ADS2 Mock Coding Challenge 2

Semester 2, 2023-24

Technical Instructions

You have 3 hours to complete this assignment. There are **three** questions, all of which need to be completed. The instructions and data sets (.csv files) can be downloaded from Blackboard Learn.

Please make an R Markdown file for your response. A template is provided. Please follow the structure set out in the template. Please remember to include your roll number (but not your name) in the author field, as well as in the name of the final document.

The final submission is a pdf knitted from the R Markdown file (if you cannot knit to pdf directly, then knit to Word and convert the outcome to a pdf file using the "Export" function in Word or another text editor).

The submission should contain explanatory text, answers to questions, all results, and all the code used to generate the results. There is one exception: When you read a .csv file and if your name is in the file path, you are allowed to hide that code chunk so that your anonymity is maintained.

You will be graded not only on your answers to the questions but also on your ability to compile a well-formatted and readable R Markdown document. It is therefore advisable to knit early and often and check that your document can be knitted without errors and that the result is in line with your expectations. If you have code chunks that take a long time to run, use the code chunk option `cache = TRUE`. This means that the results of the code chunk get saved and will be used in the next knit, instead of being computed again (provided the code chunk has not changed).

Please upload your pdf file to the assessment dropbox at the end of the assignment. We are aware that due to increased traffic when everybody uploads their file, your upload may be a few minutes past the deadline. In such cases, we will consult the time at which the pdf document was produced and use this to determine whether or not your submission counts as a late submission. If so, the same penalties apply as for other in-course assessments.

Honour Code

This is an open-book assessment. This means you are allowed to consult your previous notes and use your previous code. You are also allowed to look up commands online if you need to (though the assessment is designed in such a way that you should not need commands or methods beyond what has been taught in this class). If you use code from an online source, please state what the source is (name of site, author if possible, url, date accessed).

You are **not** allowed to work with other students on this assessment. This is why we do not allow mobile phones. Of course, because we are allowing internet access, we cannot completely rule out the possibility of you working together. But we ask that you don't.

We appeal to your sense of honour and integrity. It is wrong to cheat, so don't do it.

By submitting this assignment, you declare that this is the result of your own work and that you did not either get help from or help, other students.

If, in marking the finished work, we find evidence that students have colluded, this will be treated as a potential violation of academic integrity and brought before the ZAMO.

1. Vitamin C and tooth growth

Lack of vitamin C leads to severe health issues. It is not produced in the human body and must be supplied with food. At the same time, personnel that have limited access to fresh vegetables (sailors, spacemen, travelers, etc) may suffer from the insufficiency of this compound in their food. Thus, a vitamin C formulation that can preserve its properties for a long time is of great need.

Researchers developed such a formulation. *In vitro* tests showed its efficiency. Now, they performed an *in vivo* trial. Guinea pigs received the newly developed formulation of Vitamin C or fresh orange juice (normalized according to the concentration of vitamin C) in addition to their standard diet (`supp`). Each type of additives included three concentrations (`dose`) of vitamin C: 0.5, 1, and 2 mg/ml. The measured outcome is the tooth length (`len`) in mm (stem cells that become teeth are sensitive to vitamin C).

Questions

- Import, check, and organize the data appropriately. Reformat columns if needed.
- Plot the data in a useful way.
- Choose, justify, state the statistical hypotheses, and carry out an appropriate test to answer whether the vitamin C formula is useful.
- Present and discuss your results. Is this novel formula useful? What would you suggest doing next?

Marking (25 points total)

Import, check, and organise the data appropriately. (3 points)

- The dataset is imported and briefly checked = 2 points.
- Rearrange and reformat columns = 1 points.

The dataset is imported – 2 points The data are loaded and quickly checked:

```
teeth <- read.csv(file = "teeth.csv")
head(teeth)
```

```
##   X  len supp dose
## 1 1 3.00   VC  0.5
## 2 2 5.95   VC  0.5
## 3 3 4.25   VC  0.5
## 4 4 3.65   VC  0.5
## 5 5 3.89   VC  0.5
## 6 6 5.34   VC  0.5
```

```
str(teeth)
```

```
## 'data.frame':    60 obs. of  4 variables:
##  $ X   : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ len : num  3 5.95 4.25 3.65 3.89 5.34 5.83 5.91 3.4 4.13 ...
##  $ supp: chr  "VC" "VC" "VC" "VC" ...
##  $ dose: num  0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 ...
```

By a brief examination, you may see the following features:

- there are no NAs;
- there are no duplicated rows;
- the data structure is not good:
  - the dependent variable, `len`, is the first column, while the independent ones go after it;
  - Also `supp` is coded as a character vector;
  - `dose` is coded as a numeric vector.

Apparently, `supp` and `dose` must be grouping variables. It is reasonable to recode them and change their order. You can also check which values are in each column to make sure that there are no weird values like "" or similar.

```
teeth <- teeth %>%
  mutate(dose = factor(dose, levels = c(0.5, 1, 2), ordered = T),
         supp = as.factor(supp)) %>%
  relocate(supp, dose)

str(teeth)
```

Rearrange and reformat columns – 1 point

```
## 'data.frame':    60 obs. of  4 variables:
##  $ supp: Factor w/ 2 levels "OJ","VC": 2 2 2 2 2 2 2 2 2 2 ...
##  $ dose: Ord.factor w/ 3 levels "0.5"<"1"<"2": 1 1 1 1 1 1 1 1 1 1 ...
##  $ X   : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ len : num  3 5.95 4.25 3.65 3.89 5.34 5.83 5.91 3.4 4.13 ...
```

Now, it is fine. Relocation of the columns is optional, but it would be better to recode the independent variables.

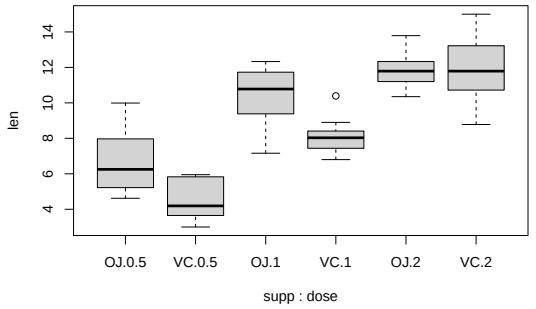
Plot the data in a useful way. (5 points)

It is a pure place for all the possible creativity: you can use boxplots, whisker plots with mean or median +/- SE/SD/CI or IQR, or the primary points. The plot must:

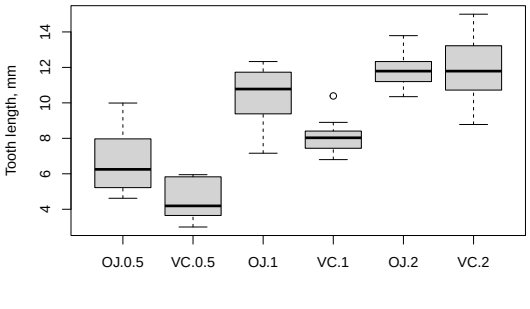
- be available at all – +1 point.
- be informative: see above – +2 points.
- nicely formatted: clear labels, nice colors – +1 point.
- with the primary data points or exceptionally good formatting – +1 point.

Let's see what I would think about each plot (Figure 1):

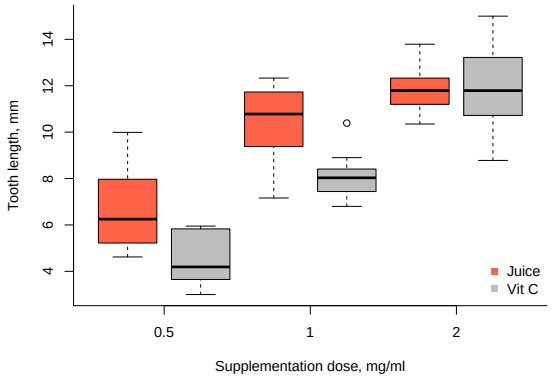
- Plot A – 3 points:
  - The graph is available (1 point);
  - It is informative (2 points);
  - Its labels are not very good, the output is also very basic, but no major issues.
- Plot B – 4 points:
  - The graph is available (1 point);



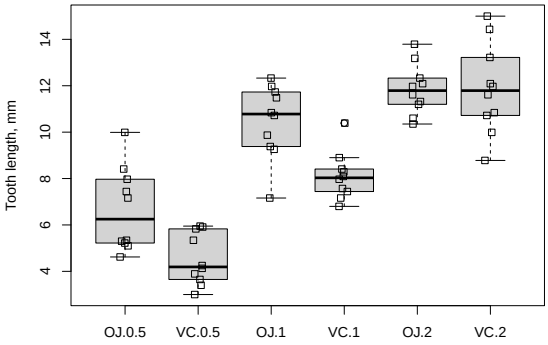
(a) An acceptable plot



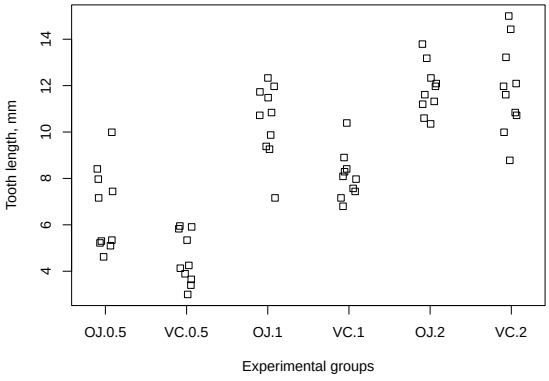
(b) A reasonably good plot



(c) A plot with a good design



(d) A plot with a nice data representation solution



(e) A very good, but simple plot

Figure 1: Some of the possible graphs to illustrate your data

  - It is informative (2 points);
  - It is properly labeled, but unassuming. But I would still consider giving a point to it (1 point).
- Plot C – 5 points:
  - The graph is available (1 point);
  - It is informative (2 points);
  - It is properly labeled, and its format is just superb (2 points).
- Plot C – 5 points:
  - The graph is available (1 point);
  - It is informative (2 points);
  - It is properly labeled, but the output is still not very beautiful (1 point);
  - There are primary data points that add credibility to the data presentation (1 point).
- Plot D – 5 points:
  - The graph is available (1 point);
  - It is informative (2 points);
  - It is properly labeled, but the output is still not very beautiful (1 point);
  - There are primary data points that add credibility to the data presentation (1 point).

Generally, `nicely formatted: clear labels, nice colors` means that it is not ugly, there are no clear faults in the presentation, the colors are not too sharp, and the labels are not too ugly. For some suboptimal plots, have a look at Figure 2.

All the graphs are not terribly bad, but there are the following issues: inappropriate labels, plot margins are too wide, two graphs instead of one, and primary points overlay each other. You can check IBMS1, semester 1, tutorial 14, Critiquing Data Visualization for more ideas.

Tables can be used as well, but it will yield 4 points at max.

Choose, justify, state the statistical hypotheses, and carry out an appropriate test to answer whether the vitamin C formula is useful. (13 points)

Choose the appropriate test – 2 points

We have 2 levels of `supp` × 3 levels of `dose` = 6 groups. It means we need to use ANOVA. As we have 2 factors, we should try to use a 2-way ANOVA if the data fit the requirements. Thus, the method of choice is a 2-way ANOVA or (if cannot run it) the Kruskal-Wallis test.

I see no reason to run ANOVA without interactions, so I would like to have a model like $len = supp + dose + interaction$. For this variant, you get 2 points.

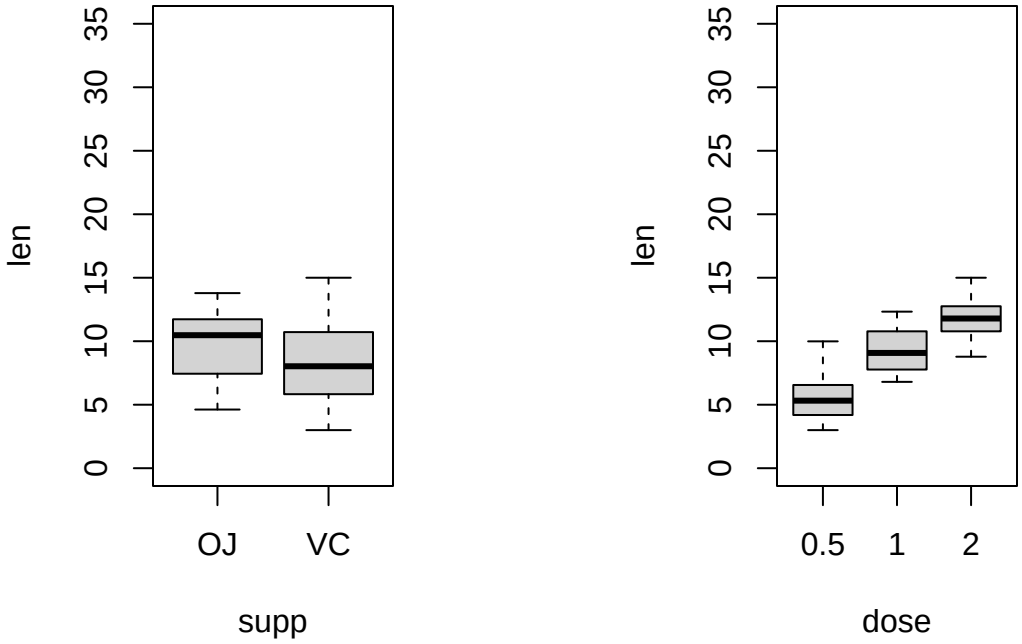
If you choose the Kruskal-Wallis test, 1-way ANOVA, or a median test, you will get 1 point (these choices are reasonable but inferior).

Other tests are wrong and will give 0 points

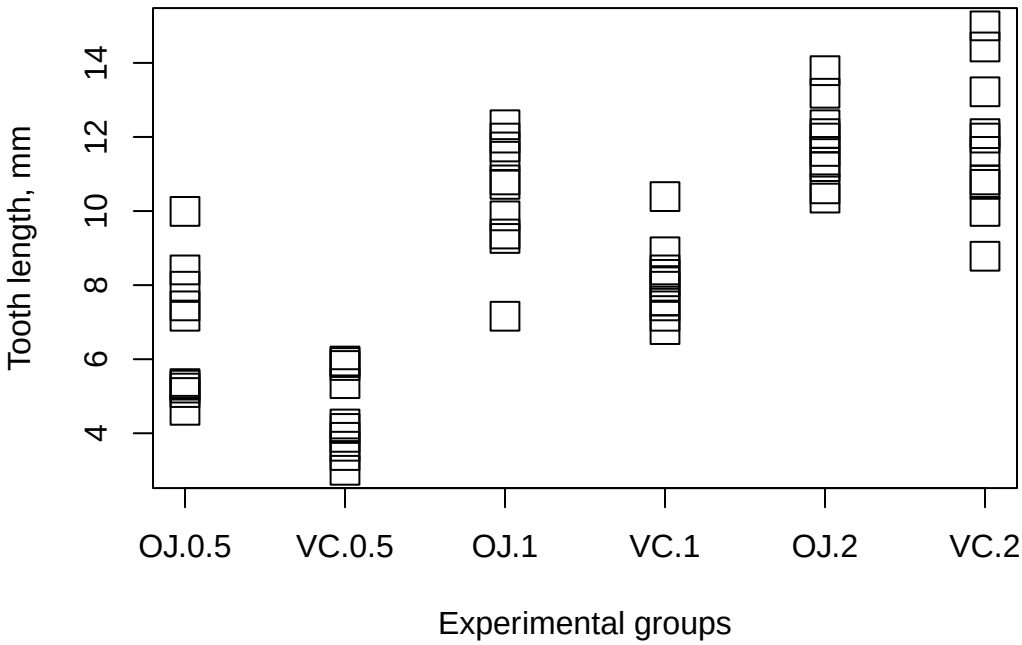
Justify your test choice – 2 points

Assumptions for a 2-way ANOVA test are:

1. Independence of observations.
   - We can assume it at once.
2. Normality of residuals:



(a) Two graphs instead of one



(b) Points are overlaid

Figure 2: Poor design choices

- Can be checked visually (`plot(anova_model, 2)`) or by running a suitable hypothesis test

3. Equality of variance:
   - Can be checked visually (`plot(anova_model, 1)`) or by running a suitable hypothesis test
4. Equal group size (have to use different types of SS calculation for the ANOVA table if this requirement is violated):
   - The group size can be noticed in the data diagnosis step

Altogether, if everything is done correctly, you get 2 points. If something on the list is missing, you get 1 point.

Only one approach must be used! Why? What will you do if you get conflicting results? If you present both approaches, you will get 1 point.

Let's see the result of the graphical method:

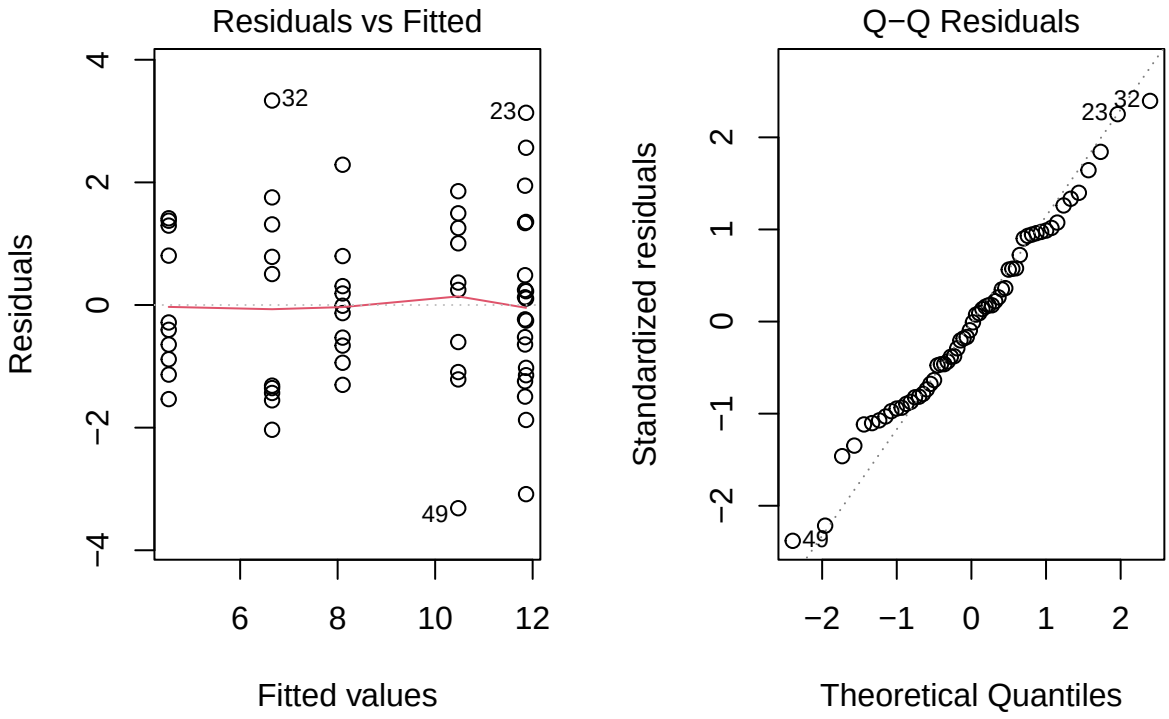


Figure 3: Assumption testing

The first plot shows the distance of residuals from the mean (is comparable across groups) and the second one shows residuals according to the normal distribution (close to the expected values).

We can use parametric ANOVA.

State the statistical hypotheses – 2 points

The correct form – 2 points

It is quite difficult to do something wrong here.

- H_0: means of different `supp` groups are the same
- H_1: means of different `supp` groups are **NOT** the same

The same for the other model elements.

The not completely correct form (still available) – 1 point

Hypothesis like:

- H_0: `supp` does not help to increase `len`
- H_1: `supp` helps to increase `len`

will be marked less.

Carry out an appropriate test to answer whether the vitamin C formula is useful. – 7 points

You run the test you chose before. In our case, it will be ANOVA with post-hoc tests. However, you may treat `dose` as a continuous quantitative predictor. It may allow you to use a linear regression as well.

If you chose the wrong test, you will get fewer points *in the step above*. But if you run it adequately and the results are reasonable, you may get full points here as well.

2-way ANOVA – 3 points

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## supp         1   33.3   33.32  15.473 0.000241 ***
## dose         2  396.0  198.02  91.965  < 2e-16 ***
## supp:dose    2   17.3    8.64   4.015 0.023683 *
## Residuals   54  116.3    2.15
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Post-hoc tests – 4 points

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = len ~ supp * dose, data = teeth)
##
## $supp
##            diff       lwr        upr     p adj
## VC-OJ -1.490333 -2.249938 -0.7307291 0.0002408
##
## $dose
##         diff      lwr      upr   p adj
## 1-0.5 3.6930 2.574698 4.811302 0.0e+00
```

```
## 2-0.5 6.2595 5.141198 7.377802 0.0e+00
## 2-1   2.5665 1.448198 3.684802 2.8e-06
##
## $`supp:dose`
##                   diff        lwr        upr     p adj
## VC:0.5-OJ:0.5 -2.120 -4.0588347 -0.1811653 0.0243952
## OJ:1-OJ:0.5    3.819  1.8801653  5.7578347 0.0000048
## VC:1-OJ:0.5    1.447 -0.4918347  3.3858347 0.2524625
## OJ:2-OJ:0.5    5.189  3.2501653  7.1278347 0.0000000
## VC:2-OJ:0.5    5.210  3.2711653  7.1488347 0.0000000
## OJ:1-VC:0.5    5.939  4.0001653  7.8778347 0.0000000
## VC:1-VC:0.5    3.567  1.6281653  5.5058347 0.0000193
## OJ:2-VC:0.5    7.309  5.3701653  9.2478347 0.0000000
## VC:2-VC:0.5    7.330  5.3911653  9.2688347 0.0000000
## VC:1-OJ:1     -2.372 -4.3108347 -0.4331653 0.0082439
## OJ:2-OJ:1      1.370 -0.5688347  3.3088347 0.3090572
## VC:2-OJ:1      1.391 -0.5478347  3.3298347 0.2929176
## OJ:2-VC:1      3.742  1.8031653  5.6808347 0.0000074
## VC:2-VC:1      3.763  1.8241653  5.7018347 0.0000066
## VC:2-OJ:2      0.021 -1.9178347  1.9598347 1.0000000
```

Present and discuss your results. Is this novel formula useful? What would you suggest doing next? (4 points)

Present and discuss your results. – 2 points

All terms show differences. That means that the formulations and their concentrations have different effects on tooth growth. Exactly:

- the new formulation is generally inferior to the fresh orange juice (~ 3.7 mm, $p < 0.001$);
- lower doses are worse than higher doses (~ 15.5 mm difference between the highest and the lowest concentration of the supplement, $p < 0.001$);
- at the highest dose, the new formulation is as good as the fresh orange juice ($p = 1$).

The highest effect can be attributed to the dose ($R^2 \approx 0.703$), but the interaction term is still detectable ($R^2 \approx 0.031$).

Altogether, the formula can be used to substitute natural dietary vitamin C, but only at a high dose.

What would you suggest doing next? – 2 points

Still, the effect of each supplementation is a bit unclear due to the lack of the non-treated group. The addition of the one would be cumbersome as we would have to give up the factorial design. It would be possible to either add a non-treated group and normalize all the other values to it or add a `dose` group with very low concentration. As the formula is functional, it is possible to run some toxicological tests, test the long-term efficiency, and go for clinical trials. It may be possible to optimize the formula further, as the response is lower than that of the fresh juice at lower doses. Possibly, more work can be spent on the bioavailability of vitamin C in the formula.

But do not boldly write: "Let's increase the sample size". What will you see if the sample size is higher? What will you do with the *even lower* p-value? Think about it. If you still decide to ask for the one, you need to explain why you would like to do that, what you would like to see, and *how much* you want to increase the sample size.

2. Mutation and survival

You work on the mutation of a certain gene (Gene_X) that likely causes developmental abnormalities in humans but is quite rare, and the precise role of the mutation is not known. You created a mouse model by introducing a similar mutation in a similar location within the murine genome.

You set several breeding pairs and crossed mice as Gene_X$^{WT/mut}$ × Gene_X$^{WT/mut}$. You recorded the genotype of the newborn mice. Your genotyping record (`genotype.csv`) includes `mouse_ID`, birth date (`BD`), `sex`, and `genotype`.

Answer the questions below, provide your analysis, and explain your results. Given the genotyping records you got, what can you say about the studied mutation?

Questions

- Import and organize the data.
- *Describe* the data in a useful way.
- What would you expect under Mendelian inheritance?
- Choose and justify the appropriate statistical test, state the statistical hypotheses, and carry the test out an appropriate test on whether the mutation affects the survival of mice.
- Present and discuss your results. What would you suggest doing next?

Marking (25 points total)

Import and organize the data. (3 points)

That's the easiest part. You need to load your data and check it. Here, nothing special.

```
genotype <- read.csv("genotype.csv")
head(genotype)
```

```
##   ID    sex genotype        BD
## 1  1 female      het 2024-2-16
## 2  2   male      het 2024-2-16
## 3  3   male      het 2024-2-16
## 4  5 female      het  2024-3-2
## 5  6 female      mut  2024-2-3
## 6  7   male      het  2024-2-3
```

```
str(genotype)
```

```
## 'data.frame':    80 obs. of  4 variables:
##  $ ID      : int  1 2 3 5 6 7 8 9 10 11 ...
##  $ sex     : chr  "female" "male" "male" "female" ...
##  $ genotype: chr  "het" "het" "het" "het" ...
##  $ BD      : chr  "2024-2-16" "2024-2-16" "2024-2-16" "2024-3-2" ...
```

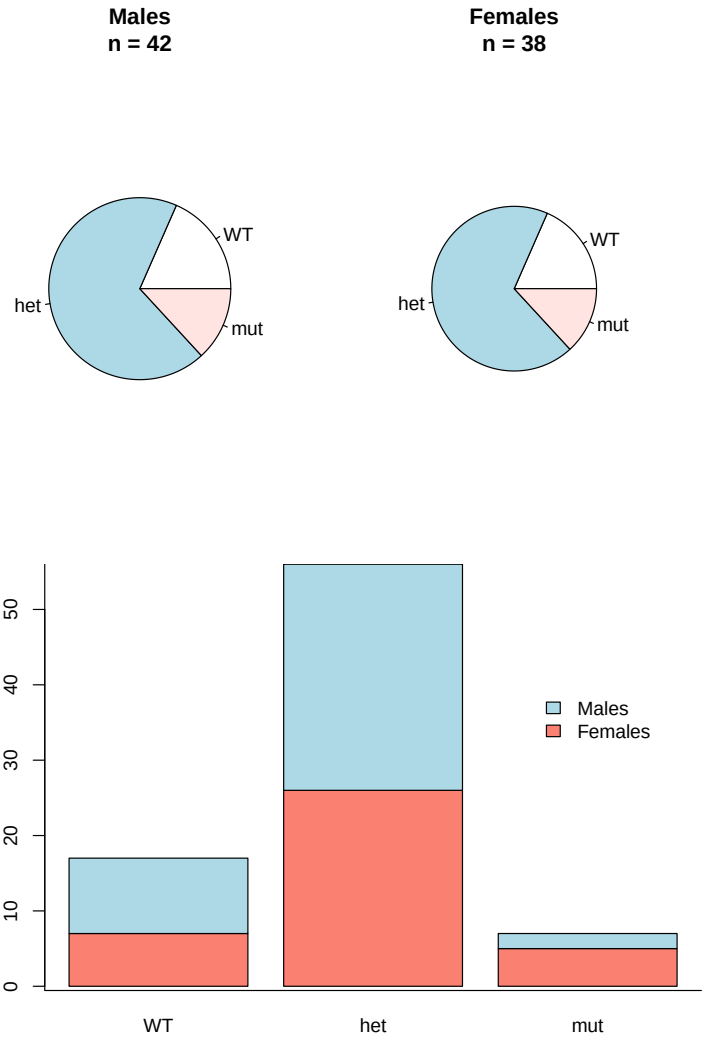
It would not harm to check which values are in the columns. But we can already see that ID seems irrelevant for further analysis. BD is also secondary. What we clearly wonder about is the distribution of `sex` × `genotype`. Thus, you can store your data in the form of a table or matrix that counts the number of values of each type.

```
##
##          WT het mut
##   female  7  26   5
##   male   10  30   2
```

***Describe* the data in a useful way. (5 points)**

In this case, you may use a plot or a table. The plot must be:

- available at all – +1 point.
- informative: see above – +2 points.
- nicely formatted: clear labels, nice colors – +2 points.



There are other choices for plots as well. Think again. Table may also work. But it must:

- be available at all – +1 point.
- include the primary numbers – +2 points.

- be informative: includes the percentages as well – +1 point.
- be nicely formatted – +1 point.

Table 1: The distribution of sex and gender in mice of different genotypes

	WT	het	mut
female	7 (8.75, %)	26 (32.5, %)	5 (6.25, %)
male	10 (12.5, %)	30 (37.5, %)	2 (2.5, %)

It is an easy, but quite illustrative choice. Scores for both options *are not* additive. You may use both, but you will get a score for only the best of them.

What would you expect under Mendelian inheritance? (4 points)

In this case, you would expect mice to have males and females as 50/50 and WT, heterozygotes, and mutant mice as 25/50/25.

Table 2: The expected distribution of sex and gender in mice of different genotypes

	WT	het	mut
Females	10	20	10
Males	10	20	10

Choose and justify the appropriate statistical test, state the statistical hypotheses, and carry the test out an appropriate test on whether the mutation affects the survival of mice. (8 points.)

Choose and justify the appropriate statistical test – 3 points

Clearly, it is an expected vs observed distribution. Thus, we need to use the χ^2 goodness-of-fit test. – 1 point.

Assumptions include: – 2 points.

- The variables must be categorical.
  - *Fits.*
- Observations must be independent.
  - Can assume from the task. *Fits.*
- Cells in the contingency table are mutually exclusive.
  - *Fits.*
- The expected value of cells should be 5 or greater in at least 80% of cells.
  - See Table 2. *Fits.*

We can run χ^2 test safely.

State the statistical hypotheses – 1 point

H_0: The data follow the expected distribution (Table 2).

H_A: The data *does not* follow the expected distribution (Table 2).

Carry test out an appropriate test – 4 points

As we need to run χ^2 for goodness-of-fit, we need to provide the expected values. In `chisq.test()`, we can do that by providing a matrix of expected probabilities under the `p` argument.

Table 3: The expected probabilities

	WT	het	mut
Females	0.125	0.25	0.125
Males	0.125	0.25	0.125

```
##
##  Chi-squared test for given probabilities
##
## data:  as.numeric(mice)
## X-squared = 16.6, df = 5, p-value = 0.005324
```

Thus, the distribution of sex and genotype deviates from the one under Mendelian inheritance law. You may wish to identify the most affected group of mice as well.

Present and discuss your results. What would you suggest doing next? (5 points)

Present and discuss your results. – 2 points

Clearly, the mutation affects the survival of mice. KO mice are only 35% ($p < 0.01$) of the expected number under Mendelian inheritance law. Moreover, mutant males and females seem to be affected differently (answer yourself how exactly).

What would you suggest doing next? – 3 points

The question is why mutant mice have a reduced survival. We may wish to identify cells that express the target gene and see if this mutation affects them and how. That's quite a bioinformatical and genomics task. I would like to see interesting suggestions. Also, it would be interesting to investigate survivors – why did they survive? Is there a special molecular pathway that allows to bypass the devastating effect of the mutation? Any creativity is welcomed.

But do not boldly write: "Let's increase the sample size". It may work here, but you need to explain why you would like to do that, what you would like to see, and how much you want to increase the sample size.

3. Coffee shop opening hours

A new coffee shop has opened on campus. Hooray! Coffee shops are normally open from 6am-5pm but the owners are aware that students often sleep later than other members of the society. After being open for one month, they run a month-long trial opening 10am-9pm to see if students prefer these times. They leave an iPad at the serving counter where customers can record if they are 'satisfied' or 'unsatisfied' with the opening times.

During the 6am-5pm opening times, the iPad records 864 presses of the 'satisfied' button by customers and 714 presses of the 'unsatisfied' button. When they change these times to 10am-9pm, they receive 980 'satisfied' pressed and 473 'unsatisfied'.

Questions

- What would be a suitable statistical test for these data and why? (6 points)
- What are your null and alternative hypotheses? (4 points)
- Are students more satisfied with the early or later opening times? (15 points)

Marking (25 points)

What would be a suitable statistical test for these data and why? (6 points)

These data are categorical but seriously lacking in independence. Students may have been customers more than once and, similarly, there are likely to be students who were customers in both trials. The two categories are therefore not exclusive either.

- Chi-squared or Fisher's exact test would be inappropriate
- Bootstrapping is the only possible alternative to take account of these complications

What are your null and alternative hypotheses? (4 points)

- Null hypothesis: there is no difference between the proportion of students who are satisfied with an early or late opening time
- Alternative hypothesis: there is a difference between the proportion of students **or** students prefer a late opening time (this would be the equivalent of a one-tailed test)

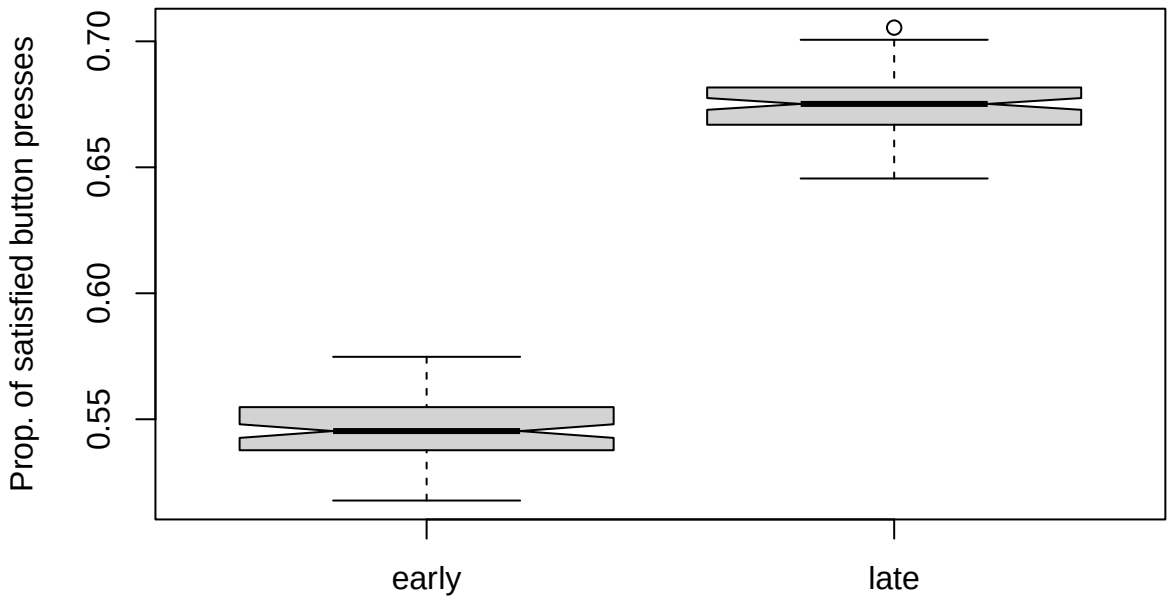
Are students more satisfied with the early or later opening times? (15 points)

```
first_satisfied <- 864
first_unsatisfied <- 714
second_satisfied <- 980
second_unsatisfied <- 473
first_bootstraps <- vector()
second_bootstraps <- vector()
first_results <- c(rep(1, first_satisfied), rep(0, first_unsatisfied))
second_results <- c(rep(1, second_satisfied), rep(0, second_unsatisfied))


for (a in 1:100) {
  first_sample <-
```

```
    mean(sample(first_results, length(first_results), replace = T))
  second_sample <-
    mean(sample(second_results, length(second_results), replace = T))

  first_bootstraps <- c(first_bootstraps, first_sample)
  second_bootstraps <- c(second_bootstraps, second_sample)
}
first_upper <- quantile(first_bootstraps, probs = c(0.975))
second_lower <- quantile(second_bootstraps, probs = c(0.025))
boxplot(
  first_bootstraps,
  second_bootstraps,
  notch = T,
  names = c('early', 'late'),
  ylab = 'Prop. of satisfied button presses'
)
```




```
first_upper < second_lower
```

```
## 97.5%
##  TRUE
```

- Yes, students clearly preferred the later times as shown by the nonoverlapping confidence intervals. This could be judged either by boxplot as here or the non-overlapping confidence intervals.

- I would also suggest we award marks here for correctly performing a chi-squared test here. We would have already penalised students for making the wrong choice of test earlier so they should not be double-penalied.

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  matrix(c(864, 714, 980, 473), ncol = 2)
## X-squared = 50.629, df = 1, p-value = 1.116e-12
```

```
## [1] 0.5840508
```

- This result again confirms a clear difference between the groups (chi-squared $p < 0.05$)
- I would only award full marks if the student reports both the significance of the test and gives some indication as to which time is preferred. Partial marks if an effect is reported but not what that effect is.

Overall presentation and R Markdown (25 points in total)

For this last part, check the following

- Was R Markdown used to knit a pdf file? (6 points)
  - The R Markdown file was knitted to a PDF or DOCX (DOCX → PDF) – 6 points.
  - The R Markdown file was created, but the report *was not* knitted. I needed to correct it a bit (a few minor LaTeX errors) – 5 points.
  - The R Markdown file was created, but the report *was not* knitted. I needed to correct it substantially (I needed to change the code slightly or some code was not closed properly) – 4 points.
  - The code was submitted as a well-formatted R script. Or R markdown required significant work – 3 points.
  - The code was submitted as an R script, but the formatting was not good. Or R markdown was just terrible. – 1-2 points.
- Is all code provided? The only exception we make is file import commands if the file path would reveal your identity. (4 points)
- Is all code provided *completely*? (4 points)

Check especially for lines of code that are too long to show up in the knit, like this one:

```
ggplot(hamster, aes(x=lifespan, fill=group)) + facet_grid(cols=vars(group)) + geom_histogram(binwidth =
```

This is a problem, because it means that the code is no longer reproducible to the reader of the knitted document. For full points, longer lines of code should be broken down, for instance like this:

```
p <- ggplot(hamster, aes(x=lifespan, fill=group))
p <- p+ facet_grid(cols=vars(group))
p <- p+ geom_histogram(binwidth = 5)
p <- p + xlab("life span (weeks)")
p <- p + scale_fill_manual(values=c("dodgerblue", "tomato1"))
p
```

- Is the code reproducible? To assess this, markers should select one of the three questions at random and try to reproduce the results. Note that here, we don't care if you chose the right analysis approach, or if your code is correct; all we care about is whether it's reproducible. (4 points)
- Is the file nicely formatted? It doesn't have to be a work of art, but it's nice if there are section headers for each of the questions (like there are in this document), so that it's clear where one question ends and the next begins. (4 points)

Such output is not welcomed:

3. ### HEADER

Text

```
# Also, the advantage of R Markdown it that allows for text,
# code, and results to nicely coexist in a file. Therefore,
# longer chunks of text (such as explanations) should be
# written as actual text, not as a comment in a code chunk
# (like this one!) - Actual text outside of code chunks is
# much easier to read.
```

- Is the writing clear? We don't care so much about smaller typos or perfect English. But the writing should be clear and understandable. It is evaluated by living persons. We still can understand only what we can read. (3 points)