

Matched pairs

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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
```

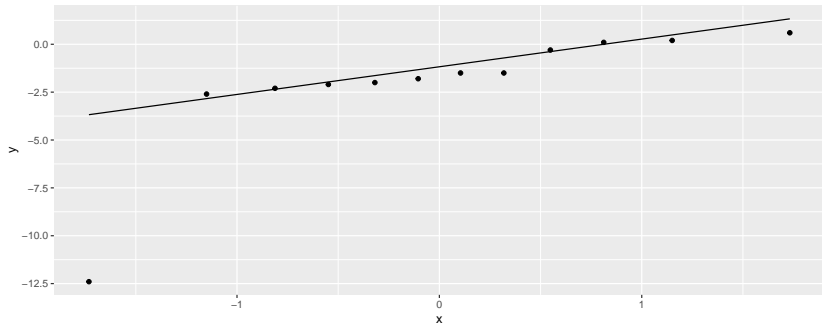
- ▶ Same P-value (0.053) and conclusion.

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
```

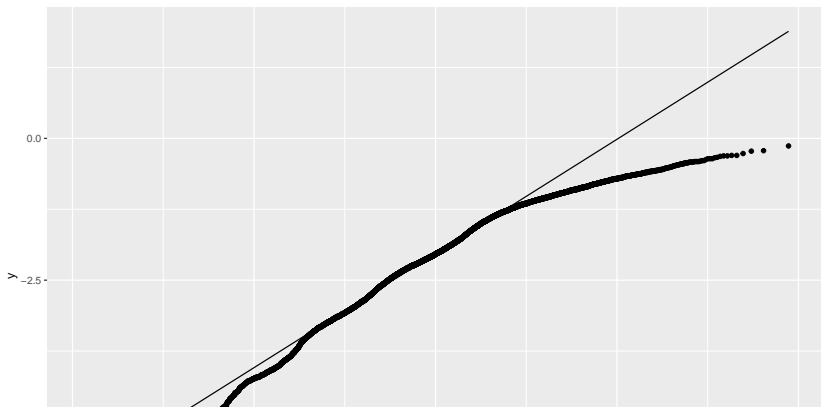
```
2          upper 0.98071289
```

```
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),  
                             size = 100)) %>%  
  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.