

## Statistical Inference: matched pairs

# Matched pairs

Some data:

subject	druga	drugb
1	2.0	3.5
2	3.6	5.7
3	2.6	2.9
4	2.6	2.4
5	7.3	9.9
6	3.4	3.3
7	14.9	16.7
8	6.6	6.0
9	2.3	3.8
10	2.0	4.0
11	6.8	9.1
12	8.5	20.9

# Matched pairs data

- Data are comparison of 2 drugs for effectiveness at reducing pain.
  - 12 subjects (cases) were arthritis sufferers
  - Response is #hours of pain relief from each drug.
- In reading example, each child tried only one reading method.
- But here, each subject tried out both drugs, giving us two measurements.
  - Possible because, if you wait long enough, one drug has no influence over effect of other.
  - Advantage: focused comparison of drugs. Compare one drug with another on same person, removes a lot of variability due to differences between people.
  - Matched pairs, requires different analysis.
- Design: randomly choose 6 of 12 subjects to get drug A first, other 6 get drug B first.

# Paired t test: reading the data

Values aligned in columns:

```
my_url <-  
  "http://www.utsc.utoronto.ca/~butler/c32/analgesic.txt"  
pain <- read_table(my_url)  
  
##  
## -- Column specification -----  
## cols(  
##   subject = col_double(),  
##   druga = col_double(),  
##   drugb = col_double()  
## )
```

# The data

pain

subject	druga	drugb
1	2.0	3.5
2	3.6	5.7
3	2.6	2.9
4	2.6	2.4
5	7.3	9.9
6	3.4	3.3
7	14.9	16.7
8	6.6	6.0
9	2.3	3.8
10	2.0	4.0
11	6.8	9.1
12	8.5	20.9

# Paired $t$ -test

```
with(pain, t.test(druga, drugb, paired = T))
```

```
##  
## Paired t-test  
##  
## data:  druga and drugb  
## t = -2.1677, df = 11, p-value = 0.05299  
## alternative hypothesis: true difference in means is not equal to  
## 95 percent confidence interval:  
## -4.29941513  0.03274847  
## sample estimates:  
## mean of the differences  
## -2.133333
```

- P-value is 0.053.
- Not quite evidence of difference between drugs.

## t-testing the differences

- Likewise, you can calculate the differences yourself and do a 1-sample t-test on them.
- First calculate a column of differences:

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

subject	druga	drugb	diff
1	2.0	3.5	-1.5
2	3.6	5.7	-2.1
3	2.6	2.9	-0.3
4	2.6	2.4	0.2
5	7.3	9.9	-2.6
6	3.4	3.3	0.1
7	14.9	16.7	-1.8
8	6.6	6.0	0.6
9	2.3	3.8	-1.5
10	2.0	4.0	-2.0
11	6.8	9.1	-2.3
12	8.5	20.9	-12.4

## t-test on the differences

- then throw them into `t.test`, testing that the mean is zero, with same result as before:

```
with(pain, t.test(diff, mu=0))
```

```
##  
## One Sample t-test  
##  
## data: diff  
## t = -2.1677, df = 11, p-value = 0.05299  
## alternative hypothesis: true mean is not equal to 0  
## 95 percent confidence interval:  
## -4.29941513 0.03274847  
## sample estimates:  
## mean of x  
## -2.133333
```

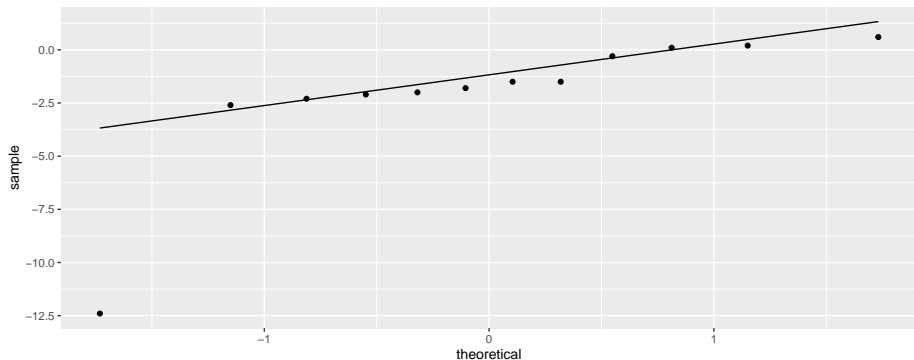


# Assessing normality

- 1-sample and 2-sample t-tests assume (each) group normally distributed.
- Matched pairs analyses assume (theoretically) that differences normally distributed.
- How to assess normality? A normal quantile plot.

# The normal quantile plot (of differences)

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



- Points should follow the straight line. Bottom left one way off, so normality questionable here: outlier.

# What to do instead?

- Matched pairs  $t$ -test based on one sample of differences
- the differences not normal (enough)
- so do *sign test* on differences, null median 0:

```
sign_test(pain, diff, 0)
```

```
## $above_below
## below above
##      9      3
##
## $p_values
##   alternative    p_value
## 1         lower 0.07299805
## 2          upper 0.98071289
## 3    two-sided 0.14599609
```

# Comments

- no evidence of any difference between drugs (P-value 0.1460)
- in  $t$ -test, the low outlier difference pulled mean difference downward and made it look more negative than it should have been
- therefore, there really isn't any difference between the drugs.