

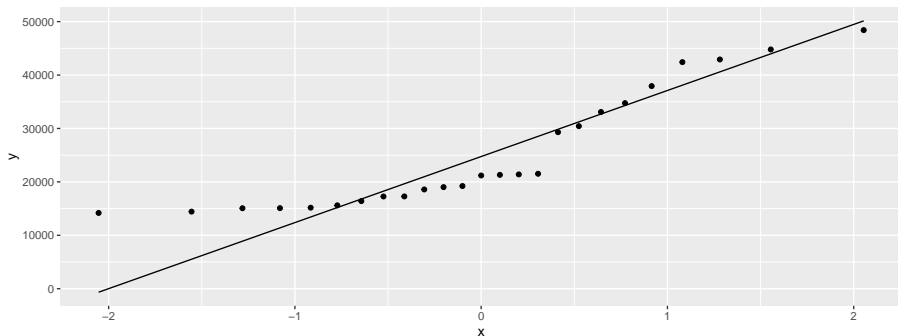
# Assumptions

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- The  $t$  procedures we have seen so far come with assumption of normally-distributed data
- but how much does that normality matter?
- Central Limit Theorem says that sampling distribution of sample mean is “approximately normal” if sample size is “large”.
- Hence same applies to difference of two sample means.
- How to use this in practice? Draw a picture and make a call about whether sample size large enough.

# Blue Jays attendances

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



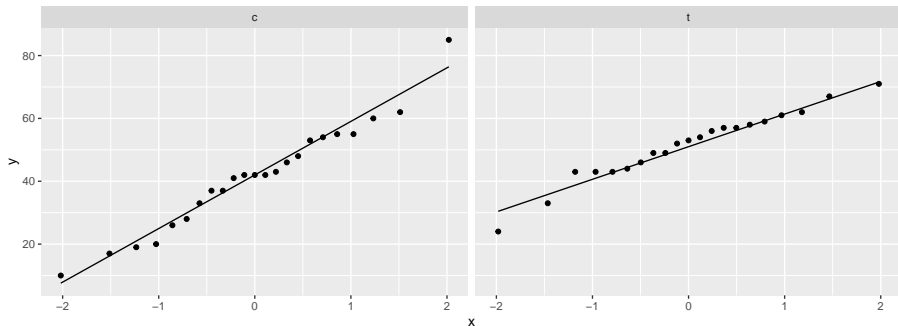
# Comments

- Distribution of attendances somewhat skewed to the right (because of the short lower tail and the sort-of curve)
- Sample size  $n = 25$  is reasonably large in Central Limit Theorem terms
- Use of  $t$  *may* be OK here despite skewed shape.

# Learning to read

- Make normal quantile plots, one for each sample:

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



# Comments

- with sample sizes over 20 in each group, these are easily normal enough to use a  $t$ -test.
- the (sampling distribution of the) difference between two sample means tends to have a more normal distribution than either sample mean individually, so that two-sample  $t$  tends to be better than you'd guess.

## Pain relief

- With matched pairs, assumption is of normality of *differences*, so work those out first:

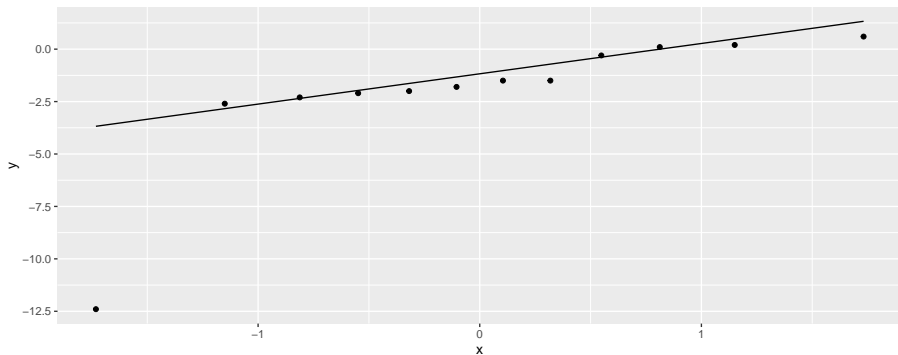
```
pain %>% mutate(diff = drug_a - drug_b) -> pain  
pain
```

```
# A tibble: 12 x 4
```

	subject	drug_a	drug_b	diff
	<dbl>	<dbl>	<dbl>	<dbl>
1	1	2	3.5	-1.5
2	2	3.6	5.7	-2.1
3	3	2.6	2.9	-0.300
4	4	2.6	2.4	0.200
5	5	7.3	9.9	-2.6
6	6	3.4	3.3	0.100
7	7	14.9	16.7	-1.80
8	8	6.6	6	0.600
9	9	2.3	3.8	-1.5
10	10	2	4	-2
11	11	6.8	9.1	-2.3
12	12	8.5	20.9	-12.4

# Normality of differences

```
ggplot(pain, aes(sample=diff)) + stat_qq() + stat_qq_line()
```





# Comments

- This is very non-normal (the low outlier)
- The sample size of  $n = 12$  is not large
- We should have concerns about our matched pairs  $t$ -test.

# Doing things properly

- The right way to use a  $t$  procedure:
  - ▶ draw a graph of our data (one of the standard graphs, or normal quantile plot)
  - ▶ use the graph to assess sufficient normality given the sample size
  - ▶ for a two-sample test, assess equality of spreads (boxplot easier for this)
  - ▶ if necessary, express our doubts about the  $t$  procedure (for now), or do a better test (later).

# Looking ahead

- Looking at a normal quantile plot and assessing it with the sample size seems rather arbitrary. Can we do better? (Yes: using the bootstrap, later.)
- What to do if the  $t$  procedure is not to be trusted? Use a different test (later):
  - ▶ one sample: sign test
  - ▶ two samples: Mood's median test
  - ▶ matched pairs: sign test on differences.
- If you have heard about the signed rank or rank sum tests: they come with extra assumptions that are usually not satisfied if normality fails.