

A Regression Example using iNZightRegression

Simon Potter, David Banks, Tom Elliott
The University of Auckland

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The `iNZightRegression` package was created to provide additional functions which provide modified output, as well as some additional functionality. This document will demonstrate the use of `iNZightRegression` for modelling some regression data.

1 Linear Models

Here, we will be using the `course.df` dataset from the `s20x` library, which contains data collected from STATS 20x students. The first function is `iNZightSummary()`, which is shown below:

```
> library(iNZightRegression)
> library(s20x)
> data(course.df)
> model_1 <- lm(Exam ~ Test + Assign + Attend, data = course.df)
> iNZightSummary(model_1)
```

Model for: Exam

Coefficients:

	Estimate	Std. Error	t value	p-value	
(Intercept)	-0.4960	3.1331	-0.158	0.874	
Test	2.6014	0.2903	8.962	1.65e-15	***
Assign	1.4804	0.2647	5.592	1.11e-07	***
Attend				0.048	*
No	0	-	-	-	
Yes	4.1047	2.0576	1.995	0.048	*

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 10.48 on 142 degrees of freedom

Multiple R-squared: 0.6919, Adjusted R-squared: 0.6854

If compared to the basic `summary()` function provided by base R, there are several differences. The main difference is the way in which factors are printed.

The baseline is included with an estimate of 0, and Type III Anova p-values are given for each factor.

Several additional arguments are demonstrated below, which allow bootstrap simulation of estimates, reordering of factors (use the most common level as the baseline), and excluding confounding variables from the output. If, for example, we are *only* interested in the effect of not attending lectures on exam marks, we could use the following function call:

```
> iNZightSummary(model_1, method = 'bootstrap',
+                 reorder.factors = TRUE, exclude = c('Test', 'Assign'))
```

Model for: Exam

Coefficients:

	Estimate	Std. Error	t value	p-value
(Intercept)	3.609	3.884	0.929	0.3544
Attend				
Yes	0	-	-	-
No	-4.105	2.135	-1.923	0.0565 .

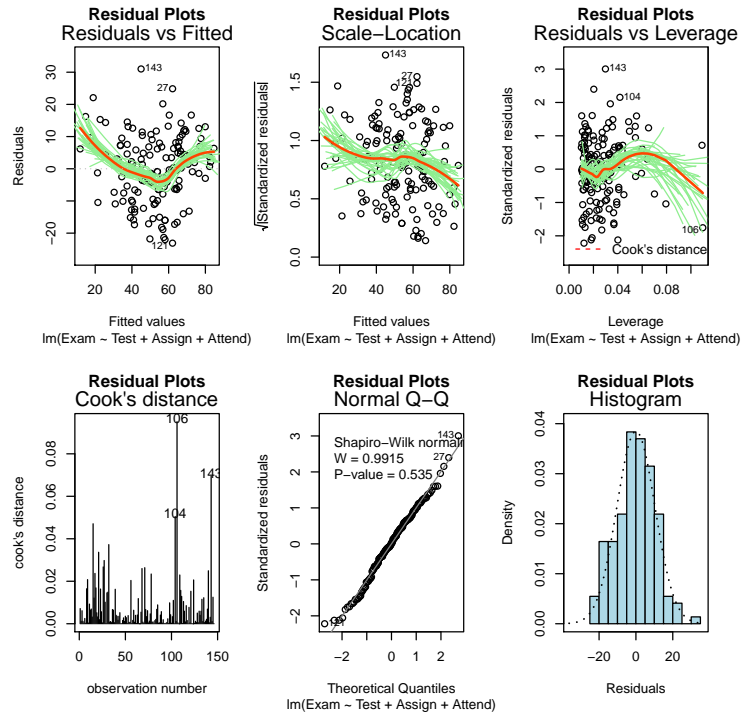
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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Summary and diagnostic plots can be produced simply by using the new `plotlm6` function, which takes several arguments. It provides 6 plots, which can be selected by the `which` argument (7 means all-in-one). Each residual plot shows a loess curve through the data, as well as a bootstrap sample of loess curves which are calculated from non-parametric bootstrap samples. The number of smoothers can be adjusted, or disabled completely as desired.

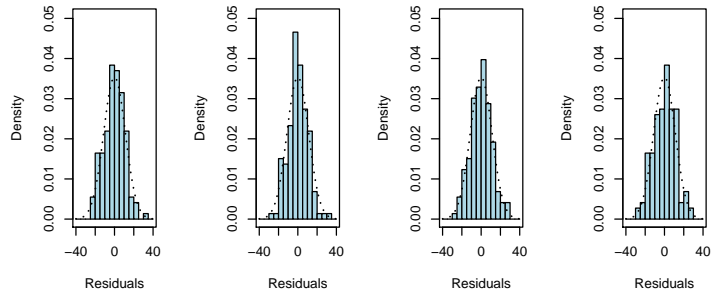
```
> plotlm6(model_1, which = 7, main = 'Residual Plots')
```



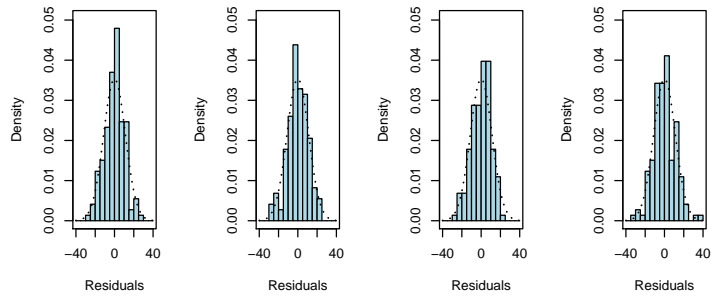
For normal data, there are also the `histogramArray` and `qqplotArray` functions, which display normally distributed (by simulation) datasets with the same mean and variance as those from the fitted model, which allow users to easily decide if the normality assumption is satisfied.

```
> histogramArray(model_1)
```

Original data Normal errors: sample 1 Normal errors: sample 2 Normal errors: sample 3

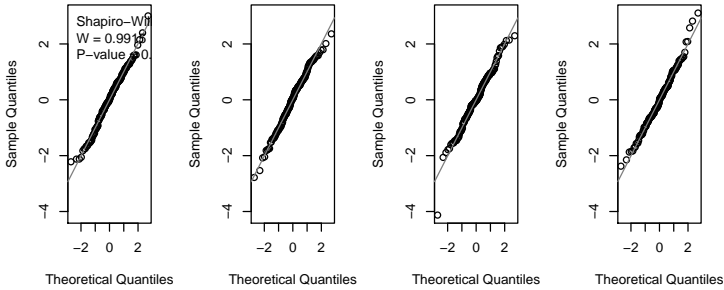


Normal errors: sample 4 Normal errors: sample 5 Normal errors: sample 6 Normal errors: sample 7



> qqplotArray(model_1)

Original data Normal errors: sample 1 Normal errors: sample 2 Normal errors: sample 3



Normal errors: sample 4 Normal errors: sample 5 Normal errors: sample 6 Normal errors: sample 7

