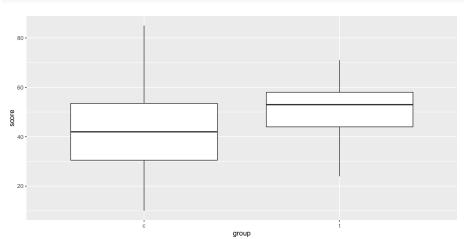


- see that normal distributions of data (or being normal enough) important
- only tools we have to assess this are histograms and maybe boxplots
- a better tool is normal quantile plot:
 - plot data against what you expect if data actually normal
 - look for points to follow a straight line, at least approx
- ggplot code: aes sample; geoms stat_qq and stat_qq_line

Kids learning to read



Each group looks normal, or at least symmetric.

Get the groups separately

```
kids %>% filter(group == "t") -> treatment
kids %>% filter(group == "c") -> control
```

to check

```
treatment %>% count(group)
```

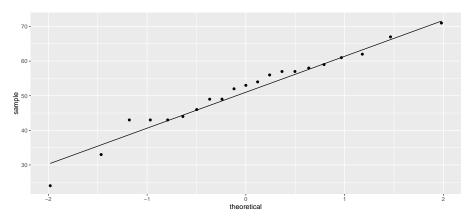
group n

```
control %>% count(group)
```

group n c 23

The treatment group

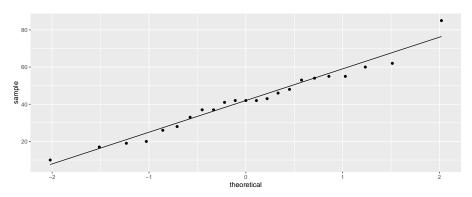
```
ggplot(treatment, aes(sample = score)) +
stat_qq() + stat_qq_line()
```



only problem here is lowest value a little too low (mild outlier).

Control group

```
ggplot(control, aes(sample = score)) +
stat_qq() + stat_qq_line()
```

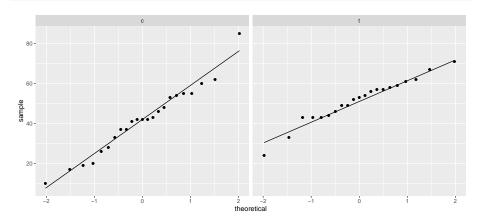


This time, highest value a little too high, but again, no real problem with normality.

Facetting more than one sample

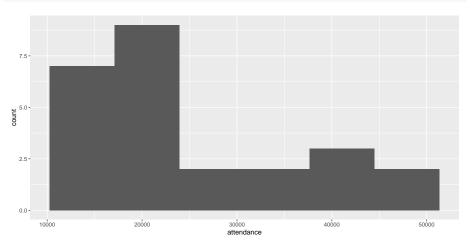
Use the whole data set and facet by groups

```
ggplot(kids, aes(sample = score)) +
stat_qq() + stat_qq_line() + facet_wrap(~group)
```



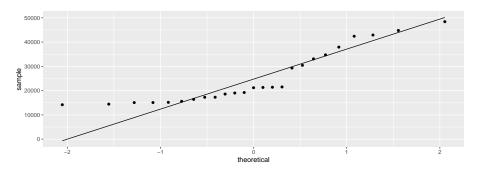
Blue Jays attendances, skewed to right

ggplot(jays, aes(x = attendance)) + geom_histogram(bins = 6)



On a normal quantile plot

```
ggplot(jays, aes(sample = attendance)) +
stat_qq() + stat_qq_line()
```



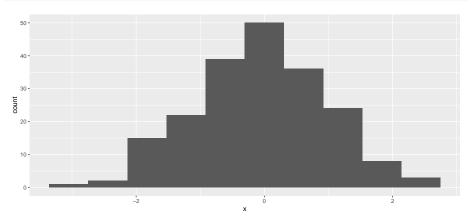
- Attendances at low end too bunched up: skewed to right.
- Right-skewness can also show up as highest values being too high, or as a curved pattern in the points.

More normal quantile plots

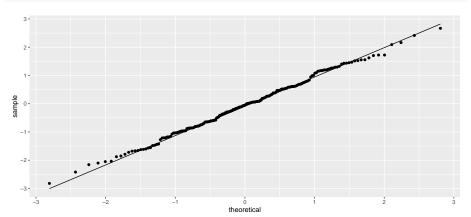
- How straight does a normal quantile plot have to be?
- There is randomness in real data, so even a normal quantile plot from normal data won't look perfectly straight.
- With a small sample, can look not very straight even from normal data.
- Looking for systematic departure from a straight line; random 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)</pre>
```



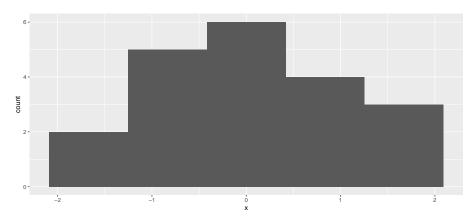




Normal data, small sample

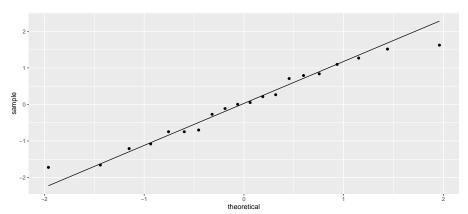
• Not so convincingly normal, but not obviously skewed:

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



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

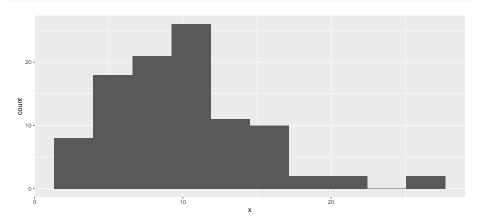
ggplot(d, aes(sample=x)) + stat_qq() + stat_qq_line()



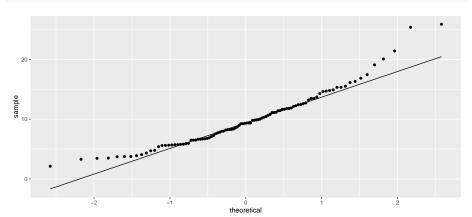
Chi-squared data, df = 10

Somewhat skewed to right:

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



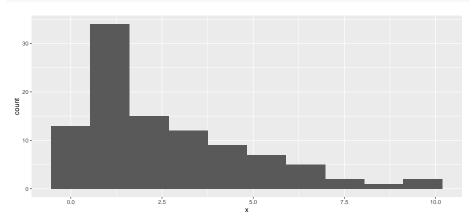
Somewhat opening-up curve:



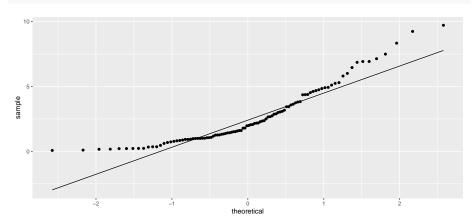
Chi-squared data, df = 3

Definitely skewed to right:

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



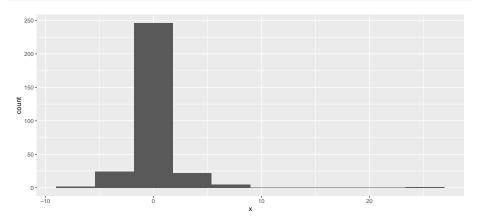
Clear upward-opening curve:



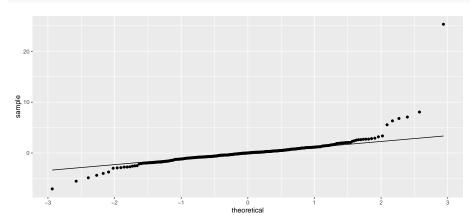
t-distributed data, df = 3

Long tails (or a very sharp peak):

```
d <- tibble(x=rt(300, 3))
ggplot(d, aes(x=x)) + geom_histogram(bins=10)</pre>
```



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



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

• short-tailed distribution OK for t (mean still good), but others problematic (depending on sample size).