

## 14.10: Checking the Normality Assumption

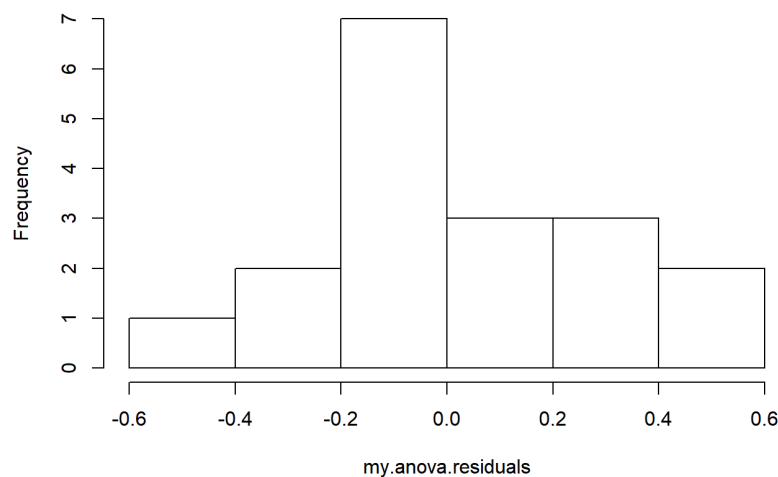
Testing the normality assumption is relatively straightforward. We covered most of what you need to know in Section 13.9. The only thing we really need to know how to do is pull out the residuals (i.e., the  $\epsilon_{ik}$  values) so that we can draw our QQ plot and run our Shapiro-Wilk test. First, let's extract the residuals. R provides a function called `residuals()` that will do this for us. If we pass our `my.anova` to this function, it will return the residuals. So let's do that:

```
my.anova.residuals <- residuals( object = my.anova ) # extract the residuals
```

We can print them out too, though it's not exactly an edifying experience. In fact, given that I'm on the verge of putting *myself* to sleep just typing this, it might be a good idea to skip that step. Instead, let's draw some pictures and run ourselves a hypothesis test:

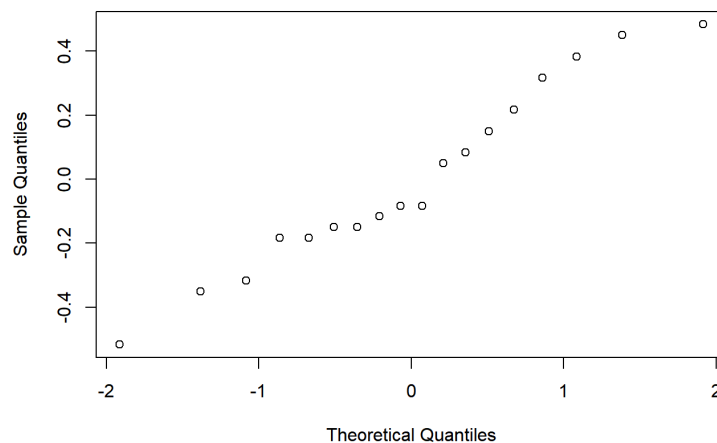
```
hist( x = my.anova.residuals ) # plot a histogram (similar to Figure @ref{fig})
```

Histogram of my.anova.residuals



```
qqnorm( y = my.anova.residuals ) # draw a QQ plot (similar to Figure @ref{fig})
```

Normal Q-Q Plot



```
shapiro.test( x = my.anova.residuals ) # run Shapiro-Wilk test
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: my.anova.residuals  
## W = 0.96019, p-value = 0.6053
```

The histogram and QQ plot are both look pretty normal to me.<sup>212</sup> This is supported by the results of our Shapiro-Wilk test ( $W=.96$ ,  $p=.61$ ) which finds no indication that normality is violated.

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