session2

February 6, 2025

1 Machine Leaning

1.1 *Lab Session 2*

[1]:
```
import pandas as pd
import numpy as np
import statistics
import seaborn as sns
import matplotlib.pyplot as plt
```

A1. Please refer to the "Purchase Data" worksheet of Lab Session Data.xlsx. Please load the data and segregate them into 2 matrices A & C (following the nomenclature of AX = C). Do the following activities.

1. What is the dimensionality of the vector space for this data?
2. How many vectors exist in this vector space?
3. What is the rank of Matrix A?
4. Using Pseudo-Inverse find the cost of each product available for sale.

[2]:
```
data1 = pd.read_excel("../questions/lab_2_data.xlsx", sheet_name=0)
data1 = data1.dropna(axis = 1) # dropping all the columsn with NaN
data1
```

[2]:

	Customer	Candies (#)	Mangoes (Kg)	Milk Packets (#)	Payment (Rs)
0	C_1	20	6	2	386
1	C_2	16	3	6	289
2	C_3	27	6	2	393
3	C_4	19	1	2	110
4	C_5	24	4	2	280
5	C_6	22	1	5	167
6	C_7	15	4	2	271
7	C_8	18	4	2	274
8	C_9	21	1	4	148
9	C_10	16	2	4	198

[3]:
```
A = data1.iloc[:, 1:-1].values # A = all the columns except first and last one
C = data1.iloc[:,-1].values.reshape(-1,1) # taking only the last column

dimensionality = A.shape[1]
```

```python
num_of_vectors = A.shape[0]
rank_A = np.linalg.matrix_rank(A)
cost_of_each = np.linalg.pinv(A) @ C
```

[4]:
```python
print("Dimensionality : ", dimensionality, "\n",
        "Number of Vectors : ", num_of_vectors, "\n",
        "Matrix Rank : ", rank_A, "\n",
        "Cost of Candy : ", cost_of_each[0].item(), "\n",
        "Cost of Mango : ", cost_of_each[1].item(), "\n",
        "Cost of Milk : ", cost_of_each[2].item(), "\n",
     )
```

```
Dimensionality :  3
 Number of Vectors :  10
 Matrix Rank :  3
 Cost of Candy :  1.0000000000000027
 Cost of Mango :  55.0
 Cost of Milk :  17.99999999999999
```

A2. Use the Pseudo-inverse to calculate the model vector X for predicting the cost of the products available with the vendor.

[5]:
```python
print("Model vector X: ")
print(cost_of_each)
```

```
Model vector X:
[[ 1.]
 [55.]
 [18.]]
```

A3. Mark all customers (in "Purchase Data" table) with payments above Rs. 200 as RICH and others as POOR. Develop a classifier model to categorize customers into RICH or POOR class based on purchase behavior.

[6]:
```python
classifications = ['RICH' if payment > 200 else 'POOR' for payment in C]
predicted_payments = A @ cost_of_each

for i in range(len(C)):
    print("Customer {}: {} (Payment: Rs. {}, Predicted: Rs. {:.2f})".format(
        i+1,
        classifications[i],
        C[i],
        predicted_payments[i].item()))
```

```
Customer 1: RICH (Payment: Rs. [386], Predicted: Rs. 386.00)
Customer 2: RICH (Payment: Rs. [289], Predicted: Rs. 289.00)
Customer 3: RICH (Payment: Rs. [393], Predicted: Rs. 393.00)
Customer 4: POOR (Payment: Rs. [110], Predicted: Rs. 110.00)
Customer 5: RICH (Payment: Rs. [280], Predicted: Rs. 280.00)
```

```
Customer 6: POOR (Payment: Rs. [167], Predicted: Rs. 167.00)
Customer 7: RICH (Payment: Rs. [271], Predicted: Rs. 271.00)
Customer 8: RICH (Payment: Rs. [274], Predicted: Rs. 274.00)
Customer 9: POOR (Payment: Rs. [148], Predicted: Rs. 148.00)
Customer 10: POOR (Payment: Rs. [198], Predicted: Rs. 198.00)
```

A4. Please refer to the data present in "IRCTC Stock Price" data sheet of the above excel file. Do the following after loading the data to your programming platform.

- Calculate the mean and variance of the Price data present in column D.
- Select the price data for all Wednesdays and calculate the sample mean. Compare the mean with the population mean and note your observations.
- Select the price data for the month of Apr and calculate the sample mean. Compare the mean with the population mean and note your observations.
- From the Chg% (available in column I) find the probability of making a loss over the stock.
- Calculate the probability of making a profit on Wednesday.
- Calculate the conditional probability of making profit, given that today is Wednesday.
- Make a scatter plot of Chg% data against the day of the week

[7]:
```python
data2 = pd.read_excel("../questions/lab_2_data.xlsx", sheet_name=1)
data2 = data2.dropna(axis=1)
data2
```

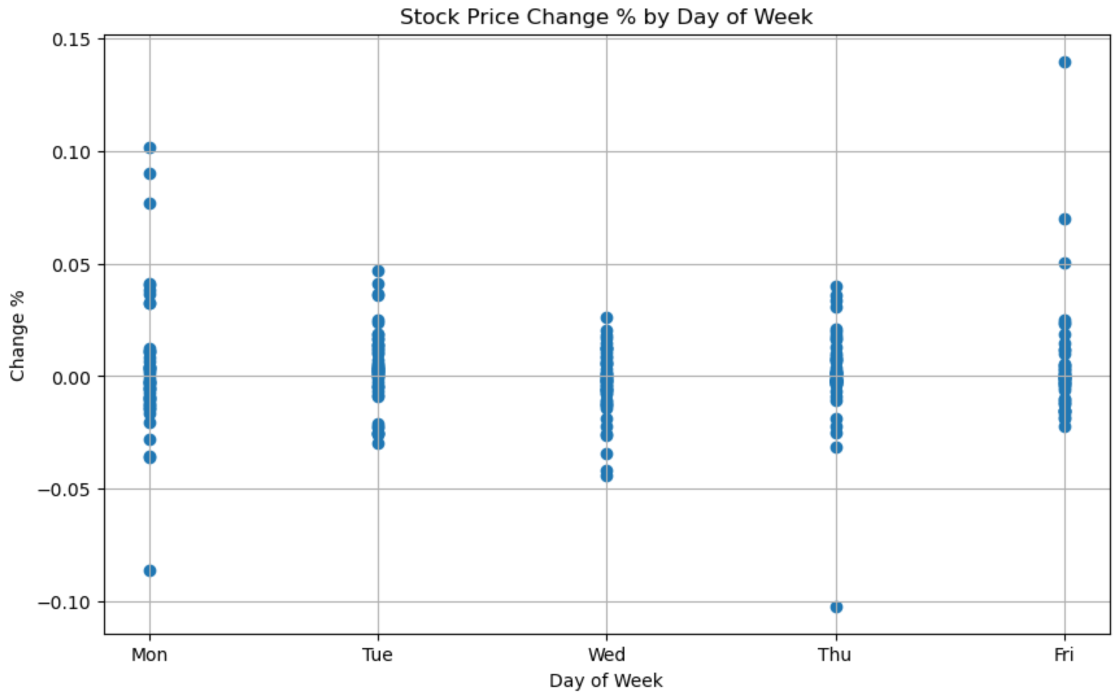
[7]:
```
             Date Month  Day    Price     Open     High      Low   Volume  \
0    Jun 29, 2021   Jun  Tue  2081.85  2092.00  2126.90  2065.05    1.67M
1    Jun 28, 2021   Jun  Mon  2077.75  2084.00  2112.45  2068.40  707.73K
2    Jun 25, 2021   Jun  Fri  2068.85  2084.35  2088.50  2053.10  475.82K
3    Jun 24, 2021   Jun  Thu  2072.95  2098.00  2098.00  2066.00  541.51K
4    Jun 23, 2021   Jun  Wed  2078.25  2102.00  2111.40  2072.00  809.62K
..            …   …   …       …       …       …       …       …
244  Jul 07, 2020   Jul  Tue  1397.40  1410.00  1411.00  1390.05  480.21K
245  Jul 06, 2020   Jul  Mon  1400.75  1405.50  1415.50  1394.00  614.93K
246  Jul 03, 2020   Jul  Fri  1405.10  1415.00  1425.00  1398.00  599.49K
247  Jul 02, 2020   Jul  Thu  1412.35  1440.00  1467.80  1395.30    2.16M
248  Jul 01, 2020   Jul  Wed  1363.05  1363.65  1377.00  1356.00  383.00K

       Chg%
0    0.0020
1    0.0043
2   -0.0020
3   -0.0026
4   -0.0023
..      …
244 -0.0024
245 -0.0031
246 -0.0051
247  0.0362
248  0.0032
```

[249 rows x 9 columns]

[8]:
```
prices = data2["Price"].values
mean_price = statistics.mean(prices)
variance_price = statistics.variance(prices)

wed_data = data2[data2["Day"] == "Wed"]
wed_price = wed_data["Price"].values
wed_mean = statistics.mean(wed_price)

apr_data = data2[data2['Month'] == "Apr"]
apr_price = apr_data["Price"].values
apr_mean = statistics.mean(apr_price)

loss_prob = len(list(filter(lambda x: x < 0, data2['Chg%']))) / len(data2)

wed_profit = len(wed_data[wed_data['Chg%'] > 0]) / len(wed_data)

total_profit_days = len(data2[data2['Chg%'] > 0])
profit_probability = total_profit_days / len(data2)

print("\nIRCTC Stock Price Analysis")
print("--------------------------")
print(f"Population Statistics:")
print(f"Mean Price: Rs. {mean_price:.2f}")
print(f"Variance: {variance_price:.2f}")

print(f"\nWednesday Statistics:")
print(f"Number of Wednesdays: {len(wed_price)}")
print(f"Wednesday Mean Price: Rs. {wed_mean:.2f}")

print(f"\nComparison:")
print(f"Difference (Population Mean - Wednesday Mean): {mean_price - wed_mean:.
↪2f}")

print(f"\nApril Statistics:")
print(f"April Mean Price: Rs. {apr_mean:.2f}")

print(f"\nComparison:")
print(f"Difference (Population Mean - April Mean): {mean_price - apr_mean:.2f}")

print(f"\nProbability of making a loss: {loss_prob:.4f}")

print(f"\nProbability of making a profit on Wednesday: {wed_profit:.4f}")

print(f"\nConditional probability of profit given Wednesday: {wed_profit:.4f}")
```

```python
print(f"Overall probability of profit: {profit_probability:.4f}\n")

day_map = {'Mon': 1, 'Tue': 2, 'Wed': 3, 'Thu': 4, 'Fri': 5}
data2['Day_Num'] = data2['Day'].map(day_map)

plt.figure(figsize=(10, 6))
plt.scatter(data2['Day_Num'], data2['Chg%'])
plt.xticks(range(1, 6), ['Mon', 'Tue', 'Wed', 'Thu', 'Fri'])
plt.xlabel('Day of Week')
plt.ylabel('Change %')
plt.title('Stock Price Change % by Day of Week')
plt.grid(True)
plt.show()
```

```
IRCTC Stock Price Analysis
--------------------------
Population Statistics:
Mean Price: Rs. 1560.66
Variance: 58732.37

Wednesday Statistics:
Number of Wednesdays: 50
Wednesday Mean Price: Rs. 1550.71

Comparison:
Difference (Population Mean - Wednesday Mean): 9.96

April Statistics:
April Mean Price: Rs. 1698.95

Comparison:
Difference (Population Mean - April Mean): -138.29

Probability of making a loss: 0.4980

Probability of making a profit on Wednesday: 0.4200

Conditional probability of profit given Wednesday: 0.4200
Overall probability of profit: 0.4980
```



A5. Data Exploration: Load the data available in "thyroid0387_UCI" worksheet. Perform the following tasks:

- Study each attribute and associated values present. Identify the datatype (nominal etc.) for the attribute.
- For categorical attributes, identify the encoding scheme to be employed.
- Study the data range for numeric variables.
- Study the presence of missing values in each attribute.
- Study presence of outliers in data.
- For numeric variables, calculate the mean and variance (or standard deviation).

[9]:
```
data3 = pd.read_excel("../questions/lab_2_data.xlsx", sheet_name=2)
data3 = data3.dropna(axis=1)
data3
```

[9]:
```
      Record ID  age sex on thyroxine query on thyroxine  \
0     840801013   29   F            f                  f
1     840801014   29   F            f                  f
2     840801042   41   F            f                  f
3     840803046   36   F            f                  f
4     840803047   32   F            f                  f
…           …   …  ..          …                 …
9167  870119022   56   M            f                  f
9168  870119023   22   M            f                  f
9169  870119025   69   M            f                  f
```

```
9170  870119027   47   F            f                  f
9171  870119035   31   M            f                  f

     on antithyroid medication sick pregnant thyroid surgery I131 treatment  \
0                            f    f        f               f              f
1                            f    f        f               f              f
2                            f    f        f               f              f
3                            f    f        f               f              f
4                            f    f        f               f              f
…                          …  …       …             …            …
9167                         f    f        f               f              f
9168                         f    f        f               f              f
9169                         f    f        f               f              f
9170                         f    f        f               f              f
9171                         f    f        f               f              f

      … TT4 measured  TT4 T4U measured   T4U FTI measured FTI TBG measured  \
0     …            f    ?            f     ?            f   ?            f
1     …            t  128            f     ?            f   ?            f
2     …            f    ?            f     ?            f   ?            t
3     …            f    ?            f     ?            f   ?            t
4     …            f    ?            f     ?            f   ?            t
…   …          …  …          …   …          …  ..          …
9167  …            t   64            t  0.83            t  77            f
9168  …            t   91            t  0.92            t  99            f
9169  …            t  113            t  1.27            t  89            f
9170  …            t   75            t  0.85            t  88            f
9171  …            t   66            t  1.02            t  65            f

     TBG referral source     Condition
0      ?           other  NO CONDITION
1      ?           other  NO CONDITION
2     11           other  NO CONDITION
3     26           other  NO CONDITION
4     36           other             S
…   ..             …           …
9167   ?             SVI  NO CONDITION
9168   ?             SVI  NO CONDITION
9169   ?             SVI             I
9170   ?           other  NO CONDITION
9171   ?           other  NO CONDITION

[9172 rows x 31 columns]
```

[10]:
```python
data3.replace('?', np.nan, inplace=True)

# Identify categorical columns
```

```python
categorical_cols = data3.select_dtypes(include=['object']).columns.tolist()

# Convert numeric columns to float
numeric_cols = [col for col in data3.columns if col not in categorical_cols]
data3[numeric_cols] = data3[numeric_cols].astype(float)

# Identify missing values
missing_values = data3.isnull().sum()

# Compute statistics for numeric attributes
numeric_stats = data3[numeric_cols].describe().T

# Label Encode binary categorical variables
binary_cols = [col for col in categorical_cols if data3[col].nunique() == 2]
for col in binary_cols:
    data3[col] = data3[col].map({'t': 1, 'f': 0})

# One-Hot Encode nominal categorical variables
nominal_cols = list(set(categorical_cols) - set(binary_cols) - {"Condition"})
data3 = pd.get_dummies(data3, columns=nominal_cols, drop_first=True)

# Data Imputation
for col in numeric_cols:
    if numeric_stats.loc[col, 'std'] / numeric_stats.loc[col, 'mean'] > 1:  # Check for outliers
        data3[col] = data3[col].fillna(data3[col].median())
    else:
        data3[col] = data3[col].fillna(data3[col].mean())

for col in categorical_cols:
    if col in data3.columns and not data3[col].mode().empty:
        data3[col] = data3[col].fillna(data3[col].mode()[0])

# Summary
print("Missing Values:\n", data3.isnull().sum())
print("\nNumeric Statistics:\n", numeric_stats)
print("\nCategorical Columns:", categorical_cols)
print("\nBinary Encoded Columns:", binary_cols)
print("\nOne-Hot Encoded Columns:", nominal_cols)
```

```
Missing Values:
 Record ID                     0
age                           0
sex                        9172
on thyroxine                  0
query on thyroxine            0
on antithyroid medication     0
sick                          0
```

```
pregnant                         0
thyroid surgery                  0
I131 treatment                   0
query hypothyroid                0
query hyperthyroid               0
lithium                          0
goitre                           0
tumor                            0
hypopituitary                    0
psych                            0
TSH measured                     0
TSH                              0
T3 measured                      0
T3                               0
TT4 measured                     0
TT4                              0
T4U measured                     0
T4U                              0
FTI measured                     0
FTI                              0
TBG measured                     0
TBG                              0
Condition                        0
referral source_SVHC             0
referral source_SVHD             0
referral source_SVI              0
referral source_WEST             0
referral source_other            0
dtype: int64

Numeric Statistics:
            count          mean           std           min           25%  \
Record ID  9172.0  8.529473e+08  7.581969e+06  8.408010e+08  8.504090e+08
age        9172.0  7.355582e+01  1.183977e+03  1.000000e+00  3.700000e+01
TSH        8330.0  5.218403e+00  2.418401e+01  5.000000e-03  4.600000e-01
T3         6568.0  1.970629e+00  8.875788e-01  5.000000e-02  1.500000e+00
TT4        8730.0  1.087003e+02  3.752267e+01  2.000000e+00  8.700000e+01
T4U        8363.0  9.760557e-01  2.003604e-01  1.700000e-01  8.600000e-01
FTI        8370.0  1.136407e+02  4.155165e+01  1.400000e+00  9.300000e+01
TBG         349.0  2.987006e+01  2.108050e+01  1.000000e-01  2.100000e+01

                    50%           75%           max
Record ID  8.510040e+08  8.607110e+08  8.701190e+08
age        5.500000e+01  6.800000e+01  6.552600e+04
TSH        1.400000e+00  2.700000e+00  5.300000e+02
T3         1.900000e+00  2.300000e+00  1.800000e+01
TT4        1.040000e+02  1.260000e+02  6.000000e+02
T4U        9.600000e-01  1.065000e+00  2.330000e+00
```

```
FTI         1.090000e+02  1.280000e+02  8.810000e+02
TBG         2.600000e+01  3.100000e+01  2.000000e+02

Categorical Columns: ['sex', 'on thyroxine', 'query on thyroxine', 'on
antithyroid medication', 'sick', 'pregnant', 'thyroid surgery', 'I131
treatment', 'query hypothyroid', 'query hyperthyroid', 'lithium', 'goitre',
'tumor', 'hypopituitary', 'psych', 'TSH measured', 'T3 measured', 'TT4
measured', 'T4U measured', 'FTI measured', 'TBG measured', 'referral source',
'Condition']

Binary Encoded Columns: ['sex', 'on thyroxine', 'query on thyroxine', 'on
antithyroid medication', 'sick', 'pregnant', 'thyroid surgery', 'I131
treatment', 'query hypothyroid', 'query hyperthyroid', 'lithium', 'goitre',
'tumor', 'hypopituitary', 'psych', 'TSH measured', 'T3 measured', 'TT4
measured', 'T4U measured', 'FTI measured', 'TBG measured']

One-Hot Encoded Columns: ['referral source']
```

```
/run/user/1000/app/org.jupyter.JupyterLab/ipykernel_1035/2432317790.py:1:
FutureWarning: Downcasting behavior in `replace` is deprecated and will be
removed in a future version. To retain the old behavior, explicitly call
`result.infer_objects(copy=False)`. To opt-in to the future behavior, set
`pd.set_option('future.no_silent_downcasting', True)`
  data3.replace('?', np.nan, inplace=True)
```

A6. Data Imputation: employ appropriate central tendencies to fill the missing values in the data variables. Employ following guidance.

- Mean may be used when the attribute is numeric with no outliers
- Median may be employed for attributes which are numeric and contain outliers
- Mode may be employed for categorical attributes

[11]:
```
for col in numeric_cols:
    if numeric_stats.loc[col, 'std'] / numeric_stats.loc[col, 'mean'] > 1:  #␣
 ↪Check for outliers
        data3[col].fillna(data3[col].median())
    else:
        data3[col].fillna(data3[col].mean())

for col in categorical_cols:
    if col in data3.columns:  # Ensure column exists
        mode_value = data3[col].mode()
        if not mode_value.empty:
            data3[col] = data3[col].fillna(mode_value[0])
data3
```

[11]:
```
        Record ID   age  sex  on thyroxine  query on thyroxine  \
0     840801013.0  29.0  NaN             0                   0
```

```
1     840801014.0  29.0  NaN            0                 0
2     840801042.0  41.0  NaN            0                 0
3     840803046.0  36.0  NaN            0                 0
4     840803047.0  32.0  NaN            0                 0
…             …    …    …           …                 …
9167  870119022.0  56.0  NaN            0                 0
9168  870119023.0  22.0  NaN            0                 0
9169  870119025.0  69.0  NaN            0                 0
9170  870119027.0  47.0  NaN            0                 0
9171  870119035.0  31.0  NaN            0                 0

      on antithyroid medication  sick  pregnant  thyroid surgery  \
0                             0     0         0                0
1                             0     0         0                0
2                             0     0         0                0
3                             0     0         0                0
4                             0     0         0                0
…                         …    …       …              …
9167                          0     0         0                0
9168                          0     0         0                0
9169                          0     0         0                0
9170                          0     0         0                0
9171                          0     0         0                0

      I131 treatment  …  FTI measured         FTI  TBG measured        TBG  \
0                  0  …             0  113.640746             0  29.870057
1                  0  …             0  113.640746             0  29.870057
2                  0  …             0  113.640746             1  11.000000
3                  0  …             0  113.640746             1  26.000000
4                  0  …             0  113.640746             1  36.000000
…              …   …          …          …            …        …
9167               0  …             1   77.000000             0  29.870057
9168               0  …             1   99.000000             0  29.870057
9169               0  …             1   89.000000             0  29.870057
9170               0  …             1   88.000000             0  29.870057
9171               0  …             1   65.000000             0  29.870057

         Condition  referral source_SVHC  referral source_SVHD  \
0     NO CONDITION                 False                 False
1     NO CONDITION                 False                 False
2     NO CONDITION                 False                 False
3     NO CONDITION                 False                 False
4                S                 False                 False
…              …                   …                   …
9167  NO CONDITION                 False                 False
9168  NO CONDITION                 False                 False
9169             I                 False                 False
```

```
9170  NO CONDITION                 False                False
9171  NO CONDITION                 False                False

      referral source_SVI  referral source_WEST  referral source_other
0                   False                 False                   True
1                   False                 False                   True
2                   False                 False                   True
3                   False                 False                   True
4                   False                 False                   True
…                   …                   …                   …
9167                 True                 False                  False
9168                 True                 False                  False
9169                 True                 False                  False
9170                False                 False                   True
9171                False                 False                   True

[9172 rows x 35 columns]
```

A7. Data Normalization / Scaling: from the data study, identify the attributes which may need normalization. Employ appropriate normalization techniques to create normalized set of data.

[12]:
```python
def handle_missing_values(df):
    # Replace '?' with NaN
    return df.replace('?', np.nan)

def custom_min_max_normalization(column):
    """Min-Max normalization: (x - min) / (max - min)"""
    col_min = column.min()
    col_max = column.max()
    return (column - col_min) / (col_max - col_min) if col_max != col_min else␣
 ↪column

def custom_z_score_normalization(column):
    """Z-score normalization: (x - mean) / standard deviation"""
    col_mean = column.mean()
    col_std = column.std()
    return (column - col_mean) / col_std if col_std != 0 else column

def custom_median_normalization(column):
    """Median-based normalization: (x - median) / IQR"""
    col_median = column.median()
    Q1 = column.quantile(0.25)
    Q3 = column.quantile(0.75)
    IQR = Q3 - Q1
    return (column - col_median) / IQR if IQR != 0 else column

def normalize_thyroid_data(data):
```

```
    # Handle missing values
    df = handle_missing_values(data)

    # Select numeric columns
    numeric_columns = ['age', 'TSH', 'T3', 'TT4', 'T4U', 'FTI', 'TBG']

    # Remove rows with all numeric columns as NaN
    df = df.dropna(subset=numeric_columns, how='all')

    # Convert to float
    df[numeric_columns] = df[numeric_columns].astype(float)

    # Fill missing values with median
    for col in numeric_columns:
        df[col] = df[col].fillna(df[col].median())

    # Create normalized datasets
    normalized_datasets = {
        'Min-Max': df.copy(),
        'Z-Score': df.copy(),
        'Median': df.copy()
    }

    # Apply normalization techniques
    for col in numeric_columns:
        normalized_datasets['Min-Max'][col] =␣
 ↪custom_min_max_normalization(df[col])
        normalized_datasets['Z-Score'][col] =␣
 ↪custom_z_score_normalization(df[col])
        normalized_datasets['Median'][col] =␣
 ↪custom_median_normalization(df[col])

    return normalized_datasets

normalized_data = normalize_thyroid_data(data3)

# Print summary statistics for each normalization method
for method, dataset in normalized_data.items():
    print(f"\n{method} Normalization Summary:")
    print(dataset[['age', 'TSH', 'T3', 'TT4']].describe())
```

```
Min-Max Normalization Summary:
               age          TSH           T3          TT4
count  9172.000000  9172.000000  9172.000000  9172.000000
mean      0.001107     0.009175     0.106999     0.178429
std       0.018069     0.043535     0.041843     0.061216
```

```
min       0.000000     0.000000     0.000000     0.000000
25%       0.000549     0.001104     0.091922     0.143813
50%       0.000824     0.002632     0.106999     0.173913
75%       0.001023     0.004708     0.119777     0.204013
max       1.000000     1.000000     1.000000     1.000000

Z-Score Normalization Summary:
                age           TSH            T3           TT4
count  9.172000e+03  9.172000e+03  9.172000e+03  9.172000e+03
mean   6.197494e-18 -2.014186e-17  1.634589e-16 -3.199456e-16
std    1.000000e+00  1.000000e+00  1.000000e+00  1.000000e+00
min   -6.128146e-02 -2.107559e-01 -2.557180e+00 -2.914728e+00
25%   -3.087546e-02 -1.854021e-01 -3.603230e-01 -5.654694e-01
50%   -1.567246e-02 -1.502969e-01  2.956366e-16 -7.376411e-02
75%   -4.692510e-03 -1.026230e-01  3.053914e-01  4.179412e-01
max    5.528187e+01  2.275914e+01  2.134196e+01  1.342081e+01

Median Normalization Summary:
               age          TSH            T3          TT4
count  9172.000000  9172.000000  9.172000e+03  9172.000000
mean      0.598575     1.815638 -2.145882e-16     0.075008
std      38.192797    12.080347  1.502146e+00     1.016869
min      -1.741935    -0.730366 -3.841258e+00    -2.888889
25%      -0.580645    -0.424084 -5.412576e-01    -0.500000
50%       0.000000     0.000000  0.000000e+00     0.000000
75%       0.419355     0.575916  4.587424e-01     0.500000
max    2111.967742   276.753927  3.205874e+01    13.722222
```

A8. Similarity Measure: Take the first 2 observation vectors from the dataset. Consider only the attributes (direct or derived) with binary values for these vectors (ignore other attributes). Calculate the Jaccard Coefficient (JC) and Simple Matching Coefficient (SMC) between the document vectors. Use first vector for each document for this. Compare the values for JC and SMC and judge the appropriateness of each of them.

$$JC = \frac{f_{11}}{f_{01} + f_{10} + f_{11}}$$

$$SMC = \frac{f_{11} + f_{00}}{f_{00} + f_{01} + f_{10} + f_{11}}$$

[13]:
```python
v1 = data3.iloc[0]
v2 = data3.iloc[1]

# Identify binary attributes
binary_attributes = [col for col in data3.columns if set(data3[col].unique()).
 ↪issubset({0, 1})]

# Initialize counters
```

```python
f11 = f10 = f01 = f00 = 0

# Iterate over binary attributes
for attr in binary_attributes:
    val1 = v1[attr]
    val2 = v2[attr]
    if val1 == 1 and val2 == 1:
        f11 += 1
    elif val1 == 1 and val2 == 0:
        f10 += 1
    elif val1 == 0 and val2 == 1:
        f01 += 1
    elif val1 == 0 and val2 == 0:
        f00 += 1

# Calculate Jaccard Coefficient (JC)
jc = f11 / (f01 + f10 + f11)

# Calculate Simple Matching Coefficient (SMC)
smc = (f11 + f00) / (f00 + f01 + f10 + f11)

print(f"Jaccard Coefficient (JC): {jc}")
print(f"Simple Matching Coefficient (SMC): {smc}")
```

```
Jaccard Coefficient (JC): 0.4
Simple Matching Coefficient (SMC): 0.88
```

A9. Cosine Similarity Measure: Now take the complete vectors for these two observations (including all the attributes). Calculate the Cosine similarity between the documents by using the second feature vector for each document.

[14]:
```python
def preprocess_data(data):
    # Replace '?' with NaN
    df = data.replace('?', np.nan)

    # Convert columns to appropriate types
    numeric_cols = ['age', 'TSH', 'T3', 'TT4', 'T4U', 'FTI', 'TBG']
    categorical_cols = [col for col in df.columns if col not in numeric_cols␣
 ↪and col != 'Record ID']

    # One-hot encode categorical columns
    df_encoded = pd.get_dummies(df, columns=categorical_cols)

    # Fill numeric missing values with median
    for col in numeric_cols:
        df_encoded[col] = df_encoded[col].fillna(df_encoded[col].median())

    return df_encoded
```

```python
def cosine_similarity(vec1, vec2):
    # Dot product
    dot_product = np.dot(vec1, vec2)

    # Magnitudes
    magnitude1 = np.linalg.norm(vec1)
    magnitude2 = np.linalg.norm(vec2)

    # Cosine similarity
    return dot_product / (magnitude1 * magnitude2)

# Preprocess data
df_processed = preprocess_data(data3)

# Select feature vectors (excluding first two rows to ensure valid comparison)
vec1 = df_processed.iloc[1].values
vec2 = df_processed.iloc[2].values

# Calculate cosine similarity
similarity = cosine_similarity(vec1, vec2)

print("Cosine Similarity:", similarity)
```

```
Cosine Similarity: 0.9999999999999997
```

[ ]:

[15]:
```python
def calculate_similarities(df_processed, first_n=20):
    # Extract first n vectors
    vectors = df_processed.iloc[:first_n].values

    # Initialize similarity matrices
    jc_matrix = np.zeros((first_n, first_n))
    smc_matrix = np.zeros((first_n, first_n))
    cos_matrix = np.zeros((first_n, first_n))

    # Calculate similarities
    for i in range(first_n):
        for j in range(first_n):
            # Binary attributes (assuming binary columns)
            binary_attrs = [col for col in df_processed.columns
                            if set(df_processed[col].unique()).issubset({0, 1})]

            # Similarity calculations
            v1 = df_processed.iloc[i]
            v2 = df_processed.iloc[j]
```

```
            # Jaccard Coefficient
            f11 = f10 = f01 = f00 = 0
            for attr in binary_attrs:
                if v1[attr] == 1 and v2[attr] == 1:
                    f11 += 1
                elif v1[attr] == 1 and v2[attr] == 0:
                    f10 += 1
                elif v1[attr] == 0 and v2[attr] == 1:
                    f01 += 1
                elif v1[attr] == 0 and v2[attr] == 0:
                    f00 += 1

            jc = f11 / (f01 + f10 + f11) if (f01 + f10 + f11) > 0 else 0
            smc = (f11 + f00) / (f00 + f01 + f10 + f11)

            # Cosine Similarity
            cos = np.dot(vectors[i], vectors[j]) / (np.linalg.norm(vectors[i])␣
 ↪* np.linalg.norm(vectors[j]))

            jc_matrix[i, j] = jc
            smc_matrix[i, j] = smc
            cos_matrix[i, j] = cos

    return jc_matrix, smc_matrix, cos_matrix

# Preprocess the data
df_processed = preprocess_data(data3)

# Calculate similarities
jc_matrix, smc_matrix, cos_matrix = calculate_similarities(df_processed)

# Create heatmap visualizations
plt.figure(figsize=(20, 16))

# Jaccard Coefficient Heatmap
plt.subplot(1, 3, 1)
sns.heatmap(jc_matrix, annot=True, cmap='YlGnBu', fmt='.2f', cbar=True)
plt.title('Jaccard Coefficient Similarity')
plt.xlabel('Vector Index')
plt.ylabel('Vector Index')

# Simple Matching Coefficient Heatmap
plt.subplot(1, 3, 2)
sns.heatmap(smc_matrix, annot=True, cmap='YlGnBu', fmt='.2f', cbar=True)
plt.title('Simple Matching Coefficient Similarity')
plt.xlabel('Vector Index')
plt.ylabel('Vector Index')
```

```python
# Cosine Similarity Heatmap
plt.subplot(1, 3, 3)
sns.heatmap(cos_matrix, annot=True, cmap='YlGnBu', fmt='.2f', cbar=True)
plt.title('Cosine Similarity')
plt.xlabel('Vector Index')
plt.ylabel('Vector Index')

plt.tight_layout()
plt.show()
```