

Model Evaluation

Contents

Overview	1
Overall Model	2
Transformation of Response Variable	3
Evaluate the Fit of the Model	5
TELEVOTE MODEL	19
Transformation of Response Variable	19
Evaluate the Fit of the Model	21
JURY MODEL	32
Transformation of Response Variable	33
Evaluate the Fit of the Model	34

Overview

This section evaluates the fit of the model's using the car package MLR requires the residuals to be $\sim \text{IID } N(0, \sigma^2)$ the residuals will be standardized for the assessment Normality Assumptions will be accessed using: i. Normality tests from the nortest package ii. Visualizations such as histograms, QQ-plots, Residual Plots and Add Variable Plots Constant Variance will be accessed using: i. non-constant variance test Multi-collinearity will be accessed using: i. variance inflation factors Outliers will be accessed using: i. Cooks Distance

```
# load relevant libraries
library(rmarkdown)
library(knitr)
library(car)
```

```
## Loading required package: carData
```

```
library(MASS)
library(nortest)
library(lmtest)
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##   as.Date, as.Date.numeric
```

```
library(dplyr)
```

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

```
## The following object is masked from 'package:MASS':
##
##   select
```

```
## 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
```

```
##-- Data --#
```

```
# load in the historic voting data for deriving the voting blocs
processed_data <- read.csv(file = "./data/processed_data.csv", header = T)
# split the televote data
televote_data <- processed_data %>% filter(Voting_Method_J == 0)
# split out the jury vote data
jury_data <- processed_data %>% filter(Voting_Method_J == 1)
```

Overall Model

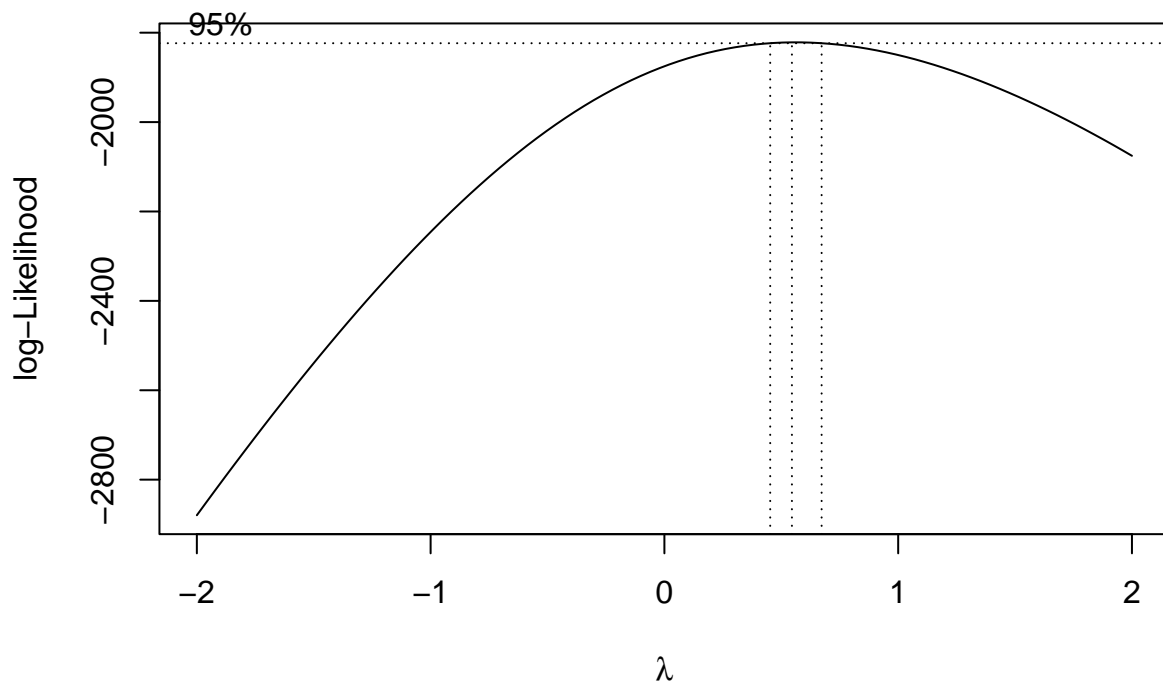
```
# load final overall model
my_model_overall <- readRDS("./models/overall_final_model.RDS")
# extract out the model coefficients
overall_model_coef <- names(my_model_overall$coefficients)[-1]
# recreate the model formula
overall_final_model_form <- as.formula(paste('Points ~', paste(overall_model_coef, collapse = ' + ')))
# generate model summary
summary(my_model_overall)
```

```
##
## Call:
## lm(formula = overall_final_model_form, data = processed_data)
##
```

```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -9.5505 -2.3301 -0.2858  2.1846  7.8517
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.7244     0.6169   6.037 2.64e-09 ***
## Average_Points    0.4798     0.1253   3.830 0.000141 ***
## acousticness      0.6959     0.1302   5.344 1.26e-07 ***
## speechiness       0.6973     0.1362   5.119 4.05e-07 ***
## METRIC_Citizens   0.3251     0.1399   2.324 0.020438 *
## TC_PerfType_Solo  1.4412     0.5613   2.568 0.010457 *
## key_0             1.2923     0.4516   2.861 0.004353 **
## CAP_DIST_km       0.2956     0.1280   2.309 0.021260 *
## OOA               1.2837     0.4512   2.845 0.004579 **
## FC_NonCOB         0.3604     0.1391   2.592 0.009766 **
## ComSONGLAN        0.2760     0.1287   2.145 0.032338 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.074 on 647 degrees of freedom
## Multiple R-squared:  0.1762, Adjusted R-squared:  0.1635
## F-statistic: 13.84 on 10 and 647 DF, p-value: < 2.2e-16
```

Transformation of Response Variable

```
# Apply box-cox transformation on the model to improve the normality assumptions
# box-cox transformation using car
bct <- MASS::boxcox(object = my_model_overall)
```



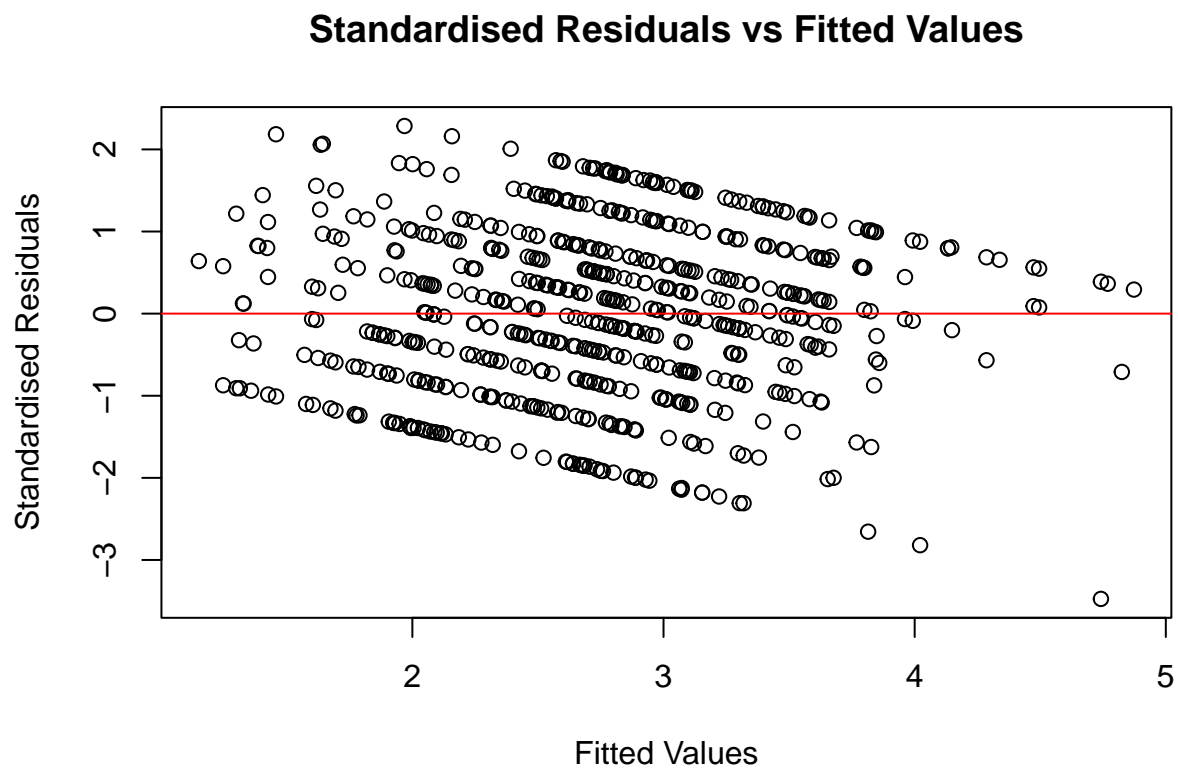
```
# find optimal box-cox power transformation power
p <- bct$x[which.max(x = bct$y)]
# transform points using the optimal power transformation
bctPoints <- (((processed_data$Points)^p) - 1)/(p)
# recreate the model formula
overall_final_model_bct_form<- as.formula(paste('bctPoints ~', paste(overall_model_coeff, collapse = ' + ')))
# refit final model with with box-cox power transformation
my_model_overall <- lm(formula = overall_final_model_bct_form, data = processed_data)
# generate model summary
summary(my_model_overall)
```

```
##
## Call:
## lm(formula = overall_final_model_bct_form, data = processed_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.7417 -1.0276  0.0449  1.1112  3.3083
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.71220    0.29239   5.856 7.55e-09 ***
## Average_Points  0.20209    0.05938   3.403 0.000706 ***
## acousticness    0.34061    0.06173   5.518 4.96e-08 ***
## speechiness     0.33666    0.06456   5.215 2.48e-07 ***
## METRIC_Citizens 0.12269    0.06630   1.851 0.064672 .
```

```
## TC_PerfType_Solo 0.69660 0.26601 2.619 0.009035 **
## key_0 0.65422 0.21405 3.056 0.002332 **
## CAP_DIST_km 0.12426 0.06069 2.048 0.041007 *
## OOA 0.62781 0.21385 2.936 0.003446 **
## FC_NonCOB 0.18387 0.06591 2.790 0.005428 **
## ComSONGLAN 0.14046 0.06099 2.303 0.021585 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.457 on 647 degrees of freedom
## Multiple R-squared: 0.169, Adjusted R-squared: 0.1562
## F-statistic: 13.16 on 10 and 647 DF, p-value: < 2.2e-16
```

Evaluate the Fit of the Model

```
# create standardize residuals
sresid <- studres(my_model_overall)
# Residual vs fits plot
plot(x = my_model_overall$fitted.values, y = sresid, main = "Standardised Residuals vs Fitted Values",
# add red horizontal line through y-axis 0
abline(h = 0, col = "red"))
```



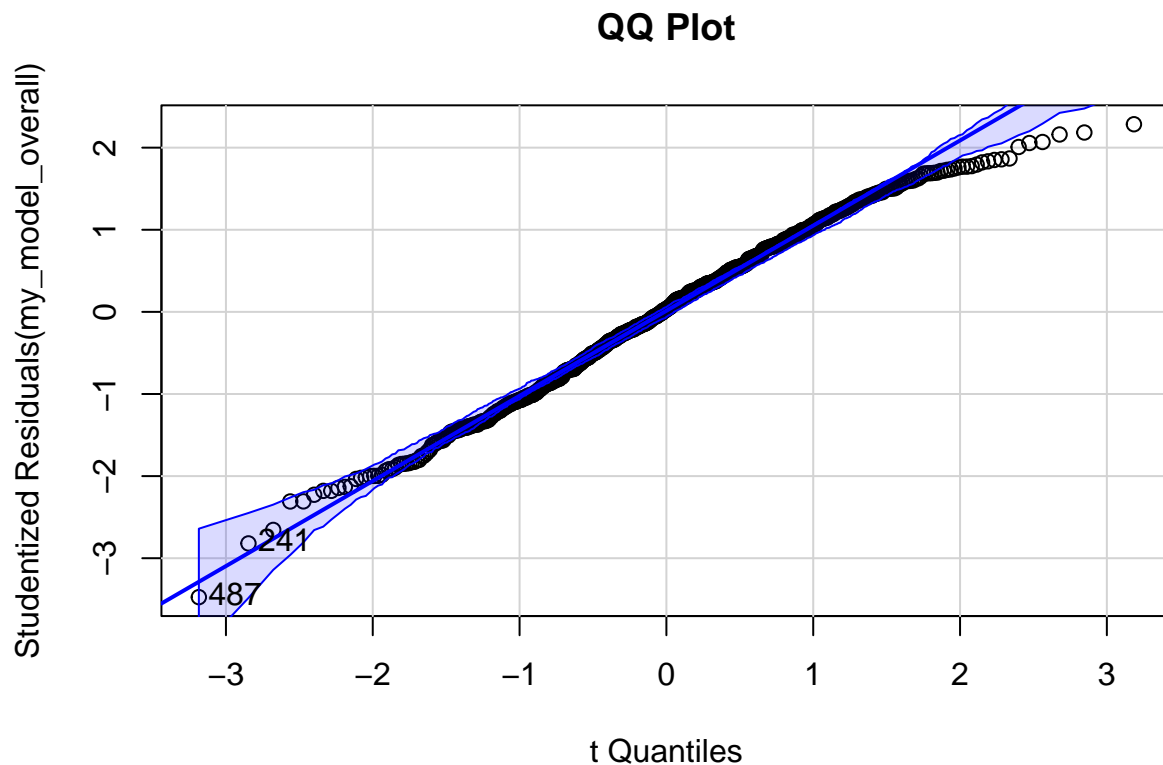
```
# Assessing Outliers
# Bonferonni p-value for most extreme obs
outlierTest(my_model_overall)
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 487 -3.473914      0.00054721      0.36006
```

```
# final outlier residuals
which(sresid < -2)
```

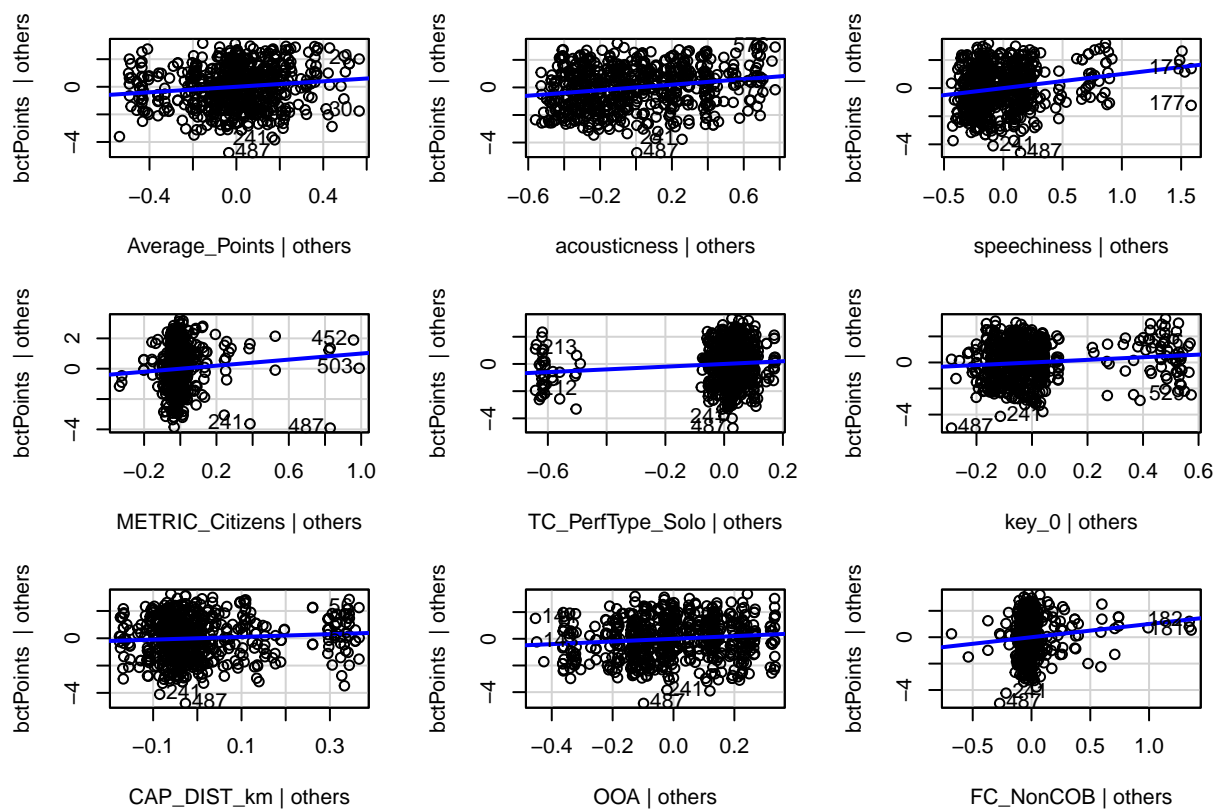
```
## 39 77 103 177 241 360 464 487 516 529 531 535 536 618
## 39 77 103 177 241 360 464 487 516 529 531 535 536 618
```

```
# qq-plot for studentized residuals
qqPlot(my_model_overall, main = "QQ Plot")
```

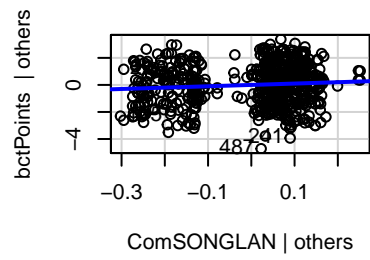


```
## [1] 241 487
```

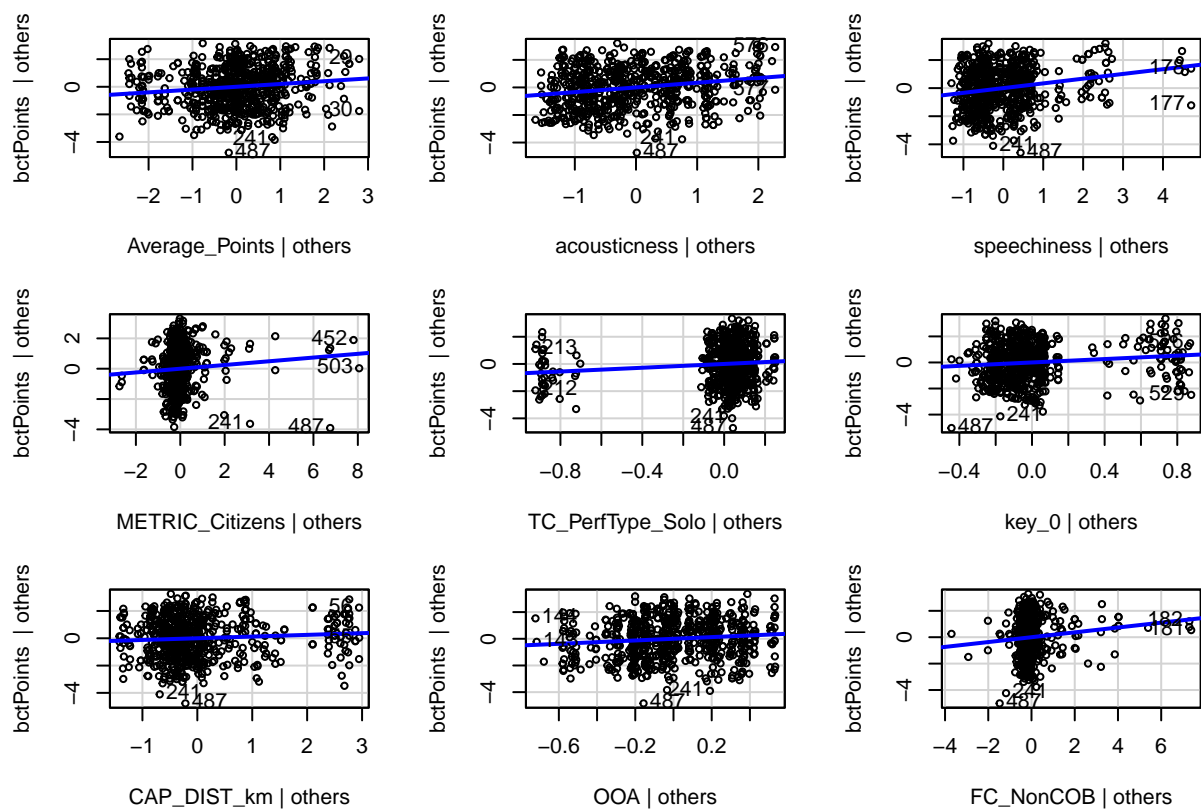
```
# leverage plots
leveragePlots(my_model_overall)
```



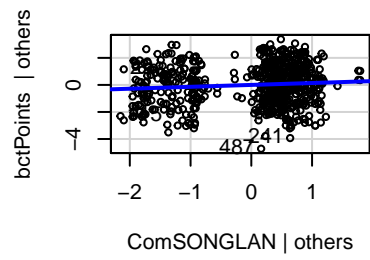
Leverage Plots



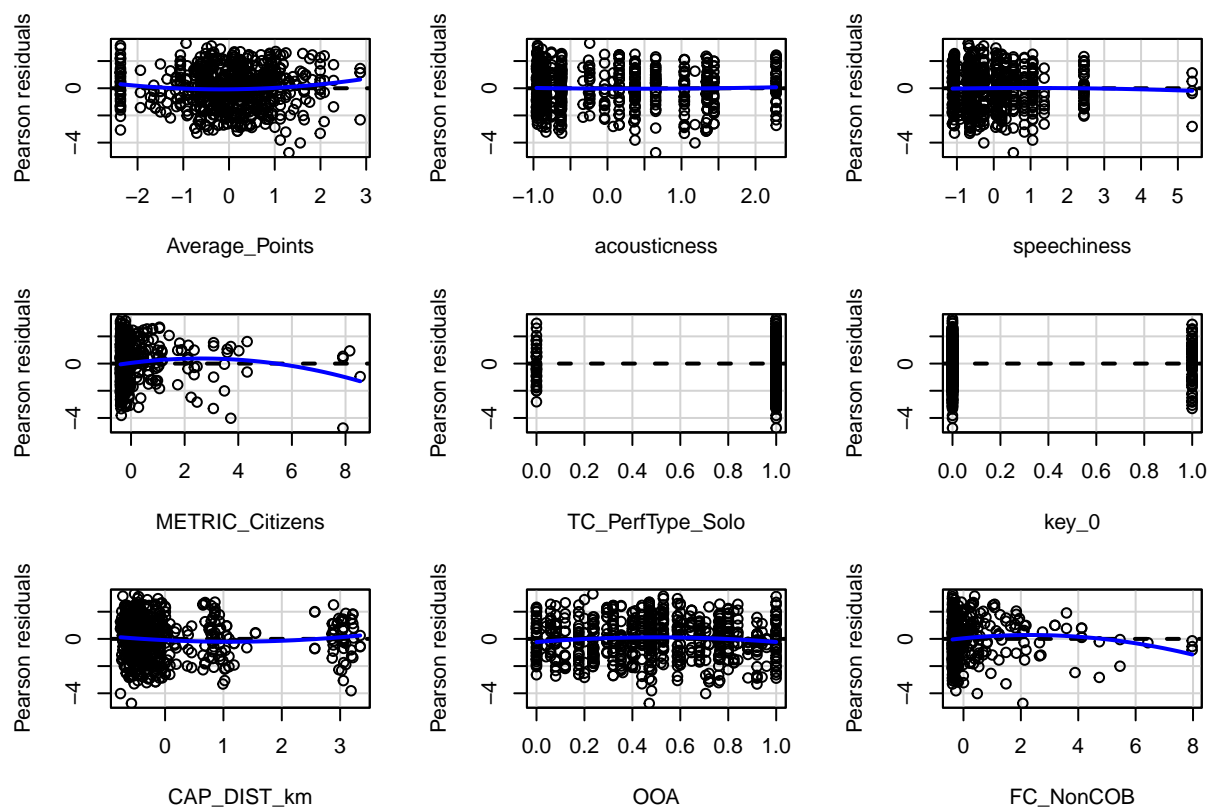
```
# Added variable Plots  
avPlots(my_model_overall)
```

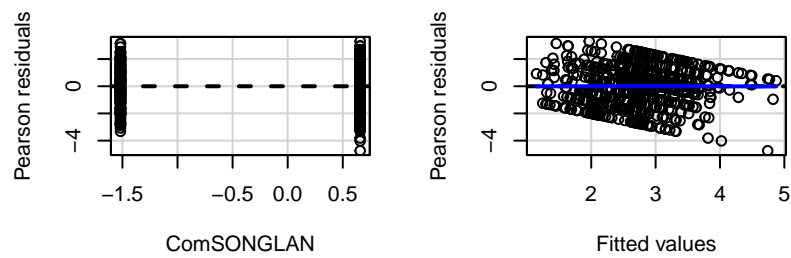



Added-Variable Plots



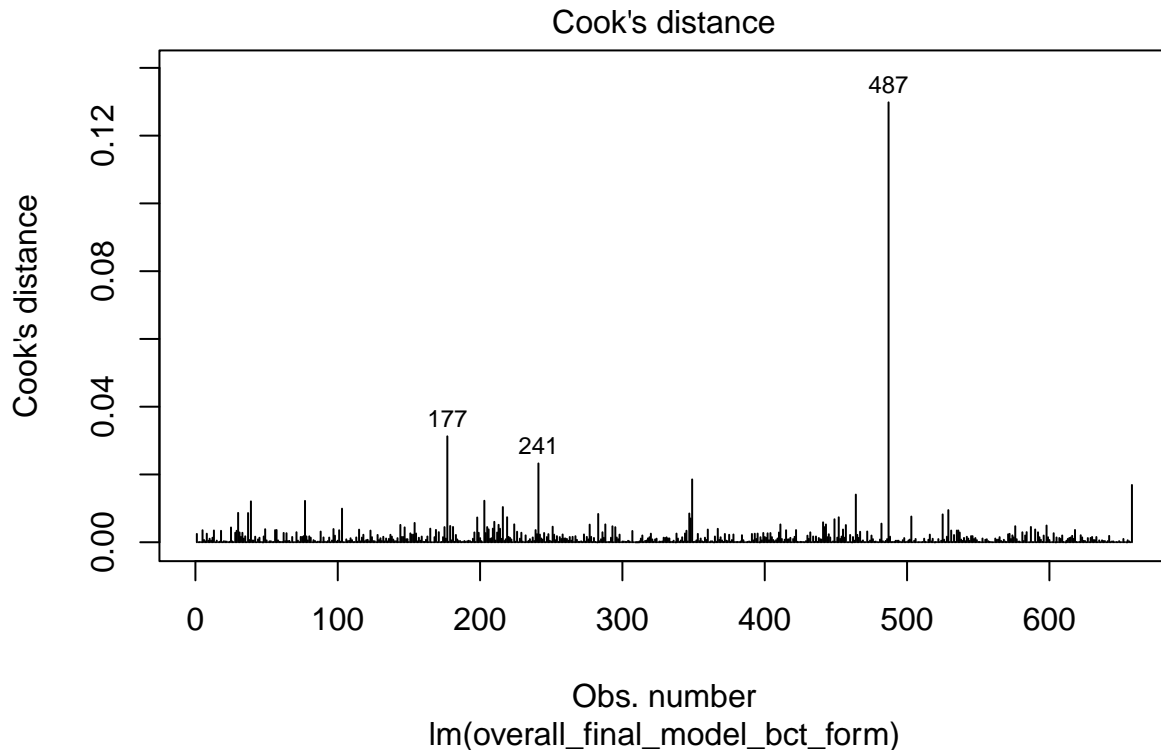
```
# Residual Plots  
residualPlots(my_model_overall)
```





```
##               Test stat Pr(>|Test stat|)
## Average_Points      2.2247      0.026443 *
## acousticness        0.5338      0.593682
## speechiness        -0.4246      0.671259
## METRIC_Citizens    -2.7460      0.006201 **
## TC_PerfType_Solo     0.7835      0.433605
## key_0                0.5665      0.571238
## CAP_DIST_km         1.8086      0.070981 .
## OOA                 -2.4388      0.015004 *
## FC_NonCOB          -2.2184      0.026874 *
## ComSONGLAN          1.2837      0.199719
## Tukey test          -0.0599      0.952216
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Cook's D plot
# identify D values > 4/(n-k-1)
cutoff <- 4/((nrow(processed_data)-length(my_model_overall$coefficients)-2))
# Crooks Distance plot
plot(my_model_overall, which = 4, cook.levels = cutoff)
```



```
# Influence Plot
```

```
influencePlot(my_model_overall, id.method = "identify", main = "Influence Plot", sub = "Circle size is p
```

```
## Warning in plot.window(...): "id.method" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "id.method" is not a graphical parameter
```

```
## Warning in axis(side = side, at = at, labels = labels, ...): "id.method" is not  
## a graphical parameter
```

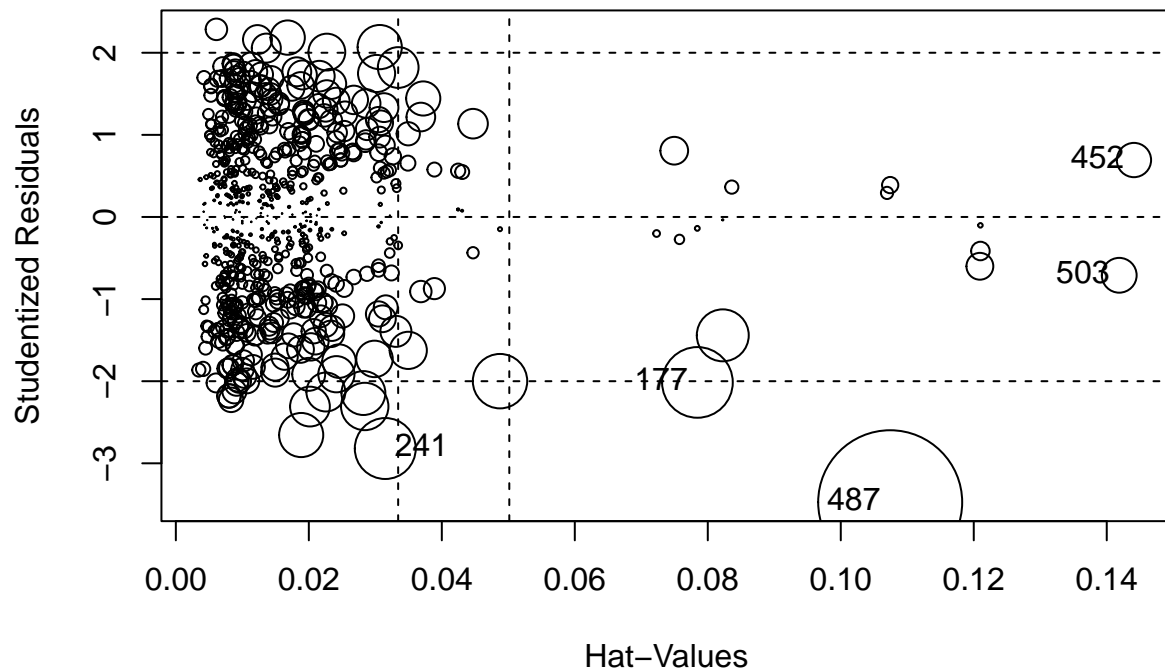
```
## Warning in axis(side = side, at = at, labels = labels, ...): "id.method" is not  
## a graphical parameter
```

```
## Warning in box(...): "id.method" is not a graphical parameter
```

```
## Warning in title(...): "id.method" is not a graphical parameter
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): "id.method" is not a  
## graphical parameter
```

Influence Plot



Circle size is proportional to Cook's Distance

StudRes	Hat	CookD	177	241	452	487	503
-2.8196641	0.0314946	0.0232539	-2.0146453	0.0784447	0.0312607	-3.4739137	0.1074300
0.1298262	-0.7100016	0.1418771	0.0073647	0.1074300	0.0075827		

Normality Test Ho: The data is normally distributed Ha: the data is not normally distributed

```
# Normality Test
shapiro.test(sresid)
```

```
##
## Shapiro-Wilk normality test
##
## data: sresid
## W = 0.99127, p-value = 0.0006293
```

```
ad.test(sresid)
```

```
##
## Anderson-Darling normality test
##
## data: sresid
## A = 1.173, p-value = 0.004584
```

```
cvm.test(sresid)
```

```
##
```

```
## Cramer-von Mises normality test
##
## data: sresid
## W = 0.16383, p-value = 0.01564
```

```
lillie.test(sresid)
```

```
##
## Lilliefors (Kolmogorov-Smirnov) normality test
##
## data: sresid
## D = 0.032825, p-value = 0.08898
```

```
pearson.test(sresid)
```

```
##
## Pearson chi-square normality test
##
## data: sresid
## P = 37.024, p-value = 0.04352
```

```
sf.test(sresid)
```

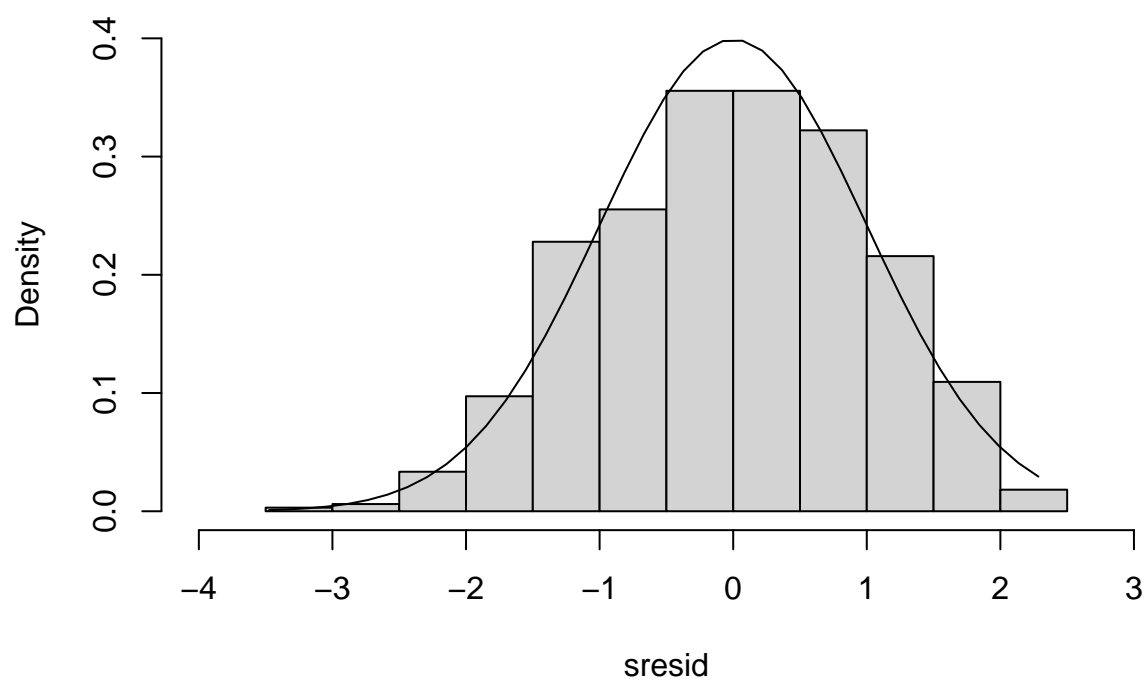
```
##
## Shapiro-Francia normality test
##
## data: sresid
## W = 0.99178, p-value = 0.001487
```

```
# the data is not normally distributed
```

```
# Histogram of residuals
```

```
hist(sresid, freq = FALSE, main = "Distribution of Standardised Residuals", ylim = c(0,0.4), xlim = c(-2,2))
xfit <- seq(min(sresid, na.rm = TRUE), max(sresid, na.rm = TRUE), length = 40)
yfit <- dnorm(xfit)
lines(xfit, yfit)
```

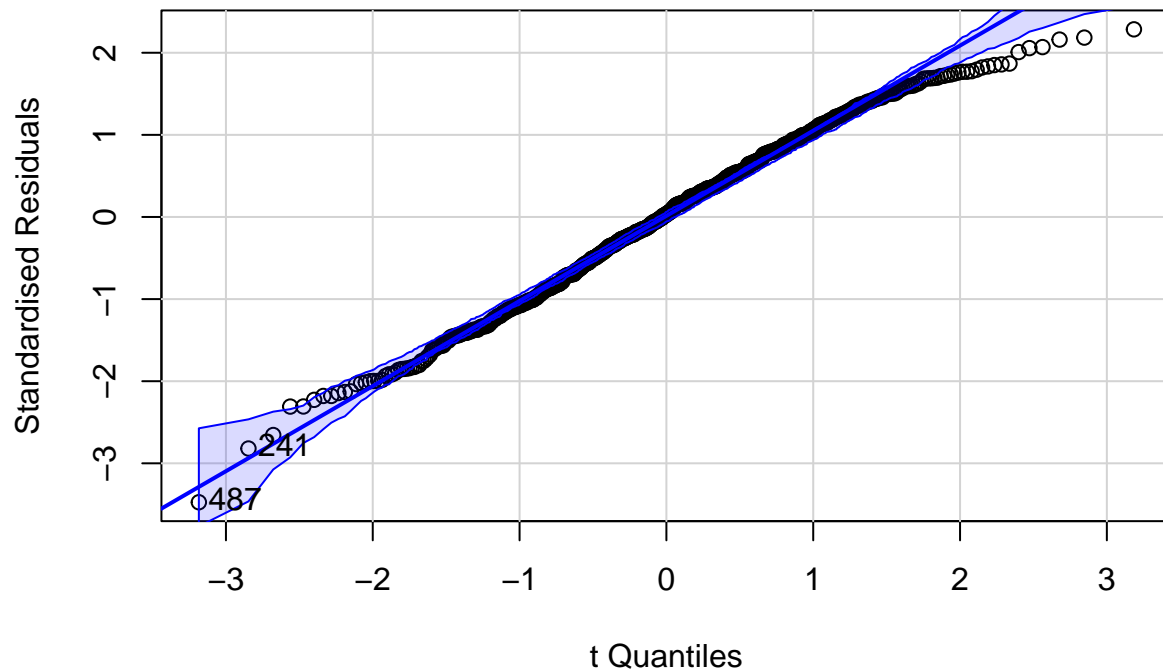
Distribution of Standardised Residuals



```
# QQ-plot of the data
```

```
qqPlot(my_model_overall, ylab = "Standardised Residuals", main = "QQ-Plot of Overall Model Standardised
```


QQ-Plot of Overall Model Standardised Residuals



```
## [1] 241 487
```

Non-Constant Error Variance Test Ho: constant error variance Ha: Non-constant error Variance

```
# Non-Constant Error Variance Test  
ncvTest(my_model_overall)
```

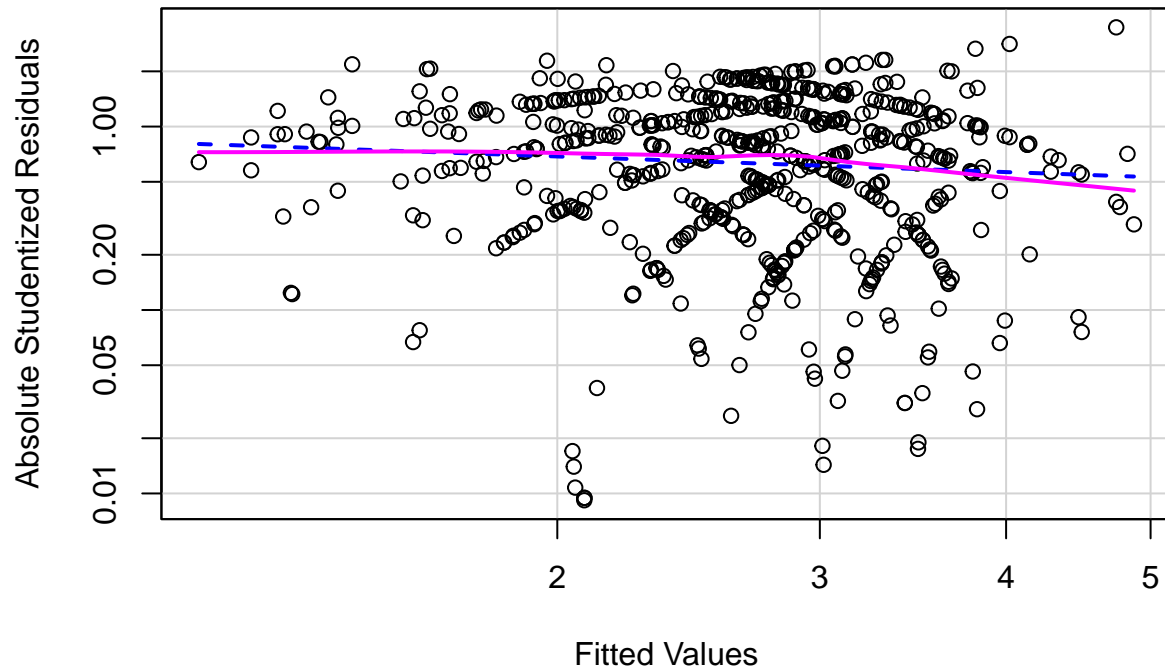
```
## Non-constant Variance Score Test  
## Variance formula: ~ fitted.values  
## Chisquare = 0.03663296, Df = 1, p = 0.84821
```

```
bptest(my_model_overall)
```

```
##  
## studentized Breusch-Pagan test  
##  
## data: my_model_overall  
## BP = 12.715, df = 10, p-value = 0.2401
```

```
# plot studentized residuals vs. fitted values  
spreadLevelPlot(my_model_overall, main = "Spread-Level Plot for Overall Model")
```

Spread–Level Plot for Overall Model



```
##
## Suggested power transformation: 1.282955
```

Variance Inflation Factors

```
vif(my_model_overall)
```

```
## Average_Points    acoustictness    speechiness    METRIC_Citizens
##      1.091139         1.179141         1.289927         1.360161
## TC_PerfType_Solo      key_0         CAP_DIST_km         OOA
##      1.104542         1.246838         1.139690         1.188927
##      FC_NonCOB      ComSONGLAN
##      1.344230         1.150996
```

```
sqrt(vif(my_model_overall)) > 2
```

```
## Average_Points    acoustictness    speechiness    METRIC_Citizens
##      FALSE         FALSE         FALSE         FALSE
## TC_PerfType_Solo      key_0         CAP_DIST_km         OOA
##      FALSE         FALSE         FALSE         FALSE
##      FC_NonCOB      ComSONGLAN
##      FALSE         FALSE
```

```
# No signs of collinearity
```

TELEVOTE MODEL

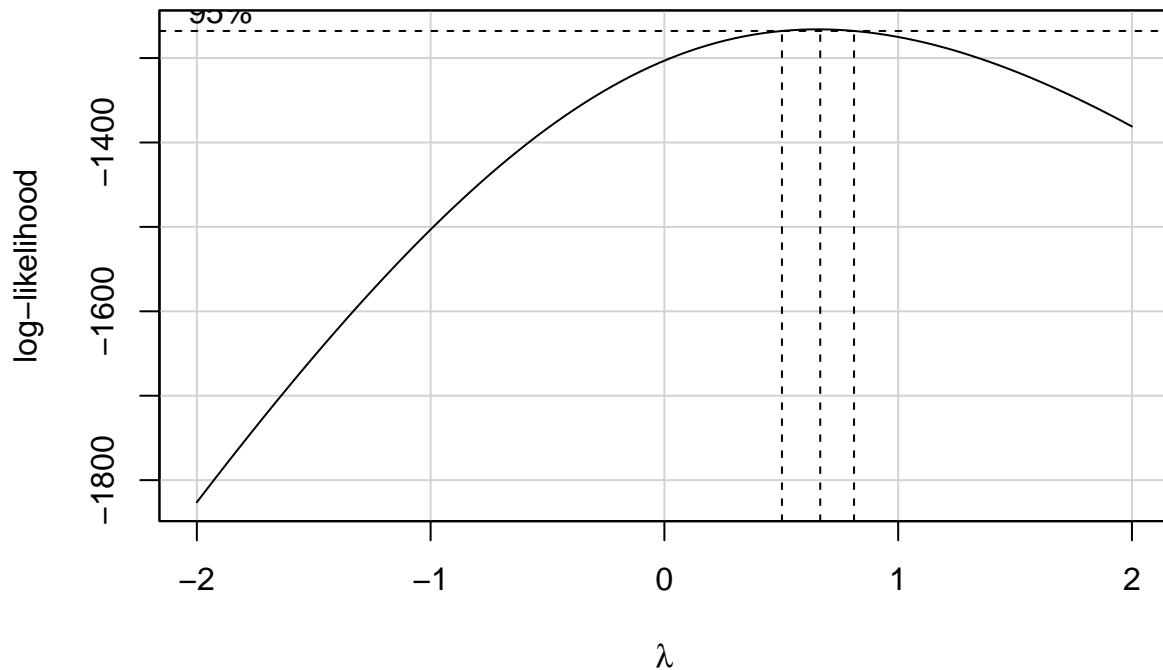
```
# load final televote model
my_model_tele <- readRDS("./models/televote_final_model.RDS")
# extract out the model coefficients
tele_model_coeff <- names(my_model_tele$coefficients)[-1]
# recreate the model formula
televote_final_model_form <- as.formula(paste('Points ~', paste(tele_model_coeff, collapse = ' + ')))
# generate model summary
summary(my_model_tele)
```

```
##
## Call:
## lm(formula = televote_final_model_form, data = televote_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.3561 -1.9688 -0.0461  1.7443  6.7011
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.1314     0.3466  14.806 < 2e-16 ***
## METRIC_Citizens  0.5344     0.1555   3.436 0.000668 ***
## Average_Points  0.8126     0.1607   5.057 7.22e-07 ***
## TC_NumNeigh     0.7464     0.1742   4.286 2.42e-05 ***
## speechiness     0.5175     0.1656   3.125 0.001943 **
## acoustichness   0.4804     0.1681   2.858 0.004550 **
## FC_NonCitizens  0.6452     0.1767   3.652 0.000304 ***
## VBlocs1_TC_13  -6.8165     2.1841  -3.121 0.001968 **
## OOA             0.8913     0.6028   1.479 0.140203
## CAP_DIST_km     0.3029     0.1726   1.755 0.080254 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.772 on 317 degrees of freedom
## Multiple R-squared:  0.3384, Adjusted R-squared:  0.3196
## F-statistic: 18.02 on 9 and 317 DF,  p-value: < 2.2e-16
```

Transformation of Response Variable

```
# Apply box-cox transformation on the model to improve the normality assumptions
# box-cox transformation using car
bct <- boxCox(object = my_model_tele)
```

Profile Log-likelihood



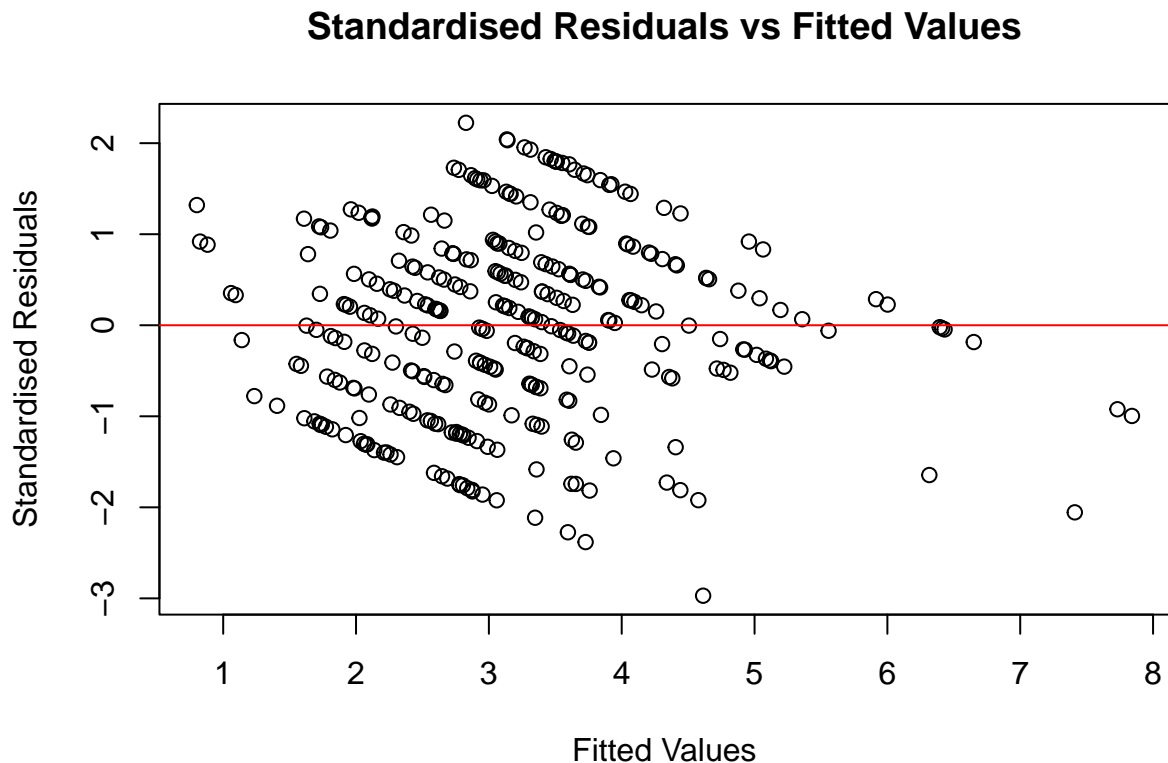
```
# find optimal box-cox power transformation power
p <- bct$x[which.max(x = bct$y)]
# transform points using the optimal power transformation
bctPoints <- (((televote_data$Points)^p) - 1)/(p)
# recreate the model formula
televote_final_model_bct_form <- as.formula(paste('bctPoints ~', paste(tele_model_coef, collapse = ' +
# refit final model with with box-cox power transformation
my_model_tele <- lm(formula = televote_final_model_bct_form, data = televote_data)
# generate model summary
summary(my_model_tele)
```

```
##
## Call:
## lm(formula = televote_final_model_bct_form, data = televote_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.6127 -1.0874  0.0907  1.1155  3.5345
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.75365    0.20088  13.708 < 2e-16 ***
## METRIC_Citizens  0.28085    0.09013   3.116 0.002000 **
## Average_Points   0.44003    0.09313   4.725 3.47e-06 ***
## TC_NumNeigh      0.44883    0.10095   4.446 1.21e-05 ***
## speechiness      0.30365    0.09599   3.163 0.001711 **
```

```
## acoustiness      0.28053      0.09743      2.879 0.004257 **
## FC_NonCitizens   0.35982      0.10241      3.514 0.000506 ***
## VBlocs1_TC_13    -3.80137      1.26592     -3.003 0.002888 **
## OOA              0.52110      0.34938      1.492 0.136818
## CAP_DIST_km       0.19110      0.10006      1.910 0.057054 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.607 on 317 degrees of freedom
## Multiple R-squared:  0.3246, Adjusted R-squared:  0.3054
## F-statistic: 16.92 on 9 and 317 DF,  p-value: < 2.2e-16
```

Evaluate the Fit of the Model

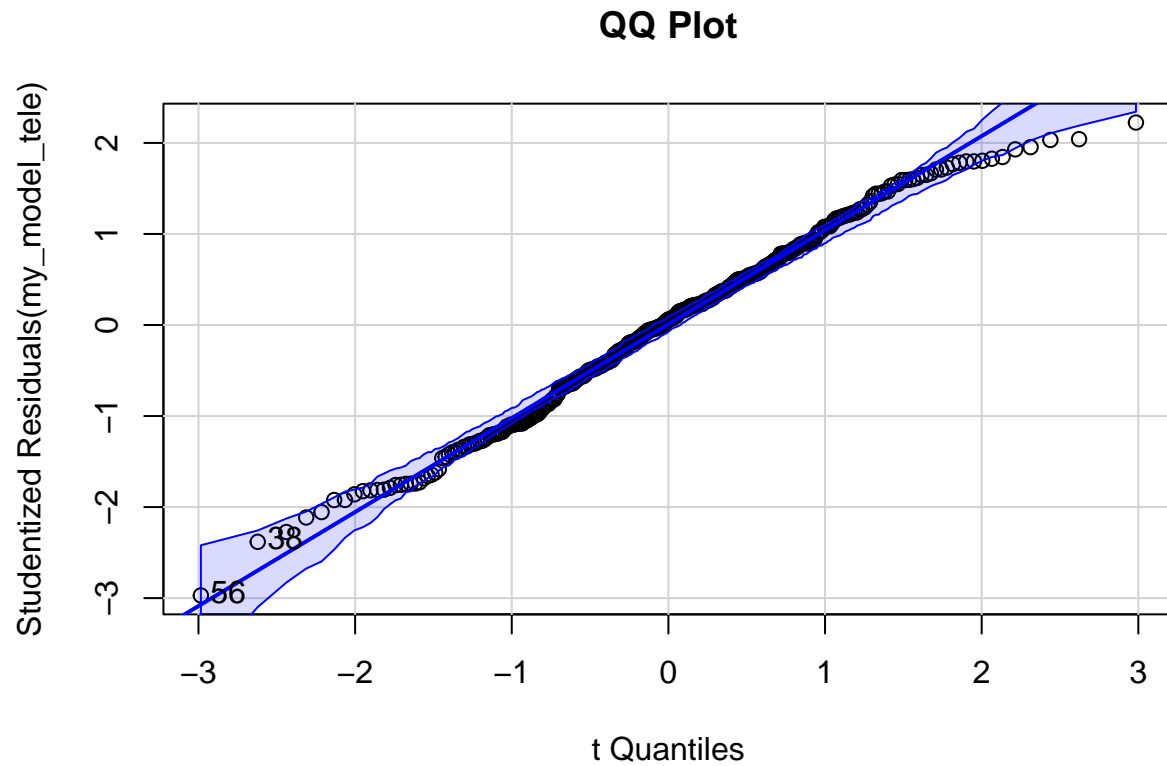
```
# create standardize residuals
sresid <- studres(my_model_tele)
# Residual vs fits plot
plot(x = my_model_tele$fitted.values, y = sresid, main = "Standardised Residuals vs Fitted Values", xlab = "Fitted Values", ylab = "Standardised Residuals")
# add red horizontal line through y-axis 0
abline(h = 0, col = "red")
```



```
# Assessing Outliers
# Bonferonni p-value for most extreme obs
outlierTest(my_model_tele)
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 56 -2.970711      0.0031989      NA
```

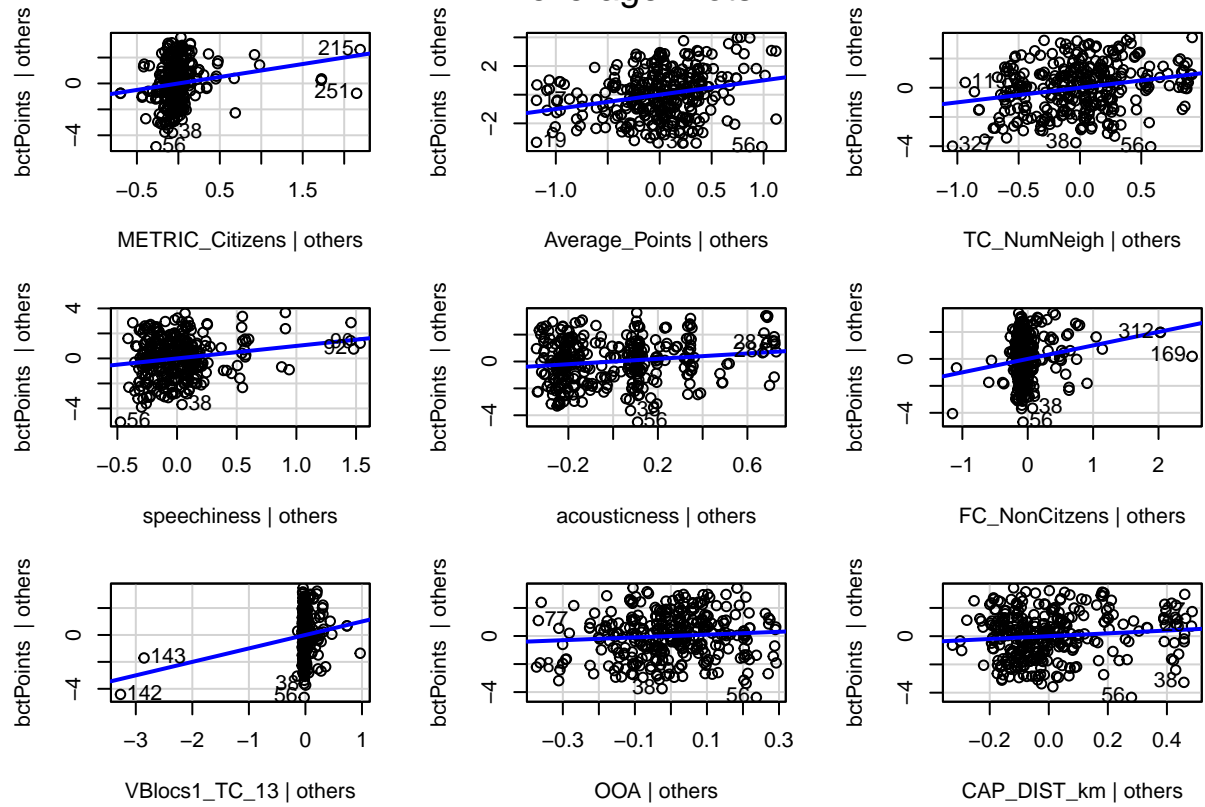
```
#qq plot for studentized residuals
qqPlot(my_model_tele, main = "QQ Plot")
```



```
## [1] 38 56
```

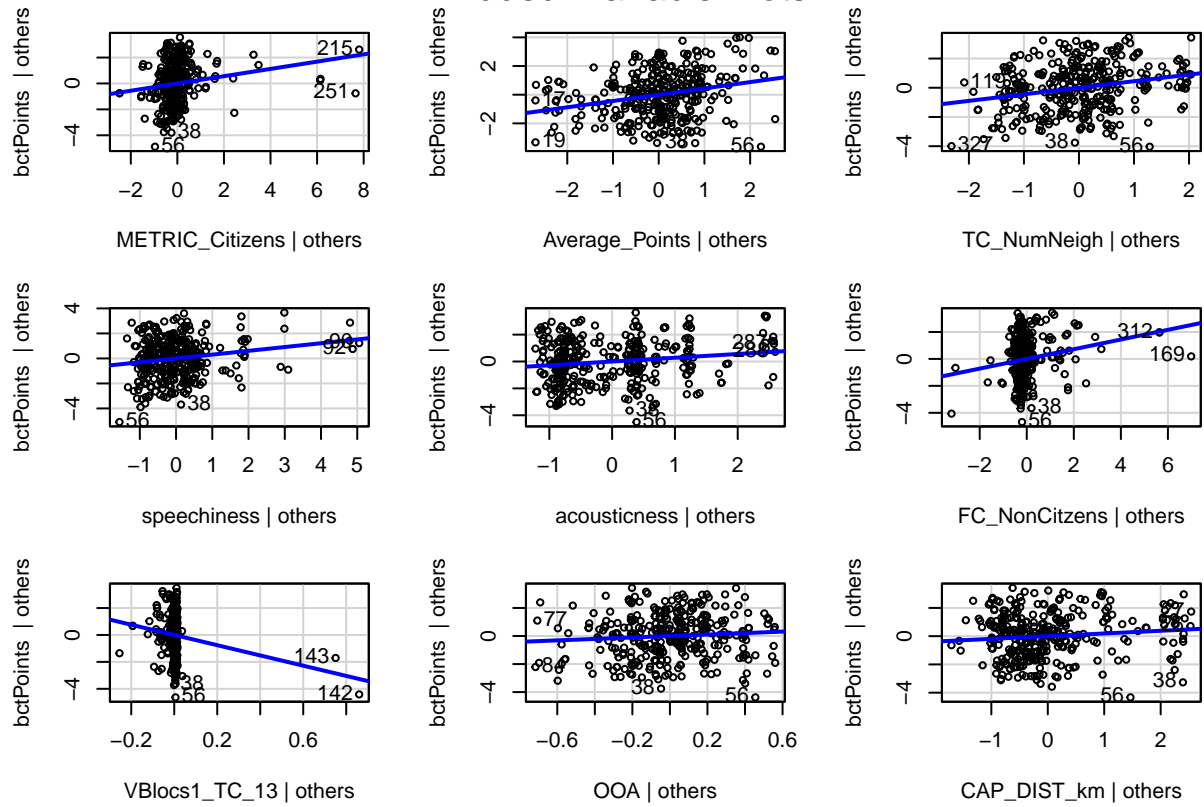
```
# leverage plots
leveragePlots(my_model_tele)
```

Leverage Plots

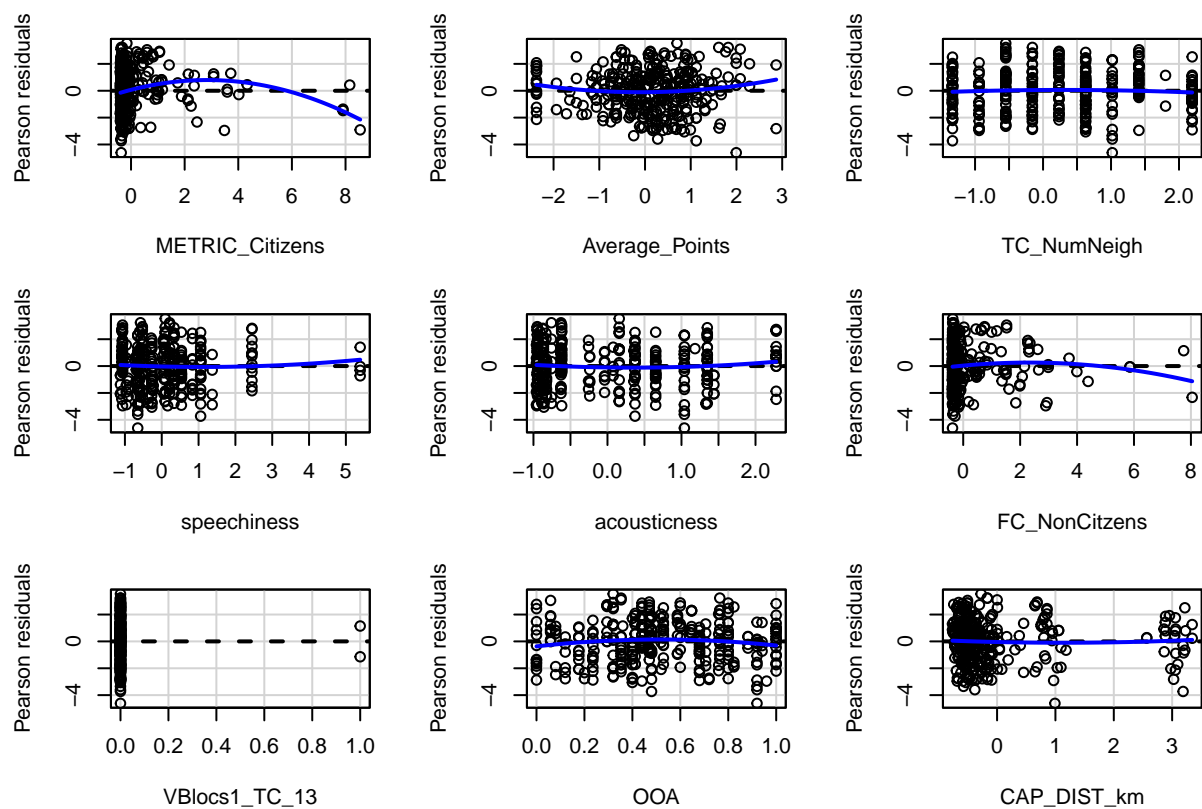


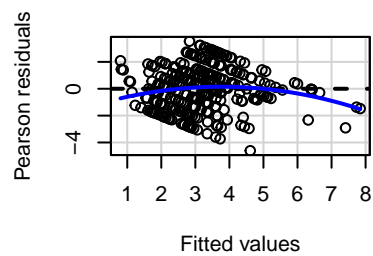
```
# Added variable Plots
avPlots(my_model_tele)
```

Added-Variable Plots



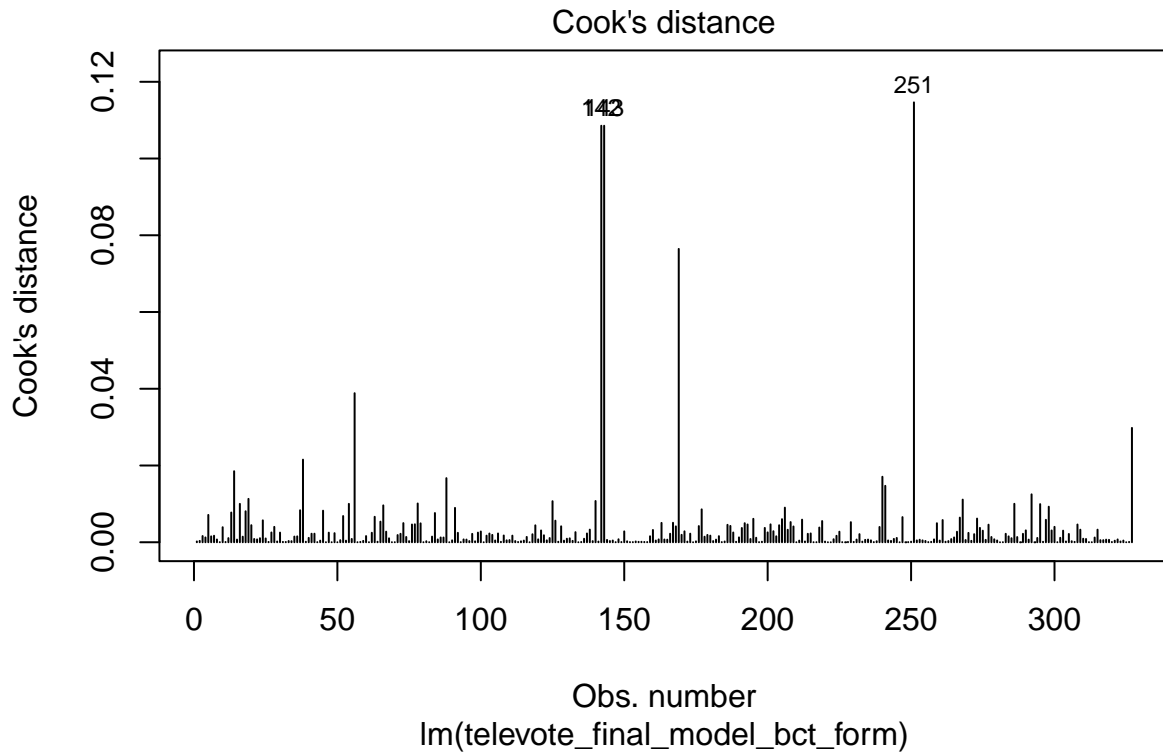
```
# Residual Plots
residualPlots(my_model_tele)
```



```
##               Test stat Pr(>|Test stat|)
## METRIC_Citizens   -4.2900      2.378e-05 ***
## Average_Points    1.8891      0.059792 .
## TC_NumNeigh       -0.7737      0.439702
## speechiness       0.8468      0.397722
## acousticness      1.3501      0.177938
## FC_NonCitizens   -1.5501      0.122130
## VBlocs1_TC_13     0.8875      0.375504
## OOA              -1.9812      0.048437 *
## CAP_DIST_km       0.5182      0.604654
## Tukey test        -3.2247      0.001261 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Cook's D plot
# identify D values > 4/(n-k-1)
cutoff <- 4/((nrow(processed_data) - length(my_model_tele$coefficients) - 2))
# Crooks Distance plot
plot(my_model_tele, which = 4, cook.levels = cutoff)
```



```
# Influence Plot
```

```
influencePlot(my_model_tele, id.method = "identify", main = "Influence Plot", sub = "Circle size is prop
```

```
## Warning in plot.window(...): "id.method" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "id.method" is not a graphical parameter
```

```
## Warning in axis(side = side, at = at, labels = labels, ...): "id.method" is not  
## a graphical parameter
```

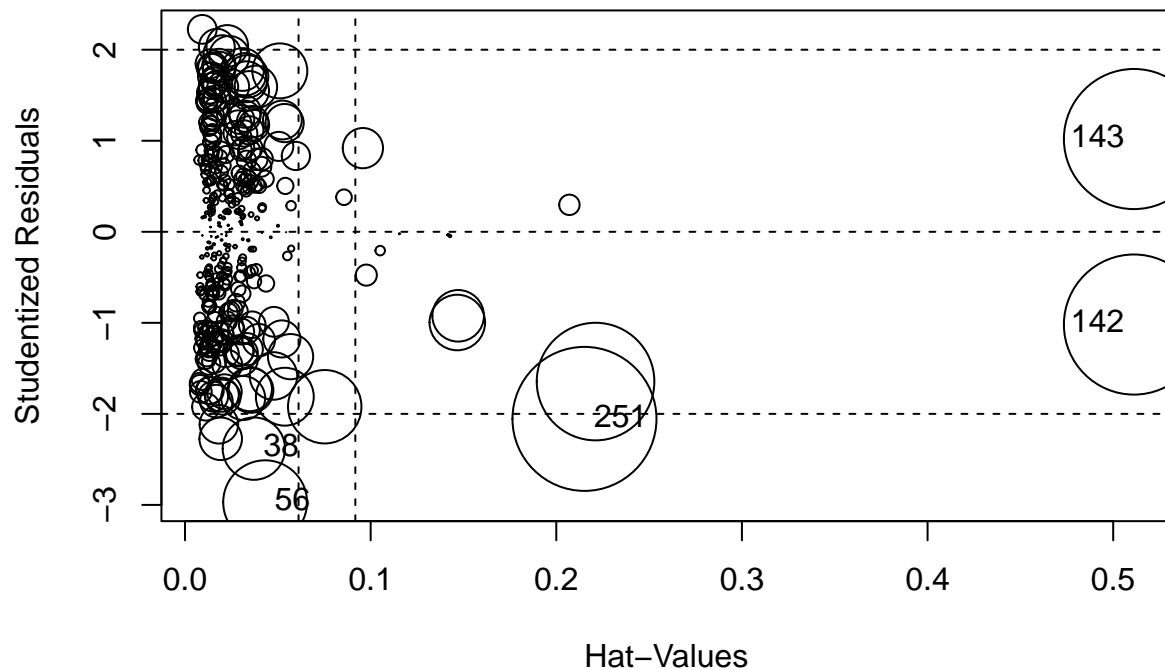
```
## Warning in axis(side = side, at = at, labels = labels, ...): "id.method" is not  
## a graphical parameter
```

```
## Warning in box(...): "id.method" is not a graphical parameter
```

```
## Warning in title(...): "id.method" is not a graphical parameter
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): "id.method" is not a  
## graphical parameter
```

Influence Plot



Circle size is proportional to Cook's Distance

StudRes	Hat	CookD	38	56	251	142	143
-2.381778	0.0370859	0.0215312	-2.970711	-2.055209	1.018872	0.5111820	0.1085464
0.0431574	0.0388459	0.1146427					

Normality Test Ho: The data is normally distributed Ha: the data is not normally distributed

```
# Normality Test
shapiro.test(sresid)
```

```
##
## Shapiro-Wilk normality test
##
## data: sresid
## W = 0.99075, p-value = 0.03758
```

```
ad.test(sresid)
```

```
##
## Anderson-Darling normality test
##
## data: sresid
## A = 0.59623, p-value = 0.1186
```

```
cvm.test(sresid)
```

```
##
```

```
## Cramer-von Mises normality test
##
## data: sresid
## W = 0.075916, p-value = 0.2334
```

```
lillie.test(sresid)
```

```
##
## Lilliefors (Kolmogorov-Smirnov) normality test
##
## data: sresid
## D = 0.038096, p-value = 0.2959
```

```
pearson.test(sresid)
```

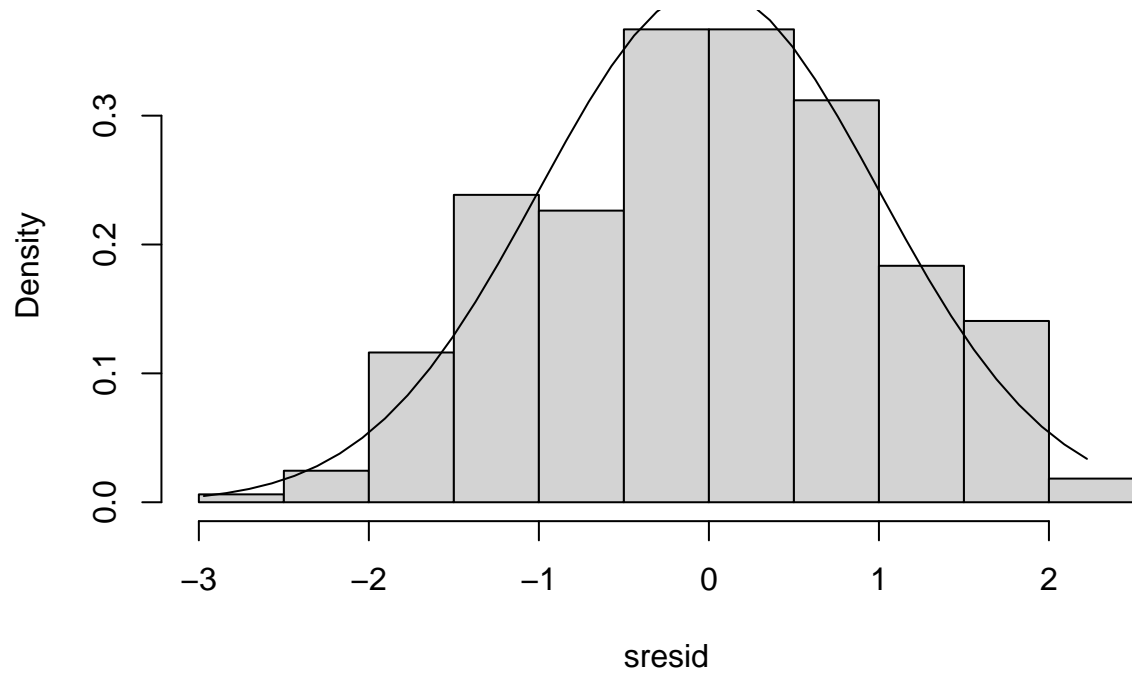
```
##
## Pearson chi-square normality test
##
## data: sresid
## P = 21.138, p-value = 0.2725
```

```
sf.test(sresid)
```

```
##
## Shapiro-Francia normality test
##
## data: sresid
## W = 0.99202, p-value = 0.07153
```

```
# the data is not normally distributed
# Histogram of residuals
hist(sresid, freq = FALSE, main = "Distribution of Studentised Residuals")
xfit <- seq(min(sresid, na.rm = TRUE), max(sresid, na.rm = TRUE), length = 40)
yfit <- dnorm(xfit)
lines(xfit, yfit)
```

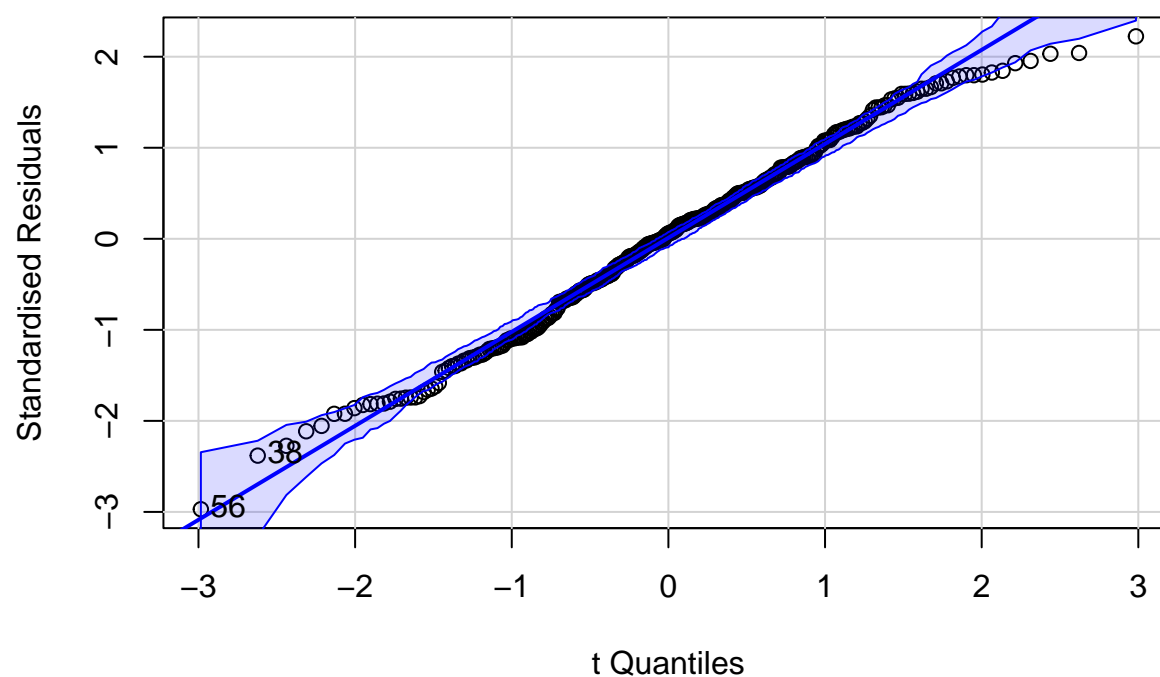
Distribution of Studentised Residuals



```
# QQ-plot of the data
```

```
qqPlot(my_model_tele, ylab = "Standardised Residuals", main = "QQ-Plot of Televote Model Standardised R
```

QQ-Plot of Televote Model Standardised Residuals



```
## [1] 38 56
```

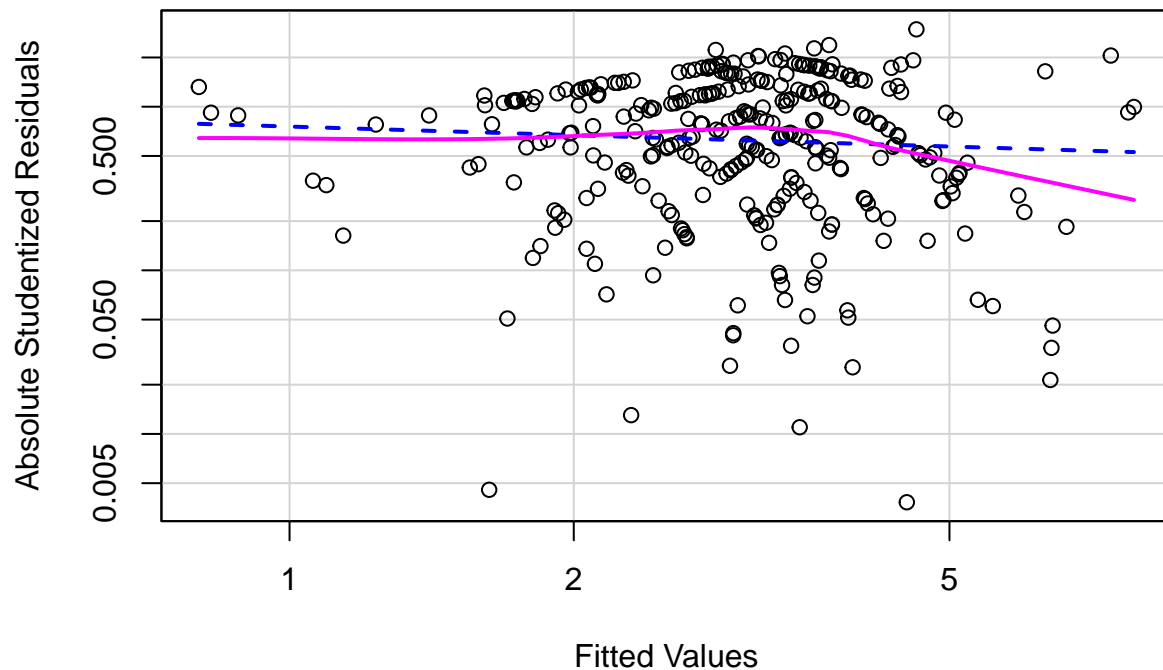
Non-Constant Error Variance Test Ho: constant error variance Ha: Non-constant error Variance

```
# Non-Constant Error Variance Test  
ncvTest(my_model_tele)
```

```
## Non-constant Variance Score Test  
## Variance formula: ~ fitted.values  
## Chisquare = 0.05524184, Df = 1, p = 0.81418
```

```
# plot studentized residuals vs. fitted values  
spreadLevelPlot(my_model_tele, main = "Spread-Level Plot for Televote Model")
```

Spread–Level Plot for Televote Model



```
##
## Suggested power transformation: 1.174411
```

```
# Variance Inflation Factors
```

```
vif(my_model_tele)
```

```
## METRIC_Citizens Average_Points TC_NumNeigh speechiness acoustiness
##      1.440215      1.072688      1.440252      1.231842      1.059780
## FC_NonCitizens VBlocs1_TC_13      OOA      CAP_DIST_km
##      1.599009      1.233766      1.147115      1.291723
```

```
sqrt(vif(my_model_tele)) > 2
```

```
## METRIC_Citizens Average_Points TC_NumNeigh speechiness acoustiness
##      FALSE      FALSE      FALSE      FALSE      FALSE
## FC_NonCitizens VBlocs1_TC_13      OOA      CAP_DIST_km
##      FALSE      FALSE      FALSE      FALSE
```

```
# No signs of collinearity
```

JURY MODEL


```

# load final televote model
my_model_jury <- readRDS("./models/jury_final_model.RDS")
# extract out the model coefficients
jury_model_coeff <- names(my_model_jury$coefficients)[-1]
# recreate the model formula
jury_final_model_form<- as.formula(paste('Points ~', paste(jury_model_coeff, collapse = ' + ')))
# generate model summary
summary(my_model_jury)

```

```

##
## Call:
## lm(formula = jury_final_model_form, data = jury_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.136 -2.494 -0.291  2.024  8.297
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.0865     0.4637   8.812 < 2e-16 ***
## CAP_DIST_km       0.6617     0.1854   3.568 0.000414 ***
## acousticness      0.5032     0.1747   2.880 0.004247 **
## speechiness       0.8932     0.2004   4.457 1.15e-05 ***
## TC_PerfType_Mixed -9.6005     3.2765 -2.930 0.003632 **
## TC_LANGFAM_Armenian -3.1767     0.9880 -3.215 0.001435 **
## VBlocs1_TC_1       3.0611     0.6177   4.956 1.17e-06 ***
## ComVBlocs1_y       -2.2750     0.6857 -3.318 0.001011 **
## VBlocs1_FC_1        0.8442     0.4283   1.971 0.049601 *
## VBlocs2_TC_1        1.5367     0.4794   3.205 0.001484 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.027 on 321 degrees of freedom
## Multiple R-squared:  0.2132, Adjusted R-squared:  0.1912
## F-statistic: 9.667 on 9 and 321 DF,  p-value: 4.405e-13

```

Transformation of Response Variable

```

# transform points using the optimal power transformation
ptPoints <- jury_data$Points^(3/4)
# Note: weird bug occurring for row name 177 / row index 88 (possibly due to column with near all zero v
jury_coeff_data <- jury_data %>% subset(select = jury_model_coeff)
jury_coeff_zero_prop <- apply(X = jury_coeff_data, MARGIN = 2, FUN = function(x) sum(x == 0)/length(x)*
jury_model_coeff <- names(which(jury_coeff_zero_prop < 99))
# recreate the model formula
jury_final_model_pt_form <- as.formula(paste('ptPoints ~', paste(jury_model_coeff, collapse = ' + ')))
# refit final model with power transformation of 3/4
# NOTE: a box cox transformation resulted in normality but also non-constant variance
my_model_jury <- lm(formula = jury_final_model_pt_form, data = jury_data)
# generate model summary
summary(my_model_jury)

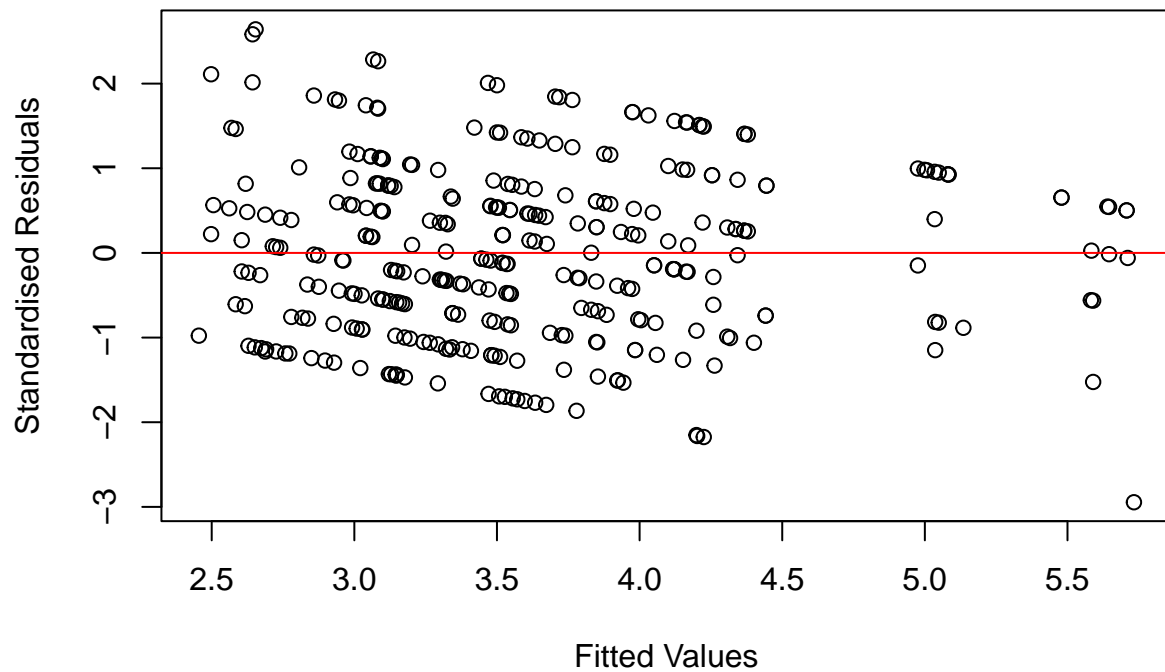
```

```
##
## Call:
## lm(formula = jury_final_model_pt_form, data = jury_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.051 -1.185 -0.045  1.071  3.804
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.73582    0.23066   11.861 < 2e-16 ***
## CAP_DIST_km       0.34953    0.09104    3.840 0.000148 ***
## acousticness      0.22920    0.08669    2.644 0.008598 **
## speechiness       0.32980    0.09305    3.544 0.000452 ***
## TC_LANGFAM_Armenian -1.49410    0.49134   -3.041 0.002553 **
## VBlocs1_TC_1       1.41307    0.30606    4.617 5.63e-06 ***
## ComVBlocs1_y      -1.03563    0.34079   -3.039 0.002569 **
## VBlocs1_FC_1       0.41954    0.21305    1.969 0.049787 *
## VBlocs2_TC_1       0.81313    0.23839    3.411 0.000730 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.506 on 322 degrees of freedom
## Multiple R-squared:  0.1852, Adjusted R-squared:  0.165
## F-statistic: 9.149 on 8 and 322 DF, p-value: 2.378e-11
```

Evaluate the Fit of the Model

```
# create standardize residuals
sresid <- studres(my_model_jury)
# Residual vs fits plot
plot(x = my_model_jury$fitted.values, y = sresid, main = "Standardised Residuals vs Fitted Values", xlab = "Fitted values", ylab = "Standardised Residuals")
# add red horizontal line through y-axis 0
abline(h = 0, col = "red")
```

Standardised Residuals vs Fitted Values

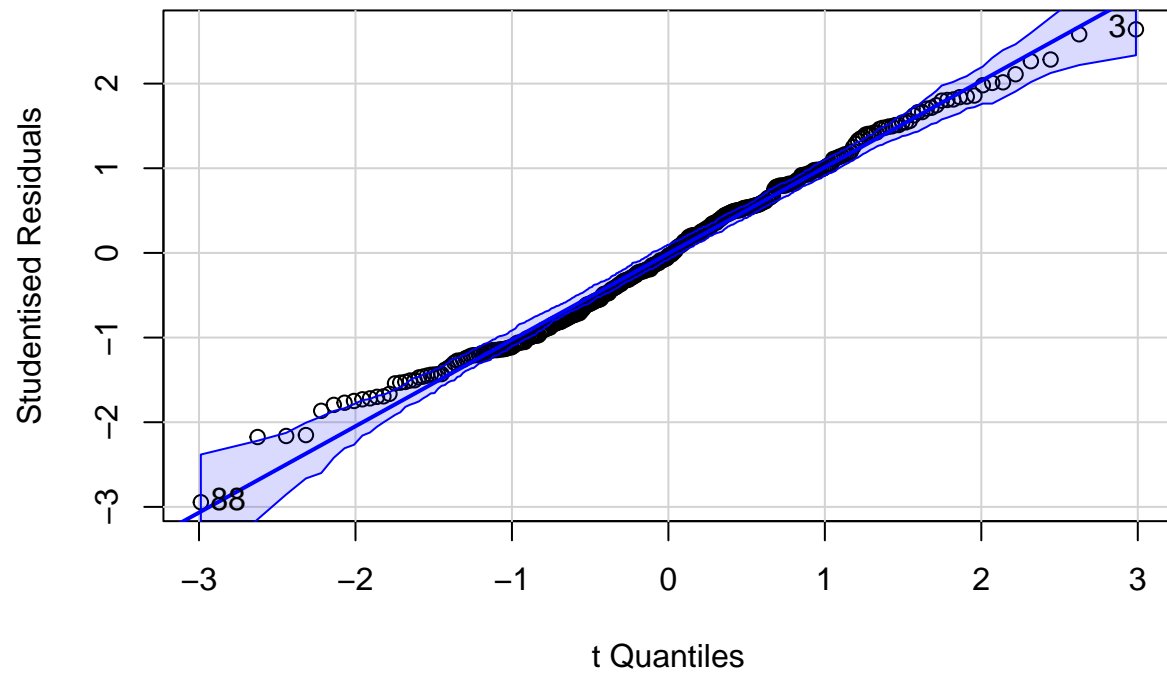


```
# Assessing Outliers  
# Bonferonni p-value for most extreme obs  
outlierTest(my_model_jury)
```

```
## No Studentized residuals with Bonferroni p < 0.05  
## Largest |rstudent|:  
##      rstudent unadjusted p-value Bonferroni p  
## 88 -2.945099      0.0034643      NA
```

```
# qq plot for studentized residuals  
qqPlot(my_model_jury, main = "QQ Plot of Studentised Residuals for Jury Vote Model", ylab = "Studentised Residuals")
```

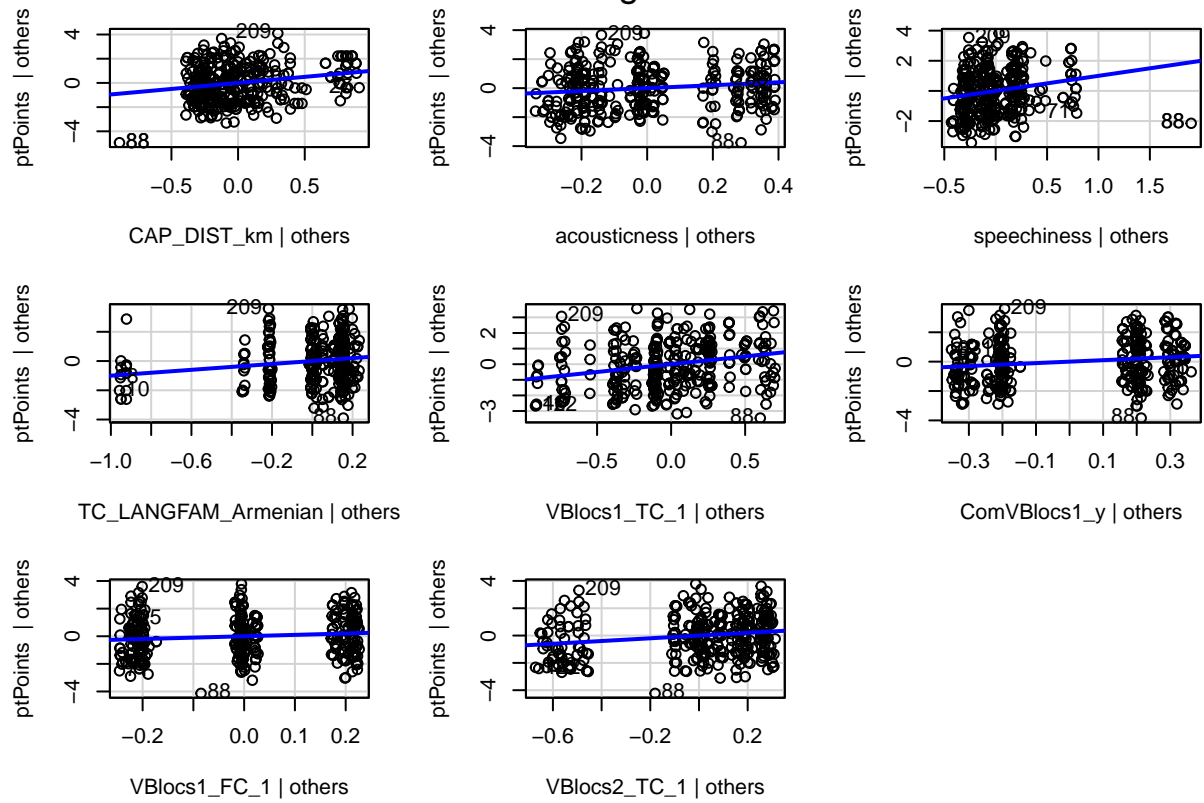
QQ Plot of Studentised Residuals for Jury Vote Model



```
## [1] 3 88
```

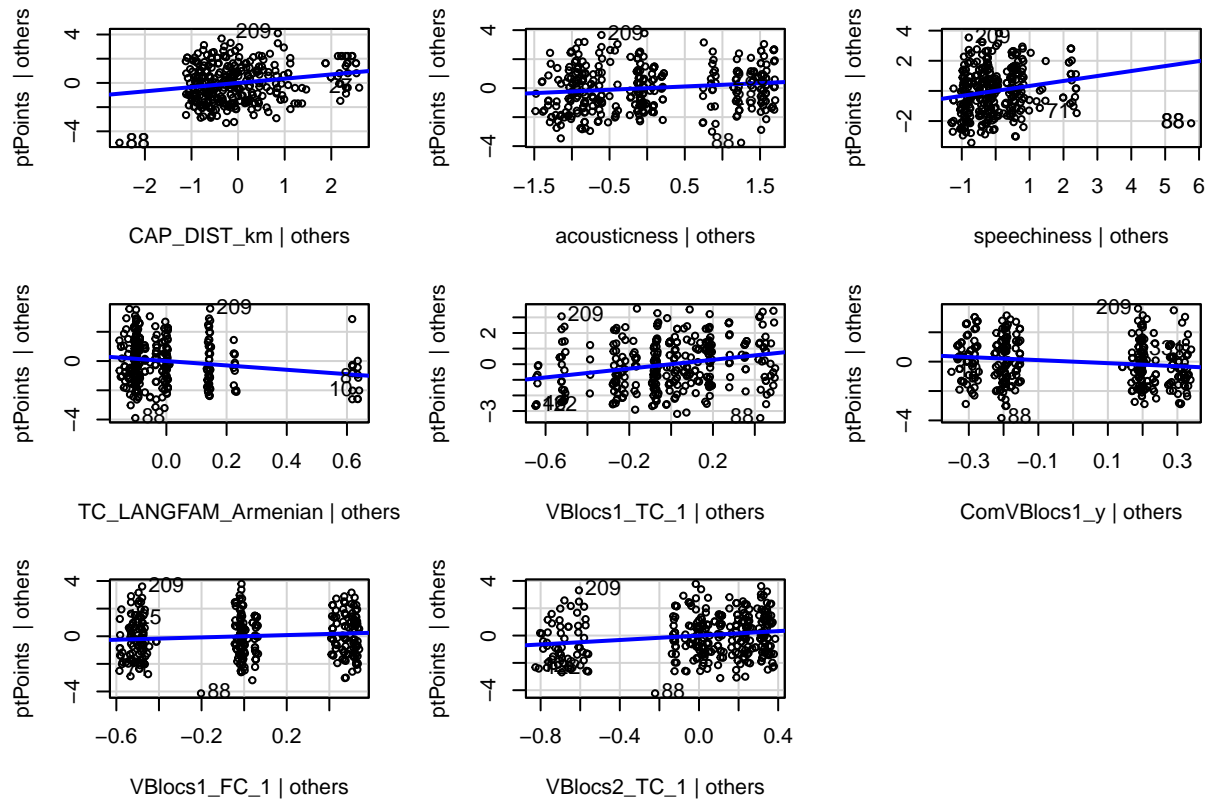
```
# leverage plots  
leveragePlots(my_model_jury)
```

Leverage Plots

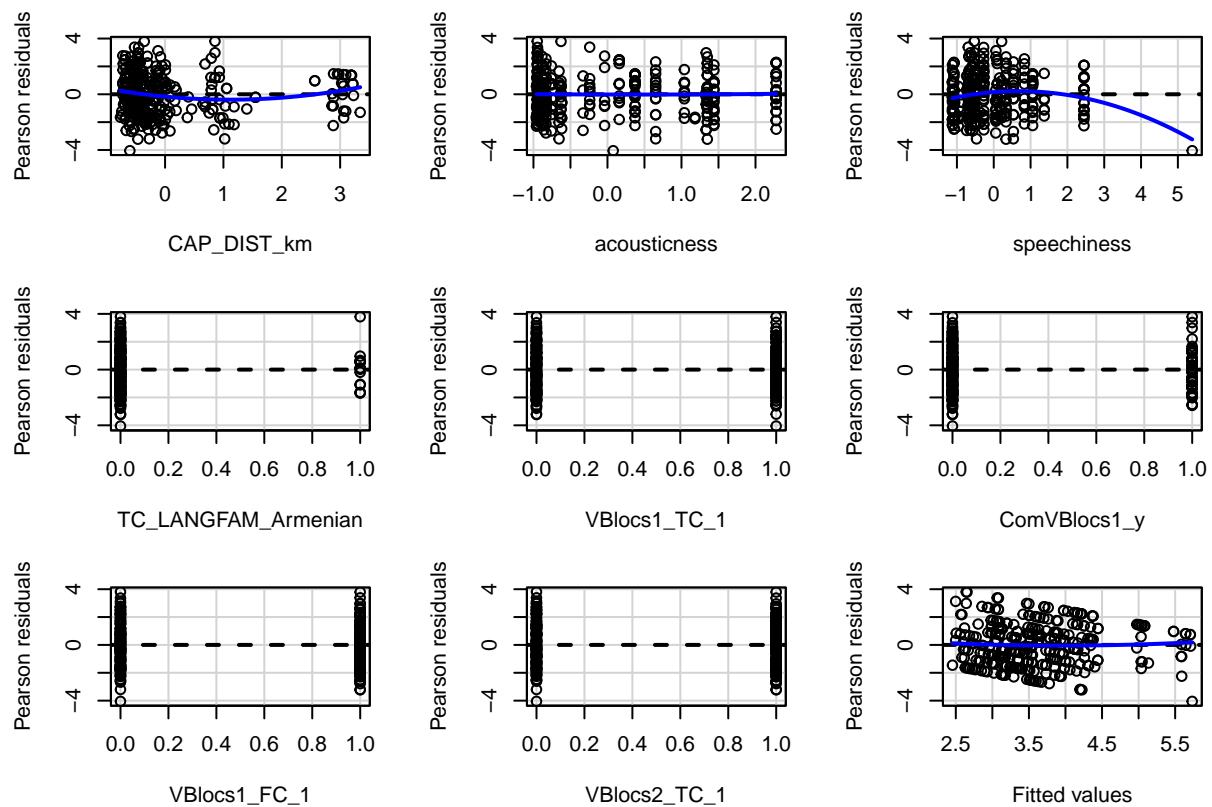


```
# Added variable Plots
avPlots(my_model_jury)
```

Added-Variable Plots

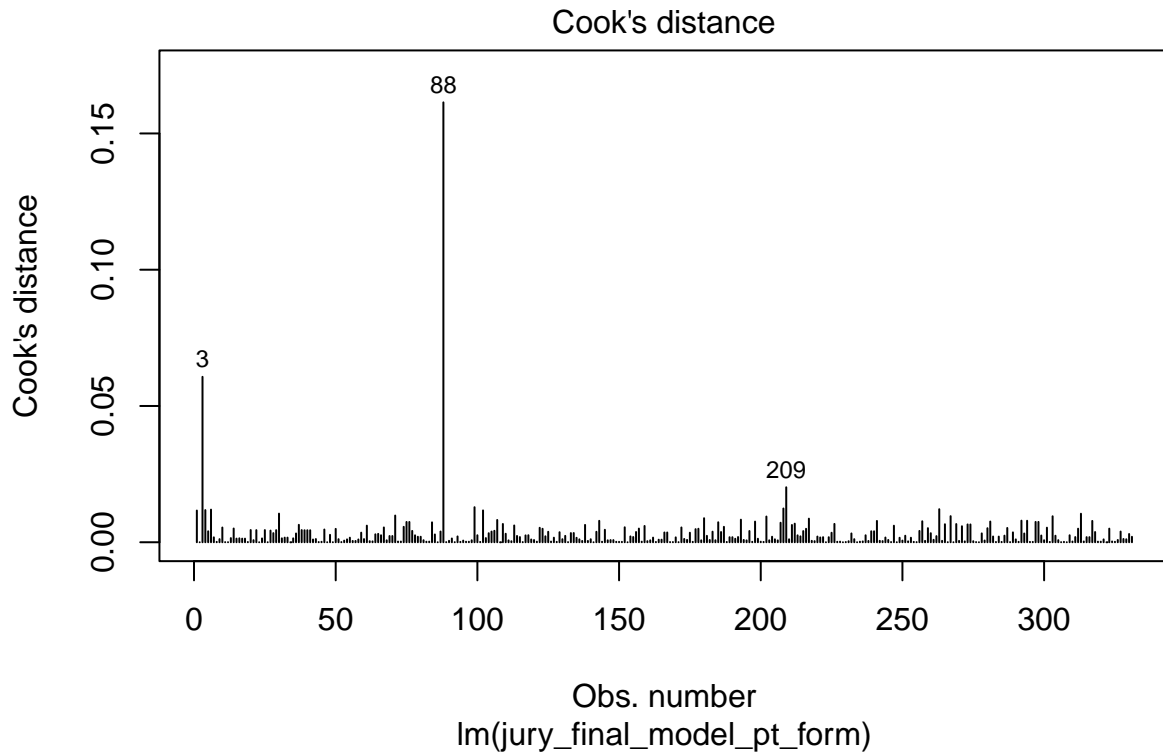


```
# Residual Plots
residualPlots(my_model_jury)
```



```
##               Test stat Pr(>|Test stat|)
## CAP_DIST_km      2.8141      0.0051936 **
## acousticness     0.1809      0.8565345
## speechiness     -3.3384      0.0009418 ***
## TC_LANGFAM_Armenian 0.6549      0.5129983
## VBlocs1_TC_1      1.4162      0.1576780
## ComVBlocs1_y     -0.1439      0.8856911
## VBlocs1_FC_1      0.2581      0.7964978
## VBlocs2_TC_1     -0.3352      0.7376926
## Tukey test        0.8966      0.3699360
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Cook's D plot
# identify D values > 4/(n-k-1)
cutoff <- 4/((nrow(processed_data) - length(my_model_jury$coefficients) - 2))
# Crooks Distance plot
plot(my_model_jury, which = 4, cook.levels = cutoff)
```



```
# Influence Plot
```

```
influencePlot(my_model_jury, id.method = "identify", main = "Influence Plot", sub = "Circle size is prop
```

```
## Warning in plot.window(...): "id.method" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "id.method" is not a graphical parameter
```

```
## Warning in axis(side = side, at = at, labels = labels, ...): "id.method" is not  
## a graphical parameter
```

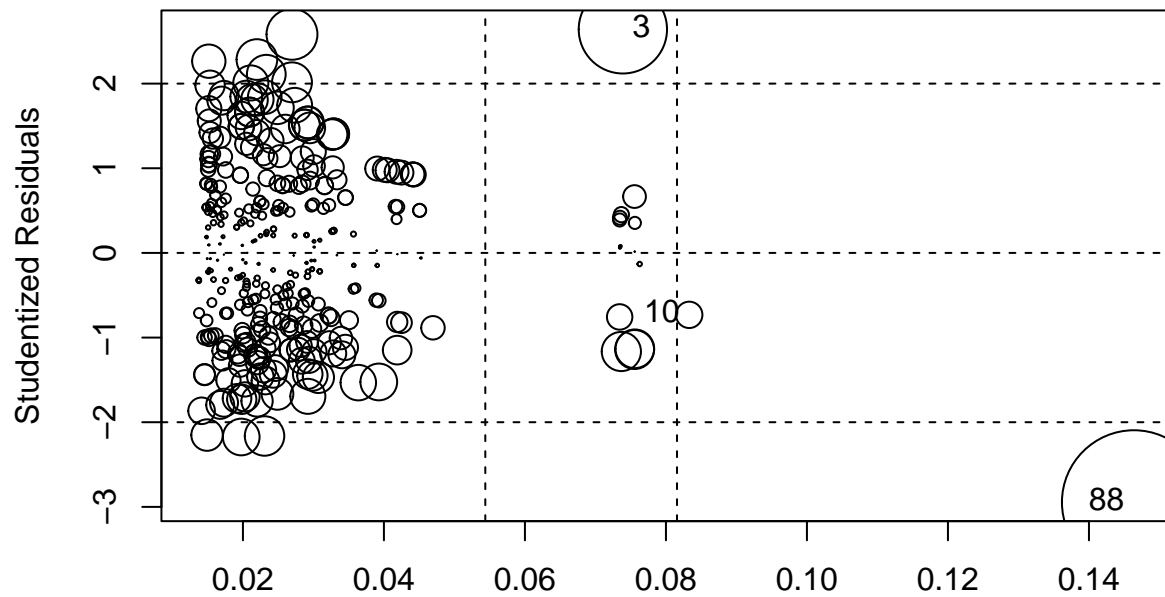
```
## Warning in axis(side = side, at = at, labels = labels, ...): "id.method" is not  
## a graphical parameter
```

```
## Warning in box(...): "id.method" is not a graphical parameter
```

```
## Warning in title(...): "id.method" is not a graphical parameter
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): "id.method" is not a  
## graphical parameter
```


Influence Plot



Hat-Values
Circle size is proportional to Cook's Distance

StudRes	Hat	CookD	Label	StudRes	Hat	CookD	Label
2.6408588	0.0738904	0.0607002	3	-0.7314985	0.0833014	0.0054105	10
-2.9450988	0.1463823	0.1614188	88				

Normality Test Ho: The data is normally distributed Ha: the data is not normally distributed

```
# Normality Test
shapiro.test(sresid)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  sresid
## W = 0.99153, p-value = 0.05511
```

```
ad.test(sresid)
```

```
##
##  Anderson-Darling normality test
##
## data:  sresid
## A = 0.89016, p-value = 0.02271
```

```
cvm.test(sresid)
```

```
##
```

```
## Cramer-von Mises normality test
##
## data:  sresid
## W = 0.13742, p-value = 0.03478
```

```
lillie.test(sresid)
```

```
##
## Lilliefors (Kolmogorov-Smirnov) normality test
##
## data:  sresid
## D = 0.047301, p-value = 0.0716
```

```
pearson.test(sresid)
```

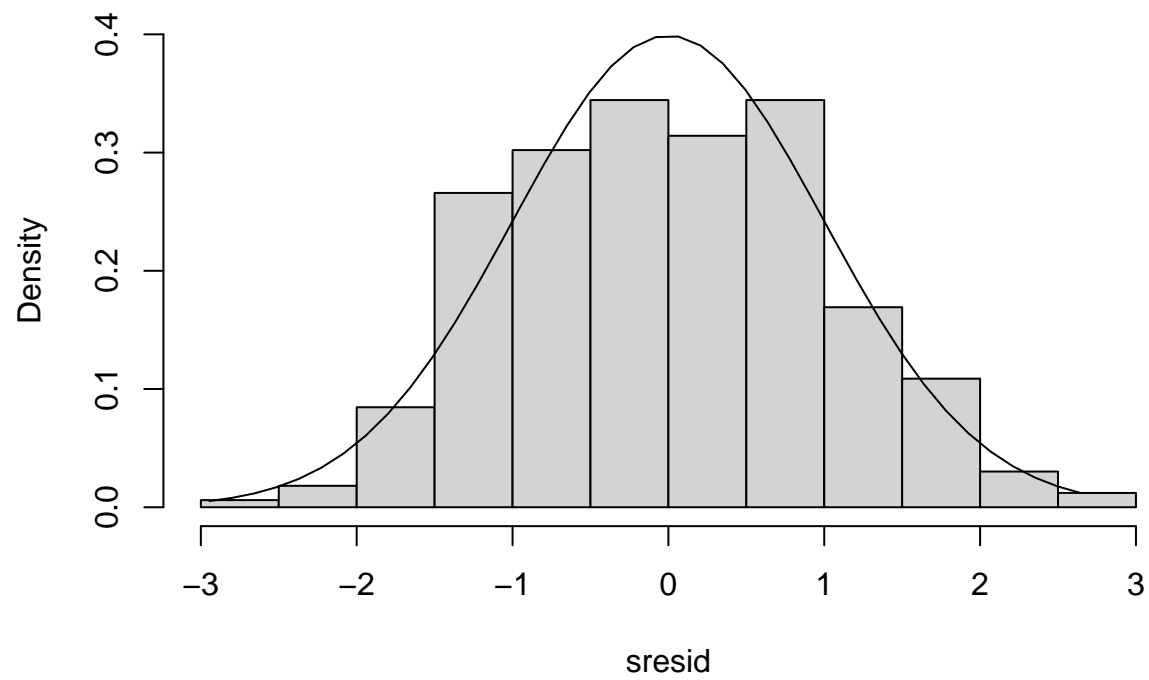
```
##
## Pearson chi-square normality test
##
## data:  sresid
## P = 30.568, p-value = 0.03228
```

```
sf.test(sresid)
```

```
##
## Shapiro-Francia normality test
##
## data:  sresid
## W = 0.99221, p-value = 0.07562
```

```
# the data is not normally distributed
# Histogram of residuals
hist(sresid, freq = FALSE, main = "Distribution of Studentised Residuals", ylim = c(0, 0.4))
xfit <- seq(min(sresid, na.rm = TRUE), max(sresid, na.rm = TRUE), length = 40)
yfit <- dnorm(xfit)
lines(xfit, yfit)
```

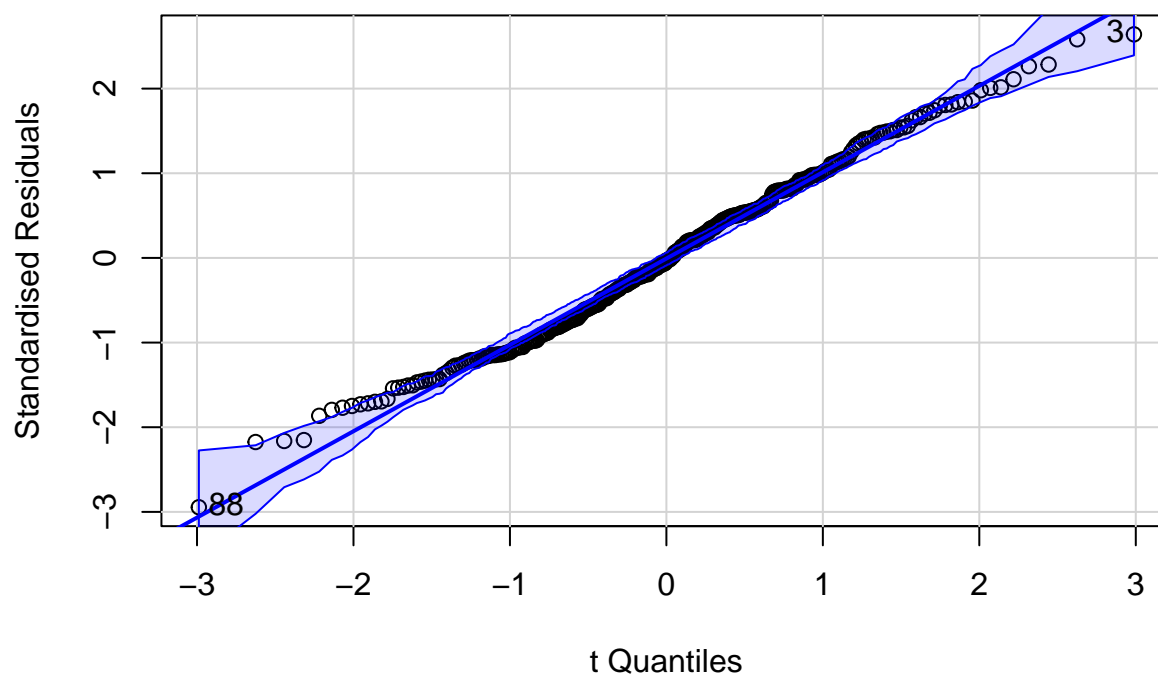
Distribution of Studentised Residuals



```
# QQ-plot of the data
```

```
qqPlot(my_model_jury, ylab = "Standardised Residuals", main = "QQ-Plot of Jury Vote Model Standardised Residuals")
```

QQ-Plot of Jury Vote Model Standardised Residuals



```
## [1] 3 88
```

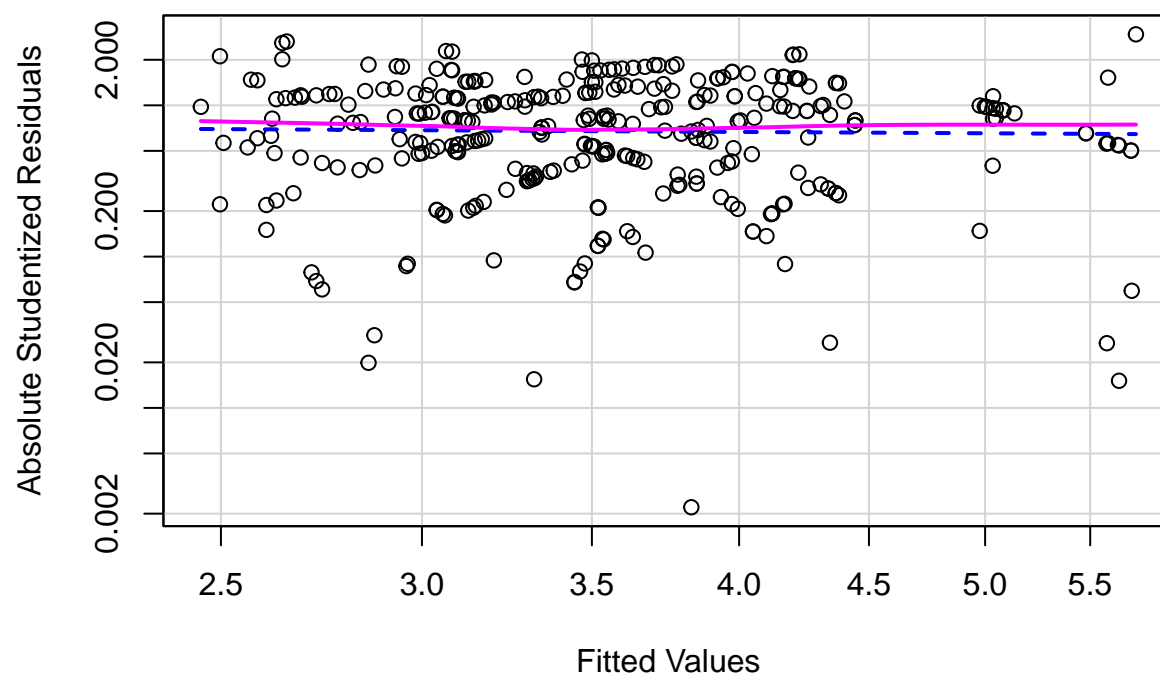
Non-Constant Error Variance Test Ho: constant error variance Ha: Non-constant error Variance

```
# Non-Constant Error Variance Test
ncvTest(my_model_jury)
```

```
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 0.2153073, Df = 1, p = 0.64264
```

```
# plot studentized residuals vs. fitted values
spreadLevelPlot(my_model_jury, main = "Spread-Level Plot for Jury Vote Model")
```

Spread–Level Plot for Jury Vote Model



```
##
## Suggested power transformation: 1.091406
```

Variance Inflation Factors

```
vif(my_model_jury)
```

```
##      CAP_DIST_km      acousticness      speechiness TC_LANGFAM_Armenian
##      1.181514      1.220899      1.187223      1.523284
##      VBlocs1_TC_1      ComVBlocs1_y      VBlocs1_FC_1      VBlocs2_TC_1
##      3.249223      2.641876      1.654895      2.067919
```

```
sqrt(vif(my_model_jury)) > 2
```

```
##      CAP_DIST_km      acousticness      speechiness TC_LANGFAM_Armenian
##      FALSE      FALSE      FALSE      FALSE
##      VBlocs1_TC_1      ComVBlocs1_y      VBlocs1_FC_1      VBlocs2_TC_1
##      FALSE      FALSE      FALSE      FALSE
```

No signs of collinearity