Lab Tutorial 6

Ladan Tazik

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Summary: The content of this tutorial has been shamelessly obtained from the textbook worksheet on *Classification II: Evaluation & Tuning*,ensuring a comprehensive understanding of model performance metrics and evaluation techniques.

Towards the end of the lab, you will find a set of assignment exercises (Assignment 5). These assignments are to be completed and submitted on Canvas.

Lab 06

After completing this week's lecture and tutorial work, you will be able to:

- Describe what a test data set is and how it is used in classification.
- Using R, evaluate classification accuracy using a test data set and appropriate metrics.
- Using R, execute cross-validation in R to choose the number of neighbours.
- In a dataset with > 2 attributes/features, perform k-nearest neighbour classification in R using the `tidymodels` package to predict the class of a test dataset.
- Describe advantages and disadvantages of the k-nearest neighbour classification algorithm.

```
### Run this cell before continuing.
library(tidyverse)
library(repr)
library(tidymodels)
options(repr.matrix.max.rows = 6)
```

Randomness and Setting Seeds

This tutorial uses functions from the `tidymodels` library, which not only allows us to perform K-nearest neighbour classification, but also allows us to evaluate how well our classification worked. In order to ensure that the steps in the worksheet are reproducible, we need to set a *seed*, i.e., a numerical "starting value," which determines the sequence of random numbers R will generate.

Below in many cells we have included a call to `set.seed`. **Do not remove these lines of code**; they are necessary to make sure the autotesting code functions properly.

The reason we have ***`set.seed`*** *in so many places is that our file is organized into cells that can be run out of order. Since things can be run out of order, the exact sequence of random values that is used in each cell is hard to determine, which makes autotesting really difficult. One drawback of calling* ***`set.seed`*** *everywhere is that the numbers that will be generated won't really be random. For the purposes of teaching and learning, that is fine here. But* ***in other data analyses outside of this course, you must call `set.seed` only once at the beginning of the analysis, so that your random numbers are actually reasonably random.***

Fruit Data Example - (Part II)

You will recognize a few of the first questions from last week's tutorial. This will help you repeat some of the fundamentals of classification before tackling the later questions in this tutorial, which integrate concepts you learned from this week's material. First, load the file `fruit_data.csv`from the previous tutorial into your notebook.

`mutate()` the `fruit_name` column such that it is a factor using `as_factor()`.

Assign your data to an object called ***`fruit_data`****.*

```
fruit_data <- read_csv("../data/fruit_data.csv") |>
              mutate(fruit_name = as.factor(fruit_name))
```

```
Rows: 59 Columns: 7
-- Column specification --------------------------------------------------------
Delimiter: ","
chr (2): fruit_name, fruit_subtype
dbl (5): fruit_label, mass, width, height, color_score

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Using `mass` and `width`, calculate the distance between the first observation and the 44th observation. *Assign your answer to an object called* ***`fruit_dist_44`***.

```
fruit_dist_44 <- fruit_data |>
  slice(1,44)|>
  select(mass, width)|>
  dist()
```

Create a `tidymodels` recipe to *standardize* (i.e., center and scale) all of the variables in the fruit dataset. Specify your recipe with class variable `fruit_name` and predictors `mass`, `width` and`height`. Name the recipe `fruit_data_recipe`. Use `set.seed(9999)`.

```
set.seed(9999)

fruit_data_recipe <- recipe(fruit_name ~ mass+width+height, data = fruit_data) |> step_cen
 step_scale(all_predictors()) |>
  prep()
```

Use `bake` to apply recipe to your original data. Save the scaled data to `scaled_fruit_data`.

```
scaled_fruit_data <- bake(fruit_data_recipe, fruit_data)
```

Evaluating the Model

To add evaluation into our classification pipeline, we:

1. Split our data into two subsets: *training data* and *testing data*.
2. Build the model & choose K using training data only (sometimes called tuning)
3. Compute accuracy by predicting labels on testing data only.

We'll now talk about each step individually.

1. Split our data into two subsets (a training and test set)

In this part, we will be partitioning `fruit_data` into a training (75%) and testing (25%) set using the `tidymodels` package. After creating the test set, we will put the test set away in a lock box and not touch it again until we have found the best k-nn classifier we can make using the *training set*. We will use the variable `fruit_name` as our class label.

To create the training and test set, first use the `initial_split` function to split `fruit_data`. Specify you want to use *75%* of the data. For the `strata` argument, place the variable we want to classify, `fruit_name`. Name the object you create `fruit_split`.

Next, pass the `fruit_split` object to the `training` and `testing` functions and name your respective objects `fruit_train` and `fruit_test`.

```
# Set the seed. Don't remove this!
set.seed(3456)

# Randomly take 75% of the data in the training set.
# This will be proportional to the different number of fruit names in the dataset.

#... <- initial_split(..., prop = ..., strata = ...)
#... <- training(...)
#... <- testing(...)
```

```
set.seed(3456)

fruit_split <- initial_split(fruit_data, prop = 0.75, strata = fruit_name)
fruit_train <- training(fruit_split)
fruit_test <- testing(fruit_split)
```

So far, we have split the training and testing datasets as well as preprocessed the data. Now, let's create our K-nearest neighbour classifier with only the training set using the `tidymodels` package. First, create the classifier by specifying that we want $K = 3$ neighbors and that we want to use the *straight-line* distance which is the same as Euclidean distance. *Assign your answer to an object called* ***`knn_spec`***.

Next, train the classifier with the training data set using the `workflow` function. This function allows you to bundle together your pre-processing, modeling, and post-processing requests. Scaffolding is provided below for you. *Assign your answer to an object called* ***`fruit_fit`***.

```
set.seed(2020) # DO NOT REMOVE

#... <- nearest_neighbor(weight_func = ..., neighbors = ...) |>
#       set_engine(...) |>
#       set_mode(...)

#... <- workflow() |>
#       add_recipe(...) |>
#       add_model(...) |>
#       fit(data = ...)
```

```r
set.seed(2020) # DO NOT REMOVE

knn_spec <- nearest_neighbor(weight_func = "rectangular", neighbors = 3) |>
      set_engine("kknn") |>
       set_mode("classification")

fruit_fit <- workflow() |>
  add_recipe(fruit_data_recipe) |>
  add_model(knn_spec) |>
  fit(data = fruit_train)

fruit_fit
```

```
== Workflow [trained] ==========================================================
Preprocessor: Recipe
Model: nearest_neighbor()

-- Preprocessor ----------------------------------------------------------------
2 Recipe Steps

* step_center()
* step_scale()

-- Model -----------------------------------------------------------------------

Call:
kknn::train.kknn(formula = ..y ~ ., data = data, ks = min_rows(3,     data, 5), kernel = ~"re

Type of response variable: nominal
Minimal misclassification: 0.1627907
Best kernel: rectangular
Best k: 3
```

Now that we have created our K-nearest neighbor classifier object, let's predict the class labels for our test set.

First, pass your fitted model and the **test dataset** to the `predict` function. Then, use the `bind_cols` function to add the column of predictions to the original test data.

Assign your answer to an object called ***`fruit_test_predictions`****.*

```r
set.seed(2020) # DO NOT REMOVE

#... <- predict(... , ...) |>
#       ...(...)
```

```r
set.seed(2020) # DO NOT REMOVE

fruit_test_predictions <- predict(fruit_fit, fruit_test) |>
  bind_cols(fruit_test)


fruit_test_predictions
```

```
# A tibble: 16 x 8
   .pred_class fruit_label fruit_name fruit_subtype     mass width height
   <fct>             <dbl> <fct>      <chr>            <dbl> <dbl>  <dbl>
 1 apple                 1 apple      granny_smith       180   8      6.8
 2 mandarin              2 mandarin   mandarin            80   5.9    4.3
 3 orange                1 apple      braeburn           178   7.1    7.8
 4 orange                1 apple      golden_delicious   164   7.3    7.7
 5 apple                 1 apple      golden_delicious   156   7.7    7.1
 6 apple                 1 apple      cripps_pink        170   7.6    7.9
 7 apple                 3 orange     selected_seconds   140   6.7    7.1
 8 apple                 3 orange     selected_seconds   164   7.2    7
 9 orange                3 orange     turkey_navel       190   7.5    8.1
10 apple                 3 orange     turkey_navel       154   7.3    7.3
11 apple                 3 orange     turkey_navel       144   6.8    7.4
12 lemon                 4 lemon      spanish_belsan     194   7.2   10.3
13 lemon                 4 lemon      spanish_belsan     200   7.3   10.5
14 lemon                 4 lemon      spanish_belsan     186   7.2    9.2
15 lemon                 4 lemon      unknown            118   5.9    8
16 lemon                 4 lemon      unknown            116   5.9    8.1
# i 1 more variable: color_score <dbl>
```

Great! We have now computed some predictions for our test datasets! From glancing at the dataframe above, it looks like most of them are correct, but wouldn't it be interesting if we could find out our classifier's accuracy?

Thankfully, the `metrics` function from the `tidymodels` package can help us. To get the statistics about the quality of our model, you need to specify the `truth` and `estimate` arguments. In the `truth` argument, you should put the column name for the true values of the response

variable. In the `estimate` argument, you should put the column name for response variable predictions.

Assign your answer to an object called ***`fruit_prediction_accuracy`****.*

```
set.seed(2020)
#... <- fruit_test_predictions |>
#         ...(truth = ..., estimate = ...)
```

```
set.seed(2020)
fruit_test_predictions |>
  metrics(truth = fruit_name, estimate = .pred_class) |>
  filter(.metric == "accuracy")
```

```
# A tibble: 1 x 3
  .metric  .estimator .estimate
  <chr>    <chr>          <dbl>
1 accuracy multiclass     0.625
```

Now, let's look at the *confusion matrix* for the classifier. This will show us a table comparing the predicted labels with the true labels.

A confusion matrix is essentially a classification matrix. The columns of the confusion matrix represent the actual class and the rows represent the predicted class (or vice versa). Shown below is an example of a confusion matrix.

		Actual Values	
		Positive	Negative
Predicted Value	Positive	True Positive	False Positive
	Negative	False Negative	True Negative

- A **true positive** is an outcome where the model correctly predicts the positive class.
- A **true negative** is an outcome where the model correctly predicts the negative class.
- A **false positive** is an outcome where the model incorrectly predicts the positive class.
- A **false negative** is an outcome where the model incorrectly predicts the negative class.

We can create a confusion matrix by using the `conf_mat` function. Similar to the `metrics` function, you will have to specify the `truth` and `estimate` arguments. *Assign your answer to an object called* ***`fruit_mat`****.*

```r
set.seed(2020) # DO NOT REMOVE

#... <- fruit_test_predictions |>
#       ...(truth = ..., estimate = ...)
```

```r
set.seed(2020)
fruit_mat <- fruit_test_predictions |>
             conf_mat(truth = fruit_name, estimate = .pred_class)
fruit_mat
```

```
          Truth
Prediction apple lemon mandarin orange
  apple        3     0        0      4
  lemon        0     5        0      0
  mandarin     0     0        1      0
  orange       2     0        0      1
```

Reading `fruit_mat`, how many observations were labelled correctly?

A. 16

B. 12

C. 10

D. 13

2. Cross-validation

The vast majority of predictive models in statistics and machine learning have parameters that you have to pick. For the past few exercises, we have had to pick the number of neighbours for the class vote, which we have done arbitraily. But, is it possible to make this selection, *i.e., tune the model, in a principled way?* Ideally, we want to pick the number of neighborurs to maximize the performance of our classifier on data *it hasn't seen yet.*

An important aspect of the tuning process is that we can, if we want to, split our training data again, train and evaluate a classifier for each split, and then choose the parameter based on all of the different results. If we just split our training data once, our best parameter choice will depend strongly on the randomness from how this single split was made. Using multiple different splits, we'll get a more robust estimate of accuracy, which will lead to a more suitable choice of the number of neighbours K to perform well on unseen data.

The idea of training and evaluating models on multiple training data splits times is called "cross-validation". In cross-validation, we split our overall training data into C evenly-sized chunks, and then iteratively use 1 chunk as the **validation set** and combine the remaining $C-1$ chunks as the **training set.** The validation set is used in a similar was as the test set, **except** that the test set is only used once at the end to report model performance whether we use model performance on the validation set to select the model during cross-validation.

We can perform a cross-validation in R using the `vfold_cv` function. To use this function, you have to identify the training set as well as specify the `v` (the number of folds) and the `strata` argument (the label variable). For this exercise, perform 5-fold cross-validation.

Assign your answer to an object called `fruit_vfold`.

```
set.seed(2020) # DO NOT REMOVE

#... <- vfold_cv(..., v = ..., strata = ...)
```

```
set.seed(2020)
fruit_vfold <- vfold_cv(fruit_train, v = 5, strata = fruit_name)
```

Now perform the workflow analysis again. You can reuse the `fruit_recipe` and `knn_spec` objects you made earlier. When you are fitting the knn model, use the `fit_resamples` function instead of the `fit` function for training. This function will allow us to run a cross-validation on each train/validation split we created in the previous question.

Assign your answer to an object called `fruit_resample_fit`.

```
set.seed(2020) # DO NOT REMOVE

#... <- workflow() |>
#       add_recipe(...) |>
#       add_model(...) |>
#       fit_resamples(resamples = ...)
```

```
set.seed(2020)
fruit_resample_fit <- workflow() |>
                      add_recipe(fruit_data_recipe) |>
                      add_model(knn_spec) |>
                      fit_resamples(resamples = fruit_vfold)
```

```
> A | warning: No observations were detected in `truth` for level(s): 'mandarin'
               Computation will proceed by ignoring those levels.

There were issues with some computations   A: x1

There were issues with some computations   A: x3
There were issues with some computations   A: x3
```

Now that we have ran a cross-validation on each train/validation split, one has to ask, how accurate was the classifier's validation across the folds? We can aggregate the *mean* and *standard error* by using the `collect_metrics` function. The standard error is essentially a measure of how uncertain we are in the mean value.

Use the `collect_metrics` function on the `fruit_resample_fit` object and assign your answer to an object called `fruit_metrics`.

```
fruit_resample_fit |>
  collect_metrics()
```

```
# A tibble: 2 x 6
  .metric  .estimator  mean     n std_err .config
  <chr>    <chr>      <dbl> <int>   <dbl> <chr>
1 accuracy multiclass 0.763     5  0.0378 Preprocessor1_Model1
2 roc_auc  hand_till  0.933     5  0.0282 Preprocessor1_Model1
```

4. Parameter value selection

Using a 5-fold cross-validation, we have established a prediction accuracy for our classifier.

If we had to improve our classifier, we have to change the parameter: number of neighbours, K. Since cross-validation helps us evaluate the accuracy of our classifier, we can use cross-validation to calculate an accuracy for each value of K in a reasonable range, and then pick the value of K that gives us the best accuracy.

The great thing about the `tidymodels` package is that it provides a very simple syntax for tuning models. Using `tune()`, each parameter in the model can be adjusted rather than given a specific value.

Create a new K-nearest neighbor model specification but instead of specifying a particular value for the `neighbors` argument, insert `tune()`.

Assign your answer to an object called ***knn_tune****.*

```
#write code
```

```
knn_tune <- nearest_neighbor(weight_func = "rectangular",
                             neighbors = tune()) |>
  set_engine("kknn") |>
  set_mode("classification")
```

Now, create a `workflow()` analysis that combines `fruit_recipe` and our new `knn_tune` model specification.

Instead of using `fit` or `fit_resamples`, we will use the `tune_grid` function to fit the model for each value in a range of parameter values. For the `resamples` argument, input the cross-validation `fruit_vfold` model we created earlier. The `grid` argument specifies that the tuning should try X amount of values of the number of neighbors K when tuning. For this exercise, use *10* K values when tuning which is specified by `k_vals`.

Finally, aggregate the mean and standard error by using the `collect_metrics` function.

Assign your answer to an object called ***knn_results****.*

```
set.seed(1234) # set the seed, don't remove this
k_vals <- tibble(neighbors = seq(from = 1, to = 10, by = 1))
#... <- workflow() |>
#       add_recipe(...) |>
#       add_model(...) |>
#       tune_grid(resamples = ..., grid = ...) |>
#       ...
```

```
set.seed(1234) # set the seed, don't remove this
k_vals <- tibble(neighbors = seq(from = 1, to = 10, by = 1))
knn_results <- workflow() |>
       add_recipe(fruit_data_recipe) |>
       add_model(knn_tune) |>
       tune_grid(resamples = fruit_vfold, grid = k_vals) |>
       collect_metrics()
```

Now, let's find the best value of the number of neighbors.

First, from `knn_results`, filter for `accuracy` from the `.metric` column.

Assign your answer to an object called ***accuracies****.*

Next, create a line plot using the `accuracies` dataset with `neighbors` on the x-axis and the `mean` on the y-axis.

Assign your answer to an object called ***`accuracy_versus_k`****.*

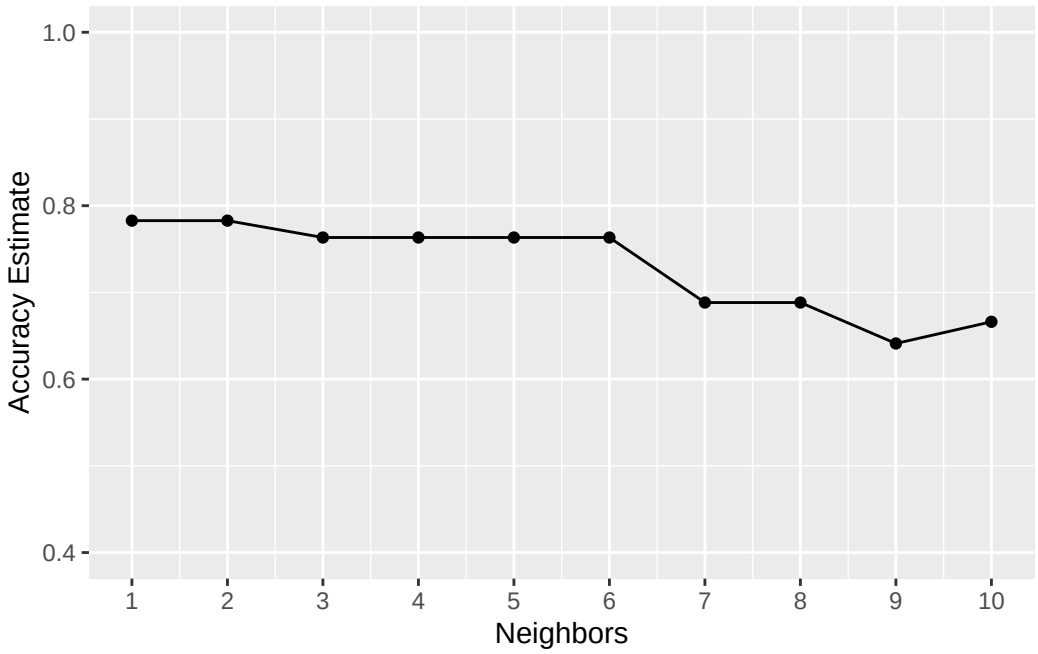
```
#... <- knn_results |>
#       filter(...)

#... <- ggplot(..., aes(x = ..., y = ...))+
#       geom_point() +
#       geom_line() +
#       labs(x = "Neighbors", y = "Accuracy Estimate") +
#       scale_x_continuous(breaks = seq(0, 14, by = 1)) +  # adjusting the x-axis
#       scale_y_continuous(limits = c(0.4, 1.0)) # adjusting the y-axis
```

```
accuracies <- knn_results |>
       filter(.metric == "accuracy")

accuracy_versus_k <- ggplot(accuracies, aes(x = neighbors, y = mean))+
       geom_point() +
       geom_line() +
       labs(x = "Neighbors", y = "Accuracy Estimate") +
       scale_x_continuous(breaks = seq(0, 14, by = 1)) +  # adjusting the x-axis
       scale_y_continuous(limits = c(0.4, 1.0)) # adjusting the y-axis

accuracy_versus_k
```



from the plot above, we can see that $K = 2$, 3, or 6 provides the highest accuracy. Larger K values result in a reduced accuracy estimate. Remember: the values you see on this plot are estimates of the true accuracy of our classifier. Although the $K = 2$, 3 or 4 value is higher than the others on this plot, that doesn't mean the classifier is necessarily more accurate with this parameter value!

Great, now you have completed a full workflow analysis with cross-validation using the `tidymodels` package! For your information, we can choose any number of folds and typically, the more we use the better our accuracy estimate will be (lower standard error). However, more folds would mean a greater computation time. In practice, C is chosen to be either 5 or 10.

Assignment 5 (Total Marks:39)

Deadline: Friday Nov 17st, 11:59 p.m

1. What does tuning a parameter mean? Is it part of testing the model? Explain. [2pts]
2. Below is an R code segment that imports the `tidymodels` and `discrim` packages, in addition to loading the `mobile_carrier_df dataset`.

```
library(tidymodels)
library(discrim)
```

```
Attaching package: 'discrim'


The following object is masked from 'package:dials':

    smoothness
```

```r
mobile_carrier_df <-
  readRDS(url('https://gmubusinessanalytics.netlify.app/data/mobile_carrier_data.rds'))
```

The `mobile_carrier_df` dataframe holds data on customers from a nationwide mobile service provider in the U.S.

In this dataset, each row corresponds to a customer and indicates whether they terminated their service. The target variable is `canceled_plan`, which is categorical with 'yes' or 'no' as possible values. The features included provide details on the customers' geographic location and their mobile phone usage patterns.

2.1 Please examine the dataset. Is there a need to convert the data type of the response variable? [1]

2.2 Construct a bar chart with ggplot2 to display the count of records per category in `canceled_plan`. Color the bars light blue and label the x and y axes appropriately. Apply the classic theme to your plot. [3]

2.3 Based on the graph, do you think this dataset is balanced? Explain your reseaoning briefly [1]

2.4 Is there any missing value in this dataset? [1]

2.5 using `tidymodels`,allocate 80% of the dataset to mobile_training for the training subset and 20% to mobile_testing for the testing subset. Ensure that the split maintains the category proportions within each subset. use `set.seed(271)`. [2]

2.6 Create a recipe by using the formula below to include only numeric variables for the predictors and `canceled_plan` as the response variable. Use proper functions to scale and center the numeric variables.[3]

```r
my_formula <- formula(canceled_plan~ number_vmail_messages+total_day_minutes+total_day_calls
```

2.7 Create 6 cross validation fold for hyper parameter tuning, name it `mobile_folds`. use the same seed; `set.seed(271)`. [1]

2.8 Specify your KNN model, set the proper parameter that allows tuning in your downstream analysis.[2]

2.9 Create a workflow by combing your model and recipe.[2]

2.10 Create a tibble of k values called `k_vals` that contains `10, 15, 25, 45, 60, 80, 100`.[1]

2.11 Now, complete your workflow by doing grid search (tune_grid()) to perform hyperparameter tuning using `k_vals` and `mobile_folds`. set seed to 314.[2]

2.12 Provide a table of the accuracy for each k.[2]

2.13 which k would you choose to be the final hyperparameter for your model? Explain your reasons. [2]

2.14 Now, create a another KNN specification (`knn25_spec`) and a seperate workflow that use best number of neighbors from prevoius to fit the model.set seed to 176.[3]

2.15 Predict the test data by the fitted model.Add the true class to the predicted dataframe.[2]

2.16 Provide a confusion matrix to evaluate the performance of your model.[1]

2.17 Calculate the Precision and recall for this classifier.[2]

3. Describe advantages and disadvantages of the k-nearest neighbour classification algorithm.[3 pts]
4. What does overfitting and underfitiing mean in machine learning? [3 pts]

General formating expectations

Code formatting. Code must appear within an R chunk with the appropriate chunk options (e.g. `echo = TRUE` unless otherwise specified)

````
```{r, echo=TRUE}
# this is some simple addition
x <- 2 + 4
x
```
````

```
[1] 6
```

or inline with text:

````
# inline R code:
This is some text with inline R code: `r mean(c(1, 2, 3, 4, 5))`.
````

which renders to: This is some text with inline R code: 3.

Text formatting Narrative and word answers should be typeset using regular text (as opposed to using using comments (preceded by `#`) within an R chunk. The use of of markdown formatting to improve readability is encouraged. Simple examples include:

- headers (second-level headers are preceded by `##`)
- *italics* (*italics* or _italics_),
- **bold** (**bold**),
- `typewritter` text (‘typewritter‘)

Labels all HTML documents should satisfy the following criteria:

- assignments should be named `assignment<x>_<y>.html` where `<x>` is replaced by the assignment number and ‘ is replaced by your student number
- Your full name, student number, assignment number, and course number should appear somewhere near the top of the rendered document
- Questions should be labeled either by the use of headers or numbered lists.

> **!** Important
>
> **Submissions in any other format (e.g. Rmd, word document) will incur a 20% penalty.**