

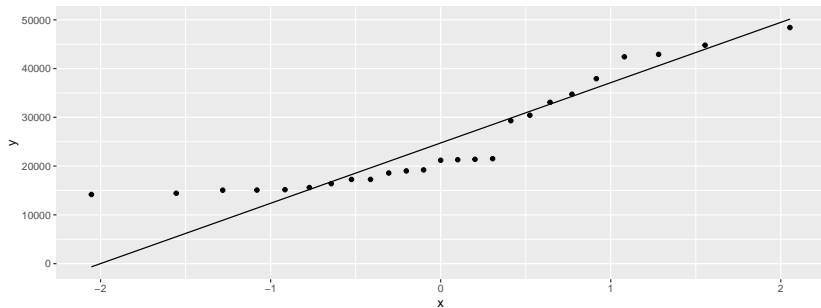
Assumptions

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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()
```



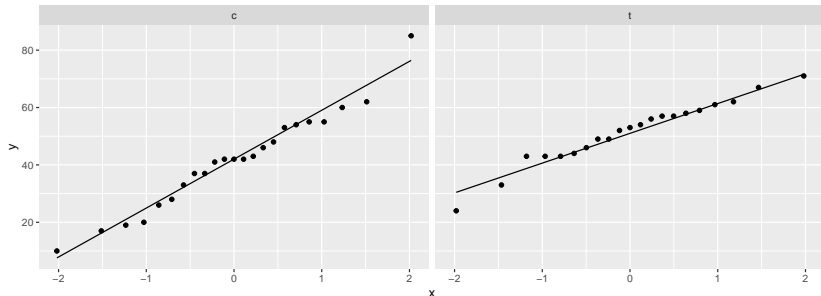
Comments

- ▶ 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:

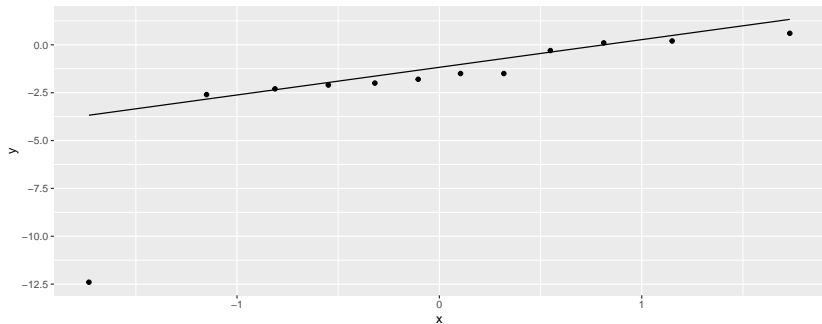
```
pain %>% mutate(diff = druga - drugb) -> pain  
pain
```

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

	subject	druga	drugb	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

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.