STATS 3DA3

Homework Assignment 6

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1. **Classification Problem Identification:** Define and describe a classification problem based on the dataset.

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

```
from ucimlrepo import fetch_ucirepo

# fetch dataset
chronic_kidney_disease = fetch_ucirepo(id=336)

# data (as pandas dataframes)
X = chronic_kidney_disease.data.features
y = chronic_kidney_disease.data.targets

# variable information
print(chronic_kidney_disease.variables)
```

```
     name     role         type demographic              description  \
0     age  Feature      Integer         Age                     None
1      bp  Feature      Integer        None           blood pressure
2      sg  Feature  Categorical        None         specific gravity
3      al  Feature  Categorical        None                  albumin
4      su  Feature  Categorical        None                    sugar
5     rbc  Feature       Binary        None          red blood cells
6      pc  Feature       Binary        None                 pus cell
7     pcc  Feature       Binary        None          pus cell clumps
8      ba  Feature       Binary        None                 bacteria
```

9	bgr	Feature	Integer	None	blood glucose random	
10	bu	Feature	Integer	None	blood urea	
11	sc	Feature	Continuous	None	serum creatinine	
12	sod	Feature	Integer	None	sodium	
13	pot	Feature	Continuous	None	potassium	
14	hemo	Feature	Continuous	None	hemoglobin	
15	pcv	Feature	Integer	None	packed cell volume	
16	wbcc	Feature	Integer	None	white blood cell count	
17	rbcc	Feature	Continuous	None	red blood cell count	
18	htn	Feature	Binary	None	hypertension	
19	dm	Feature	Binary	None	diabetes mellitus	
20	cad	Feature	Binary	None	coronary artery disease	
21	appet	Feature	Binary	None	appetite	
22	pe	Feature	Binary	None	pedal edema	
23	ane	Feature	Binary	None	anemia	
24	class	Target	Binary	None	ckd or not ckd	

	units	missing_values
0	year	yes
1	mm/Hg	yes
2	None	yes
3	None	yes
4	None	yes
5	None	yes
6	None	yes
7	None	yes
8	None	yes
9	mgs/dl	yes
10	mgs/dl	yes
11	mgs/dl	yes
12	mEq/L	yes
13	mEq/L	yes

```
14           gms            yes
15          None            yes
16     cells/cmm            yes
17  millions/cmm            yes
18          None            yes
19          None            yes
20          None            yes
21          None            yes
22          None            yes
23          None            yes
24          None             no
```

```
all_data = pd.concat([X,y],axis=1)
```

```
all_data
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc	r
0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	...	44.0	7800.0	5
1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	38.0	6000.0	N
2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	423.0	...	31.0	7500.0	N
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117.0	...	32.0	6700.0	3
4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	106.0	...	35.0	7300.0	4
...	...	...	...	...	...	...	...	...	...	...	...	...	...	.
395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	140.0	...	47.0	6700.0	4
396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	75.0	...	54.0	7800.0	6
397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	100.0	...	49.0	6600.0	5
398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	114.0	...	51.0	7200.0	5
399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	131.0	...	53.0	6800.0	6

Answer: Based on the loaded dataset, the classification problem can be identified as determining whether a patient has chronic kidney disease (CKD) or not. The dataset contains various measurements and test results that could potentially indicate the presence of CKD in patients.

2. **Variable Transformation:** Implement any transformations chosen or justify the absence of such modifications.

Answer: To clean the data for further analysis, the following transformations are applied:

- Binary categories like "yes"/"no" will be mapped to 1/0.
- Other categorical variables with more than two categories will be converted to numerical codes.

```
from sklearn.preprocessing import LabelEncoder, StandardScaler
from sklearn.impute import SimpleImputer


# Applying label encoding to categorical variables
# keep missing value
label_encoders = {}
miss_placeholder = 'missing'
numerical_col = list(all_data.select_dtypes(include=['int32', 'float64']))
categorical_col = list(all_data.select_dtypes(include=['object']).columns)
le = LabelEncoder()
for col in categorical_col:
    all_data[col] = all_data[col].fillna(miss_placeholder)
    if miss_placeholder in all_data[col]:
        all_data[col] = le.fit_transform(all_data[col].astype(str))
        placeholder_index = le.transform([miss_placeholder])[0]
        all_data[col].replace(placeholder_index,np.nan, inplace=True)
    else:
        all_data[col] = le.fit_transform(all_data[col].astype(str))


# use 1 for have ckd, 0 for not having ckd
all_data['class'].replace(0,1, inplace=True)
all_data['class'].replace(2,0, inplace=True)
```

3. **Dataset Overview:** Provide a detailed description of the dataset, covering variables, summaries, observation counts, data types, and distributions (at least three statements).

```
all_data.describe().transpose()
```

	count	mean	std	min	25%	50%	75%	max
age	391.0	51.483376	17.169714	2.000	42.00	55.00	64.50	90.000
bp	388.0	76.469072	13.683637	50.000	70.00	80.00	80.00	180.000
sg	353.0	1.017408	0.005717	1.005	1.01	1.02	1.02	1.025
al	354.0	1.016949	1.352679	0.000	0.00	0.00	2.00	5.000
su	351.0	0.450142	1.099191	0.000	0.00	0.00	0.00	5.000
rbc	400.0	1.385000	0.687719	0.000	1.00	2.00	2.00	2.000
pc	400.0	1.457500	0.793579	0.000	1.00	2.00	2.00	2.000
pcc	400.0	1.095000	0.325946	0.000	1.00	1.00	1.00	2.000
ba	400.0	1.045000	0.251262	0.000	1.00	1.00	1.00	2.000
bgr	356.0	148.036517	79.281714	22.000	99.00	121.00	163.00	490.000
bu	381.0	57.425722	50.503006	1.500	27.00	42.00	66.00	391.000
sc	383.0	3.072454	5.741126	0.400	0.90	1.30	2.80	76.000
sod	313.0	137.528754	10.408752	4.500	135.00	138.00	142.00	163.000
pot	312.0	4.627244	3.193904	2.500	3.80	4.40	4.90	47.000
hemo	348.0	12.526437	2.912587	3.100	10.30	12.65	15.00	17.800
pcv	329.0	38.884498	8.990105	9.000	32.00	40.00	45.00	54.000
wbcc	294.0	8406.122449	2944.474190	2200.000	6500.00	8000.00	9800.00	26400.000
rbcc	269.0	4.707435	1.025323	2.100	3.90	4.80	5.40	8.000
htn	400.0	1.362500	0.491628	0.000	1.00	1.00	2.00	2.000
dm	400.0	2.332500	0.497557	0.000	2.00	2.00	3.00	3.000
cad	400.0	1.080000	0.289499	0.000	1.00	1.00	1.00	2.000
appet	400.0	0.412500	0.808689	0.000	0.00	0.00	0.00	2.000
pe	400.0	1.187500	0.397163	0.000	1.00	1.00	1.00	2.000
ane	400.0	1.147500	0.362038	0.000	1.00	1.00	1.00	2.000
class	400.0	0.625000	0.484729	0.000	0.00	1.00	1.00	1.000

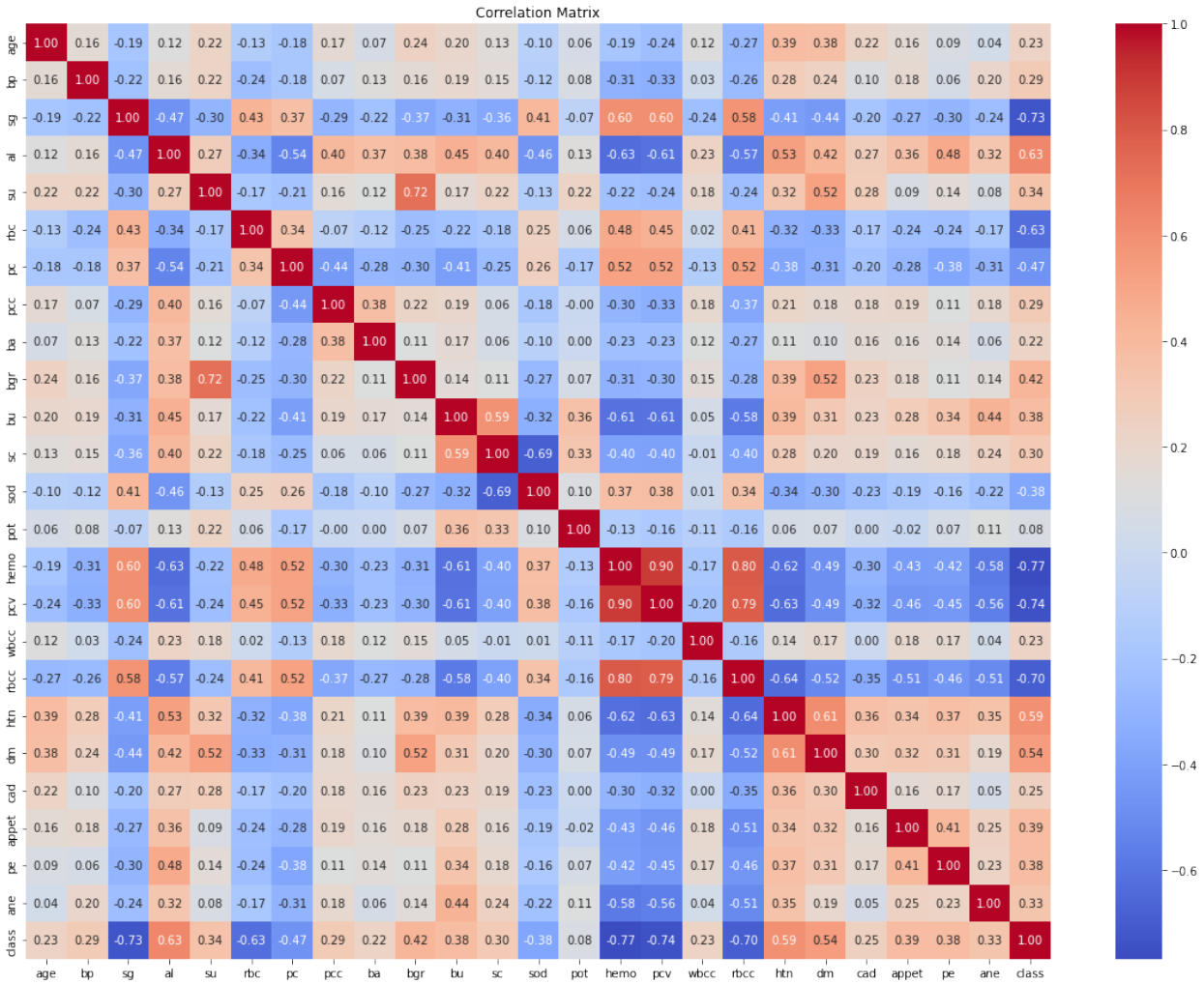
Answer:

- Observation Count and Variables: The dataset contains 400 rows and 25 columns

- Clinical measurements might contain outliers, particularly in variables like blood glucose random which can vary widely depending on the patient's condition and dietary intake.
- Patients' age might range widely, from young children to elderly, affecting the kidney function differently across ages

4. **Association Between Variables:** Analyze variable relationships and their implications for feature selection or extraction (at least three statements).

```
correlation_matrix = all_data.corr()
plt.figure(figsize=(20,15))
sns.heatmap(correlation_matrix, annot=True, fmt=".2f", cmap='coolwarm')
plt.title('Correlation Matrix')
plt.show()
```



Answer:

- Serum Creatinine (Sc) and Blood Urea (Bu): Another significant positive correlation is observed between 'sc' and 'bu', which could indicate a combined impact of these variables on kidney health, as both are commonly used indicators of renal function.
- Specific Gravity (Sg) and Albumin (Al): There's a negative correlation between 'sg' and 'al', which might be interpreted that higher levels of albumin in the urine (a sign of kidney disease) are often associated with lower urine specific gravity, perhaps due to the kidneys' reduced ability to concentrate urine.
- Blood Pressure (Bp) and Serum Creatinine (Sc): A moderate positive correlation is seen between 'bp' and 'sc', suggesting that higher blood pressure is associated with higher serum creatinine levels, which is a common clinical pattern observed in patients with chronic kidney conditions.

5. **Missing Value Analysis and Handling:** Implement your strategy for identifying and addressing missing values in the dataset, or provide reasons for not addressing them.

Answer:

For numerical variables, we can use mean or median imputation.

For categorical variables, we can use the most frequent value (mode) for imputation.

```
for col in numerical_col:
    all_data[col] = all_data[col].fillna(np.mean(all_data[col]))
for col in categorical_col:
    all_data[col] = all_data[col].fillna(all_data[col].value_counts().idxmax())
```

6. **Outlier Analysis:** Implement your approach for identifying and managing outliers, or provide reasons for not addressing them.

The outliers should be kept. In medical datasets, what appears to be an outlier could be a critical rare case that's essential for a predictive model to learn from.

7. **Sub-group Analysis:** Explore potential sub-groups within the data, employing appropriate data science methods to find the sub-groups of patients and visualize the sub-groups. The sub-group analysis must not include the labels (for CKD patients and healthy controls).

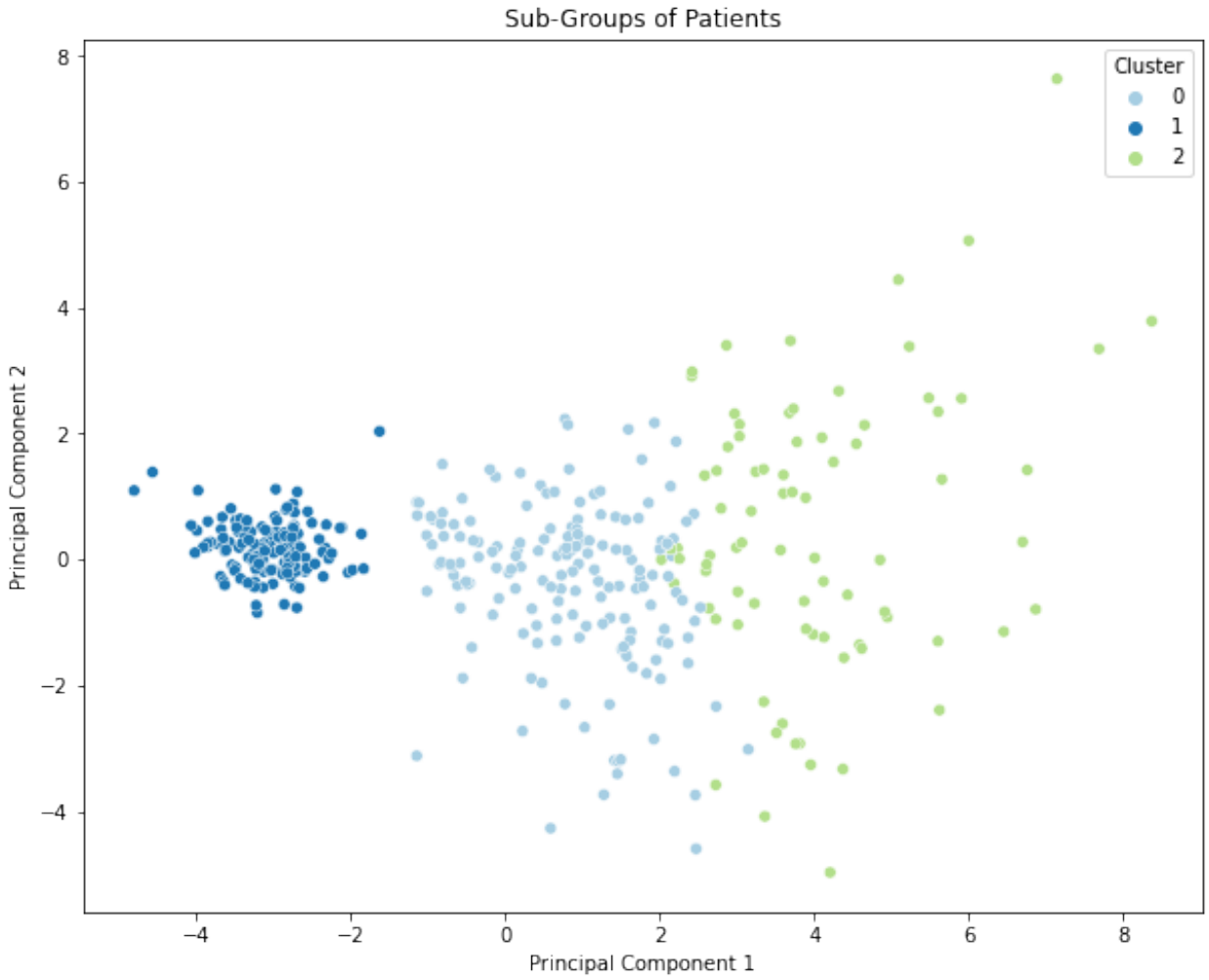
```
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans
from sklearn.decomposition import PCA
import matplotlib.pyplot as plt
import seaborn as sns
```

```
scaler = StandardScaler()
all_data_scaled = scaler.fit_transform(all_data)

# Apply K-Means clustering
k_mean = KMeans(n_clusters=3, random_state=1)
clusters = k_mean.fit_predict(all_data_scaled)

# Apply PCA for visualization
pca = PCA(n_components=2)
principal_components = pca.fit_transform(all_data_scaled)

# Visualize clusters
plt.figure(figsize=(10, 8))
sns.scatterplot(x=principal_components[:, 0], y=principal_components[:, 1], hue=clusters, pale
plt.title('Sub-Groups of Patients')
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.legend(title='Cluster')
plt.show()
```



From the result, it can be seen the green cluster is a clear sub-group of the dataset.

8. **Data Splitting:** Segregate 30% of the data for testing, using a random seed of 1. Use the remaining 70% for training and model selection.

```
from sklearn.model_selection import train_test_split
X = all_data.drop('class', axis=1)
y = all_data['class']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=1, strati
```

9. **Classifier Choices:** Identify the two classifiers you have chosen and justify your selections.

Answer:

- Logistic Regression: This model is favored for its simplicity and interpretability, making it an excellent choice for scenarios such as in medical diagnostics. Its efficiency in computation and ability to provide probabilities for outcomes is particularly useful in binary classification tasks.
- Random Forest: Ideal for handling complex, nonlinear data relationships without extensive pre-processing, Random Forests are robust against overfitting due to their ensemble approach that averages predictions across multiple decision trees.

10. **Performance Metrics:** Outline the two metrics for comparing the performance of the classifiers.

Answer:

- AUC-ROC AUC-ROC is useful for binary classification problems, especially when classes are imbalanced. It provides a single measure of overall model performance and can compare different models' performance without setting a classification threshold. Higher AUC values indicate better model performance.
- F1 Score The F1 score is the harmonic mean of precision (the ratio of true positives to the sum of true and false positives) and recall (the ratio of true positives to the sum of true positives and false negatives). It balances the trade-off between precision and recall.

11. **Feature Selection/Extraction:** Implement methods to enhance the performance of at least one classifier in (9). The answer for this question can be included in (12).
12. **Classifier Comparison:** Utilize the selected metrics to compare the classifiers based on the test set. Discuss your findings (at least two statements).

```
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import roc_auc_score, f1_score, roc_curve



# Initialize the two classifiers
log_reg = LogisticRegression()
random_forest = RandomForestClassifier(random_state=1)
```

```
# Train the logistic regression classifier
log_reg.fit(X_train, y_train)

# Train the random forest classifier
random_forest.fit(X_train, y_train)

# Make predictions with both classifiers
y_pred_lr = log_reg.predict(X_test)
y_pred_rf = random_forest.predict(X_test)

y_pred_proba_lr = log_reg.predict_proba(X_test)[:, 1]
y_pred_proba_rf = random_forest.predict_proba(X_test)[:, 1]

# Calculate ROC AUC
roc_auc_lr = roc_auc_score(y_test, y_pred_proba_lr)
roc_auc_rf = roc_auc_score(y_test, y_pred_proba_rf)

# Calculate F1 Scores
f1_score_lr = f1_score(y_test, y_pred_lr)
f1_score_rf = f1_score(y_test, y_pred_rf)

print(f'Logistic Regression ROC score: {roc_auc_lr:.4f}')
print(f'Random Forest ROC score: {roc_auc_rf:.4f}')
print(f'Logistic Regression F1 score: {f1_score_lr:.4f}')
print(f'Random Forest F1 score: {f1_score_rf:.4f}')
```

```
Logistic Regression ROC score: 0.9876
Random Forest ROC score: 1.0000
Logistic Regression F1 score: 0.9530
Random Forest F1 score: 1.0000
```

Compare the result, Random Forest is better than logestic regression.

13. **Interpretable Classifier Insight:** After re-training the interpretable classifier with all available data, analyze and interpret the significance of predictor variables in the context of the data and the challenge (at least two statements).

```
feature_importance = pd.DataFrame(log_reg.coef_[0], index=X_train.columns, columns=['Coefficien
print(feature_importance.sort_values(by='Coefficient', ascending=False))
```

```
       Coefficient
sc        0.158424
al        0.144894
sod       0.102454
appet     0.056116
bp        0.047509
bgr       0.041562
htn       0.040796
pe        0.038069
dm        0.034479
bu        0.024944
su        0.016794
pcc       0.015932
ane       0.015852
cad       0.012012
ba        0.010071
sg        0.002993
wbcc      0.000177
pot      -0.005023
age      -0.022394
pc       -0.043374
rbcc     -0.059370
rbc      -0.101766
hemo     -0.242584
```

```
pcv       -0.502294
```

- negative coefficient for hemoglobin points to its critical role in CKD diagnosis. Lower hemoglobin levels, which occur with anemia associated with kidney disease, significantly increase the likelihood of CKD. This connection emphasizes the kidney's role in producing hormones that stimulate red blood cell production.
- The negative coefficient for Red Blood Cell Count (rbc) suggests that a lower red blood cell count is associated with higher odds of CKD.
- The positive coefficient for serum creatinine (sc) indicates that higher levels of creatinine in the blood are associated with an increased risk of CKD. Elevated creatinine levels often signal reduced kidney function, as creatinine is a waste product filtered out by healthy kidneys.

15. **Team Contributions:** Document each team member's specific contributions related to the questions above.

- Yuchen Wang did question 1-7
- Shilin Wang did question 8-16

16. **Link** to the public GitHub repository.

https://github.com/wangy773/STATS-3DA3-A6