

HW 12 regression in r

Problem 2

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Problem 2: Application Problems

Note that some details are missing for all the following examples, the problems lack a complete explanation, and the code may need adequate comments. In this form, you must present a proper mathematical formulation, a brief background of the problem (and its bibliographical references) and, a much better explanation.

- The olsrr package
 - a. Introduction to olsrr (<https://olsrr.rsquaredacademy.com/articles/intro.html>)
 - b. Variable Selection Methods (https://olsrr.rsquaredacademy.com/articles/variable_selection.html)
 - c. Residual Diagnostics (https://olsrr.rsquaredacademy.com/articles/residual_diagnostics.html)
 - d. Heteroscedasticity (<https://olsrr.rsquaredacademy.com/articles/heteroskedasticity.html>)
 - e. Measures of Influence (https://olsrr.rsquaredacademy.com/articles/influence_measures.html)
 - f. Collinearity Diagnostics, Model Fit & Variable Contribution (https://olsrr.rsquaredacademy.com/articles/regression_diagnostics.html)
- The blorr package
 - a. A Short Introduction to the blorr Package (<https://blorr.rsquaredacademy.com/articles/introduction.html>)

Introduction to olsrr

This document is a quick start guide to the tools offered by olsrr. Other vignettes provide more details on specific topics: - Residual Diagnostics: Includes plots to examine residuals to validate OLS assumptions - Variable selection: Different variable selection procedures such as all possible regression, best subset regression, stepwise regression, stepwise forward regression and stepwise backward regression - Heteroskedasticity: Tests for heteroskedasticity include bartlett test, breusch pagan test, score test and f

test - Measures of influence: Includes 10 different plots to detect and identify influential observations -
Collinearity diagnostics: VIF, Tolerance and condition indices to detect collinearity and plots for assessing
model fit and contributions of variables

This example uses **mtcars** dataset. This dataset contains a subset of the fuel economy data that the EPA makes available on <https://fuelconomy.gov/> (<https://fuelconomy.gov/>). It contains only models which had a new release every year between 1999 and 2008 - this was used as a proxy for the popularity of the car.

A data frame with 234 rows and 11 variables:

- manufacturer: manufacturer name
- model: model name
- displ: engine displacement, in litres
- year: year of manufacture
- cyl: number of cylinders
- trans: type of transmission
- drv: the type of drive train, where f = front-wheel drive, r = rear wheel drive, 4 = 4wd
- cty: city miles per gallon
- hwy: highway miles per gallon
- fl: fuel type
- class: "type" of car

Regression

Hide

```
library(olsrr)
```

```
Attaching package: 'olsrr'
```

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

```
  cement
```

```
The following object is masked from 'package:datasets':
```

```
  rivers
```

Hide

```
ols_regress(mpg ~ disp + hp + wt + qsec, data = mtcars)
```

Model Summary							
R	0.914	RMSE	2.409				
R-Squared	0.835	MSE	6.875				
Adj. R-Squared	0.811	Coef. Var	13.051				
Pred R-Squared	0.771	AIC	159.070				
MAE	1.858	SBC	167.864				
RMSE: Root Mean Square Error MSE: Mean Square Error MAE: Mean Absolute Error AIC: Akaike Information Criteria SBC: Schwarz Bayesian Criteria							
ANOVA							
	Sum of Squares	DF	Mean Square	F	Sig.		
Regression	940.412	4	235.103	34.195	0.0000		
Residual	185.635	27	6.875				
Total	1126.047	31					
Parameter Estimates							
model	Beta	Std. Error	Std. Beta	t	Sig	lower	upper
(Intercept)	27.330	8.639		3.164	0.004	9.604	45.055
disp	0.003	0.011	0.055	0.248	0.806	-0.019	0.025
hp	-0.019	0.016	-0.212	-1.196	0.242	-0.051	0.013
wt	-4.609	1.266	-0.748	-3.641	0.001	-7.206	-2.012
qsec	0.544	0.466	0.161	1.166	0.254	-0.413	1.501

In the presence of interaction terms in the model, the predictors are scaled and centered before computing the standardized betas. `ols_regress()` will detect interaction terms automatically but in case you have created a new variable instead of using the inline function `*`, you can indicate the presence of interaction

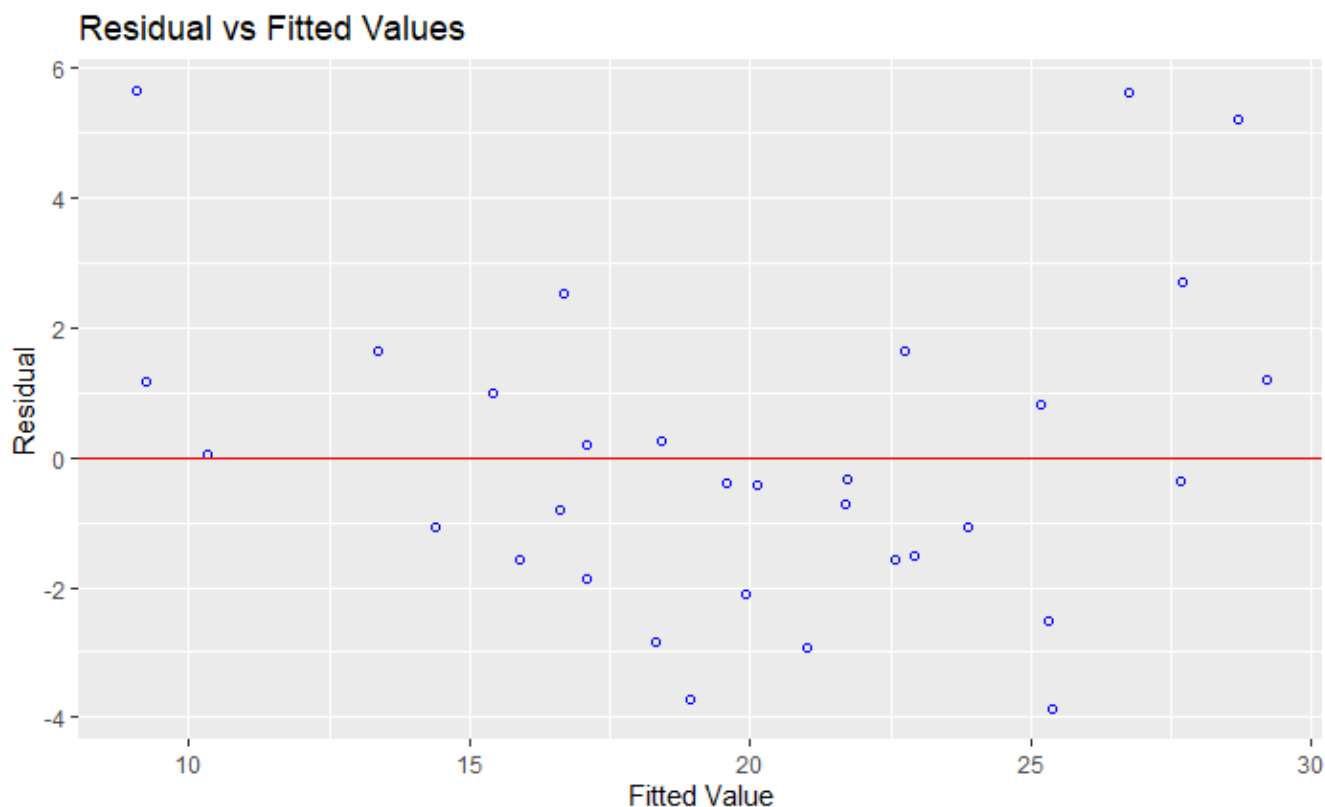
terms by setting `iterm` to `TRUE`.

Residual vs Fitted Values Plot

Plot to detect non-linearity, unequal error variances, and outliers. Each point is the error in each vector. Red line just marks the 0 to have a visual benchmark.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_resid_fit(model)
```



DFBETAs Panel

DFBETAs measure the difference in each parameter estimate with and without the influential observation. `dfbetas_panel` creates plots to detect influential observations using DFBETAs.

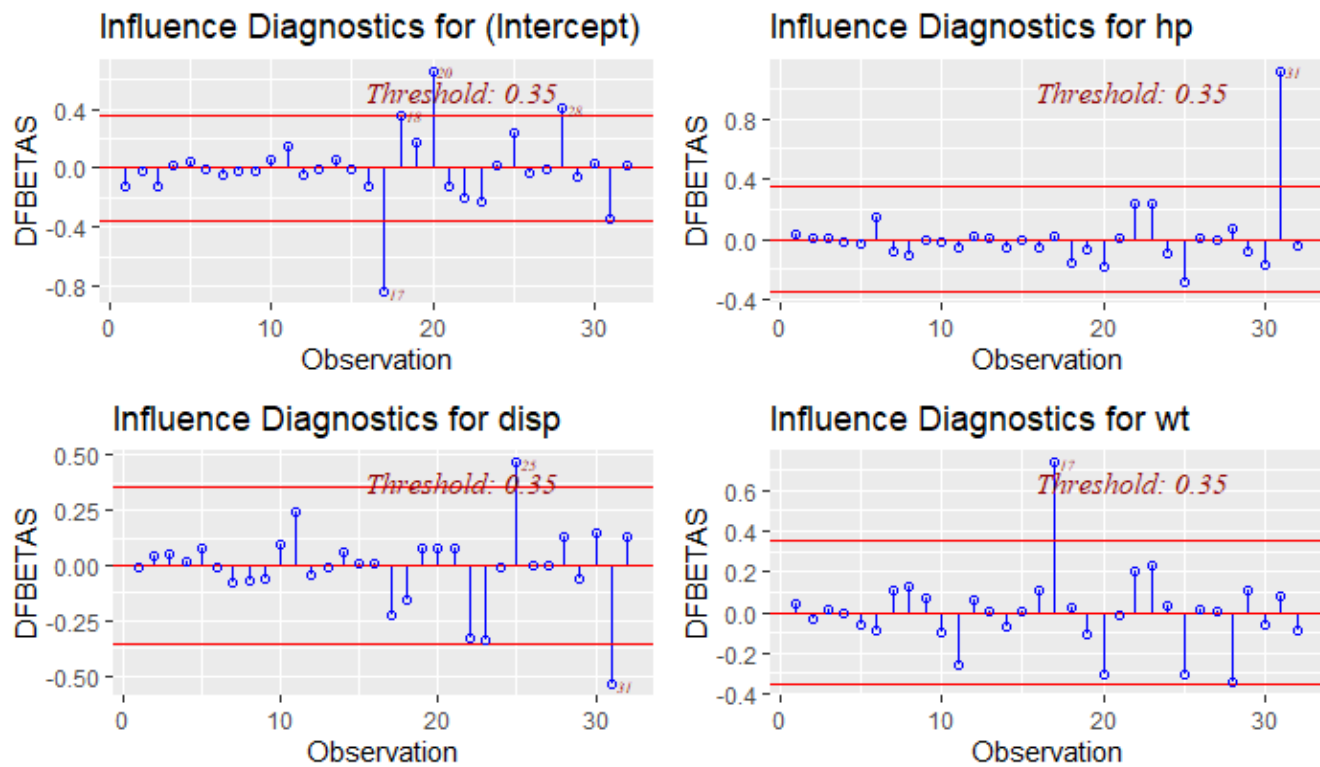
Belsley, Kuh, and Welsch MATH sugirieron una estadística que indica cuanto el coeficiente de regresión estimado b_i cambia, en unidades de desviaciones estándar, si la i — *ésima* observación fuera eliminada. La estadística es

$$DFBETAS_{i,j} = \frac{b_i - b_{j(i)}}{\sqrt{s_i^2 C_{jj}}}$$

Donde $MATH$ es la varianza del coeficiente de regresión b_j calculada sin la i — *ésima* observación. Un valor grande de $DFBETAS_{j,i}$ indica que la i — *ésima* observación tiene una considerable influencia sobre el j — *ésimo* coeficiente de regresión b_j . reference
(http://red.unal.edu.co/cursos/ciencias/2007315/html/un6/cont_12_73.html)

Hide

```
model <- lm(mpg ~ disp + hp + wt, data = mtcars)
ols_plot_dfbetas(model)
```



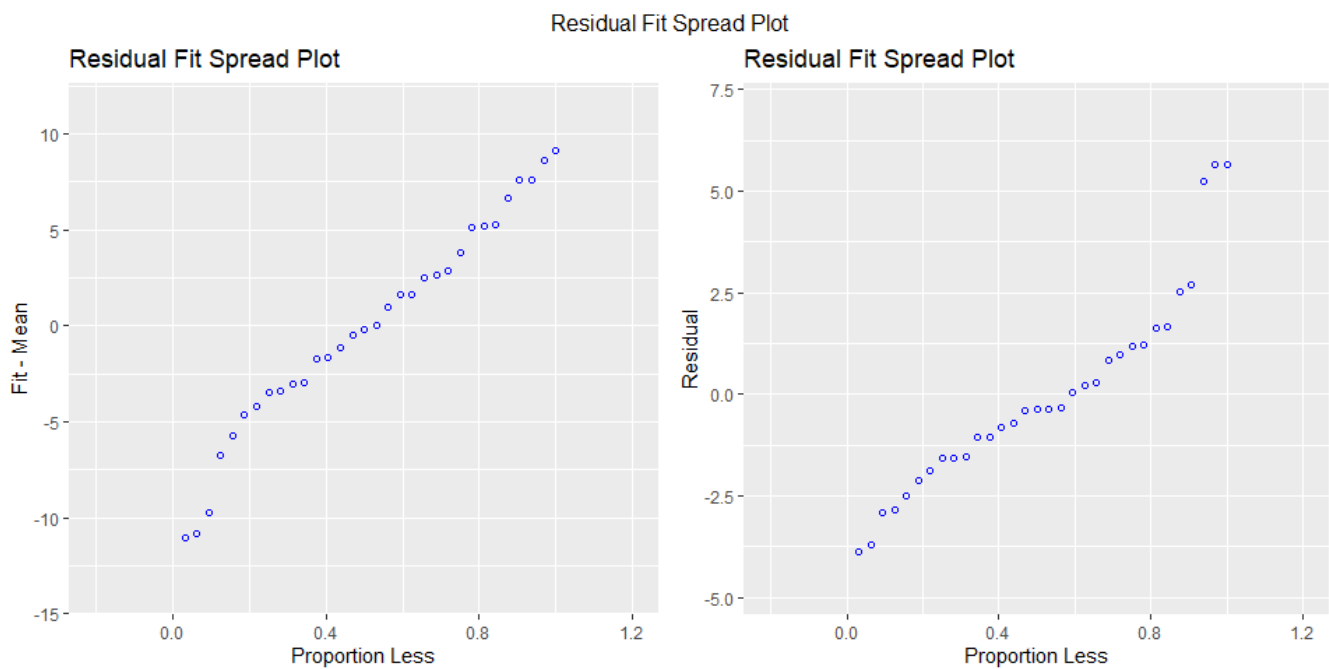
Residual Fit Spread Plot

Plot to detect non-linearity, influential observations and outliers.

Each spread plot is a graph of centered data values plotted against the estimated cumulative probability. Thus, spread plots are similar to a (rotated) plot of the empirical cumulative distribution function. reference (<https://blogs.sas.com/content/iml/2013/06/12/interpret-residual-fit-spread-plot.html>)

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_resid_fit_spread(model)
```



Breusch Pagan Test

Breusch Pagan test is used to test for heteroskedasticity (non-constant error variance). It tests whether the variance of the errors from a regression is dependent on the values of the independent variables. It is a χ^2 test.

Null hypothesis implies the variance is constant and using an alpha of 0.05 then in this case we reject the null hypothesis because p-value is 0.23

Hide

```
model <- lm(mpg ~ disp + hp + wt + drat, data = mtcars)
ols_test_breusch_pagan(model)
```

Breusch Pagan Test for Heteroskedasticity

Ho: the variance is constant

Ha: the variance is not constant

Data

Response : mpg

Variables: fitted values of mpg

Test Summary

```
DF          = 1
Chi2        = 1.429672
Prob > Chi2 = 0.231818
```

Collinearity Diagnostics

collinearity, in statistics, correlation between predictor variables (or independent variables), such that they express a linear relationship in a regression model. When predictor variables in the same regression model are correlated, they cannot independently predict the value of the dependent variable.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_coll_diag(model)
```

Tolerance and Variance Inflation Factor

Variables <chr>	Tolerance <dbl>	VIF <dbl>
disp	0.1252279	7.985439
hp	0.1935450	5.166758
wt	0.1445726	6.916942
qsec	0.3191708	3.133119
4 rows		

Eigenvalue and Condition Index

Eigenvalue <dbl>	Condition Index <dbl>	intercept <dbl>	disp <dbl>	hp <dbl>	wt <dbl>
4.721487187	1.000000	0.000123237	0.001132468	0.001413094	0.0005253393
0.216562203	4.669260	0.002617424	0.036811051	0.027751289	0.0002096014
0.050416837	9.677242	0.001656551	0.120881424	0.392366164	0.0377028008
0.010104757	21.616057	0.025805998	0.777260487	0.059594623	0.7017528428
0.001429017	57.480524	0.969796790	0.063914571	0.518874831	0.2598094157
5 rows					

Stepwise Regression

Build regression model from a set of candidate predictor variables by entering and removing predictors based on p values, in a stepwise manner until there is no variable left to enter or remove any more.

Here p-value and Akaike Information Criterion are used to decide which model is the best in each step of the algorithm.

Variable Selection

[Hide](#)

```
# stepwise regression
model <- lm(y ~ ., data = surgical)
ols_step_both_p(model)
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	802.606	806.584	646.794	0.00000	0.00000
1	liver_test (+)	771.875	777.842	616.009	0.45454	0.44405
2	alc_heavy (+)	761.439	769.395	605.506	0.56674	0.54975
3	enzyme_test (+)	750.509	760.454	595.297	0.65900	0.63854
4	pindex (+)	735.715	747.649	582.943	0.75015	0.72975
5	bcs (+)	730.620	744.543	579.638	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig.	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914

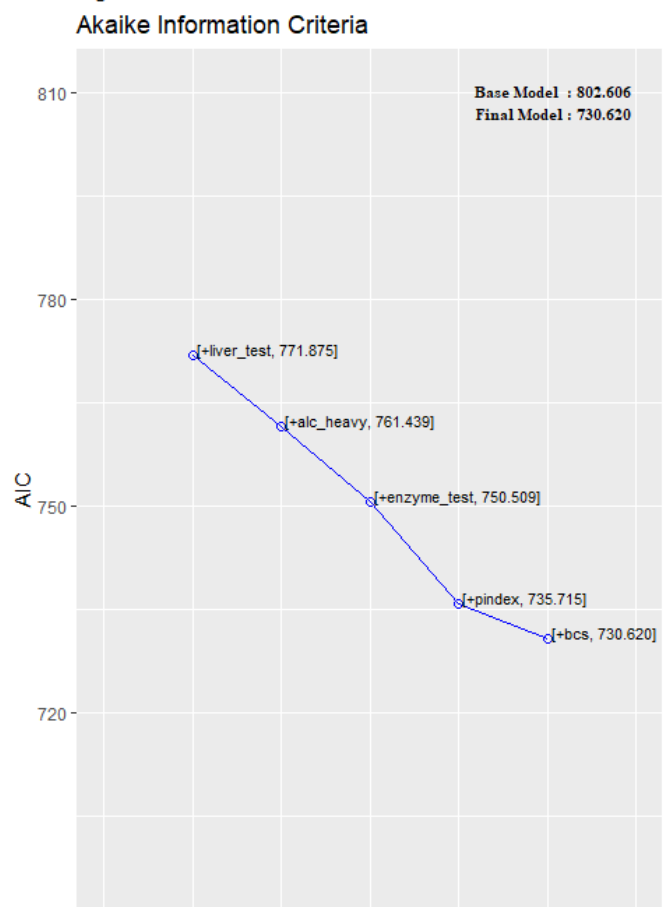
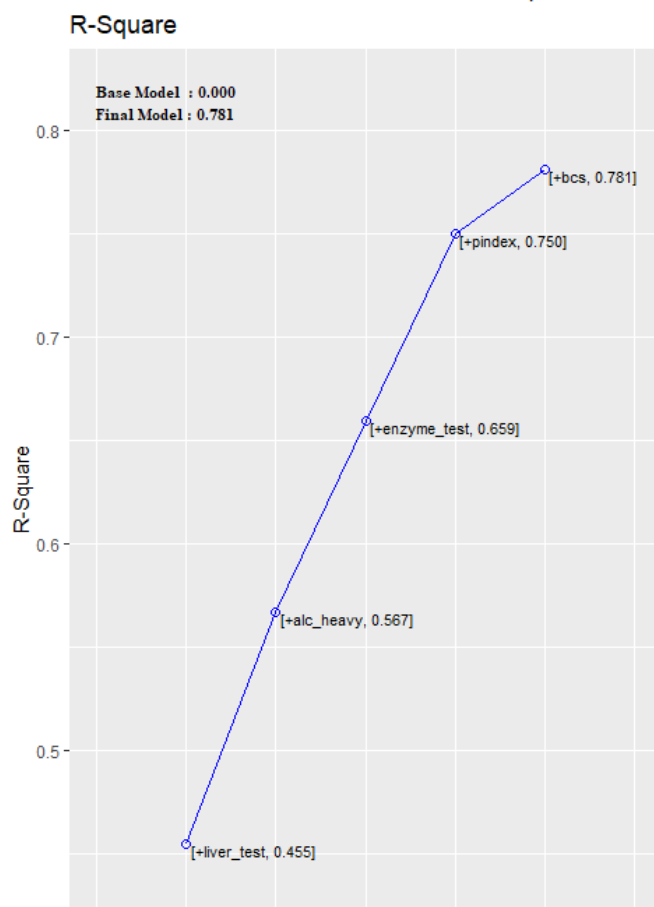
-758.746						
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
138.779						
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
461.878						
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
13.077						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						
bcs	59.864	23.060	0.241	2.596	0.012	13.498
106.230						

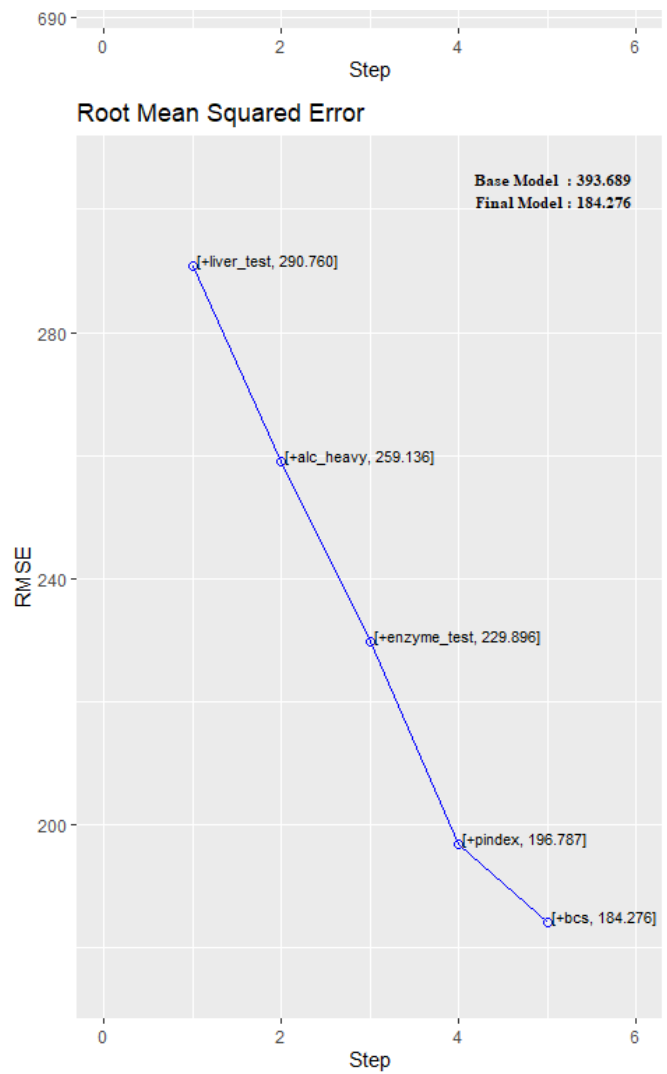
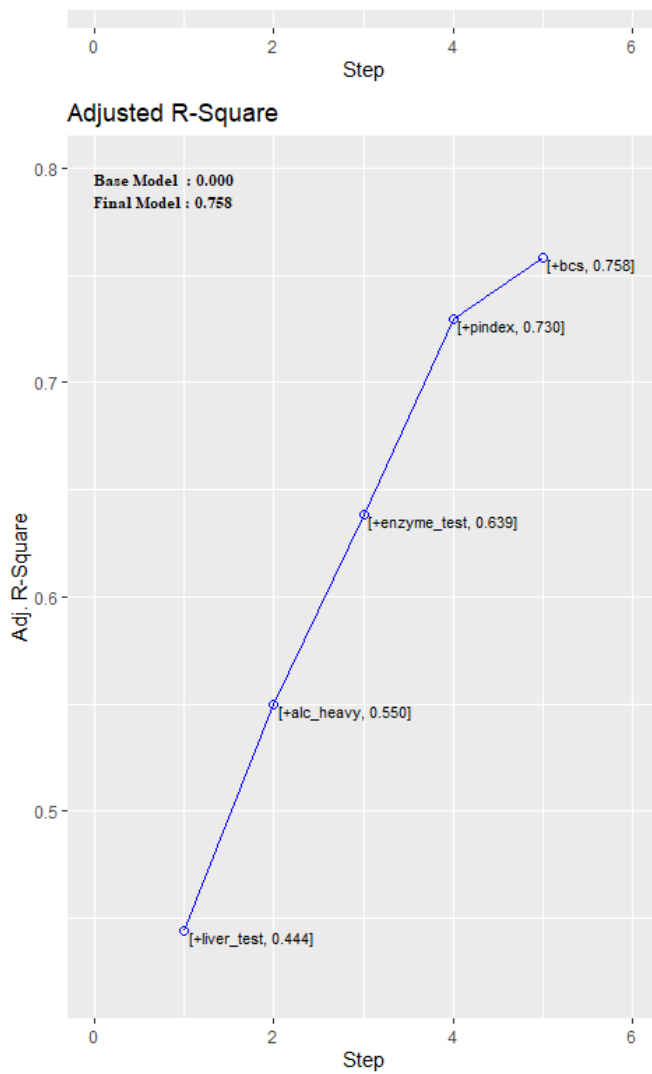
Plot

Hide

```
model <- lm(y ~ ., data = surgical)
k <- ols_step_both_p(model)
plot(k)
```

Stepwise Both Direction Regression





Stepwise AIC Backward Regression

Build regression model from a set of candidate predictor variables by removing predictors based on Akaike Information Criteria, in a stepwise manner until there is no variable left to remove any more.

Variable Selection

Hide

```
# stepwise aic backward regression
model <- lm(y ~ ., data = surgical)
k <- ols_step_backward_aic(model)
k
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Full Model	736.390	756.280	586.665	0.78184	0.74305
1	alc_mod	734.407	752.308	583.884	0.78177	0.74856
2	gender	732.494	748.406	581.290	0.78142	0.75351
3	age	730.620	744.543	578.844	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

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Parameter Estimates

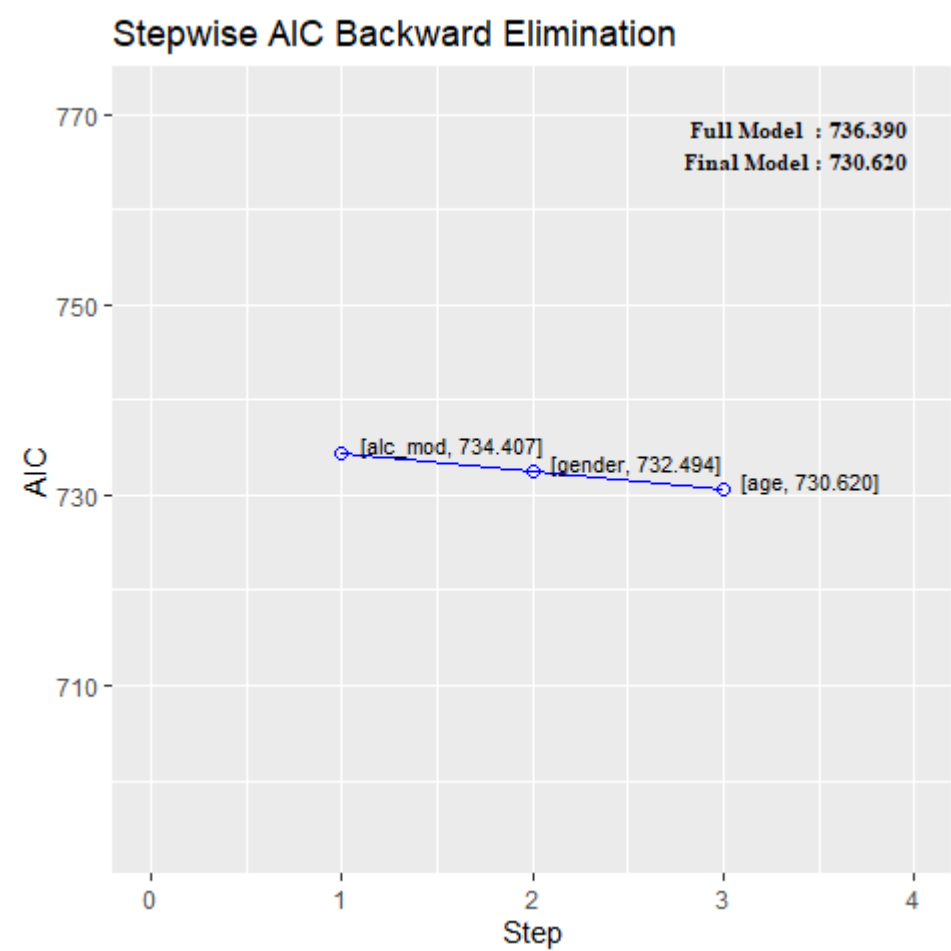
model	Beta	Std. Error	Std. Beta	t	Sig.	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914
-758.746						
bcs	59.864	23.060	0.241	2.596	0.012	13.498

106.230						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
13.077						
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
138.779						
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
461.878						

Plot

Hide

```
model <- lm(y ~ ., data = surgical)
k <- ols_step_backward_aic(model)
plot(k)
```



Variable Selection Methods

Attaching package: 'ggplot2'

The following object is masked from 'Auto':

mpg

Attaching package: 'goftest'

The following objects are masked from 'package:nortest':

ad.test, cvm.test

Introduction

All Possible Regression

All subset regression tests, all possible subsets of the set of potential independent variables. If there are K potential independent variables (besides the constant), then there are 2^K distinct subsets of them to be tested. For example, if you have 10 candidate independent variables, the number of subsets to be tested is 2^{10} , which is 1024, and if you have 20 candidate variables, the number is 2^{20} , which is more than one million.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_step_all_possible(model)
```

	Index <int>	N <int>	Predictors <chr>	R-Square <dbl>	Adj. R-Square <dbl>	Mallow's Cp <dbl>
3	1	1	wt	0.7528328	0.7445939	0.70869536
1	2	1	disp	0.7183433	0.7089548	0.67512054
2	3	1	hp	0.6024373	0.5891853	0.50969578
4	4	1	qsec	0.1752963	0.1478062	0.07541973
8	5	2	hp wt	0.8267855	0.8148396	0.78108710
10	6	2	wt qsec	0.8264161	0.8144448	0.77856272
6	7	2	disp wt	0.7809306	0.7658223	0.72532105
5	8	2	disp hp	0.7482402	0.7308774	0.69454380
7	9	2	disp qsec	0.7215598	0.7023571	0.66395284

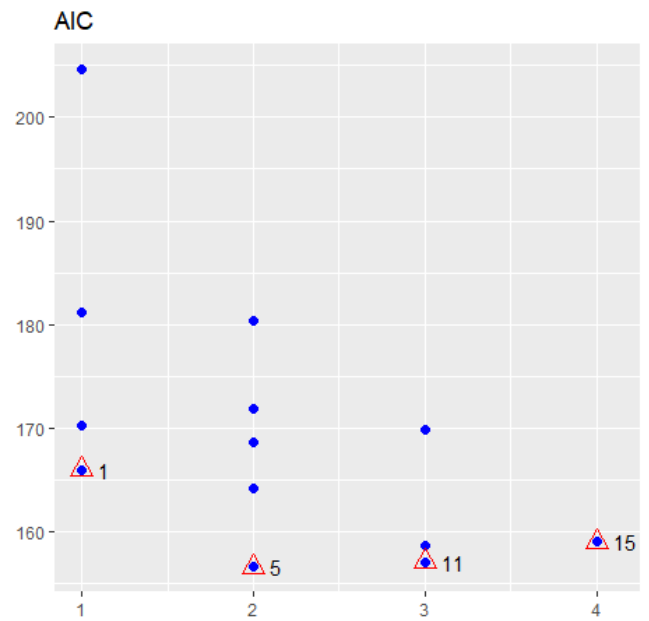
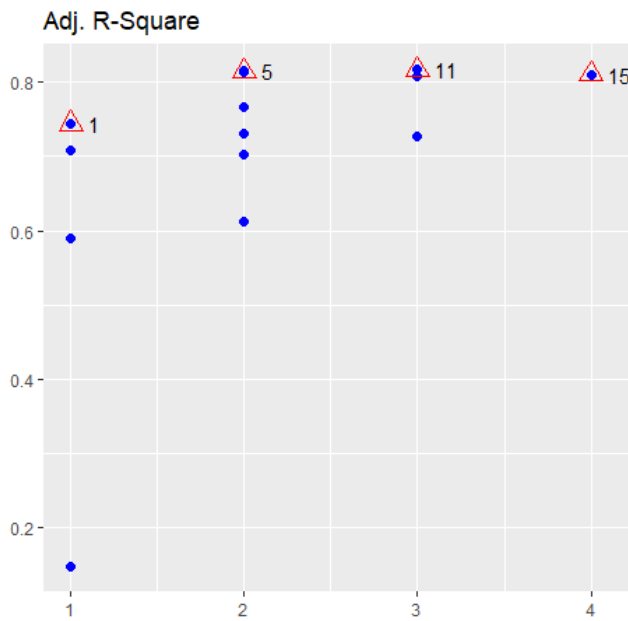
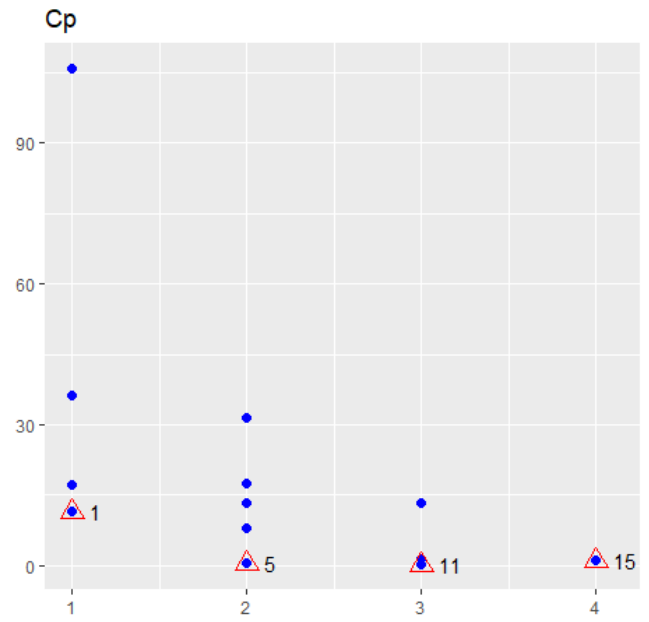
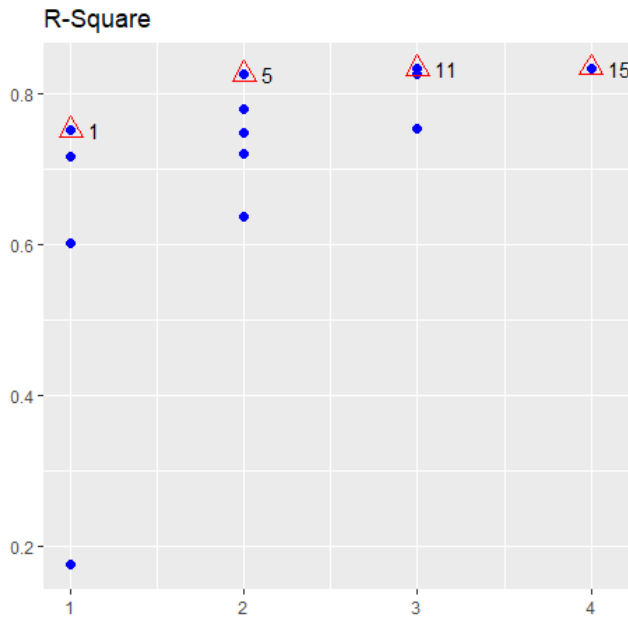
Index <int>	N <int>	Predictors <chr>	R-Square <dbl>	Adj. R-Square <dbl>	Mallow's Cp <dbl>
9	10	2 hp qsec	0.6368769	0.6118339	0.52014395
1-10 of 15 rows				Previous	1 2 Next

The `plot` method shows the panel of fit criteria for all possible regression methods.

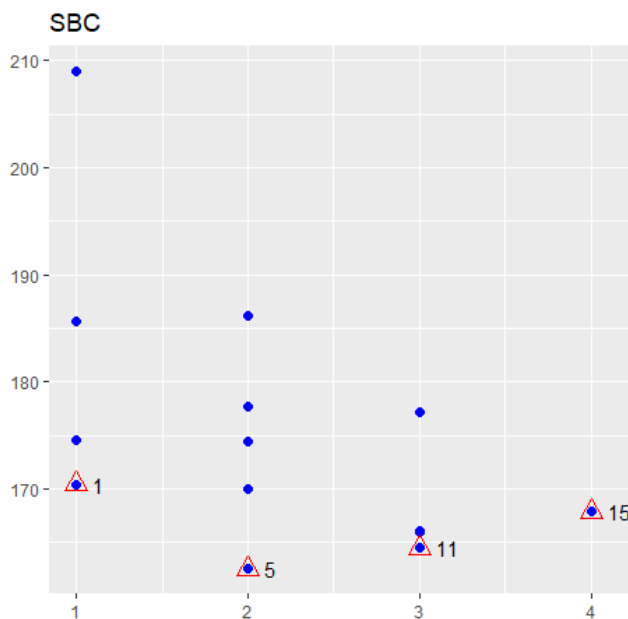
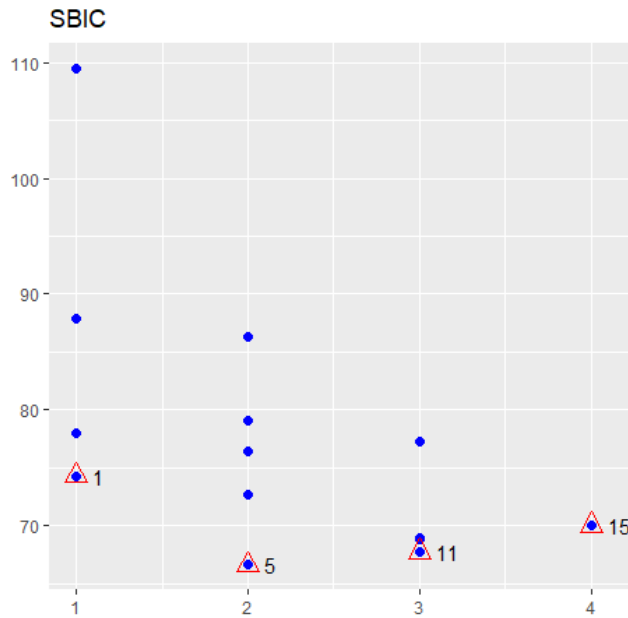
Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
k <- ols_step_all_possible(model)
plot(k)
```

All Possible Regression



All Possible Regression



Best Subset Regression

Select the subset of predictors that do the best at meeting some well-defined objective criterion, such as having the largest R^2 value or the smallest MSE, Mallows's C_p or AIC.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_step_best_subset(model)
```

Best Subsets Regression										

Model	Index	Predictors								

	1	wt								
	2	hp wt								
	3	hp wt qsec								
	4	disp hp wt qsec								

Subsets Regression Summary										

Model	R-Square	Adj. R-Square	Pred R-Square	C(p)	AIC	SBIC	SBC	MSEP	FPE	HSP

1	0.7528	0.7446	0.7087	12.4809	166.0294	74.2916	170.4266	296.9167	9.8572	0.31
99	0.2801									
2	0.8268	0.8148	0.7811	2.3690	156.6523	66.5755	162.5153	215.5104	7.3563	0.24
02	0.2091									
3	0.8348	0.8171	0.782	3.0617	157.1426	67.7238	164.4713	213.1929	7.4756	0.24
61	0.2124									
4	0.8351	0.8107	0.771	5.0000	159.0696	70.0408	167.8640	220.8882	7.9497	0.26
44	0.2259									

AIC: Akaike Information Criteria										
SBIC: Sawa's Bayesian Information Criteria										
SBC: Schwarz Bayesian Criteria										
MSEP: Estimated error of prediction, assuming multivariate normality										
FPE: Final Prediction Error										
HSP: Hocking's Sp										
APC: Amemiya Prediction Criteria										

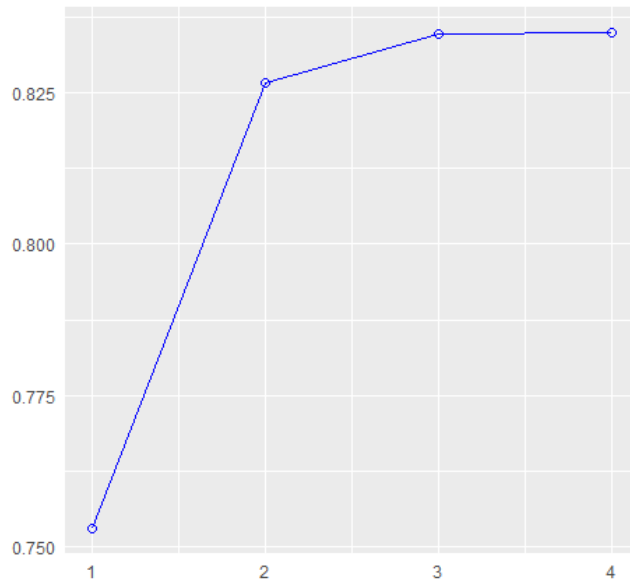
The `plot` method shows the panel of fit criteria for best subset regression methods.

Hide

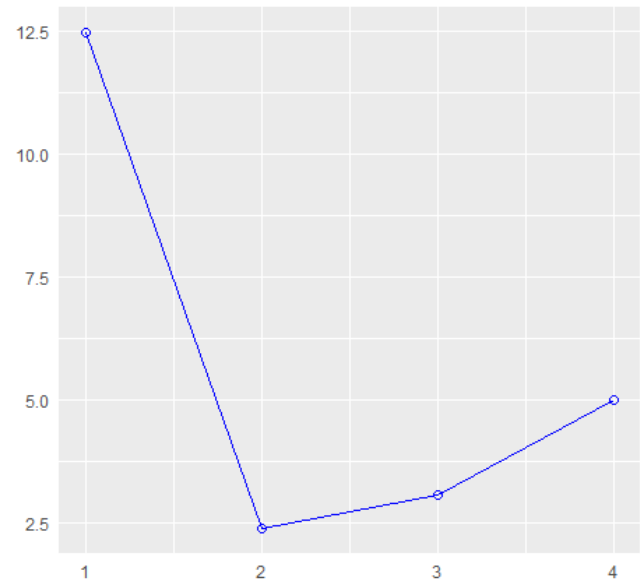
```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
k <- ols_step_best_subset(model)
plot(k)
```


Best Subset Regression

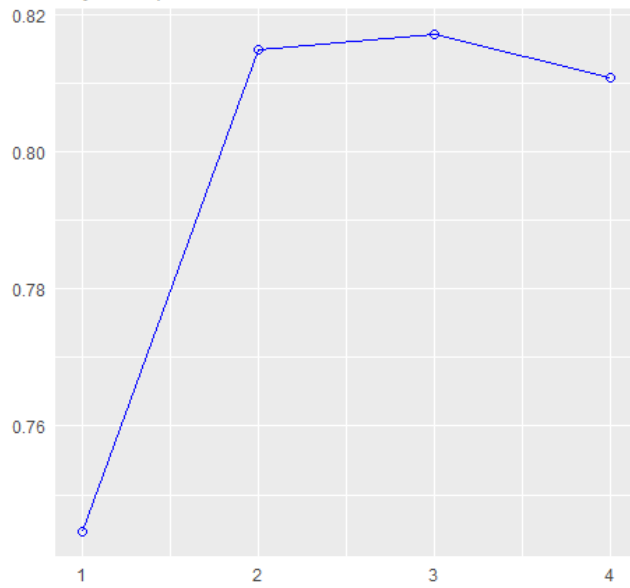
R-Square



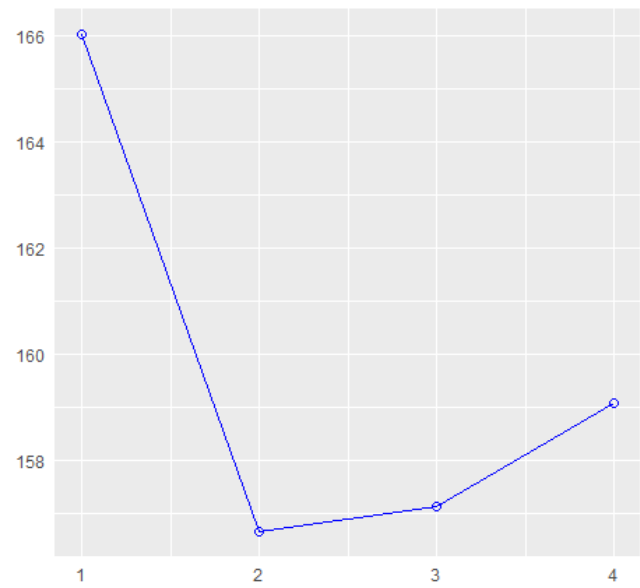
C(p)



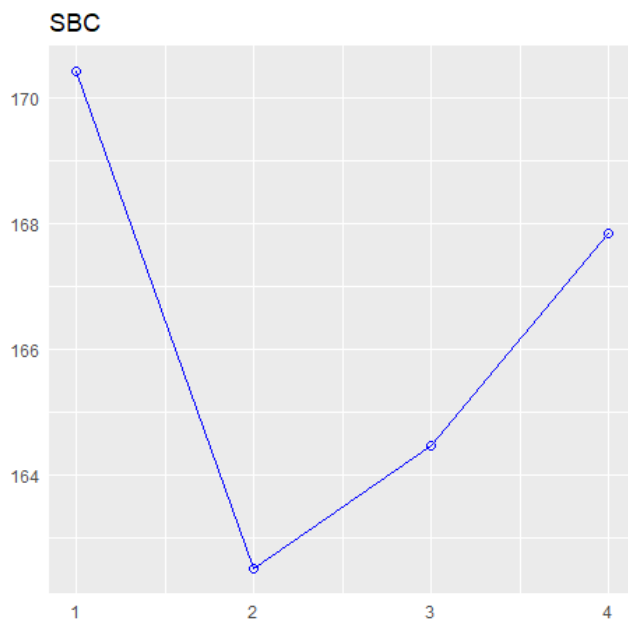
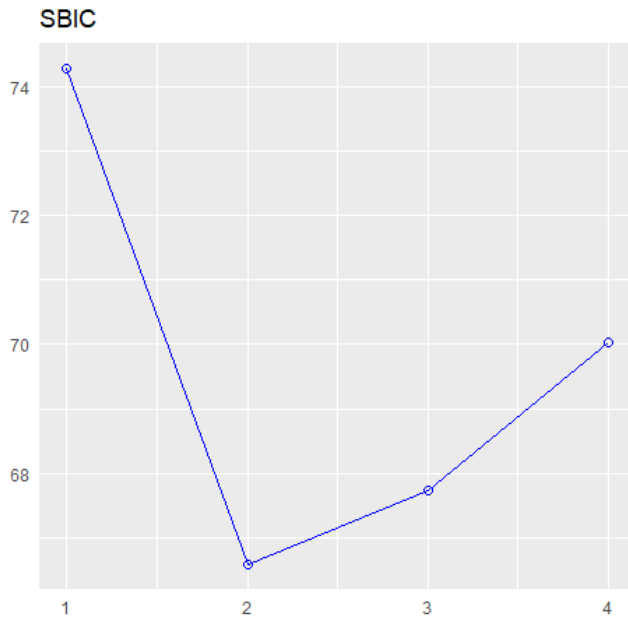
Adj. R-Square



AIC



Best Subset Regression



Stepwise Forward Regression

Build regression model from a set of candidate predictor variables by entering predictors based on p values, in a stepwise manner until there is no variable left to enter any more. The model should include all the candidate predictor variables. If details is set to TRUE , each step is displayed.

Variable Selection

Hide

```
# stepwise forward regression
model <- lm(y ~ ., data = surgical)
ols_step_forward_p(model)
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	802.606	806.584	646.794	0.00000	0.00000
1	liver_test	771.875	777.842	616.009	0.45454	0.44405
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RMSE: Root Mean Square Error

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MAE: Mean Absolute Error

AIC: Akaike Information Criteria

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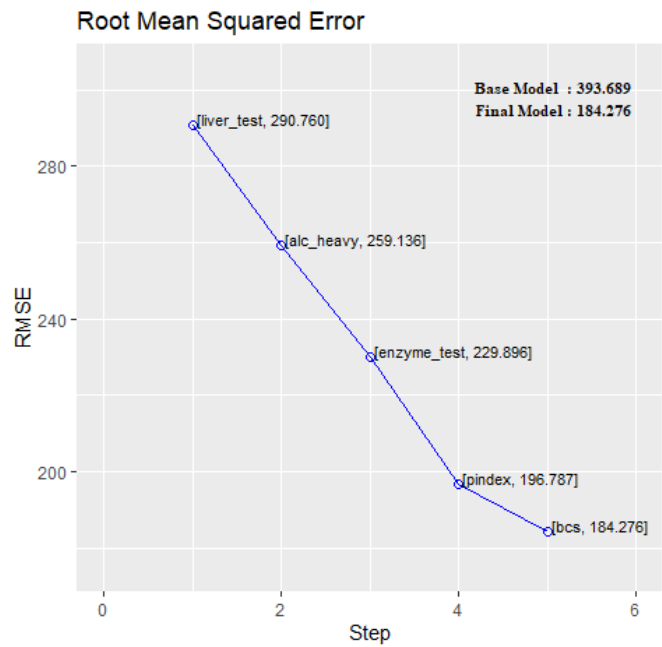
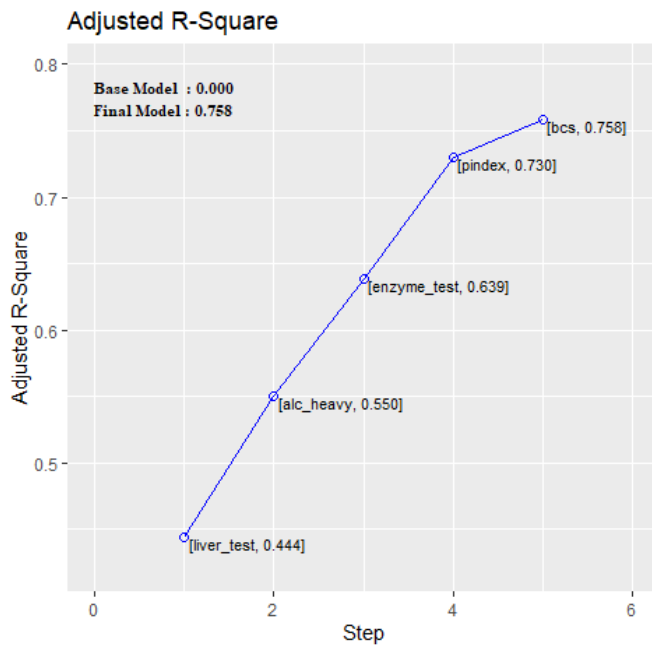
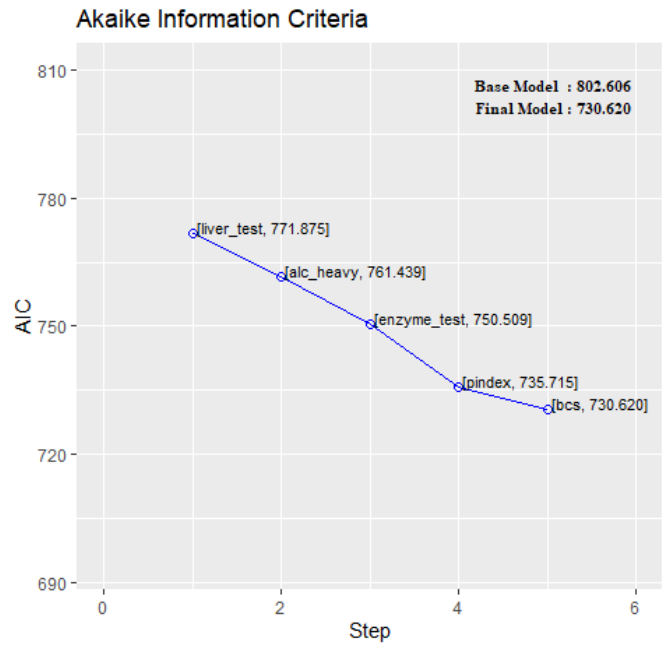
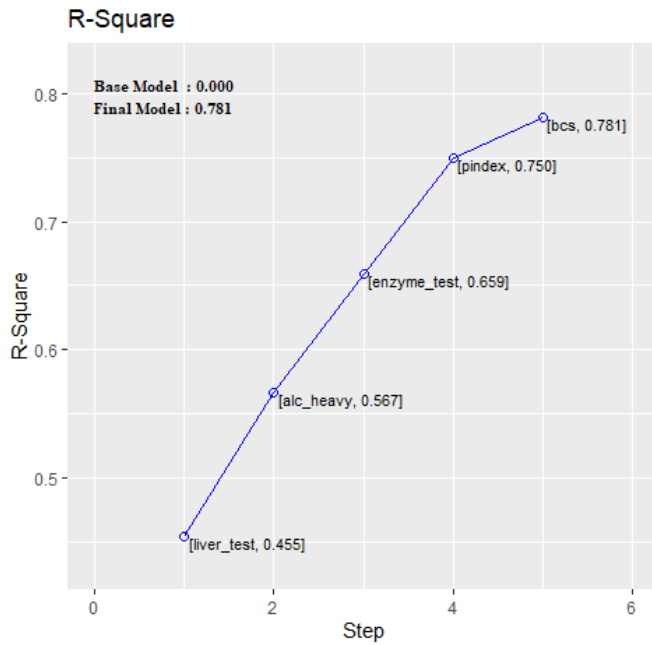
-758.746						
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
138.779						
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
461.878						
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
13.077						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						
bcs	59.864	23.060	0.241	2.596	0.012	13.498
106.230						

Plot

Hide

```
model <- lm(y ~ ., data = surgical)
k <- ols_step_forward_p(model)
plot(k)
```


Stepwise Forward Regression



Detailed Output

Hide

```
# stepwise forward regression
model <- lm(y ~ ., data = surgical)
ols_step_forward_p(model, details = TRUE)
```

Forward Selection Method

Candidate Terms:

1. bcs
2. pindex
3. enzyme_test
4. liver_test
5. age
6. gender
7. alc_mod
8. alc_heavy

Step => 0

Model => $y \sim 1$

R2 => 0

Initiating stepwise selection...

Selection Metrics Table

Predictor	Pr(> t)	R-Squared	Adj. R-Squared	AIC
liver_test	0.00000	0.455	0.444	771.875
enzyme_test	0.00000	0.334	0.322	782.629
pindex	0.00155	0.177	0.161	794.100
alc_heavy	0.00172	0.174	0.158	794.301
bcs	0.01025	0.120	0.103	797.697
alc_mod	0.19286	0.032	0.014	802.828
gender	0.20972	0.030	0.011	802.956
age	0.39073	0.014	-0.005	803.834

Step => 1

Selected => liver_test

Model => $y \sim \text{liver_test}$

R2 => 0.455

Selection Metrics Table

Predictor	Pr(> t)	R-Squared	Adj. R-Squared	AIC
alc_heavy	0.00065	0.567	0.550	761.439
enzyme_test	0.00089	0.562	0.544	762.077
pindex	0.07087	0.489	0.469	770.387
alc_mod	0.10979	0.481	0.461	771.141

gender	0.79395	0.455	0.434	773.802
age	0.83908	0.455	0.434	773.831
bcs	0.93062	0.455	0.433	773.867

```
-----
Step      => 2
Selected  => alc_heavy
Model     => y ~ liver_test + alc_heavy
R2        => 0.567
```

Selection Metrics Table

Predictor	Pr(> t)	R-Squared	Adj. R-Squared	AIC
enzyme_test	0.00057	0.659	0.639	750.509
pindex	0.00961	0.622	0.599	756.125
bcs	0.55687	0.570	0.544	763.063
age	0.58269	0.569	0.544	763.110
alc_mod	0.91757	0.567	0.541	763.428
gender	0.93799	0.567	0.541	763.433

```
-----
Step      => 3
Selected  => enzyme_test
Model     => y ~ liver_test + alc_heavy + enzyme_test
R2        => 0.659
```

Selection Metrics Table

Predictor	Pr(> t)	R-Squared	Adj. R-Squared	AIC
pindex	1e-04	0.750	0.730	735.715
bcs	0.21294	0.670	0.643	750.782
alc_mod	0.75743	0.660	0.632	752.403
age	0.77290	0.660	0.632	752.416
gender	0.99197	0.659	0.631	752.509

```
-----
Step      => 4
Selected  => pindex
Model     => y ~ liver_test + alc_heavy + enzyme_test + pindex
R2        => 0.75
```

Selection Metrics Table

Predictor	Pr(> t)	R-Squared	Adj. R-Squared	AIC
bcs	0.01248	0.781	0.758	730.620
age	0.86220	0.750	0.724	737.680

gender	0.96390	0.750	0.724	737.712
alc_mod	0.97040	0.750	0.724	737.713

```
-----
Step      => 5
Selected  => bcs
Model     => y ~ liver_test + alc_heavy + enzyme_test + pindex + bcs
R2        => 0.781
```

Selection Metrics Table

Predictor	Pr(> t)	R-Squared	Adj. R-Squared	AIC
age	0.74164	0.781	0.754	732.494
gender	0.80666	0.781	0.753	732.551
alc_mod	0.94086	0.781	0.753	732.614

No more variables to be added.

Variables Selected:

```
=> liver_test
=> alc_heavy
=> enzyme_test
=> pindex
=> bcs
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	802.606	806.584	646.794	0.00000	0.00000
1	liver_test	771.875	777.842	616.009	0.45454	0.44405
2	alc_heavy	761.439	769.395	605.506	0.56674	0.54975
3	enzyme_test	750.509	760.454	595.297	0.65900	0.63854
4	pindex	735.715	747.649	582.943	0.75015	0.72975
5	bcs	730.620	744.543	579.638	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839

Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error
MSE: Mean Square Error
MAE: Mean Absolute Error
AIC: Akaike Information Criteria
SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
pindex	8.924	1.808	0.380	4.935	0.000	5.288
bcs	59.864	23.060	0.241	2.596	0.012	13.498

Stepwise Backward Regression

Build regression model from a set of candidate predictor variables by removing predictors based on p values, in a stepwise manner until there is no variable left to remove any more. The model should include all the candidate predictor variables. If details is set to TRUE , each step is displayed.

Variable Selection

[Hide](#)

```
# stepwise backward regression  
model <- lm(y ~ ., data = surgical)  
ols_step_backward_p(model)
```


Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Full Model	736.390	756.280	586.665	0.78184	0.74305
1	alc_mod	734.407	752.308	584.276	0.78177	0.74856
2	gender	732.494	748.406	581.938	0.78142	0.75351
3	age	730.620	744.543	579.638	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

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ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig.	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914 -758.746
bcs	59.864	23.060	0.241	2.596	0.012	13.498

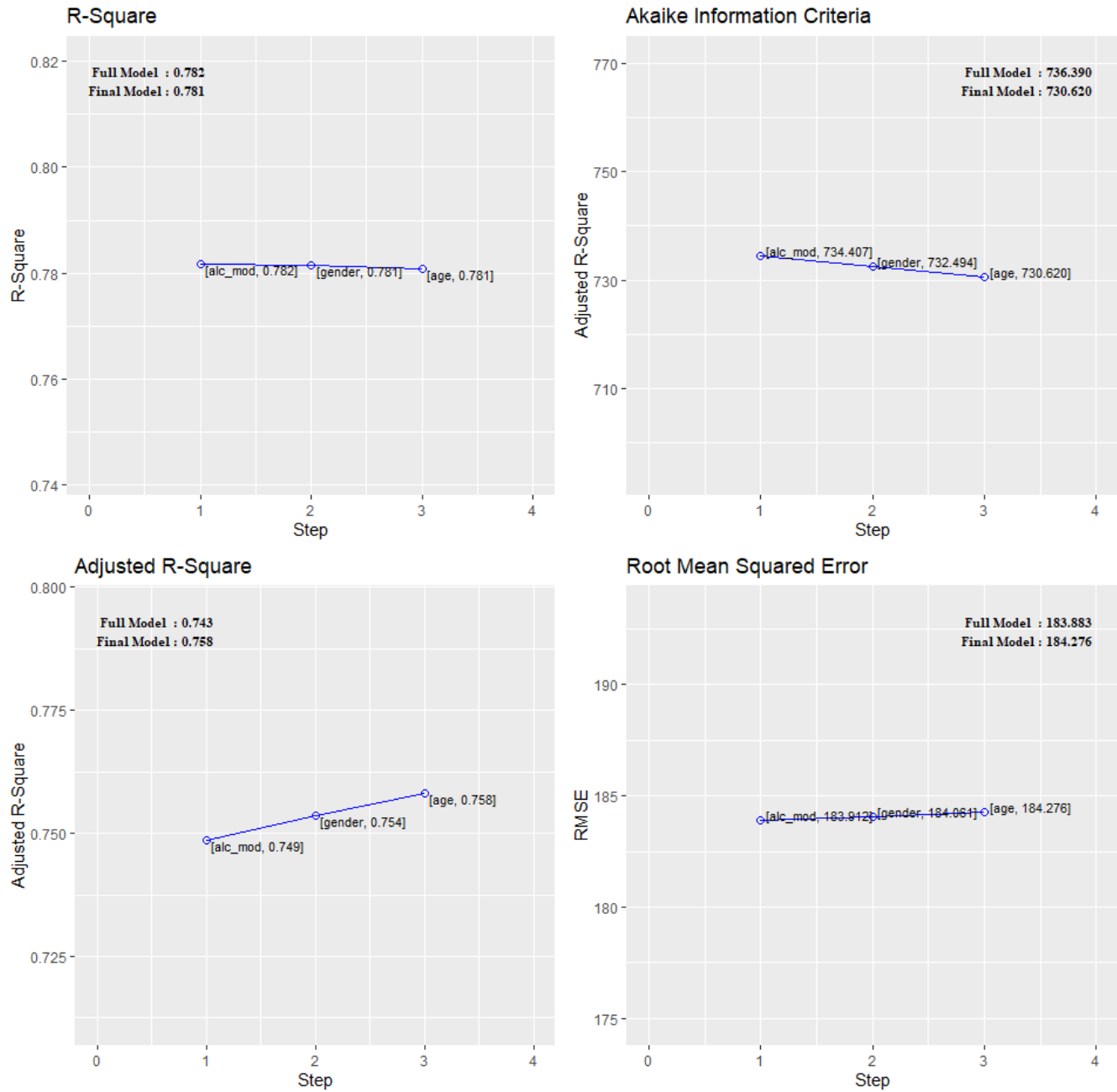
106.230						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
13.077						
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
138.779						
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
461.878						

Plot

Hide

```
model <- lm(y ~ ., data = surgical)
k <- ols_step_backward_p(model)
plot(k)
```


Stepwise Backward Regression



Detailed Output

Hide

```
# stepwise backward regression
model <- lm(y ~ ., data = surgical)
ols_step_backward_p(model, details = TRUE)
```

Backward Elimination Method

Candidate Terms:

1. bcs
2. pindex
3. enzyme_test
4. liver_test
5. age
6. gender
7. alc_mod
8. alc_heavy

Step => 0

Model => $y \sim \text{bcs} + \text{pindex} + \text{enzyme_test} + \text{liver_test} + \text{age} + \text{gender} + \text{alc_mod} + \text{alc_heavy}$

R2 => 0.782

Initiating stepwise selection...

Step => 1

Removed => alc_mod

Model => $y \sim \text{bcs} + \text{pindex} + \text{enzyme_test} + \text{liver_test} + \text{age} + \text{gender} + \text{alc_heavy}$

R2 => 0.78177

Step => 2

Removed => gender

Model => $y \sim \text{bcs} + \text{pindex} + \text{enzyme_test} + \text{liver_test} + \text{age} + \text{alc_heavy}$

R2 => 0.78142

Step => 3

Removed => age

Model => $y \sim \text{bcs} + \text{pindex} + \text{enzyme_test} + \text{liver_test} + \text{alc_heavy}$

R2 => 0.78091

No more variables to be removed.

Variables Removed:

=> alc_mod

=> gender

=> age

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Full Model	736.390	756.280	586.665	0.78184	0.74305
1	alc_mod	734.407	752.308	584.276	0.78177	0.74856
2	gender	732.494	748.406	581.938	0.78142	0.75351
3	age	730.620	744.543	579.638	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

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MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914
-758.746						
bcs	59.864	23.060	0.241	2.596	0.012	13.498
106.230						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419

```

13.077
  liver_test      58.064      40.144      0.156      1.446      0.155      -22.652
138.779
  alc_heavy      317.848      71.634      0.314      4.437      0.000      173.818
461.878
-----
-----

```

Stepwise Regression

Build regression model from a set of candidate predictor variables by entering and removing predictors based on p values, in a stepwise manner until there is no variable left to enter or remove any more. The model should include all the candidate predictor variables. If details is set to `TRUE`, each step is displayed.

Variable Selection

Hide

```

# stepwise regression
model <- lm(y ~ ., data = surgical)
ols_step_both_p(model)

```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	802.606	806.584	646.794	0.00000	0.00000
1	liver_test (+)	771.875	777.842	616.009	0.45454	0.44405
2	alc_heavy (+)	761.439	769.395	605.506	0.56674	0.54975
3	enzyme_test (+)	750.509	760.454	595.297	0.65900	0.63854
4	pindex (+)	735.715	747.649	582.943	0.75015	0.72975
5	bcs (+)	730.620	744.543	579.638	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig.	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914

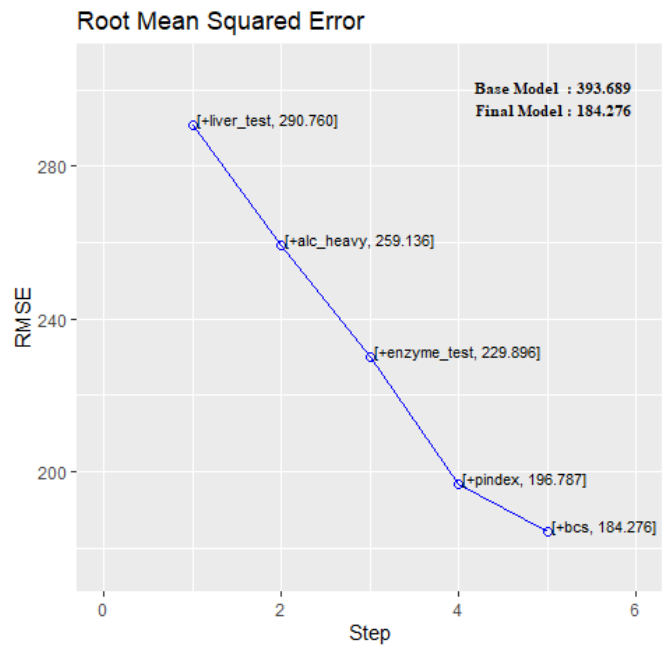
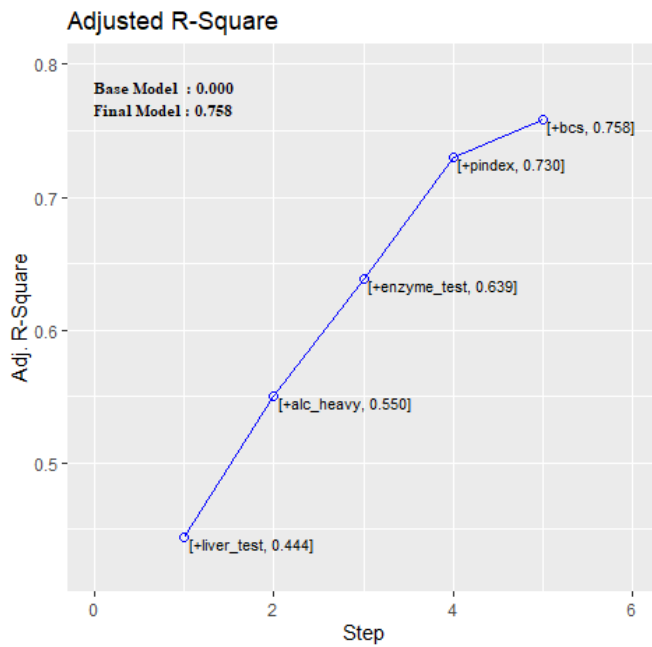
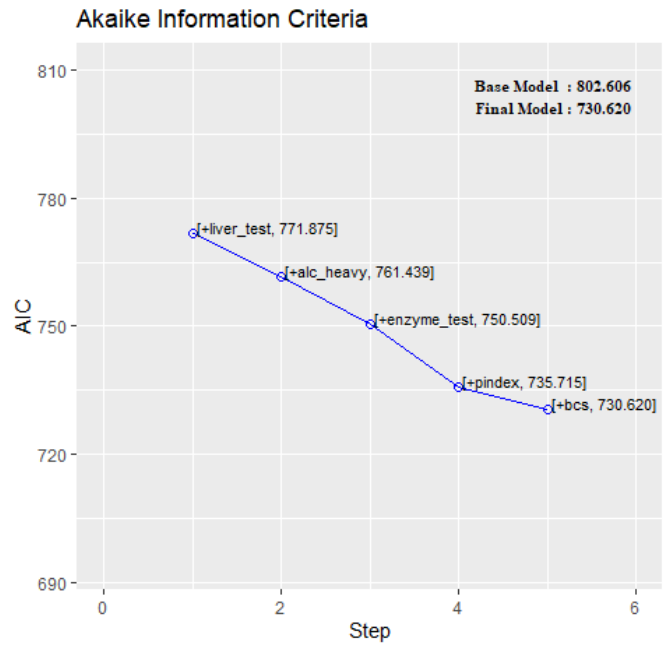
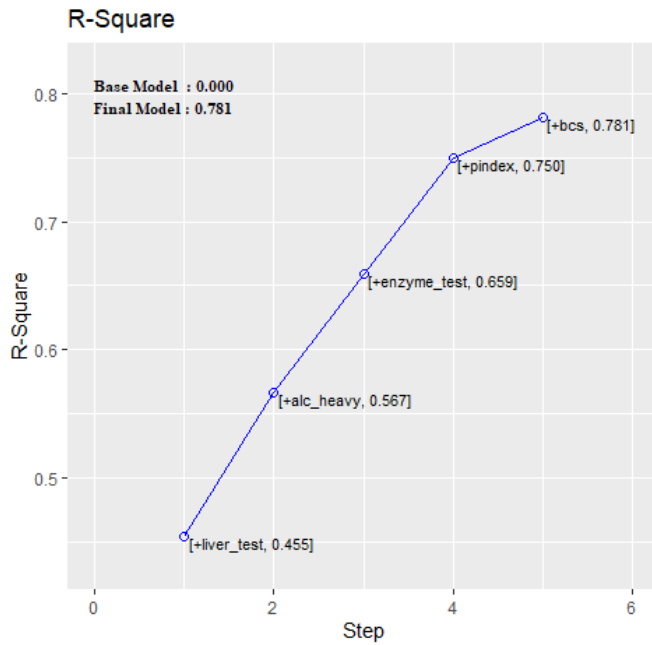
-758.746						
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
138.779						
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
461.878						
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
13.077						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						
bcs	59.864	23.060	0.241	2.596	0.012	13.498
106.230						

Plot

Hide

```
model <- lm(y ~ ., data = surgical)
k <- ols_step_both_p(model)
plot(k)
```


Stepwise Both Direction Regression



Detailed Output

Hide

```
# stepwise regression
model <- lm(y ~ ., data = surgical)
ols_step_both_p(model, details = TRUE)
```

Stepwise Selection Method

Candidate Terms:

1. bcs
2. pindex
3. enzyme_test
4. liver_test
5. age
6. gender
7. alc_mod
8. alc_heavy

Step => 0
Model => y ~ 1
R2 => 0

Initiating stepwise selection...

Step => 1
Selected => liver_test
Model => y ~ liver_test
R2 => 0.455

Step => 2
Selected => alc_heavy
Model => y ~ liver_test + alc_heavy
R2 => 0.567

Step => 3
Selected => enzyme_test
Model => y ~ liver_test + alc_heavy + enzyme_test
R2 => 0.659

Step => 4
Selected => pindex
Model => y ~ liver_test + alc_heavy + enzyme_test + pindex
R2 => 0.75

Step => 5
Selected => bcs
Model => y ~ liver_test + alc_heavy + enzyme_test + pindex + bcs
R2 => 0.781

No more variables to be added or removed.

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	802.606	806.584	646.794	0.00000	0.00000
1	liver_test (+)	771.875	777.842	616.009	0.45454	0.44405
2	alc_heavy (+)	761.439	769.395	605.506	0.56674	0.54975
3	enzyme_test (+)	750.509	760.454	595.297	0.65900	0.63854
4	pindex (+)	735.715	747.649	582.943	0.75015	0.72975
5	bcs (+)	730.620	744.543	579.638	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914 -758.746

liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
138.779						
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
461.878						
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
13.077						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						
bcs	59.864	23.060	0.241	2.596	0.012	13.498
106.230						

Stepwise AIC Forward Regression

Build regression model from a set of candidate predictor variables by entering predictors based on Akaike Information Criteria, in a stepwise manner until there is no variable left to enter any more.

The model should include all the candidate predictor variables. If details is set to TRUE , each step is displayed.

Variable Selection

Hide

```
# stepwise aic forward regression
model <- lm(y ~ ., data = surgical)
ols_step_forward_aic(model)
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	802.606	806.584	646.794	0.00000	0.00000
1	liver_test	771.875	777.842	616.009	0.45454	0.44405
2	alc_heavy	761.439	769.395	605.506	0.56674	0.54975
3	enzyme_test	750.509	760.454	595.297	0.65900	0.63854
4	pindex	735.715	747.649	582.943	0.75015	0.72975
5	bcs	730.620	744.543	579.638	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

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AIC: Akaike Information Criteria

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ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

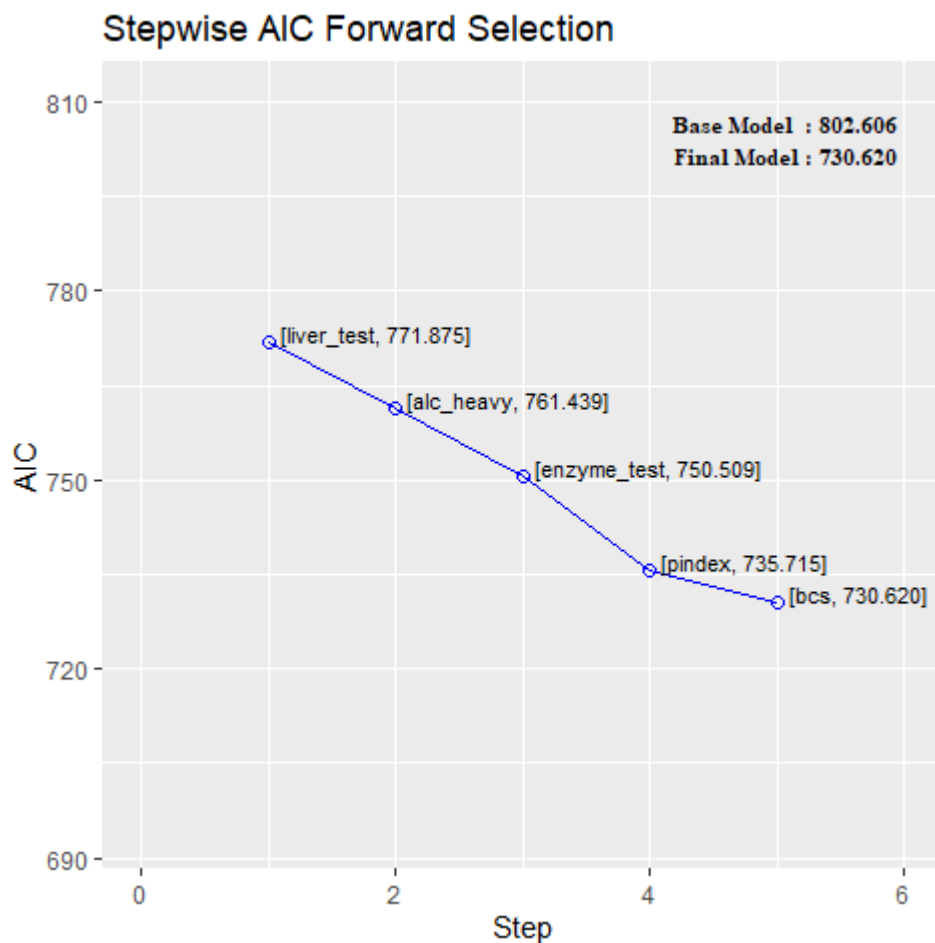
model	Beta	Std. Error	Std. Beta	t	Sig.	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914

-758.746						
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
138.779						
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
461.878						
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
13.077						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						
bcs	59.864	23.060	0.241	2.596	0.012	13.498
106.230						

Plot

Hide

```
model <- lm(y ~ ., data = surgical)
k <- ols_step_forward_aic(model)
plot(k)
```



Detailed Output

Hide

```
# stepwise aic forward regression  
model <- lm(y ~ ., data = surgical)  
ols_step_forward_aic(model, details = TRUE)
```

Forward Selection Method

Candidate Terms:

1. bcs
2. pindex
3. enzyme_test
4. liver_test
5. age
6. gender
7. alc_mod
8. alc_heavy

Step => 0
Model => y ~ 1
AIC => 802.606

Initiating stepwise selection...

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
liver_test	1	771.875	777.842	616.009	0.45454	0.44405
enzyme_test	1	782.629	788.596	626.220	0.33435	0.32154
pindex	1	794.100	800.067	637.196	0.17680	0.16097
alc_heavy	1	794.301	800.268	637.389	0.17373	0.15784
bcs	1	797.697	803.664	640.655	0.12010	0.10318
alc_mod	1	802.828	808.795	645.601	0.03239	0.01378
gender	1	802.956	808.923	645.725	0.03009	0.01143
age	1	803.834	809.801	646.572	0.01420	-0.00476

Step => 1
Added => liver_test
Model => y ~ liver_test
AIC => 771.8753

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
alc_heavy	1	761.439	769.395	605.506	0.56674	0.54975
enzyme_test	1	762.077	770.033	606.090	0.56159	0.54440
pindex	1	770.387	778.343	613.737	0.48866	0.46861
alc_mod	1	771.141	779.097	614.435	0.48147	0.46113

gender	1	773.802	781.758	616.901	0.45528	0.43391
age	1	773.831	781.787	616.928	0.45498	0.43361
bcs	1	773.867	781.823	616.961	0.45462	0.43323

Step => 2
 Added => alc_heavy
 Model => y ~ liver_test + alc_heavy
 AIC => 761.4394

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
enzyme_test	1	750.509	760.454	595.297	0.65900	0.63854
pindex	1	756.125	766.070	600.225	0.62163	0.59892
bcs	1	763.063	773.008	606.379	0.56975	0.54394
age	1	763.110	773.055	606.421	0.56938	0.54354
alc_mod	1	763.428	773.373	606.704	0.56683	0.54084
gender	1	763.433	773.378	606.709	0.56679	0.54080

Step => 3
 Added => enzyme_test
 Model => y ~ liver_test + alc_heavy + enzyme_test
 AIC => 750.5089

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
pindex	1	735.715	747.649	582.943	0.75015	0.72975
bcs	1	750.782	762.716	595.377	0.66973	0.64277
alc_mod	1	752.403	764.337	596.743	0.65967	0.63189
age	1	752.416	764.350	596.755	0.65959	0.63180
gender	1	752.509	764.443	596.833	0.65900	0.63116

Step => 4
 Added => pindex
 Model => y ~ liver_test + alc_heavy + enzyme_test + pindex
 AIC => 735.7146

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
bcs	1	730.620	744.543	579.638	0.78091	0.75808
age	1	737.680	751.603	585.012	0.75030	0.72429

gender	1	737.712	751.635	585.036	0.75016	0.72413
alc_mod	1	737.713	751.636	585.037	0.75015	0.72413

```
-----
Step      => 5
Added     => bcs
Model     => y ~ liver_test + alc_heavy + enzyme_test + pindex + bcs
AIC       => 730.6204
```

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
age	1	732.494	748.406	581.938	0.78142	0.75351
gender	1	732.551	748.463	581.978	0.78119	0.75325
alc_mod	1	732.614	748.526	582.023	0.78093	0.75297

No more variables to be added.

Variables Selected:

```
=> liver_test
=> alc_heavy
=> enzyme_test
=> pindex
=> bcs
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	802.606	806.584	646.794	0.00000	0.00000
1	liver_test	771.875	777.842	616.009	0.45454	0.44405
2	alc_heavy	761.439	769.395	605.506	0.56674	0.54975
3	enzyme_test	750.509	760.454	595.297	0.65900	0.63854
4	pindex	735.715	747.649	582.943	0.75015	0.72975
5	bcs	730.620	744.543	579.638	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839

Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error
MSE: Mean Square Error
MAE: Mean Absolute Error
AIC: Akaike Information Criteria
SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
pindex	8.924	1.808	0.380	4.935	0.000	5.288
bcs	59.864	23.060	0.241	2.596	0.012	13.498

Stepwise AIC Backward Regression

Build regression model from a set of candidate predictor variables by removing predictors based on Akaike Information Criteria, in a stepwise manner until there is no variable left to remove any more. The model should include all the candidate predictor variables. If details is set to TRUE , each step is displayed.

Variable Selection

[Hide](#)

```
# stepwise aic backward regression
model <- lm(y ~ ., data = surgical)
k <- ols_step_backward_aic(model)
k
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Full Model	736.390	756.280	586.665	0.78184	0.74305
1	alc_mod	734.407	752.308	583.884	0.78177	0.74856
2	gender	732.494	748.406	581.290	0.78142	0.75351
3	age	730.620	744.543	578.844	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig.	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914 -758.746
bcs	59.864	23.060	0.241	2.596	0.012	13.498

106.230						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
13.077						
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
138.779						
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
461.878						

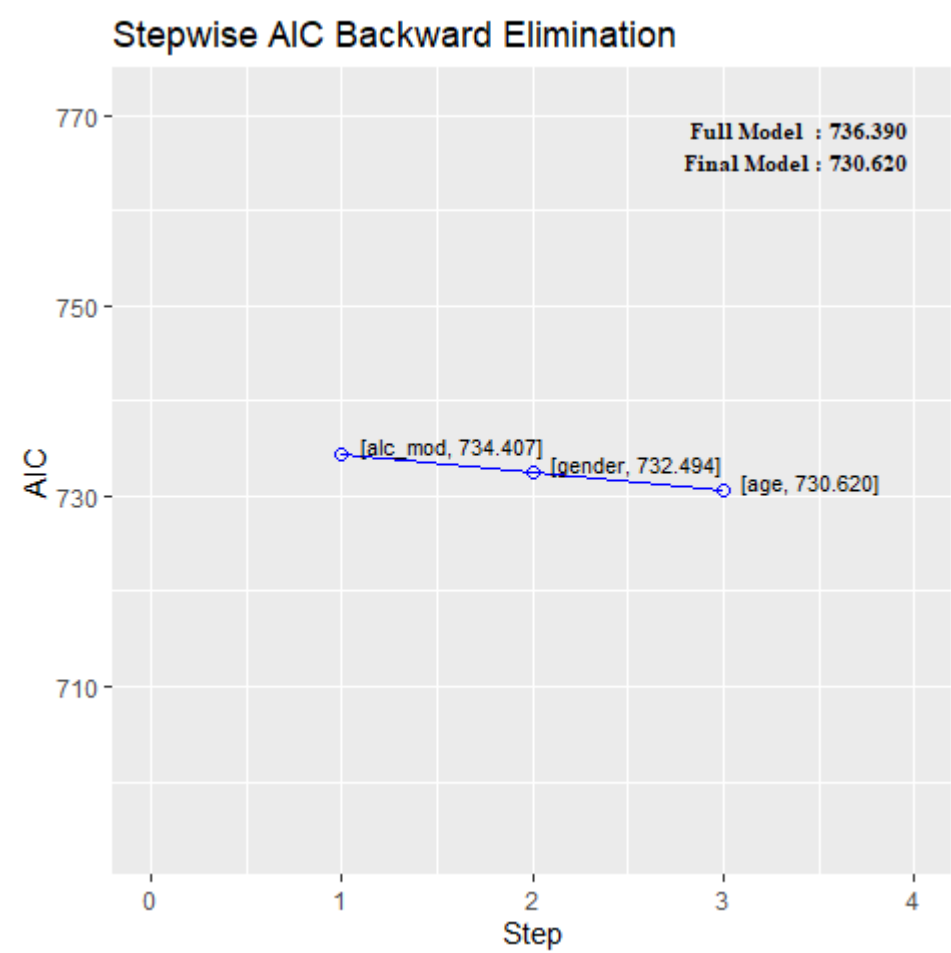
Plot

Hide

```

model <- lm(y ~ ., data = surgical)
k <- ols_step_backward_aic(model)
plot(k)

```



Detailed Output

Hide


```
# stepwise aic backward regression  
model <- lm(y ~ ., data = surgical)  
ols_step_backward_aic(model, details = TRUE)
```

Backward Elimination Method

Candidate Terms:

1. bcs
2. pindex
3. enzyme_test
4. liver_test
5. age
6. gender
7. alc_mod
8. alc_heavy

Step => 0

Model => $y \sim \text{bcs} + \text{pindex} + \text{enzyme_test} + \text{liver_test} + \text{age} + \text{gender} + \text{alc_mod} + \text{alc_heavy}$

AIC => 736.3899

Initiating stepwise selection...

Table: Removing Existing Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
alc_mod	1	734.407	752.308	584.276	0.78177	0.74856
gender	1	734.478	752.379	584.323	0.78148	0.74823
age	1	734.544	752.445	584.367	0.78121	0.74792
liver_test	1	735.878	753.779	585.255	0.77574	0.74162
bcs	1	741.677	759.577	589.203	0.75032	0.71233
alc_heavy	1	749.210	767.111	594.541	0.71294	0.66926
pindex	1	756.624	774.525	600.014	0.67070	0.62059
enzyme_test	1	763.557	781.458	605.318	0.62559	0.56861

Step => 1

Removed => alc_mod

Model => $y \sim \text{bcs} + \text{pindex} + \text{enzyme_test} + \text{liver_test} + \text{age} + \text{gender} + \text{alc_heavy}$

AIC => 734.4068

Table: Removing Existing Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
gender	1	732.494	748.406	581.938	0.78142	0.75351
age	1	732.551	748.463	581.978	0.78119	0.75325
liver_test	1	733.921	749.833	582.951	0.77556	0.74691

bcs	1	739.677	755.589	587.106	0.75032	0.71845
alc_heavy	1	750.486	766.398	595.217	0.69499	0.65605
pindex	1	754.759	770.671	598.530	0.66987	0.62773
enzyme_test	1	761.595	777.507	603.950	0.62532	0.57749

Step => 2

Removed => gender

Model => y ~ bcs + pindex + enzyme_test + liver_test + age + alc_heavy

AIC => 732.4942

Table: Removing Existing Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
age	1	730.620	744.543	579.638	0.78091	0.75808
liver_test	1	732.339	746.262	580.934	0.77382	0.75026
bcs	1	737.680	751.603	585.012	0.75030	0.72429
alc_heavy	1	748.486	762.409	593.500	0.69499	0.66322
pindex	1	752.777	766.700	596.959	0.66976	0.63536
enzyme_test	1	759.596	773.518	602.553	0.62532	0.58629

Step => 3

Removed => age

Model => y ~ bcs + pindex + enzyme_test + liver_test + alc_heavy

AIC => 730.6204

Table: Removing Existing Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
liver_test	1	730.924	742.858	579.087	0.77136	0.75269
bcs	1	735.715	747.649	582.943	0.75015	0.72975
alc_heavy	1	747.181	759.114	592.362	0.69104	0.66582
pindex	1	750.782	762.716	595.377	0.66973	0.64277
enzyme_test	1	757.971	769.905	601.477	0.62270	0.59190

No more variables to be removed.

Variables Removed:

=> alc_mod

=> gender

=> age

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Full Model	736.390	756.280	586.665	0.78184	0.74305
1	alc_mod	734.407	752.308	583.884	0.78177	0.74856
2	gender	732.494	748.406	581.290	0.78142	0.75351
3	age	730.620	744.543	578.844	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914
-758.746						
bcs	59.864	23.060	0.241	2.596	0.012	13.498
106.230						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						

enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
13.077						
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
138.779						
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
461.878						

Stepwise AIC Regression

Build regression model from a set of candidate predictor variables by entering and removing predictors based on Akaike Information Criteria, in a stepwise manner until there is no variable left to enter or remove any more. The model should include all the candidate predictor variables. If details is set to TRUE , each step is displayed.

Variable Selection

Hide

```
# stepwise aic regression
model <- lm(y ~ ., data = surgical)
ols_step_both_aic(model)
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	802.606	806.584	646.794	0.00000	0.00000
1	liver_test (+)	771.875	777.842	616.009	0.45454	0.44405
2	alc_heavy (+)	761.439	769.395	605.506	0.56674	0.54975
3	enzyme_test (+)	750.509	760.454	595.297	0.65900	0.63854
4	pindex (+)	735.715	747.649	582.943	0.75015	0.72975
5	bcs (+)	730.620	744.543	579.638	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	6535804.090	5	1307160.818	34.217	0.0000
Residual	1833716.447	48	38202.426		
Total	8369520.537	53			

Parameter Estimates

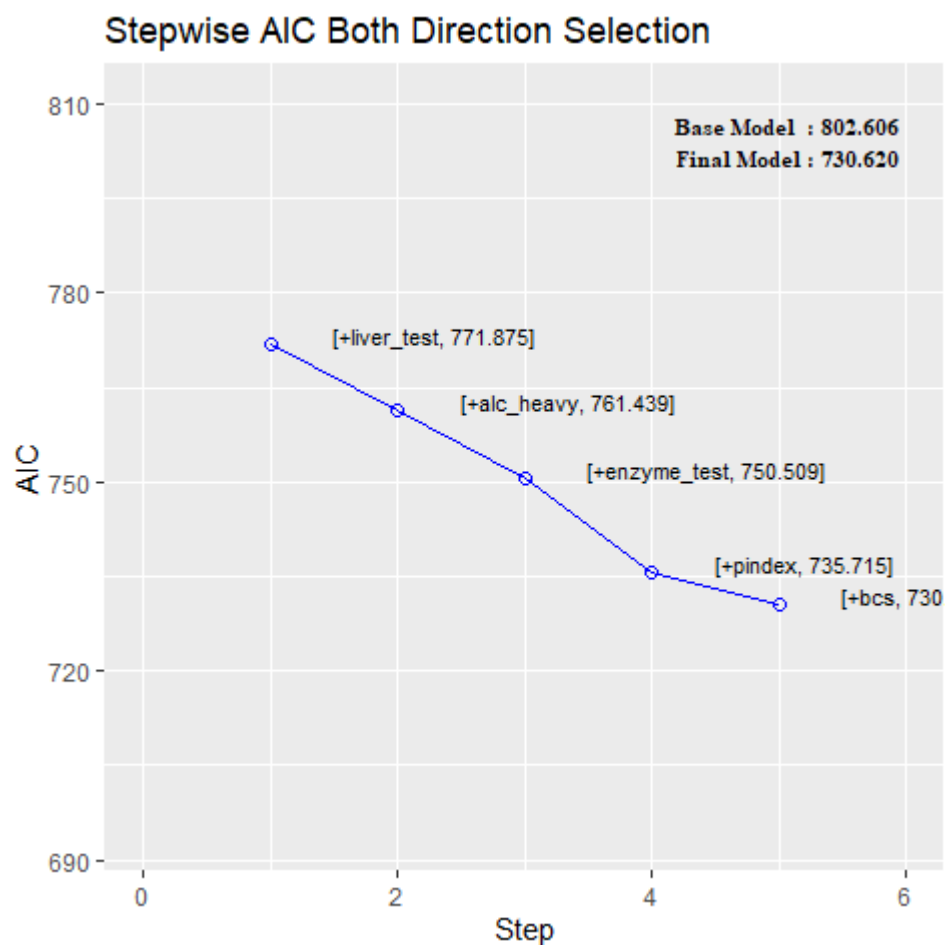
model	Beta	Std. Error	Std. Beta	t	Sig.	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914

-758.746						
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652
138.779						
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818
461.878						
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419
13.077						
pindex	8.924	1.808	0.380	4.935	0.000	5.288
12.559						
bcs	59.864	23.060	0.241	2.596	0.012	13.498
106.230						

Plot

Hide

```
model <- lm(y ~ ., data = surgical)
k <- ols_step_both_aic(model)
plot(k)
```



Detailed Output

Hide

```
# stepwise aic regression  
model <- lm(y ~ ., data = surgical)  
ols_step_both_aic(model, details = TRUE)
```


Stepwise Selection Method

Candidate Terms:

1. bcs
2. pindex
3. enzyme_test
4. liver_test
5. age
6. gender
7. alc_mod
8. alc_heavy

Step => 0
Model => y ~ 1
AIC => 802.606

Initiating stepwise selection...

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
bcs	1	797.697	803.664	640.655	0.12010	0.10318
pindex	1	794.100	800.067	637.196	0.17680	0.16097
enzyme_test	1	782.629	788.596	626.220	0.33435	0.32154
liver_test	1	771.875	777.842	616.009	0.45454	0.44405
age	1	803.834	809.801	646.572	0.01420	-0.00476
gender	1	802.956	808.923	645.725	0.03009	0.01143
alc_mod	1	802.828	808.795	645.601	0.03239	0.01378
alc_heavy	1	794.301	800.268	637.389	0.17373	0.15784

Step => 1
Added => liver_test
Model => y ~ liver_test
AIC => 771.8753

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
bcs	1	773.867	781.823	616.961	0.45462	0.43323
pindex	1	770.387	778.343	613.737	0.48866	0.46861
enzyme_test	1	762.077	770.033	606.090	0.56159	0.54440
age	1	773.831	781.787	616.928	0.45498	0.43361

gender	1	773.802	781.758	616.901	0.45528	0.43391
alc_mod	1	771.141	779.097	614.435	0.48147	0.46113
alc_heavy	1	761.439	769.395	605.506	0.56674	0.54975

Step => 2
Added => alc_heavy
Model => y ~ liver_test + alc_heavy
AIC => 761.4394

Table: Removing Existing Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
liver_test	1	794.301	800.268	637.389	0.17373	0.15784
alc_heavy	1	771.875	777.842	616.009	0.45454	0.44405

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
bcs	1	763.063	773.008	606.379	0.56975	0.54394
pindex	1	756.125	766.070	600.225	0.62163	0.59892
enzyme_test	1	750.509	760.454	595.297	0.65900	0.63854
age	1	763.110	773.055	606.421	0.56938	0.54354
gender	1	763.433	773.378	606.709	0.56679	0.54080
alc_mod	1	763.428	773.373	606.704	0.56683	0.54084

Step => 3
Added => enzyme_test
Model => y ~ liver_test + alc_heavy + enzyme_test
AIC => 750.5089

Table: Removing Existing Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
liver_test	1	773.555	781.511	616.671	0.45777	0.43650
alc_heavy	1	762.077	770.033	606.090	0.56159	0.54440
enzyme_test	1	761.439	769.395	605.506	0.56674	0.54975

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
bcs	1	750.782	762.716	595.377	0.66973	0.64277

pindex	1	735.715	747.649	582.943	0.75015	0.72975
age	1	752.416	764.350	596.755	0.65959	0.63180
gender	1	752.509	764.443	596.833	0.65900	0.63116
alc_mod	1	752.403	764.337	596.743	0.65967	0.63189

Step => 4
 Added => pindex
 Model => y ~ liver_test + alc_heavy + enzyme_test + pindex
 AIC => 735.7146

Table: Removing Existing Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
liver_test	1	748.167	758.112	593.257	0.67347	0.65388
alc_heavy	1	755.099	765.044	599.321	0.62875	0.60647
enzyme_test	1	756.125	766.070	600.225	0.62163	0.59892
pindex	1	750.509	760.454	595.297	0.65900	0.63854

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
bcs	1	730.620	744.543	579.638	0.78091	0.75808
age	1	737.680	751.603	585.012	0.75030	0.72429
gender	1	737.712	751.635	585.036	0.75016	0.72413
alc_mod	1	737.713	751.636	585.037	0.75015	0.72413

Step => 5
 Added => bcs
 Model => y ~ liver_test + alc_heavy + enzyme_test + pindex + bcs
 AIC => 730.6204

Table: Removing Existing Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
liver_test	1	730.924	742.858	579.087	0.77136	0.75269
alc_heavy	1	747.181	759.114	592.362	0.69104	0.66582
enzyme_test	1	757.971	769.905	601.477	0.62270	0.59190
pindex	1	750.782	762.716	595.377	0.66973	0.64277
bcs	1	735.715	747.649	582.943	0.75015	0.72975

Table: Adding New Variables

Predictor	DF	AIC	SBC	SBIC	R2	Adj. R2
age	1	732.494	748.406	581.938	0.78142	0.75351
gender	1	732.551	748.463	581.978	0.78119	0.75325
alc_mod	1	732.614	748.526	582.023	0.78093	0.75297

No more variables to be added or removed.

Variables Selected:

=> liver_test
=> alc_heavy
=> enzyme_test
=> pindex
=> bcs

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	802.606	806.584	646.794	0.00000	0.00000
1	liver_test (+)	771.875	777.842	616.009	0.45454	0.44405
2	alc_heavy (+)	761.439	769.395	605.506	0.56674	0.54975
3	enzyme_test (+)	750.509	760.454	595.297	0.65900	0.63854
4	pindex (+)	735.715	747.649	582.943	0.75015	0.72975
5	bcs (+)	730.620	744.543	579.638	0.78091	0.75808

Final Model Output

Model Summary

R	0.884	RMSE	184.276
R-Squared	0.781	MSE	38202.426
Adj. R-Squared	0.758	Coef. Var	27.839
Pred R-Squared	0.700	AIC	730.620
MAE	137.656	SBC	744.543

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.	
Regression	6535804.090	5	1307160.818	34.217	0.0000	
Residual	1833716.447	48	38202.426			
Total	8369520.537	53				

Parameter Estimates						
model	Beta	Std. Error	Std. Beta	t	Sig	lower upper
(Intercept)	-1178.330	208.682		-5.647	0.000	-1597.914 -758.746
liver_test	58.064	40.144	0.156	1.446	0.155	-22.652 138.779
alc_heavy	317.848	71.634	0.314	4.437	0.000	173.818 461.878
enzyme_test	9.748	1.656	0.521	5.887	0.000	6.419 13.077
pindex	8.924	1.808	0.380	4.935	0.000	5.288 12.559
bcs	59.864	23.060	0.241	2.596	0.012	13.498 106.230

Notes on stepwise

A fundamental problem with stepwise regression is that some real explanatory variables that have causal effects on the dependent variable may happen to not be statistically significant, while nuisance variables may be coincidentally significant. As a result, the model may fit the data well in-sample, but do poorly out-of-sample.

Many Big-Data researchers believe that, the larger the number of possible explanatory variables, the more useful is stepwise regression for selecting explanatory variables. The reality is that stepwise regression is less effective the larger the number of potential explanatory variables. Stepwise regression does not solve the Big-Data problem of too many explanatory variables. Big Data exacerbates the failings of stepwise regression. reference (<https://journalofbigdata.springeropen.com/articles/10.1186/s40537-018-0143-6>)

Residual Diagnostics

Introduction

olsrr offers tools for detecting violation of standard regression assumptions. Here we take a look at residual diagnostics. The standard regression assumptions include the following about residuals/errors:

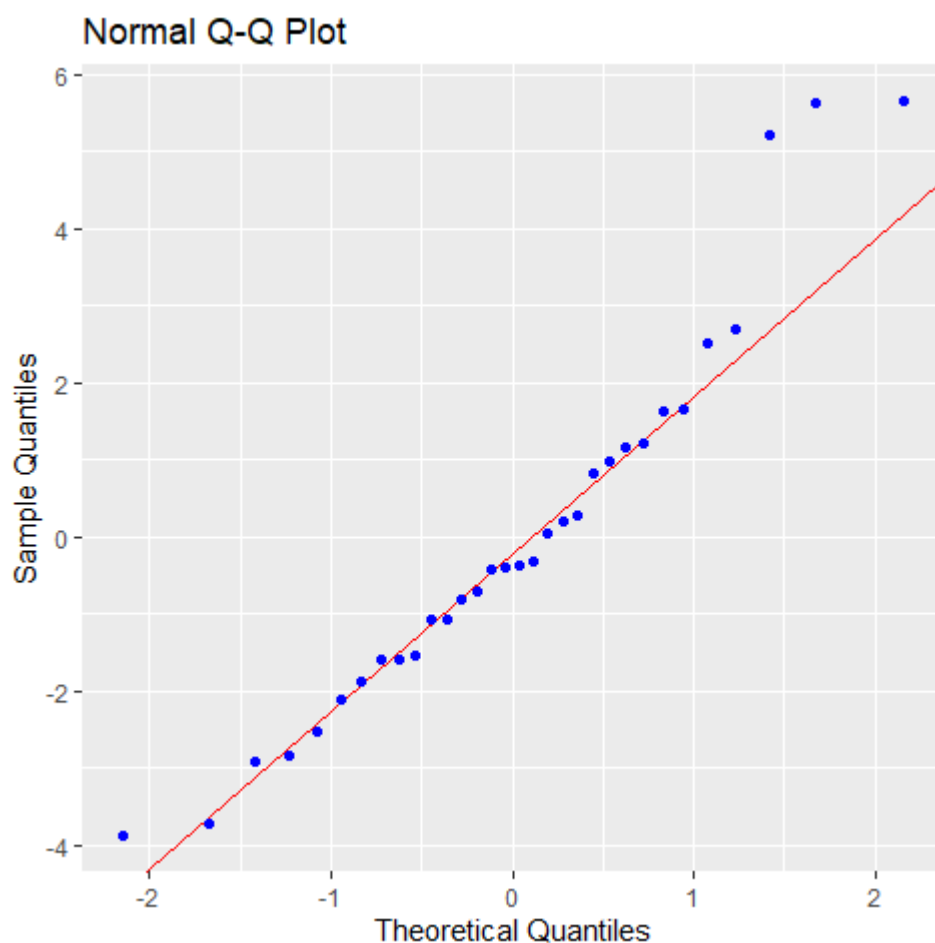
- The error has a normal distribution (normality assumption).
- The errors have mean zero.
- The errors have same but unknown variance (homoscedasticity assumption).
- The error are independent of each other (independent errors assumption).

Residual QQ Plot

Graph for detecting violation of normality assumption.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_resid_qq(model)
```



Residual Normality Test

Test for detecting violation of normality assumption.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_test_normality(model)
```

```
-----
      Test           Statistic      pvalue
-----
Shapiro-Wilk         0.9366         0.0600
Kolmogorov-Smirnov    0.1152         0.7464
Cramer-von Mises      2.8122         0.0000
Anderson-Darling      0.5859         0.1188
-----
```

Correlation between observed residuals and expected residuals under normality.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_test_correlation(model)
```

```
[1] 0.970066
```

Residual vs Fitted Values Plot

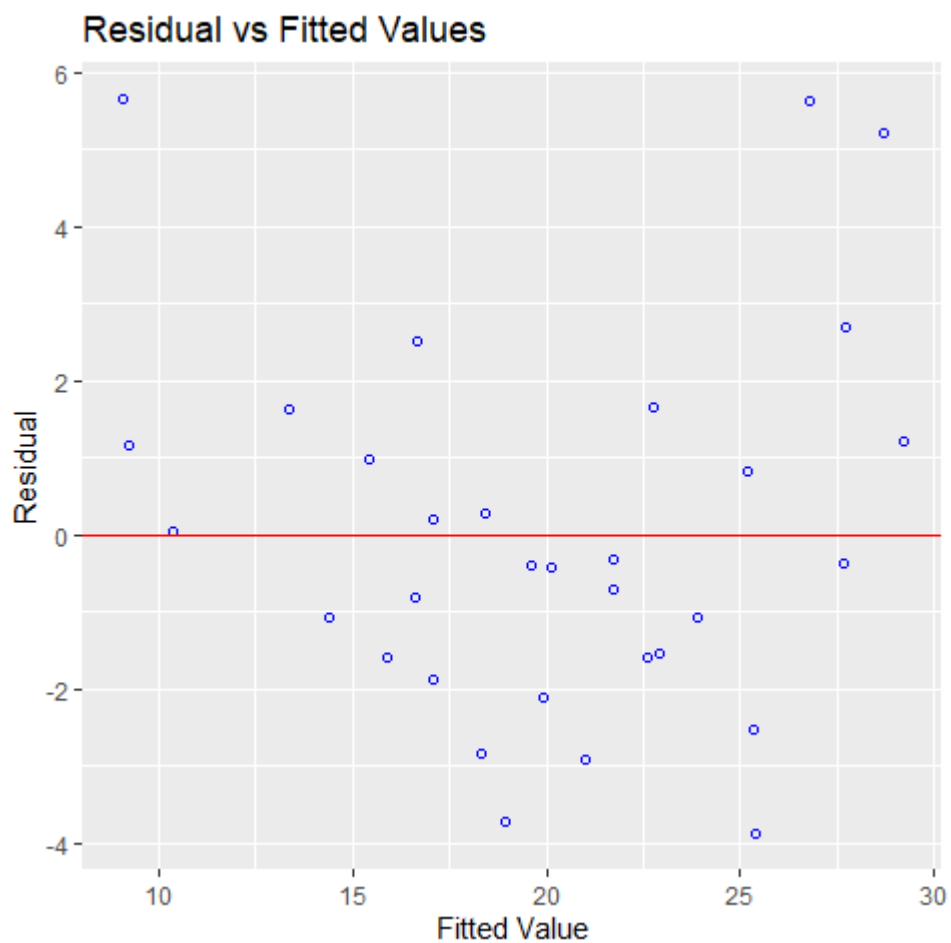
It is a scatter plot of residuals on the y axis and fitted values on the x axis to detect non-linearity, unequal error variances, and outliers.

Characteristics of a well behaved residual vs fitted plot:

- The residuals spread randomly around the 0 line indicating that the relationship is linear.
- The residuals form an approximate horizontal band around the 0 line indicating homogeneity of error variance.
- No one residual is visibly away from the random pattern of the residuals indicating that there are no outliers.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_resid_fit(model)
```

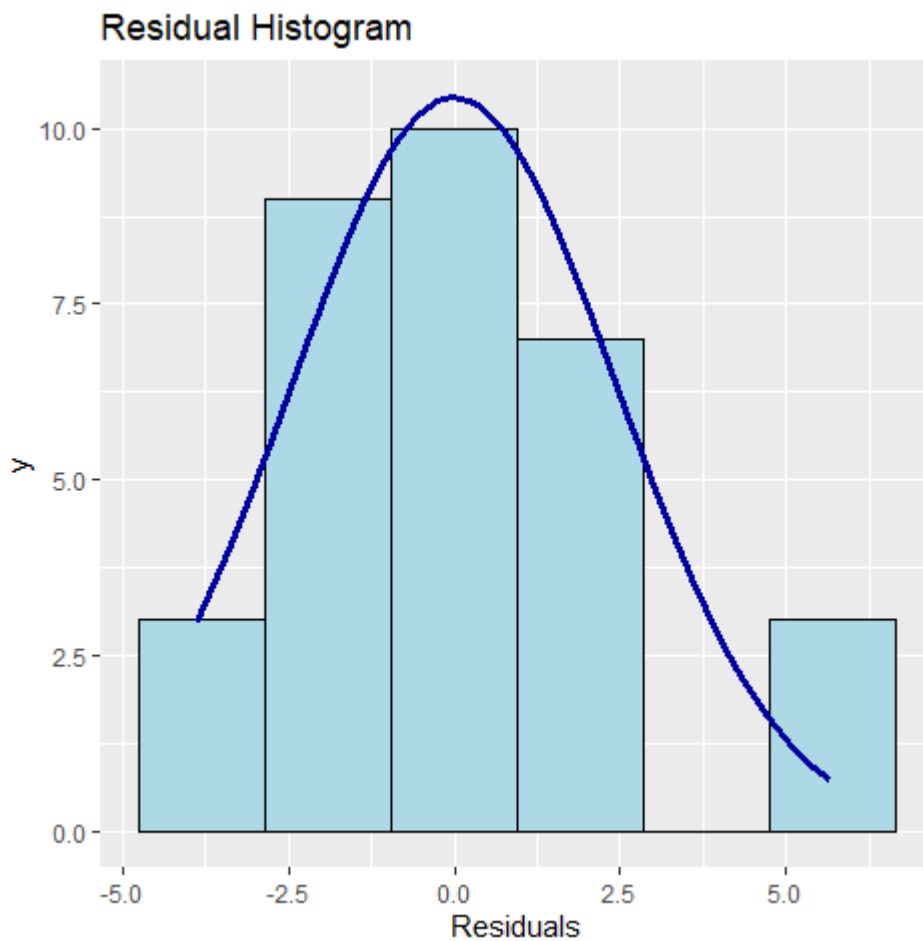


Residual Histogram

Histogram of residuals for detecting violation of normality assumption.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_resid_hist(model)
```

Heteroscedasticity

Introduction

One of the assumptions made about residuals/errors in OLS regression is that the errors have the same but unknown variance. This is known as constant variance or homoscedasticity. When this assumption is violated, the problem is known as heteroscedasticity.

Consequences of Heteroscedasticity

- The OLS estimators and regression predictions based on them remains unbiased and consistent.
- The OLS estimators are no longer the BLUE (Best Linear Unbiased Estimators) because they are no longer efficient, so the regression predictions will be inefficient too.
- Because of the inconsistency of the covariance matrix of the estimated regression coefficients, the tests of hypotheses, (t-test, F-test) are no longer valid.

olsrr provides the following 4 tests for detecting heteroscedasticity:

- Bartlett Test
- Breusch Pagan Test
- Score Test
- F Test

Bartlett Test

Bartlett's test is used to test if variances across samples is equal. It is sensitive to departures from normality. The Levene test is an alternative test that is less sensitive to departures from normality.

You can perform the test using 2 continuous variables, one continuous and one grouping variable, a formula or a linear model.

Use grouping variable

Hide

```
ols_test_bartlett(hsb, 'read', group_var = 'female')
```

Bartlett's Test of Homogeneity of Variances

Ho: Variances are equal across groups

Ha: Variances are unequal for atleast two groups

Test Summary

DF	=	1
Chi2	=	0.1866579
Prob > Chi2	=	0.6657129

Using variables

Hide

```
ols_test_bartlett(hsb, 'read', 'write')
```

Bartlett's Test of Homogeneity of Variances

Ho: Variances are equal across groups

Ha: Variances are unequal for atleast two groups

Data

Variables: read write

Test Summary

DF	=	1
Chi2	=	1.222871
Prob > Chi2	=	0.2687979

Breusch Pagan Test

Breusch Pagan Test was introduced by Trevor Breusch and Adrian Pagan in 1979. It is used to test for heteroskedasticity in a linear regression model and assumes that the error terms are normally distributed. It tests whether the variance of the errors from a regression is dependent on the values of the independent variables. It is a χ^2 test.

You can perform the test using the fitted values of the model, the predictors in the model and a subset of the independent variables. It includes options to perform multiple tests and p value adjustments. The options for p value adjustments include Bonferroni, Sidak and Holm's method.

Use fitted values of the model

Hide

```
model <- lm(mpg ~ disp + hp + wt + drat, data = mtcars)
ols_test_breusch_pagan(model)
```

Breusch Pagan Test for Heteroskedasticity

Ho: the variance is constant

Ha: the variance is not constant

Data

Response : mpg

Variables: fitted values of mpg

Test Summary

DF	=	1
Chi2	=	1.429672
Prob > Chi2	=	0.231818

Use independent variables of the model

Hide

```
model <- lm(mpg ~ disp + hp + wt + drat, data = mtcars)
ols_test_breusch_pagan(model, rhs = TRUE)
```

Breusch Pagan Test for Heteroskedasticity

Ho: the variance is constant

Ha: the variance is not constant

Data

Response : mpg

Variables: disp hp wt drat

Test Summary

```
DF          =      4
Chi2        =      1.513808
Prob > Chi2  =      0.8241927
```

Use independent variables of the model and perform multiple tests

Hide

```
model <- lm(mpg ~ disp + hp + wt + drat, data = mtcars)
ols_test_breusch_pagan(model, rhs = TRUE, multiple = TRUE)
```

Breusch Pagan Test for Heteroskedasticity

Ho: the variance is constant

Ha: the variance is not constant

Data

Response : mpg

Variables: disp hp wt drat

Test Summary (Unadjusted p values)

Variable	chi2	df	p
disp	1.2355345	1	0.2663334
hp	0.9209878	1	0.3372157
wt	1.2529988	1	0.2629805
drat	1.1668486	1	0.2800497
simultaneous	1.5138083	4	0.8241927

Bonferroni p value Adjustment

[Hide](#)

```
model <- lm(mpg ~ disp + hp + wt + drat, data = mtcars)
ols_test_breusch_pagan(model, rhs = TRUE, multiple = TRUE, p.adj = 'bonferroni')
```

Breusch Pagan Test for Heteroskedasticity

Ho: the variance is constant

Ha: the variance is not constant

Data

Response : mpg

Variables: disp hp wt drat

Test Summary (Bonferroni p values)

Variable	chi2	df	p

disp	1.2355345	1	1.0000000
hp	0.9209878	1	1.0000000
wt	1.2529988	1	1.0000000
drat	1.1668486	1	1.0000000

simultaneous	1.5138083	4	0.8241927

Sidak p value Adjustment

[Hide](#)

```
model <- lm(mpg ~ disp + hp + wt + drat, data = mtcars)
ols_test_breusch_pagan(model, rhs = TRUE, multiple = TRUE, p.adj = 'sidak')
```

Breusch Pagan Test for Heteroskedasticity

Ho: the variance is constant

Ha: the variance is not constant

Data

Response : mpg

Variables: disp hp wt drat

Test Summary (Sidak p values)

Variable	chi2	df	p
disp	1.2355345	1	0.7102690
hp	0.9209878	1	0.8070305
wt	1.2529988	1	0.7049362
drat	1.1668486	1	0.7313356
simultaneous	1.5138083	4	0.8241927

Holm's p value Adjustment

Hide

```
model <- lm(mpg ~ disp + hp + wt + drat, data = mtcars)
ols_test_breusch_pagan(model, rhs = TRUE, multiple = TRUE, p.adj = 'holm')
```

Breusch Pagan Test for Heteroskedasticity

Ho: the variance is constant

Ha: the variance is not constant

Data

Response : mpg

Variables: disp hp wt drat

Test Summary (Holm's p values)

Variable	chi2	df	p
disp	1.2355345	1	0.7990002
hp	0.9209878	1	0.3372157
wt	1.2529988	1	1.0000000
drat	1.1668486	1	0.5600994
simultaneous	1.5138083	4	0.8241927

Score Test

Test for heteroskedasticity under the assumption that the errors are independent and identically distributed (i.i.d.). You can perform the test using the fitted values of the model, the predictors in the model and a subset of the independent variables.

Use fitted values of the model

[Hide](#)

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_test_score(model)
```

Score Test for Heteroskedasticity

Ho: Variance is homogenous

Ha: Variance is not homogenous

Variables: fitted values of mpg

Test Summary

DF	=	1
Chi2	=	0.5163959
Prob > Chi2	=	0.4723832

Use independent variables of the model

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_test_score(model, rhs = TRUE)
```

Score Test for Heteroskedasticity

Ho: Variance is homogenous

Ha: Variance is not homogenous

Variables: disp hp wt qsec

Test Summary

DF	=	4
Chi2	=	2.039404
Prob > Chi2	=	0.7285114

Specify variables

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_test_score(model, vars = c('disp', 'hp'))
```


Score Test for Heteroskedasticity

Ho: Variance is homogenous

Ha: Variance is not homogenous

Variables: disp hp

Test Summary

DF	=	2
Chi2	=	0.9983196
Prob > Chi2	=	0.6070405

F Test

F Test for heteroskedasticity under the assumption that the errors are independent and identically distributed (i.i.d.). You can perform the test using the fitted values of the model, the predictors in the model and a subset of the independent variables.

Use fitted values of the model

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_test_f(model)
```

F Test for Heteroskedasticity

Ho: Variance is homogenous

Ha: Variance is not homogenous

Variables: fitted values of mpg

Test Summary

Num DF	=	1
Den DF	=	30
F	=	0.4920617
Prob > F	=	0.4884154

Use independent variables of the model

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_test_f(model, rhs = TRUE)
```

F Test for Heteroskedasticity

Ho: Variance is homogenous

Ha: Variance is not homogenous

Variables: disp hp wt qsec

Test Summary

Num DF = 4

Den DF = 27

F = 0.4594694

Prob > F = 0.7647271

Specify variables

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_test_f(model, vars = c('disp', 'hp'))
```

F Test for Heteroskedasticity

Ho: Variance is homogenous

Ha: Variance is not homogenous

Variables: disp hp

Test Summary

Num DF = 2

Den DF = 29

F = 0.4669306

Prob > F = 0.631555

Measures of Influence

Introduction

It is possible for a single observation to have a great influence on the results of a regression analysis. It is therefore important to detect influential observations and to take them into consideration when interpreting the results.

olsrr offers the following tools to detect influential observations:

- Cook's D Bar Plot
- Cook's D Chart
- DFBETAs Panel
- DFFITs Plot
- Studentized Residual Plot
- Standardized Residual Chart
- Studentized Residuals vs Leverage Plot
- Deleted Studentized Residual vs Fitted Values Plot
- Hadi Plot
- Potential Residual Plot

Cook's D Bar Plot

Bar Plot of Cook's distance to detect observations that strongly influence fitted values of the model. Cook's distance was introduced by American statistician R Dennis Cook in 1977. It is used to identify influential data points. It depends on both the residual and leverage i.e it takes it account both the **x** value and **y** value of the observation.

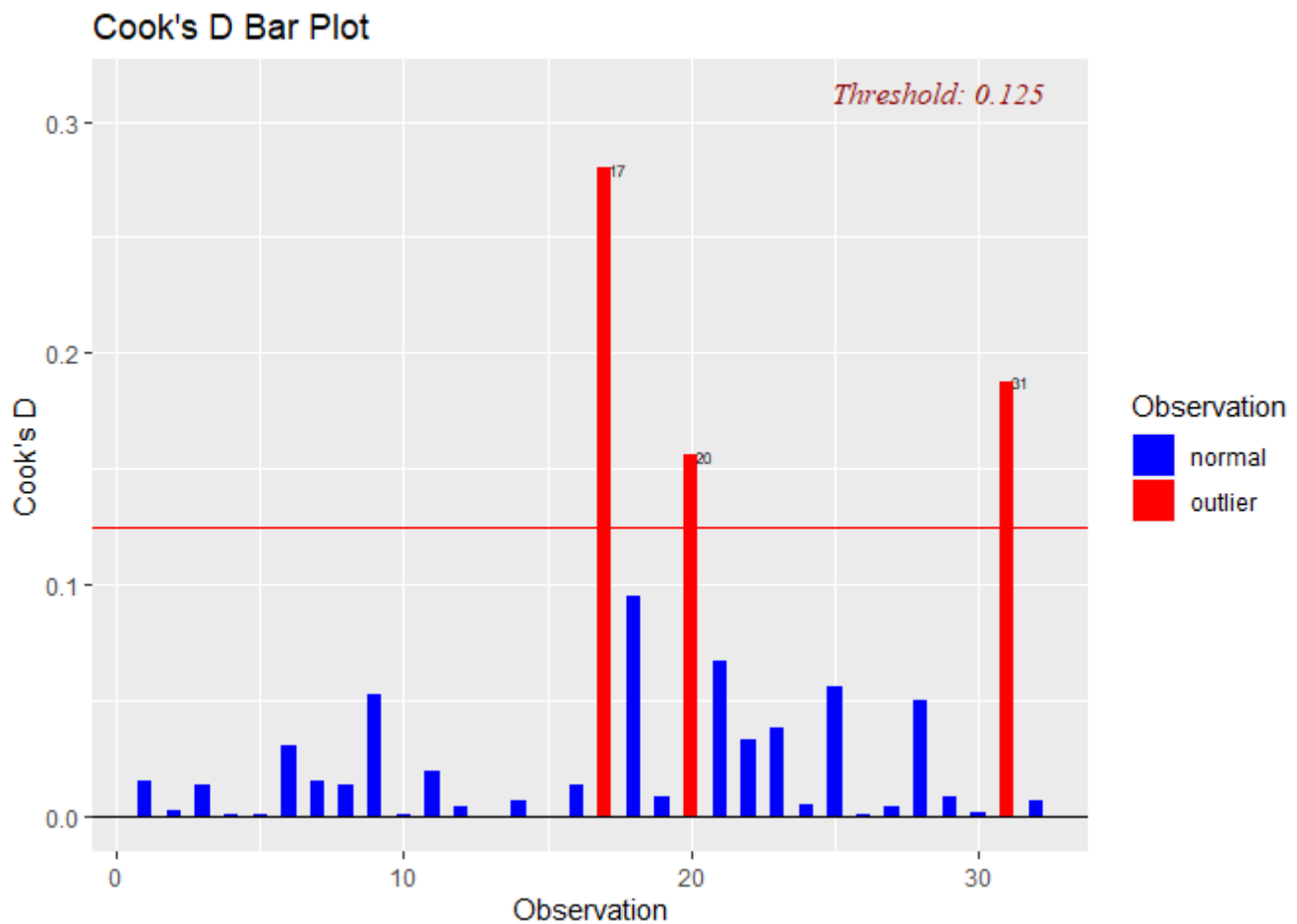
Steps to compute Cook's distance:

- delete observations one at a time.
- refit the regression model on remaining $(n - 1)$ observations
- examine how much all of the fitted values change when the i th observation is deleted.

A data point having a large cook's d indicates that the data point strongly influences the fitted values.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_cooksd_bar(model)
```

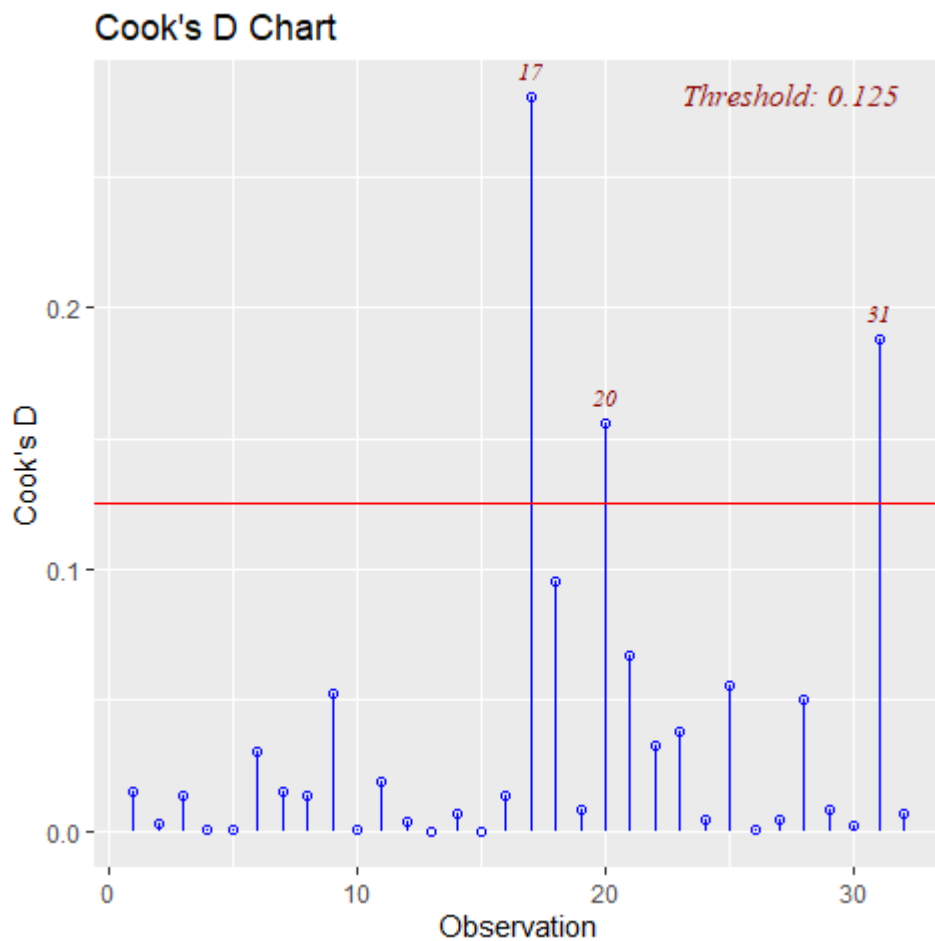


Cook's D Chart

Chart of Cook's distance to detect observations that strongly influence fitted values of the model.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_cooksd_chart(model)
```



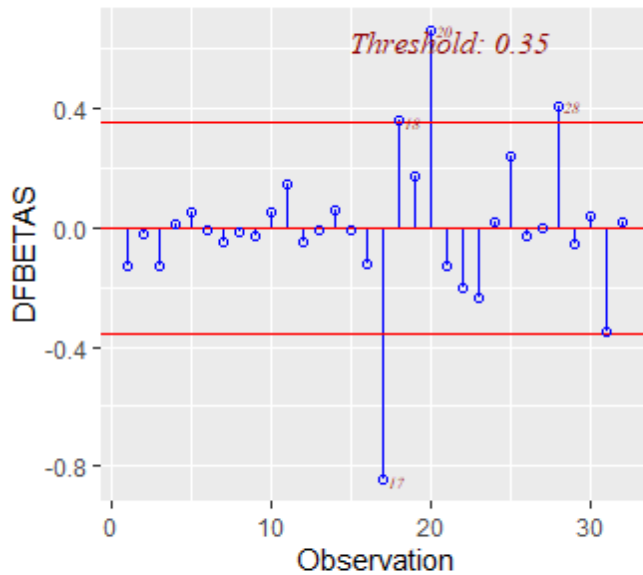
DFBETAs Panel

DFBETA measures the difference in each parameter estimate with and without the influential point. There is a DFBETA for each data point i.e if there are n observations and k variables, there will be $n * k$ DFBETAs. In general, large values of DFBETAS indicate observations that are influential in estimating a given parameter. Belsley, Kuh, and Welsch recommend 2 as a general cutoff value to indicate influential observations and $\frac{2}{\sqrt{n}}$ as a size-adjusted cutoff.

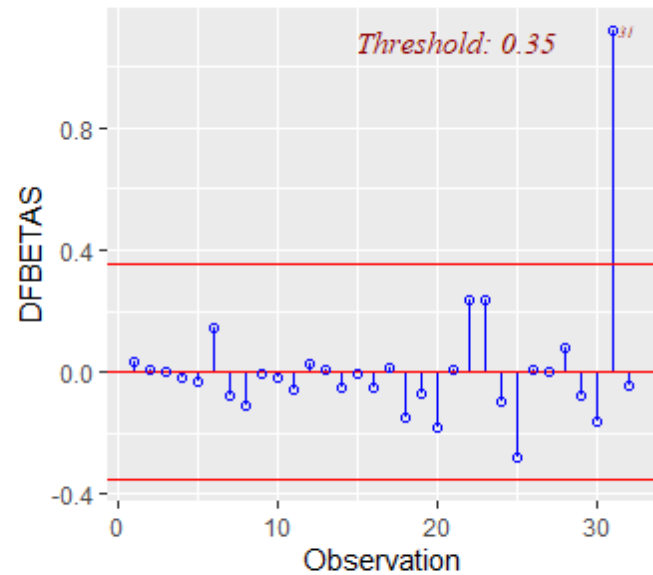
Hide

```
model <- lm(mpg ~ disp + hp + wt, data = mtcars)
ols_plot_dfbetas(model)
```

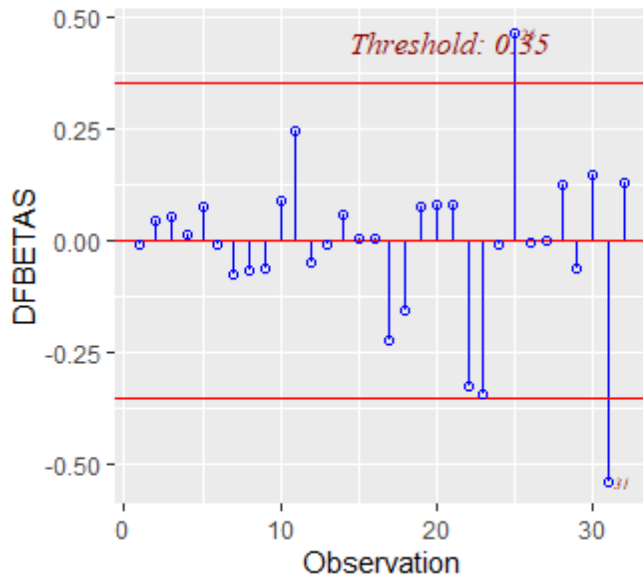

Influence Diagnostics for (Intercept)



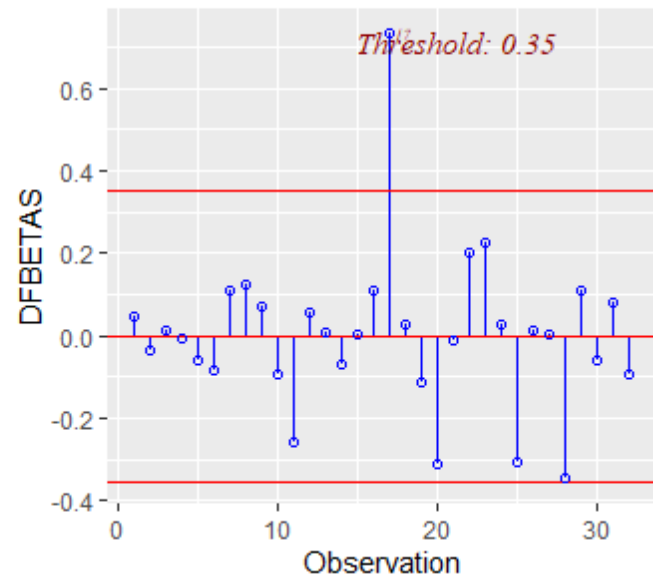
Influence Diagnostics for hp



Influence Diagnostics for disp



Influence Diagnostics for wt



DFFITS Plot

Proposed by Welsch and Kuh (1977). It is the scaled difference between the i^{th} fitted value obtained from the full data and the i^{th} fitted value obtained by deleting the i^{th} observation. DFFIT - difference in fits, is used to identify influential data points. It quantifies the number of standard deviations that the fitted value changes when the i th data point is omitted.

Steps to compute DFFITs:

- delete observations one at a time.
- refit the regression model on remaining $\{n - 1\}$ observations
- examine how much all of the fitted values change when the i th observation is deleted.

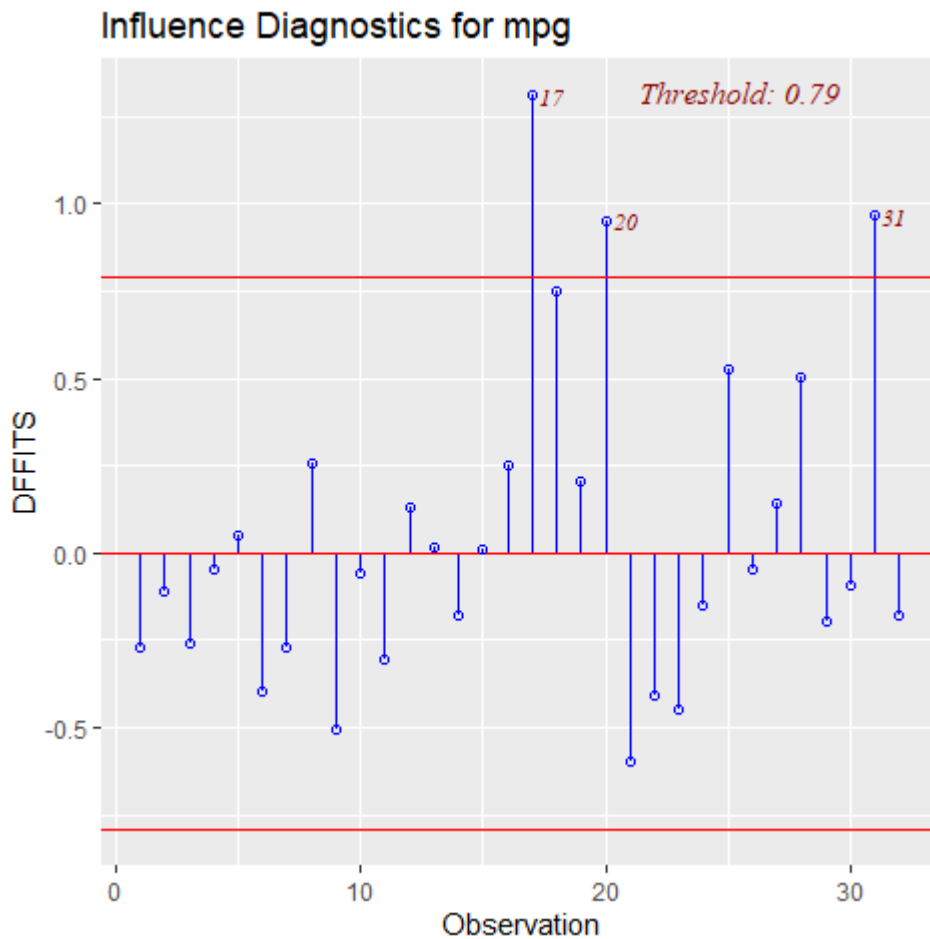
An observation is deemed influential if the absolute value of its DFFITS value is greater than:

$$2 * \frac{\sqrt{(p+1)}}{(n-p-1)}$$

where n is the number of observations and p is the number of predictors including intercept.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_dffits(model)
```

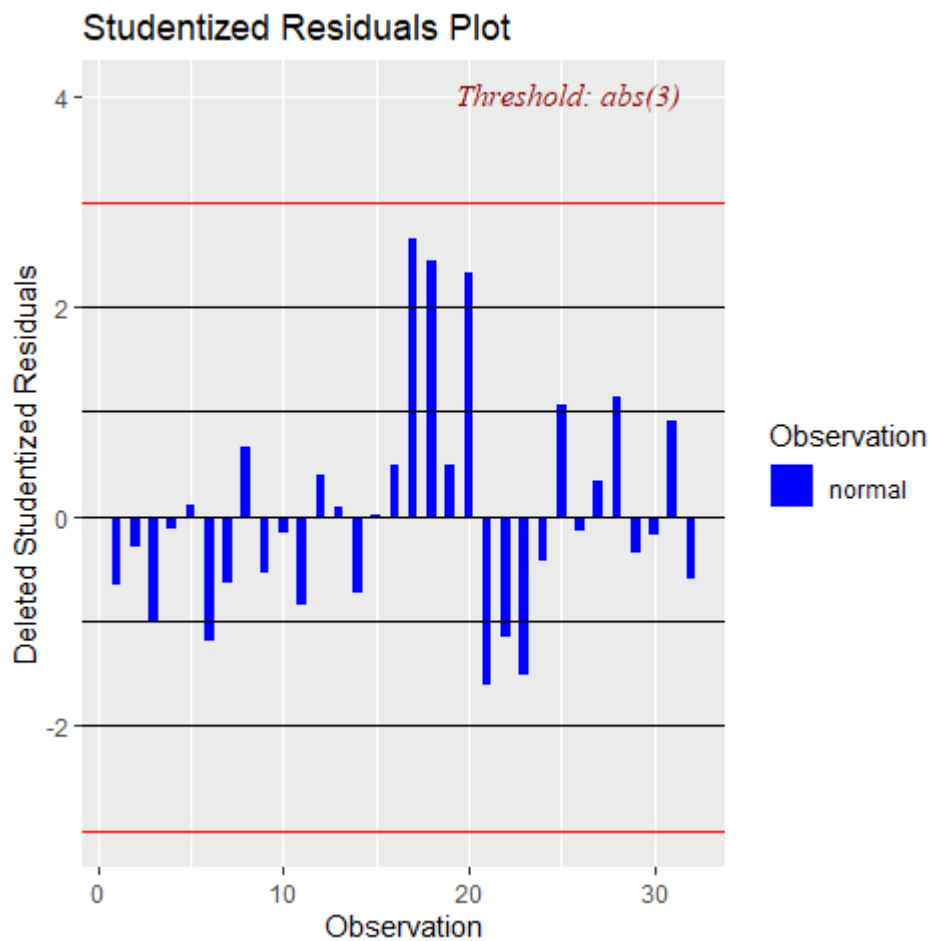


Studentized Residual Plot

Plot for detecting outliers. Studentized deleted residuals (or externally studentized residuals) is the deleted residual divided by its estimated standard deviation. Studentized residuals are going to be more effective for detecting outlying Y observations than standardized residuals. If an observation has an externally studentized residual that is larger than 3 (in absolute value) we can call it an outlier.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_resid_stud(model)
```

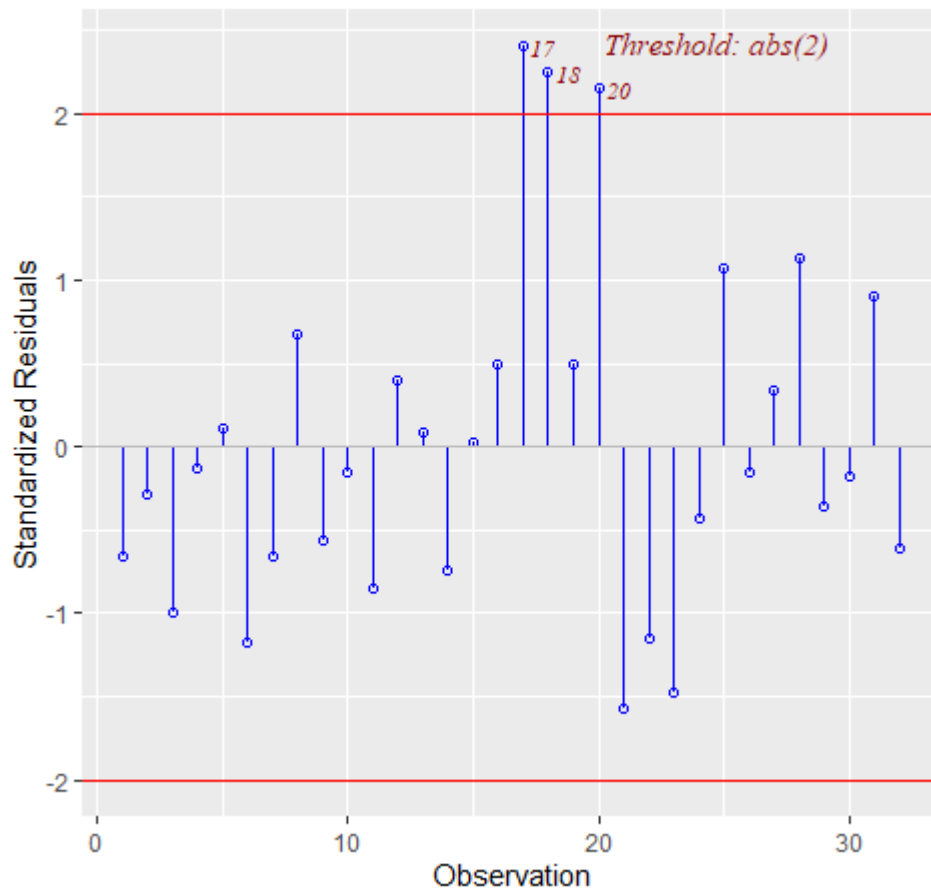
Standardized Residual Chart

Chart for detecting outliers. Standardized residual (internally studentized) is the residual divided by estimated standard deviation.

[Hide](#)

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_resid_stand(model)
```

Standardized Residuals Chart



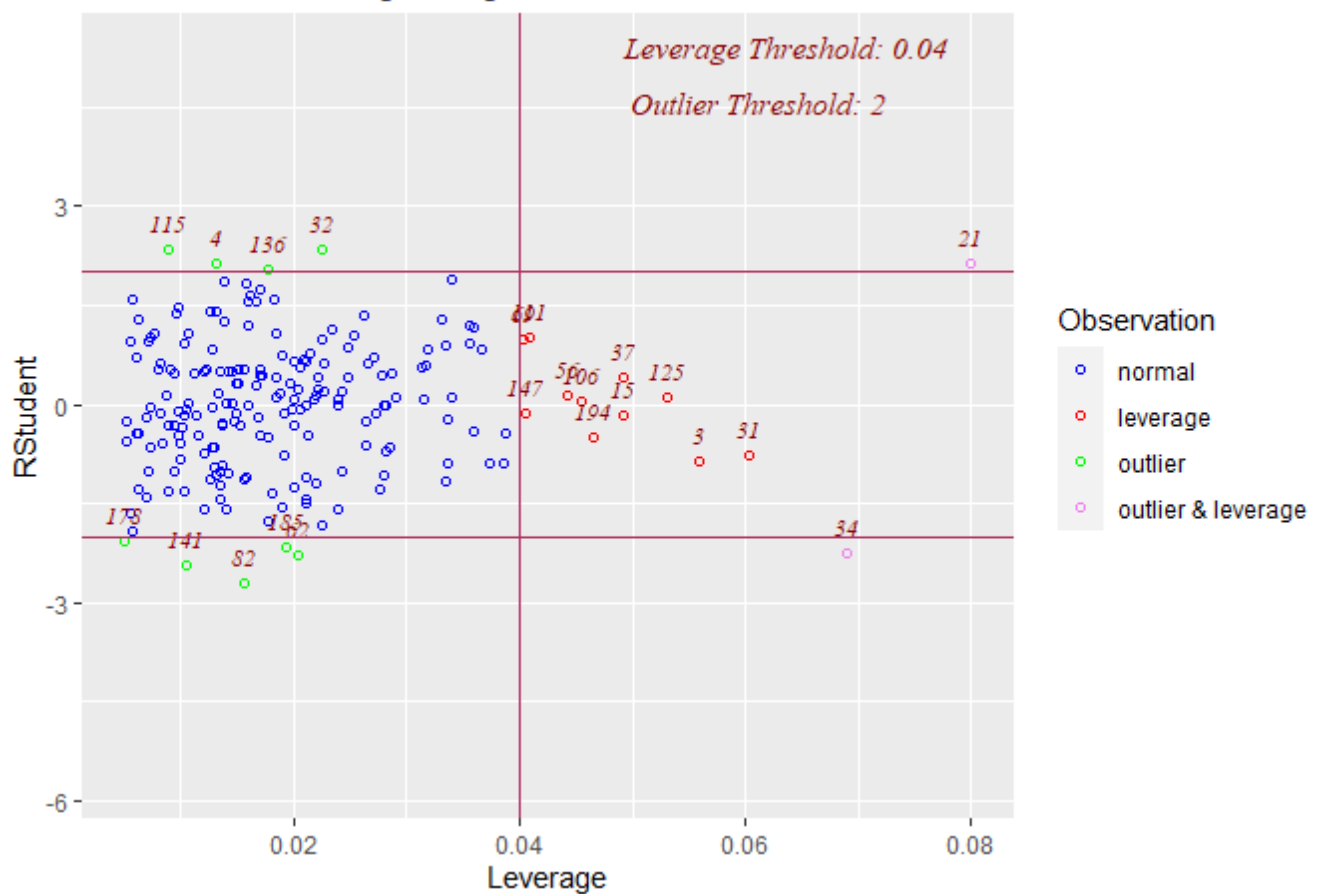
Studentized Residuals vs Leverage Plot

Graph for detecting influential observations.

Hide

```
model <- lm(read ~ write + math + science, data = hsb)
ols_plot_resid_lev(model)
```

Outlier and Leverage Diagnostics for read

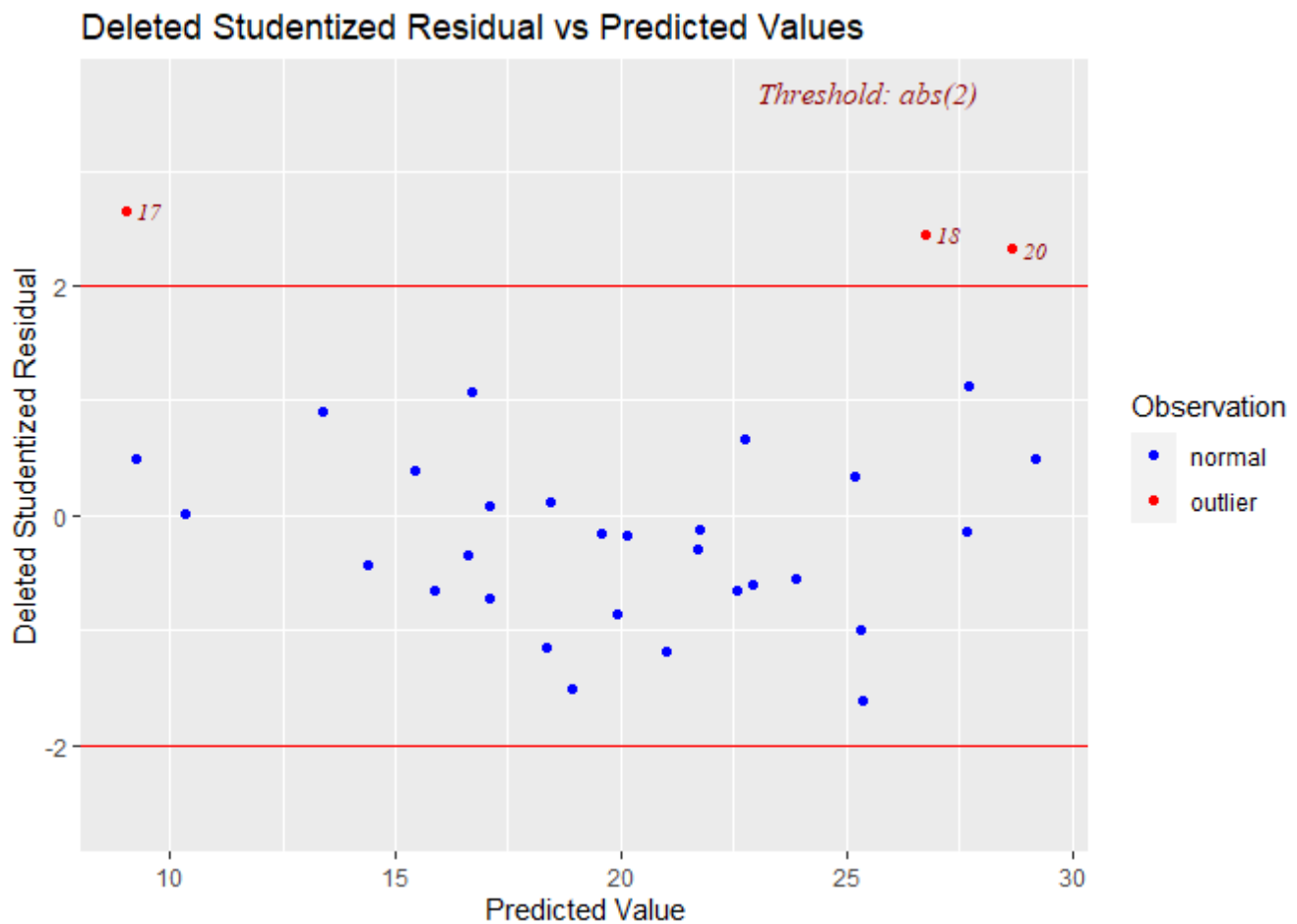


Deleted Studentized Residual vs Fitted Values Plot

Graph for detecting outliers.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_resid_stud_fit(model)
```

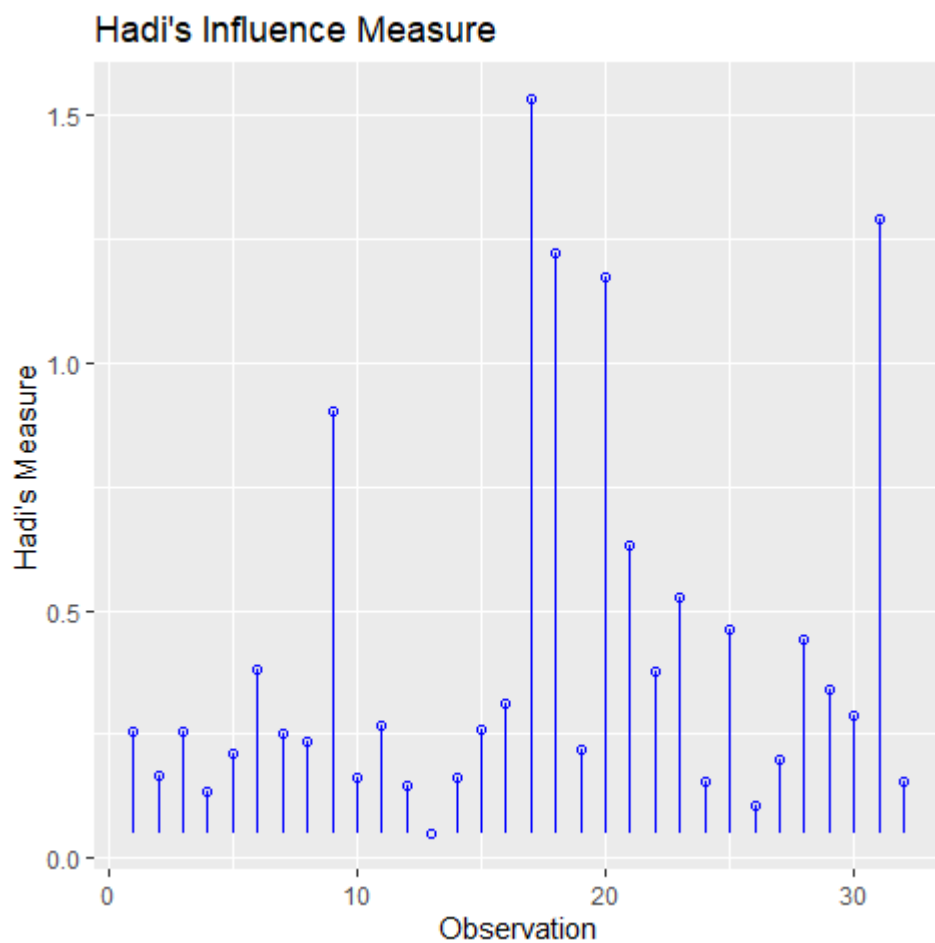


Hadi Plot

Hadi's measure of influence based on the fact that influential observations can be present in either the response variable or in the predictors or both. The plot is used to detect influential observations based on Hadi's measure.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_hadi(model)
```

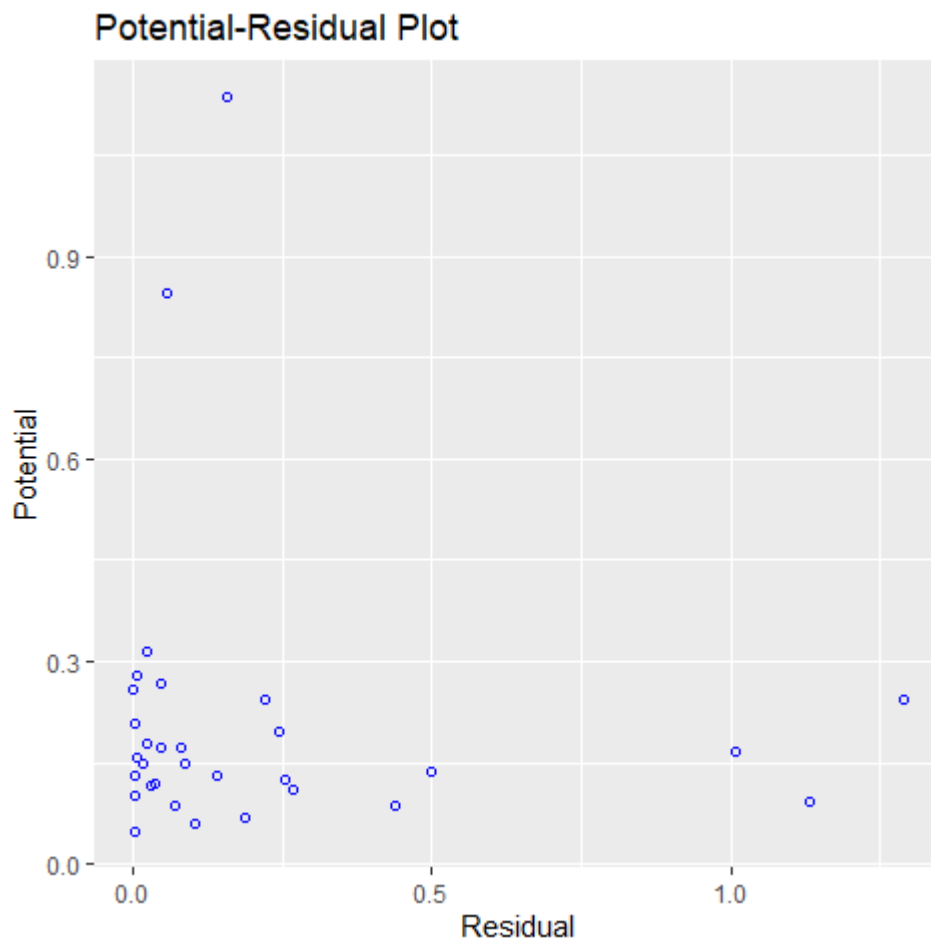


Potential Residual Plot

Plot to aid in classifying unusual observations as high-leverage points, outliers, or a combination of both.

[Hide](#)

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_resid_pot(model)
```



Collinearity Diagnostics, Model Fit & Variable Contribution

Collinearity Diagnostics

Collinearity implies two variables are near perfect linear combinations of one another. Multicollinearity involves more than two variables. In the presence of multicollinearity, regression estimates are unstable and have high standard errors.

VIF

Variance inflation factors measure the inflation in the variances of the parameter estimates due to collinearities that exist among the predictors. It is a measure of how much the variance of the estimated regression coefficient β_k is “inflated” by the existence of correlation among the predictor variables in the model. A VIF of 1 means that there is no correlation among the k th predictor and the remaining predictor variables, and hence the variance of β_k is not inflated at all. The general rule of thumb is that VIFs exceeding 4 warrant further investigation, while VIFs exceeding 10 are signs of serious multicollinearity requiring correction.

Steps to calculate VIF:

- Regress the k^{th} predictor on rest of the predictors in the model.
- Compute the R_k^2

$$VIF = \frac{1}{1 - R_k^2} = \frac{1}{Tolerance}$$

[Hide](#)

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_vif_tol(model)
```

Variables <chr>	Tolerance <dbl>	VIF <dbl>
disp	0.1252279	7.985439
hp	0.1935450	5.166758
wt	0.1445726	6.916942
qsec	0.3191708	3.133119
4 rows		

Tolerance

Percent of variance in the predictor that cannot be accounted for by other predictors.

Steps to calculate tolerance:

- Regress the k^{th} predictor on rest of the predictors in the model.
- Compute the R_k^2

$$Tolerance = 1 - R_k^2$$

Condition Index

Most multivariate statistical approaches involve decomposing a correlation matrix into linear combinations of variables. The linear combinations are chosen so that the first combination has the largest possible variance (subject to some restrictions we won't discuss), the second combination has the next largest variance, subject to being uncorrelated with the first, the third has the largest possible variance, subject to being uncorrelated with the first and second, and so forth. The variance of each of these linear combinations is called an eigenvalue. Collinearity is spotted by finding 2 or more variables that have large proportions of variance (.50 or more) that correspond to large condition indices. A rule of thumb is to label as large those condition indices in the range of 30 or larger.

[Hide](#)

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_eigen_cindex(model)
```

Eigenvalue <dbl>	Condition Index <dbl>	intercept <dbl>	disp <dbl>	hp <dbl>	wt <dbl>

Eigenvalue <dbl>	Condition Index <dbl>	intercept <dbl>	disp <dbl>	hp <dbl>	wt <dbl>	
4.721487187	1.000000	0.000123237	0.001132468	0.001413094	0.0005253393	C
0.216562203	4.669260	0.002617424	0.036811051	0.027751289	0.0002096014	C
0.050416837	9.677242	0.001656551	0.120881424	0.392366164	0.0377028008	C
0.010104757	21.616057	0.025805998	0.777260487	0.059594623	0.7017528428	C
0.001429017	57.480524	0.969796790	0.063914571	0.518874831	0.2598094157	C
5 rows						

Collinearity Diagnostics

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_coll_diag(model)
```

Tolerance and Variance Inflation Factor

Variables <chr>	Tolerance <dbl>	VIF <dbl>
disp	0.1252279	7.985439
hp	0.1935450	5.166758
wt	0.1445726	6.916942
qsec	0.3191708	3.133119
4 rows		

Eigenvalue and Condition Index

Eigenvalue <dbl>	Condition Index <dbl>	intercept <dbl>	disp <dbl>	hp <dbl>	wt <dbl>	
4.721487187	1.000000	0.000123237	0.001132468	0.001413094	0.0005253393	C
0.216562203	4.669260	0.002617424	0.036811051	0.027751289	0.0002096014	C
0.050416837	9.677242	0.001656551	0.120881424	0.392366164	0.0377028008	C

Eigenvalue <dbl>	Condition Index <dbl>	intercept <dbl>	disp <dbl>	hp <dbl>	wt <dbl>	
0.010104757	21.616057	0.025805998	0.777260487	0.059594623	0.7017528428	0
0.001429017	57.480524	0.969796790	0.063914571	0.518874831	0.2598094157	0
5 rows						

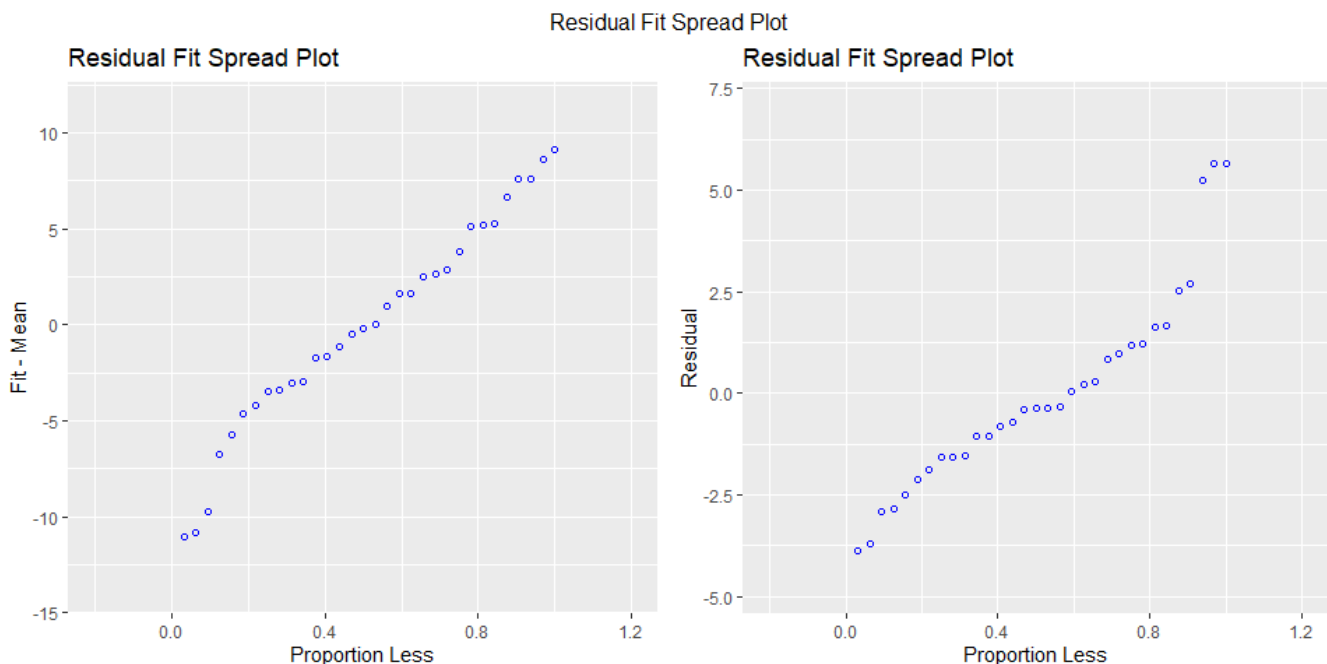
Model Fit Assessment

Residual Fit Spread Plot

Plot to detect non-linearity, influential observations and outliers. Consists of side-by-side quantile plots of the centered fit and the residuals. It shows how much variation in the data is explained by the fit and how much remains in the residuals. For inappropriate models, the spread of the residuals in such a plot is often greater than the spread of the centered fit.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_resid_fit_spread(model)
```



Part & Partial Correlations

Correlations

Relative importance of independent variables in determining **Y**. How much each variable uniquely contributes to R^2 over and above that which can be accounted for by the other predictors.

Zero Order

Pearson correlation coefficient between the dependent variable and the independent variables.

Part

Unique contribution of independent variables. How much R^2 will decrease if that variable is removed from the model?

Partial

How much of the variance in **Y**, which is not estimated by the other independent variables in the model, is estimated by the specific variable?

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_correlations(model)
```

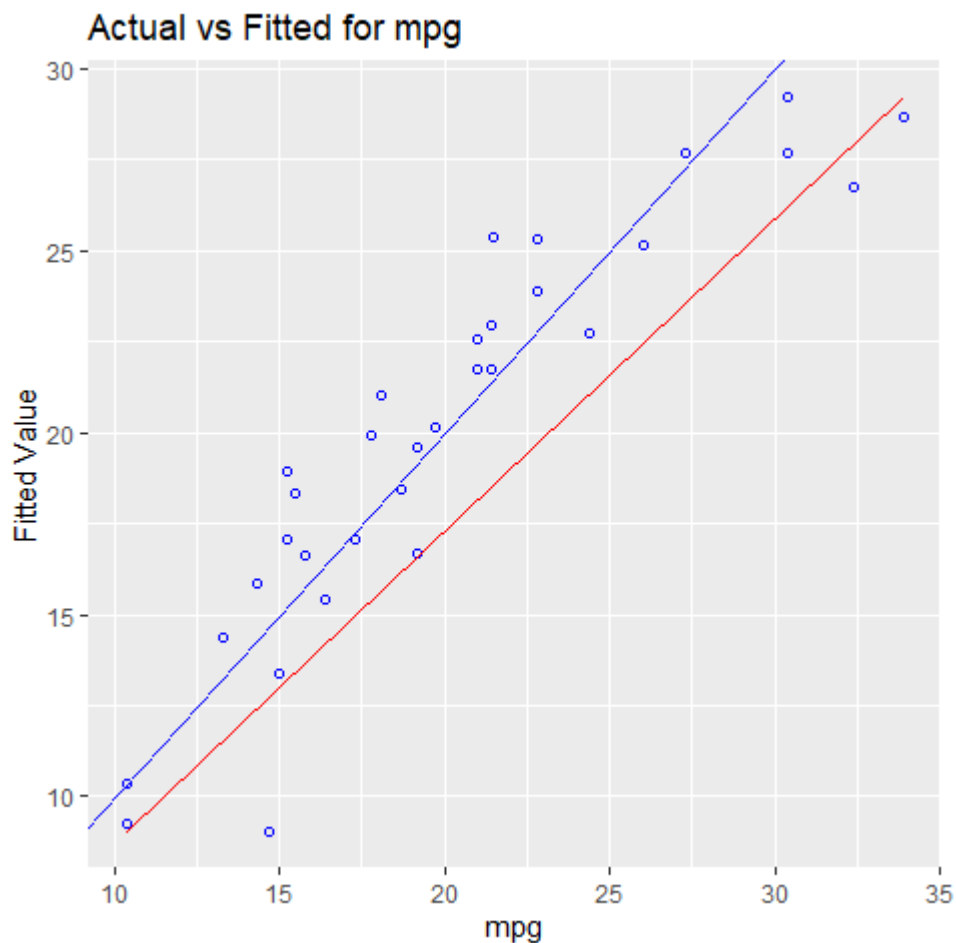
Correlations			
Variable	Zero Order	Partial	Part
disp	-0.848	0.048	0.019
hp	-0.776	-0.224	-0.093
wt	-0.868	-0.574	-0.285
qsec	0.419	0.219	0.091

Observed vs Predicted Plot

Plot of observed vs fitted values to assess the fit of the model. Ideally, all your points should be close to a regressed diagonal line. Draw such a diagonal line within your graph and check out where the points lie. If your model had a high R Square, all the points would be close to this diagonal line. The lower the R Square, the weaker the Goodness of fit of your model, the more foggy or dispersed your points are from this diagonal line.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_obs_fit(model)
```



Lack of Fit F Test

Assess how much of the error in prediction is due to lack of model fit. The residual sum of squares resulting from a regression can be decomposed into 2 components:

- Due to lack of fit
- Due to random variation

If most of the error is due to lack of fit and not just random error, the model should be discarded and a new model must be built. The lack of fit F test works only with simple linear regression. Moreover, it is important that the data contains repeat observations i.e. replicates for at least one of the values of the predictor x. This test generally only applies to datasets with plenty of replicates.

Hide

```
model <- lm(mpg ~ disp, data = mtcars)
ols_pure_error_anova(model)
```

Lack of Fit F Test

Response : mpg
Predictor: disp

Analysis of Variance Table

	DF	Sum Sq	Mean Sq	F Value	Pr(>F)
disp	1	808.8885	808.8885	314.0095	1.934413e-17
Residual	30	317.1587	10.57196		
Lack of fit	25	304.2787	12.17115	4.724824	0.04563623
Pure Error	5	12.88	2.576		

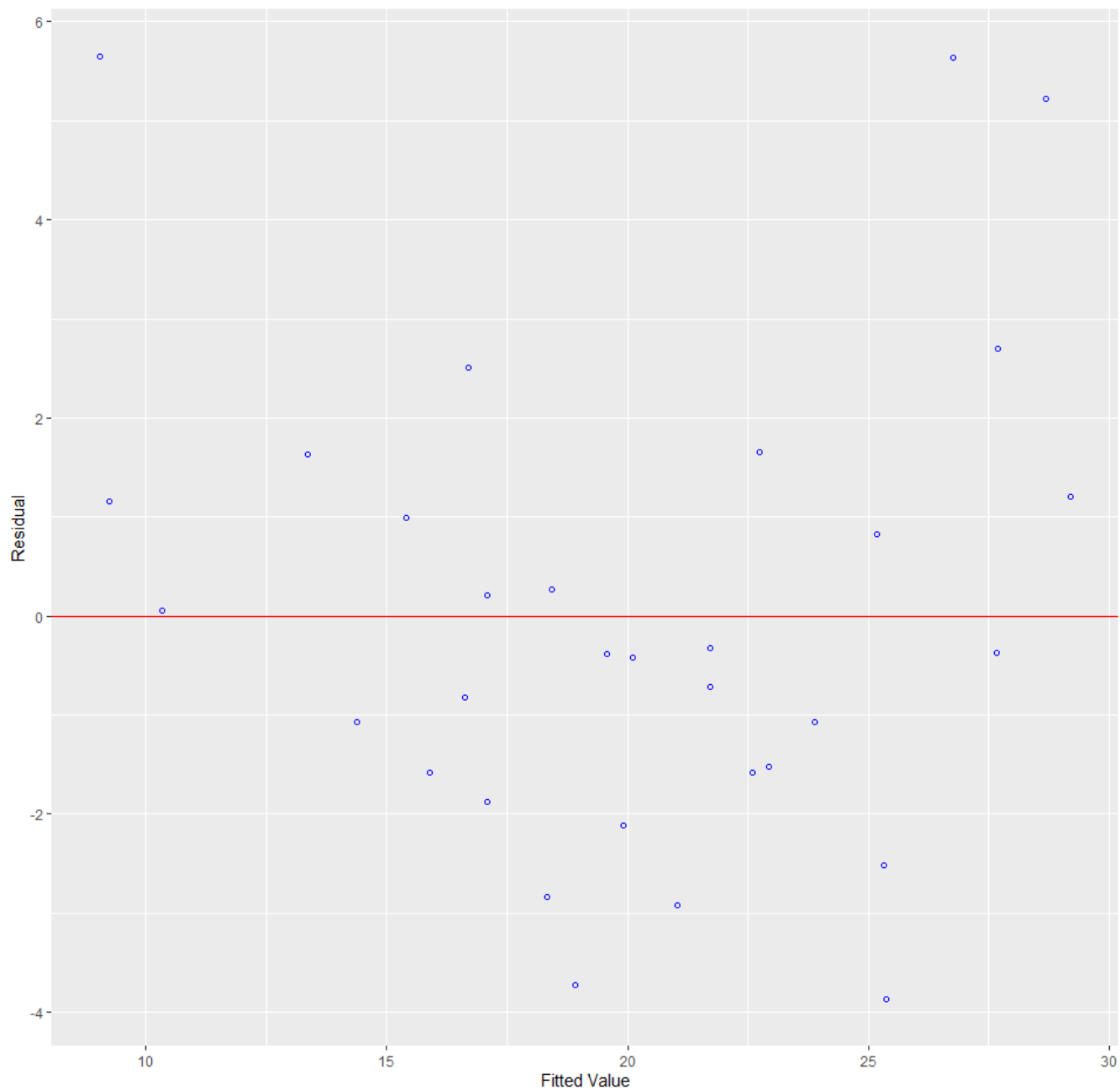
Diagnostics Panel

Panel of plots for regression diagnostics

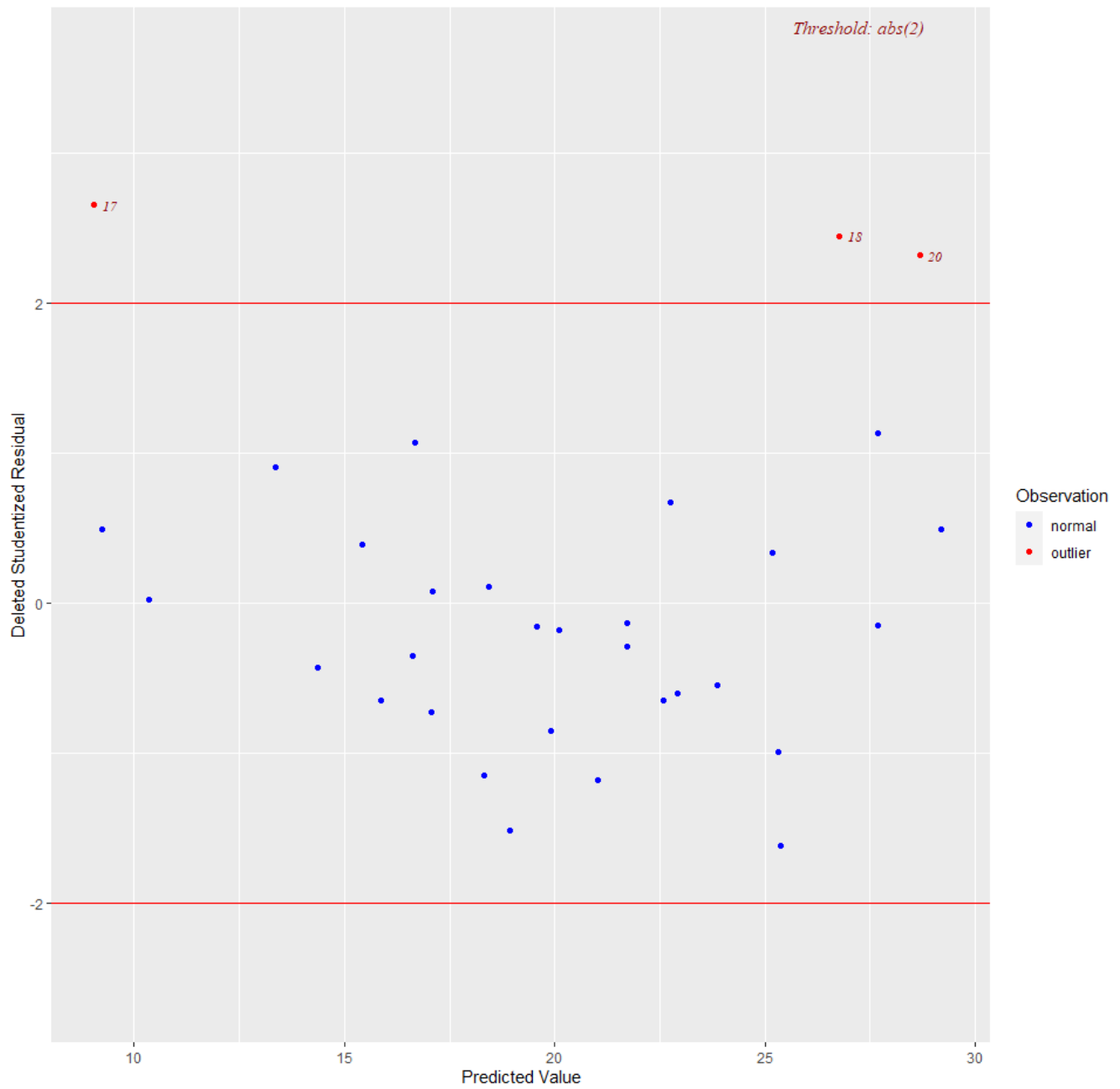
Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_diagnostics(model)
```

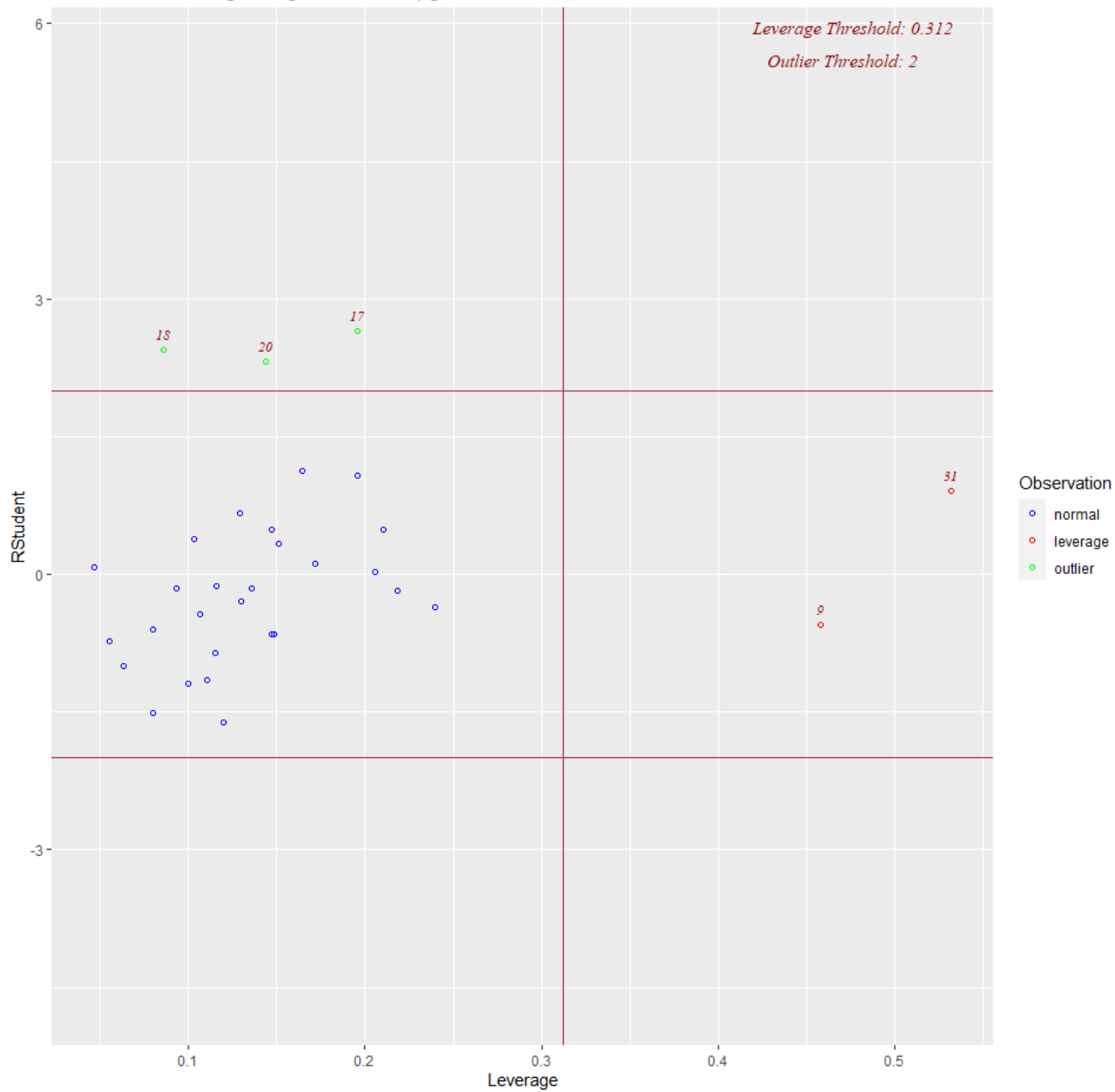
Residual vs Fitted Values



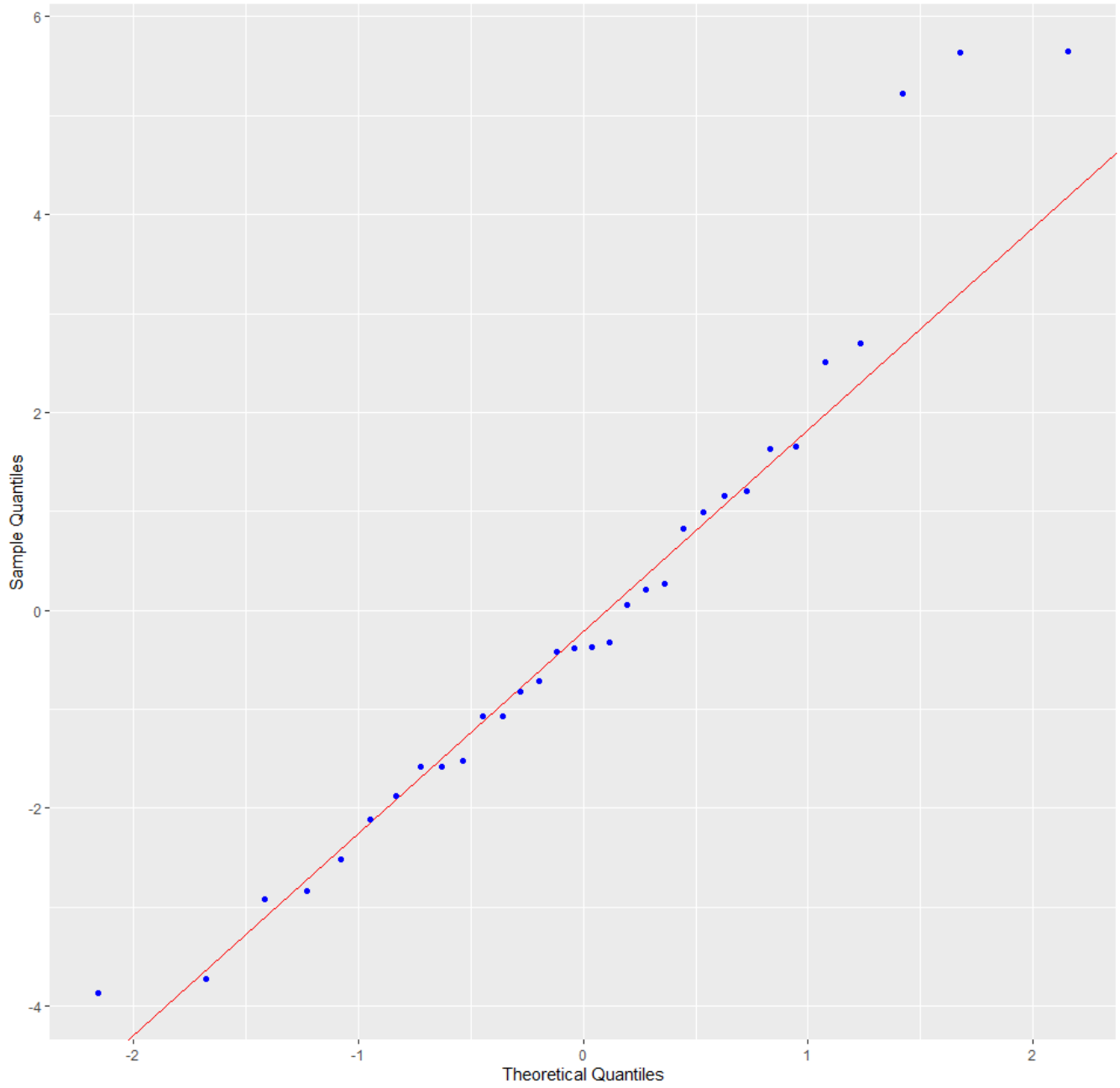
Deleted Studentized Residual vs Predicted Values



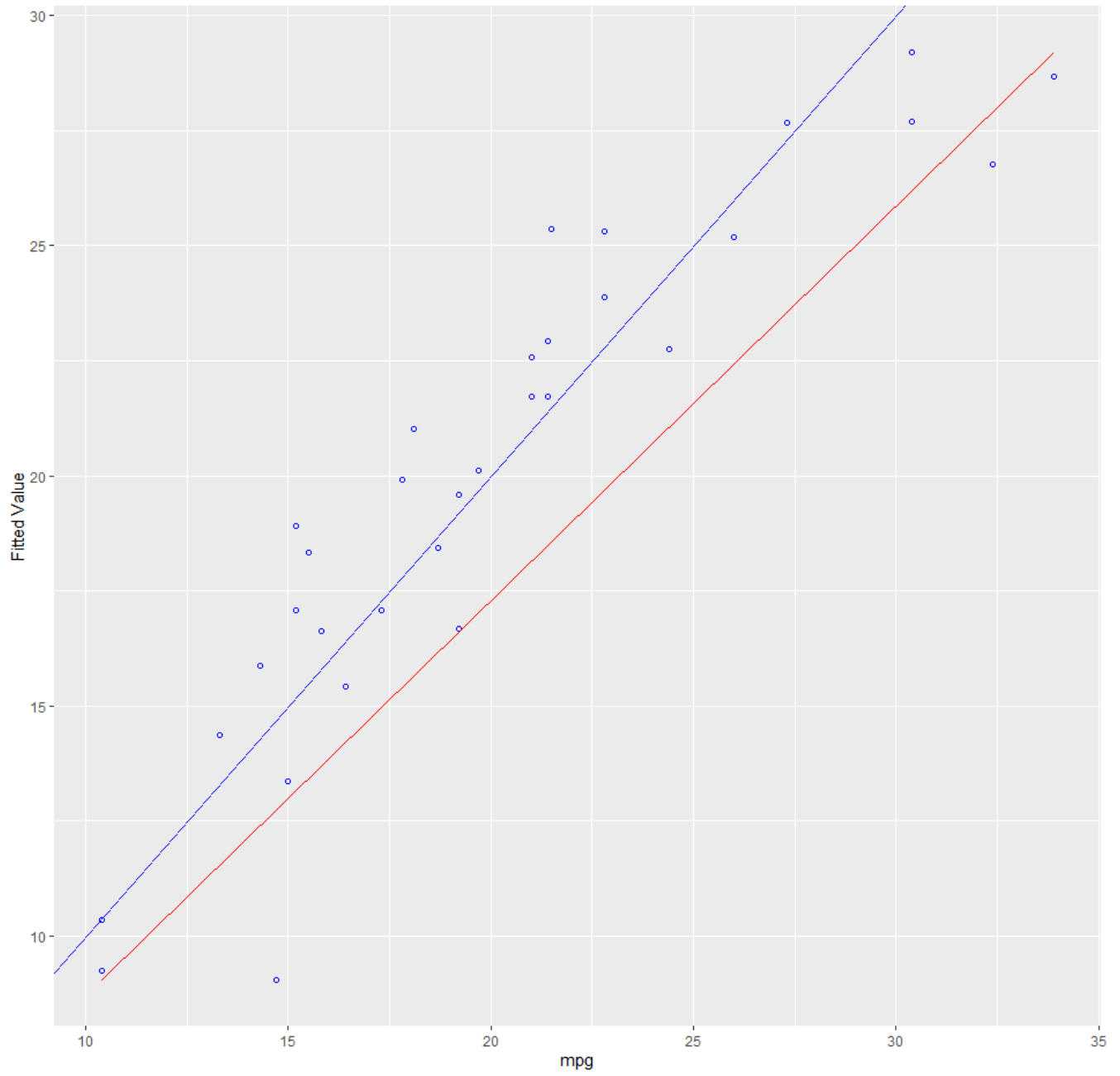
Outlier and Leverage Diagnostics for mpg



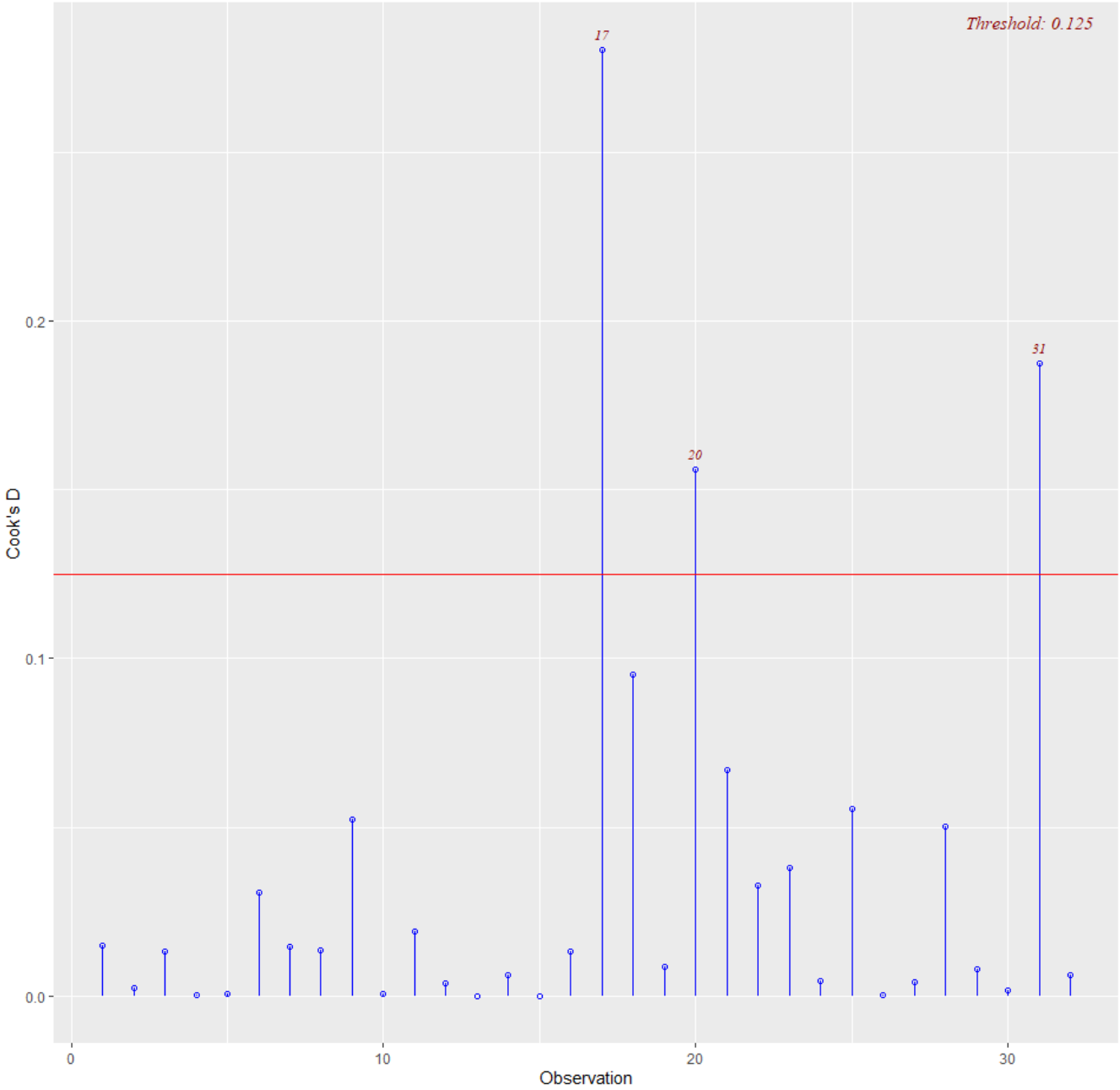
Normal Q-Q Plot



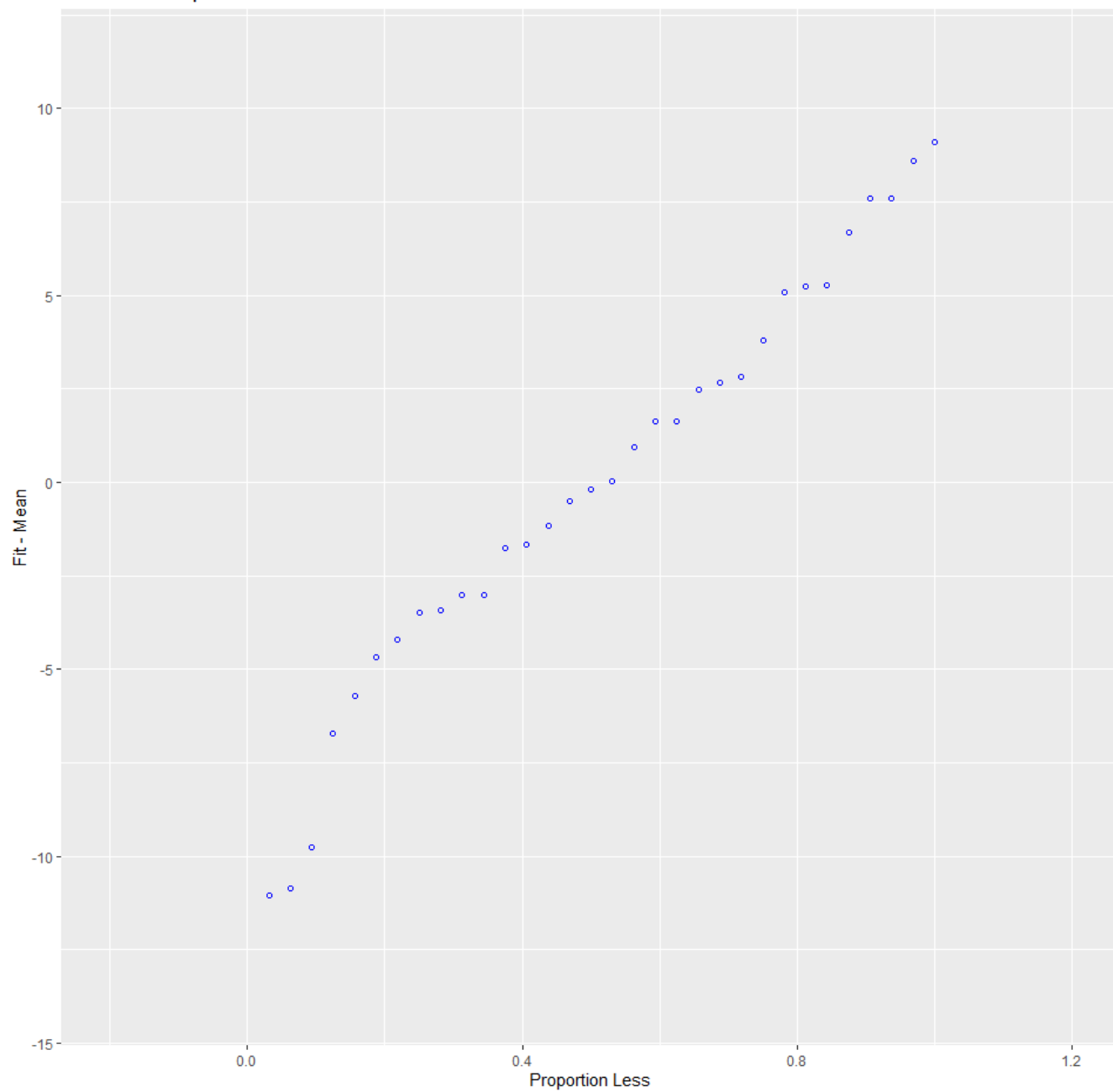
Actual vs Fitted for mpg



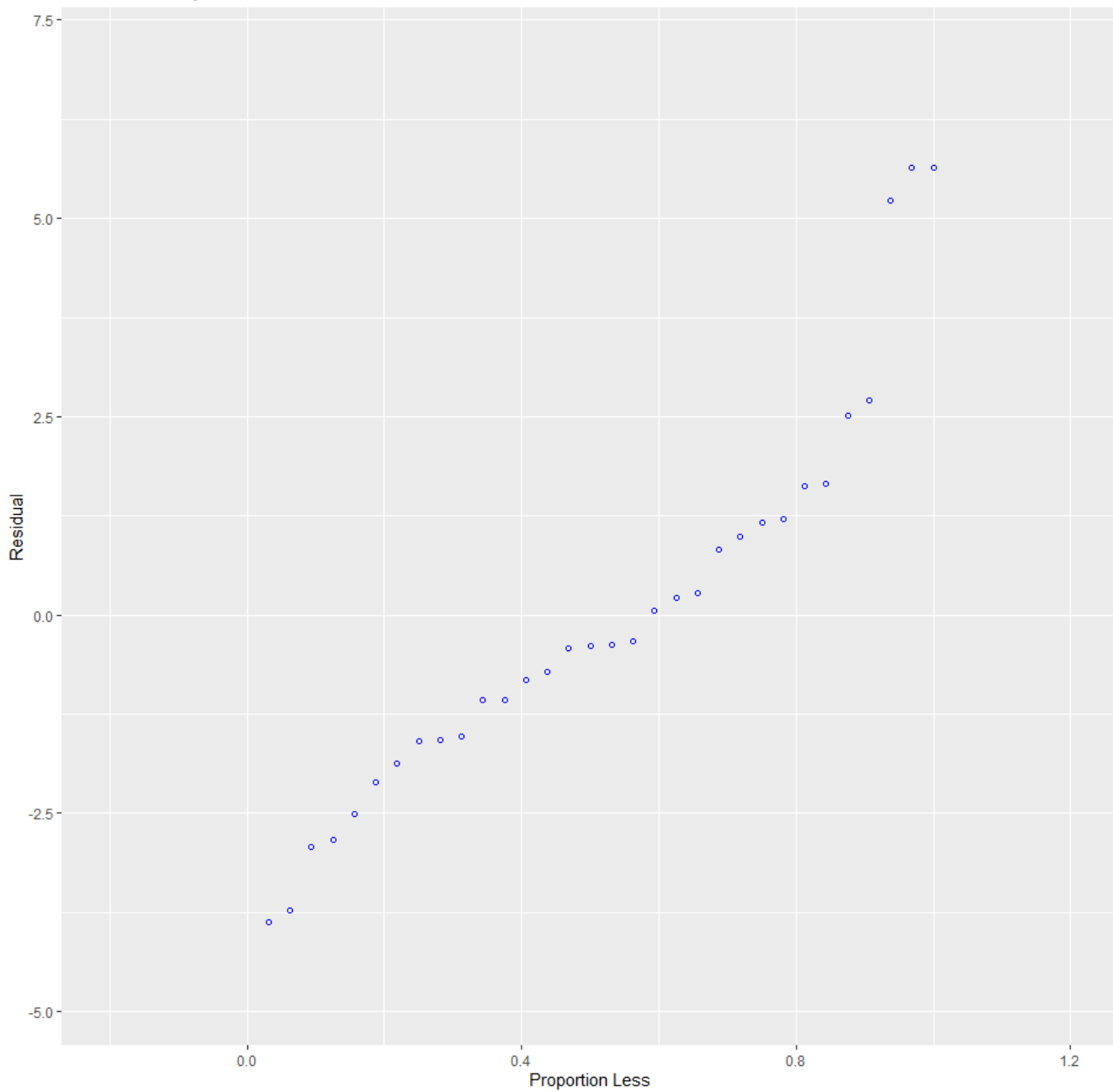
Cook's D Chart



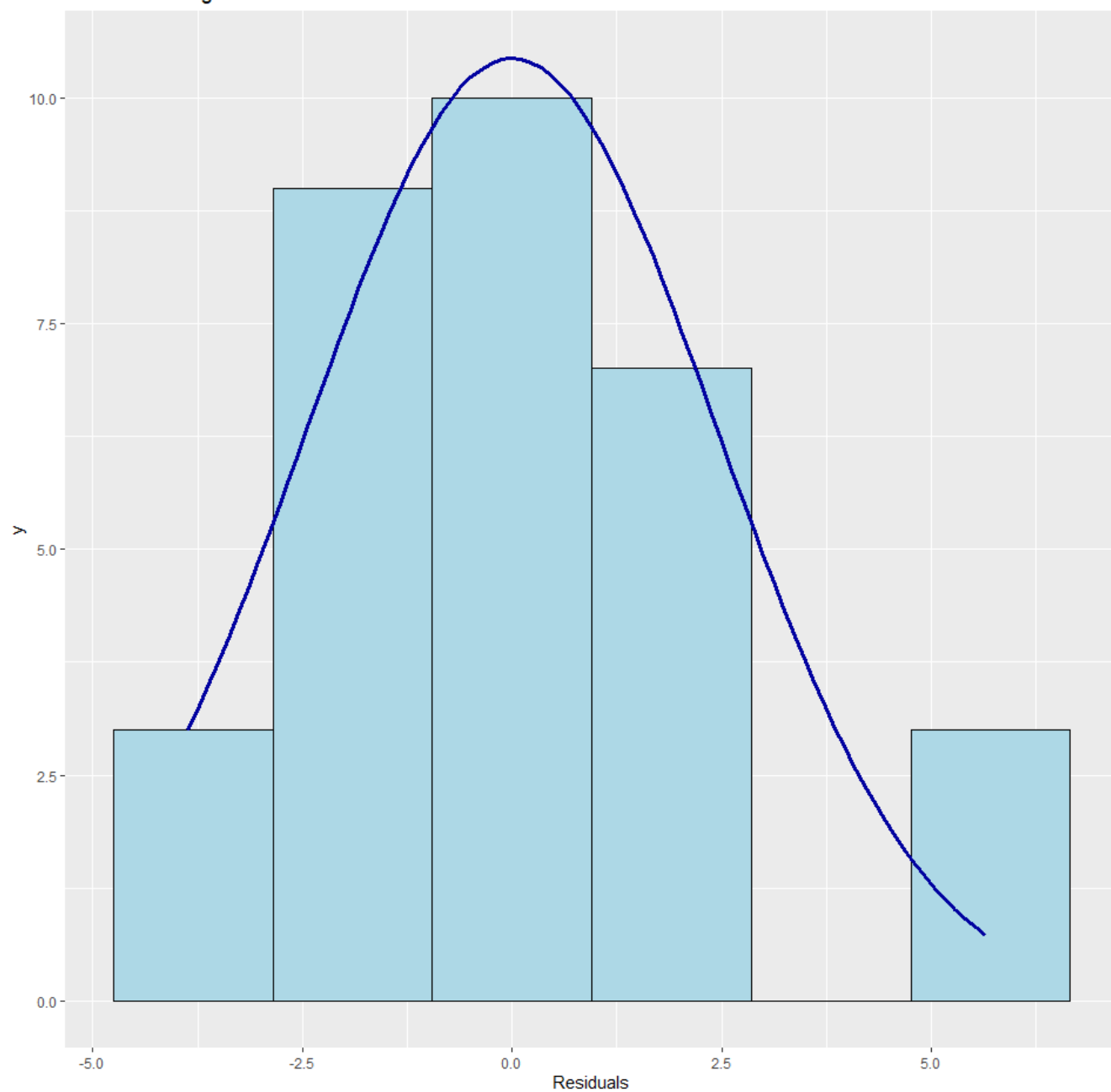
Residual Fit Spread Plot



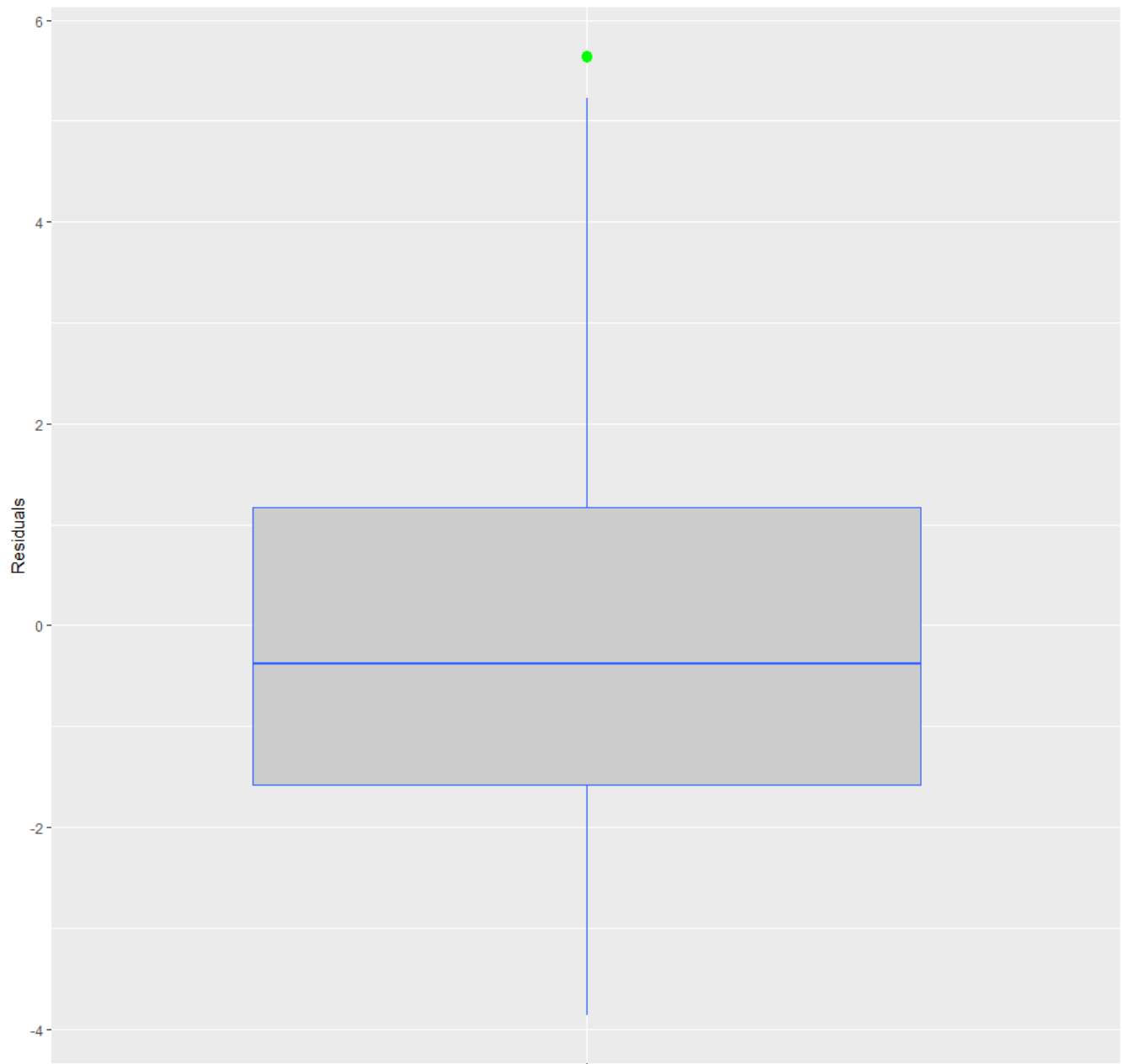
Residual Fit Spread Plot



Residual Histogram

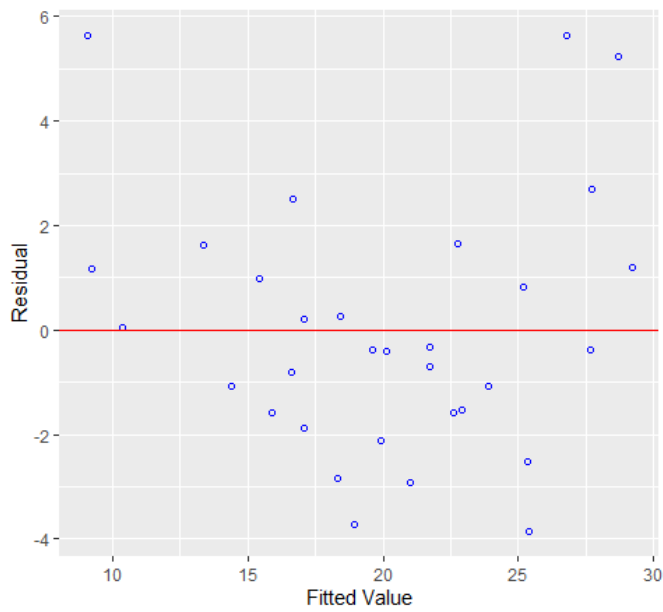


Residual Box Plot

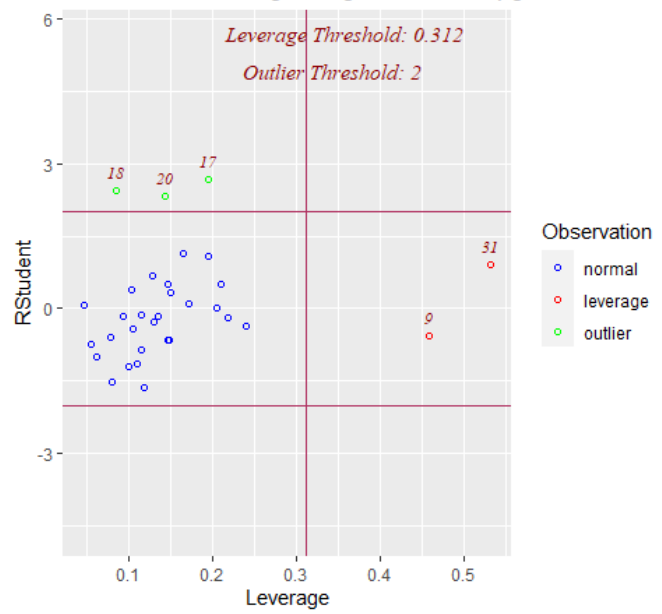


Regression Diagnostics

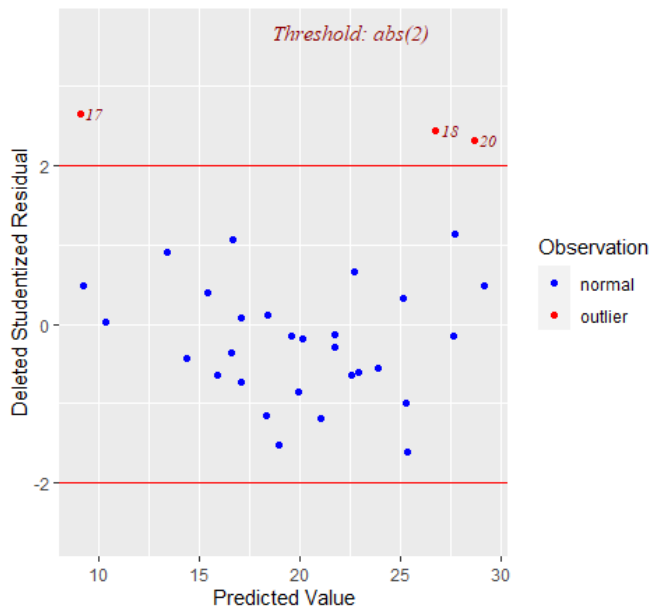
Residual vs Fitted Values



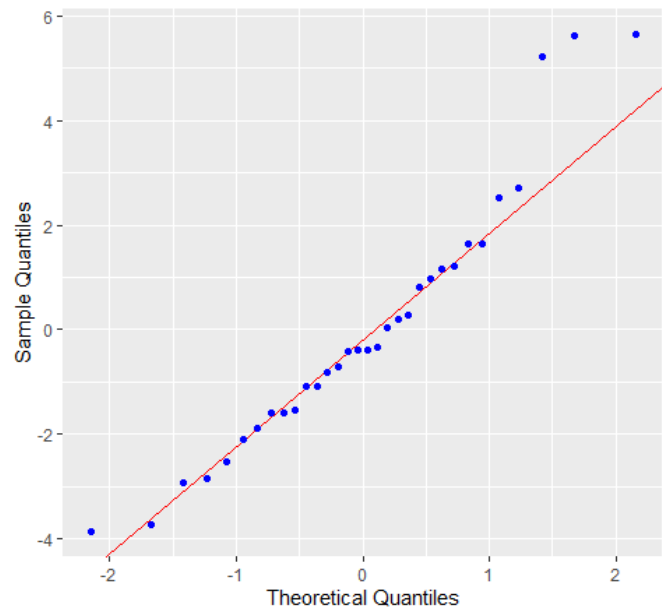
Outlier and Leverage Diagnostics for mpg



Deleted Studentized Residual vs Predicted Values

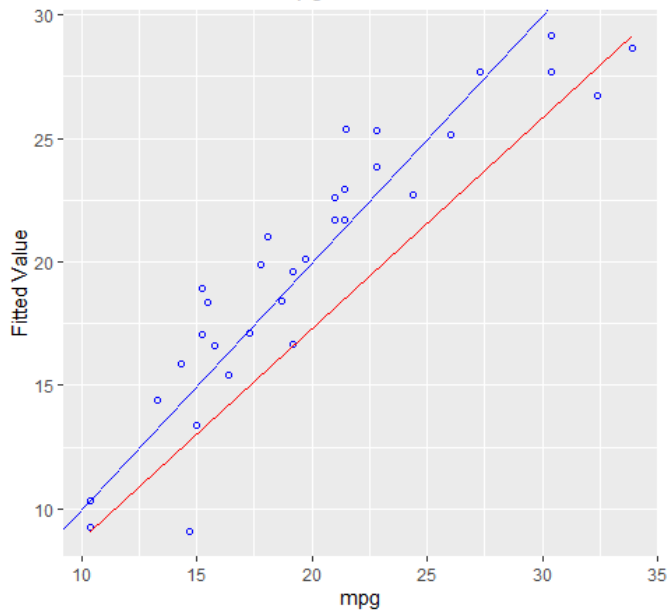


Normal Q-Q Plot

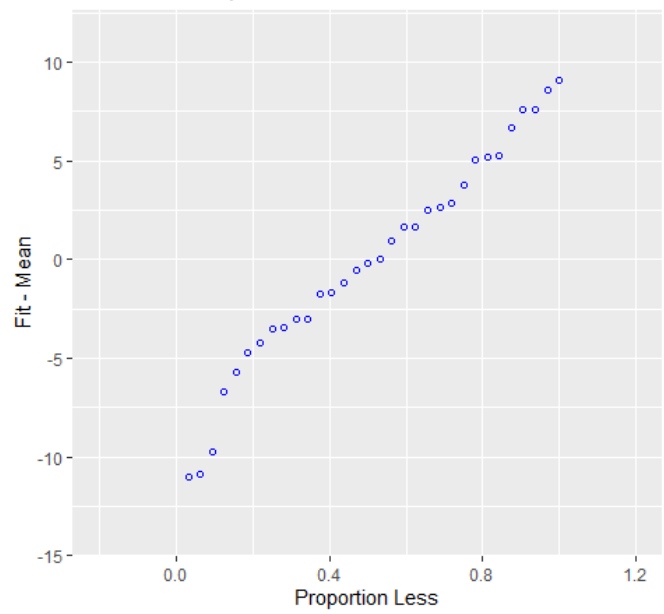


Regression Diagnostics

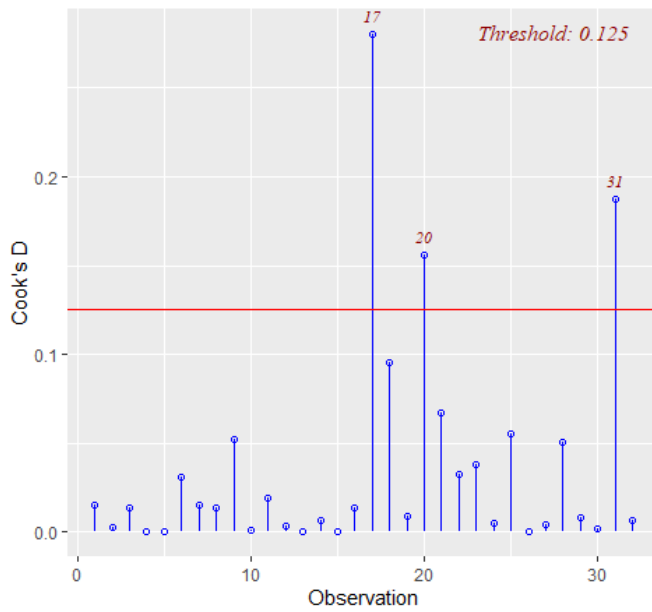
Actual vs Fitted for mpg



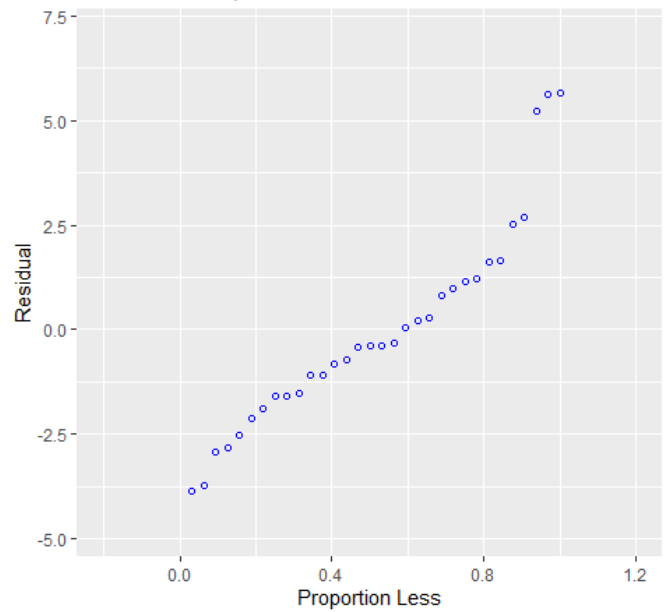
Residual Fit Spread Plot



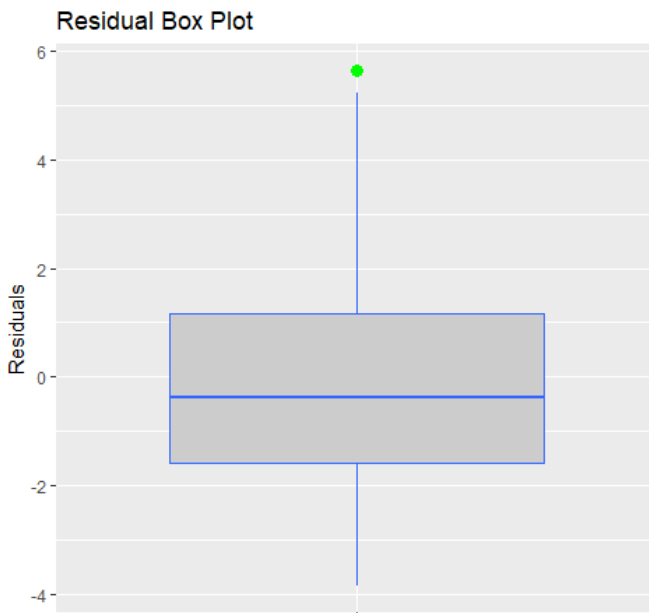
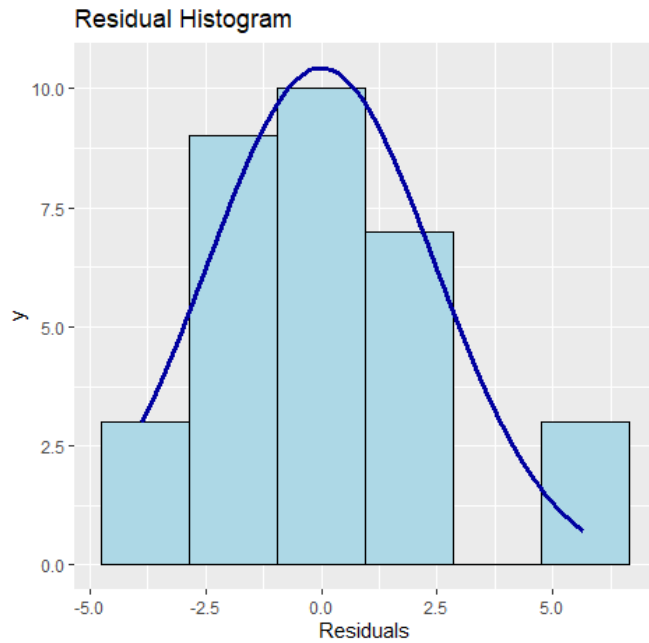
Cook's D Chart



Residual Fit Spread Plot



Regression Diagnostics



Variable Contributions

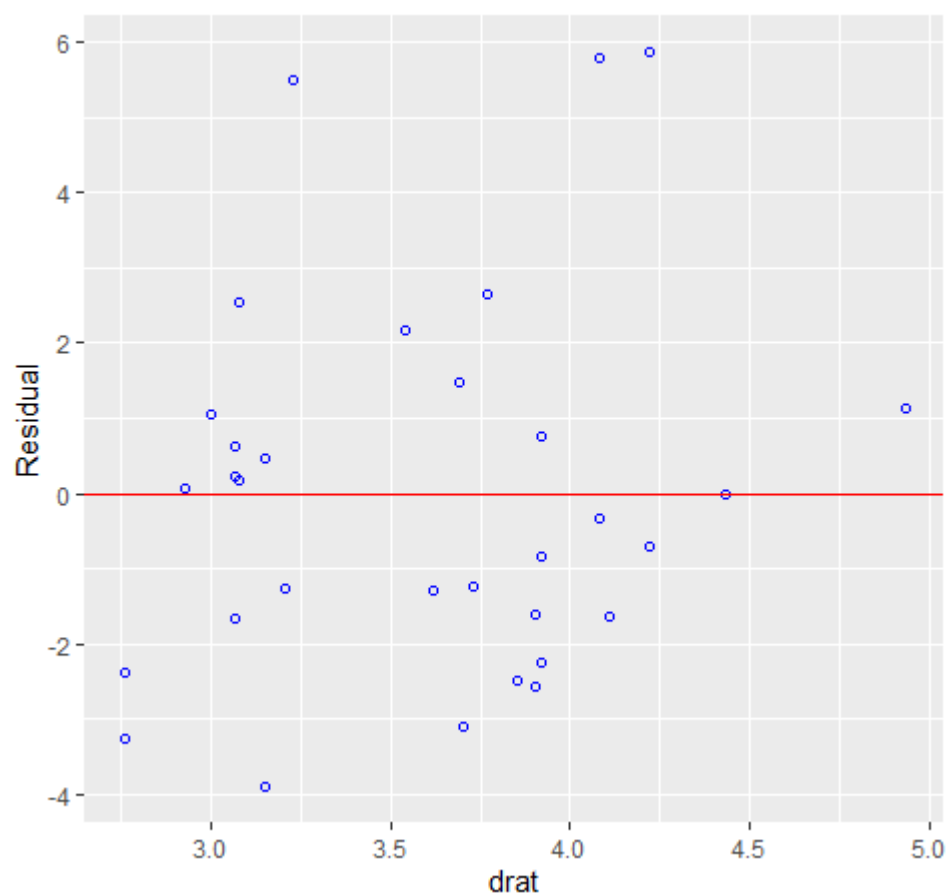
Residual vs Regressor Plots

Graph to determine whether we should add a new predictor to the model already containing other predictors. The residuals from the model is regressed on the new predictor and if the plot shows non random pattern, you should consider adding the new predictor to the model.

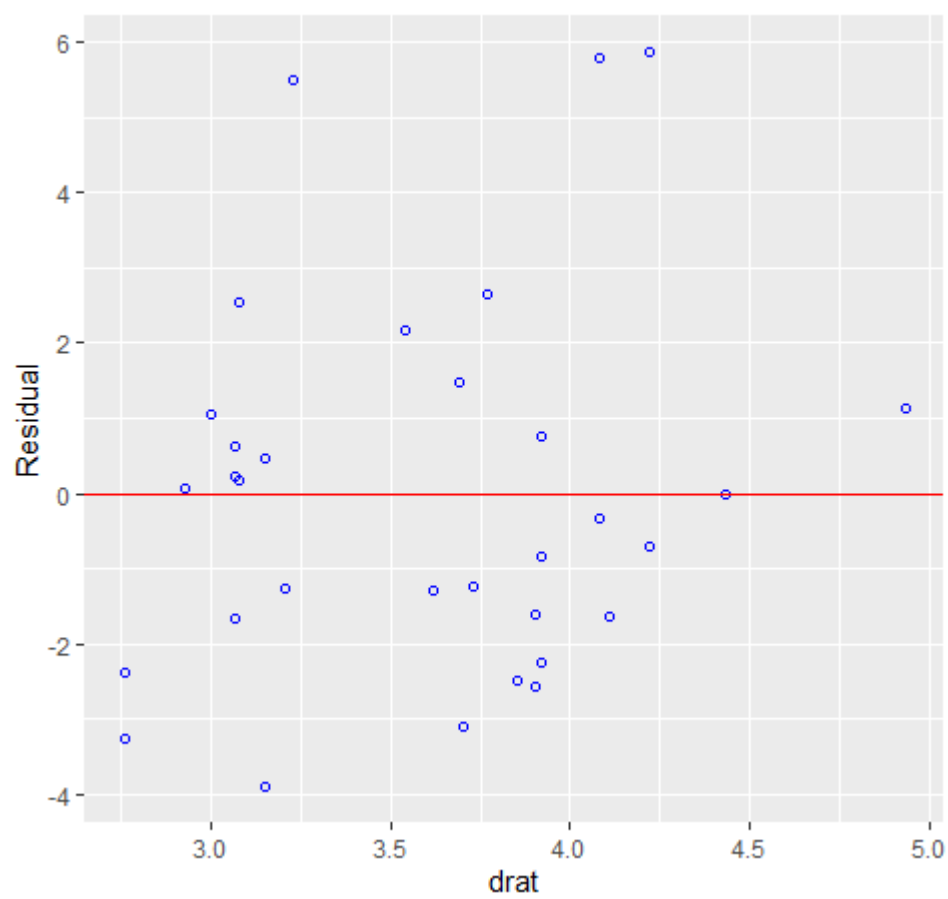
Hide

```
model <- lm(mpg ~ disp + hp + wt, data = mtcars)
ols_plot_resid_regressor(model, 'drat')
```

Residual vs drat



Residual vs drat



Added Variable Plot

Added variable plot provides information about the marginal importance of a predictor variable X_k , given the other predictor variables already in the model. It shows the marginal importance of the variable in reducing the residual variability.

The added variable plot was introduced by Mosteller and Tukey (1977). It enables us to visualize the regression coefficient of a new variable being considered to be included in a model. The plot can be constructed for each predictor variable.

Let us assume we want to test the effect of adding/removing variable X from a model. Let the response variable of the model be Y

Steps to construct an added variable plot:

- Regress Y on all variables other than X and store the residuals (Y residuals).
- Regress X on all the other variables included in the model (X residuals).
- Construct a scatter plot of Y residuals and X residuals.

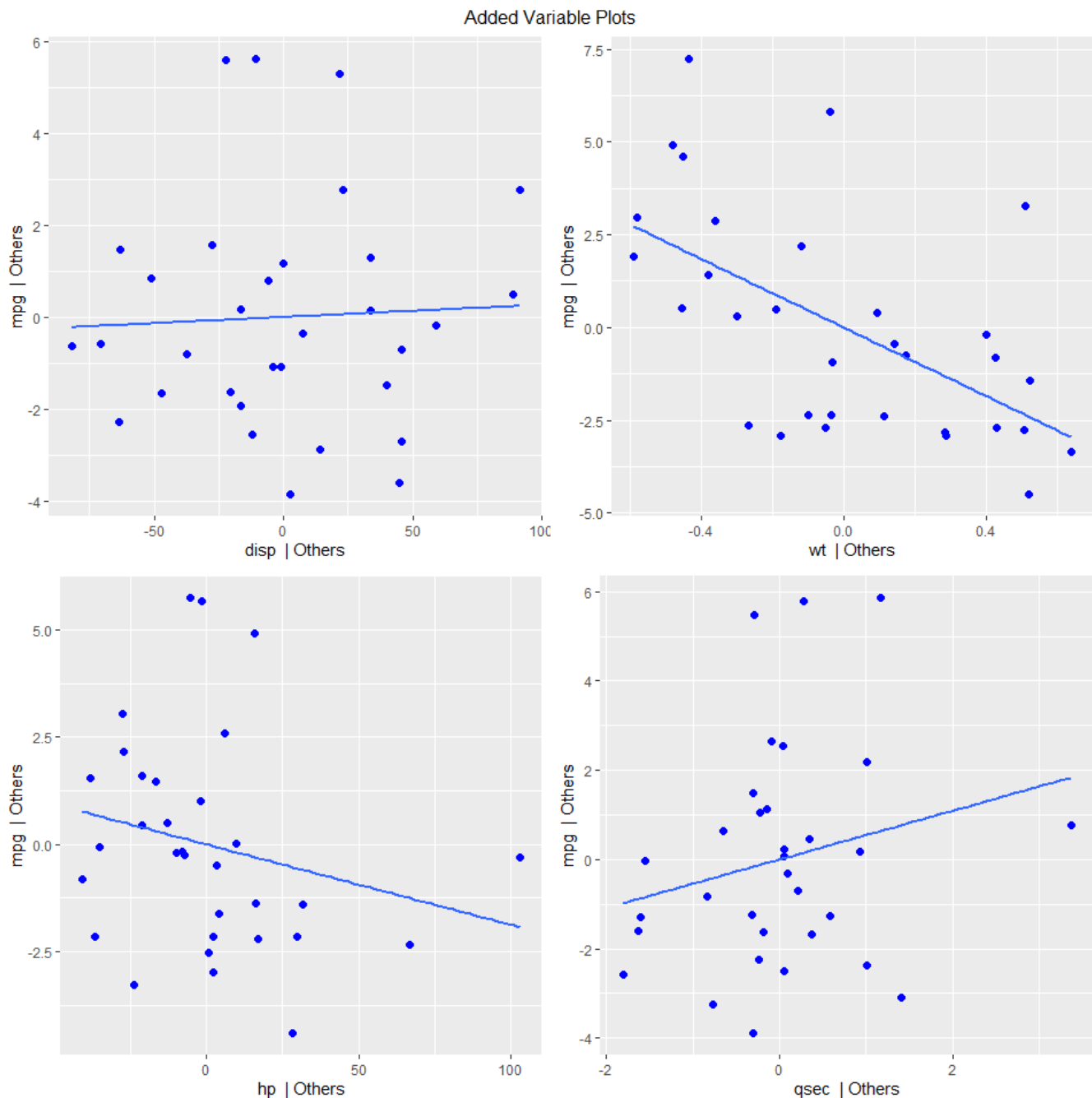
What do the Y and X residuals represent? The Y residuals represent the part of Y not explained by all the variables other than X . The X residuals represent the part of X not explained by other variables. The slope of the line fitted to the points in the added variable plot is equal to the regression coefficient when Y is regressed on all variables including X .

A strong linear relationship in the added variable plot indicates the increased importance of the contribution of X to the model already containing the other predictors.

Hide

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_added_variable(model)
```

```
`geom_smooth()` using formula 'y ~ x'
`geom_smooth()` using formula 'y ~ x'
`geom_smooth()` using formula 'y ~ x'
`geom_smooth()` using formula 'y ~ x'
```

Residual Plus Component Plot

The residual plus component plot was introduced by Ezekeil (1924). It was called as Partial Residual Plot by Larsen and McCleary (1972). Hadi and Chatterjee (2012) called it the residual plus component plot.

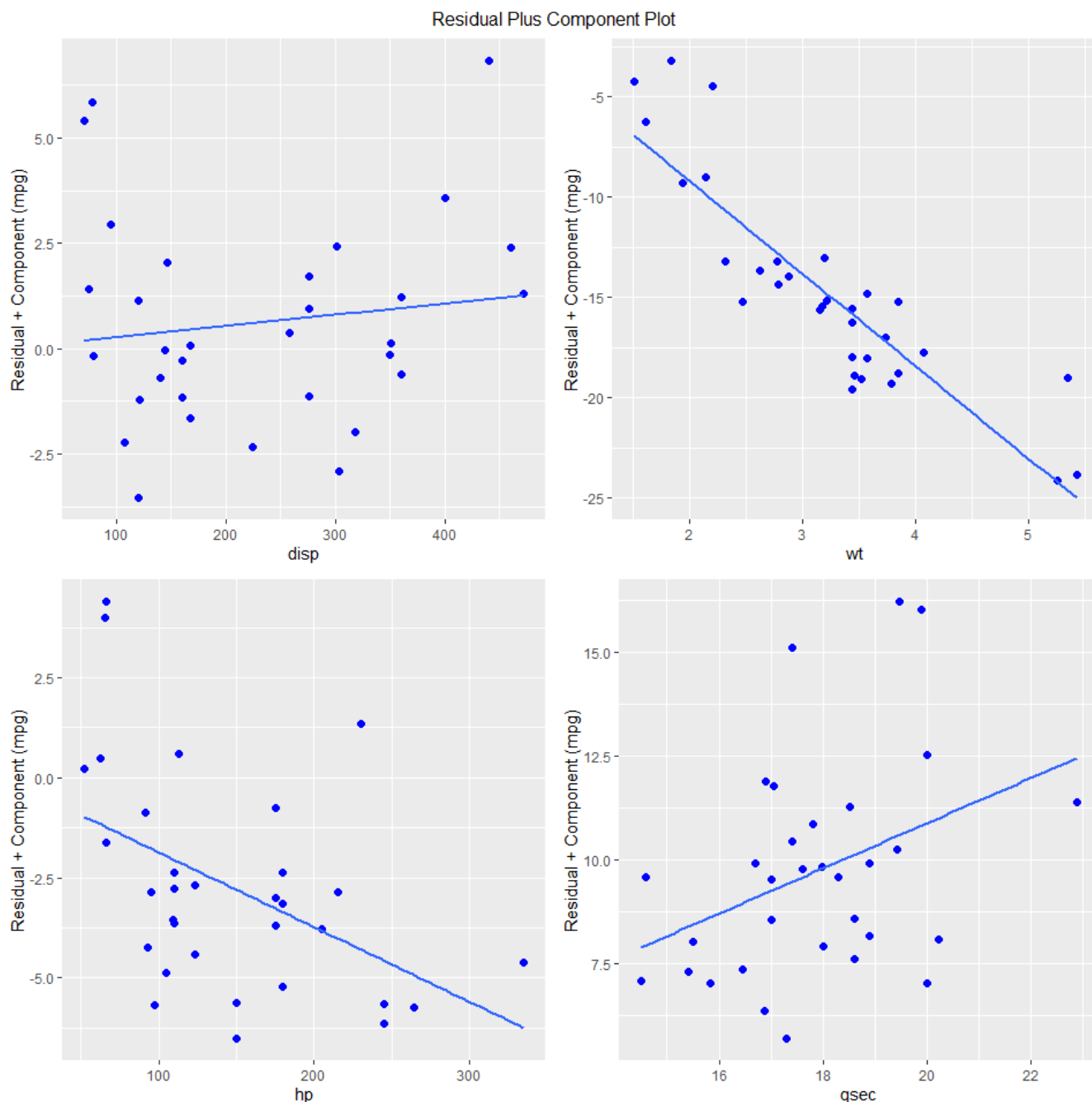
Steps to construct the plot:

- Regress **Y** on all variables including **X** and store the residuals (**e**).
- Multiply **e** with regression coefficient of **X** (**eX**).
- Construct scatter plot of **eX** and **X**

The residual plus component plot indicates whether any non-linearity is present in the relationship between **Y** and **X** and can suggest possible transformations for linearizing the data.

```
model <- lm(mpg ~ disp + hp + wt + qsec, data = mtcars)
ols_plot_comp_plus_resid(model)
```

```
`geom_smooth()` using formula 'y ~ x'
`geom_smooth()` using formula 'y ~ x'
`geom_smooth()` using formula 'y ~ x'
`geom_smooth()` using formula 'y ~ x'
```



A Short Introduction to the blorr Package

Introduction

The **blorr** package offers tools for building and validating binary logistic regression models. It is most suitable for beginner/intermediate R users and those who teach statistics using R. The API is very simple and most of the functions take either a `data.frame` / `tibble` or a `model` as input. **blorr** uses consistent prefix **blr_** for easy tab completion.

Installation

You can install **blorr** using:

Hide

```
install.packages("blorr")
```

The documentation of the package can be found at <https://blorr.rsquaredacademy.com> (<https://blorr.rsquaredacademy.com>). This vignette gives a quick tour of the package.

Libraries

The following libraries are used in the examples in the vignette:

Hide

```
library(blorr)
```

```
Warning: package 'blorr' was built under R version 4.1.3
Registered S3 method overwritten by 'data.table':
  method      from
print.data.table
```

Hide

```
library(magrittr)
```

Data

To demonstrate the features of blorr, we will use the bank marketing data set. The data is related with direct marketing campaigns of a Portuguese banking institution. The marketing campaigns were based on phone calls. Often, more than one contact to the same client was required, in order to access if the product (bank term deposit) would be ('yes') or not ('no') subscribed. It contains a random sample (~4k) of the original data set which can be found at <https://archive.ics.uci.edu/ml/datasets/bank+marketing> (<https://archive.ics.uci.edu/ml/datasets/bank+marketing>).

Bivariate Analysis

Let us begin with careful bivariate analysis of each possible variable and the outcome variable. We will use information value and likelihood ratio chi square test for selecting the initial set of predictors for our model. The bivariateanalysis is currently available for categorical predictors only.

Hide

```
blr_bivariate_analysis(bank_marketing, y, job, marital, education, default,
  housing, loan, contact, poutcome)
```


Bivariate Analysis				
Variable	Information Value	LR Chi Square	LR DF	LR p-value
job	0.16	75.2690	11	0.0000
marital	0.05	21.6821	2	0.0000
education	0.05	25.0466	3	0.0000
default	0.02	6.0405	1	0.0140
housing	0.16	72.2813	1	0.0000
loan	0.06	26.6615	1	0.0000
contact	0.31	124.3834	2	0.0000
poutcome	0.53	270.6450	3	0.0000

Weight of Evidence & Information Value

Weight of evidence (WoE) is used to assess the relative risk of different attributes for a characteristic and as a means to transform characteristics into variables. It is also a very useful tool for binning. The WoE for any group with average odds is zero. A negative WoE indicates that the proportion of defaults is higher for that attribute than the overall proportion and indicates higher risk.

The information value is used to rank order variables in terms of their predictive power. A high information value indicates a high ability to discriminate. Values for the information value will always be positive and may be above 3 when assessing highly predictive characteristics. Characteristics with information values less than 0.10 are typically viewed as weak, while values over 0.30 are sought after.

Hide

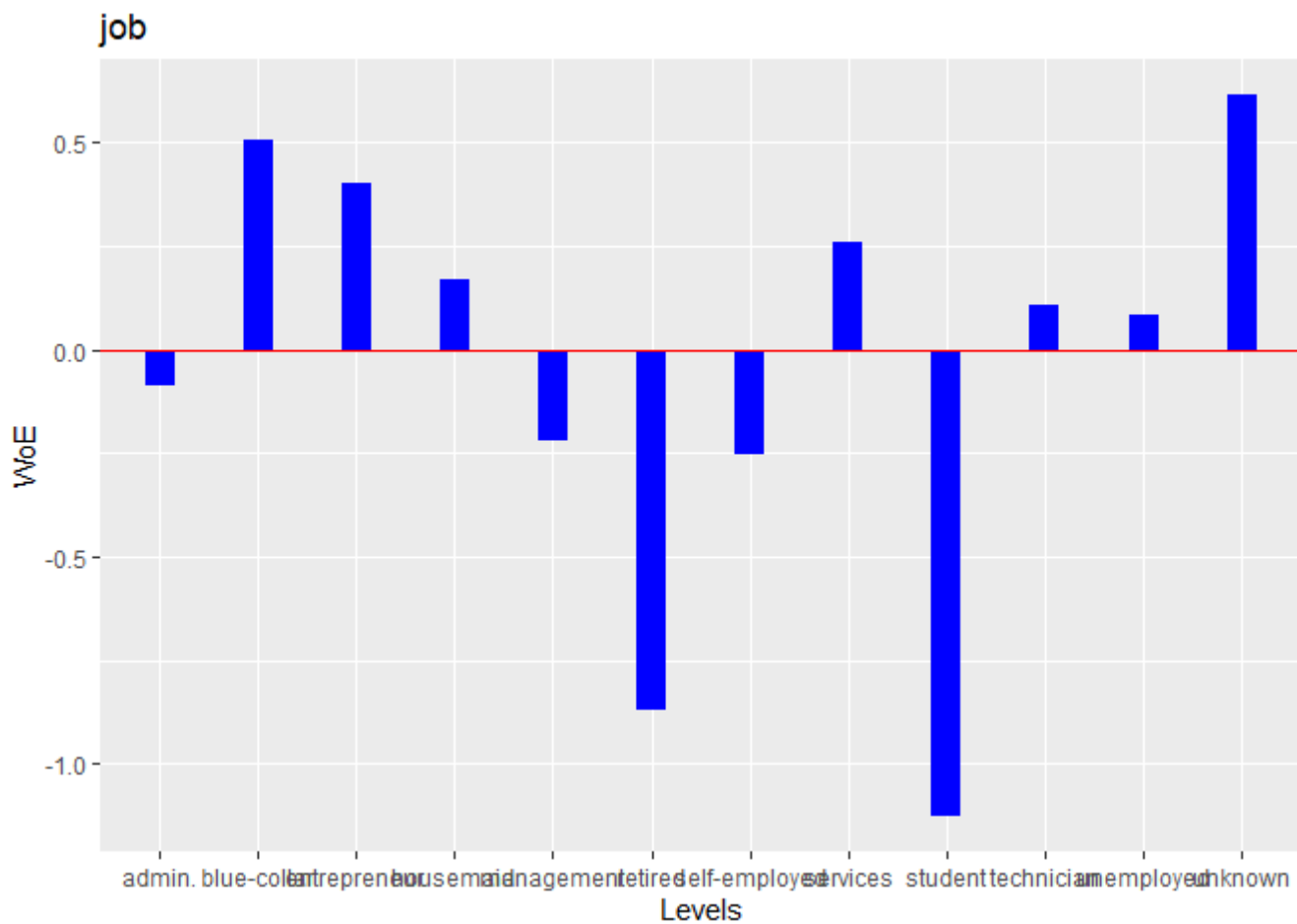
```
blr_woe_iv(bank_marketing, job, y)
```

Weight of Evidence						
levels	count_0s	count_1s	dist_0s	dist_1s	woe	iv
management	809	130	0.20	0.25	-0.22	0.01
technician	682	79	0.17	0.15	0.11	0.00
entrepreneur	139	12	0.03	0.02	0.40	0.00
blue-collar	937	73	0.23	0.14	0.51	0.05
unknown	29	2	0.01	0.00	0.61	0.00
retired	152	47	0.04	0.09	-0.87	0.05
admin.	433	61	0.11	0.12	-0.09	0.00
services	392	39	0.10	0.08	0.26	0.01
self-employed	132	22	0.03	0.04	-0.26	0.00
unemployed	126	15	0.03	0.03	0.08	0.00
housemaid	110	12	0.03	0.02	0.17	0.00
student	63	25	0.02	0.05	-1.13	0.04
Information Value						
Variable	Information Value					
job	0.1594					

Plot

Hide

```
k <- blr_woe_iv(bank_marketing, job, y)
plot(k)
```



Multiple Variables

We can generate the weight of evidence and information value for multiple variables using `blr_woe_iv_stats()` .

Hide

```
blr_woe_iv_stats(bank_marketing, y, job, marital, education)
```

Variable: job

Weight of Evidence

levels	count_0s	count_1s	dist_0s	dist_1s	woe	iv
management	809	130	0.20	0.25	-0.22	0.01
technician	682	79	0.17	0.15	0.11	0.00
entrepreneur	139	12	0.03	0.02	0.40	0.00
blue-collar	937	73	0.23	0.14	0.51	0.05
unknown	29	2	0.01	0.00	0.61	0.00
retired	152	47	0.04	0.09	-0.87	0.05
admin.	433	61	0.11	0.12	-0.09	0.00
services	392	39	0.10	0.08	0.26	0.01
self-employed	132	22	0.03	0.04	-0.26	0.00
unemployed	126	15	0.03	0.03	0.08	0.00
housemaid	110	12	0.03	0.02	0.17	0.00
student	63	25	0.02	0.05	-1.13	0.04

Information Value

Variable	Information Value
job	0.1594

Variable: marital

Weight of Evidence

levels	count_0s	count_1s	dist_0s	dist_1s	woe	iv
married	2467	273	0.62	0.53	0.15	0.01
single	1079	191	0.27	0.37	-0.32	0.03
divorced	458	53	0.11	0.10	0.11	0.00

Information Value

Variable	Information Value
marital	0.0464

Variable: education

Weight of Evidence

levels	count_0s	count_1s	dist_0s	dist_1s	woe	iv
tertiary	1104	195	0.28	0.38	-0.31	0.03
secondary	2121	231	0.53	0.45	0.17	0.01
unknown	154	25	0.04	0.05	-0.23	0.00
primary	625	66	0.16	0.13	0.20	0.01

Information Value

Variable	Information Value
education	0.0539

`blr_woe_iv()` and `blr_woe_iv_stats()` are currently available for categorical predictors only.

Stepwise Selection

For the initial/ first cut model, all the independent variables are put into the model. Our goal is to include a limited number of independent variables (5-15) which are all significant, without sacrificing too much on the model performance. The rationale behind not-including too many variables is that the model would be over fitted and would become unstable when tested on the validation sample. The variable reduction is done using forward or backward or stepwise variable selection procedures. We will use `blr_step_aic_both()` to shortlist predictors for our model.

Model

Hide

```
model <- glm(y ~ ., data = bank_marketing, family = binomial(link = 'logit'))
```

Selection Summary

Hide

```
blr_step_aic_both(model)
```

Stepwise Selection Method

Candidate Terms:

1 . age
2 . job
3 . marital
4 . education
5 . default
6 . balance
7 . housing
8 . loan
9 . contact
10 . day
11 . month
12 . duration
13 . campaign
14 . pdays
15 . previous
16 . poutcome

Variables Entered/Removed:

- duration added
- poutcome added
- month added
- contact added
- housing added
- loan added
- campaign added
- marital added
- education added
- age added

No more variables to be added or removed.

Stepwise Summary

Variable	Method	AIC	BIC	Deviance

duration	addition	2674.384	2687.217	2670.384
poutcome	addition	2396.014	2428.097	2386.014
month	addition	2274.109	2376.773	2242.109
contact	addition	2207.884	2323.381	2171.884
housing	addition	2184.550	2306.463	2146.550
loan	addition	2171.972	2300.302	2131.972

campaign	addition	2164.164	2298.910	2122.164
marital	addition	2158.524	2306.103	2112.524
education	addition	2155.837	2322.666	2103.837
age	addition	2154.272	2327.517	2100.272

Plot

Hide

```
model %>%  
  blr_step_aic_both() %>%  
  plot()
```

Stepwise Selection Method

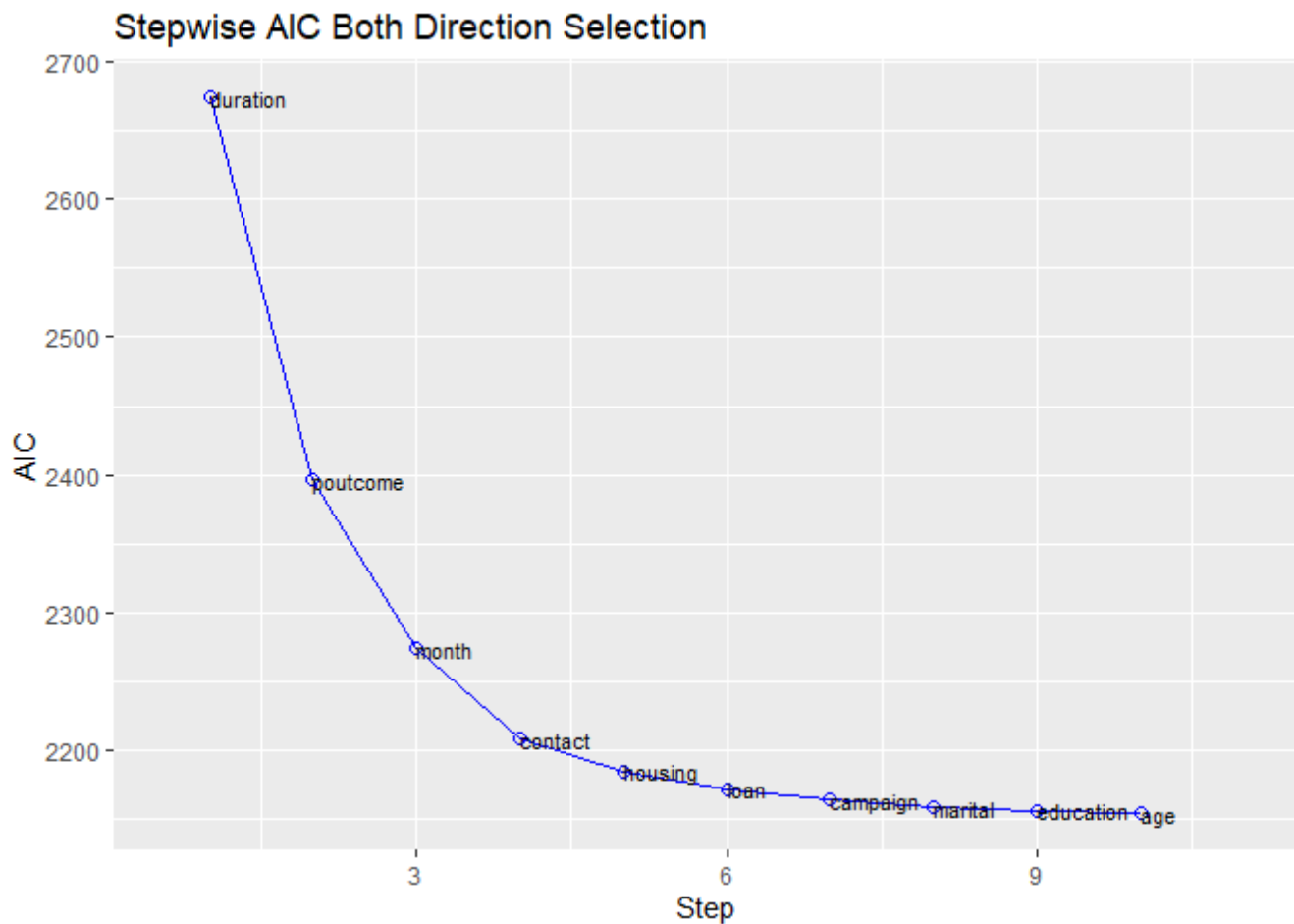
Candidate Terms:

- 1 . age
- 2 . job
- 3 . marital
- 4 . education
- 5 . default
- 6 . balance
- 7 . housing
- 8 . loan
- 9 . contact
- 10 . day
- 11 . month
- 12 . duration
- 13 . campaign
- 14 . pdays
- 15 . previous
- 16 . poutcome

Variables Entered/Removed:

- duration added
- poutcome added
- month added
- contact added
- housing added
- loan added
- campaign added
- marital added
- education added
- age added

No more variables to be added or removed.



Regression Output

Model

We can use bivariate analysis and stepwise selection procedure to shortlist predictors and build the model using the `glm()`. The predictors used in the below model are for illustration purposes and not necessarily shortlisted from the bivariate analysis and variable selection procedures.

Hide

```
model <- glm(y ~ age + duration + previous + housing + default +  
            loan + poutcome + job + marital, data = bank_marketing,  
            family = binomial(link = 'logit'))
```

Use `blr_regress()` to generate comprehensive regression output. It accepts either of the following

- model built using `glm()`
- model formula and data

Using Model

Let us look at the output generated from `blr_regress()` :

Hide

```
blr_regress(model)
```

- Creating model overview.
- Creating response profile.
- Extracting maximum likelihood estimates.
- Estimating concordant and discordant pairs.

Model Overview

Data Set	Resp Var	Obs.	Df. Model	Df. Residual	Convergence
data	y	4521	4520	4498	TRUE

Response Summary

Outcome	Frequency	Outcome	Frequency
0	4004	1	517

Maximum Likelihood Estimates

Parameter	DF	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1	-5.1347	0.3728	-13.7729	0.0000
age	1	0.0096	0.0067	1.4299	0.1528
duration	1	0.0042	2e-04	20.7853	0.0000
previous	1	-0.0357	0.0392	-0.9089	0.3634
housingno	1	0.7894	0.1232	6.4098	0.0000
defaultyes	1	-0.8691	0.6919	-1.2562	0.2091
loanno	1	0.6598	0.1945	3.3925	7e-04
poutcomefailure	1	0.6085	0.2012	3.0248	0.0025
poutcomeother	1	1.1354	0.2700	4.2057	0.0000
poutcomesuccess	1	3.2481	0.2462	13.1913	0.0000
jobtechnician	1	-0.2713	0.1806	-1.5019	0.1331
jobentrepreneur	1	-0.7041	0.3809	-1.8486	0.0645
jobblue-collar	1	-0.6132	0.1867	-3.2851	0.0010
jobunknown	1	-0.9932	0.8226	-1.2073	0.2273
jobretired	1	0.3197	0.2729	1.1713	0.2415
jobadmin.	1	0.1120	0.2001	0.5599	0.5755
jobservices	1	-0.1750	0.2265	-0.7728	0.4397
jobself-employed	1	-0.1408	0.3009	-0.4680	0.6398
jobunemployed	1	-0.6581	0.3432	-1.9174	0.0552
jobhousemaid	1	-0.7456	0.3932	-1.8963	0.0579
jobstudent	1	0.1927	0.3433	0.5613	0.5746
maritalsingle	1	0.5451	0.1387	3.9299	1e-04
maritaldivorced	1	-0.1989	0.1986	-1.0012	0.3167

Association of Predicted Probabilities and Observed Responses

% Concordant	0.8886	Somers' D	0.7773
% Discordant	0.1114	Gamma	0.7773
% Tied	0.0000	Tau-a	0.1575
Pairs	2070068	c	0.8886

If you want to examine the odds ratio estimates, set `odd_conf_limit` to `TRUE`. The odds ratio estimates are not explicitly computed as we observed considerable increase in computation time when dealing with large data sets.

Using Formula

Let us use the model formula and the data set to generate the above results.

Hide

```
blr_regress(y ~ age + duration + previous + housing + default +
            loan + poutcome + job + marital, data = bank_marketing)
```

- Creating model overview.
- Creating response profile.
- Extracting maximum likelihood estimates.
- Estimating concordant and discordant pairs.

Model Overview

Data Set	Resp Var	Obs.	Df. Model	Df. Residual	Convergence
data	y	4521	4520	4498	TRUE

Response Summary

Outcome	Frequency	Outcome	Frequency
0	4004	1	517

Maximum Likelihood Estimates

Parameter	DF	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1	-5.1347	0.3728	-13.7729	0.0000
age	1	0.0096	0.0067	1.4299	0.1528
duration	1	0.0042	2e-04	20.7853	0.0000
previous	1	-0.0357	0.0392	-0.9089	0.3634
housingno	1	0.7894	0.1232	6.4098	0.0000
defaultyes	1	-0.8691	0.6919	-1.2562	0.2091
loanno	1	0.6598	0.1945	3.3925	7e-04
poutcomefailure	1	0.6085	0.2012	3.0248	0.0025
poutcomeother	1	1.1354	0.2700	4.2057	0.0000
poutcomesuccess	1	3.2481	0.2462	13.1913	0.0000
jobtechnician	1	-0.2713	0.1806	-1.5019	0.1331
jobentrepreneur	1	-0.7041	0.3809	-1.8486	0.0645
jobblue-collar	1	-0.6132	0.1867	-3.2851	0.0010
jobunknown	1	-0.9932	0.8226	-1.2073	0.2273
jobretired	1	0.3197	0.2729	1.1713	0.2415
jobadmin.	1	0.1120	0.2001	0.5599	0.5755
jobservices	1	-0.1750	0.2265	-0.7728	0.4397
jobself-employed	1	-0.1408	0.3009	-0.4680	0.6398
jobunemployed	1	-0.6581	0.3432	-1.9174	0.0552
jobhousemaid	1	-0.7456	0.3932	-1.8963	0.0579
jobstudent	1	0.1927	0.3433	0.5613	0.5746
maritalsingle	1	0.5451	0.1387	3.9299	1e-04
maritaldivorced	1	-0.1989	0.1986	-1.0012	0.3167

Association of Predicted Probabilities and Observed Responses

```

-----
% Concordant      0.8886      Somers' D      0.7773
% Discordant      0.1114      Gamma         0.7773
% Tied            0.0000      Tau-a         0.1575
Pairs            2070068      c             0.8886
-----

```

Model Fit Statistics

Model fit statistics are available to assess how well the model fits the data and to compare two different models. The output includes likelihood ratio test, AIC, BIC and a host of pseudo r-squared measures. You can read more about pseudo r-squared at <https://stats.idre.ucla.edu/other/mult-pkg/faq/general/faq-what-are-pseudo-r-squareds/> (<https://stats.idre.ucla.edu/other/mult-pkg/faq/general/faq-what-are-pseudo-r-squareds/>).

Single Model

Hide

```
blr_model_fit_stats(model)
```

Model Fit Statistics

```

-----
Log-Lik Intercept Only:    -1607.330    Log-Lik Full Model:    -1123.340
Deviance(4498):           2246.679    LR(22):                967.980
                               Prob > LR:                0.000
MCFadden's R2             0.301    McFadden's Adj R2:     0.287
ML (Cox-Snell) R2:        0.193    Cragg-Uhler(Nagelkerke) R2: 0.379
McKelvey & Zavoina's R2:  0.388    Efron's R2:            0.278
Count R2:                 0.904    Adj Count R2:          0.157
BIC:                      2440.259    AIC:                   2292.679
-----

```

Model Validation

Confusion Matrix

In the event of deciding a cut-off point on the probability scores of a logistic regression model, a confusion matrix is created corresponding to a particular cut-off. The observations with probability scores above the cut-off score are predicted to be events and those below the cut-off score, as non-events. The confusion matrix, a 2X2 table, then calculates the number of correctly classified and miss-classified observations.

Hide

```
blr_confusion_matrix(model, cutoff = 0.5)
```

Confusion Matrix and Statistics

Reference		
Prediction	0	1
0	3920	352
1	84	165

Accuracy : 0.9036

No Information Rate : 0.8856

Kappa : 0.3851

McNemars's Test P-Value : 0.0000

Sensitivity : 0.3191

Specificity : 0.9790

Pos Pred Value : 0.6627

Neg Pred Value : 0.9176

Prevalence : 0.1144

Detection Rate : 0.0365

Detection Prevalence : 0.0551

Balanced Accuracy : 0.6491

Precision : 0.6627

Recall : 0.3191

'Positive' Class : 1

The validity of a cut-off is measured using sensitivity, specificity and accuracy.

- **Sensitivity:** The % of correctly classified events out of all events = $TP / (TP + FN)$
- **Specificity:** The % of correctly classified non-events out of all non-events = $TN / (TN + FP)$
- **Accuracy:** The % of correctly classified observation over all observations = $(TP + TN) / (TP + FP + TN + FN)$
- *True Positive (TP):* Events correctly classified as events.
- *True Negative (TN):* Non-Events correctly classified as non-events.
- *False Positive (FP):* Non-events miss-classified as events.
- *False Negative (FN):* Events miss-classified as non-events.

For a standard logistic model, the higher is the cut-off, the lower will be the sensitivity and the higher would be the specificity. As the cut-off is decreased, sensitivity will go up, as then more events would be captured. Also, specificity will go down, as more non-events would miss-classified as events. Hence a trade-off is done based on the requirements. For example, if we are looking to capture as many events as possible, and we can afford to have miss-classified non-events, then a low cut-off is taken.

Hosmer Lemeshow Test

Hosmer and Lemeshow developed a goodness-of-fit test for logistic regression models with binary responses. The test involves dividing the data into approximately ten groups of roughly equal size based on the percentiles of the estimated probabilities. The observations are sorted in increasing order of their estimated probability of having an even outcome. The discrepancies between the observed and expected number of observations in these groups are summarized by the Pearson chi-square statistic, which is then compared to chi-square distribution with t degrees of freedom, where t is the number of groups minus 2. Lower values of Goodness-of-fit are preferred.

Hide

```
blr_test_hosmer_lemeshow(model)
```

Partition for the Hosmer & Lemeshow Test

Group	Total	def = 1		def = 0	
		Observed	Expected	Observed	Expected
1	453	2	5.14	451	447.86
2	452	3	8.63	449	443.37
3	452	4	11.88	448	440.12
4	452	7	15.29	445	436.71
5	452	14	19.39	438	432.61
6	452	10	24.97	442	427.03
7	452	31	33.65	421	418.35
8	452	62	49.74	390	402.26
9	452	128	88.10	324	363.90
10	452	256	260.21	196	191.79

Goodness of Fit Test

Chi-Square	DF	Pr > ChiSq
52.9942	8	0.0000

Gains Table & Lift Chart

A lift curve is a graphical representation of the % of cumulative events captured at a specific cut-off. The cut-off can be a particular decile or a percentile. Similar, to rank ordering procedure, the data is in descending order of the scores and is then grouped into deciles/percentiles. The cumulative number of observations and events are then computed for each decile/percentile. The lift curve is the created using the cumulative % population as the x-axis and the cumulative percentage of events as the y-axis.

Hide

```
blr_gains_table(model)
```

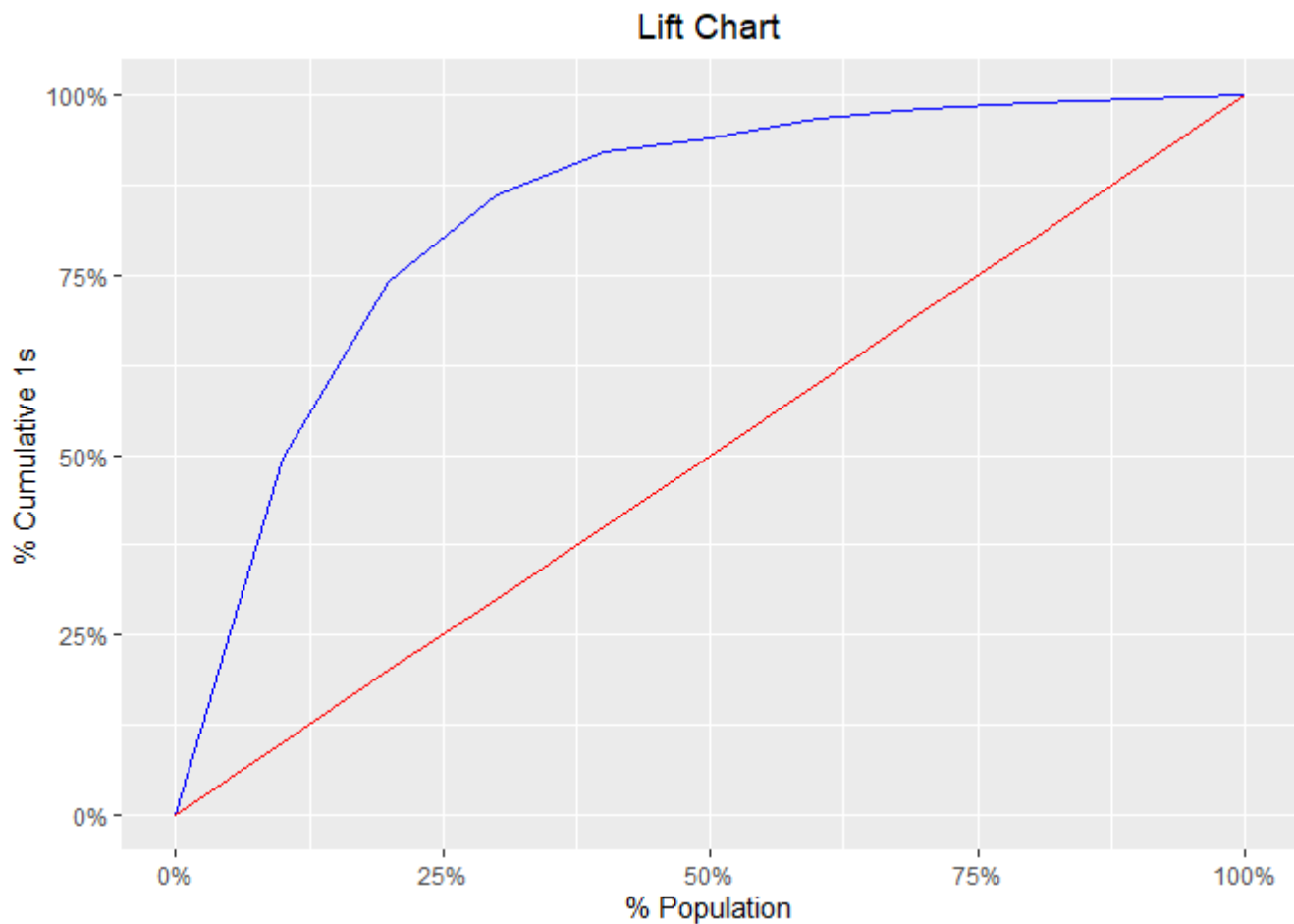

decile <dbl>	total <int>	1 <int>	0 <int>	ks <dbl>	tp <int>	tn <int>	fp <int>	fn <int>	sensitivity <dbl>	
1	452	256	196	44.62134	256	3808	196	261	49.51644	
2	452	128	324	61.28765	384	3484	520	133	74.27466	
3	452	62	390	63.53965	446	3094	910	71	86.26692	
4	452	31	421	59.02130	477	2673	1331	40	92.26306	
5	452	10	442	49.91657	487	2231	1773	30	94.19729	
6	452	14	438	41.68544	501	1793	2211	16	96.90522	
7	452	7	445	31.92552	508	1348	2656	9	98.25919	
8	452	4	448	21.51040	512	900	3104	5	99.03288	
9	452	3	449	10.87689	515	451	3553	2	99.61315	
10	453	2	451	0.00000	517	0	4004	0	100.00000	

1-10 of 10 rows | 1-10 of 12 columns

Lift Chart

Hide

```
model %>%
  blr_gains_table() %>%
  plot()
```

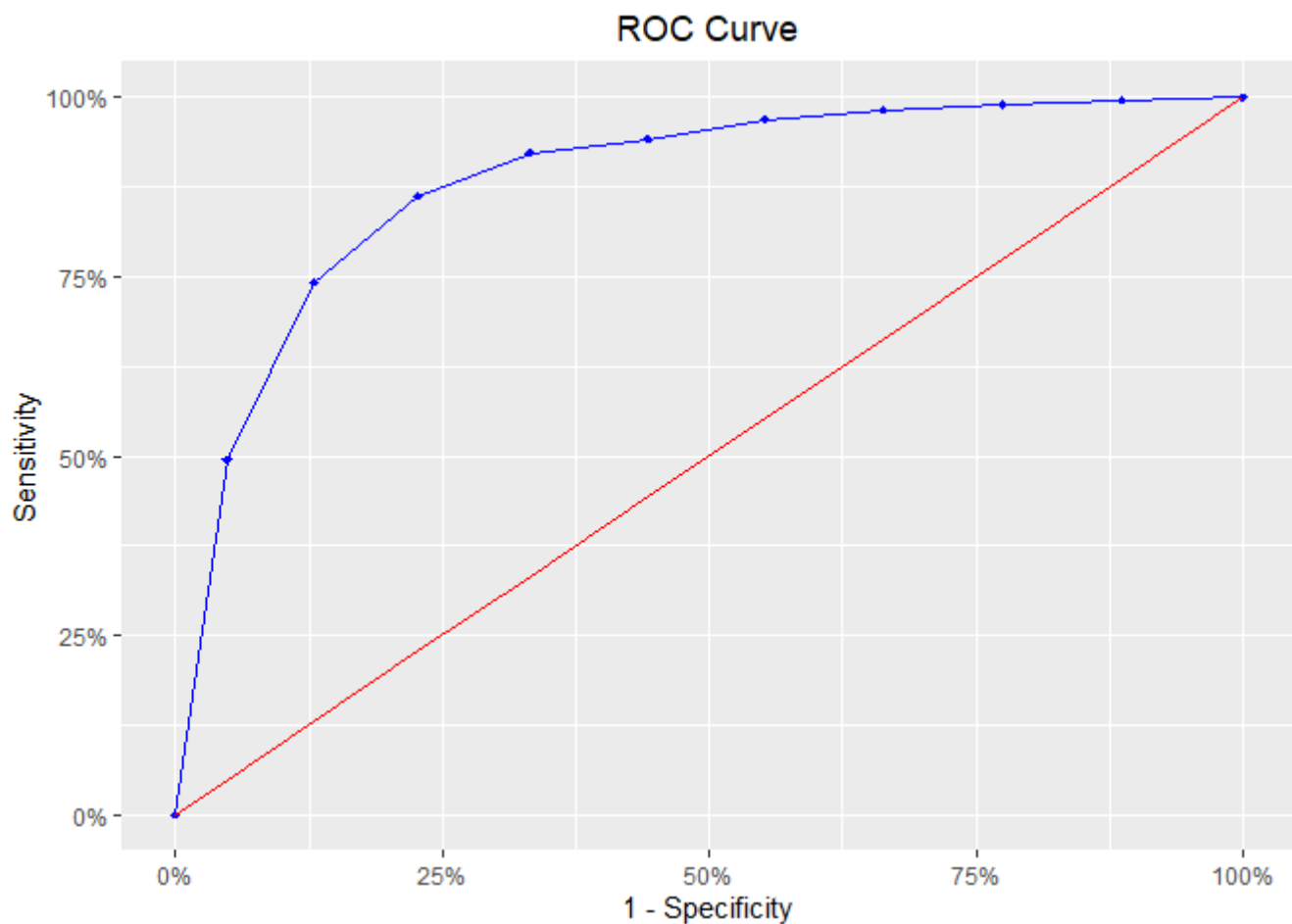


ROC Curve

ROC curve is a graphical representation of the validity of cut-offs for a logistic regression model. The ROC curve is plotted using the sensitivity and specificity for all possible cut-offs, i.e., all the probability scores. The graph is plotted using sensitivity on the y-axis and 1-specificity on the x-axis. Any point on the ROC curve represents a sensitivity X (1-specificity) measure corresponding to a cut-off. The area under the ROC curve is used as a validation measure for the model – the bigger the area the better is the model.

Hide

```
model %>%  
  blr_gains_table() %>%  
  blr_roc_curve()
```

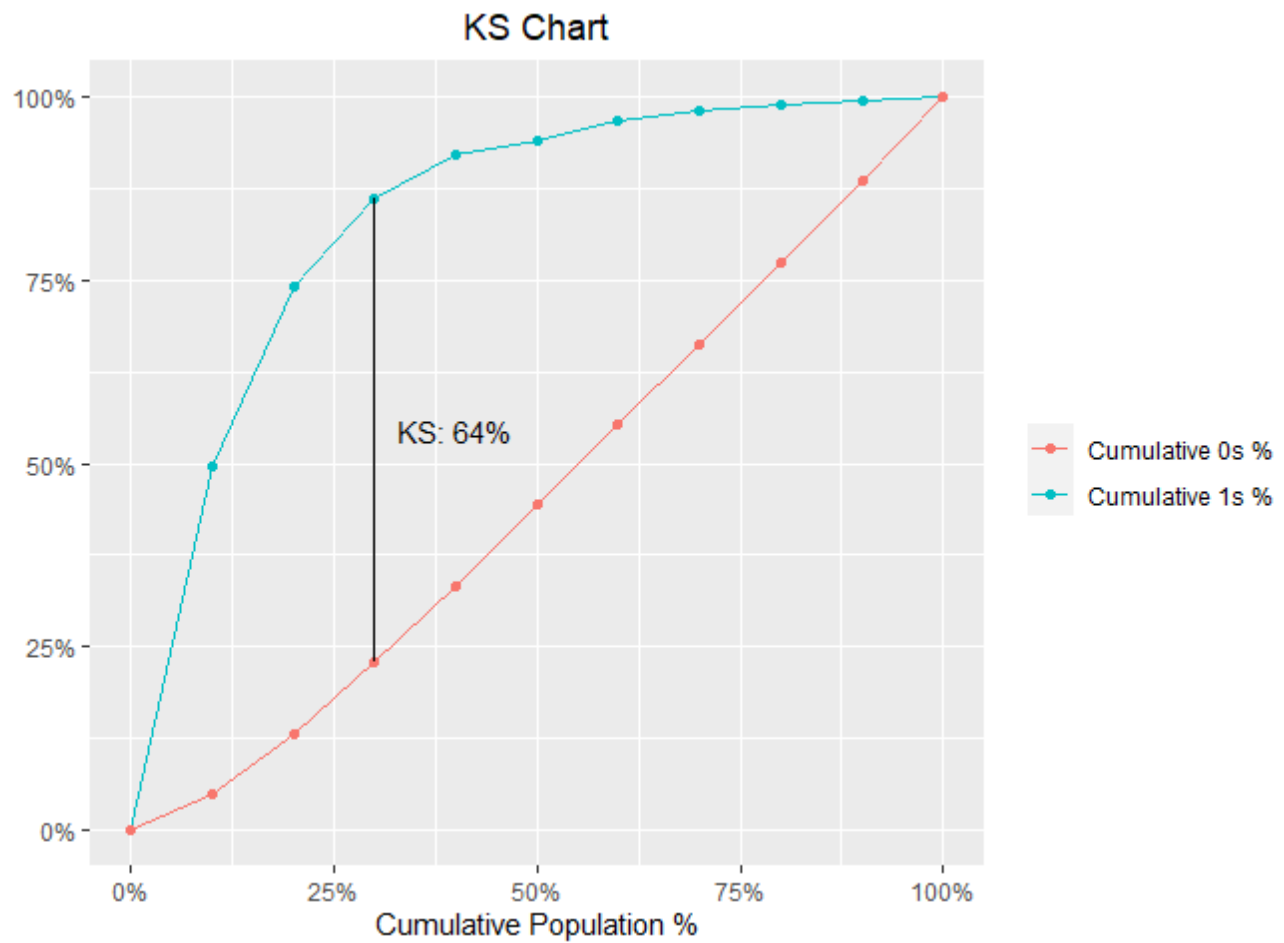


KS Chart

The KS Statistic is again a measure of model efficiency, and it is created using the lift curve. The lift curve is created to plot % events. If we also plot % non-events on the same scale, with % population at x-axis, we would get another curve. The maximum distance between the lift curve for events and that for non-events is termed as KS. For a good model, KS should be big (≥ 0.3) and should occur as close to the event rate as possible.

Hide

```
model %>%  
  blr_gains_table() %>%  
  blr_ks_chart()
```

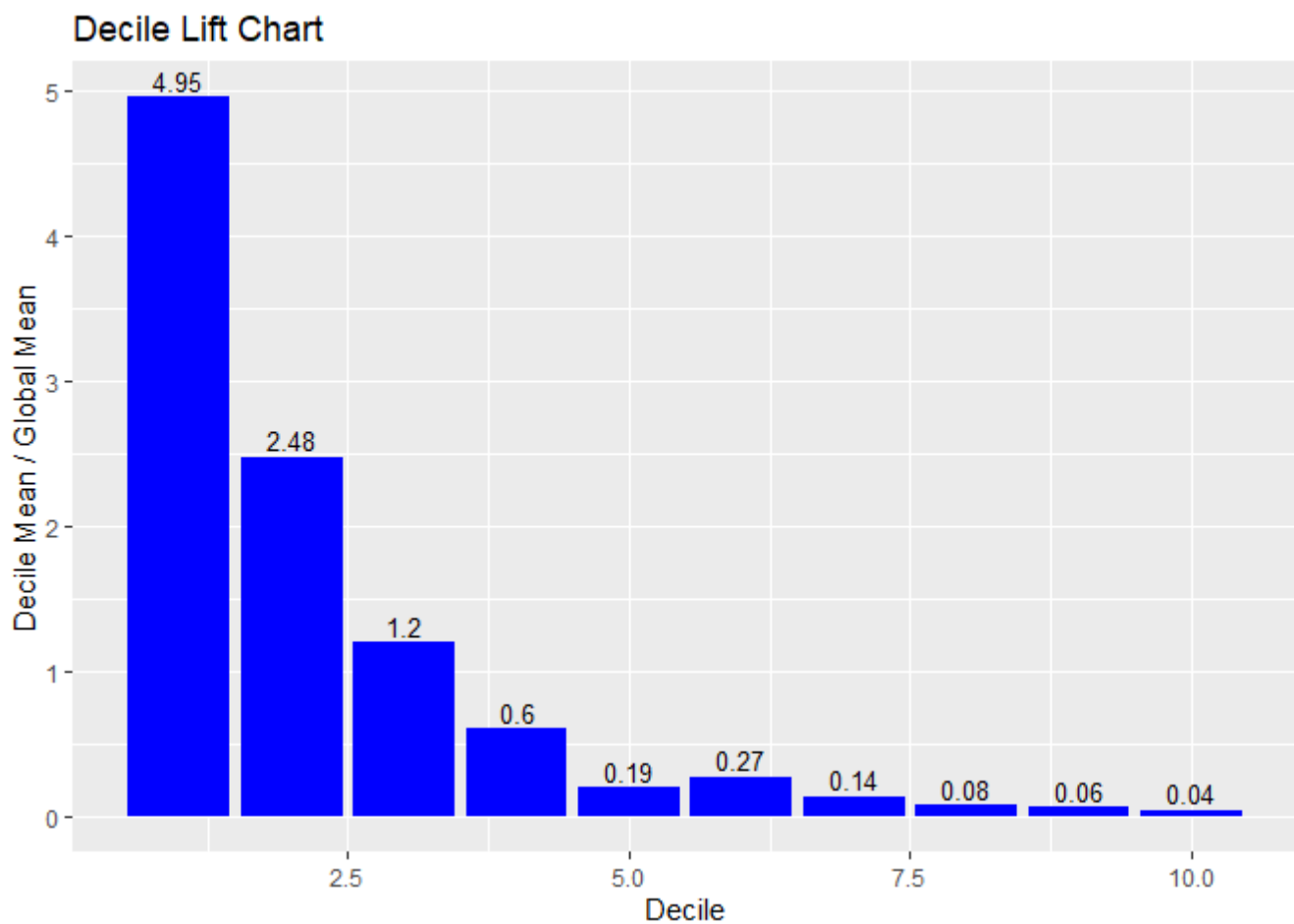


Decile Lift Chart

The decile lift chart displays the lift over the global mean event rate for each decile. For a model with good discriminatory power, the top deciles should have an event/conversion rate greater than the global mean.

[Hide](#)

```
model %>%  
  blr_gains_table() %>%  
  blr_decile_lift_chart()
```

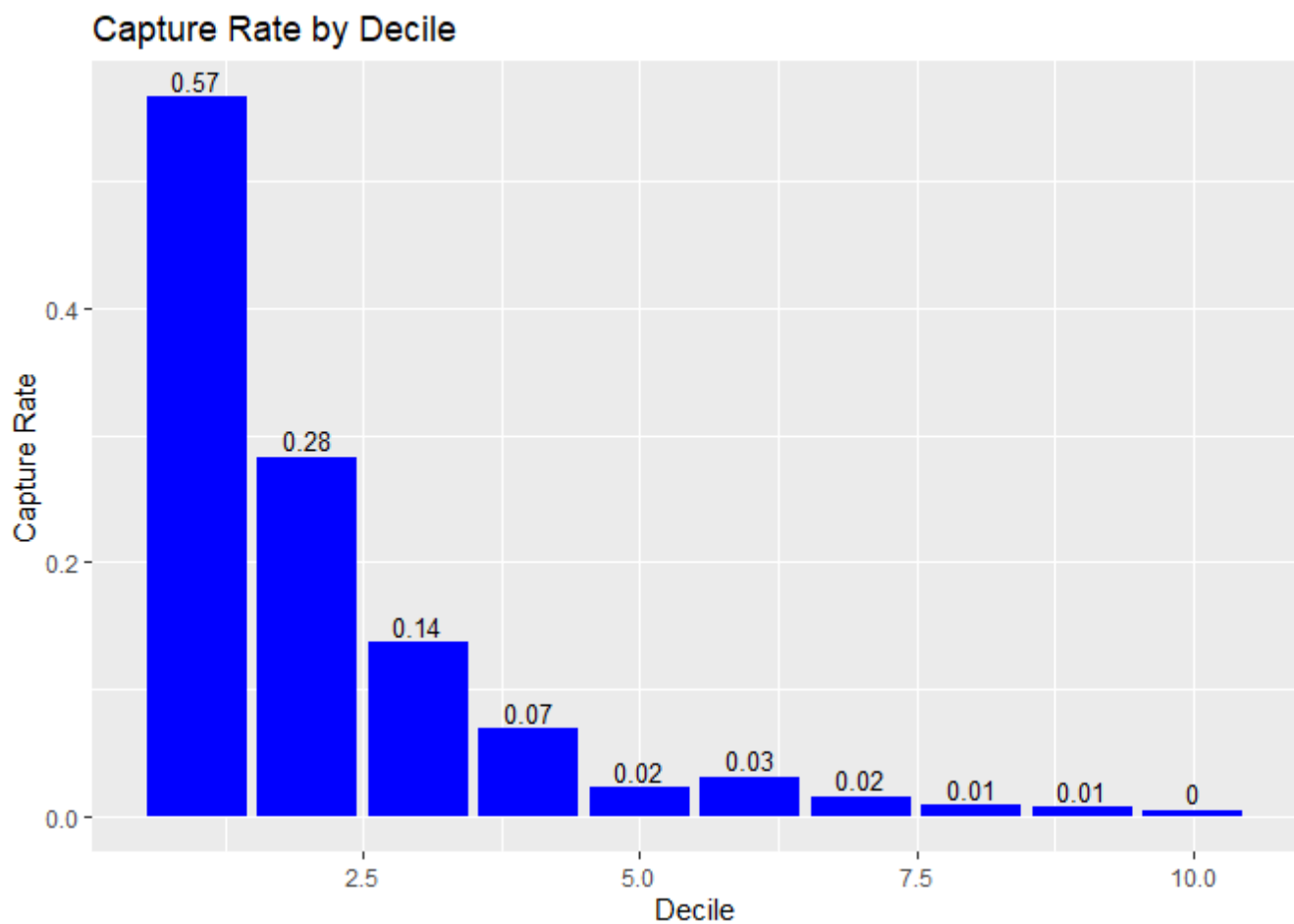


Capture Rate by Decile

If the model has good discriminatory power, the top deciles should have a higher event/conversion rate compared to the bottom deciles.

[Hide](#)

```
model %>%  
  blr_gains_table() %>%  
  blr_decile_capture_rate()
```

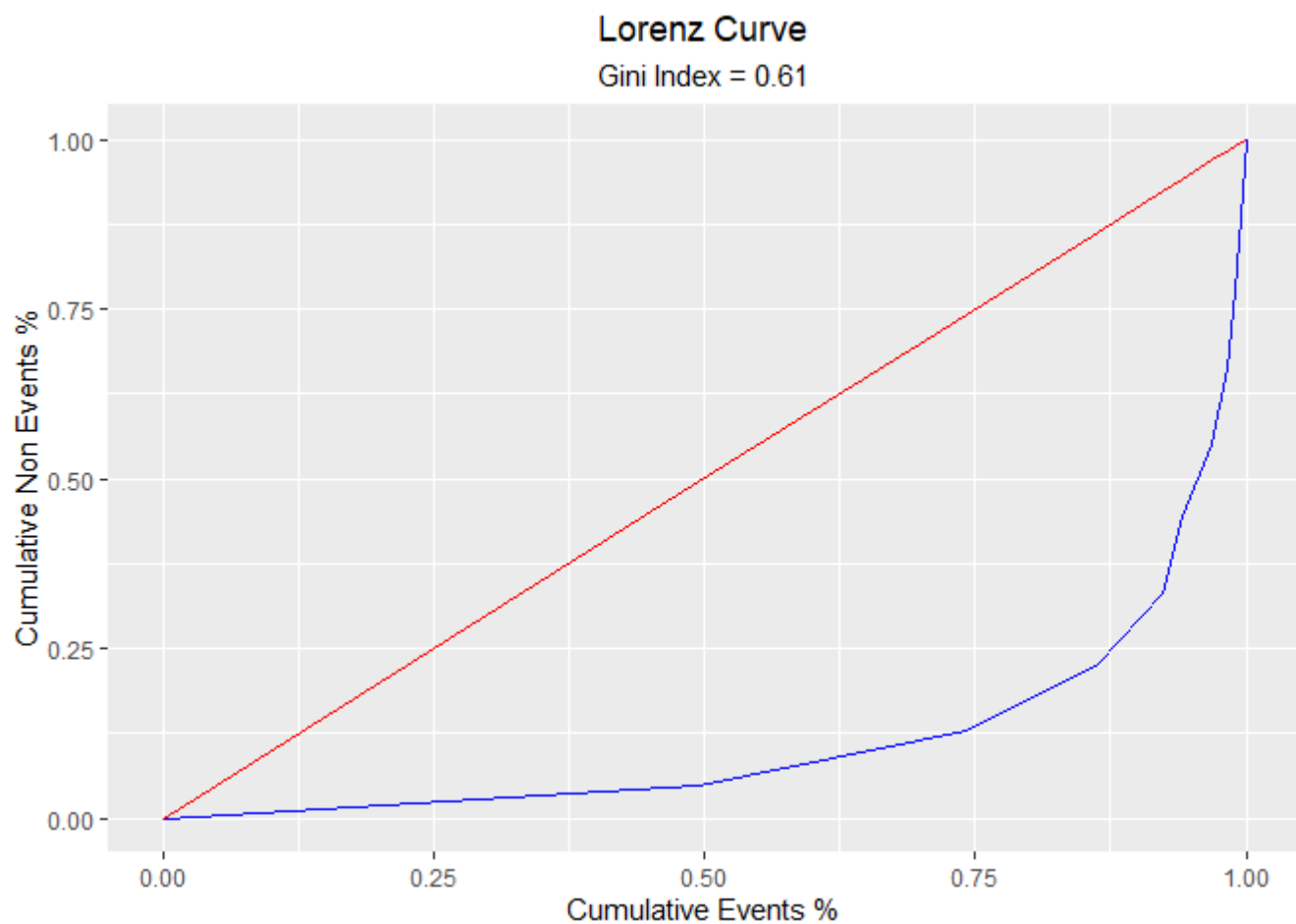


Lorenz Curve

The Lorenz curve is a simple graphic device which illustrates the degree of inequality in the distribution of the variable concerned. It is a visual representation of inequality used to measure the discriminatory power of the predictive model.

[Hide](#)

```
blr_lorenz_curve(model)
```



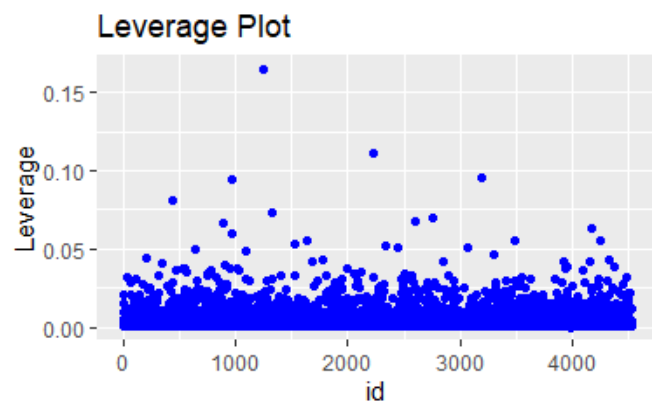
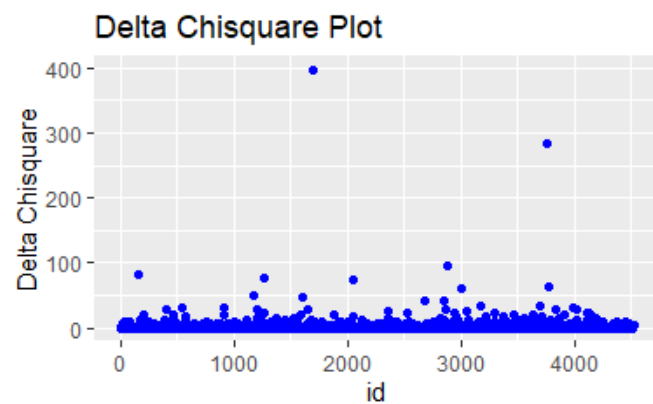
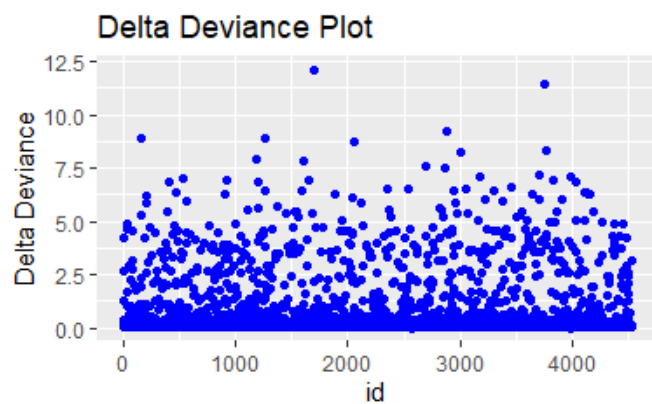
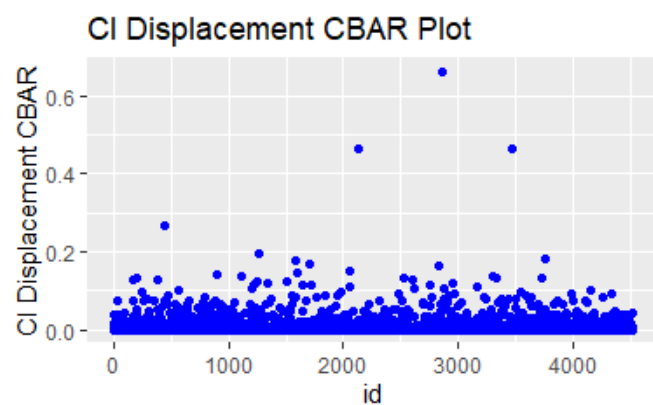
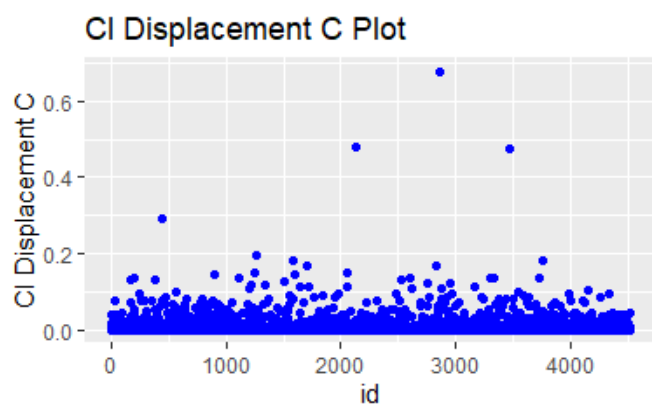
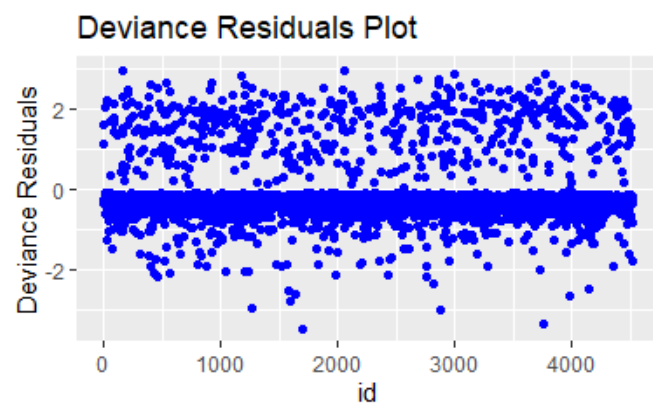
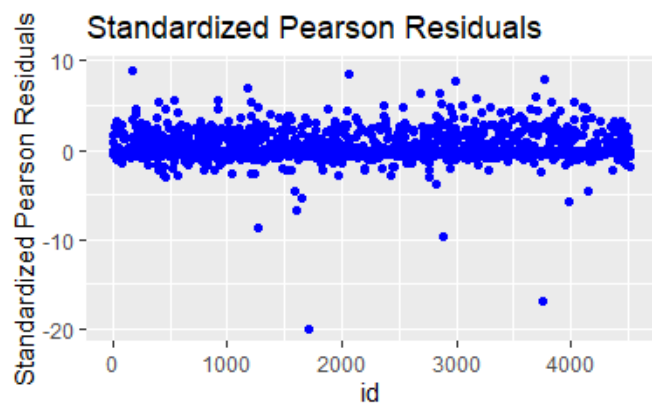
Residual & Influence Diagnostics

blorr can generate 22 plots for residual, influence and leverage diagnostics.

Influence Diagnostics

Hide

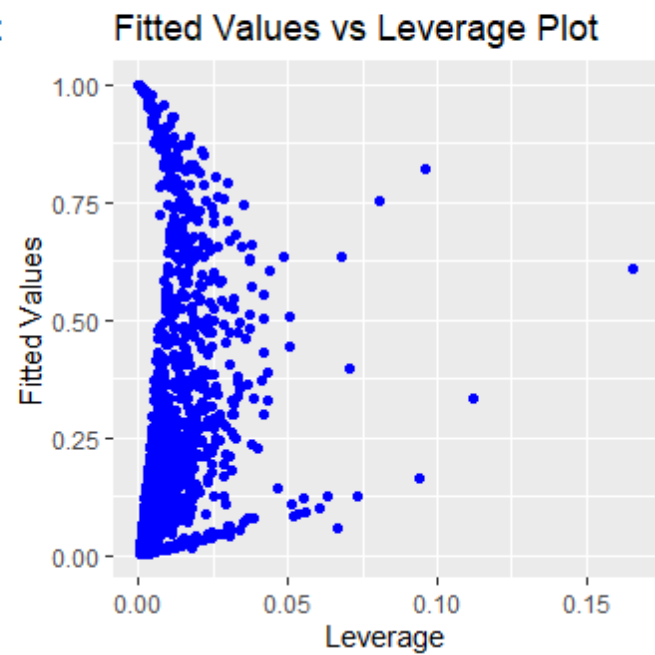
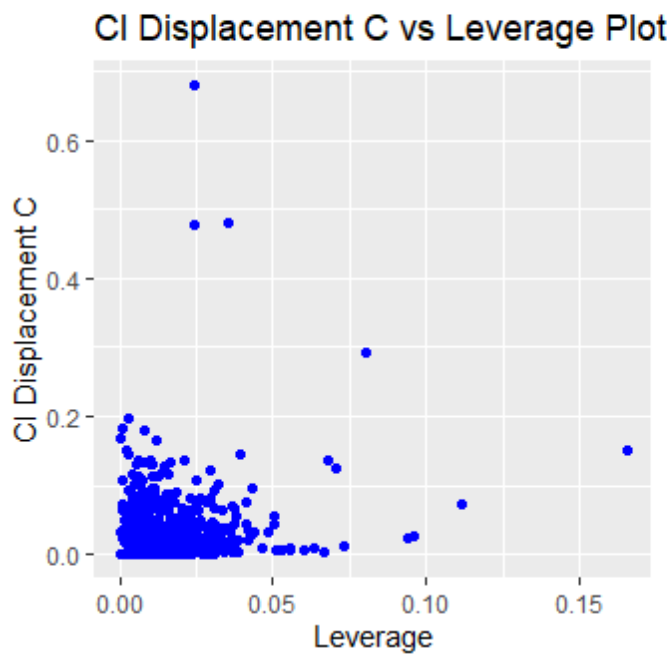
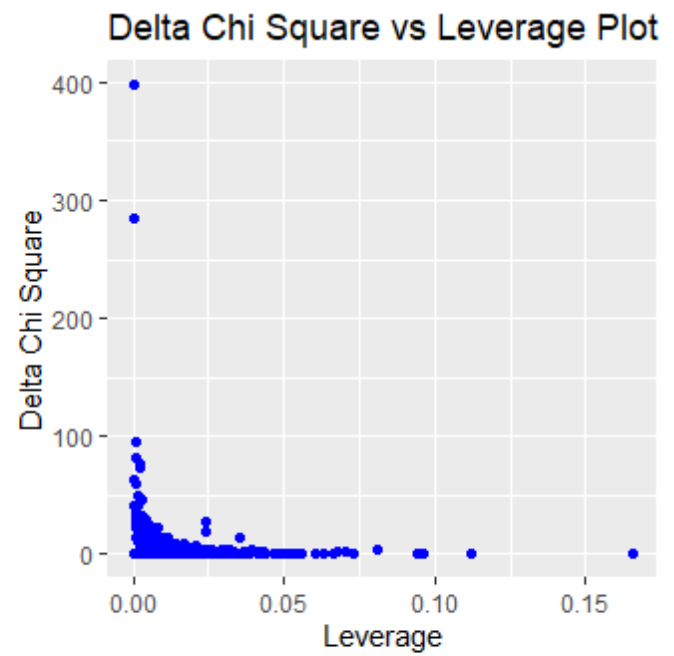
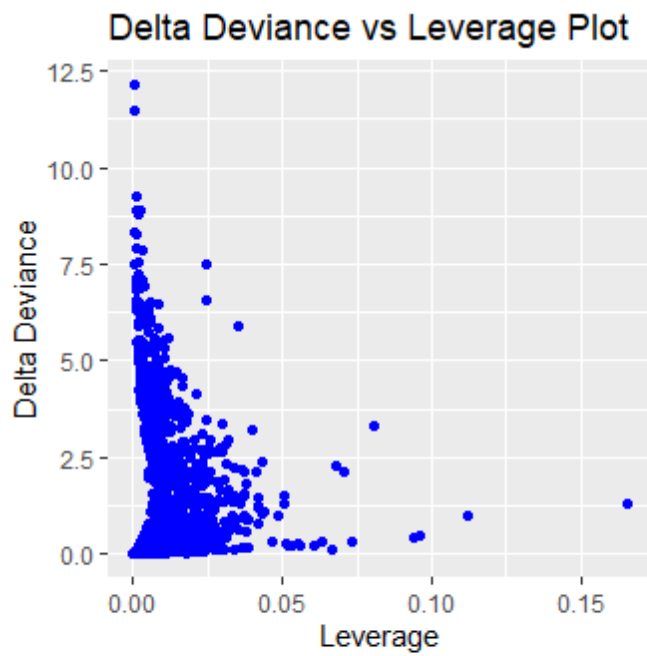
```
blr_plot_diag_influence(model)
```



Leverage Diagnostics

Hide

```
blr_plot_diag_leverage(model)
```

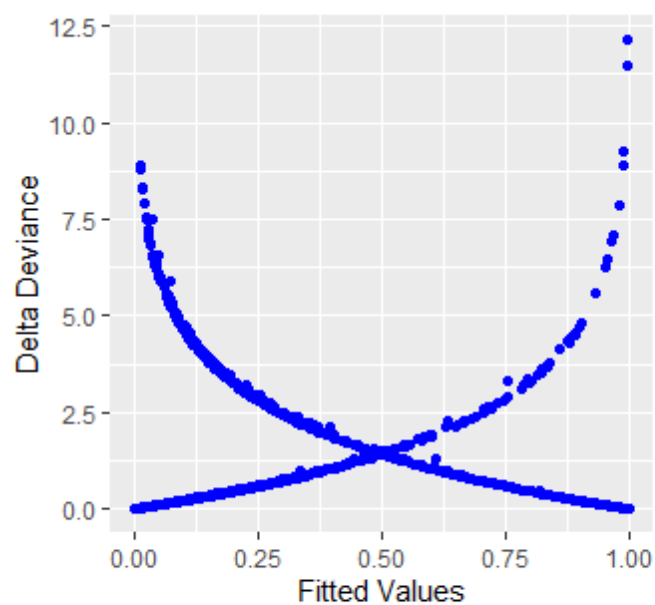



Fitted Values Diagnostics

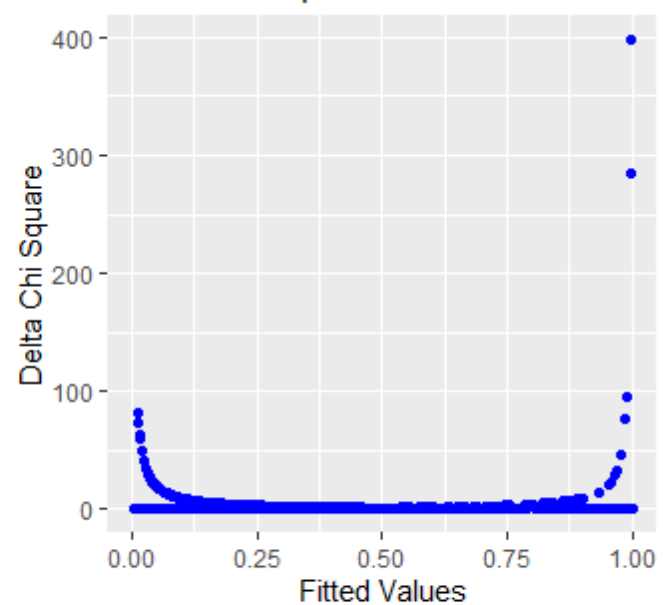
Hide

```
blr_plot_diag_fit(model)
```

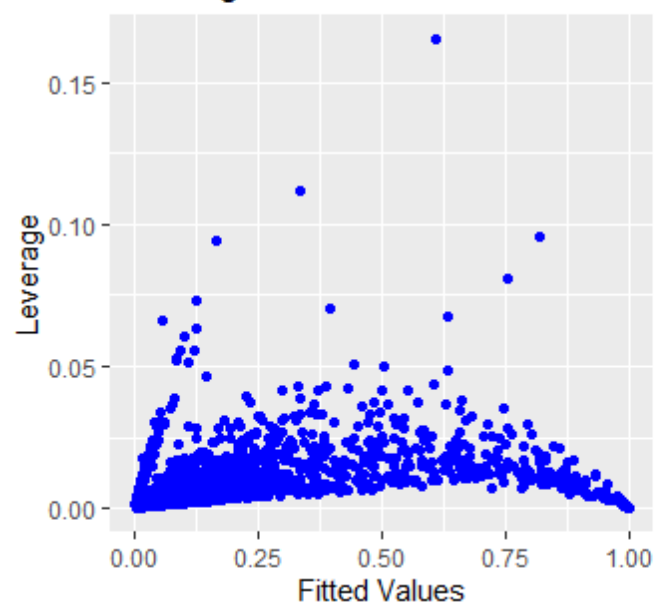
Delta Deviance vs Fitted Values Plc



Delta Chi Square vs Fitted Values F



Leverage vs Fitted Values



CI Displacement C vs Fitted Values I

