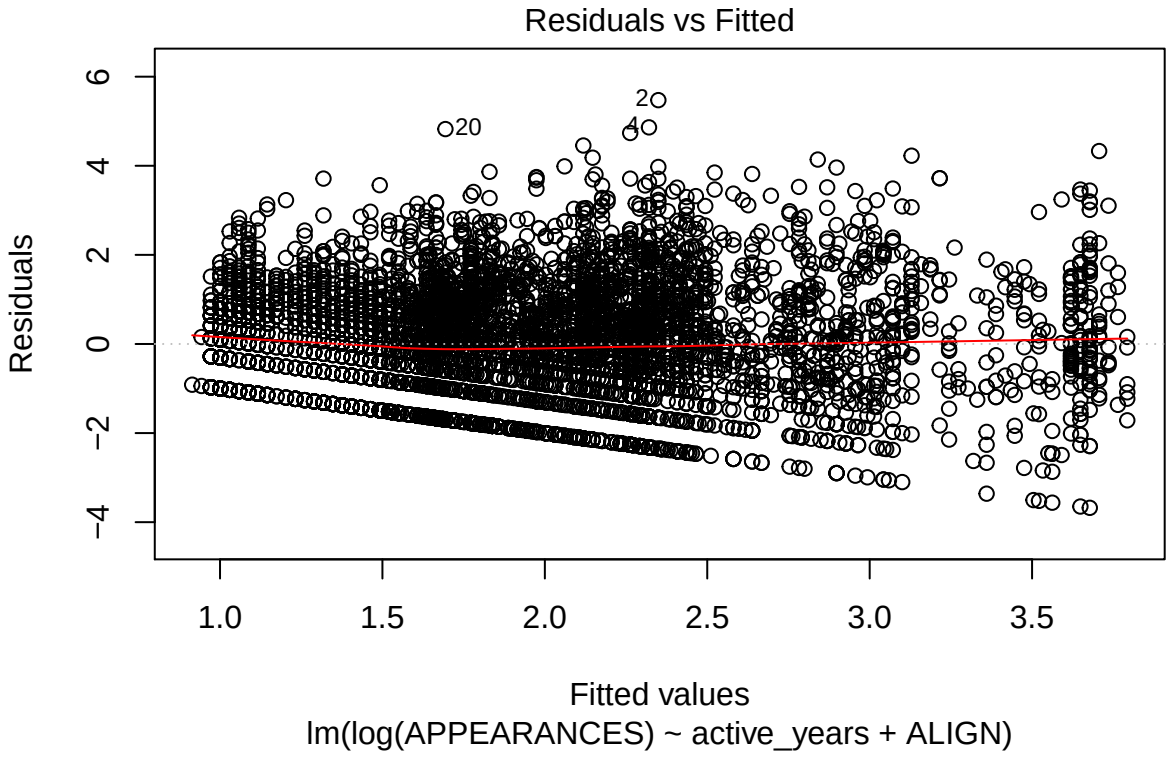
Se aggiungiamo un altro anno di attività, ci aspettiamo che il numero di apparizioni cresca del 3%

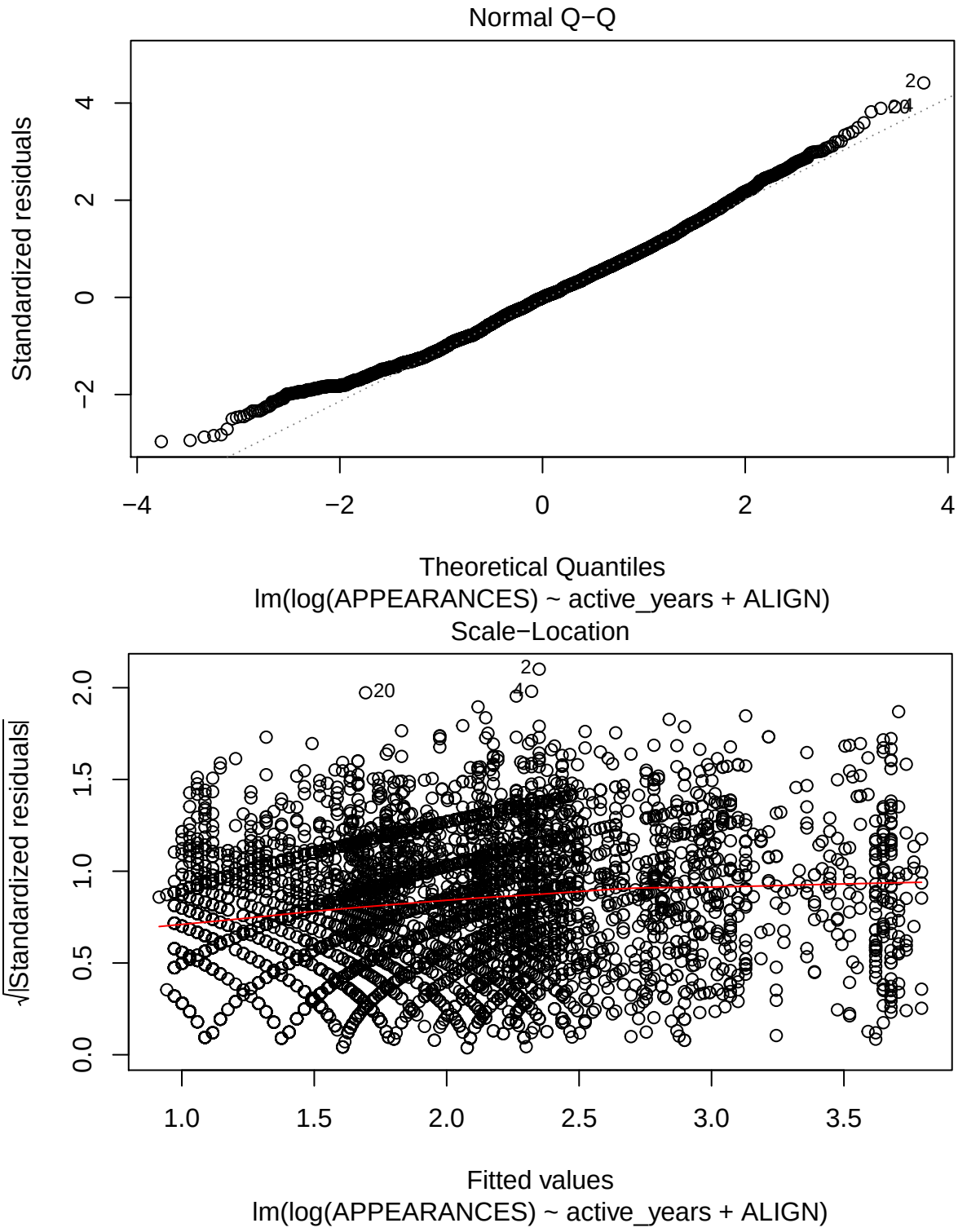
```
m3 <- lm(data=dc, log(APPEARANCES) ~ active_years + ALIGN)

summary(m3)
```

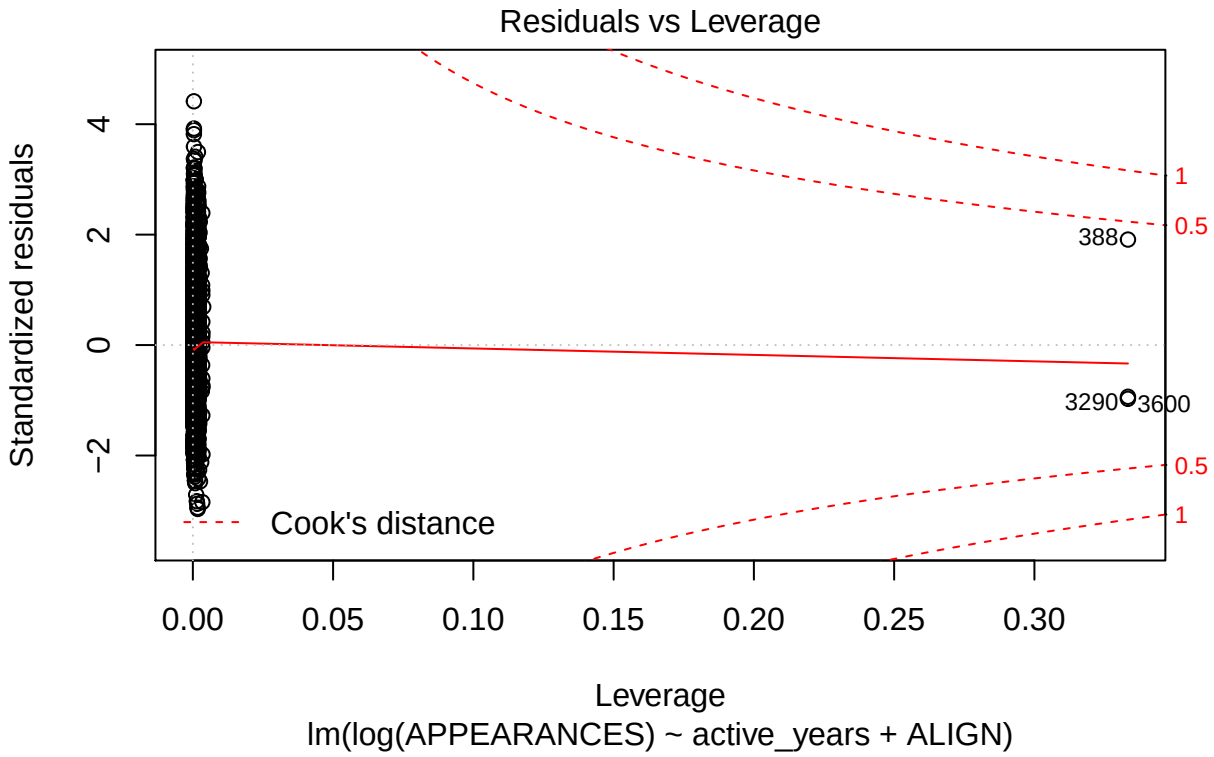
```
##
```

```
## Call:
## lm(formula = log(APPEARANCES) ~ active_years + ALIGN, data = dc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.6776 -0.9429 -0.0091  0.7971  5.4730
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)               0.9142744  0.0315861  28.945   <2e-16 ***
## active_years              0.0288729  0.0009689  29.800   <2e-16 ***
## ALIGNGood Characters      0.6555994  0.0340508  19.254   <2e-16 ***
## ALIGNNeutral Characters 0.5281561  0.0583511   9.051   <2e-16 ***
## ALIGNReformed Criminals 1.2482256  0.7163524   1.742   0.0815 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.24 on 5918 degrees of freedom
##   (973 observations deleted due to missingness)
## Multiple R-squared:  0.1936, Adjusted R-squared:  0.193
## F-statistic: 355.1 on 4 and 5918 DF,  p-value: < 2.2e-16
```

```
plot(m3)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(log(APPEARANCES) ~ active_years + ALIGN)
Scale−Location
√|Standardized residuals|
Fitted values
lm(log(APPEARANCES) ~ active_years + ALIGN)



Se aggiungiamo un altro anno di attività, ci aspettiamo che il numero di apparizioni cresca del 3%.

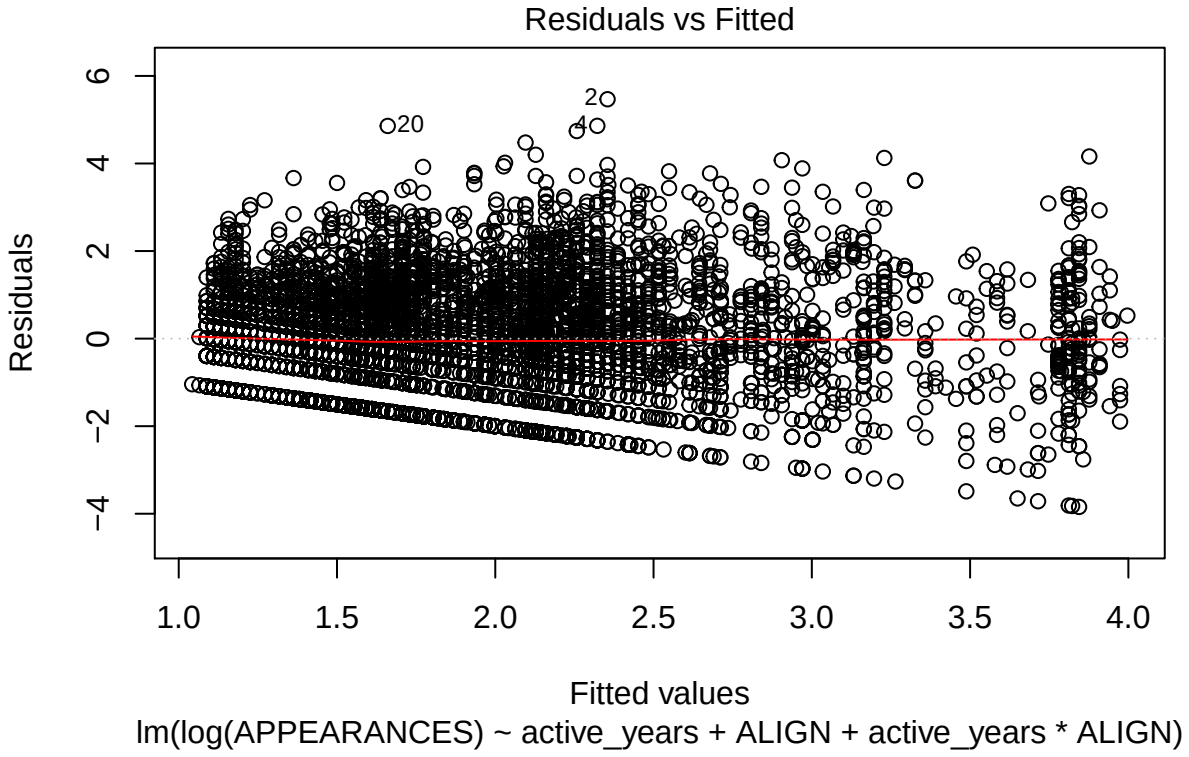
https://www.youtube.com/watch?v=wXC2kViEGz8

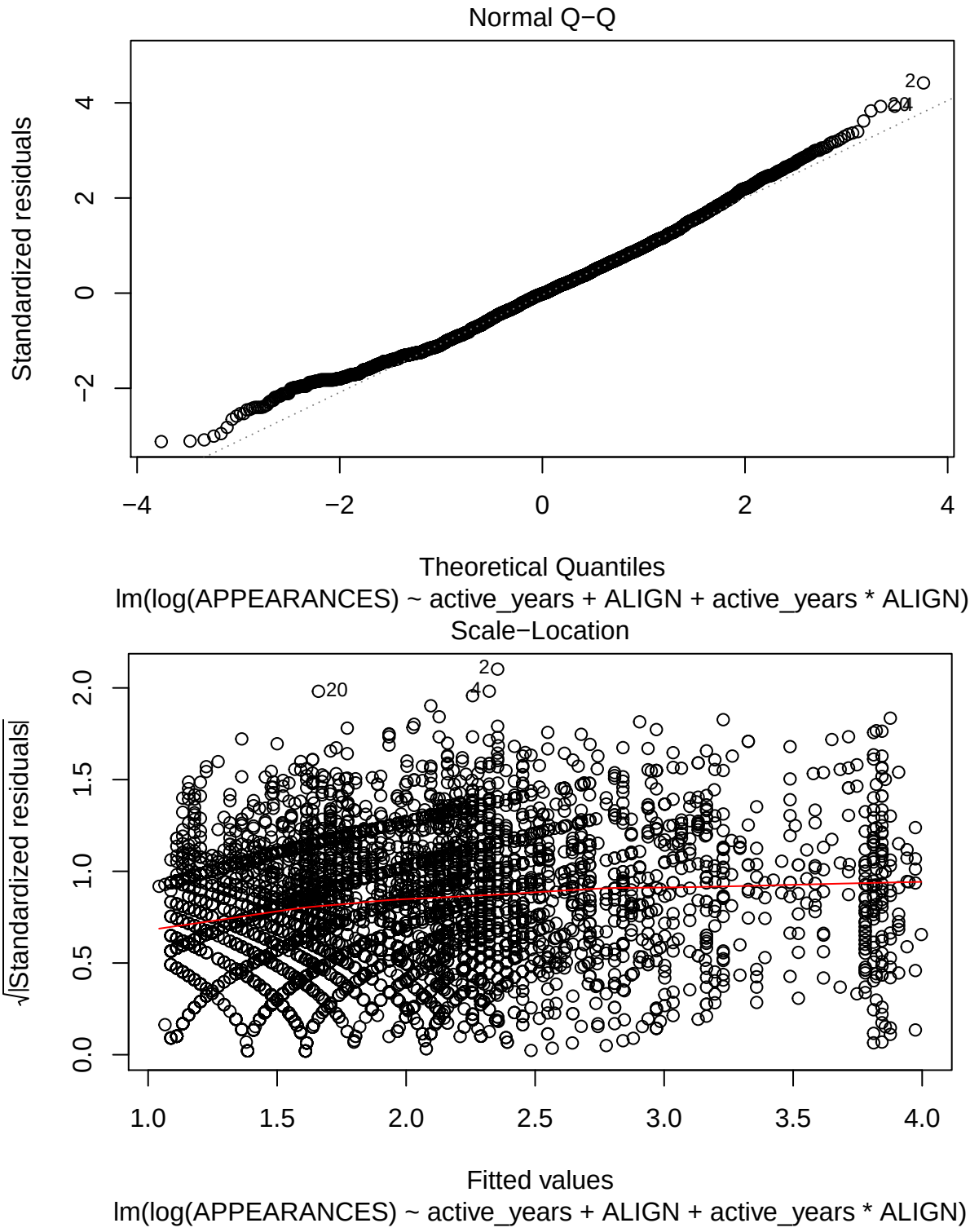
```
m4 <- lm(data=dc, log(APPEARANCES) ~ active_years + ALIGN + active_years*ALIGN)

summary(m4)
```

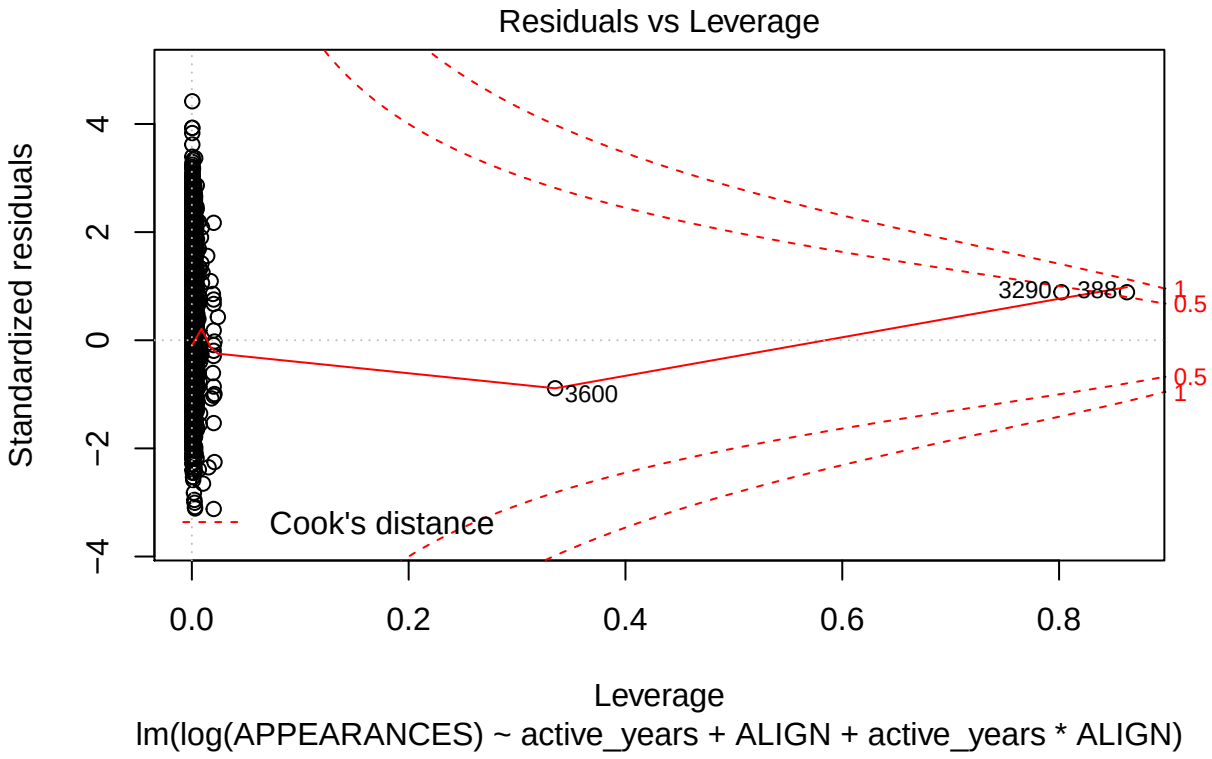
```
##
## Call:
## lm(formula = log(APPEARANCES) ~ active_years + ALIGN + active_years *
##     ALIGN, data = dc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.8442 -0.9037 -0.0126  0.8020  5.4677
##
## Coefficients:
##                                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)                            1.042552   0.040777  25.567  < 2e-16
## active_years                           0.022880   0.001548  14.782  < 2e-16
## ALIGNGood Characters                   0.437866   0.058237   7.519 6.36e-14
## ALIGNNeutral Characters                0.268121   0.099289   2.700  0.00694
## ALIGNReformed Criminals                5.071996   2.437474   2.081  0.03749
## active_years:ALIGNGood Characters      0.009501   0.002043   4.652 3.37e-06
## active_years:ALIGNNeutral Characters   0.012005   0.003685   3.258  0.00113
## active_years:ALIGNReformed Criminals -0.263465   0.158876  -1.658  0.09731
##
## (Intercept)                           ***
## active_years                          ***
## ALIGNGood Characters                  ***
```

```
## ALIGNNeutral Characters              **
## ALIGNReformed Criminals              *
## active_years:ALIGNGood Characters    ***
## active_years:ALIGNNeutral Characters **
## active_years:ALIGNReformed Criminals .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.237 on 5915 degrees of freedom
##   (973 observations deleted due to missingness)
## Multiple R-squared:  0.1974, Adjusted R-squared:  0.1964
## F-statistic: 207.8 on 7 and 5915 DF,  p-value: < 2.2e-16
```

```
plot(m4)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(log(APPEARANCES) ~ active_years + ALIGN + active_years * ALIGN)
Scale−Location
√|Standardized residuals|
Fitted values
lm(log(APPEARANCES) ~ active_years + ALIGN + active_years * ALIGN)



LOGISTIC REGRESSION

https://datascienceplus.com/perform-logistic-regression-in-r/

```
dc_class <- dc %>%
  filter((ALIGN == "Bad Characters" | ALIGN == "Good Characters") &
           (SEX == "Female Characters" | SEX == "Male Characters")) %>%
  select(name, ALIGN, SEX, APPEARANCES, active_years) %>%
  na.omit

l1 <- glm(data = dc_class, ALIGN ~ SEX, family = "binomial")

summary(l1)
```

```
##
## Call:
## glm(formula = ALIGN ~ SEX, family = "binomial", data = dc_class)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.378  -1.104  -1.104   1.253   1.253
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          0.45981    0.05364   8.572   <2e-16 ***
## SEXMale Characters -0.63598    0.06273 -10.139   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 7316.9  on 5277  degrees of freedom
## Residual deviance: 7212.0  on 5276  degrees of freedom
## AIC: 7216
##
## Number of Fisher Scoring iterations: 4
```

```
post_l1 <- predict(l1, type = "response")

ALIGN_pred <- ifelse(post_l1>0.5,  "Good Characters", "Bad  Characters")

misClasificError <- mean(ALIGN_pred != dc_class$ALIGN)
print(paste('Accuracy',1-misClasificError))
```

```
## [1] "Accuracy 0.170140204622963"
```

```
table(dc_class$ALIGN)
```

```
##
##     Bad Characters    Good Characters Neutral Characters
##               2641               2637                  0
## Reformed Criminals
##                  0
```

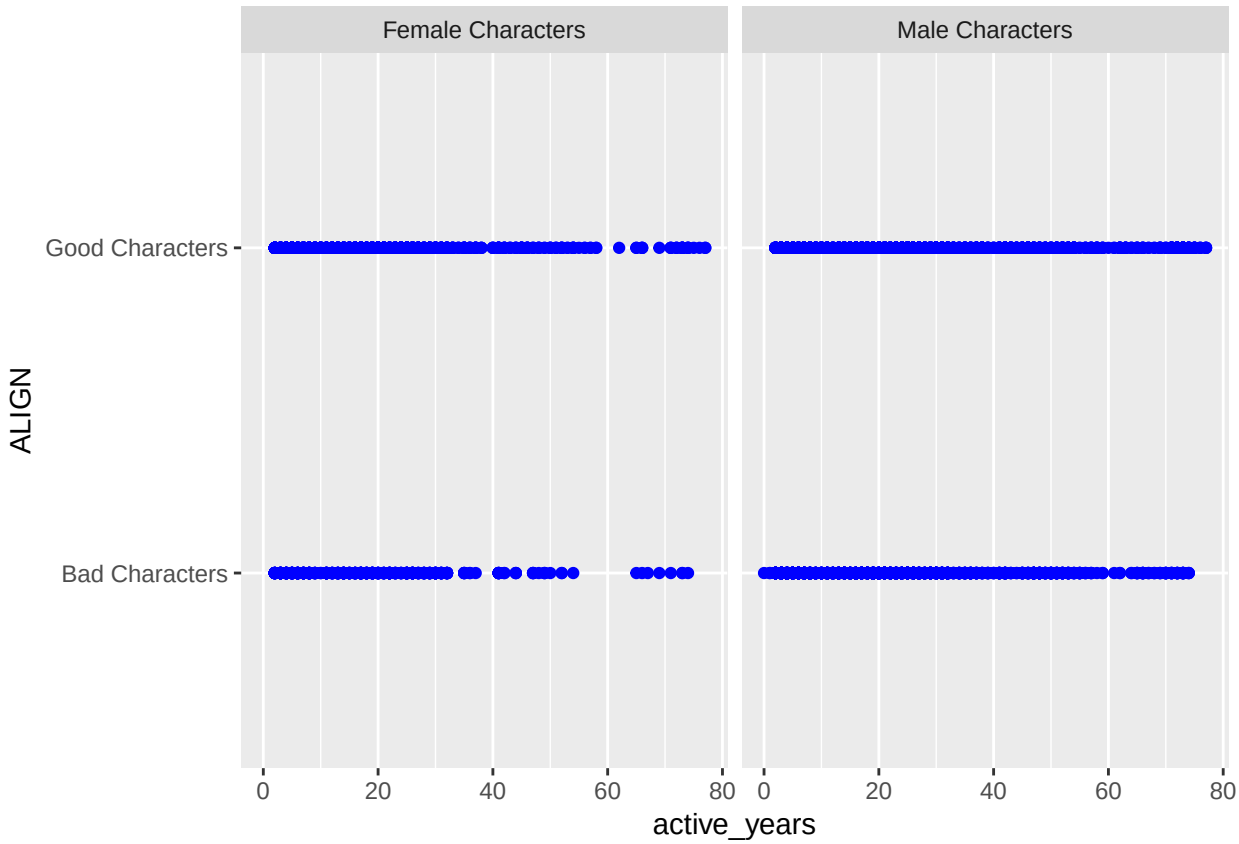
```
table(ALIGN_pred)
```

```
## ALIGN_pred
## Bad  Characters Good Characters
##            3813            1465
```

```
table(dc_class$ALIGN, ALIGN_pred)
```

```
##                     ALIGN_pred
##                      Bad  Characters Good Characters
##   Bad Characters                2074             567
##   Good Characters               1739             898
##   Neutral Characters               0               0
##   Reformed Criminals               0               0
```

```
ggp <- ggplot(data = dc_class, mapping = aes(x = active_years, y = ALIGN)) +
  geom_point(colour="blue") +
  #geom_line(mapping = aes(x = active_years, y = ALIGN), colour="red") +
  facet_wrap(facets = ~SEX)
print(ggp)
```




```
l2 <- glm(data = dc_class, ALIGN ~ SEX + active_years, family = "binomial")

summary(l2)
```

```
##
## Call:
## glm(formula = ALIGN ~ SEX + active_years, family = "binomial",
##     data = dc_class)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.7874  -1.1054  -0.9442   1.1572   1.4225
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          0.122198   0.063490   1.925   0.0543 .
## SEXMale Characters -0.715899   0.063810 -11.219   <2e-16 ***
## active_years         0.016877   0.001713   9.851   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 7316.9  on 5277  degrees of freedom
## Residual deviance: 7111.5  on 5275  degrees of freedom
## AIC: 7117.5
##
```

```
## Number of Fisher Scoring iterations: 4
```

```
post_l2 <- predict(l2, type = "response")

ALIGN_pred_l2 <- ifelse(post_l2>0.5,  "Good Characters", "Bad  Characters")

misClasificError <- mean(ALIGN_pred_l2 != dc_class$ALIGN)
print(paste('Accuracy',1-misClasificError))
```

```
## [1] "Accuracy 0.255778704054566"
```

```
table(dc_class$ALIGN, ALIGN_pred_l2)
```

```
##                     ALIGN_pred_l2
##                      Bad  Characters Good Characters
##   Bad Characters                1723              918
##   Good Characters               1287             1350
##   Neutral Characters               0                0
##   Reformed Criminals               0                0
```

```
anova(l2, test="Chisq")
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: ALIGN
##
## Terms added sequentially (first to last)
##
##
##              Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                          5277     7316.9
## SEX           1   104.90      5276     7212.0 < 2.2e-16 ***
## active_years  1   100.47      5275     7111.5 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
l3 <- glm(data = dc_class, ALIGN ~ SEX + active_years + APPEARANCES, family = "binomial")
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
summary(l3)
```

```
##
## Call:
## glm(formula = ALIGN ~ SEX + active_years + APPEARANCES, family = "binomial",
##     data = dc_class)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.3715  -1.0378  -0.9422   1.1578   1.4308
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          0.068231   0.064948   1.051    0.293
## SEXMale Characters -0.676379   0.064748 -10.446  < 2e-16 ***
## active_years         0.007528   0.001866   4.036 5.45e-05 ***
```

```
## APPEARANCES         0.014712   0.001346  10.929  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 7316.9  on 5277  degrees of freedom
## Residual deviance: 6888.4  on 5274  degrees of freedom
## AIC: 6896.4
##
## Number of Fisher Scoring iterations: 6
```

```
post_l3 <- predict(l3, type = "response")

ALIGN_pred_l3 <- ifelse(post_l3>0.5,  "Good Characters", "Bad  Characters")

misClasificError <- mean(ALIGN_pred_l3 != dc_class$ALIGN)
print(paste('Accuracy',1-misClasificError))
```

```
## [1] "Accuracy 0.257104964001516"
```

```
table(dc_class$ALIGN, ALIGN_pred_l3)
```

```
##                     ALIGN_pred_l3
##                      Bad  Characters Good Characters
##   Bad Characters                1862             779
##   Good Characters               1280            1357
##   Neutral Characters               0               0
##   Reformed Criminals               0               0
```

```
anova(l3, test="Chisq")
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: ALIGN
##
## Terms added sequentially (first to last)
##
##
##              Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                          5277     7316.9
## SEX           1   104.90      5276     7212.0 < 2.2e-16 ***
## active_years  1   100.47      5275     7111.5 < 2.2e-16 ***
## APPEARANCES   1   223.06      5274     6888.4 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DECISION TREE

https://gormanalysis.com/decision-trees-in-r-using-rpart/

```
library(rpart)
```

```r
table(iris$Species)
```

```
##
##     setosa versicolor  virginica
##         50         50         50
```

```r
iris_tree <- rpart(Species ~ ., method = "class", data = iris)

print(iris_tree)
```

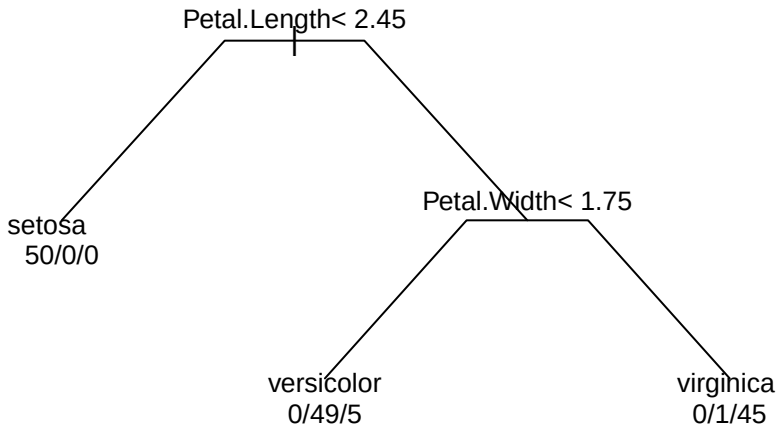
```
## n= 150
##
## node), split, n, loss, yval, (yprob)
##       * denotes terminal node
##
## 1) root 150 100 setosa (0.33333333 0.33333333 0.33333333)
##   2) Petal.Length< 2.45 50   0 setosa (1.00000000 0.00000000 0.00000000) *
##   3) Petal.Length>=2.45 100  50 versicolor (0.00000000 0.50000000 0.50000000)
##     6) Petal.Width< 1.75 54   5 versicolor (0.00000000 0.90740741 0.09259259) *
##     7) Petal.Width>=1.75 46   1 virginica (0.00000000 0.02173913 0.97826087) *
```

```r
summary(iris_tree)
```

```
## Call:
## rpart(formula = Species ~ ., data = iris, method = "class")
##   n= 150
##
##     CP nsplit rel error xerror       xstd
## 1 0.50      0      1.00   1.18 0.05017303
## 2 0.44      1      0.50   0.62 0.06031031
## 3 0.01      2      0.06   0.11 0.03192700
##
## Variable importance
##  Petal.Width Petal.Length Sepal.Length  Sepal.Width
##           34           31           21           14
##
## Node number 1: 150 observations,    complexity param=0.5
##   predicted class=setosa      expected loss=0.6666667  P(node) =1
##     class counts:    50    50    50
##    probabilities: 0.333 0.333 0.333
##   left son=2 (50 obs) right son=3 (100 obs)
##   Primary splits:
##       Petal.Length < 2.45 to the left,  improve=50.00000, (0 missing)
##       Petal.Width  < 0.8  to the left,  improve=50.00000, (0 missing)
##       Sepal.Length < 5.45 to the left,  improve=34.16405, (0 missing)
##       Sepal.Width  < 3.35 to the right, improve=19.03851, (0 missing)
##   Surrogate splits:
##       Petal.Width  < 0.8  to the left,  agree=1.000, adj=1.00, (0 split)
##       Sepal.Length < 5.45 to the left,  agree=0.920, adj=0.76, (0 split)
##       Sepal.Width  < 3.35 to the right, agree=0.833, adj=0.50, (0 split)
##
## Node number 2: 50 observations
##   predicted class=setosa      expected loss=0  P(node) =0.3333333
##     class counts:    50     0     0
##    probabilities: 1.000 0.000 0.000
```

```
##
## Node number 3: 100 observations,    complexity param=0.44
##   predicted class=versicolor  expected loss=0.5  P(node) =0.6666667
##     class counts:     0    50    50
##    probabilities: 0.000 0.500 0.500
##   left son=6 (54 obs) right son=7 (46 obs)
##   Primary splits:
##       Petal.Width  < 1.75 to the left,  improve=38.969400, (0 missing)
##       Petal.Length < 4.75 to the left,  improve=37.353540, (0 missing)
##       Sepal.Length < 6.15 to the left,  improve=10.686870, (0 missing)
##       Sepal.Width  < 2.45 to the left,  improve= 3.555556, (0 missing)
##   Surrogate splits:
##       Petal.Length < 4.75 to the left,  agree=0.91, adj=0.804, (0 split)
##       Sepal.Length < 6.15 to the left,  agree=0.73, adj=0.413, (0 split)
##       Sepal.Width  < 2.95 to the left,  agree=0.67, adj=0.283, (0 split)
##
## Node number 6: 54 observations
##   predicted class=versicolor  expected loss=0.09259259  P(node) =0.36
##     class counts:     0    49     5
##    probabilities: 0.000 0.907 0.093
##
## Node number 7: 46 observations
##   predicted class=virginica   expected loss=0.02173913  P(node) =0.3066667
##     class counts:     0     1    45
##    probabilities: 0.000 0.022 0.978
```

```
plot(iris_tree, compress = T, margin = 0.2, branch = 0.3)
text(iris_tree, use.n = T, digits = 3, cex = 0.8)
```




```
printcp(iris_tree)
```

```
##
## Classification tree:
## rpart(formula = Species ~ ., data = iris, method = "class")
##
## Variables actually used in tree construction:
## [1] Petal.Length Petal.Width
##
## Root node error: 100/150 = 0.66667
##
## n= 150
```

```
##
##     CP nsplit rel error xerror     xstd
## 1 0.50      0      1.00   1.18 0.050173
## 2 0.44      1      0.50   0.62 0.060310
## 3 0.01      2      0.06   0.11 0.031927
```

```
iris_pred <- predict(iris_tree, type = "class")

table(iris_pred, iris$Species)
```

```
##
## iris_pred    setosa versicolor virginica
##   setosa         50          0         0
##   versicolor      0         49         5
##   virginica       0          1        45
```

```
misClasificError <- mean(iris_pred != iris$Species)
print(paste('Accuracy',1-misClasificError))
```

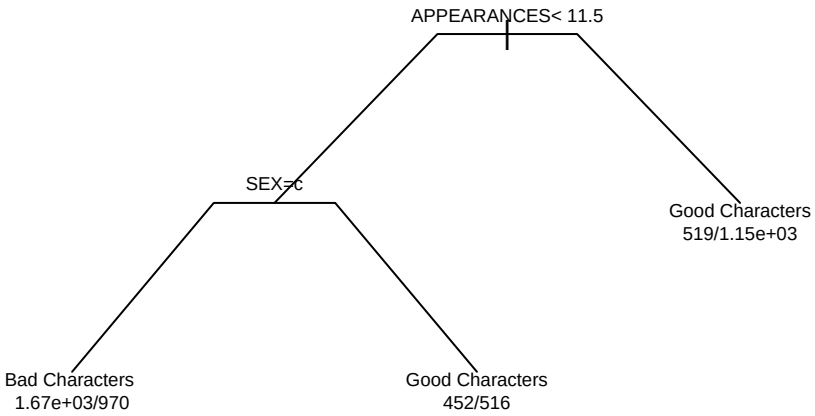
```
## [1] "Accuracy 0.96"
```

```
align_tree <- rpart(ALIGN ~ SEX + active_years + APPEARANCES, method = "class", data = dc_class)

summary(align_tree)
```

```
## Call:
## rpart(formula = ALIGN ~ SEX + active_years + APPEARANCES, data = dc_class,
##     method = "class")
##   n= 5278
##
##          CP nsplit rel error    xerror       xstd
## 1 0.2396663      0 1.0000000 1.0303375 0.01376908
## 2 0.0242700      1 0.7603337 0.7701934 0.01340452
## 3 0.0100000      2 0.7360637 0.7561623 0.01335732
##
## Variable importance
##  APPEARANCES          SEX active_years
##           75           16            9
##
## Node number 1: 5278 observations,    complexity param=0.2396663
##   predicted class=Bad Characters   expected loss=0.4996211  P(node) =1
##     class counts:  2641  2637
##    probabilities: 0.500 0.500
##   left son=2 (3608 obs) right son=3 (1670 obs)
##   Primary splits:
##       APPEARANCES  < 11.5 to the left,  improve=175.64190, (0 missing)
##       SEX          splits as  R-L-,     improve= 52.10742, (0 missing)
##       active_years < 22.5 to the left,  improve= 35.48814, (0 missing)
##   Surrogate splits:
##       active_years < 39.5 to the left,  agree=0.722, adj=0.12, (0 split)
##
## Node number 2: 3608 observations,    complexity param=0.02427
##   predicted class=Bad Characters   expected loss=0.4118625  P(node) =0.6835923
##     class counts:  2122  1486
##    probabilities: 0.588 0.412
##   left son=4 (2640 obs) right son=5 (968 obs)
```

```
##   Primary splits:
##       SEX          splits as  R-L-,     improve=38.86330, (0 missing)
##       APPEARANCES  < 4.5  to the left,  improve=20.28753, (0 missing)
##       active_years < 22.5 to the left,  improve=14.12867, (0 missing)
##
## Node number 3: 1670 observations
##   predicted class=Good Characters  expected loss=0.3107784  P(node) =0.3164077
##     class counts:   519  1151
##    probabilities: 0.311 0.689
##
## Node number 4: 2640 observations
##   predicted class=Bad Characters   expected loss=0.3674242  P(node) =0.5001895
##     class counts:  1670   970
##    probabilities: 0.633 0.367
##
## Node number 5: 968 observations
##   predicted class=Good Characters  expected loss=0.4669421  P(node) =0.1834028
##     class counts:   452   516
##    probabilities: 0.467 0.533
```

```
plot(align_tree, uniform = T, compress = T, margin = 0.2, branch = 0.3)
text(align_tree, use.n = T, digits = 3, cex = 0.6)
```




```
align_pred_tree <- predict(align_tree, type = "class")

table(align_pred_tree, dc_class$ALIGN)
```

```
##
## align_pred_tree      Bad Characters Good Characters Neutral Characters
##   Bad Characters               1670             970                   0
##   Good Characters               971            1667                   0
##   Neutral Characters              0               0                   0
##   Reformed Criminals              0               0                   0
##
## align_pred_tree      Reformed Criminals
##   Bad Characters                     0
##   Good Characters                    0
##   Neutral Characters                 0
##   Reformed Criminals                 0
```

```
misClasificError <- mean(align_pred_tree != dc_class$ALIGN)
print(paste('Accuracy',1-misClasificError))
```

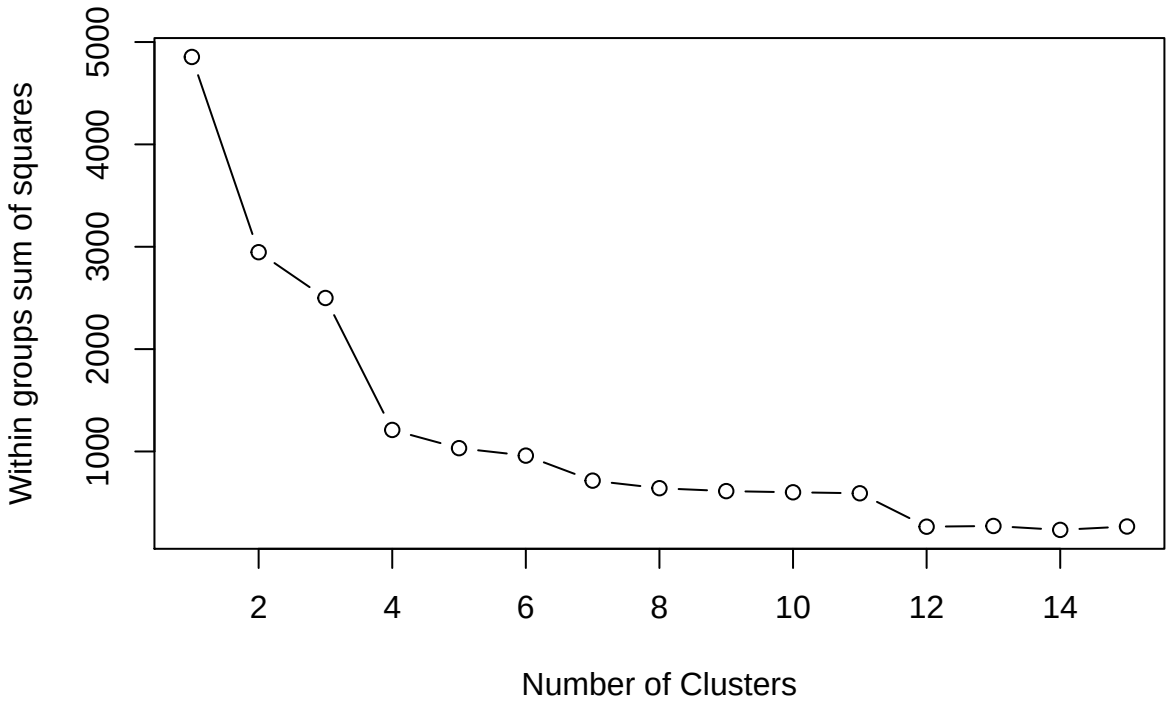
```
## [1] "Accuracy 0.632247063281546"
```

Training and test dataset

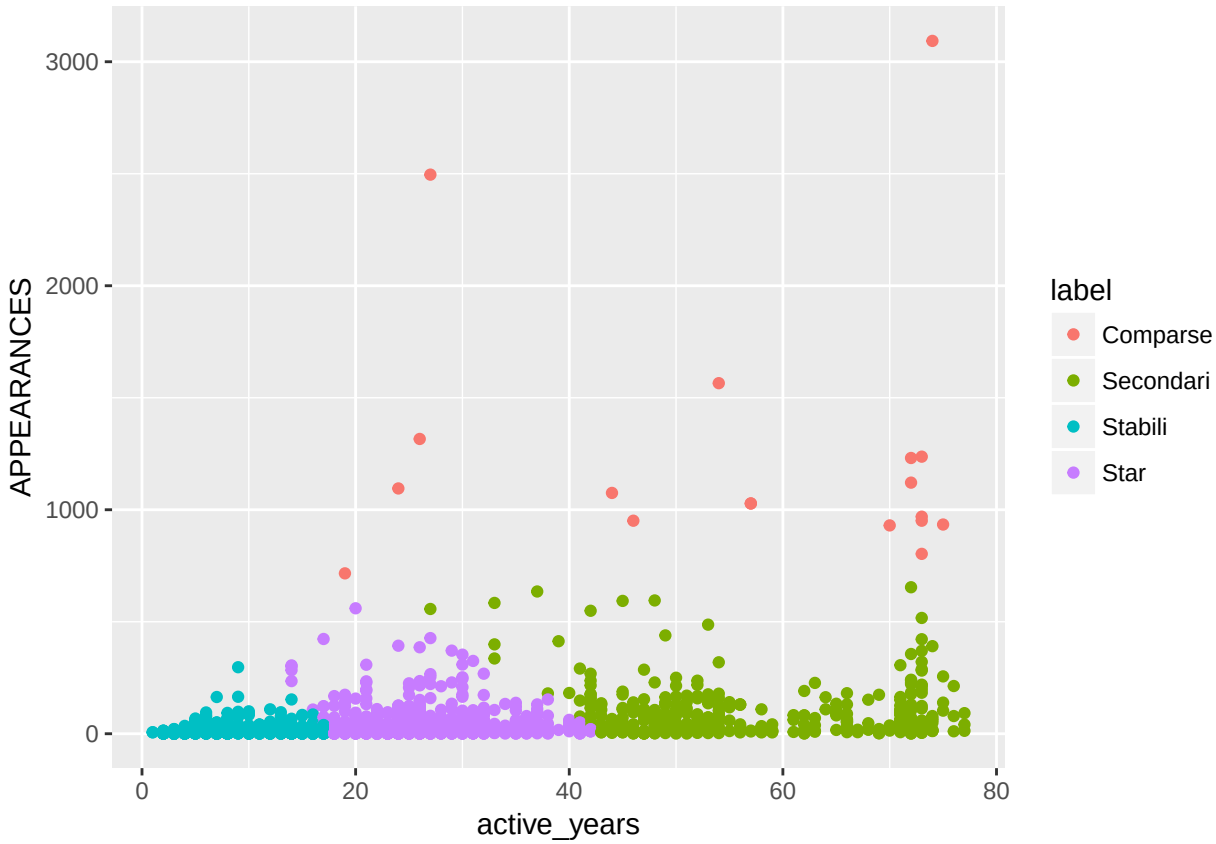
```
train <- sample(nrow(dc_class), 4800)
dc_train <- dc_class[train,]
dc_test <- dc_class[-train,]
```

CLUSTER

```
dc_full <- dc %>%
  select(name, ALIGN, EYE, HAIR, SEX, ALIVE, APPEARANCES, active_years, YEAR) %>%
  na.omit()

dc_cluster <-dc_full %>%
  select(active_years, APPEARANCES) %>%
  scale() %>%
  as.data.frame()


# Finding cluster number through Within groups sum of squares
wss <- (nrow(dc_cluster)-1)*sum(apply(dc_cluster,2,var))
for (i in 2:15){
  wss[i] <- sum(kmeans(dc_cluster, centers=i)$withinss)
  }
plot(1:15, wss, type="b", xlab="Number of Clusters", ylab="Within groups sum of squares")
```



```r
# Let's try 4

set.seed(1234)

# K-Means Cluster Analysis
fit <- kmeans(dc_cluster, 4) # 4 cluster solution
# append cluster assignment
dc_full <- data.frame(dc_full, cluster = as.factor(fit$cluster))




# CLUSTERS MEANS

# Stats
cluster_stats <- dc_full %>%
  group_by(cluster) %>%
  summarise(count = n(),
            perc = paste0(round(n()/nrow(dc_full)*100,2),"%"),
            avg_appear = mean(APPEARANCES),
            avg_year = mean(active_years))

### LABELS MAY BE DIFFERENT!!

dc_full <- dc_full %>%
  mutate(label = case_when(
    cluster == 1 ~ "Stabili",
    cluster == 2 ~ "Star",
    cluster == 3 ~ "Comparse",
    cluster == 4 ~ "Secondari"
  ))

ggplot(data = dc_full, aes(x = active_years, y = APPEARANCES, col = label)) +
  geom_point()
```




```
star <- dc_full %>%
  filter(label == "Star")
```