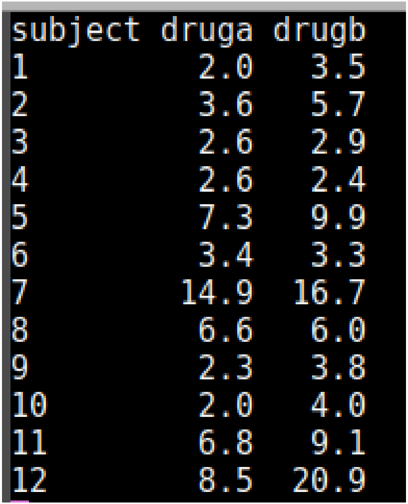
Matched pairs

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
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-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 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 = 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
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 
```

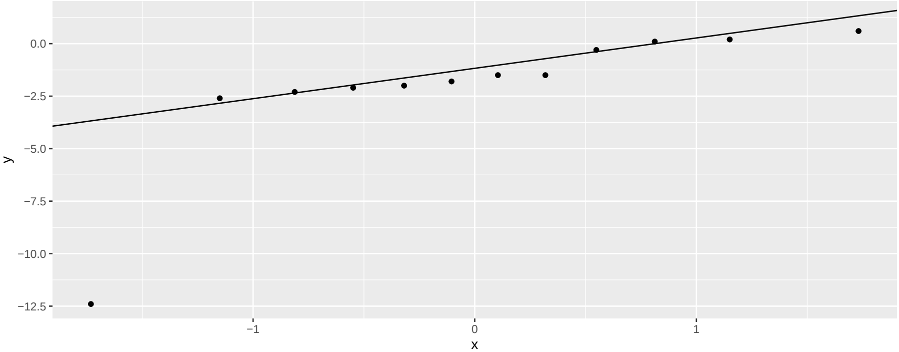
- Same P-value (0.053) and conclusion.

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)
```

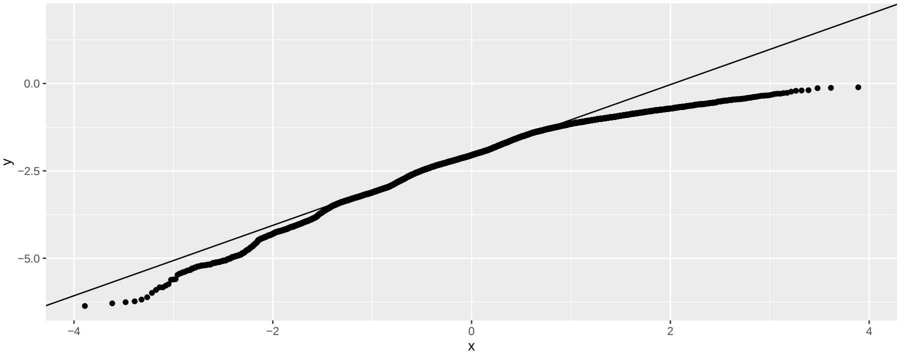
```
$above_below
below above
    9     3

$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.