Drawing graphs

Our data

- To illustrate making graphs, we need some data.
- Data on 202 male and female athletes at the Australian Institute of Sport.
- Variables:
    - categorical: Sex of athlete, sport they play
    - quantitative: height (cm), weight (kg), lean body mass, red and white blood cell counts, haematocrit and haemoglobin (blood), ferritin concentration, body mass index, percent body fat.
- Values separated by tabs (which impacts reading in).

Packages for this section

```r
library(tidyverse)
```

Reading data into R

- Use read_tsv ("tab-separated values"), like read_csv.
- Data in ais.txt:

```
my_url <- "http://ritsokiguess.site/datafiles/ais.txt"
athletes <- read_tsv(my_url)
```

The data (some)

```
athletes
```

```
# A tibble: 202 x 13
   Sex    Sport    RCC   WCC    Hc    Hg  Ferr   BMI   SSF `%
   <chr>  <chr>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
 1 female Netball  4.56  13.3  42.2  13.6    20  19.2  49
 2 female Netball  4.15   6    38    12.7    59  21.2 110.
 3 female Netball  4.16   7.6  37.5  12.3    22  21.4  89
 4 female Netball  4.32   6.4  37.7  12.3    30  21.0  98.3
 5 female Netball  4.06   5.8  38.7  12.8    78  21.8 122.
 6 female Netball  4.12   6.1  36.6  11.8    21  21.4  90.4
 7 female Netball  4.17   5    37.4  12.7   109  21.5 107.
 8 female Netball  3.8    6.6  36.5  12.4   102  24.4 157.
 9 female Netball  3.96   5.5  36.3  12.4    71  22.6 101.
10 female Netball  4.44   9.7  41.4  14.1    64  22.8 126.
# i 192 more rows
# i 1 more variable: Wt <dbl>
```

Types of graph

Depends on number and type of variables:

Categorical	Quantitative	Graph
1	0	bar chart
0	1	histogram
2	0	grouped bar charts
1	1	side-by-side boxplots
0	2	scatterplot
2	1	grouped boxplots
1	2	scatterplot with points identified by group (eg. by colour)

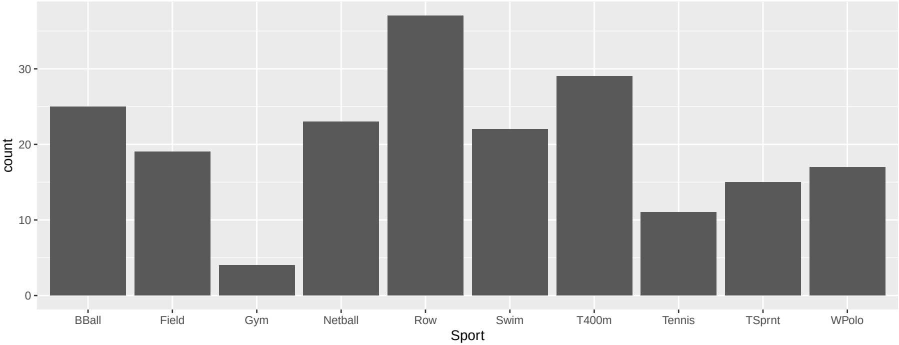
With more (categorical) variables, might want *separate plots by groups*. This is called `facetting` in R.

ggplot

- R has a standard graphing procedure ggplot, that we use for all our graphs.
- Use in different ways to get precise graph we want.
- Let's start with bar chart of the sports played by the athletes.

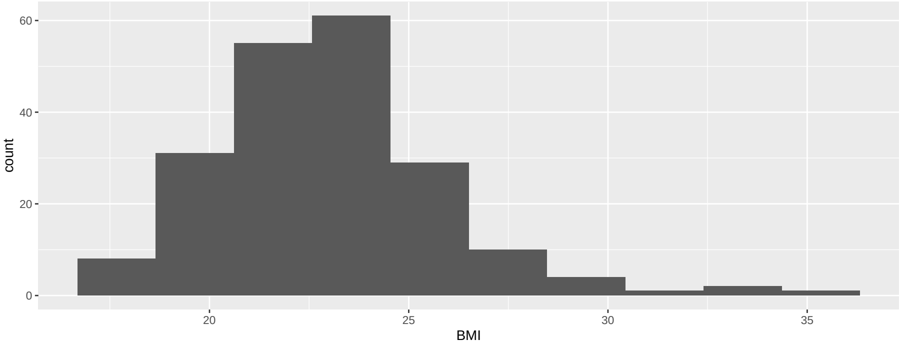
Bar chart

```
ggplot(athletes, aes(x = Sport)) + geom_bar()
```



Histogram of body mass index

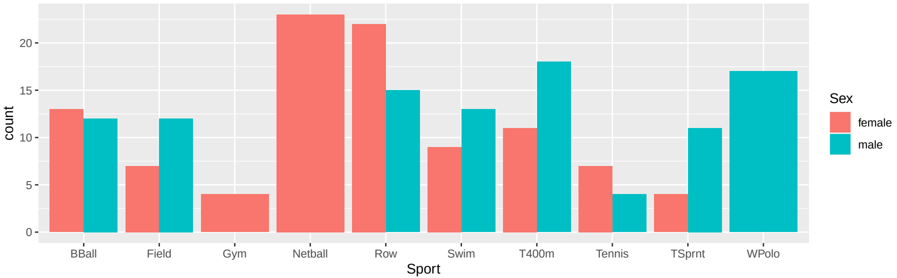
```
ggplot(athletes, aes(x = BMI)) + geom_histogram(bins = 10)
```



Which sports are played by males and females?

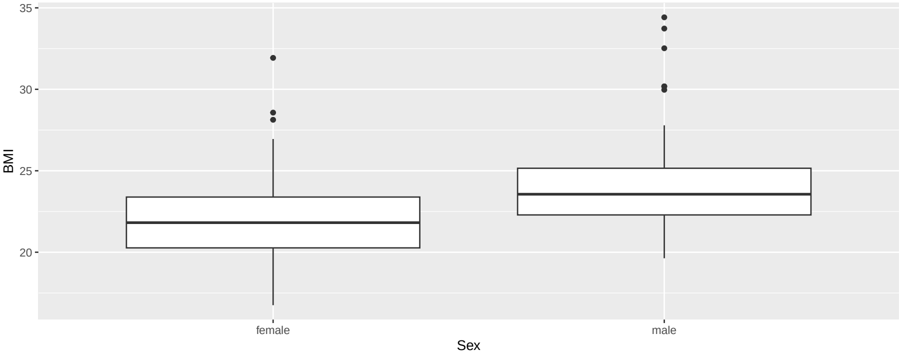
Grouped bar chart:

```
ggplot(athletes, aes(x = Sport, fill = Sex)) +
  geom_bar(position = "dodge")
```



BMI by gender

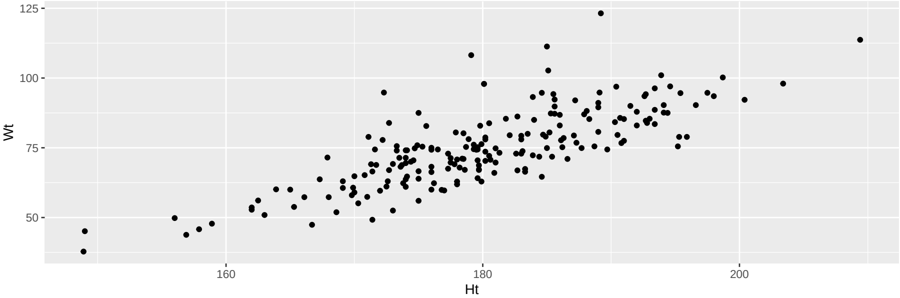
```
ggplot(athletes, aes(x = Sex, y = BMI)) + geom_boxplot()
```



Height vs. weight

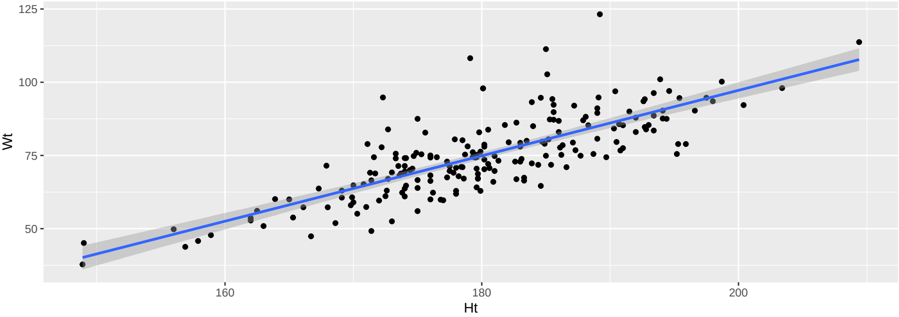
Scatterplot:

```
ggplot(athletes, aes(x = Ht, y = Wt)) + geom_point()
```



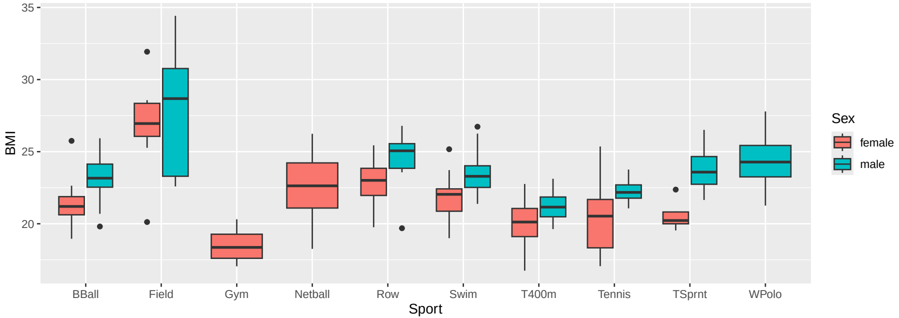
With regression line

```
ggplot(athletes, aes(x = Ht, y = Wt)) +
  geom_point() + geom_smooth(method = "lm")
```



BMI by sport and gender

```
ggplot(athletes, aes(x = Sport, y = BMI, fill = Sex)) +
  geom_boxplot()
```

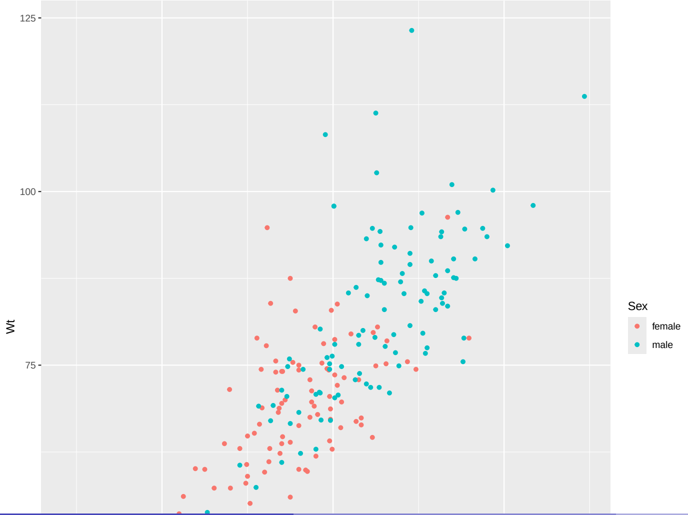


A variation that uses `colour` instead of `fill`:

```
ggplot(athletes, aes(x = Sport, y = BMI, colour = Sex)) +
  geom_boxplot()
```

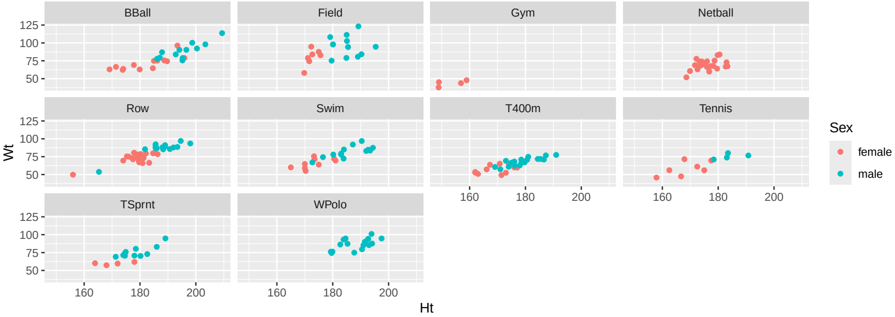
Height and weight by gender

```
ggplot(athletes, aes(x = Ht, y = Wt, colour = Sex)) +
  geom_point()
```



Height by weight by gender for each sport, with facets

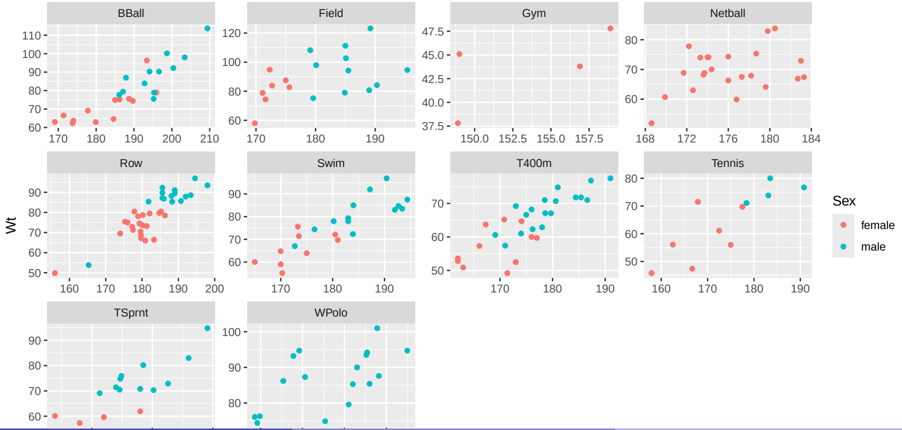
```
ggplot(athletes, aes(x = Ht, y = Wt, colour = Sex)) +
  geom_point() + facet_wrap(~Sport)
```



Filling each facet

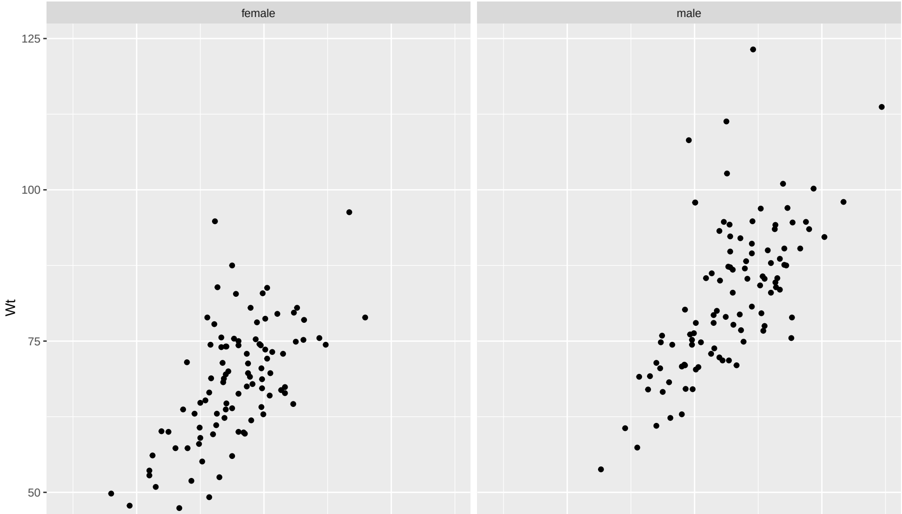
Default uses same scale for each facet. To use different scales for each facet, this:

```
ggplot(athletes, aes(x = Ht, y = Wt, colour = Sex)) +
  geom_point() + facet_wrap(~Sport, scales = "free")
```



Another view of height vs weight

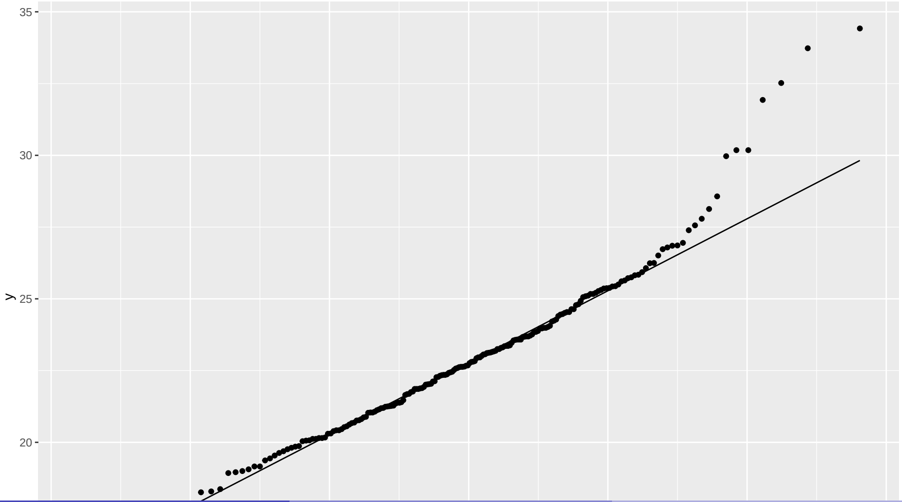
```
ggplot(athletes, aes(x = Ht, y = Wt)) +
  geom_point() + facet_wrap(~ Sex)
```



Normal quantile plot

For assessing whether a column has a normal distribution or not:

```
ggplot(athletes, aes(sample = BMI)) + stat_qq() + stat_qq_line
```



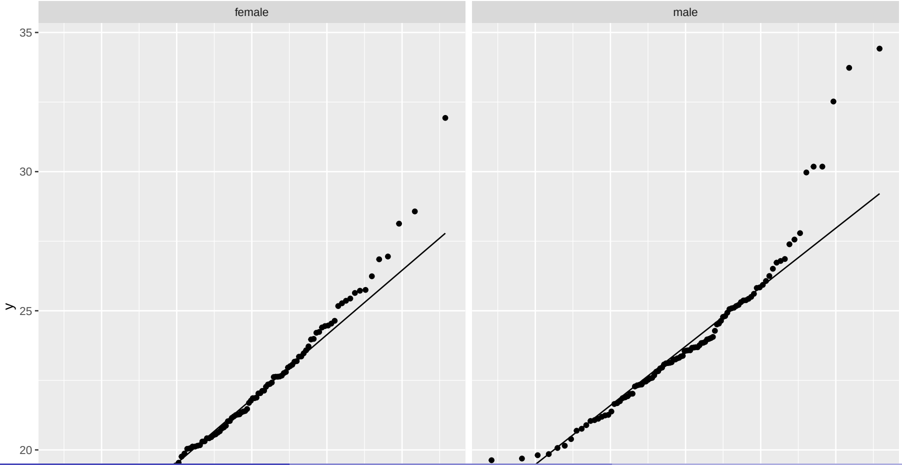
Comments

- Data on y-axis
- on x-axis, the z-scores you would expect if normal distribution correct
- if the points follow the line, distribution is normal
- the way in which the points *don't* follow line tell you about how the distribution is not normal
- in this case, the highest values are too high (long upper tail).

Facetting

Male and female athletes' BMI separately:

```
ggplot(athletes, aes(sample = BMI)) + stat_qq() + stat_qq_line
  facet_wrap(~ Sex)
```



Comments

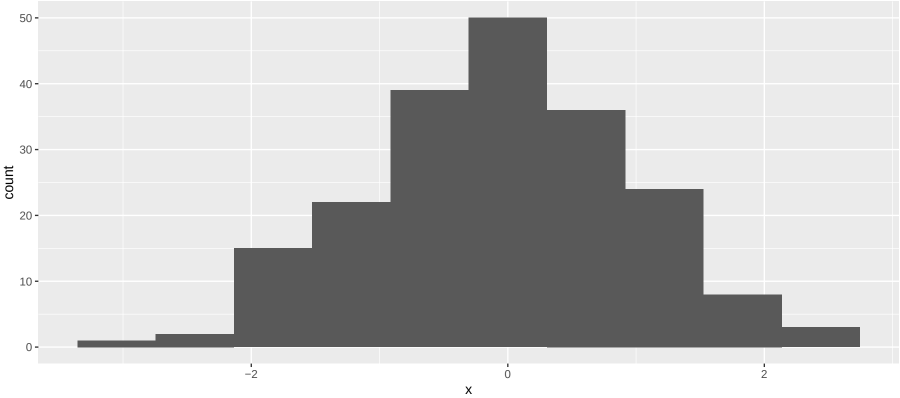
- The distribution of BMI for females is closer to normal, with only the highest few values being too high
- The distribution of BMI values for males might even be right-skewed: not only are the upper values too high, but some of the lowest ones are not low enough.

More normal quantile plots

- How straight does a normal quantile plot have to be?
- There is randomness in real data, so even a normal quantile plot from normal data won't look perfectly straight.
- With a small sample, can look not very straight even from normal data.
- Looking for systematic departure from a straight line; random wiggles ought not to concern us.
- Look at some examples where we know the answer, so that we can see what to expect.

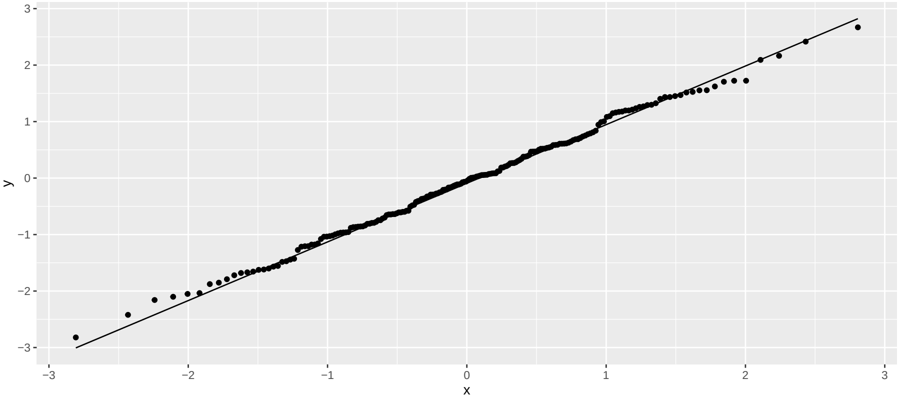
Normal data, large sample

```
d <- tibble(x=rnorm(200))
ggplot(d, aes(x=x)) + geom_histogram(bins=10)
```



The normal quantile plot

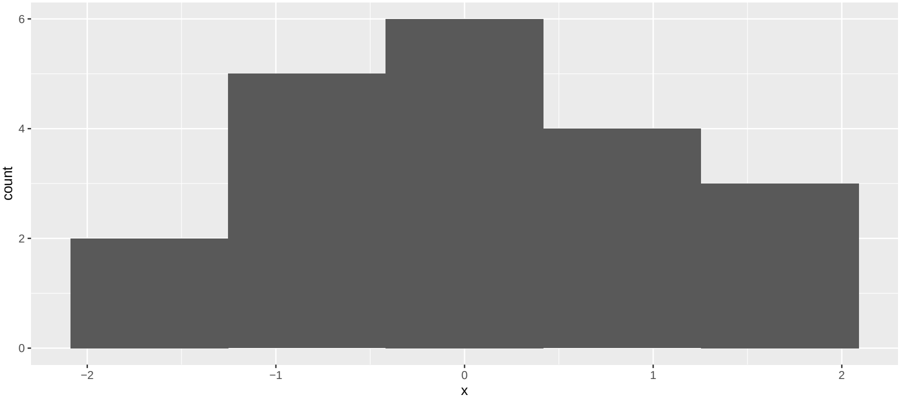
```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



Normal data, small sample

- Not so convincingly normal, but not obviously skewed:

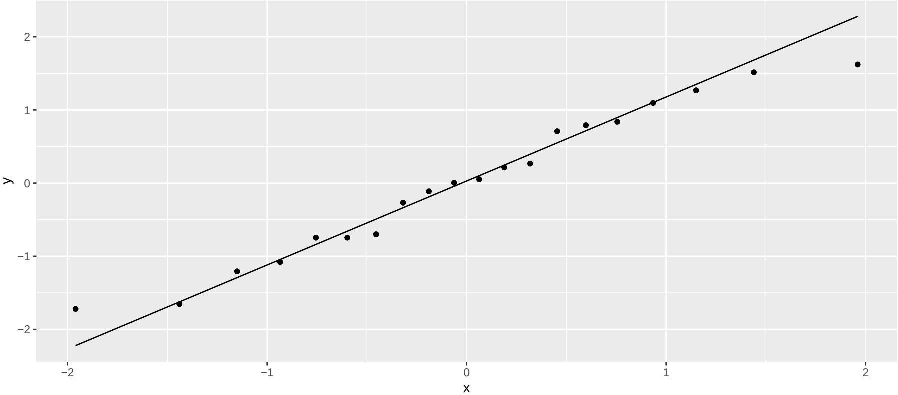
```
d <- tibble(x=rnorm(20))
ggplot(d, aes(x=x)) + geom_histogram(bins=5)
```



The normal quantile plot

Good, apart from the highest and lowest points being slightly off. I'd call this good:

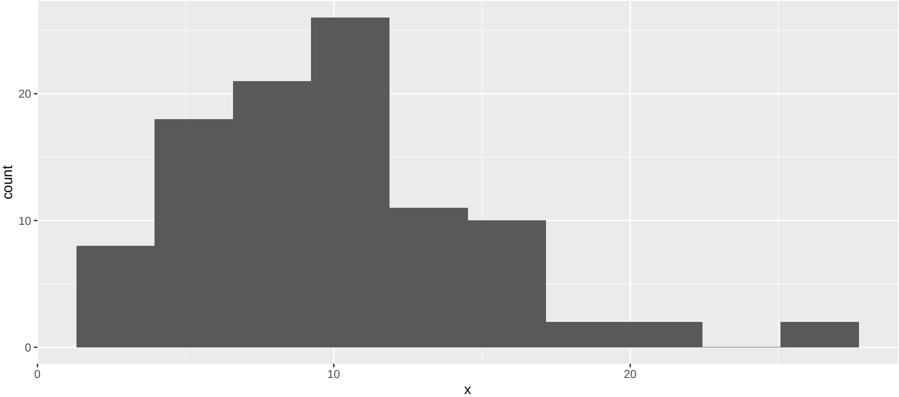
```
ggplot(d, aes(sample=x)) + stat_qq() + stat_qq_line()
```



Chi-squared data, $df = 10$

Somewhat skewed to right:

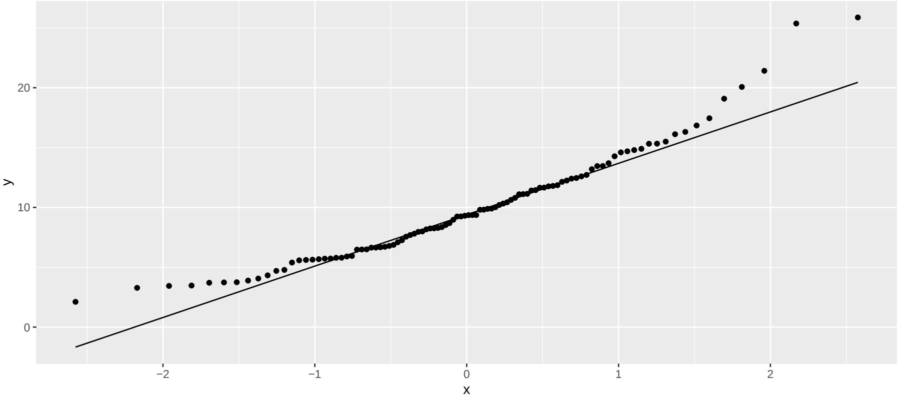
```
d <- tibble(x=rchisq(100, 10))
ggplot(d,aes(x=x)) + geom_histogram(bins=10)
```



The normal quantile plot

Somewhat opening-up curve:

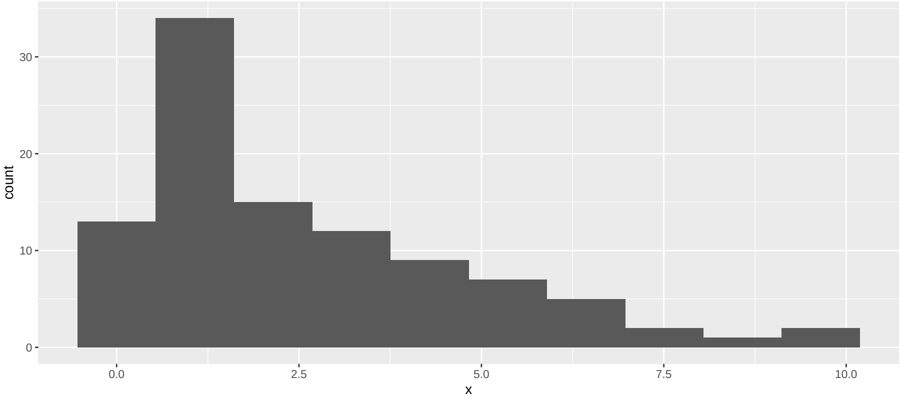
```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



Chi-squared data, df = 3

Definitely skewed to right:

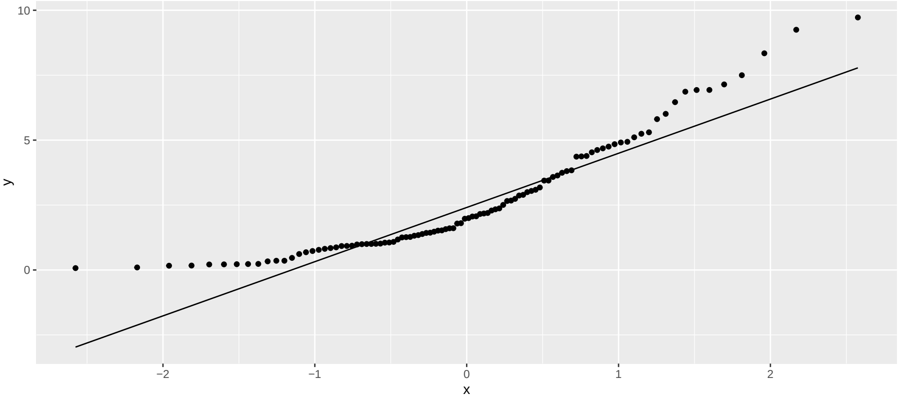
```
d <- tibble(x=rchisq(100, 3))
ggplot(d, aes(x=x)) + geom_histogram(bins=10)
```



The normal quantile plot

Clear upward-opening curve:

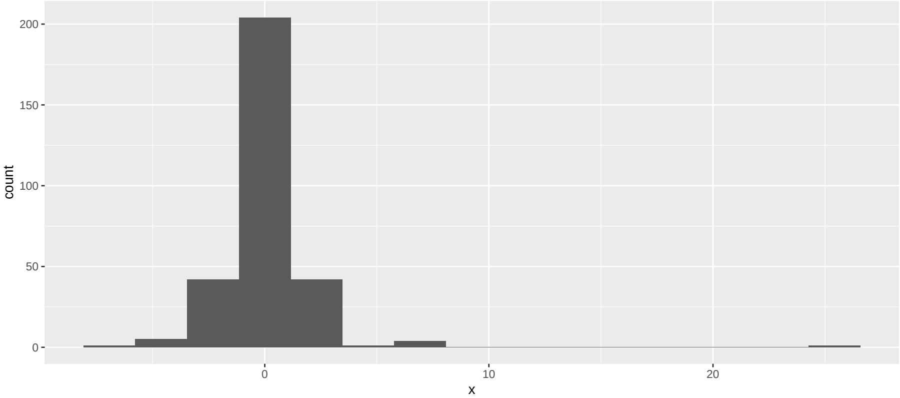
```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



t-distributed data, df = 3

Long tails (or a very sharp peak):

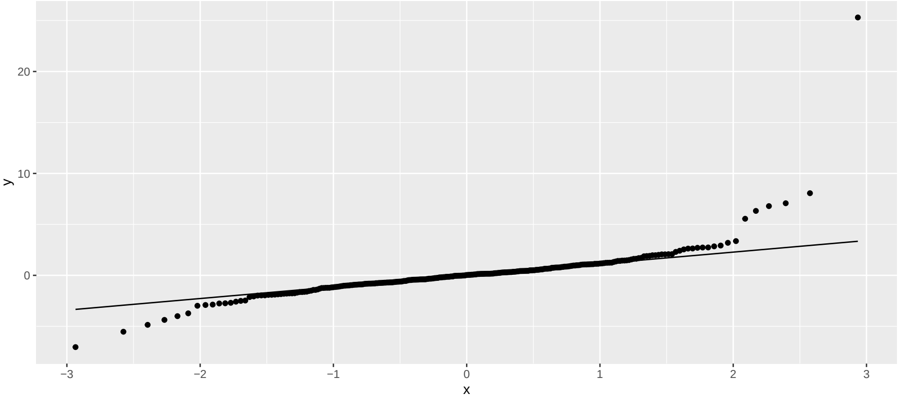
```
d <- tibble(x=rt(300, 3))
ggplot(d, aes(x=x)) + geom_histogram(bins=15)
```



The normal quantile plot

Low values too low and high values too high for normal.

```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



Summary

On a normal quantile plot:

- points following line (with some small wiggles): normal.
- kind of deviation from a straight line indicates kind of nonnormality:
  - a few highest point(s) too high and/or lowest too low: outliers
  - else see how points at each end off the line:

	High points	
Low points	**Too low**	**Too high**
Too low	Skewed left	Long tails
Too high	Short tails	Skewed right