# 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

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- 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.

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## 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.

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### **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 %>% slice(1:6) # display first six rows
```

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#### Paired t-test

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

Paired t-test

```
data: druga and drugb
t = -2.1677, df = 11, p-value = 0.05299
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
   -4.29941513   0.03274847
```

sample estimates:

-2.133333

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

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### 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 %>% slice(1:5)
```

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#### 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.

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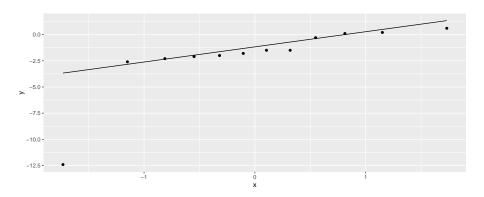
## Assessing normality

- 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.

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## 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.

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#### 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:

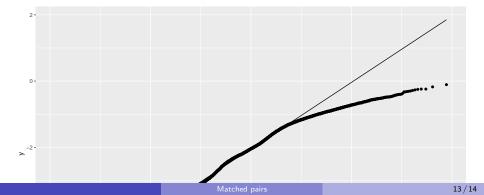
sign\_test(pain, diff, 0)

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### 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.

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