# DSCI 6607 - Fall 2024

#### Assignment 4\*

### Question 1

Consider sales\_data.csv with the following columns: [20 points]

- a. Load the dataset in python and ensure that the Date column is converted to a datetime format.
- b. Add a new column Profit where: If the Region is "North", the profit is Revenue \* 0.3. If the Region is "South", the profit is Revenue \* 0.4. For all other regions, the profit is Revenue \* 0.25.
- c. For each Product, calculate the total units sold and the average profit per unit sold. Store this information in a new DataFrame.
- d. Filter the original dataset to include only rows where: The Date falls in the year 2023. The Revenue is above the median revenue for all rows.
- e. For the filtered dataset: Group the data by Region and calculate the total Profit and Units Sold for each region. Sort the grouped data in descending order of total Profit.
- f. Export the grouped data to a new CSV file called region\_summary.csv.

```
sales_data = pd.read_csv('sales_data.csv')
sales_data.head()
```

#### Question 2

You are provided with a dataset in R that contains information about monthly sales, categorized by product and region, in a messy format. [20 points]

- a. Separate the Product.Region column into two new columns: Product and Region.
- b. Transform the dataset so that each Product becomes a column, and the Sales values are summarized by Month and Region (reshape the data from long to wide format).
- c. Calculate an additional column for each row in the final dataset, representing the total sales across all products for the combination of Month and Region.
- d. Filter the dataset to include only rows where the total sales exceed the average total sales across all rows.
- $e. \ \ Sort\ the\ resulting\ dataset\ by\ \texttt{Month}\ and\ \texttt{Region}, and\ save\ it\ to\ a\ CSV\ file\ called\ \texttt{tidy\_sales\_data.csv}.$

```
messy_sales_data <- read_csv('messy_sales_data.csv')
head(messy_sales_data)</pre>
```

 $<sup>^*</sup>$ This content is protected and may not be shared, uploaded, or distributed without written permission from Dr. Armin Hatefi.

#### Question 3

Load the movies.csv from your directory in R. For data set, see the lecture notes. [20 points]

- a. Plot the side-by-side histograms of the movie scores for the top three genres.
- b. Plot the side-by-side boxplots of the movie scores for the top three genres.

```
movies_data <- read_csv('movies.csv')
head(movies_data)</pre>
```

## Question 4

Download the following data:

download.file("https://raw.githubusercontent.com/biocorecrg/CRG\_RIntroduction/master/ex12\_normalized\_in")

- 1. Read file into object intenseData.
- 2. Using ggplot, create a simple scatter plot representing gene expression of sampleB on the x-axis and 'sampleH on the y-axis.
- 3. Add a column to the data frame intenseData (call this column expr\_limits), that will be filled the following way: if the expression of a gene is > 13 in both sampleB and sampleH, set to the value in expr\_limits to high if the expression of a gene is < 6 in both sampleB and sampleH, set it to low if different, set it to normal.
- 4. Color the points of the scatter plot according to the newly created column expr\_limits. Save that plot in the object p.
- 5. Add a layer to **p** in order to change the points colors to blue (for low), grey (for normal) and red (for high). Save this plot in the object **p2**.
- 6. Save p2 in a pdf file. [20 points]

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Due on Tuesday, November 26, by 11 pm

Have fun!