Lab Tutorial 5

Ladan Tazik

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Summary:

Towards the end of the lab, you will find a set of assignment exercises (Assignment 4). These assignments are to be completed and submitted on Canvas.

Lab 05

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

- Recognize situations where a simple classifier would be appropriate for making predictions.
- Explain the k-nearest neighbor classification algorithm.
- Interpret the output of a classifier.
- Compute, by hand, the distance between points when there are two explanatory variables/predictors.
- Perform k-nearest neighbour classification in R using `tidymodels` to predict the class of a single new observation.

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

Classification for Breast Cancer dataset

Breast cancer can be diagnosed by performing a biopsy, a process where tissue is removed from the body and examined for the presence of disease. Traditionally these procedures were quite invasive; modern methods such as fine needle aspiration, used to collect the present data set, extract only a small amount of tissue and are less invasive.

Based on a digital image of each breast tissue sample collected for this data set, ten different variables were measured for each cell nucleus in the image (items 3–12 of the list of variables below), and then the mean for each variable across the nuclei was recorded. Each image additionally was given a unique ID and a diagnosis by a physician. Therefore, the total set of variables per image in this data set is:

1. ID: identification number
2. Class: the diagnosis (M = malignant or B = benign)
3. Radius: the mean of distances from center to points on the perimeter
4. Texture: the standard deviation of gray-scale values
5. Perimeter: the length of the surrounding contour
6. Area: the area inside the contour
7. Smoothness: the local variation in radius lengths
8. Compactness: the ratio of squared perimeter and area
9. Concavity: severity of concave portions of the contour
10. Concave Points: the number of concave portions of the contour
11. Symmetry: how similar the nucleus is when mirrored
12. Fractal Dimension: a measurement of how "rough" the perimeter is.

Suppose we have past data of cancer tumour cell diagnosis labelled "benign" and "malignant". Do you think a new cell with Concavity = 3.3 and Perimeter = 0.2 would be malignant? How did you decide?

Question 0.1: What kind of data analysis question is this?

- descriptive
- exploratory
- predictive
- inferential
- causal

> `Predictive`

The breast cancer data for the next part have been **standardized (centred and scaled)** for you already. We will implement these steps later, but for now, know the data has been standardized. Therefore the variables are unitless and hence why we have zero and negative values for variables like Radius.

Question 0.2

Read the `clean-wdbc-data.csv` file (found in the `data` module on Canvas) using the `read_csv()` function into the notebook and store it as a data frame. Name it `cancer`.

```r
cancer <- read_csv("https://irene.vrbik.ok.ubc.ca/data/clean-wdbc-data.csv")
```

```
Rows: 569 Columns: 12
-- Column specification --------------------------------------------------------
Delimiter: ","
chr  (1): Class
dbl (11): ID, Radius, Texture, Perimeter, Area, Smoothness, Compactness, Con...

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.
```

```r
glimpse(cancer)
```

```
Rows: 569
Columns: 12
$ ID                <dbl> 842302, 842517, 84300903, 84348301, 84358402, 843786~
$ Class             <chr> "M", "M", "M", "M", "M", "M", "M", "M", "M", "M", "M~
$ Radius            <dbl> 1.8850310, 1.8043398, 1.5105411, -0.2812170, 1.29743~
$ Texture           <dbl> -1.35809849, -0.36887865, -0.02395331, 0.13386631, -~
$ Perimeter         <dbl> 2.30157548, 1.53377643, 1.34629062, -0.24971958, 1.3~
$ Area              <dbl> 1.999478159, 1.888827020, 1.455004298, -0.549537693,~
$ Smoothness        <dbl> 1.306536657, -0.375281748, 0.526943750, 3.391290721,~
$ Compactness       <dbl> 2.61436466, -0.43006581, 1.08198014, 3.88997467, -0.~
$ Concavity         <dbl> 2.10767182, -0.14661996, 0.85422232, 1.98783917, 0.6~
$ Concave_points    <dbl> 2.29405760, 1.08612862, 1.95328166, 2.17387323, 0.72~
$ Symmetry          <dbl> 2.7482041, -0.2436753, 1.1512420, 6.0407261, -0.8675~
$ Fractal_dimension <dbl> 1.93531174, 0.28094279, 0.20121416, 4.93067187, -0.3~
```

Question 0.3 True or False:

After looking at the first six rows of the `cancer` data fame, suppose we asked you to predict the variable "area" for a new observation. **Is this a classification problem?**

Note

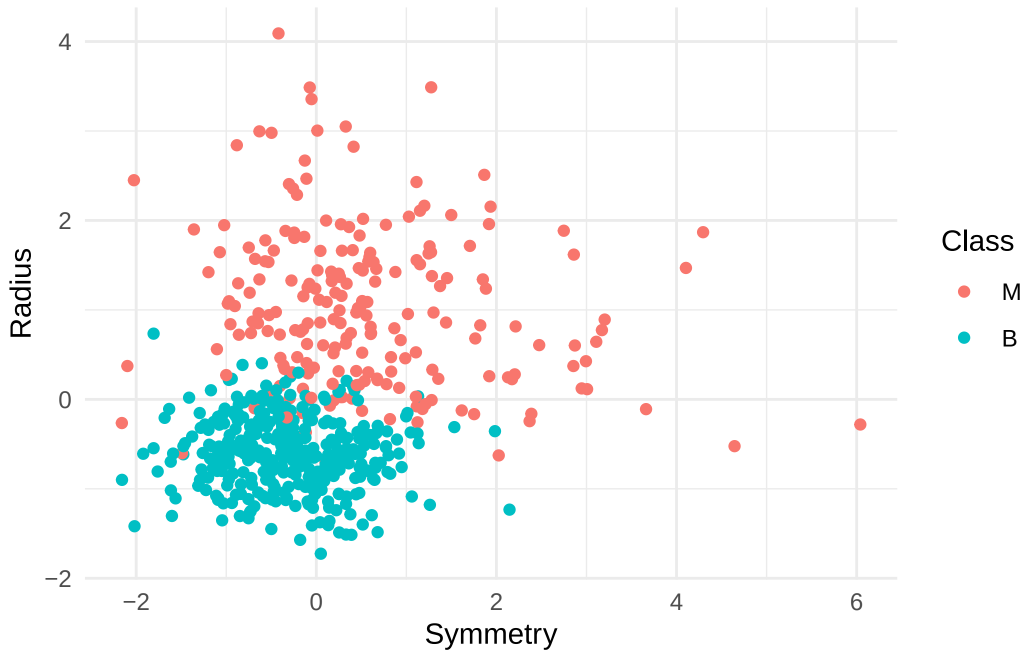
Look at the values in the Area column - are they categorical? Remember, classification problems involve predicting class labels for categorical data.

We will be treating `Class` as a categorical variable, so Let's convert it into a factor using the `as_factor()` function.

```
cancer <- cancer |>
  mutate(Class = as_factor(Class))
```

Question 0.5 Create a scatterplot of the data with `Symmetry` on the x-axis and `Radius` on the y-axis. Modify your aesthetics by colouring for `Class`. As you create this plot, ensure you follow the guidelines for creating effectxfruiive visualizations. In particular, note on the plot axes whether the data is standardized or not. Assign your plot to an object called `cancer_plot`.

```
cancer_plot <- cancer |>
               ggplot(aes(x = Symmetry, y = Radius, color = Class)) +
               geom_point()+
                theme_minimal()
cancer_plot
```



Just by looking at the scatterplot above, how would you classify an observation with `Symmetry` = 1 and `Radius` = 1 (Benign or Malignant)?

Note

Looking at the location of (1,1) the data point is Malignant.

K-nearest neighbours classification

Predict the label / class for a new observation using the K closest points from our dataset.

The following steps are the backbone of KNN classification method:

1. Compute the distance between the new observation and each observation in our *training set.*Recall from your reading, the training dataset is the sample of data used to fit the model.
2. Sort the data in ascending order according to the distances
3. Choose the top K rows as "neighbours"
4. Assign the label/class for the new observation based on majority votes from "neighbors".

1. Compute Distances

Let's compute the distance between the first and second observation in the breast cancer dataset using the explanatory variables/predictors `Symmetry` and `Radius`. Recall we can calculate the distance between two points using the following formula:

$$Distance = \sqrt{(a_x - b_x)^2 + (a_y - b_y)^2}$$

Question 1.1

First, extract the coordinates for the two observations and assign them to objects called:

- `ax` (Symmetry value for the first row)
- `ay` (Radius value for the first row)
- `bx` (Symmetry value for the second row)
- `by` (Radius value for the second row).

Scaffolding for ***`ax`*** *is given.* > Note we are using the function `pull()` because we want the numeric value (and object) as our output rather than a `tibble` type object so we can do calculations later on. You can verify the object type in R with the `class()` function. Check the class of `ax` with and without the `pull()` function and see what you get! Use `?pull` to learn more.

```
# ax <- slice(cancer, 1) |>     pull(Symmetry)
```

```
ax <- slice(cancer, 1) |>     pull(Symmetry)

ay <- slice(cancer, 1) |>     pull(Radius)

bx <- slice(cancer, 2) |>     pull(Symmetry)

by <- slice(cancer, 2) |>     pull(Radius)
```

Question 1.2 Plug the coordinates into the distance equation. Assign your answer to an object called `answer1.2`.

```
#... <- sqrt((... - ...)^... + (... - ...)^...)
```

```
answer1.2 <- sqrt(( ax-bx )^2 + (ay - by)^2)
```

Question 1.3

Now we'll do the same thing *with 3 explanatory variables/predictors*: `Symmetry`, `Radius` and `Concavity`. Again, use the first two rows in the data set as the points you are calculating the distance between (point *a* is row 1, and point *b* is row 2).

Find the coordinates for the third variable (Concavity) and assign them to objects called `az` and `bz`. Use the scaffolding given in **Question 1.1** as a guide.

```
az <- slice(cancer, 1) |>     pull(Concavity)

bz <- slice(cancer, 2) |>     pull(Concavity)
```

Question 1.4

Again, calculate the distance between the first and second observation in the breast cancer dataset using 3 explanatory variables/predictors: `Symmetry`, `Radius` and `Concavity`.

Assign your answer to an object called `answer1.4`. Use the scaffolding given to calculate `answer1.2` as a guide.

```
answer1.4 <- sqrt((ax-bx)^2 + (ay - by)^2 +(az-bz)^2)
```

Question 1.5

Let's do this without explicitly making coordinate variables!

Create a vector of the coordinates for each point. Name one vector `point_a` and the other vector `point_b`. Within the vector, the order of coordinates should be: `Symmetry`, `Radius`, `Concavity`.

Fill in the `...` in the cell below.

> Here will use `select` and `as.numeric` instead of `pull` because we need to get the numeric values of 3 columns. `pull`, that we used previously, only works to extract the numeric values from a single column.

```r
# This is only the scaffolding for one vector
# You need to make another one for row number 2!

#... <- slice(cancer, 1) |>
#    select(..., Radius, ...) |>
#    as.numeric()
```

```r
point_a <- slice(cancer, 1) |> select(Symmetry, Radius, Concavity) |> as.numeric()

point_b <- slice(cancer, 2) |> select(Symmetry, Radius, Concavity) |> as.numeric()
```

Question 1.6

Compute the squared differences between the two vectors, `point_a` and `point_b`. The result should be a vector of length 3 named `dif_square`. *Hint:* `^` *is the exponent symbol in R.*

```r
dif_square <- (point_a - point_b)^2
```

Question 1.6.1

Sum the squared differences between the two vectors, `point_a` and `point_b`. The result should be a single number named `dif_sum`.

Hint: the `sum` *function in R returns the sum of the elements of a vector*

```r
dif_sum <- sum(dif_square)
```

Question 1.6.2

Square root the sum of your squared differences. The result should be a double named `root_dif_sum`.

```r
root_dif_sum <- sqrt(dif_sum)
```

Question 1.6.3

If we have more than a few points, calculating distances as we did in the previous questions is VERY tedious. Let's use the `dist()` function to find the distance between the first and second observation in the breast cancer dataset using Symmetry, Radius and Concavity.

Fill in the ... in the cell below.

Assign your answer to an object called `dist_cancer_two_rows`.

```
# ... <- cancer  |>
#    slice(1,2)  |>
#    select(..., ..., Concavity)  |>
#    dist()
# your code
```

```
dist_cancer_two_rows <- cancer |>
  slice(1,2)|>
  select(Symmetry, Radius, Concavity)|>
  dist()
```

Question 1.6.4 True or False:

Compare `answer1.4`, `root_dif_sum`, and `dist_cancer_two_rows`.

Are they all the same value?

Note: We can go beyond 3 predictors

For two observations u, v, each with m variables (columns) labelled $1, \ldots, m$,

Distance $= \sqrt{(u_1 - v_1)^2 + (u_2 - v_2)^2 + \cdots + (u_m - v_m)^2}$

Aside from that, it's the same algorithm!

2.A Simple Example Done Manually

Question 2.0.0

Let's take a random sample of 5 observations from the breast cancer dataset using the `sample_n` function. To make this random sample reproducible, we will use `set.seed(20)`. This means that the random number generator will start at the same point each time when we run the code and we will always get back the same random samples.

We will focus on the predictors Symmetry and Radius only. Thus, we will need to select the columns `Symmetry` and `Radius` and `Class`. Save these 5 rows and 3 columns to a data frame named `small_sample`.

Fill in the ... in the scaffolding provided below.

```
#set.seed(20)
#... <- sample_n(cancer, 5) |>
```

```
#    select(...)
```

```
set.seed(20)

small_sample<- sample_n(cancer, 5) |> select(Symmetry, Radius, Class)
```

Question 2.0.1

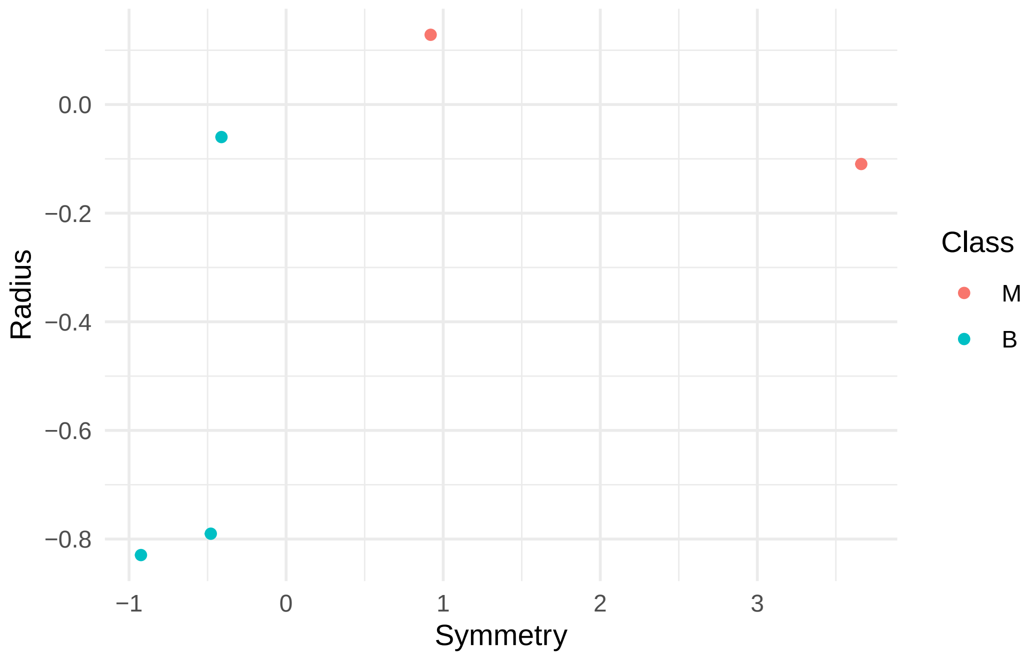
Finally, create a scatter plot where `Symmetry` is on the x-axis, and `Radius` is on the y-axis. Color the points by `Class`. Name your plot `small_sample_plot`.

Fill in the `...` in the scaffolding provided below.

As you create this plot, ensure you follow the guidelines for creating effective visualizations. In particular, note on the plot axes whether the data is standardized or not.

```
#... <- ...|>
#    ggplot(...) +
#        geom_...() +
#        ...
```

```
set.seed(20)
small_sample_plot <- small_sample |>
  ggplot(aes(x = Symmetry, y = Radius, color = Class)) +
  geom_point()+
  theme_minimal()
small_sample_plot
```



Question 2.1

Suppose we are interested in classifying a new observation with `Symmetry = 0.5` and `Radius = 0`, but unknown `Class`. Using the `small_sample` data frame, add another row with `Symmetry = 0.5`, `Radius = 0`, and `Class = "unknown"`.

Fill in the `...` in the scaffolding provided below.

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

```
#... <- ... |>
#    add_row(Symmetry = ..., ... = 0, Class = ...)
```

```
newData <- small_sample|> add_row(Symmetry = 0.5, Radius = 0, Class = "unknown")
```

Question 2.2

Compute the distance between each pair of the 6 observations in the `newData` dataframe using the `dist()` function based on two variables: `Symmetry` and `Radius`. Fill in the `...` in the scaffolding provided below.

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

```
# ... <- newData |>
#    select(..., ...) |>
#    ...() |>
#    as.matrix()
```

```
dist_matrix <- newData |>
  slice(1:6) |>
  select(Symmetry, Radius) |>
  dist() |>
  as.matrix()
```

Question 2.3 Multiple Choice:

In the table above, the row and column numbers reflect the row number from the data frame the `dist` function was applied to. Thus numbers 1 - 5 were the points/observations from rows 1 - 5 in the `small_sample` data frame. Row 6 was the new observation that we do not know the diagnosis class for. The values in `dist_matrix` are the distances between the points of the row and column number. For example, the distance between the point 2 and point 4 is 4.196683. And the distance between point 3 and point 3 (the same point) is 0.

Which observation is the nearest to our new point?

```
order(dist_matrix[6, c(1:5)]) #exclude the last column since it's the distance with itself

# The smallest value is at 5 so observation 5
```

Question 2.4 Multiple Choice:

Use the K-nearest neighbour classification algorithm with K = 1 to classify the new observation using your answers to **Questions 2.2 & 2.3**. Is the new data point predicted to be benign or malignant?

```
small_sample$Class[5]  #  look at the class of row 5
```

Question 2.5 Multiple Choice:

Using your answers to **Questions 2.2 & 2.3**, what are the three closest observations to your new point?

A. 1, 3, 2

B. 5, 1, 4

C. 5, 2, 4

D. 3, 4, 2

```
#B
```

Question 2.6 Multiple Choice:

We will now use the K-nearest neighbour classification algorithm with K = 3 to classify the new observation using your answers to **Questions 2.2 & 2.3**. Is the new data point predicted to be benign or malignant?

```
small_sample$Class[c(5,1,4)]  #
```

```
[1] M B B
Levels: M B
```

```
# 2/3 is B so the predicted class is B
```

Question 2.7

Compare your answers in 2.4 and 2.6. Are they the same?

Standardizing Data

When using K-nearest neighbour classification, the scale of each variable (i.e., its size and range of values) matters. Since the classifier predicts classes by identifying observations that are nearest to it, any variables that have a large scale will have a much larger effect than variables with a small scale. But just because a variable has a large scale doesn't mean that it is more important for making accurate predictions. - For example, suppose you have a data set with two attributes, height (in feet) and weight (in pounds).

$$distance1 = \sqrt{(202-200)^2 + (6-6)^2} = 2$$

$$distance2 = \sqrt{(200-200)^2 + (8-6)^2} = 2$$

Here if we calculate the distance we get 2 in both cases! A difference of 2 pounds is not that big, but a different in 2 feet is a lot.

So how we adjust that? What if one variable is much larger than the other?

Standardize: shift (center) and scale so that the average is 0 and the standard deviation is 1.

When all variables in a data set have a mean (center) of 0 and a standard deviation (scale) of 1, we say that the data have been **standardized**. standardizing the data can change things in an important way when we are using predictive algorithms. As a rule of thumb, standardizing your data should be a part of the preprocessing you do before any predictive modelling / analysis.

Introduction to the `tidymodels` package in R

Now that we understand how K-nearest neighbours (k-nn) classification works, let's get familar with the `tidymodels` R package. The benefit of using `tidymodels` is that it will keep our code simple, readable and accurate. Coding less and in a tidier format means that there is less chance for errors to occur.

`tidymodels` is a collection of packages and handles computing distances, standardization, balancing, and prediction for us!

Remember to install and load the the package `tidymodels`.

```r
library(tidyverse)
library(tidymodels)
options(repr.matrix.max.rows = 6)
```

1. Preprocess the data

In `tidymodels`, the `recipes` package is named after cooking terms.

1. Make a `recipe` to specify the predictors/response and preprocess the data.`recipe()`: Main argument in the formula.

Arguments: - formula - data

2. `prep()` & `bake()`: you can also `prep` and `bake` a recipe to see what the preprocessing does!

More specifically;

- The `prep()` function computes everything so that the preprocessing steps can be executed
- The `bake()` function takes a recipe and applies it to data and returns data

visit https://recipes.tidymodels.org/reference/index.html to see all the preprocessing steps.

Note: If you want to extract the pre-processed dataset: you can `prep()` and `bake()` but extracting the pre-processed data isn't necessary for the data analysis pipeline, since this will be done under the hood when the model is fit. We talk more about fitting the model in a bit.

We'll again focus on `Radius` and `Symmetry` as the two predictors. This time, we would like to predict the class of a new observation with `Symmetry = 1` and `Radius = 0`. This one is a bit tricky to do visually from the plot above, and so is a motivating example for us to compute the prediction using k-nn with the `tidymodels` package. Let's use `K = 7`.

Fill in `...` below for classifying the class of a tumor based on Symmetry and Radius variables.

```
# Standardize the cancer data
tumor_recipe <- recipe(... ~ ... + ..., data=cancer) |>
                 step_center(...) |>
                 step_scale(...) |>
                 prep() #just in case you want to save the scaled data
tumor_recipe
```

- first argument "Model formula"
- Left hand side of ~: "response" / thing we are trying to predict (can selectively remove, but another step)
- Right hand side: whatever columns you want to use as predictors (could use a . to use everything as a predictor)
- second argument: data frame
- pre-processing steps to standardize data

```r
tumor_recipe <- recipe(Class ~ Symmetry + Radius, data=cancer) |>
                  step_center(all_predictors()) |>
                  step_scale(all_predictors()) |>
                  prep()
tumor_recipe
```

```
-- Recipe ----------------------------------------------------------------------



-- Inputs


Number of variables by role


outcome:   1
predictor: 2
```

```
-- Training information

Training data contained 569 data points and no incomplete rows.



-- Operations

* Centering for: Symmetry, Radius | Trained

* Scaling for: Symmetry, Radius | Trained
```

You can find a full set of all the steps and variable selection functions on the recipe reference page

2. Build a model specification (`model_spec`) to specify the model and training algorithm

1. **model type**: kind of model you want to fit
2. **arguments**: model parameter values
3. **engine**: underlying package the model should come from
4. **mode**: type of prediction (some packages can do both classification and regression)

Question 3.1

Create a **model specification** for K-nearest neighbours classification by using the `nearest_neighbor()` function. Specify that we want to set `k = 7` and use the *straight-line distance*. Furthermore, specify the *computational engine* to be `"kknn"` for training the model with the `set_engine()` function. Finally, identify that this is a *classification* problem with the `set_mode()` function.

Name your model specification `knn_spec`.

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

```
knn_spec <- nearest_neighbor(weight_func = "gaussian", neighbors = 7) |>
      set_engine("kknn") |>
       set_mode("classification")

#or
#knn_spec <- nearest_neighbor(mode = "classification", engine = "kknn", weight_func = "gau
```

3. Put them together in a workflow and then `fit` it

Question 3.2

To train the model on the breast cancer dataset, pass `knn_spec` and the `cancer` dataset to the `fit()` function. Specify `Class` as your target variable and the `Symmetry` and `Radius` variables as your predictors. Name your fitted model as `knn_fit`.

```
# ... <- ... |>
#         fit(... ~ Symmetry + ..., data = ...)
```

```
knn_fit <- knn_spec |>
        fit(Class ~ Symmetry + Radius, data = cancer)
```

4. Predict a new class label using `predict`

Question 4.1

Now we will make our prediction on the `Class` of a new observation with a `Symmetry` of 1 and a `Radius` of 0. First, create a tibble with these variables and values and call it `new_obs`. Next, use the `predict()` function to obtain our prediction by passing `knn_fit` and `new_obs` to it. Name your predicted class as `class_prediction`.

```
#... <- tibble(... = 1,... = 0)
#... <- predict(..., ...)
```

```
new_obs <- tibble(Symmetry = 1,Radius = 0)
class_prediction <- predict(knn_fit, new_obs)
class_prediction
```

```
# A tibble: 1 x 1
  .pred_class
  <fct>
```

```
1 M
```

Question 4.2

Let's perform K-nearest neighbour classification again, but with three predictors. Use the `tidymodels` package and `K = 7` to classify a new observation where we measure `Symmetry = 1`, `Radius = 0` and `Concavity = 1`.

- Pass the same `knn_spec` from before to `fit`, but this time specify `Symmetry`, `Radius`, and `Concavity` as the predictors. Store the output in `knn_fit_2`.
- store the new observation values in an object called `new_obs_2`
- store the output of `predict` in an object called `class_prediction_2`

```
knn_fit2 <- knn_spec |>
        fit(Class ~ Symmetry + Radius + Concavity, data = cancer)

new_obs2 <- tibble(Symmetry = 1,Radius = 0, Concavity = 1)
class_prediction_2 <- predict(knn_fit2, new_obs2)
class_prediction_2
```

```
# A tibble: 1 x 1
  .pred_class
  <fct>
1 M
```

We may want to use our recipe across several steps as we train and test our model. To simplify this process, we can use a model workflow, which pairs a model and recipe together

```
tumor_workflow <- workflow() |>
    add_recipe(...) |>
    add_model(...)

tumor_fit <- ... |>
    fit(data=cancer)

tumor_workflow
```

```
tumor_workflow <- workflow() |>
    add_recipe(tumor_recipe) |>
    add_model(knn_spec)
```

```
tumor_fit <- tumor_workflow |>
    fit(data=cancer)
```

Assignment 4

Deadline: Wednesday Nov 1st, 11:59 p.m

1. Before applying k-nearest neighbour to a classification task, we need to scale the data. What is the purpose of this step? [1pt]

    a. To help speed up the knn algorithm.

    b. To convert all data observations to numeric values.

    c. To ensure all data observations will be on a comparable scale and contribute equal shares to the calculation of the distance between points.

    d. None of the above.

2. **Fruit Dataset**

In the agricultural industry, cleaning, sorting, grading, and packaging food products are all necessary tasks in the post-harvest process. Products are classified based on appearance, size and shape, attributes which helps determine the quality of the food. Sorting can be done by humans, but it is tedious and time consuming. Automatic sorting could help save time and money. Images of the food products are captured and analysed to determine visual characteristics.

The dataset contains observations of fruit described with four features 1- mass (in g) 2- width (in cm) 3- height (in cm) 4- color score (on a scale from 0 - 1).

2.1- Load the file, `fruit_data.csv`, into your workspace.`mutate()` the `fruit_name` column such that it is a *factor* using the `as_factor()` function. Assign your data to an object called `fruit_data`. [2pt]

2.2- Which of the columns should we treat as categorical variables?[1pt]

a. Fruit label, width, fruit subtype

b. Fruit name, color score, height

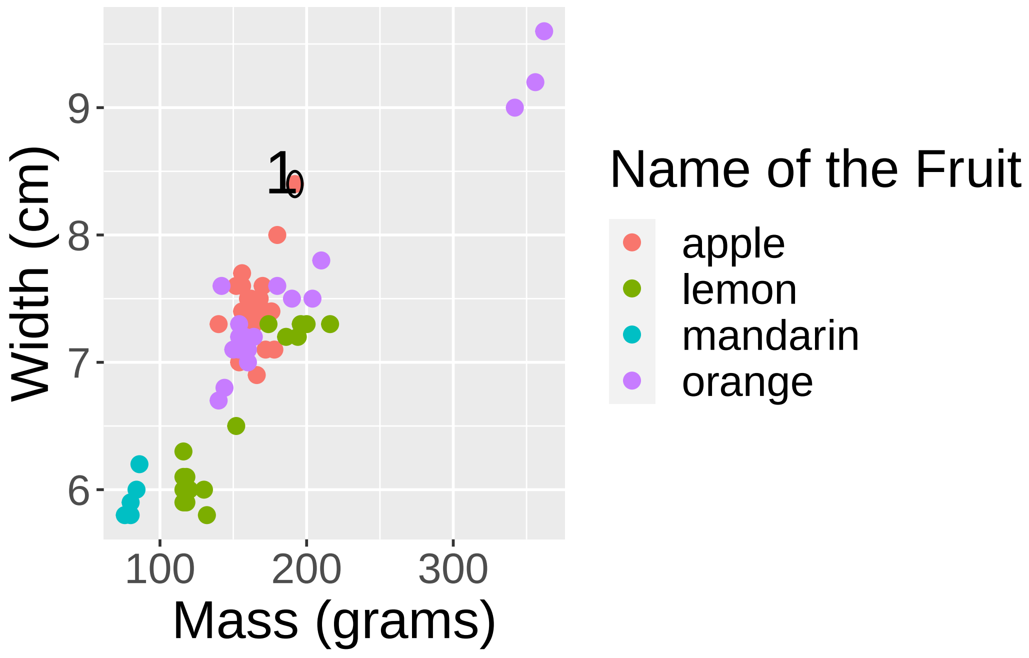
c. Fruit label, fruit subtype, fruit name

d. Color score, mass, width

2.3- Run the cell below, and find the nearest neighbour based on mass and width to the first observation just by looking at the scatterplot (the first observation has been circled for you). [1]

```r
# Run this cell.
options(repr.plot.width=10, repr.plot.height=7)
point1 <- c(192, 8.4)
point2 <- c(180, 8)
point44 <- c(194, 7.2)

fruit_data |>
    ggplot(aes(x=mass,
               y= width,
               colour = fruit_name)) +
        labs(x = "Mass (grams)",
             y = "Width (cm)",
            colour = 'Name of the Fruit') +
        geom_point(size = 2.5) +
        annotate("path",
                 x=point1[1] + 5*cos(seq(0,2*pi,length.out=100)),
                 y=point1[2] + 0.1*sin(seq(0,2*pi,length.out=100))) +
        annotate("text", x = 183, y =  8.5, label = "1", size = 8) +
        theme(text = element_text(size = 20))
```



Based on the graph generated, what is the `fruit_name` of the closest data point to the one circled?

a. apple

b. lemon

c. mandarin

d. orange

2.3 Using mass and width, calculate the distance between the first observation and the second observation.Assign your answer to an object called `fruit_dist_2`.[1]

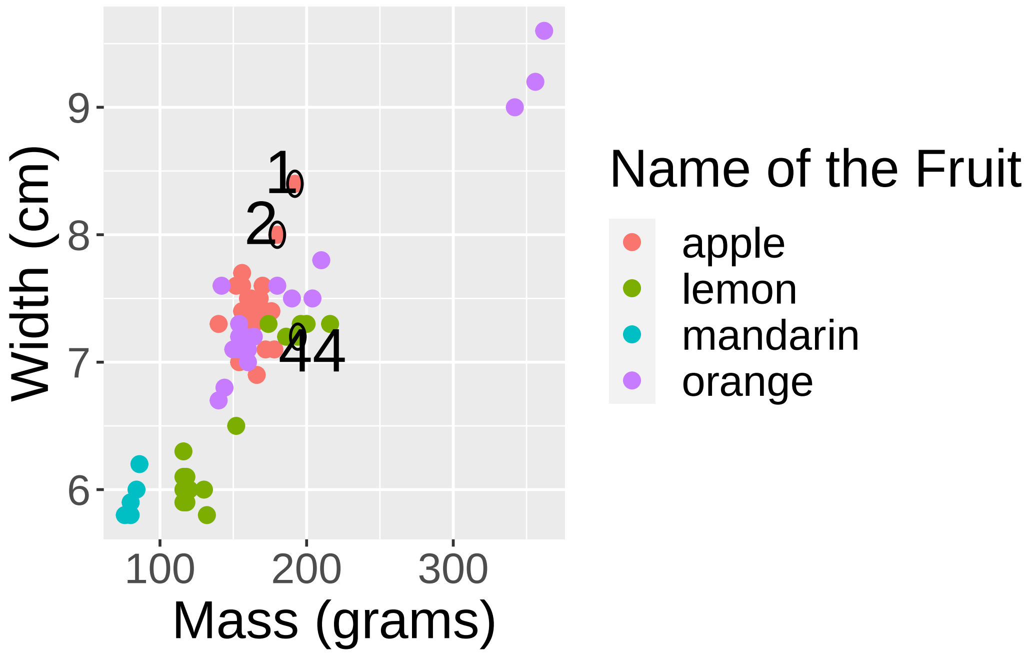
2.4 Calculate the distance between the first and the the 44th observation in the fruit dataset using the mass and width variables. Assign your answer to an object called `fruit_dist_44`.[1]

2.5 these three observations are circled on the plot from earlier.

```
options(repr.plot.width = 10, repr.plot.height = 7)

# Run this cell.
point1 <- c(192, 8.4)
point2 <- c(180, 8)
point44 <- c(194, 7.2)

fruit_data |>
    ggplot(aes(x = mass,
               y = width,
               colour = fruit_name)) +
        labs(x = "Mass (grams)",
             y = "Width (cm)",
            colour = 'Name of the Fruit') +
        geom_point(size = 2.5) +
        theme(text = element_text(size = 20)) +
        annotate("path",
                 x=point1[1] + 5*cos(seq(0,2*pi,length.out=100)),
                 y=point1[2] + 0.1*sin(seq(0,2*pi,length.out=100))) +
        annotate("text", x = 183, y =  8.5, label = "1", size = 8) +
        annotate("path",
                 x=point2[1] + 5*cos(seq(0,2*pi,length.out=100)),
                 y=point2[2] + 0.1*sin(seq(0,2*pi,length.out=100))) +
        annotate("text", x = 169, y =  8.1, label = "2", size = 8) +
        annotate("path",
                 x=point44[1] + 5*cos(seq(0,2*pi,length.out=100)),
                y=point44[2]+0.1*sin(seq(0,2*pi,length.out=100))) +
    annotate("text", x = 204, y =  7.1, label = "44", size = 8)
```



The distance between the first and second observation is 12.01 and the distance between the first and 44th observation is 2.33. By the formula, observation 1 and 44 are closer, however, if we look at the scatterplot the distance of the first observation to the second observation appears closer than to the 44th observation.

Which of the following statements is correct? [1]

A. A difference of 12 g in mass between observation 1 and 2 is large compared to a difference of 1.2 cm in width between observation 1 and 44. Consequently, mass will drive the classification results, and width will have less of an effect.

B. If we measured mass in kilograms, then we'd get different nearest neighbours.

C. We should standardize the data so that all variables will be on a comparable scale.

D. All of the above.

2.6 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`, `height`, and `color_score`. Name the recipe `fruit_data_recipe`.[3]

```r
# Set the seed. Don't remove this!
set.seed(9999)
#your solution
```

2.6.1 Use `bake` to apply recipe to your original data. Save the scaled data to `scaled_fruit_data`. [1]

2.7 Let's repeat **Question 2.3 and 2.4** with the scaled variables:

2.7.1 calculate the distance with the scaled mass and width variables between observations 1 and 2.[1]

2.7.2 calculate the distances with the scaled mass and width variables between observations 1 and 44. [1]

After you do this, think about how these distances compared to the distances you computed in **Question 1.2 and 1.3** for the same points.

Assign your answers to objects called `distance_2` and `distance_44` respectively.

2.8 Make a scatterplot of scaled mass on the horizontal axis and scaled color score on the vertical axis to show this relationship for each fruit name. (hint: use faceting). Ensure proper labeling for the x and y axes and color the data points using 'lightblue'." [4]

Assign your plot to an object called `fruit_plot`.

2.9 Make another scatterplot of scaled mass on the horizontal axis and scaled color score on the vertical axis and color the datapoints based of their fruit name. [1]

Assign your plot to an object called `fruit_plot2`.

2.10 Suppose we have a new observation in the fruit dataset with scaled mass 0.5 and scaled color score 0.5. Just by looking at the scatterplot, how would you classify this observation using K-nearest neighbours if you use K = 3? Explain how you arrived at your answer. [1]

2.11 Use the `tidymodels` package to predict `fruit_name` for another new observation. The new observation we are interested in has mass 150g and color score 0.73.

First, create the K-nearest neighbour model specification. Specify that we want $K = 5$ neighbors, `set_engine` to be `"kknn"`, and that each neighboring point should have the same weight when voting. Name this model specification as `my_knn`.

Then create a new recipe named `fruit_data_recipe_2` that centers and scales the predictors, but only uses `mass` and `color_score` as predictors.

Combine this with your recipe from before in a `workflow`, and fit to the `fruit_data` dataset.

Name the fitted model `fruit_fit`. [8]

Use `set.seed(9999)` at first

2.12 Create a new tibble where `mass = 150` and `color_score = 0.73` and call it `new_fruit`. Then, pass `fruit_fit` and `new_fruit` to the `predict` function to predict the class for the new fruit observation. Save your prediction to an object named `fruit_predicted`.

3. **Wheat Seed Dataset**

X-ray images can be used to analyze and sort seeds. In this data set, we have 7 measurements from x-ray images from 3 varieties of wheat seeds (Kama, Rosa and Canadian). The data set is available here: https://archive.ics.uci.edu/ml/machine-learning-databases/00236/seeds_dataset.txt

The seven measurements were taken below for each wheat kernel: 1. area A, 2. perimeter P, 3. compactness C = 4*pi*A/P^2, 4. length of kernel, 5. width of kernel, 6. asymmetry coefficient 7. length of kernel groove.

The last column in the data set is the variety label. The mapping for the numbers to varieties is listed below:

- 1 == Kama
- 2 == Rosa
- 3 == Canadian

3.1 Download the dataset directly from this URL using the read_table2() function. This function is especially useful when the columns are separated by one or more white spaces. Please take note that the dataset lacks column names, so be sure to set the appropriate parameter to handle this. [1]

3.2 We provide a string list of column names from the information above. Assign it to the dataset so each column gets it's name. [1]

```
mycol_names <- c("area", "perimeter", "compactness", "length", "width", "asymmetry_coeffic
```

3.3 Explore the dataset and determine the number of observations within each variety label. Be sure to enforce type correction for the variety label column. [2]

```
# Set the seed. Don't remove this!
set.seed(9999)

#This is the new observation to predict
new_seed <- tibble(area = 12.1,
                        perimeter = 14.2,
                        compactness = 0.9,
                        length = 4.9,
                        width = 2.8,
                        asymmetry_coefficient = 3.0,
                              groove_length = 5.1)
```

3.4 Similar to the question before, by using KNN with K = 4 and using all the features as predictors, What is the predicted class for the `new_seed` observation?(preprocess data as needed) [8]

A. Kama

B. Rosa

C. Canadian

General formating expectations

Code formatting (1 point). 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 (1 point) 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 (1 point) 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.