

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

## Matched pairs 1/2

- ▶ 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.

## Matched pairs 2/2

- ▶ 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.

# Packages

```
library(tidyverse)  
library(smmr) # for a sign test later
```

## Reading the data

Values aligned in columns:

```
my_url <-  
  "http://ritsokiguess.site/datafiles/analgesic.txt"  
pain <- read_table(my_url)  
pain
```

```
# A tibble: 12 x 3  
  subject druga drugb  
    <dbl> <dbl> <dbl>  
1       1     2   3.5  
2       2   3.6   5.7  
3       3   2.6   2.9  
4       4   2.6   2.4  
5       5   7.3   9.9  
6       6   3.4   3.3  
7       7  14.9  16.7  
8       8   6.6    6  
9       9   2.3   3.8
```

## Paired $t$ -test

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

Paired  $t$ -test

data: druga and drugb

$t = -2.1677$ ,  $df = 11$ ,  $p\text{-value} = 0.05299$

alternative hypothesis: true mean difference is not equal to 0

95 percent confidence interval:

-4.29941513 0.03274847

sample estimates:

mean difference

-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 then do a 1-sample t-test on them.

```
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
```



## 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
```

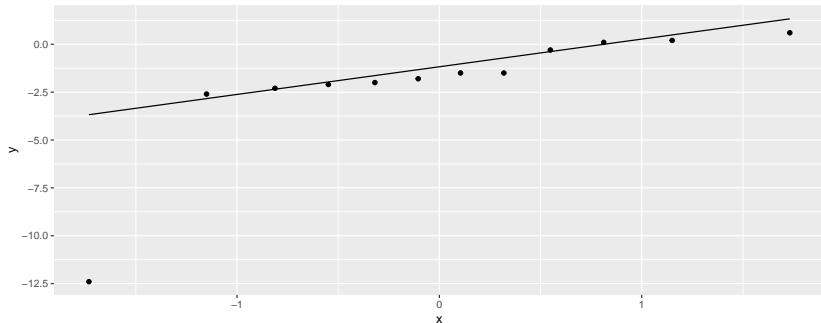
- ▶ Same P-value (0.053) and conclusion.

## 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
```

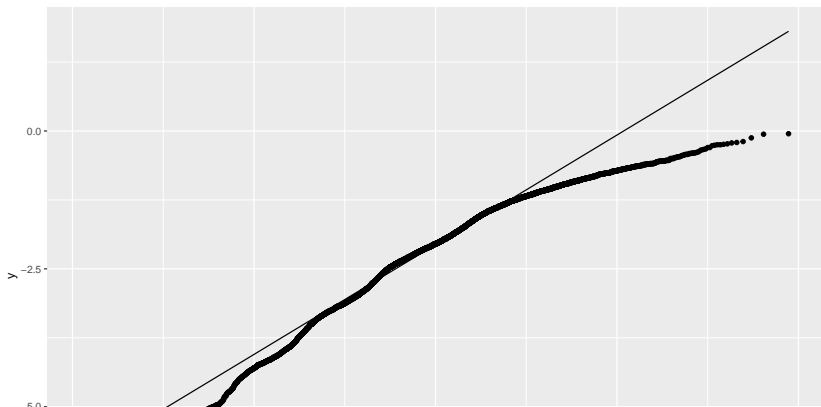
```
2         upper 0.98071289
```

```
3    two-sided 0.14599609
```

## Did we need to worry about that outlier?

Bootstrap sampling distribution of sample mean differences:

```
tibble(sim = 1:10000) %>%  
  rowwise() %>%  
  mutate(my_sample = list(sample(pain$diff, replace = TRUE))  
  mutate(my_mean = mean(my_sample)) %>%  
  ggplot(aes(sample = my_mean)) + stat_qq() + stat_qq_line
```



## 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.