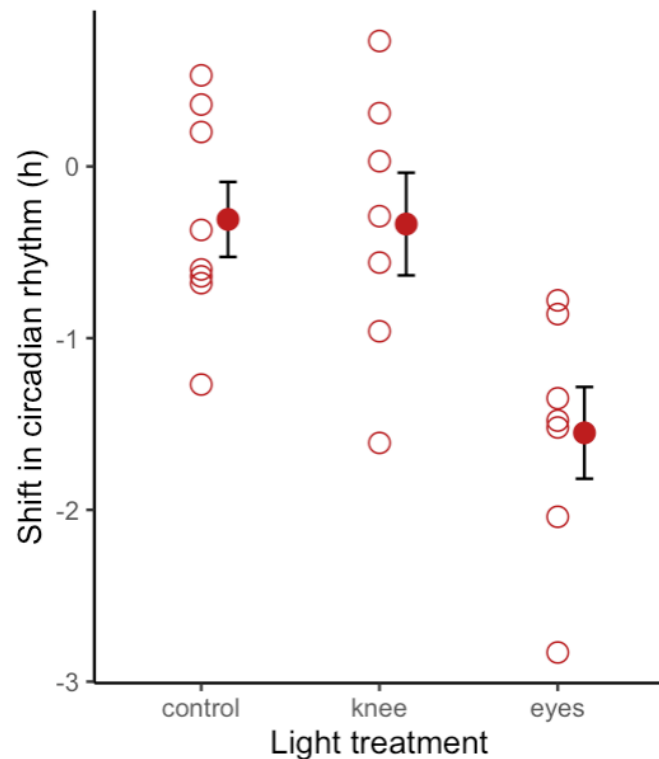# THE ANALYSIS OF VARIANCE (ANOVA)
for comparing multiple sample means (groups or treatments)

H_0: The samples come from statistical populations with the same mean, i.e., $\mu_{control} = \mu_{knee} = \mu_{eyes}$.

H_A: At least two samples come from different statistical populations with different means.

P-value (ANOVA) = 0.00447

Research conclusion: Light treatment influences shifts in circadian rhythm.
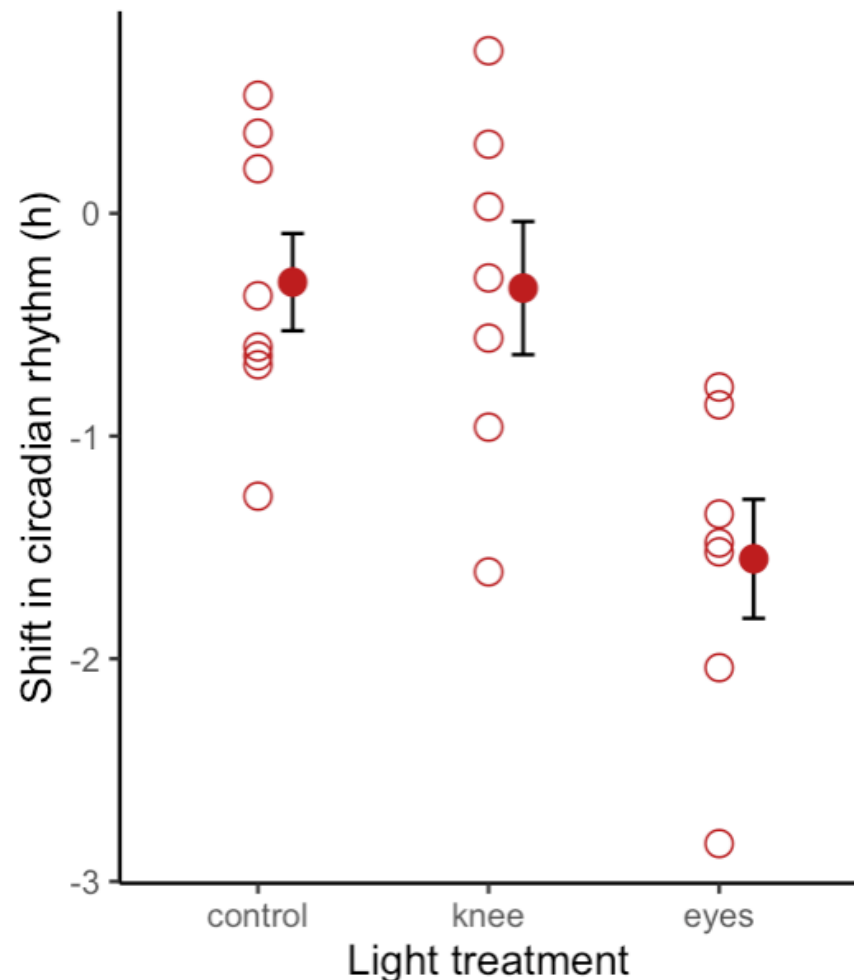
ANOVA

Research conclusion: Light treatment influences shifts in circadian rhythm.

How does light treatment influence shifts in circadian rhythm?

How do we know which group means differ from one another?

Why not simply not contrast all pairs of means using a two-sample mean t-test?

"The knees who say night" Control vs. knee; control vs. eyes; knee vs. eyes?

After ANOVA:

- Multiple testing and post hoc tests.

- The concept of family wise type I error and why we conduct ANOVAs first instead of two-sample t-tests!

Multiple testing survey (BIOL322); anonymous
survey - it will close on Thursday Nov. 10 (5pm)

Results will be used to demonstrate the statistical principles of multiple testing

last number of your street address · Multiple choice

○ Odd number ✕

○ Even number ✕

○ Add option or add "Other"

Required

Your birthday is an odd or even number (the actual day; not month or year) *

○ Odd number

○ Even number

Do you like soccer? *

	1	2	3	4	5	
Deslike	○	○	○	○	○	Love it

Do you like video games? *

	1	2	3	4	5	
Deslike	○	○	○	○	○	Love it

Do you like eating out? *

|	1	2	3	4	5	
Deslike	○	○	○	○	○	Love it

Classroom survey:
Would you expect odd- and even
day born individuals
to differ in their preferences?

Birthday and preferences
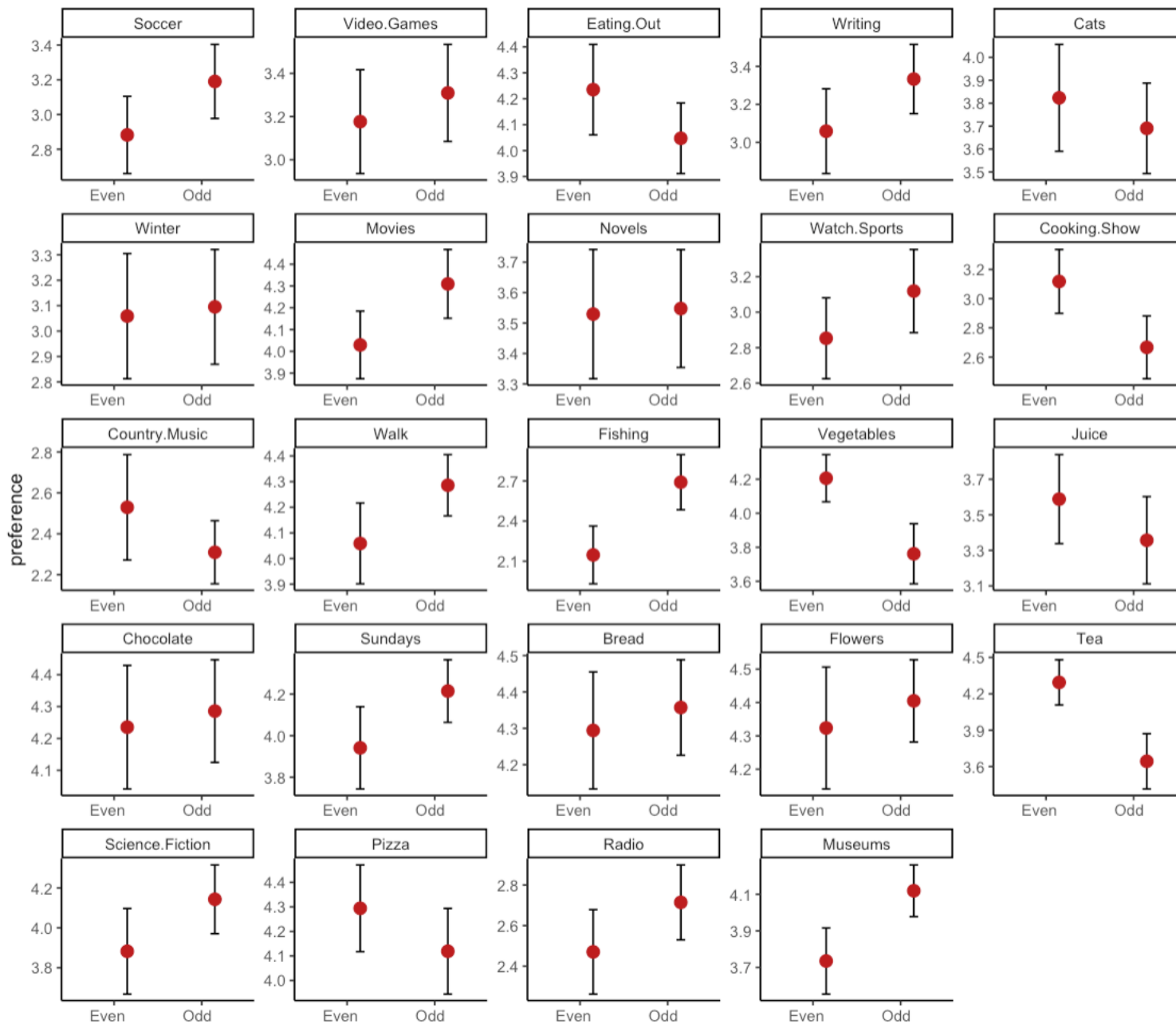
One should not have any theoretical basis for preferences to vary among groups other than by chance alone!

Contrast between odd and even-day born individuals - probability of rejection based on a two-sample t test (odd *versus* even)

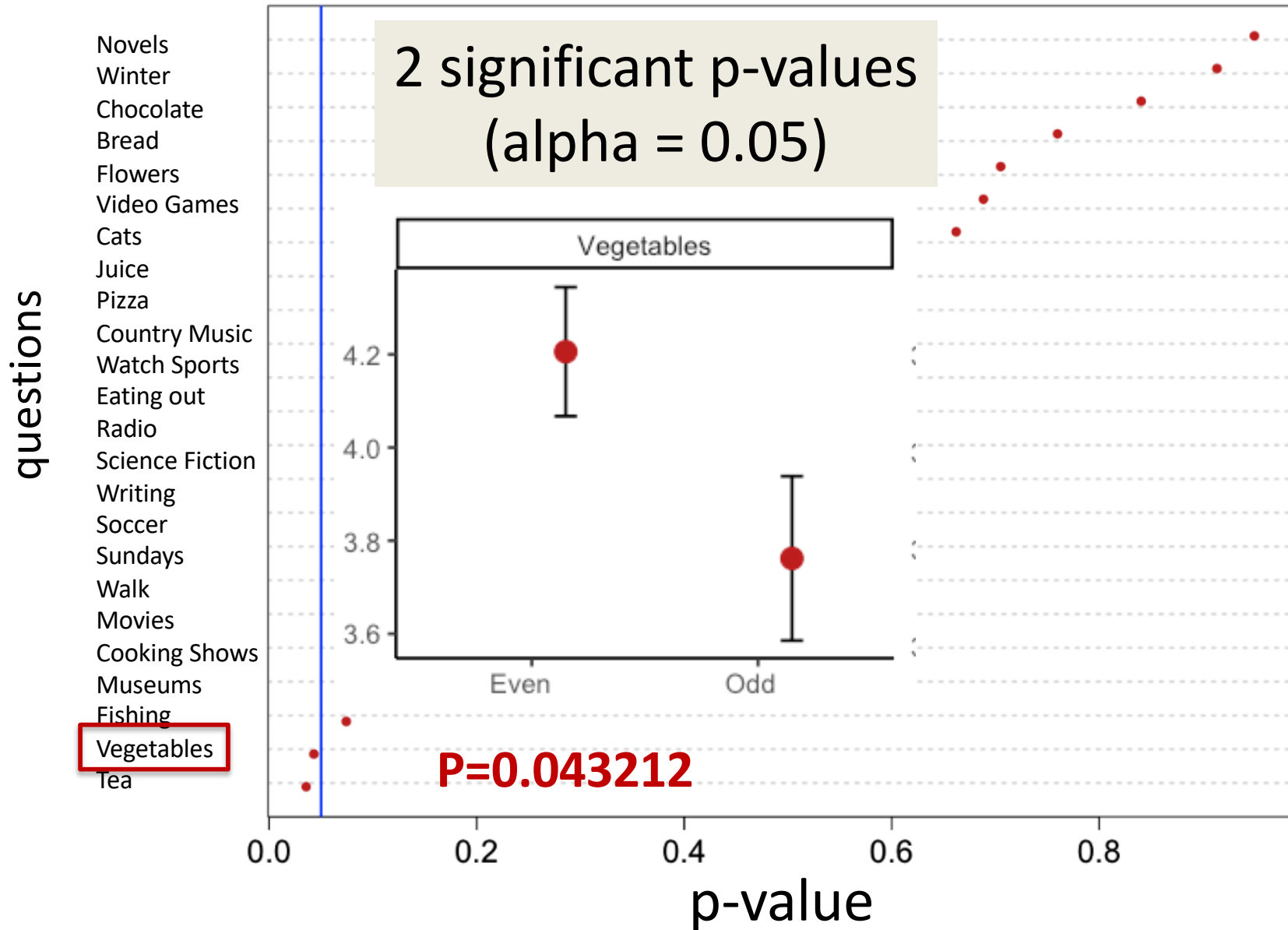2 significant p-values (alpha = 0.05)
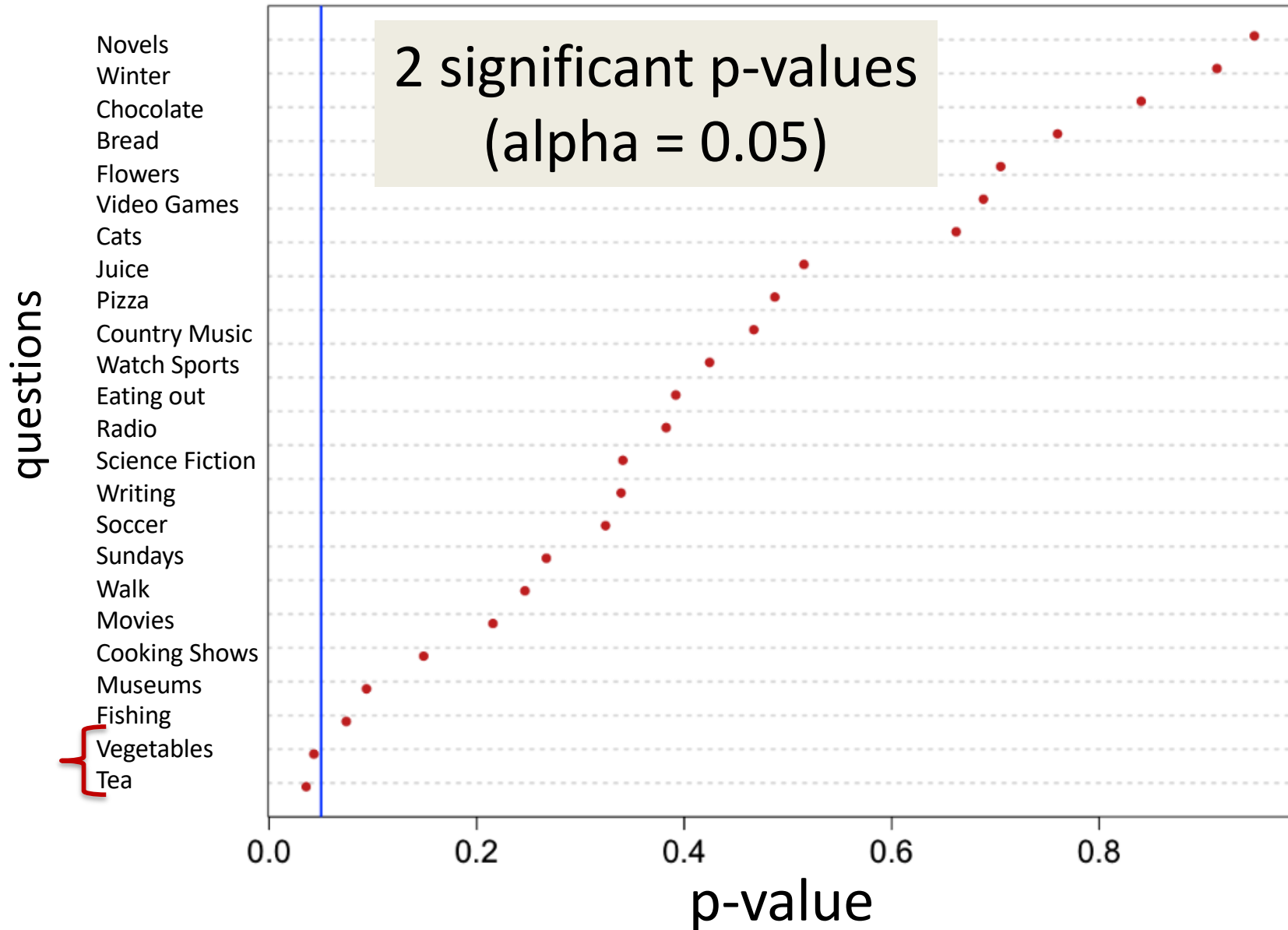
Contrast between odd and even-day born individuals - probability of rejection based on a two-sample t test (odd *versus* even)

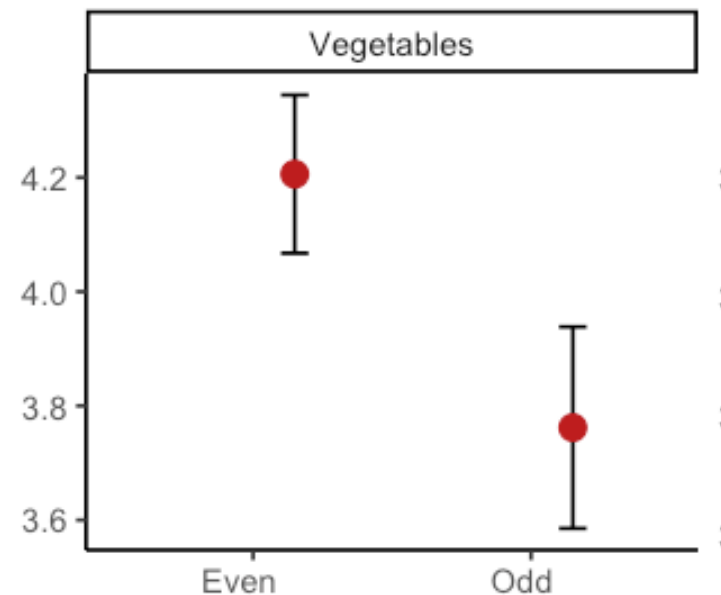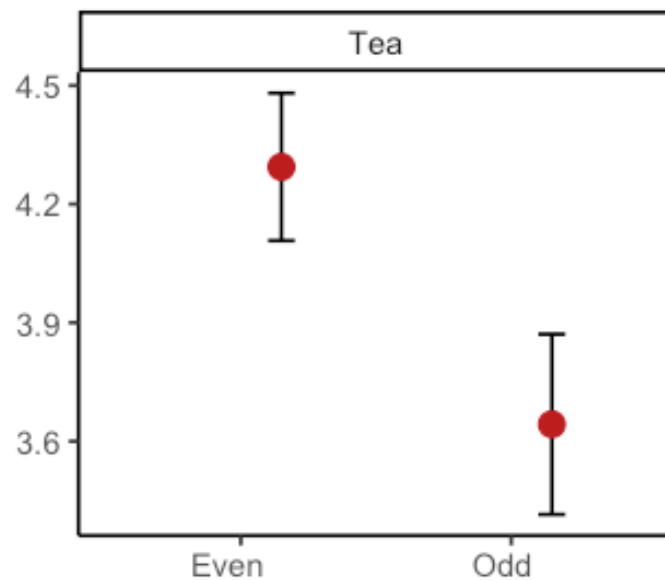Contrast between odd and even-day born individuals - probability of rejection based on a two-sample t test (odd *versus* even)

2 significant p-values (alpha = 0.05)

P=0.043212
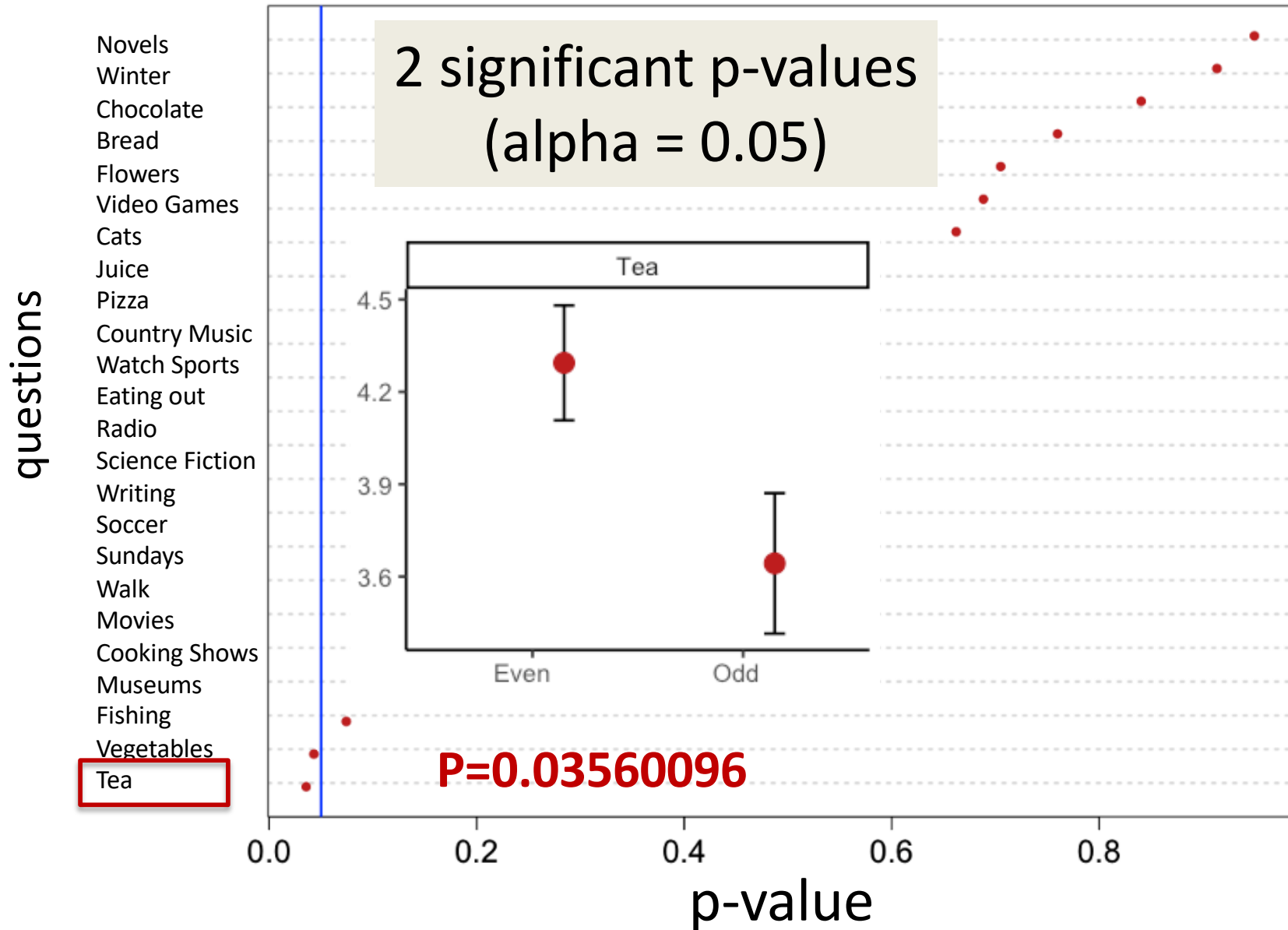
Birthday and Preferences:
We were even able to observe an association between liking tea and liking eating vegetables (in a plausible direction) simply by separating individuals according to their birthdays.

How can that be?

Another example of significance when there should be none

A simulated randomized clinical trial in coronary artery disease was conducted to illustrate the need for clinical judgment and modern statistical methods in assessing therapeutic claims in studies of complex diseases.

In this example, **1073 consecutive**, medically treated coronary artery disease patients from the Duke University data bank were randomized into **two groups**. The groups were reasonably comparable and, as expected, **there was no overall difference in survival between the two groups**.

Another example of significance when there should be none

1073 heart disease patients were **RANDOMLY** placed into two groups; no statistical difference was found in survival (not surprising given that they were randomly placed into groups as an exercise to demonstrate the issues with multiple testing) between the two groups.

1073 patients

536 patients

537 patients

Statistical test contrasting the two groups in terms of their survival was non-significant.

Another example of significance when there should be none

A simulated randomized clinical trial in coronary artery disease was conducted to illustrate the need for clinical judgment and modern statistical methods in assessing therapeutic claims in studies of complex diseases.

In this example, **1073 consecutive**, medically treated coronary artery disease patients from the Duke University data bank were randomized into **two groups**. The groups were reasonably comparable and, as expected, **there was no overall difference in survival between the two groups**.

But when patients were further subdivided into 18 prognostic categories, in a subgroup of 397 patients characterized by three-vessel disease and an abnormal left ventricular contraction, however, survival of group 1 patients was significantly different from that of group 2 patients.

Another example of significance when there should be none

But when individuals between the two groups were then contrasted for their differences in survival according to **18 prognostic categories** (heart morphology used to predict the likely outcome of a heart condition), for one of the categories the two groups differed in their survival. Any difference in survival should be due to chance alone as individuals were randomly divided into these categories.

Statistical tests across 18 prognostic categories

Another example of significance when there should be none

A simulated randomized clinical trial in coronary artery disease was conducted to illustrate the need for clinical judgment and modern statistical methods in assessing therapeutic claims in studies of complex diseases.
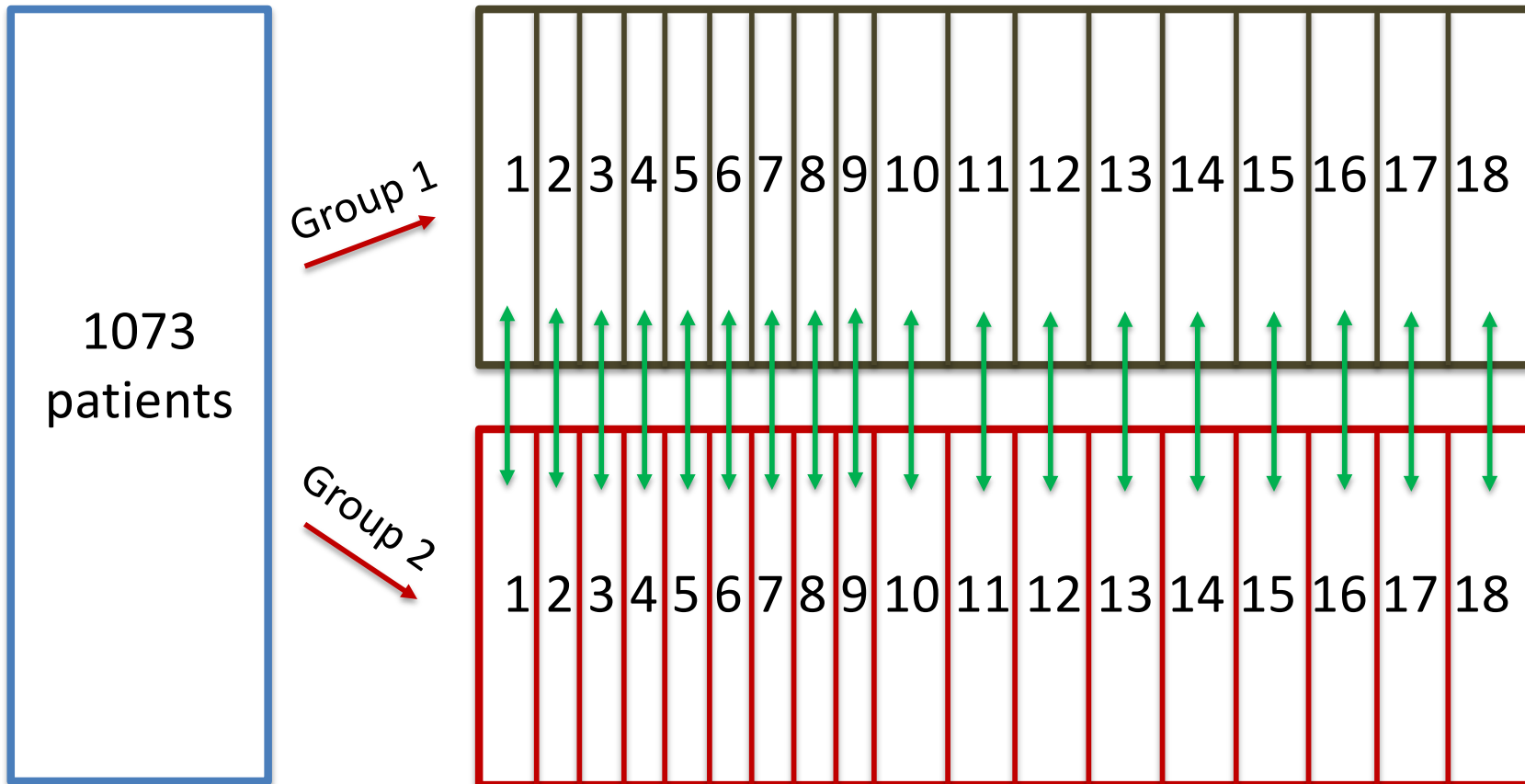
In this example, **1073 consecutive**, medically treated coronary artery disease patients from the Duke University data bank were randomized into **two groups**. The groups were reasonably comparable and, as expected, **there was no overall difference in survival between the two groups**.

But when patients were further subdivided into 18 prognostic categories, in a subgroup of 397 patients characterized by three-vessel disease and an abnormal left ventricular contraction, however, survival of group 1 patients was significantly different from that of group 2 patients.

Multivariable adjustment procedures revealed that the difference resulted from the combined effect of small imbalances in the distribution of several prognostic factors. Clinicians must exercise careful judgment in attributing such results to an efficacious therapy, as they may be due to chance or to inadequate baseline comparability of the groups.

Another example of significance when there should be none

- Patients grouped according as "three-vessel disease and an abnormal left ventricular contraction" were found to have differences between in survival between the two groups.
- However, patients were randomly assigned to each of the two groups in the beginning (i.e., survival *versus* non-survival).
- ***How did that happen?***
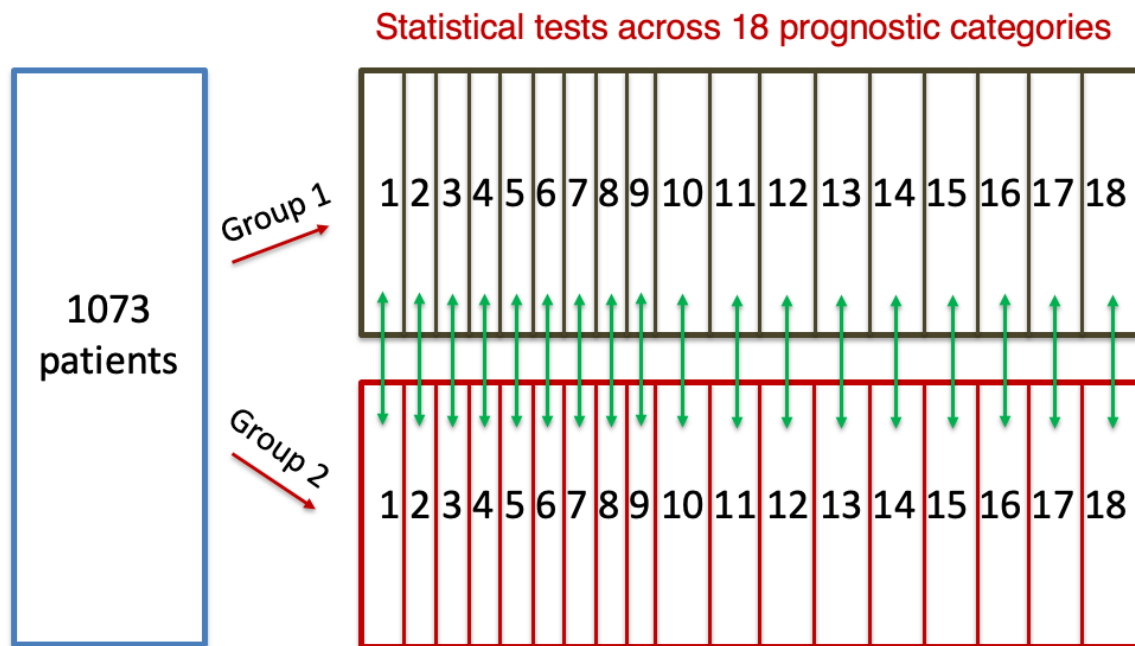
Statistical tests across 18 prognostic categories

Another example of significance when there should be none

- 1073 heart disease patients were randomly placed into two groups; no difference was found in survival (not surprising) between the two groups.
[akin to BIOL322 students divided according to their "birthdays"]

- Individuals within each group were then contrasted according to 18 prognostic categories (heart morphology used to predict the likely outcome of a heart condition). **[prognostics are akin to our 24 questions]**

- Individuals between the two groups were then contrasted for their differences in survival (any difference in survival should be due to chance alone as individuals were randomly divided into these categories). **[p-values for a test comparing the two groups]**

- Patients grouped according as "three-vessel disease and an abnormal left ventricular contraction" were found to have differences between in survival between the two groups. **[students differ in their preferences for drinking tea and eating vegetables]**

- However, patients were randomly assigned to each of the two groups in the beginning (i.e., survival versus non-survival). **[one should not expect differences related to odd/even birthdays]**

- **How did that happen?**

Let's take a break - 2 minutes

Remembering how the sampling distribution under the null hypothesis is built (conceptually)

observed data

test statistic of interest
(here t statistic)

$\pm$ observed t-value

$$t = \frac{\bar{Y}_1 - \bar{Y}_2}{SE_{\bar{Y}_1 - \bar{Y}_2}}$$

model assuming
H_0 as true
$(\mu_1 = \mu_2)$

$\bar{Y}_1$
$\bar{Y}_2$
$\bar{Y}_3$
...
$\bar{Y}_\infty$

sampling distribution of t
values under H_0

Infinite or very large
number of simulated data
(i.e., number of samples
from the population)

simulated data assuming a normally
distributed population (μ and σ are not
important; any combination leads to the
same t distribution); samples taken
respecting sample size of the observed
data.

probability

$-\infty$

∞

-4   -2   0   2   4

Number of standard deviations away from the
theoretical parameter assumed under H_0

Why when comparing multiple means, one should start with an ANOVA and not by two-sample t-tests?
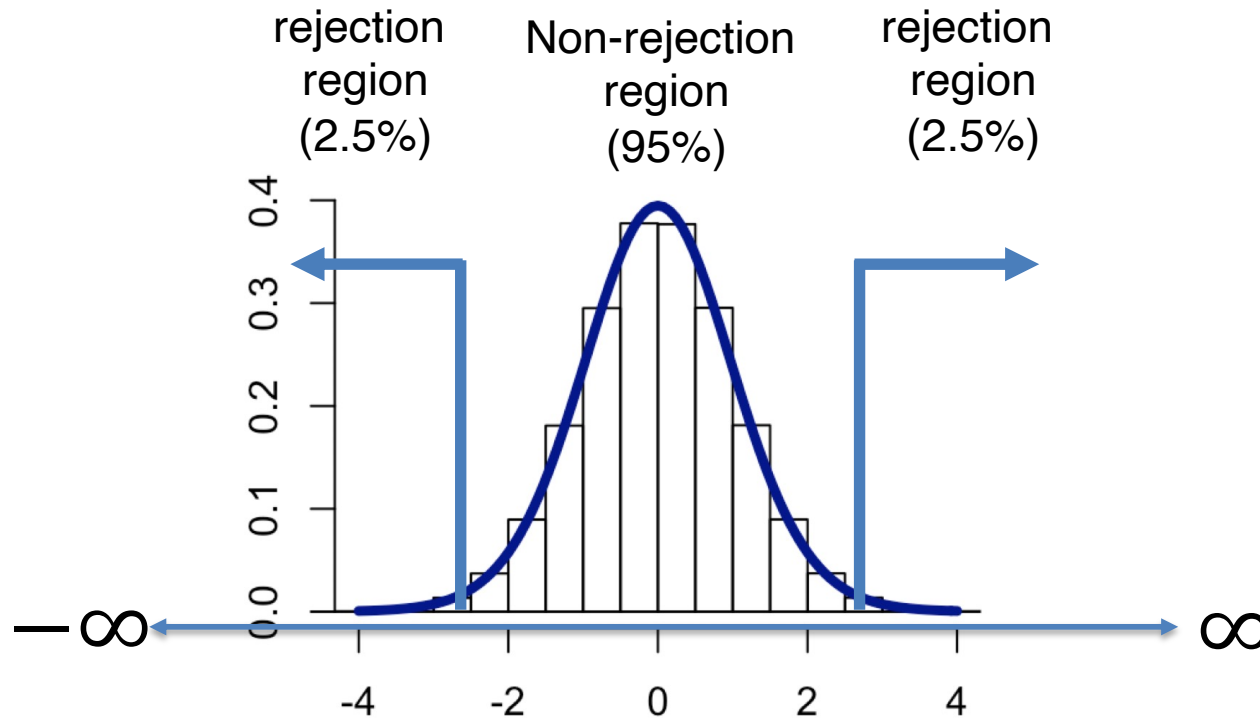
All the infinite t values are possible under H_0, even the ones in the rejection region (they have a probability of alpha=0.05 to be sampled).

If you conduct one or multiple tests, your probability of committing a type I error is still 0.05 (or another chosen alpha)

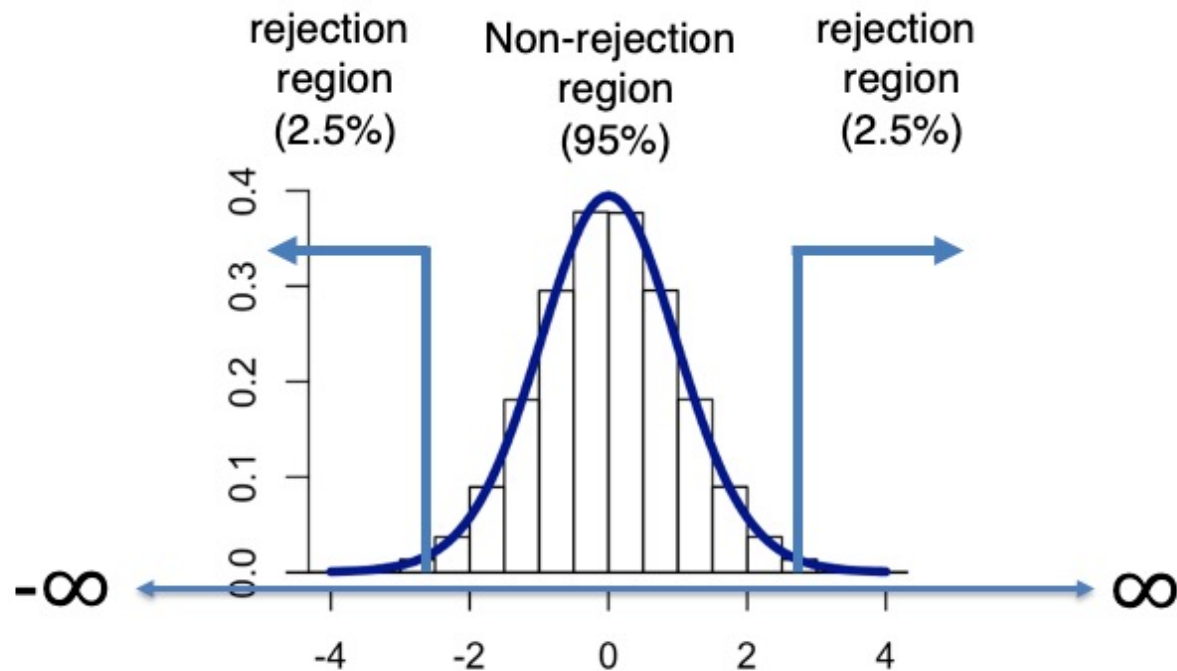**From tutorial 9:** There is a small statistical price to pay when inferring from samples: we need to accept a small risk of committing one sort of error [i.e., type I error] to avoid a bigger risk of committing another sort of error [i.e., type II error].

All the infinite t values are possible under H_0, even the ones in the rejection region (they have a probability of alpha=0.05 to be sampled).

If we conduct one or multiple tests, our probability of committing a type I error is alpha (say 0.05, i.e., 5%). In other words, rejecting the null hypothesis when (in reality) is true.

| rejection region (2.5%) | Non-rejection region (95%) | rejection region (2.5%) |

All the infinite t values are possible under H_0, even the ones in the rejection region (they have a probability of alpha=0.05 to be sampled).
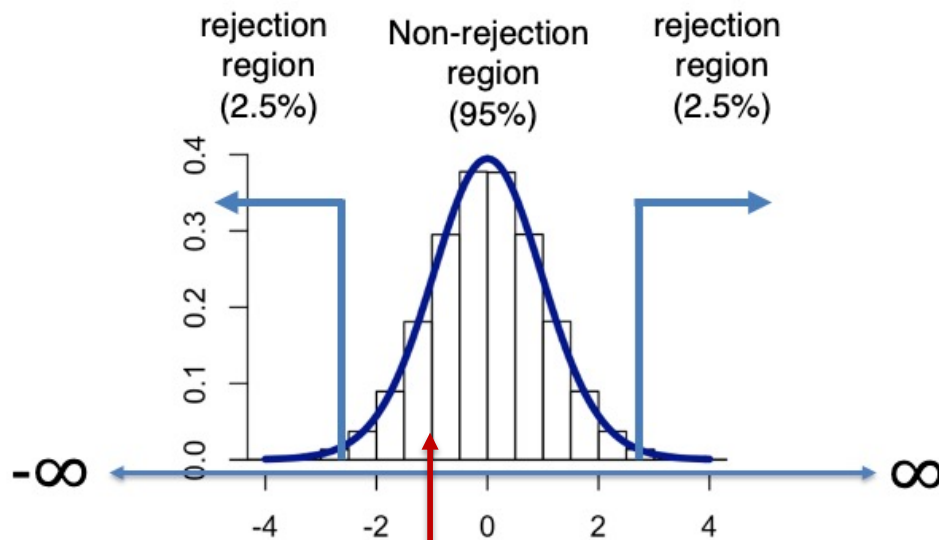
Then is likely (95% chance) that the test will not be significant (i.e., p-value < 0.05) by pure chance (as throwing a dart without aiming at the distribution)

Let's assume that the null hypothesis is indeed true (like in our student survey and the heart study).

If we conduct one or multiple tests, our probability of committing a type I error is alpha (say 0.05, i.e., 5%). In other words, rejecting the null hypothesis when (in reality) is true.
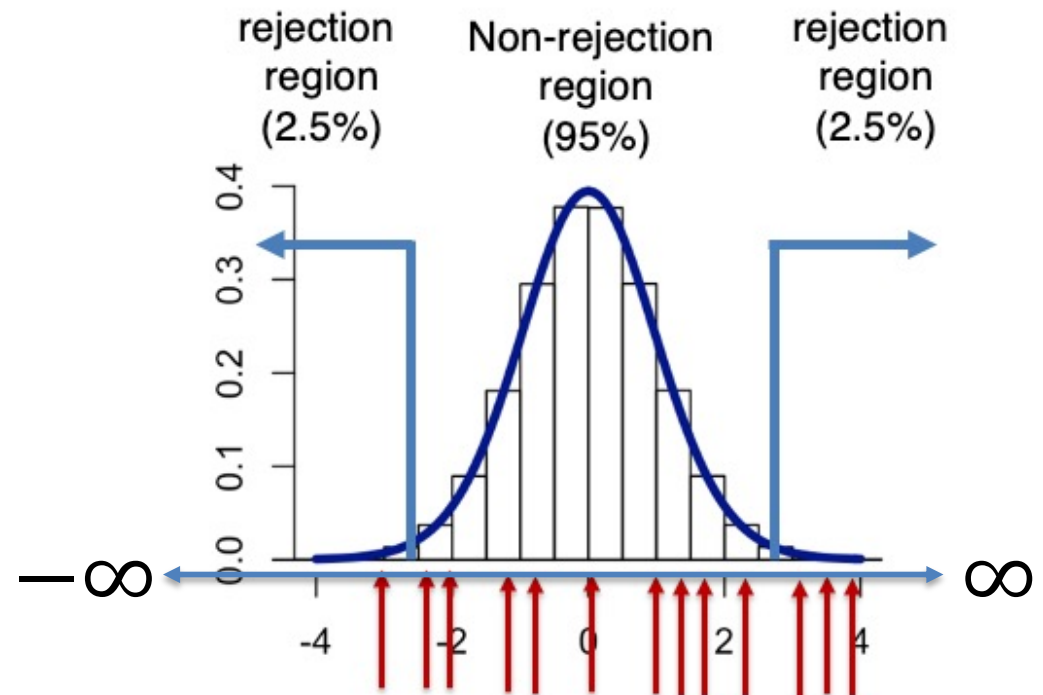

But throwing multiple darts without aiming at the distribution, one has 5% chance of hitting a rejection (i.e., a p-value < alpha).

All the infinite t values are possible under H_0, even the ones in the rejection region (they have a probability of alpha=0.05 to be sampled)

Why when comparing multiple means one should start with an ANOVA and not multiple t-test – because they inflate the number of false positive tests
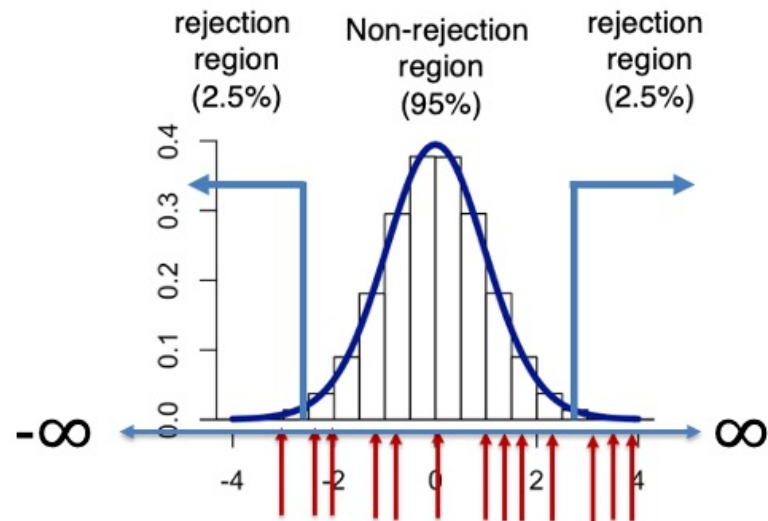
If you conduct too many tests, you will eventually, by chance alone, hit a t value that is in the rejection region. Remember that the sampling distribution contains all infinite values for the t statistic measuring the difference between two sample means assuming that H_0 is true.

Because we eliminate implausible (low probability) values in the sampling distribution assuming the null hypothesis as true; assuming an alpha value to establish the rejection area, then it is obvious that if one conducts too many tests, one will eventually commit Type I errors for a given alpha (i.e., increase the number of false positive tests – reject when in reality one should not).

Would you expect odd- and even day born individuals to differ in their preferences?

odd-day even-day born	dislike 1	2	3	4	Love it 5
			X		
1) Do you like soccer?	X				
2) Do you like playing video games?			X		
3) Do you like eating out?					
4) Do you enjoy writting?					
5) Do you like cats?			X		
6) Do you like to watch movies?				X	
7) Do you like to read novels?					

……

21) Do you like science fiction?	X				
22) Do you like pizza?		X			
23) Do you like to listen to the radio?			X		
24) Do you like museums?		X			

rejection region (2.5%)   Non-rejection region (95%)   rejection region (2.5%)

If we set an alpha of 0.05, i.e., acceptance area of 95% (0.95), then the chance of finding at least one significant test when you should not (i.e., false positive) out of 24 tests (groups) is:

$$1-0.95^{24} = 0.708$$

70.1% chance of finding at least 1 significant difference between odd and even born individuals in their preferences when H_0 is true!

Would you expect odd- and even day born individuals to differ in their preferences?

| | dislike | | | | Love it |
odd-day even-day born	1	2	3	4	5
			X		
1) Do you like soccer?	X				
2) Do you like playing video games?			X		
3) Do you like eating out?					
4) Do you enjoy writting?					
5) Do you like cats?			X		
6) Do you like to watch movies?					X
7) Do you like to read novels?					

......

21) Do you like science fiction?	X				
22) Do you like pizza?		X			
23) Do you like to listen to the radio?				X	
24) Do you like museums?			X		

$1-0.95^{24}=0.708$

70.1% chance of finding at least 1 significant test when all H_0 are true!

2 tests were in fact significant.

2 significant p-values (alpha = 0.05)
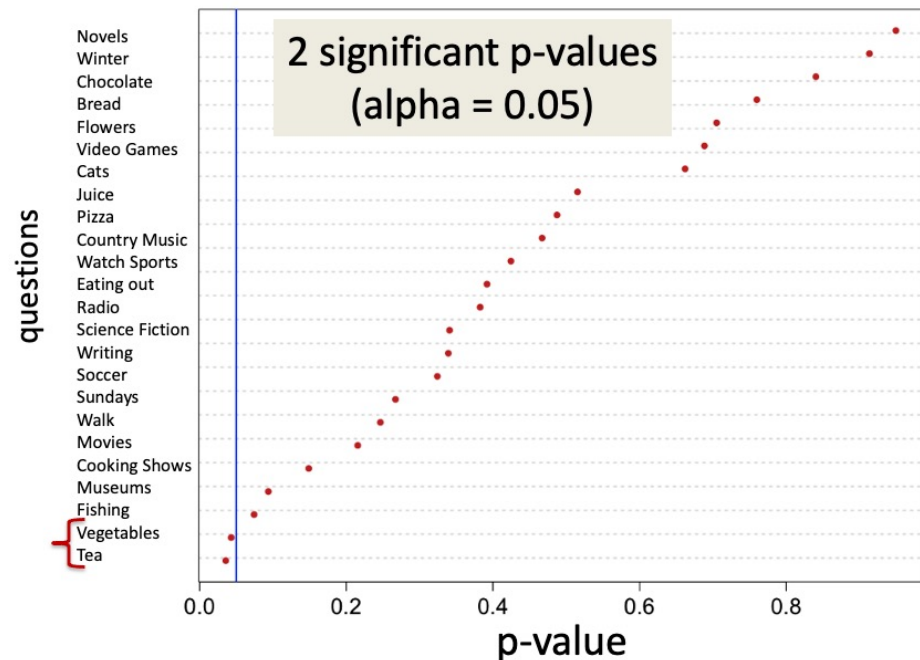
Let's assume that 100 tests were conducted:

If we set an alpha of 0.05, i.e., acceptance area of 95% (0.95), then the chance of finding at least one significant test when you should not (i.e., false positive) out of 100 tests (groups) is:

$$1\text{-}0.95^{100} = 0.994$$

99.4% chance of finding at least 1 significant difference between group 1 and group 2 when H_0 is true!

SO, 100% chance if you conduct 100 tests on samples that are expected to vary just due to chance alone (i.e., for which the null hypothesis H_0 is true).

If we set an alpha of 0.05, i.e., acceptance area of 95% (0.95), then the chance of finding at least one significant test when you should not (i.e., false positive) out of 1 test is obviously the original alpha:

$1 - 0.95^1 = 0.05$

5% chance of finding at least 1 significant test when H_0 is true!
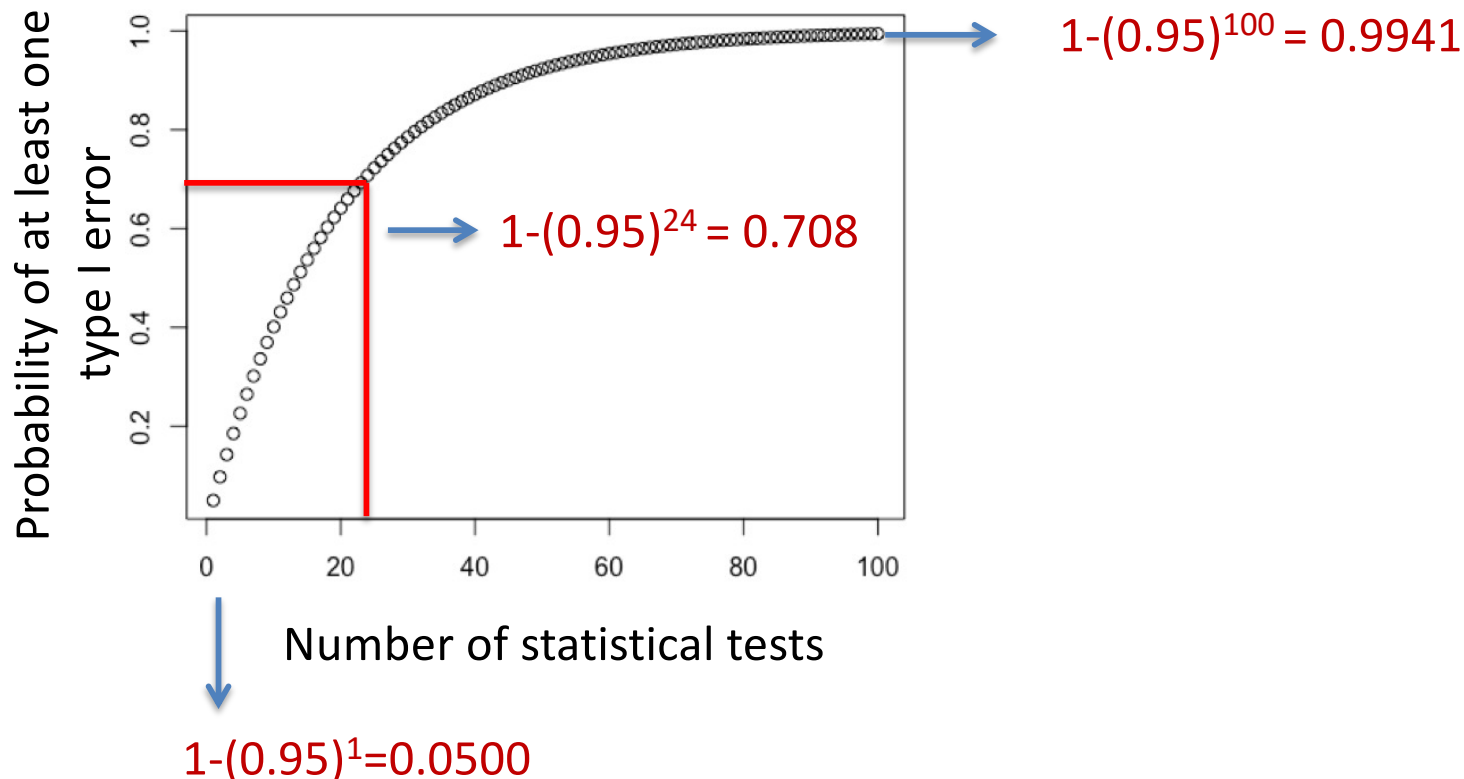

Probability of at least one type I error
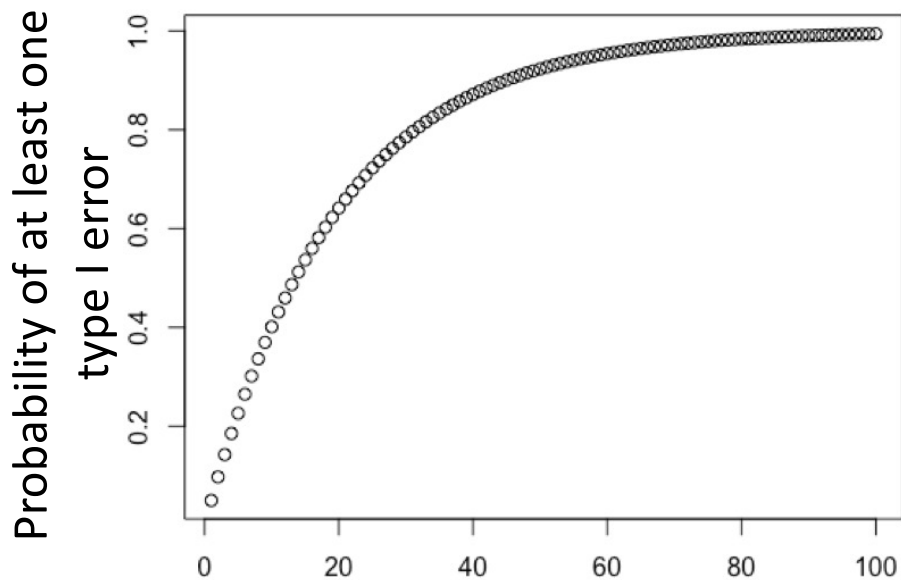
Number of statistical tests

$1 - (0.95)^1 = 0.0500$

If we set an alpha of 0.05, i.e., acceptance area of 95% (0.95), then the chance of finding at least one significant test when you should not (i.e., false positive) out of 24 tests is:

$1-0.95^{24}=0.708$

70.1% chance of finding at least 1 significant test when H_0 is true!

$1-(0.95)^{100} = 0.9941$

$1-(0.95)^{24} = 0.708$

Number of statistical tests

Probability of at least one type I error

$1-(0.95)^{1}=0.0500$

Let's take a break – 2 minutes

The goal of performing an ANOVA before is to protect one against inflated type I errors due to multiple pairwise testing.

When ANOVA is significant, which pairs of means can be "honestly" considered significant?

We need then a way to control for the possibility of inflated type I errors due to multiple testing:
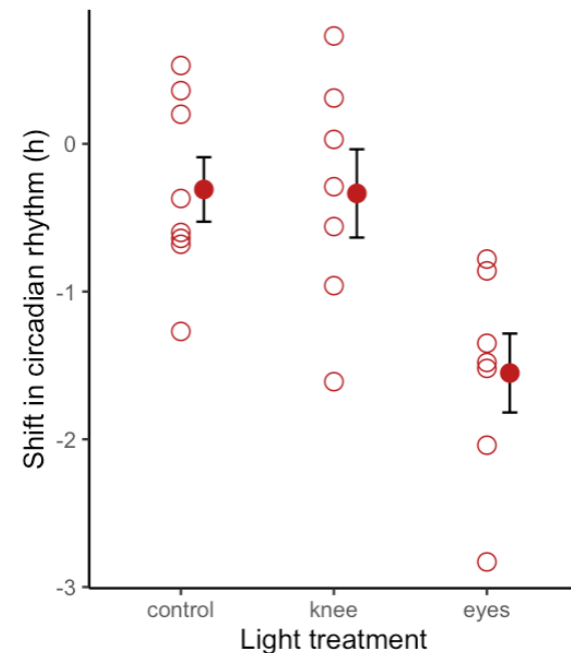
The Tukey's honest test.

THE ANALYSIS OF VARIANCE (ANOVA) for comparing multiple sample means (groups)

H$_0$: The samples come from statistical populations with the same mean, i.e., $\mu_{control} = \mu_{knee} = \mu_{eyes}$.

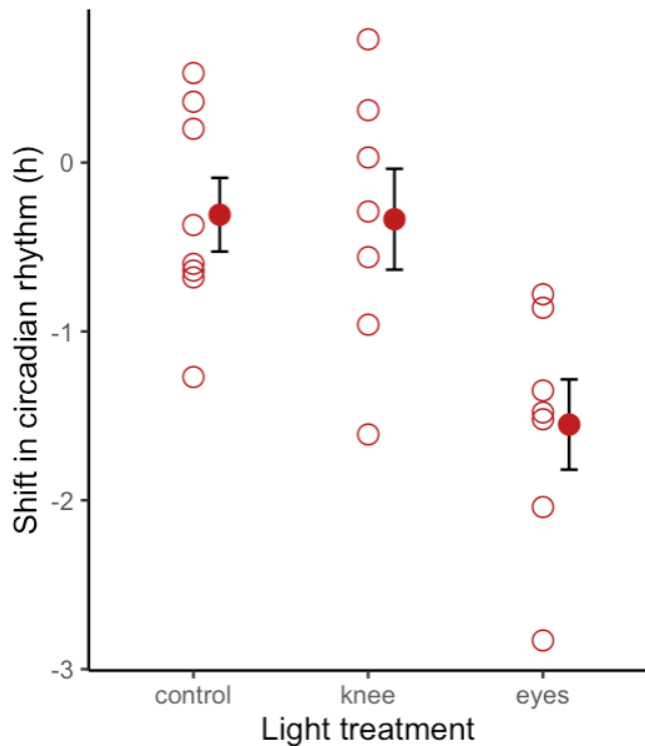**H$_A$:** At least two samples come from different statistical populations with different means.

When ANOVA is significant, which pairs of means can be "honestly" considered significant?

How many pairs of means are possible to be contrasted (i.e., differences between means)?

$$\binom{r}{2} = \frac{r!}{2!(r-2)!} = \frac{r(r-1)}{2}$$

$$\frac{3(3-1)}{2} = 3$$

Control – Knee
Control – Eyes
Knee - Eyes

3 mean pairs (contrasts)

The post-hoc (after ANOVA) - Tukey's honest test

There is a pair of hypotheses for each pair of means as follows:

H_0: $\mu_i = \mu_j$ for each pair $i \neq j$

H_A: $\mu_i \neq \mu_j$ for each pair

i and j stand for the subscripts of the groups

(treatments) being compared.

Control – Knee
Control – Eyes
Knee - Eyes

3 mean pairs (contrasts)

Tukey's honest test in R

```
> circadianANOVA <- aov(shift ~ treatment, data = circadian)
> posthoc <- TukeyHSD(circadianANOVA, conf.level=0.95)
> posthoc
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = shift ~ treatment, data = circadian)

$treatment
                    diff        lwr        upr      p adj
eyes-control -1.24267857 -2.1682364 -0.3171207 0.0078656
knee-control -0.02696429 -0.9525222  0.8985936 0.9969851
knee-eyes     1.21571429  0.2598022  2.1716263 0.0116776
```

Tukey's honest test in R: we often use letters (a, b, c., etc) to show on graphs the means that are different and similar.

```
> circadianANOVA <- aov(shift ~ treatment, data = circadian)
> posthoc <- TukeyHSD(circadianANOVA, conf.level=0.95)
> posthoc
   Tukey multiple comparisons of means
     95% family-wise confidence level

Fit: aov(formula = shift ~ treatment, data = circadian)

$treatment
                    diff         lwr         upr       p adj
eyes-control  -1.24267857  -2.1682364  -0.3171207  0.0078656
knee-control  -0.02696429  -0.9525222   0.8985936  0.9969851
knee-eyes      1.21571429   0.2598022   2.1716263  0.0116776
```
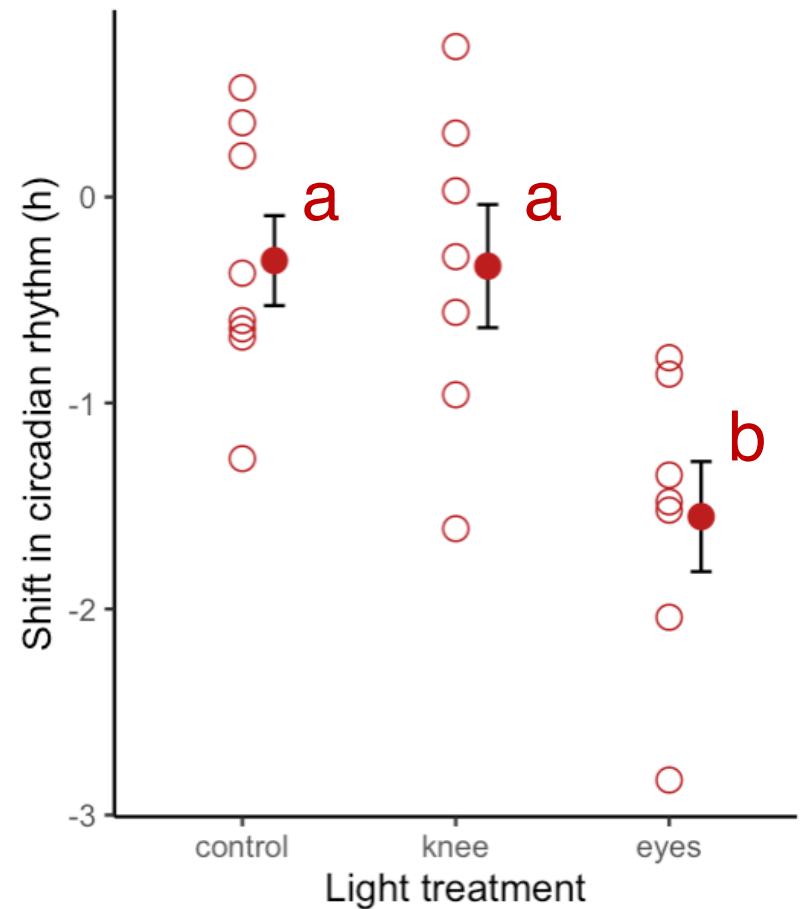
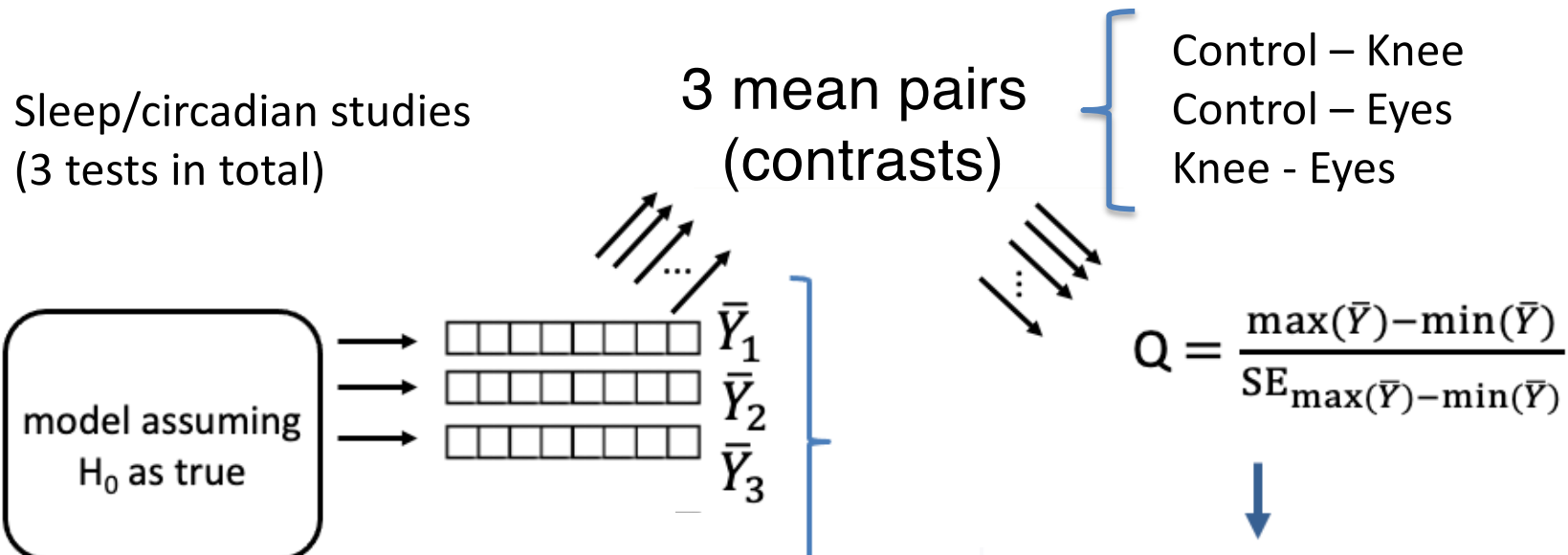The test statistic for the Tukey Test is calculated as:

$$Q = \frac{|\bar{X}_i - \bar{X}_j|}{SE}$$

$$SE_{i-j} = \sqrt{\frac{s_{p(i,j)}^2}{2}\left(\frac{1}{n_A} + \frac{1}{n_B}\right)}$$

$$s_{p(i,j)}^2 = \frac{df_i s_i^2 + df_j s_j^2}{df_i + df_j}$$

The quantity s_p^2 is called the pooled sample variance and is the average of the sample variances weighted by their degrees of freedom.

Q is then contrasted against a distribution built from the largest possible difference between the two-sample means given the number of two-sample tests and assuming H_0 as true.

Sleep/circadian studies
(3 tests in total)

3 mean pairs
(contrasts)

Control – Knee
Control – Eyes
Knee - Eyes

model assuming
H_0 as true

$\bar{Y}_1$
$\bar{Y}_2$
$\bar{Y}_3$

$$Q = \frac{max(\bar{Y}) - min(\bar{Y})}{SE_{max(\bar{Y}) - min(\bar{Y})}}$$

Infinite or very large
number of simulated data
(i.e., number of samples
from the population)

By picking the single largest difference (i.e., most significant) to build the Q distribution, we then assure that only 1 test will be significant when H_0 is true, thus controlling for inflated Type I errors due to multiple testing.
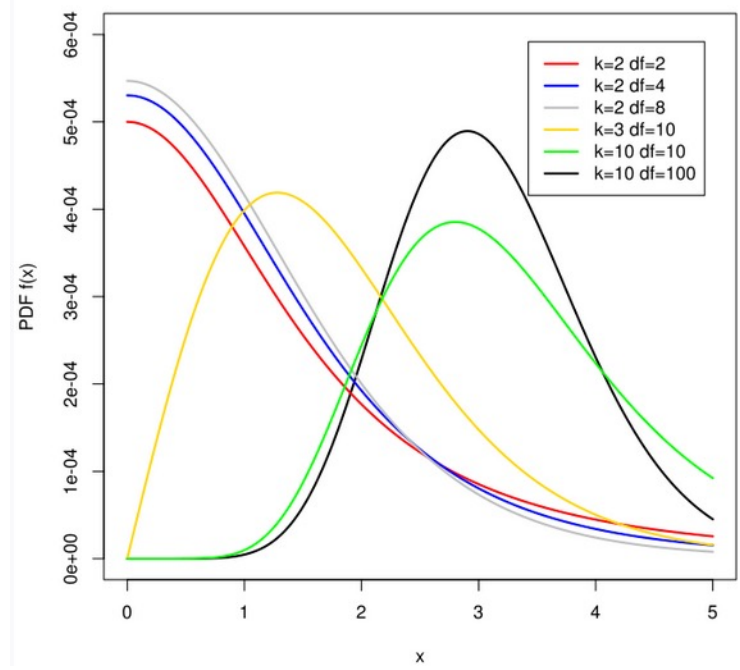
PDF f(x)

k=2 df=2
k=2 df=4
k=2 df=8
k=3 df=10
k=10 df=10
k=10 df=100

Q is then contrasted against a distribution built from the largest possible difference between the two-sample means given the number of two-sample tests and assuming H0 as true.
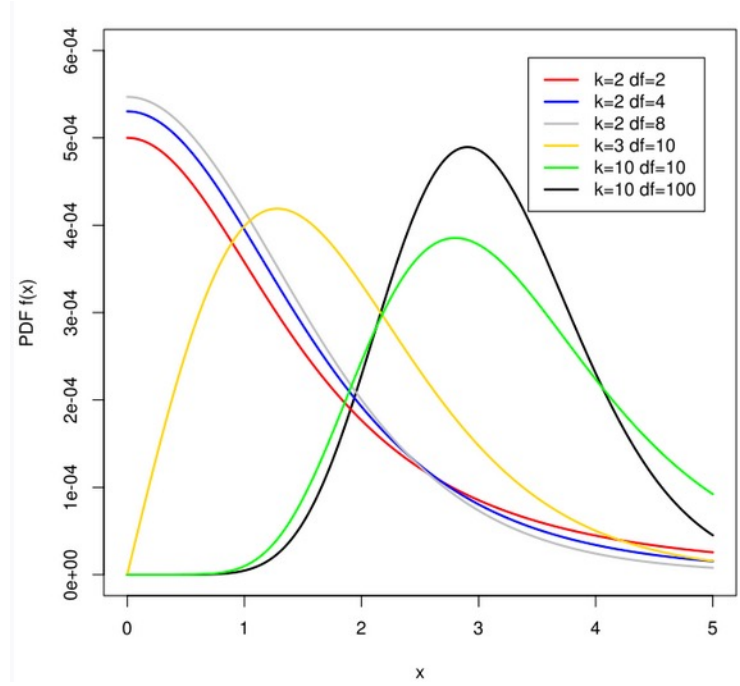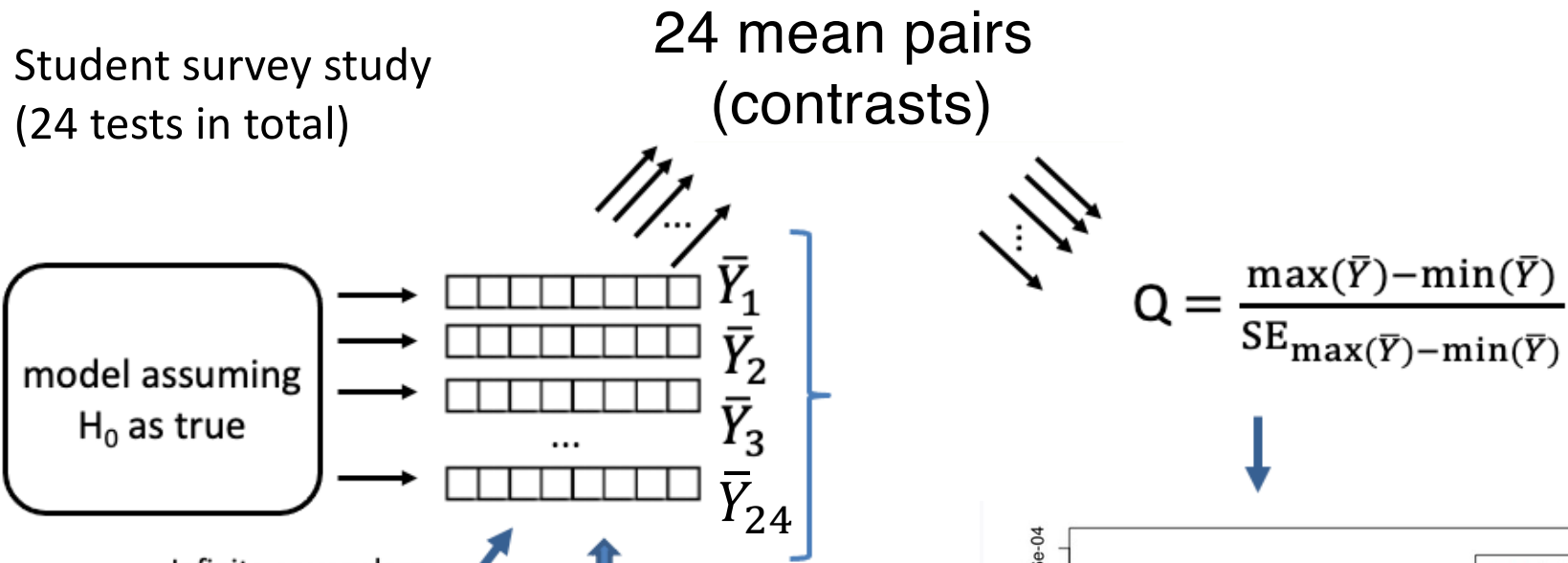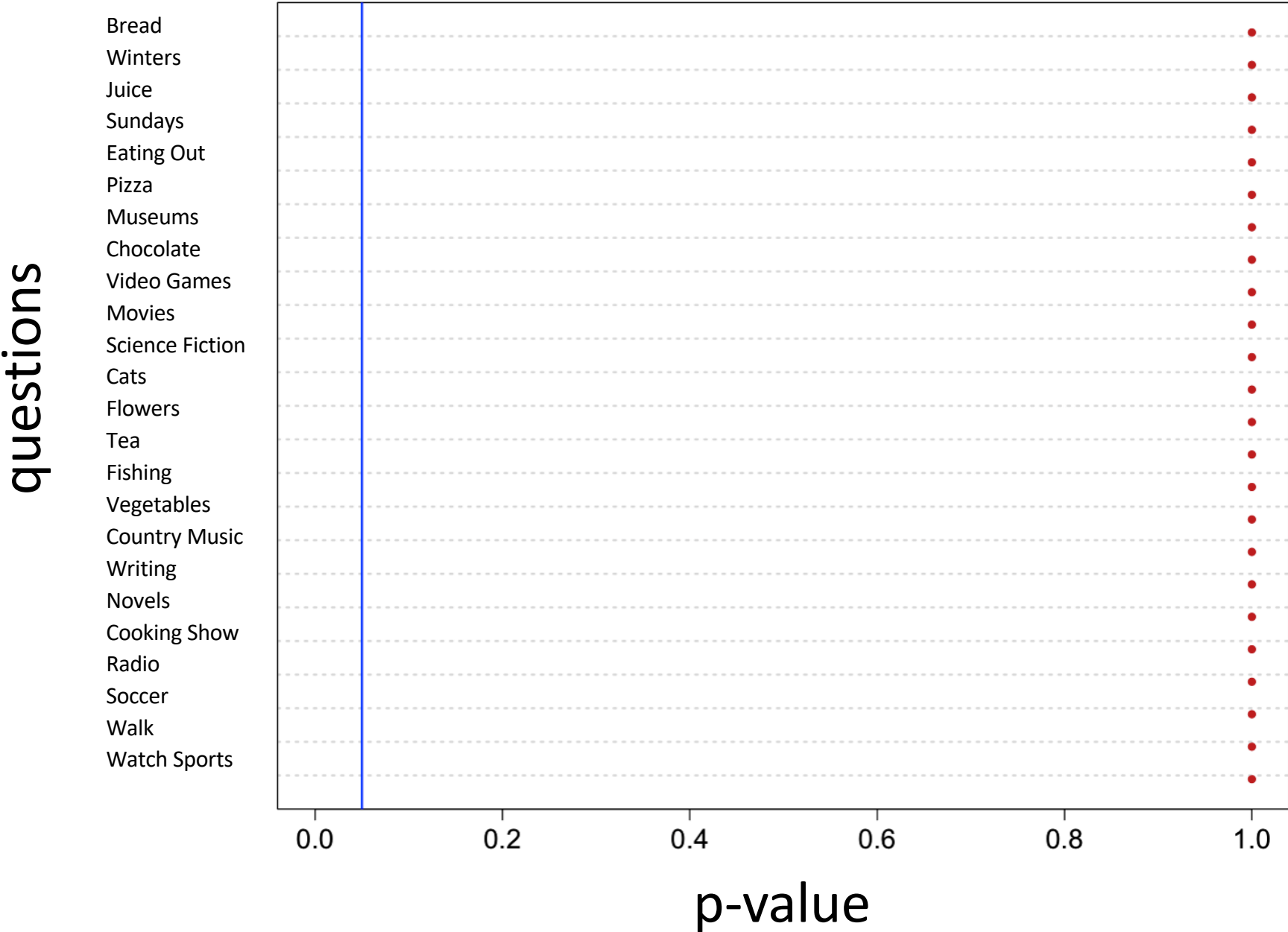
Student survey study
(24 tests in total)

24 mean pairs (contrasts)

model assuming H_0 as true

$\bar{Y}_1$
$\bar{Y}_2$
$\bar{Y}_3$
...
$\bar{Y}_{24}$

$$Q = \frac{\max(\bar{Y}) - \min(\bar{Y})}{SE_{\max(\bar{Y}) - \min(\bar{Y})}}$$

Infinite or very large number of simulated data (i.e., number of samples from the population)

simulated data assuming a normally distributed population (μ and σ are not important; any combination leads to the same t distribution); samples taken respecting number of groups and sample size of each group.

PDF f(x)

- k=2 df=2
- k=2 df=4
- k=2 df=8
- k=3 df=10
- k=10 df=10
- k=10 df=100

No difference from the survey detected as significant after the Tukey test

ANOVA & the Tukey-test:

Assumptions:

- Each of the samples (observations within groups) is a random sample from its population.

- The variable (shift in circadian rhythm) is normally distributed in each (treatment) population.

- The variances are equal among all statistical populations from which the treatments were sampled.

Testing differences in variances among populations - The Levene's test (too complex to understand its calculation for BIOL322 level but it is important to know its existence, utility and how to apply it in R). Hypotheses for the Levene's test:

H_0: $\sigma^2_{control} = \sigma^2_{knee} = \sigma^2_{eye}$

H_A: At least one population variance (σ^2) is different from another population variance or other population variances.

We need to generate evidence towards H_0 to apply an ANOVA to the data at hands.

Testing differences in variances among populations - The Levene's test

H₀: $\sigma^2_{control} = \sigma^2_{knee} = \sigma^2_{eye}$

H$_A$: At least one population variance (σ^2) is different from another population variance or other population variances.
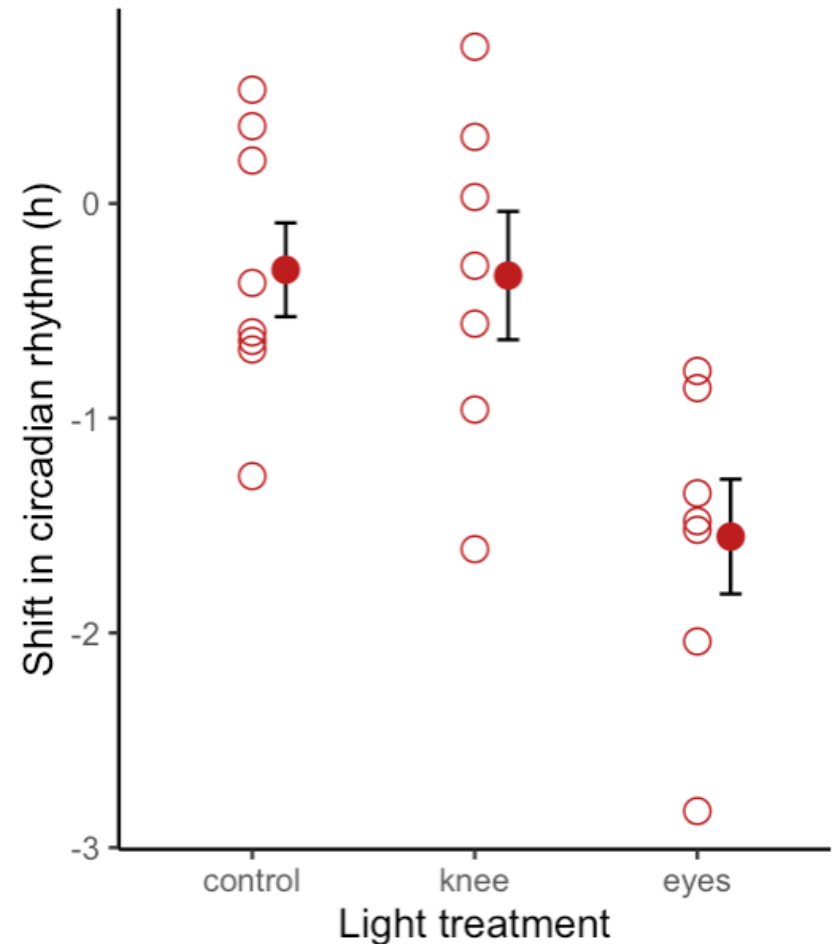
Levene's test:

Assumptions:

- Each of the samples (observations within groups) is a random sample from its population.

- The variable (shift in circadian rhythm) is normally distributed in each (treatment) population.

Testing differences in variances among populations - The Levene's test (too complex for BIOL322 level but it is important to know its existence, utility and how to apply it in R). Hypotheses for the Levene's test

```
leveneTest(shift ~ factor(treatment), data=circadian)
Levene's Test for Homogeneity of Variance (center = median)
      Df  F value  Pr(>F)
group  2   0.1586  0.8545
       19
```

P = 0.8545. Based on an alpha = 0.05, we should not reject the null hypothesis that: $\sigma^2_{control} = \sigma^2_{knee} = \sigma^2_{eye}$

Therefore, we should feel confident to conduct a standard ANOVA to the data (there is a Welch-like ANOVA).