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 5	2.6	2.4
	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 3 / 14

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</pre>
```

```
# A tibble: 12 \times 3
  subject druga drugb
    <dbl> <dbl> <dbl>
                3.5
           2
       2 3.6 5.7
3
       3 2.6 2.9
       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 2.3 3.8
10
      10 2 4
11
      11 6.8 9.1
           8.5 20.9
12
      12
```

Matched pairs

6/14

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 (
95 percent confidence interval:
-4.29941513 0.03274847
```

- sample estimates: mean difference
 - -2.133333

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

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t-testing the differences

 Or, 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> <dbl>
           2
                3.5 - 1.5
       2 3.6 5.7 -2.1
3
       3 2.6 2.9 -0.300
       4 2.6 2.4 0.200
5
       5 7.3 9.9 -2.6
6
       6 3.4 3.3 0.100
          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
```

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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.

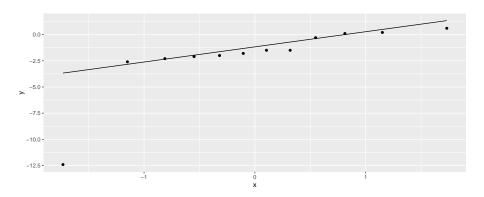
Assessing normality

- 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:

```
$above_below
below above
    9    3

$p_values
    alternative    p_value
1    lower 0.07299805
2    upper 0.98071289
3    two-sided 0.14599609
```

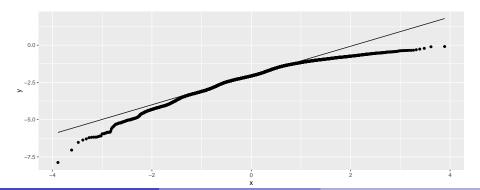
sign_test(pain, diff, 0)

Matched pairs 12 / 14

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()
```



Matched pairs

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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