Day 17: Nonparametric tests - Supplemental material

BSTA 511/611

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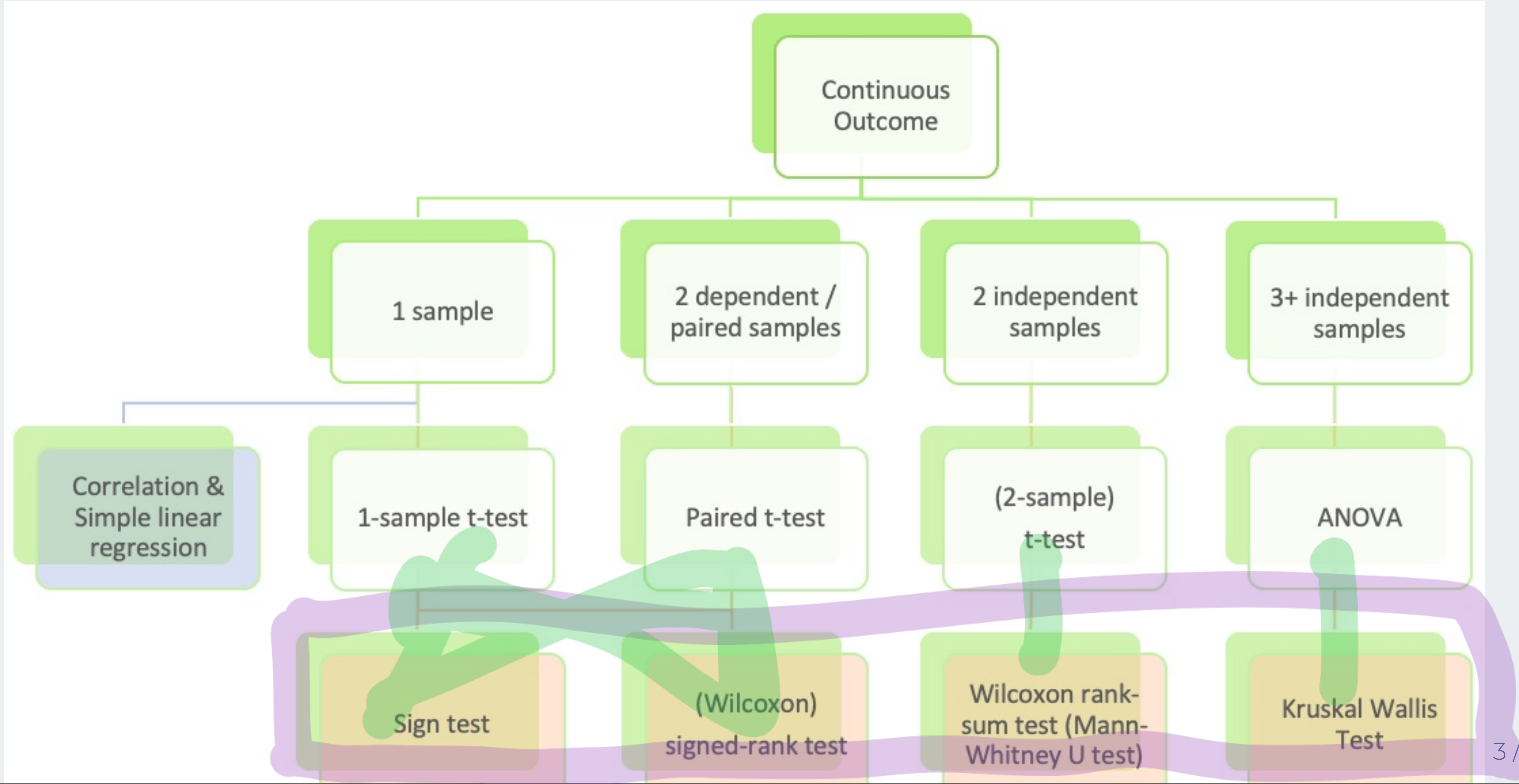
MoRitz's tip: write "nice" R code

Check out the tidyverse style guide: https://style.tidyverse.org/index.html

Especially, Chapter 4: Pipes and Chapter 5: ggplot2

```
```{r}
employ<-employ%>%mutate(disability=factor(disability),disability=fct_relevel(disability,"none"),disability=fct_recode(disability,amputation="amputee"))
summary(employ)
```
```

vs.

```
```{r}
employ <- employ %>%
  mutate(
    disability = factor(disability),
# make "none" the first level
      disability = fct_relevel(disability,
                               "none"),
# change level name amputee to amputation
      disability = fct_recode(disability,
                              amputation = "amputee"))
summary(employ)
```
```

```
```{r}
ggplot(employ,aes(x=disability,y=score,fill=disability,color=disability))+geom_dotplot(binaxis="y",alpha=.5)+geom_hline(aes(yintercept=mean(score)),lty="dashed")+stat_summary(fun="mean",geom="point",size=3,color="grey33",alpha=1)+theme(legend.position="none")
```
```

vs.

```
```{r}
ggplot(employ,
       aes(x = disability, y=score,
           fill = disability,
           color = disability)) +
  geom_dotplot(binaxis = "y", alpha =.5) +
  geom_hline(aes(yintercept = mean(score)),
             lty = "dashed") +
  stat_summary(fun = "mean",
               geom = "point",
               size = 3,
               color = "grey33",
               alpha =1)  +
  theme(legend.position = "none")
```
```

Where are we?


Continuous Outcome
1 sample
2 dependent / paired samples
2 independent samples
3+ independent samples
Correlation & Simple linear regression
1-sample t-test
Paired t-test
(2-sample) t-test
ANOVA
Sign test
(Wilcoxon) signed-rank test
Wilcoxon rank-sum test (Mann-Whitney U test)
Kruskal Wallis Test

Goals for today (Supplemental material)

- Why us a nonparametric approach?
- What the following tests are & when to use them

- **Sign test**
  - for paired data or single samples
- **(Wilcoxon) sign-rank test**
  - for paired data or single samples
  - accounts for sizes of differences
- **Wilcoxon Rank-sum test**
  - for two independent samples
  - a.k.a **Mann-Whitney U test**
- **Kruskal-Wallis test**
  - nonparametric ANOVA test

- How to use R for each test & interpret the results

Additional resource

- Chapter 13: Nonparametric tests of Pagano's *Principles of Biostatistics*, 2022 edition
- Can download chapter from OHSU library eBook at https://ebookcentral.proquest.com/lib/ohsu/detail.action?docID=6950388&pq-origsite=primo

Nonparametric tests

Background: parametric vs nonparametric

- Prior inference of means methods had conditions assuming the underlying population(s) was (were) normal (or at least approximately normal).
- Normal distribution is completely described (parameterized) by two parameters: μ and σ.
- The first was often the parameter of interest, while the latter was assumed known (Z-test) or estimated (t-tests).

- The above are therefore described as **parametric** procedures.

- **Nonparametric** procedures
    - Make fewer assumptions about the structure of the underlying population from which the samples were collected.
    - Work well when distributional assumptions are in doubt.

The good and the bad about nonparametric tests

Good

- Fewer assumptions
- Tests are based on ranks
  - Therefore outliers have no greater influence than non-outliers.
  - Since tests are based on ranks we can apply these procedures to ordinal data
    - (where means and standard deviations are not meaningful).

Drawbacks

- Less powerful than parametric tests (due to loss of information when data are converted to ranks)
- While the test is easy, it may require substantial (computer) work to develop a confidence interval [by "inverting" the test].
- Theory was developed for continuous data (where ties are not possible); if population or data contain many ties, then a correction to the procedures must be implemented.
- Some procedures have "large" and "small" sample versions; the small sample versions require special tables or a computer.

Sign test

For paired data or single samples

Example: Intraocular pressure of glaucoma patients

- Intraocular pressure of glaucoma patients is often reduced by treatment with adrenaline.
- A **new synthetic drug** is being considered, but it is more expensive than the **current adrenaline alternative**.
- 7 glaucoma patients were treated with both drugs:
  - one eye with adrenaline and
  - the other with the synthetic drug
- **Reduction in pressure** was recorded in each eye after following treatment (larger numbers indicate greater reduction)

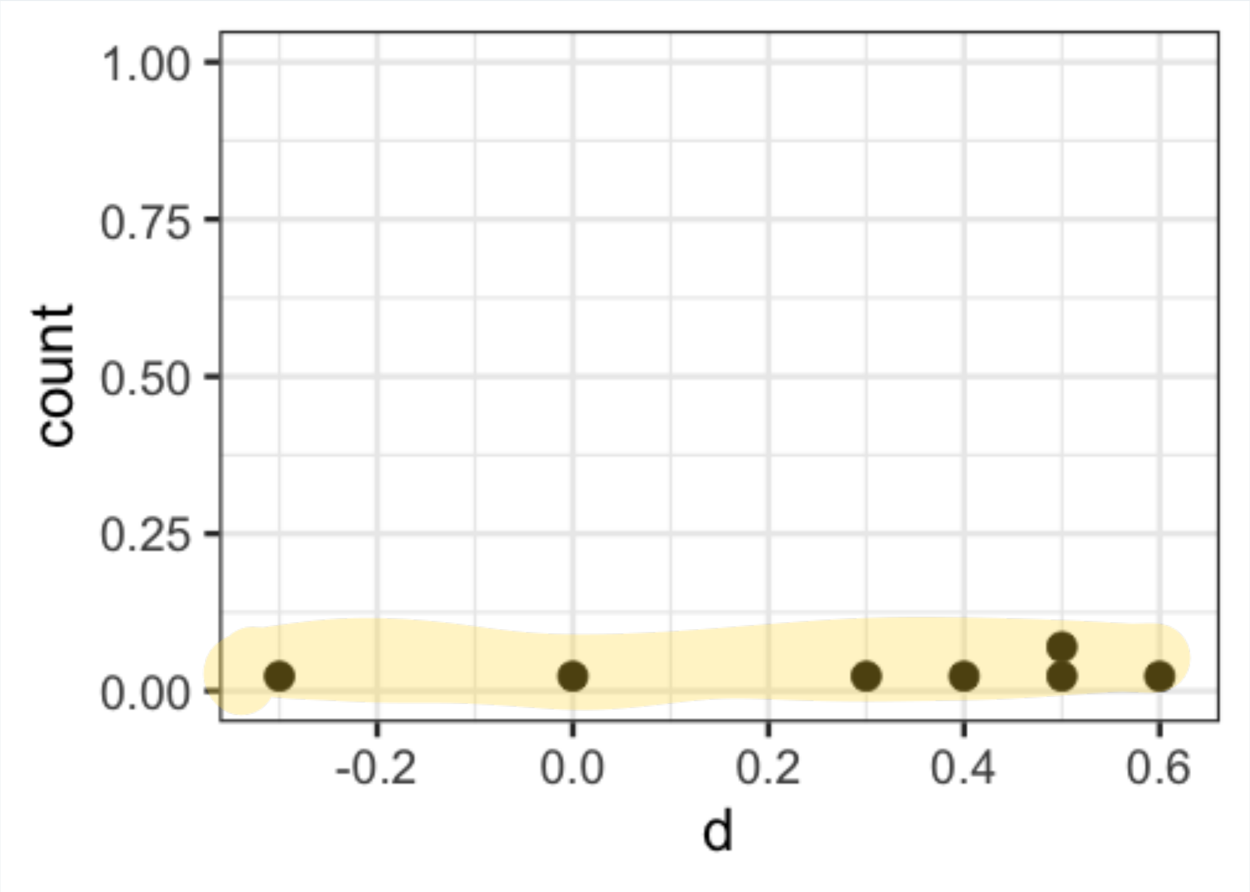
Patient	Adren	Synth	d	Sign
1	3.5	3.2	-0.3	-
2	2.6	3.1	0.5	+
3	3.0	3.3	0.3	+
4	1.9	2.4	0.5	+
5	2.9	2.9	0.0	NA
6	2.4	2.8	0.4	+
7	2.0	2.6	0.6	+

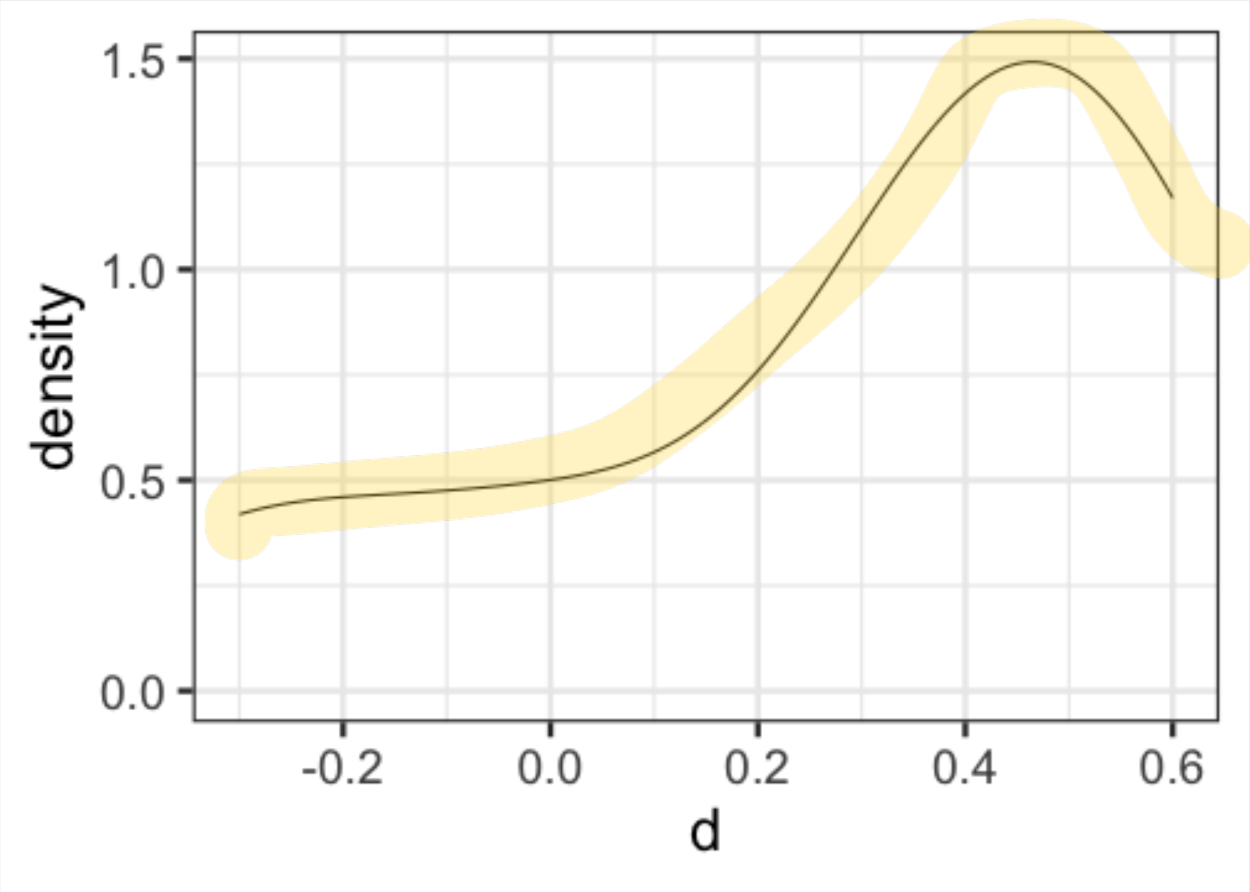
$n=6$

- **d** is the difference in reduction of pressure: **Synth - Adren**
- **Sign** is
  - + if the difference is positive and
  - − if the difference is negative

Visualize the differences

Visualize the differences in reduction of pressure d : **Synth - Adren**





Hypotheses & "statistic" (Sign test)

Hypotheses

H_0 : The median difference in the population is 0
H_a : The median difference in the population is NOT 0

Patient	Adren	Synth	d	Sign
1	3.5	3.2	-0.3	-
2	2.6	3.1	0.5	+
3	3.0	3.3	0.3	+
4	1.9	2.4	0.5	+
~~5~~	~~2.9~~	~~2.9~~	~~0.0~~	~~NA~~
6	2.4	2.8	0.4	+
7	2.0	2.6	0.6	+

"Statistic"

D^+ = number of positive differences
D^- = number of negative differences

What are D^+ and D^- for our example?

$D^+ = 5$

$D^- = 1$

Exact p-value (Sign test)

- If the median difference is 0 (H_0 is true) , then
  - half the population consists of positive differences
  - while half have negative differences.
- Let $p = P(\text{neg. diff.}) = P(\text{pos. diff.}) = 0.5$

- If the median difference is 0 (H_0 is true),
  - then a sample of n differences
    - behaves like n trials in a binomial experiment
    - where "success" is analogous to seeing a positive difference.
  - By symmetry ($p = 0.5$), the same distribution applies to negative differences, i.e.,

$$D^+ \text{ and } D^- \sim \text{Bin}(n, p = 0.5)$$

- Thus the (exact) p-value is calculated using the Binomial distribution

Glaucoma example (exact) p-value

$\binom{n}{k} p^k (1-p)^{n-k}$

$\binom{n}{k} .5^k (.5)^{n-k} = \binom{n}{k} .5^n$

- 7 differences:
  - 1 negative (D^-)
  - 5 were positive (D^+) $P(D^+ \geq 5)$
  - 1 difference is 0 and is discarded
- Thus the effective sample size is $n = 6$.

$D^- \sim \text{Bin}(n = 6, p = 0.5)$

$\binom{n}{k} = \frac{n!}{k!(n-k)!} = \binom{n}{n-k}$

$$p - value = P(D^- \leq 1)$$

$$= P(D^- = 0) + P(D^- = 1)$$

$$= \frac{6!}{0!6!}(0.5)^6 + \frac{6!}{1!5!}(0.5)^6$$

$$\approx 0.1094$$

One-sided p-value = probability that we would see 1 or fewer negative signs among the $n = 6$ differences, if the median difference is really 0

Two-sided p-value = 2 × One-sided p-value

$$p - value \times 2 \approx 0.2188$$

```
# 2-sided p-value: 2*P(D^- <= 1)
2*pbinom(1, size = 6, p = 0.5)
```

≤ 1

```
## [1] 0.21875
```

Sign test in R: Glaucoma example

Below we create the dataset as a tibble (and add the signs):

```
IOP <- tibble(
  Patient = 1:7,
  Adren = c(3.5, 2.6, 3, 1.9, 2.9, 2.4, 2),
  Synth = c(3.2, 3.1, 3.3, 2.4, 2.9, 2.8, 2.6)
  ) %>%
  mutate(d = Synth - Adren,
    Sign = case_when(
      d < 0 ~ "-",
      d > 0 ~ "+"))
```

```
IOP %>% gt()
```

Patient	Adren	Synth	d	Sign
1	3.5	3.2	-0.3	-
2	2.6	3.1	0.5	+
3	3.0	3.3	0.3	+
4	1.9	2.4	0.5	+
5	2.9	2.9	0.0	NA
6	2.4	2.8	0.4	+
7	2.0	2.6	0.6	+

Recall we're testing the population median.
Here's the sample median:

```
median(IOP$d)
```

```
## [1] 0.4
```

Sign test in R: Glaucoma example (specifying both columns)

```
library(BSDA)  # new package!! Make sure to first install it
# Can't "tidy" the output
SIGN.test(x = IOP$Synth, y = IOP$Adren, alternative = "two.sided", conf.level = 0.95)
```

Don't need to specify paired.

```
##
##  Dependent-samples Sign-Test
##
## data:  IOP$Synth and IOP$Adren
## S = 5, p-value = 0.2187
## alternative hypothesis: true median difference is not equal to 0
## 95 percent confidence interval:
##  -0.2057143  0.5685714
## sample estimates:
## median of x-y
##           0.4
##
## Achieved and Interpolated Confidence Intervals:
##
##                   Conf.Level  L.E.pt U.E.pt
## Lower Achieved CI     0.8750  0.0000 0.5000
## Interpolated CI       0.9500 -0.2057 0.5686
## Upper Achieved CI     0.9844 -0.3000 0.6000
```

$S = D^+$

Sign test in R: Glaucoma example (specifying differences)

```
# Note output calls this a "One-sample Sign-Test"
SIGN.test(x = IOP$d, alternative = "two.sided", conf.level = 0.95)
```

```
##
##      One-sample Sign-Test
##
## data:  IOP$d
## s = 5, p-value = 0.2187
## alternative hypothesis: true median is not equal to 0
## 95 percent confidence interval:
##  -0.2057143  0.5685714
## sample estimates:
## median of x
##         0.4
##
## Achieved and Interpolated Confidence Intervals:
##
##                   Conf.Level  L.E.pt U.E.pt
## Lower Achieved CI     0.8750  0.0000 0.5000
## Interpolated CI       0.9500 -0.2057 0.5686
## Upper Achieved CI     0.9844 -0.3000 0.6000
```

Conclusion

Recall the hypotheses to the sign test:

H_0 : The median population difference in reduction of intraocular pressure in treatment with adrenaline vs. new synthetic drug is 0.

H_a : The median population difference in reduction of intraocular pressure in treatment with adrenaline vs. new synthetic drug is NOT 0.

- Significance level: α = 0.05
- p-value = 0.2188 > .05 → FtR

Conclusion:

The median difference in reduction of intraocular pressure between eyes being treated with the synthetic drug and adrenaline for seven glaucoma patients was 0.4 (95% CI: -0.2, 0.6). There is insufficient evidence the reduction in intraocular pressure differs when using the synthetic drug and adrenaline (2-sided sign test p-value = 0.219).

Sign test with large samples: p-value normal approximation

- If the sample size is large, say greater than 20,
    - then binomial probabilities can be approximated using normal probabilities
- Normal approximation:

$$\mu = np = n(0.5) = n/2$$
$$\sigma = \sqrt{np(1-p)} = \sqrt{n(0.5)(0.5)} = \sqrt{n}/2$$

- Thus we have the test statistic:

$$z = \frac{D^{-} - n/2}{\sqrt{n}/2}$$

- With access to a computer, it's better to use the exact binomial probabilities instead of the normal approximation.

Sign test with one sample

- One can use the sign test when testing just one sample.
- Note that we did this when in R, when running the sign test using just the differences.
- For one sample, we can specify the null population median value:

H_0 : The population median is m
H_a : The population median is NOT m

Example: Run sign test for paired data with null $m = 0.7$:

```
SIGN.test(x = IOP$d, md = 0.7, alternative = "two.sided", conf.level = 0.95)
```

```
##
##      One-sample Sign-Test
##
## data:  IOP$d
## s = 0, p-value = 0.01563
## alternative hypothesis: true median is not equal to 0.7
## 95 percent confidence interval:
##  -0.2057143  0.5685714
## sample estimates:
## median of x
```

0.4

(Wilcoxon) Signed-rank test

For paired data or single samples;
accounts for sizes of differences

(Wilcoxon) Signed-rank test

- Like the sign test, the (Wilcoxon) signed-rank test is used for
  - paired samples (i.e., a single set of differences) or
  - a one-sample comparison against a specified value
- However, this test *does* make use of information concerning the size of the differences.

Hypotheses

H_0 : the population is **symmetric around some value** $\tilde{\mu}_0$
H_a : the population is **not symmetric around some value** $\tilde{\mu}_0$

Don't have to be normal.

- Even if the population has a mean/median equal to $\tilde{\mu}_0$, the test may reject the null if the population isn't symmetric, thus only use if the data (differences) are symmetric.
- If the population is symmetric
  - then the mean and median coincide,
  - thus often the null hypothesis is phrased in terms of the median difference being 0

Example: calculate signed ranks

- Rank the absolute values of the differences from smallest to largest
- For ties, take the average of the highest and lowest tied ranks
  - I.e. if ranks 3-7 are tied, then assign (3+7)/2 = 5 as the rank
- Then calculate the signed ranks as +/- the rank depending on whether the sign is +/-

```
IOP_ranks <- IOP %>%
  mutate(abs_d = abs(d)) %>%
  arrange(abs_d) %>%
  mutate(
    Rank = c(NA, 1.5, 1.5, 3, 4.5, 4.5, 6),
    Signed_rank = case_when(
      d < 0 ~ -Rank,
      d > 0 ~ Rank))
```

```
IOP_ranks %>% gt()
```

Patient	Adren	Synth	d	Sign	abs_d	Rank		Signed_rank
~~5~~	~~2.9~~	~~2.9~~	~~0.0~~	~~NA~~	~~0.0~~	~~NA~~		~~NA~~
1	3.5	3.2	-0.3	-	0.3	1.5	1,2	-1.5
3	3.0	3.3	0.3	+	0.3	1.5	1,2	1.5
6	2.4	2.8	0.4	+	0.4	3.0	3	3.0
2	2.6	3.1	0.5	+	0.5	4.5	4,5	4.5
4	1.9	2.4	0.5	+	0.5	4.5	4,5	4.5
7	2.0	2.6	0.6	+	0.6	6.0	6	6.0

Test statistic (Wilcoxon) Signed-rank test

If the null is true:

- The population is symmetric around some point ($\tilde{\mu}_0 = 0$, typically), and
- The **overall size of the positive ranks should be about the same as the overall size of negative ranks**.

Note:

- The sum of the ranks $1, 2, \ldots, n$ is always $n(n+1)/2$,
- which can be broken down as the
  - sum of the positive ranks (T^+)
  - plus the sum of the negative ranks (T^-)

Thus, any of the following can be used as a test statistic and will lead to the same conclusion:

- T^+
- T^-
- T^+ - T^-
- $T_{min} = \min(T^+, T^-)$

Example: calculate sums of signed ranks

```
IOP_ranks %>% gt()
```

Patient	Adren	Synth	d	Sign	abs_d	Rank	Signed_rank
~~5~~	~~2.9~~	~~2.9~~	~~0.0~~	~~NA~~	~~0.0~~	~~NA~~	~~NA~~
1	3.5	3.2	-0.3	-	0.3	1.5	-1.5
3	3.0	3.3	0.3	+	0.3	1.5	1.5
6	2.4	2.8	0.4	+	0.4	3.0	3.0
2	2.6	3.1	0.5	+	0.5	4.5	4.5
4	1.9	2.4	0.5	+	0.5	4.5	4.5
7	2.0	2.6	0.6	+	0.6	6.0	6.0

- Sum of the positive ranks
  - T^+ = 1.5 + 3 + 4.5 + 4.5 + 6 = 19.5
- Sum of the negative ranks
  - T^- = -1.5
- The sum of the ranks $1, 2, \ldots, n$ is always $n(n+1)/2$:
  - $n(n+1)/2 = 6(7)/2 = 21$
  - $T^+ + |T^-| = 19.5 + |-1.5| = 21$

Exact p-value (Wilcoxon) Signed-rank test (fyi) (1/2)

- **Exact p-value** is preferable
  - This is the default method in R's `wilcox.test()`
    - if the samples contain less than 50 finite values
    - and **there are no ties**
      - *R will automatically use normal approximation method if there are ties*
- *We will not be calculating the exact p-value "by hand." We will be using R for this.*

$$p - value = 2 * P(\min(T^+, T^-) \leq t)$$

- t is the smaller of the calculated sums of the positive and negative ranks
- To calculate the exact p-value, we need the probability of each possible sum of ranks.

Exact p-value (Wilcoxon) Signed-rank test (fyi) (2/2)

- To calculate the exact p-value, we need the probability of each possible sum of ranks:
  - list all possible combinations of positive and negative ranks for the sample size,
  - calculate the sum of the positive ranks (T^+) for each possible combination (or T^-), and
  - then figure out the probability of each possible T^+ (assuming all combinations are equally likely)

Example when $n = 3$: (from https://online.stat.psu.edu/stat415/lesson/20/20.2)

	1	-1	1	1	-1	-1	1	-1
T^+, T^-	2	2	-2	2	-2	2	-2	-2
	3	3	3	-3	3	-3	-3	-3
W	6	5	4	$\boxed{3}$	$\boxed{3}$	2	1	0
	T^+	T^+						T^+

- $P(W = 0) = 1/8$, because there is only one way that $W = 0$
- $P(W = 1) = 1/8$, because there is only one way that $W = 1$
- $P(W = 2) = 1/8$, because there is only one way that $W = 2$
- $P(W = 3) = 2/8$, because there are two ways that $W = 3$
- $P(W = 4) = 1/8$, because there is only one way that $W = 4$
- $P(W = 5) = 1/8$, because there is only one way that $W = 5$
- $P(W = 6) = 1/8$, because there is only one way that $W = 6$

See https://online.stat.psu.edu/stat415/lesson/20/20.2 for more details.

$T^+ = 2 \rightarrow \mathbb{P}(T^+ \leq 2) = 1/8 + 1/8 + 1/8 = 3/8$

Normal approx. p-value (Wilcoxon) Signed-rank test (fyi)

- **Normal approximation** method:
  - If the number of non-zero differences is at least 16, then a normal approximation can be used.
  - Have the option to apply a continuity correct (default) or not
- *We will not be calculating the p-value "by hand." We will be using R for this.*

Test statistic:

$$Z_{T_{min}} = \frac{T_{min} - \frac{n(n+1)}{4}}{\sqrt{\frac{n(n+1)(2n+1)}{24}}}$$

- $T_{min} = \min(T^+, T^-)$
- n = sample size
- Test statistic $Z_{T_{min}}$ follows a standard normal distribution $N(0,1)$
- Use normal distribution to calculate p-value

See https://online.stat.psu.edu/stat415/lesson/20/20.2 for more details.

(Wilcoxon) Signed-rank test in R: Glaucoma example

"Attempt" with exact p-value & specifying columns for paired data

```
# Exact p-value
wilcox.test(x = IOP$Synth, y = IOP$Adren, paired = TRUE,
    alternative = c("two.sided"), mu = 0,
    exact = TRUE)
```

```
## Warning in wilcox.test.default(x = IOP$Synth, y = IOP$Adren, paired = TRUE, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(x = IOP$Synth, y = IOP$Adren, paired = TRUE, :
## cannot compute exact p-value with zeroes
```

```
##
##     Wilcoxon signed rank test with continuity correction
##
## data:  IOP$Synth and IOP$Adren
## V = 19.5, p-value = 0.07314
## alternative hypothesis: true location shift is not equal to 0
```

Normal approx.

(Wilcoxon) Signed-rank test in R: Glaucoma example

"Attempt" with exact p-value & running one sample test with differences

```
# Exact p-value
wilcox.test(x = IOP$d,
        alternative = c("two.sided"), mu = 0,
        exact = TRUE, correct = TRUE)
```

null value

```
## Warning in wilcox.test.default(x = IOP$d, alternative = c("two.sided"), :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(x = IOP$d, alternative = c("two.sided"), :
## cannot compute exact p-value with zeroes
```

```
##
##     Wilcoxon signed rank test with continuity correction
##
## data:  IOP$d
## V = 19.5, p-value = 0.07314
## alternative hypothesis: true location is not equal to 0
```

(Wilcoxon) Signed-rank test in R: Glaucoma example

"Attempt" with approximate p-value & specifying columns for paired data

```
# Normal approximation with continuity correction
wilcox.test(x = IOP$Synth, y = IOP$Adren, paired = TRUE,
        alternative = c("two.sided"), mu = 0,
        exact = FALSE, correct = TRUE)
```

```
##
##     Wilcoxon signed rank test with continuity correction
##
## data:  IOP$Synth and IOP$Adren
## V = 19.5, p-value = 0.07314
## alternative hypothesis: true location shift is not equal to 0
```

No more warnings!! However,... should we be using the normal approximation here?

Conclusion

Recall the hypotheses to the (Wilcoxon) Signed-rank test:

H_0 : the population difference in reduction of intraocular pressure in treatment with adrenaline vs. new synthetic drug is **symmetric around** $\tilde{\mu}_0 = 0$
H_a : the population difference in reduction of intraocular pressure in treatment with adrenaline vs. new synthetic drug is **not symmetric around** $\tilde{\mu}_0 = 0$

- Significance level: $\alpha = 0.05$
- p-value = 0.07314 Normal approx. (ties → not exact)

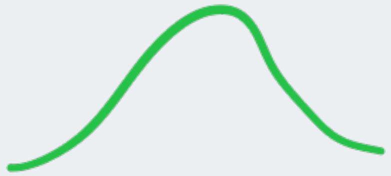
$> .05$

Conclusion:

There is insufficient evidence the differences in reduction in intraocular pressure differs between the synthetic drug and adrenaline are symmetric about 0 (2-sided Wilcoxon signed rank test p-value = 0.07314)

However,...

$n \geq 16$ $(n = 6)$



Need symmetric data → skewed left

Sign test
(wilcoxon) sign-rank test } 1-sample or paired samples

Wilcoxon rank-sum test

For two independent samples
a.k.a Mann-Whitney U test

Wilcoxon rank-sum test

- The nonparametric alternative to the two-sample t-test
  - used to analyze two samples selected from separate (independent) populations
- Also called the Mann-Whitney U test.

- Unlike the signed-rank test, there is no need to assume symmetry

- Necessary **condition** is that the two populations being compared
  - have the **same shape** (both right skewed, both left skewed, both symmetric, etc.),
  - so any noted difference is due to a shift in the median

- Since they have the same shape, when summarizing the test, we can describe the results in terms of a difference in medians.

Hypotheses:

H_0 : the two populations have the same median
H_a : the two populations do NOT have the same median

Example

Dr. Priya Chaudhary (OHSU) examined the evoked membrane current of dental sensory neurons (in rats) under control conditions and a mixture of capsaicin plus capsazepine (CPZ). J. Dental Research} 80:1518--23, 2001.

```
CPZdata <- tibble(
  control = c(3024, 2164, 864, 780, 125, 110),
  cap_CPZ = c(426, 232, 130, 94, 75, 55)
  )

CPZdata %>%
  get_summary_stats(type = "median") %>%
  gt()
```

variable	n	median
control	6	822
cap_CPZ	6	112

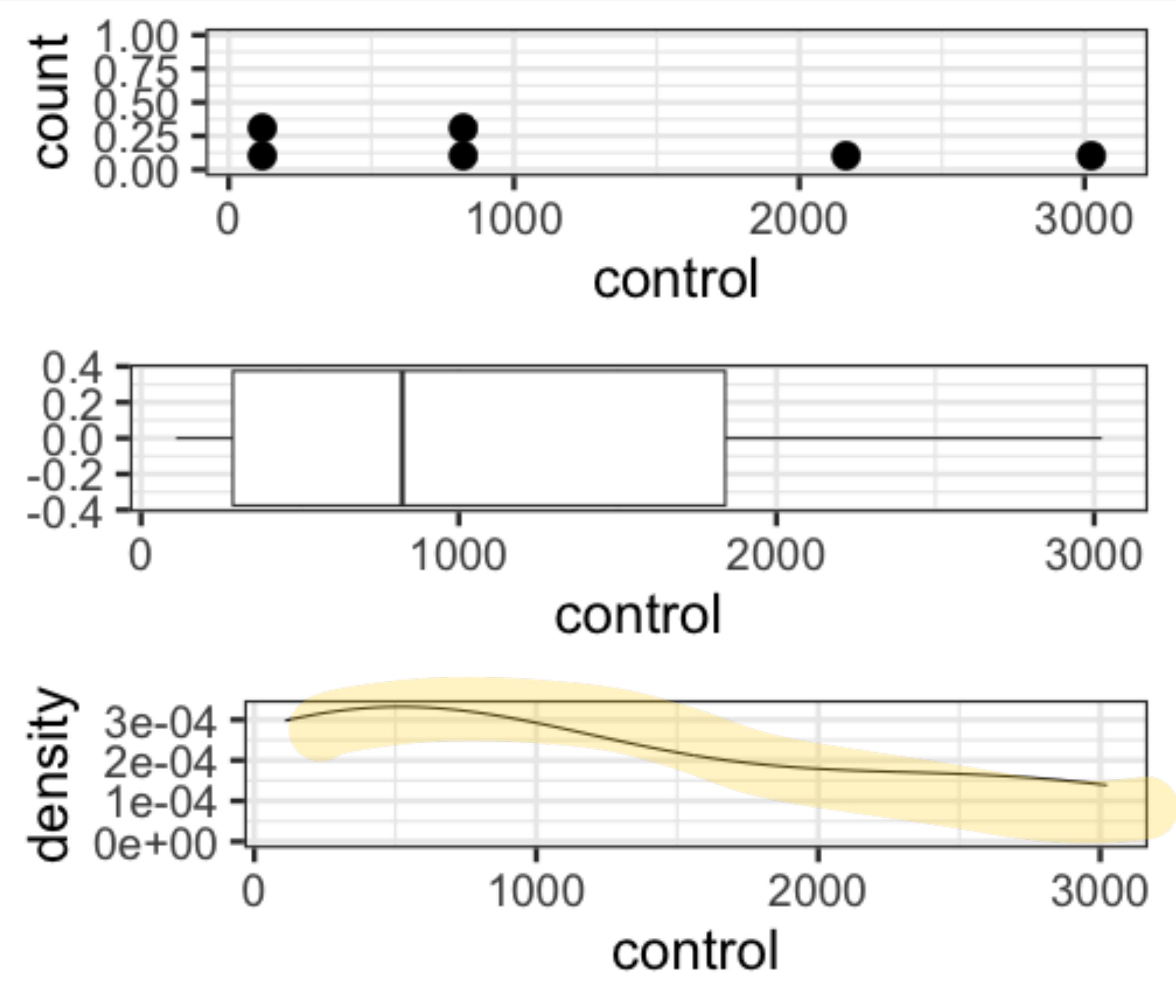
```
CPZdata %>% gt()
```

control	cap_CPZ
3024	426
2164	232
864	130
780	94
125	75
110	55

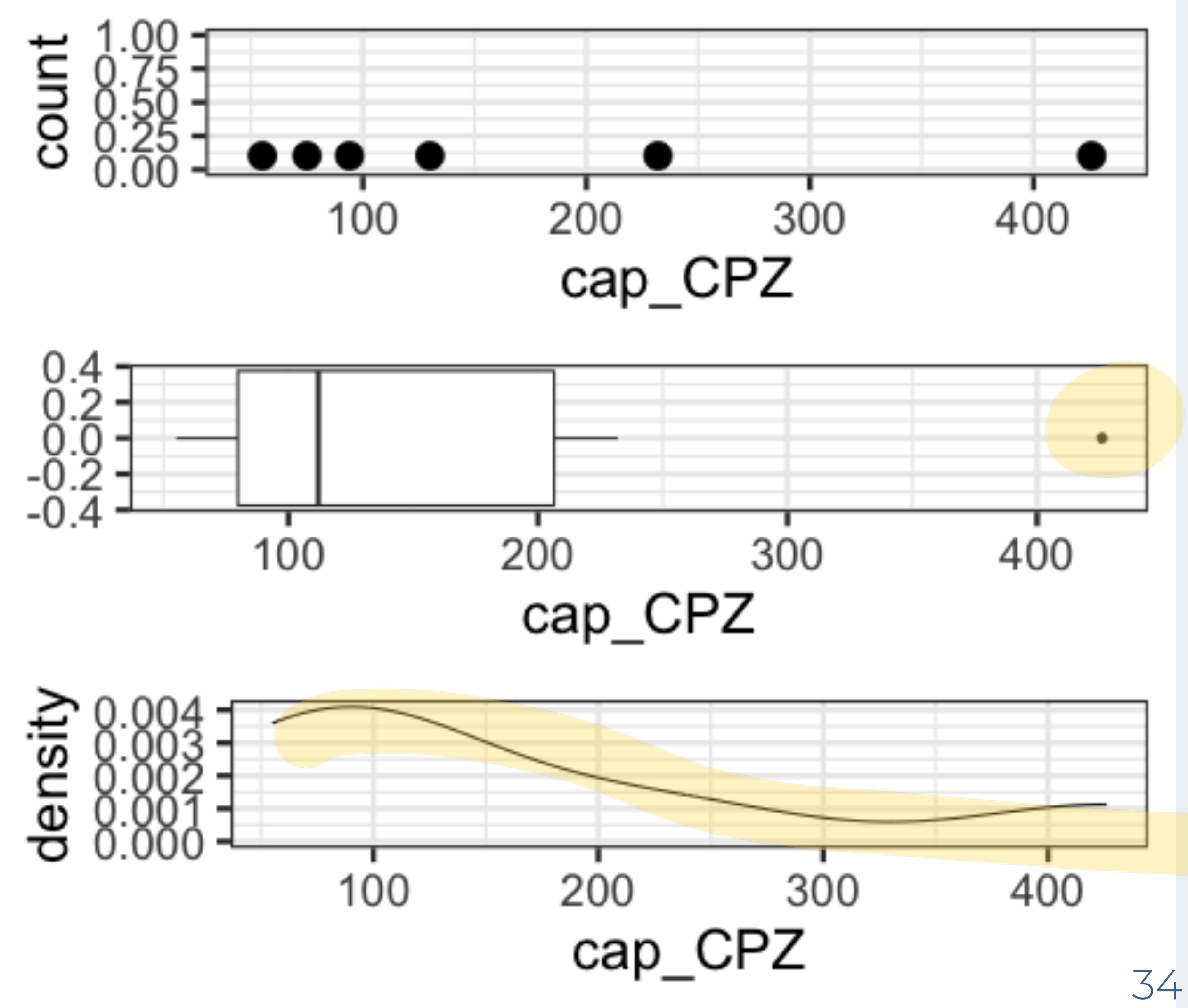
Visualize the data

Do the independent samples have the same distribution?

Control group



Cap + CPZ group



Calculating ranks and test statistic W

1. Combine the two samples together (keep track of which observations came from each sample).
2. Rank the full set of $N = n_1 + n_2$ observations.
   - If ties exist, assign average ranks to the tied values (as with the signed-rank test).
3. Sum the ranks corresponding to those observations from the smaller sample.
   - This is a time-saving step; you could also have used the larger sample.
   - Call this sum W.

$$W_{CPZ} = 1 + 2 + 3 + 6 + 7 + 8 = 27$$

$$W_{control} = 4 + 5 + 9 + 10 + 11 + 12 = 51$$

Group	Current	Rank
cap_CPZ	55	1
cap_CPZ	75	2
cap_CPZ	94	3
control	110	4
control	125	5
cap_CPZ	130	6
cap_CPZ	232	7
cap_CPZ	426	8
control	780	9
control	864	10
control	2164	11
control	3024	12

In our example, both groups have equal n; choose either for computing W.

Exact p-value approach (fyi)

- **If n_1, n_2 are both less than 10, then use an exact test**,
  - otherwise use the large-sample normal approximation.
  - However, exact method can only be done if **no ties** are present
- p-value is the probability of getting a rank sum W as extreme or more extreme than the observed one.
  - Multiply the 1-tail probability by 2 for the 2-tailed probability

$$p - value = 2 \cdot P(W_{CPZ} \leq 27)$$

- To calculate $P(W_{CPZ} \leq 27)$,
  - we need to enumerate all possible sets ranks for the sample size,
  - calculate the sum of ranks for each set of possible ranks,
  - and then the probability for each sum (assuming each set of ranks is equally likely).

- *We will not be calculating the p-value "by hand." We will be using R for this.*

Normal approximation approach (fyi)

If the null hypothesis is true, then the mean of the sum of the ranks from the smaller-sized group will be

$$\mu_W = \frac{n_s \cdot (n_s + n_l + 1)}{2},$$

with a standard deviation of

$$\sigma_W = \sqrt{\frac{n_s \cdot n_l \cdot (n_s + n_l + 1)}{12}}.$$

Provided both groups are large (≥ 10),

$$Z = \frac{W - \mu_W}{\sigma_W} \approx Normal(0, 1)$$

Example:

We have $W = 27$ and $n_l = n_s = 6$:

$$\mu_W = \frac{6 \cdot (6 + 6 + 1)}{2} = 39$$

$$\sigma_W = \sqrt{\frac{6 \cdot 6 \cdot (6 + 6 + 1)}{12}} = \sqrt{39} \approx 6.2450$$

$$z \approx \frac{27 - 39}{6.2450} = -1.921538$$

The two-sided p-value is

$$p = 2 \cdot P(Z < -1.921538) = 0.05466394$$

R code for creating ranks on previous slide

```
CPZdata
```

```
## # A tibble: 6 × 2
##   control cap_CPZ
##     <dbl>   <dbl>
## 1    3024     426
## 2    2164     232
## 3     864     130
## 4     780      94
## 5     125      75
## 6     110      55
```

```
CPZdata_long <- CPZdata %>%
  pivot_longer(cols = c(control,cap_CPZ),
               names_to = "Group",
               values_to = "Current") %>%
  arrange(Current) %>%
  mutate(Rank = 1:12)
```

```
CPZdata_long %>% gt()
```

Group	Current	Rank
cap_CPZ	55	1
cap_CPZ	75	2
cap_CPZ	94	3
control	110	4
control	125	5
cap_CPZ	130	6
cap_CPZ	232	7
cap_CPZ	426	8
control	780	9
control	864	10
control	2164	11
control	3024	12

Wilcoxon rank-sum test in R: with wide data

```
glimpse(CPZdata)
```

```
## Rows: 6
## Columns: 2
## $ control <dbl> 3024, 2164, 864, 780, 125, 110
## $ cap_CPZ <dbl> 426, 232, 130, 94, 75, 55
```

Exact p-value

default:
paired =FALSE

```
wilcox.test(x = CPZdata$cap_CPZ, y = CPZdata$control,
            alternative = c("two.sided"), mu = 0,
            exact = TRUE)
```

```
##
##      Wilcoxon rank sum exact test
##
## data:  CPZdata$cap_CPZ and CPZdata$control
## W = 6, p-value = 0.06494
## alternative hypothesis: true location shift is not equal to 0
```

Wilcoxon rank-sum test in R: with wide data

Normal approximation p-value without CC

```
wilcox.test(x = CPZdata$cap_CPZ, y = CPZdata$control,
    alternative = c("two.sided"), mu = 0,
    exact = FALSE, correct = FALSE) %>% tidy() %>% gt()
```

statistic	p.value	method	alternative
6	0.05466394	Wilcoxon rank sum test	two.sided

Normal approximation p-value with CC

```
wilcox.test(x = CPZdata$cap_CPZ, y = CPZdata$control,
    alternative = c("two.sided"), mu = 0,
    exact = FALSE, correct = TRUE) %>% tidy() %>% gt()
```

statistic	p.value	method	alternative
6	0.06555216	Wilcoxon rank sum test with continuity correction	two.sided

Wilcoxon rank-sum test in R: with long data

Make data long (if it's not already long):

```
CPZdata_long <- CPZdata %>%
  pivot_longer(cols = c(control,cap_CPZ),
               names_to = "Group",
               values_to = "Current")

head(CPZdata_long)
```

```
## # A tibble: 6 × 2
##   Group   Current
##   <chr>     <dbl>
## 1 control    3024
## 2 cap_CPZ     426
## 3 control    2164
## 4 cap_CPZ     232
## 5 control     864
## 6 cap_CPZ     130
```

Exact p-value RV ~ EV

```
wilcox.test(Current ~ Group,
            data = CPZdata_long,
            alternative = c("two.sided"),
            mu = 0,
            exact = TRUE) %>%
  tidy() %>% gt()
```

statistic	p.value	method	alternative
6	0.06493506	Wilcoxon rank sum exact test	two.sided

Conclusion

Recall the hypotheses to the (Wilcoxon) Signed-rank test:

H_0 : the control and treated populations have the same median
H_a : the control and treated populations do NOT have the same median

- Significance level: α = 0.05
- p-value = 0.06494

Conclusion:

There is suggestive but inconclusive evidence that the evoked membrane current of dental sensory neurons (in rats) differs between the control group and the group exposed to a mixture of capsaicin plus capsazepine (2-sided Wilcoxon rank-sum test p-value = 0.06494).

Kruskal-Wallis test

Nonparametric ANOVA test

Kruskal-Wallis test: nonparametric ANOVA test

- Recall that an ANOVA tests means from more than 2 groups
- Conditions for ANOVA include
  - Sample sizes in each group group are large (each $n \geq 30$),
    - OR the data are relatively normally distributed in each group
  - Variability is "similar" in all group groups
- If these conditions are in doubt, or if the response is ordinal, then the Kruskal-Wallis test is an alternative.

μ $\tilde{\mu}$ $\mu, \hat{\mu}$ sample

$$\begin{aligned} H_0 &: \text{pop median}_1 = \text{pop median}_2 = \ldots = \text{pop median}_k \\ \text{vs. } H_A &: \text{At least one pair pop median}_i \neq \text{pop median}_j \text{ for } i \neq j \end{aligned}$$

- K-W test is an extension of the (Wilcoxon) rank-sum test to more than 2 groups
  - With $k = 2$ groups, the K-W test is the same as the rank-sum test

K-W test statistic: H (fyi)

$$H = \frac{12}{N(N+1)} \sum_{i=1}^{k} \frac{R_i^2}{n_i} - 3(N+1)$$

- k is the number of groups,
- n_i is the number of observations in group i
- $N = n_1 + \ldots + n_k$ is the total number of observations across all groups,
- R_i is the sum of ranks for group i

The test statistic H has a Chi-squared distribution with $k-1$ degrees of freedom:

$$H \sim \chi^2_{k-1}$$

Ranks are calculated similarly to the (Wilcoxon) rank-sum test.

Ranks for the K-W test

1. Combine the k samples together (keep track of which observations came from each sample).
2. Rank the full set of $N = n_1 + \ldots + n_k$ observations.
   - If ties exist, assign average ranks to the tied values (as with the signed-rank test).
3. Then sum the ranks within each of the k groups
   - Label the sums of the ranks for each group as $R_1, \ldots + R_k$.

If H_0 is true, we expect the populations to have the same medians, and thus the ranks to be similar as well.

Example: Ozone levels by month (1/2)

- `airquality` data included in base R - no need to load it
- Daily air quality measurements in New York, May to September 1973.
- Question: do ozone levels differ by month?

```
glimpse(airquality)
```

```
## Rows: 153
## Columns: 6
## $ Ozone   <int> 41, 36, 12, 18, NA, 28, 23, 19, 8, NA, 7, 16, 11, 14, 18, 14, …
## $ Solar.R <int> 190, 118, 149, 313, NA, NA, 299, 99, 19, 194, NA, 256, 290, 27…
## $ Wind    <dbl> 7.4, 8.0, 12.6, 11.5, 14.3, 14.9, 8.6, 13.8, 20.1, 8.6, 6.9, 9…
## $ Temp    <int> 67, 72, 74, 62, 56, 66, 65, 59, 61, 69, 74, 69, 66, 68, 58, 64…
## $ Month   <int> 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5,…
## $ Day     <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,…
```

Example: Ozone levels by month (2/2)

NO

```
Oz_mnth <- airquality %>%
  group_by(Month) %>%
  get_summary_stats(Ozone,
    show = c("n", "mean", "median", "sd"))
Oz_mnth %>% gt()
```

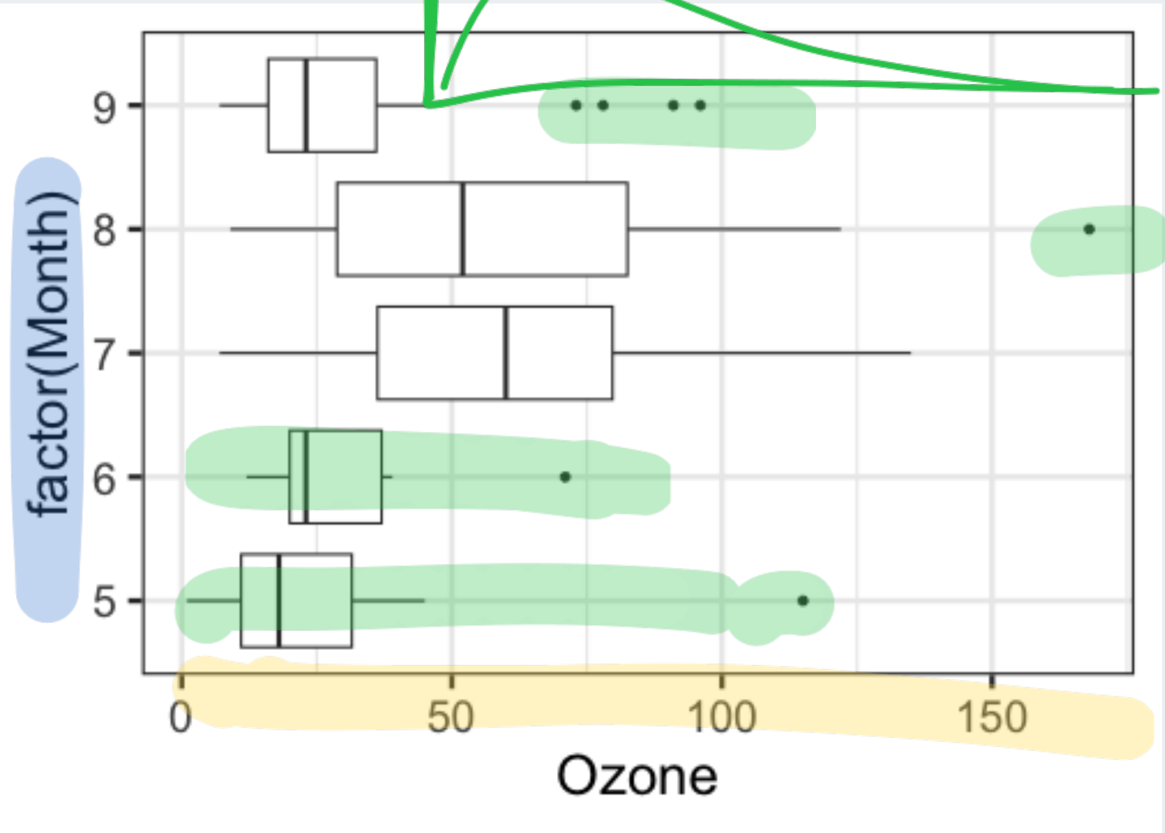
Month	variable	n	mean	median	sd
5	Ozone	26	23.615	18	22.224
6	Ozone	9	29.444	23	18.208
7	Ozone	26	59.115	60	31.636
8	Ozone	26	59.962	52	39.681
9	Ozone	29	31.448	23	24.142

```
max(Oz_mnth$sd) / min(Oz_mnth$sd)
```

```
## [1] 2.179317
```

> 2

```
ggplot(airquality,
       aes(x = Ozone, y = factor(Month))) +
  geom_boxplot()
```



Example: calculate ranks (fyi) (1/2)

```
ranks_Oz_mnth <- airquality %>%
  select(Ozone, Month)

summary(ranks_Oz_mnth)
```

```
##      Ozone             Month      
##  Min.   :  1.00   Min.   :5.000  
##  1st Qu.: 18.00   1st Qu.:6.000  
##  Median : 31.50   Median :7.000  
##  Mean   : 42.13   Mean   :6.993  
##  3rd Qu.: 63.25   3rd Qu.:8.000  
##  Max.   :168.00   Max.   :9.000  
##  NA's   :37
```

```
ranks_Oz_mnth <- ranks_Oz_mnth %>%
  drop_na(Ozone) %>%
  arrange(Ozone) %>%
  mutate(Rank = 1:nrow(.))
```

Ranks below do not take into account ties!!

```
ranks_Oz_mnth
```

```
##       Ozone Month Rank
## 1         1     5    1
## 2         4     5    2
## 3         6     5    3
## 4         7     5    4
## 5         7     7    5
## 6         7     9    6
## 7         8     5    7
## 8         9     8    8
## 9         9     8    9
## 10        9     9   10
## 11       10     7   11
## 12       11     5   12
## 13       11     5   13
## 14       11     5   14
## 15       12     5   15
## 16       12     6   16
```

Example: calculate ranks (fyi) (2/2)

Ranks below do not take into account ties!!

```
ranks_Oz_mnth
```

```
##       Ozone Month Rank
## 1         1     5    1
## 2         4     5    2
## 3         6     5    3
## 4         7     5    4
## 5         7     7    5
## 6         7     9    6
## 7         8     5    7
## 8         9     8    8
## 9         9     8    9
## 10        9     9   10
## 11       10     7   11
## 12       11     5   12
## 13       11     5   13
## 14       11     5   14
## 15       12     5   15
## 16       12     6   16
```

Sum of ranks for each group: (not taking into account ties!!)

```
ranks_Oz_mnth %>%
  group_by(Month) %>%
  summarise(sumRank = sum(Rank))
```

```
## # A tibble: 5 × 2
##   Month sumRank
##   <int>   <int>
## 1     5     939
## 2     6     434
## 3     7    2023
## 4     8    1956
## 5     9    1434
```

R_1
R_2
$\vdots$
R_5

K-W test in R

RV ~ EV   y ~ x

DV ~ IV

```
kruskal.test(Ozone ~ Month, data = airquality)
```

```
## 
##      Kruskal-Wallis rank sum test
## 
## data:  Ozone by Month
## Kruskal-Wallis chi-squared = 29.267, df = 4, p-value = 6.901e-06
```

<.05

```
kruskal.test(Ozone ~ Month, data = airquality) %>% tidy() %>% gt()
```

statistic	p.value	parameter	method
29.26658	6.900714e-06	4	Kruskal-Wallis rank sum test

There is sufficient evidence that the median ozone levels are different in at least two months from May - September, 1973 in New York City ($p < 0.001$; Kruskal-Wallis test).

- (fyi) Since the K-W test is significant, follow-up with pairwise (Wilcoxon) rank-sum tests using a multiple comparison procedure to identify which months have different medians.

Permutation tests & bootstrapping

another option to consider

Permutation tests & bootstrapping

- In some cases we saw that the conditions failed or the sample size was too small for a normal approximation and there were ties in ranks preventing us from using an exact method.
- Another nonparametric option to consider is a permutation test or bootstrapping.
- If you're interested in learning more about this approach, check out the ModernDive Statistical Inference via Data Science book by Chester Ismay and Albert Kim.
    - Ch 7: Sampling
    - Ch 8: Bootstrapping and Confidence Intervals
    - Ch 9: Hypothesis Testing