

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
11	6.8	9.1
12	8.5	20.9

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
10      10     2     4
11      11    6.8    9.1
12      12    8.5   20.9
```

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

- Or, calculate the differences yourself and then do a 1-sample t-test on them.

```
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
```


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
```

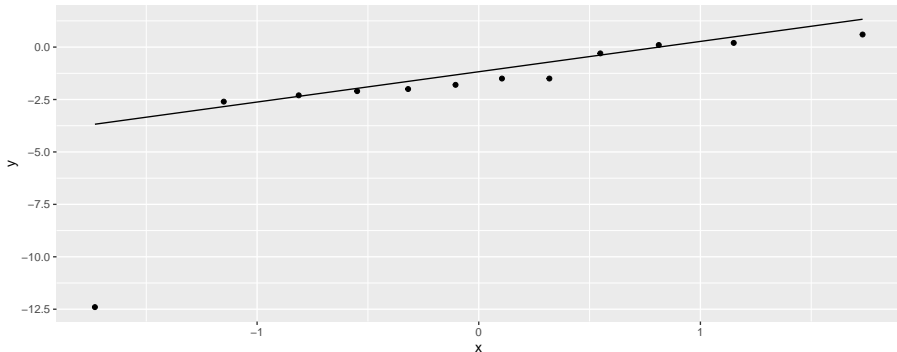
- Same P-value (0.053) and conclusion.

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
```

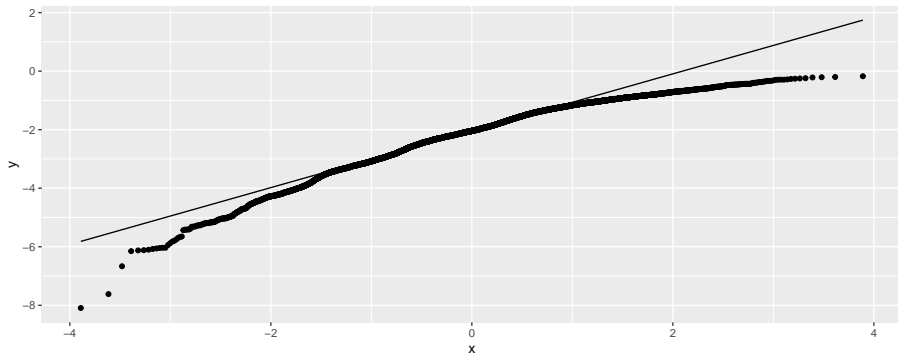
```
2          upper 0.98071289
```

```
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.