

R Tutorial-11

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You may [click here](#) to access the .qmd file.

In this issue, we

- investigate whether a t -test appears justified, and
- use the **sign test**

As best I can ascertain from the opening to [Chapter 9](#), the research question will be this: Do surgical masks reduce the number of copies of influenza virus in fine particle droplets?

The data, taken from a 2013 study and found in `fosdata::masks`, contains virus counts when subjects exhaled into a collection device over a 30-minute period. Each subject had two runs (so this is matched-pairs data), one wearing a surgical mask, and the other without. The relevant columns are named `mask_fine` and `no_mask_fine`.

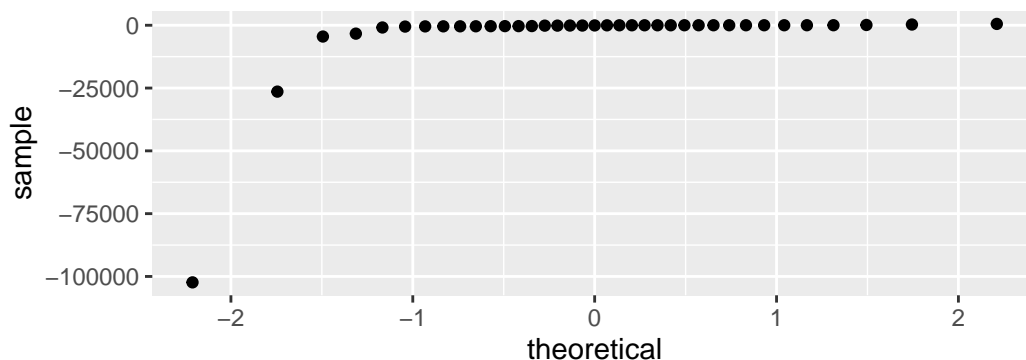
Testing normality

As the data is matched pairs, we are interested in the difference

```
no_mask_fine - mask_fine
```

We use a normal quantile plot as an indicator of whether these values follow a normal distribution:

```
gf_qq(~(mask_fine - no_mask_fine), data=masks)
```



The data does not fall along a straight line well enough to consider them as having a *normal* distribution.

Is the sample size large enough?

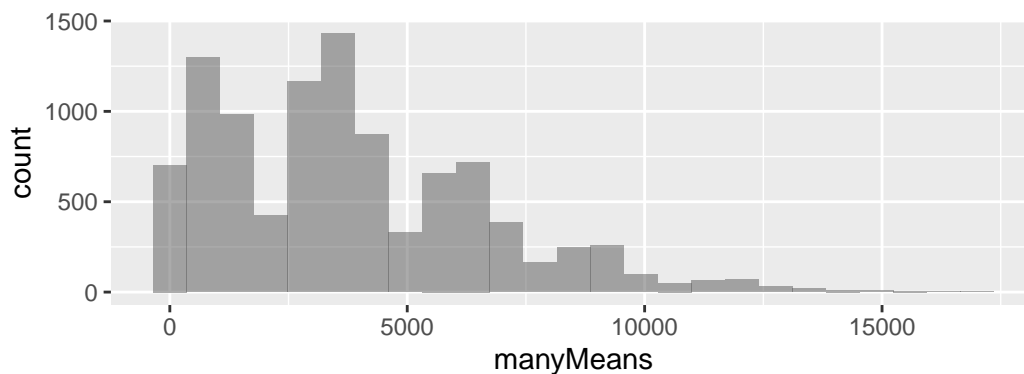
Of course, 1-sample t -tests are **robust** in the sense that they work reasonably well even when the sample is drawn from a non-normal population, so long as the sample size is large enough? Our sample is of size

```
nrow(masks)
```

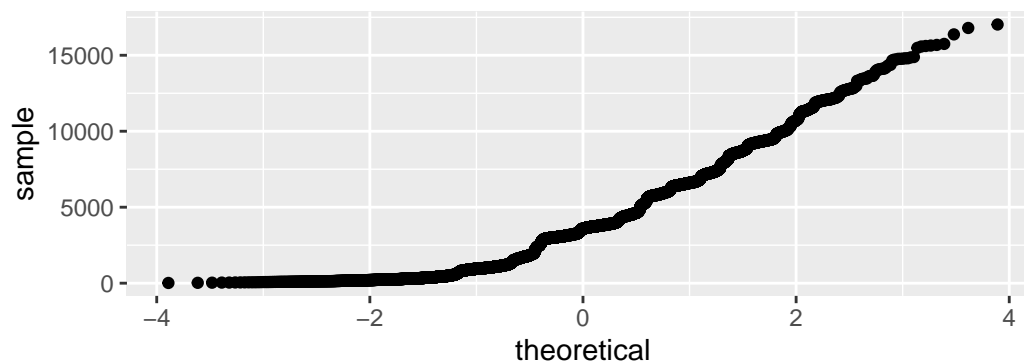
```
[1] 37
```

Perhaps that is large enough. We might produce a bootstrap distribution of sample mean differences and see if it appears to be normal. If it were, that would give us some reason to think the sample size $n = 37$ is large enough.

```
manyMeans = replicate(10000,  
                      mean(~(no_mask_fine-mask_fine), data=resample(masks))  
                      )  
gf_histogram(~manyMeans)
```



```
gf_qq(~manyMeans)
```



The lack of normality for the sampling distribution of bootstrap means raises the concern that $n = 37$ is not large enough. We can run a 1-sample t -test, even so, but the values it produces may be meaningless.

The Sign Test

[Note: This is not the test discussed in the textbook when treating this data. It is somewhat simpler than the methods of Chapter 9 (a chapter we are skipping).] The idea of a **sign test**: If there were really no difference in virus counts under the two treatments, then the **sign** of the difference should be something like a coin toss, having a negative sign about half the time, a positive one the other half. Ties can and do happen, and sometimes it seems justified eliminating those cases before proceeding with a sign test.

```
subset(masks, select=c(no_mask_fine, mask_fine))
```

	no_mask_fine	mask_fine
1	4	16
2	37	7
3	13	7
4	154	38
5	181	30
6	34	30
7	126587	24239
8	0	3
9	10	294
10	533	5
11	39087	12665
12	37	144
13	4	0
14	2	0
15	21	24
16	0	0
17	433	78
18	479	22
19	2057	1640
20	8	15
21	0	0
22	7	0
23	3888	541
24	895	8
25	672	245
26	32	10
27	787	454
28	11	0
29	230	761
30	666	319
31	556	181
32	5206	711
33	217	54
34	113	0
35	443	8

36	19	9
37	75	0

Note that Subjects 16 and 21 contributed virus counts of 0 under both treatments. They must have been completely free of influenza virus, and the difference $0 - 0 = 0$ for such a subject is not germane to the research question. We make a new data frame from the old, leaving out these cases (as well as variables we do not use).

```
modifiedMasks = subset(masks[c(-16, -21), ], select=c(no_mask_fine, mask_fine))
modifiedMasks$diff = modifiedMasks$no_mask_fine - modifiedMasks$mask_fine
```

```
modifiedMasks
```

	no_mask_fine	mask_fine	diff
1	4	16	-12
2	37	7	30
3	13	7	6
4	154	38	116
5	181	30	151
6	34	30	4
7	126587	24239	102348
8	0	3	-3
9	10	294	-284
10	533	5	528
11	39087	12665	26422
12	37	144	-107
13	4	0	4
14	2	0	2
15	21	24	-3
17	433	78	355
18	479	22	457
19	2057	1640	417
20	8	15	-7
22	7	0	7
23	3888	541	3347
24	895	8	887
25	672	245	427
26	32	10	22
27	787	454	333
28	11	0	11
29	230	761	-531
30	666	319	347
31	556	181	375
32	5206	711	4495
33	217	54	163
34	113	0	113
35	443	8	435

36	19	9	10
37	75	0	75

The new data frame keeps the 35 subjects from the other rows.

To conduct the sign test, we

- count the number of positive (or, equivalently, the number of negative) results
- we take as our null hypothesis the belief that the proportion of positive results, under the assumption that masks do not reduce the exhalation of virus particles, is $p = 0.5$
- we use `pbinom()` to obtain a P -value

```
sum(modifiedMasks$diff < 0)
```

```
[1] 7
```

Under the null hypothesis, the count of negative results should be binomial with probability $p = 0.5$. How extreme is a count of 7? In 35 trials, we would look for an expected count of

$$np = (35)(0.5) = 17.5.$$

Things at least as extreme as 7, when the null hypothesis is true, consist of counts 7 and below, as well as counts 28 and above.

```
pbinom(7, 35, 0.5) + 1-pbinom(27, 35, 0.5)
```

```
[1] 0.0005082604
```

Knowing the numbers—7 failures out of 35 tries, with a supposed probability of 0.5—one can use `binom.test()` to produce the same P -value:

```
binom.test(7, 35, 0.5)
```

```
data: 7 out of 35
number of successes = 7, number of trials = 35, p-value = 0.0005083
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.08440602 0.36937884
sample estimates:
probability of success
          0.2
```

Notes:

- The sign test ignores the size of the differences, paying attention only to whether a result is a success or not (as measured by whether it has a positive or negative sign)
- For the research question, one might argue that if masks make a difference, then virus counts are going to be, on average, *smaller* while wearing a mask. This would imply having a 1-sided alternative, thereby taking as our P -value only the cumulative probability in the left tail: `pbinom(7, 35, 0.5)`
- When journalist Alex Berenson wrote his treatise, in November of 2020, “Unreported Truths About Covid-19 and Lockdowns: Part 3: Masks”, he cited this [Study from 2020](#) that conducted meta-analysis on all of the *clinical trials* that could be found in the world at that time (there were only 10, dating back to 1946) testing whether wearers of masks outside hospital settings offered protection against transmission of the flu. That is a different research question than the one addressed above. The discussion section of the 2020 study states, “We did not find evidence that surgical-type face masks are effective in reducing laboratory-confirmed influenza transmission, either when worn by infected persons (source control) or by persons in the general community to reduce their susceptibility.”

Lobsters (Your opportunity to try the sign test)

The package **abd** contains a data set called **Lobsters**. Lobsters were captured and moved to a new location. After settling in, the angle between the axial ray drawn from tail through eyes of a lobster, and the ray from the lobster’s current location back to its “home” site was measured. These angles, measured in degrees, are found in the **orientation** column of the data frame. An angle between (-89°) and 89° might be an indication that the lobster has an innate sense of where its home lies. State null and alternative hypotheses, then use a binomial test to assess the evidence against the null hypothesis. Draw a conclusion based on a significance level $\alpha = 0.05$. A lobster at 90° or (-90°) might be considered a throw-away data point, much as the “tie” cases above.