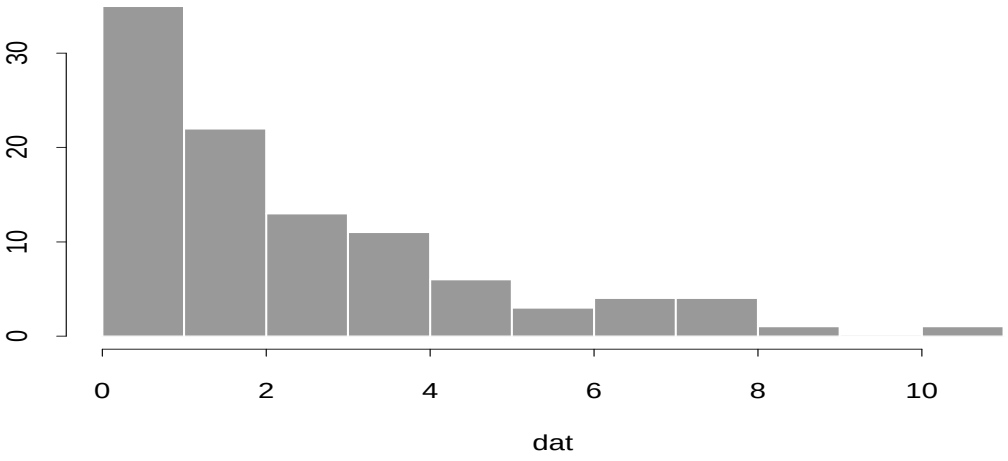
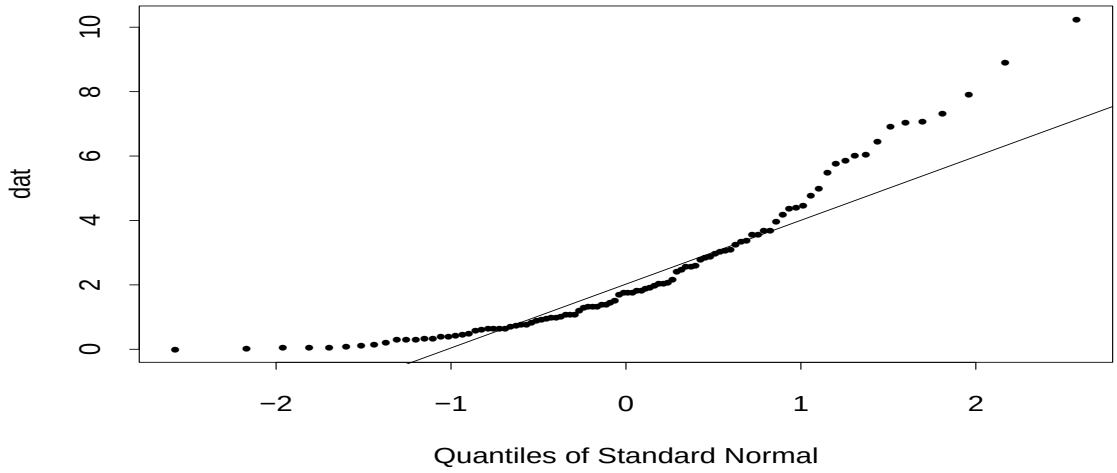
Assessing Normality of a Sample

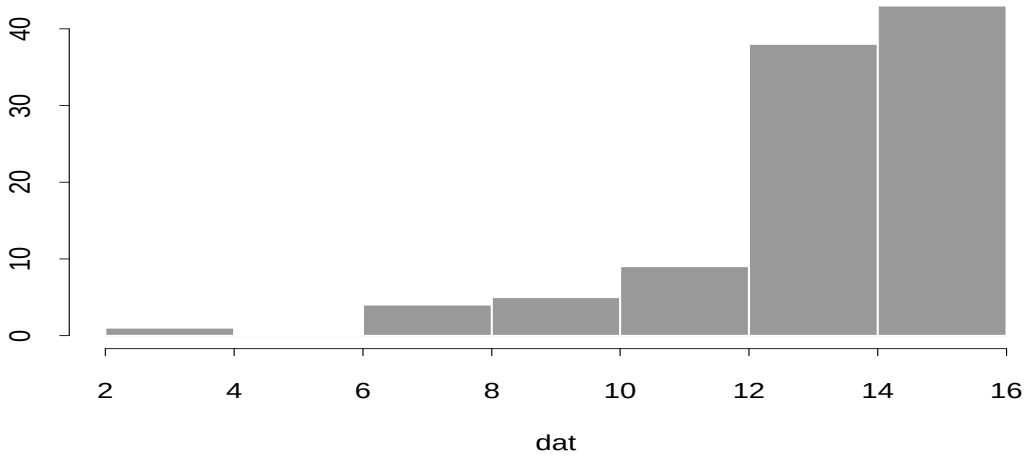
- normal *quantile* plots can be used to assess whether the data could have come from a normal distribution
- these plots are also called *QQ* or *normal scores* plots
- the sorted values are plotted against the values we would expect to get if the sample came from a normal distribution
- a straight line in this plot indicates that the data are normally distributed
- outliers show up as values distant from the overall pattern
- curvature indicates departure from normality *e.g.* skewness
- the NSCORES command in MINITAB can be used to produce the values to be plotted against the data

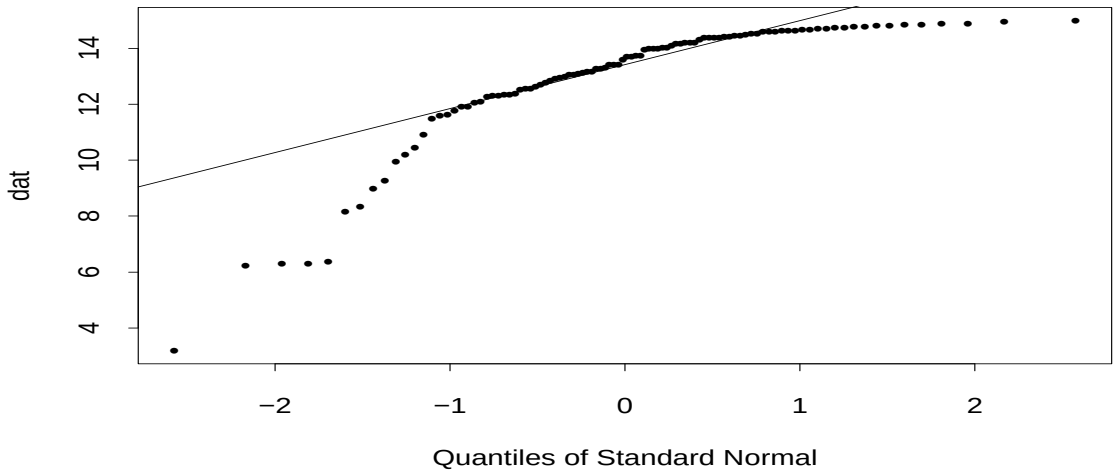
- the curvature in the normal scores plot can reveal the shape of distribution
- if the distribution is skewed to the right, the nscores plot curves up at both the left and the right



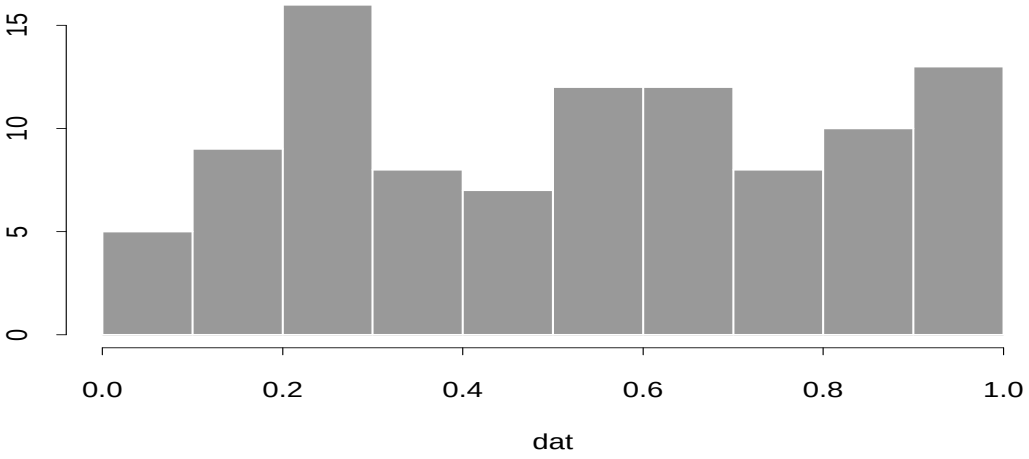


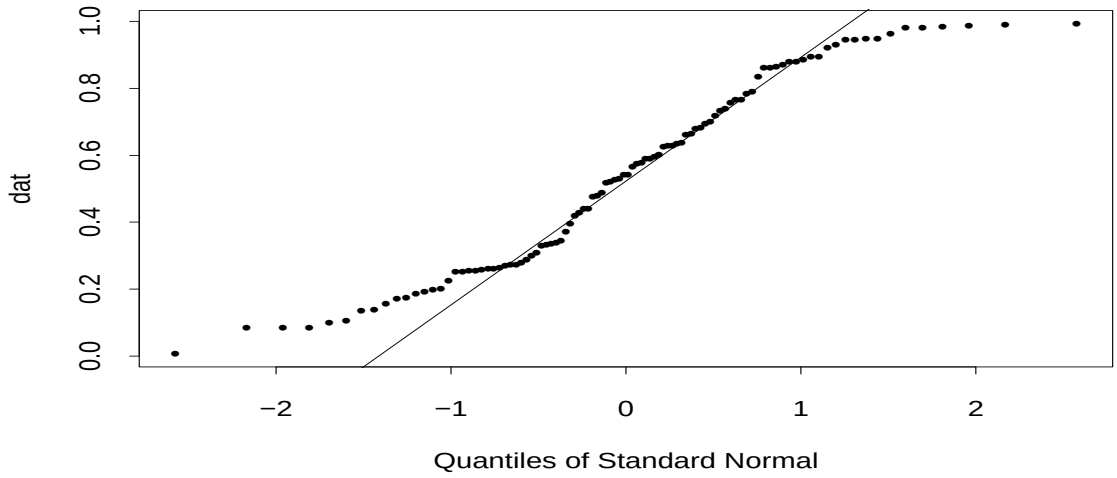
- if the distribution is skewed to the left, the nscores plot curves down at each end





- if the distribution has a flatter peak than the normal, the normal scores plot curves up at the left and down at the right





Example: The normal scores plot for residuals from the data on golf balls is shown below. Alternatively the residuals can be saved (in C3 for example) and the plot obtained using the commands

```
MTB > NSOR C3 C4
MTB > PLOT C3*C4
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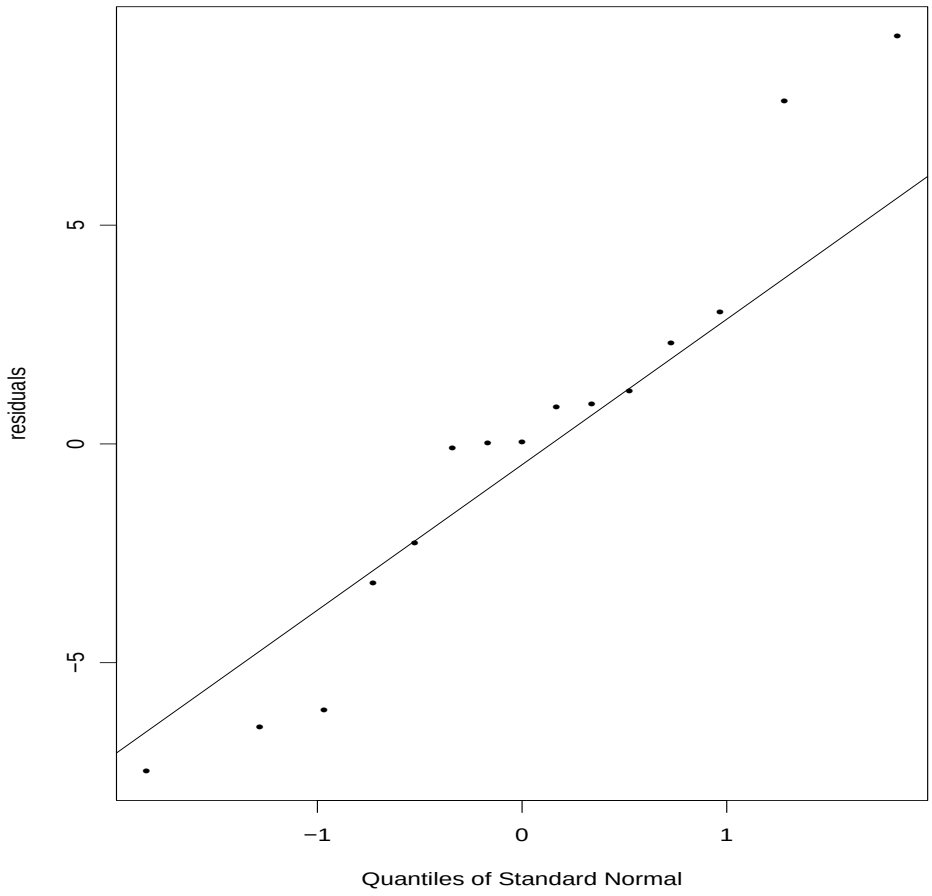
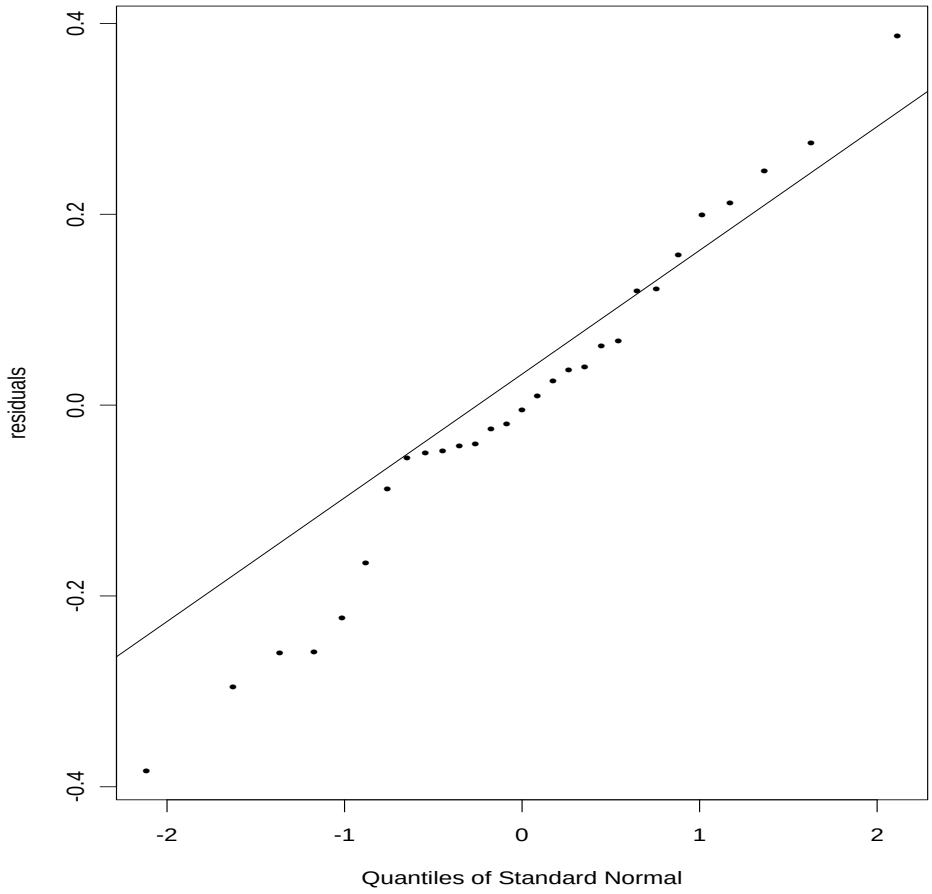


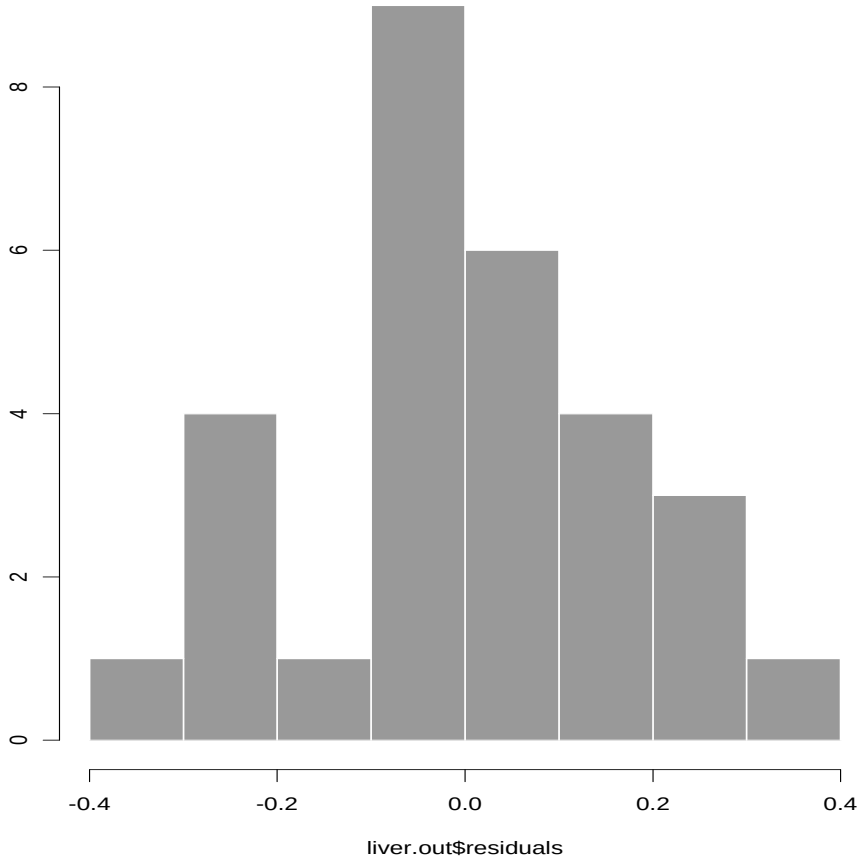
- the points are fairly close to a straight line

- there is no evidence of a departure from normality
- a plot like this can be plotted directly from the pull-down menu for the One-Way command under the Graphs button. This plot uses a probability scale rather than a quantile scale, but the idea is the same - a straight line indicates normality.

Example: For the liver weight data, the normal scores plot of the residuals is shown below.



- the normal scores are quite close to the straight line except in the left tail
- a histogram indicates that many of the negative residuals are close to zero rather than spread out over the interval from -.4 to 0


0
2
4
6
8
-0.4
-0.2
0.0
0.2
0.4
liver.out$residuals