STATS 3DA3

Homework Assignment 6

Jianghan Sun (400189997), Zhen Ye (400363186)

2024-04-14

1

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

# 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
ckd = pd.concat([chronic_kidney_disease.data.features ,chronic_kidney_disease.data.targets],ax

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
```

```
ckd.head(10)
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc
0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	...	44.0	7800.0
1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	38.0	6000.0
2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	423.0	...	31.0	7500.0
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117.0	...	32.0	6700.0
4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	106.0	...	35.0	7300.0
5	60.0	90.0	1.015	3.0	0.0	NaN	NaN	notpresent	notpresent	74.0	...	39.0	7800.0
6	68.0	70.0	1.010	0.0	0.0	NaN	normal	notpresent	notpresent	100.0	...	36.0	NaN
7	24.0	NaN	1.015	2.0	4.0	normal	abnormal	notpresent	notpresent	410.0	...	44.0	6900.0
8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	present	notpresent	138.0	...	33.0	9600.0
9	53.0	90.0	1.020	2.0	0.0	abnormal	abnormal	present	notpresent	70.0	...	29.0	12100.0

From the dataset we've been given, our main task is to determine whether someone has chronic kidney disease (CKD) or not. The dataset includes various measurements and test results which might help us identify whether a patient has CKD.

2

To prepare the data for analysis

- categorical variables should be translated into numerical variables. LableEncoder is used.

- Records with missing values is removed

```
from sklearn.preprocessing import LabelEncoder

# remove NaN values
ckd_transform = ckd.dropna()

# Applying label encoding to categorical variables
label_encoders = {}
categorical_col = list(ckd_transform.select_dtypes(include=['object']).columns)
le = LabelEncoder()
for col in categorical_col:
    if col == 'class':
        ckd_transform[col] = ckd_transform[col].apply(lambda x: 0 if 'not' in x else 1)
    else:
        ckd_transform[col] = le.fit_transform(ckd_transform[col].astype(str))
```

```
ckd_transform.head(10)
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc	rbcc	htn	dm	cad	ap
3	48.0	70.0	1.005	4.0	0.0	1	0	1	0	117.0	...	32.0	6700.0	3.9	1	0	0	1
9	53.0	90.0	1.020	2.0	0.0	0	0	1	0	70.0	...	29.0	12100.0	3.7	1	1	0	1
11	63.0	70.0	1.010	3.0	0.0	0	0	1	0	380.0	...	32.0	4500.0	3.8	1	1	0	1
14	68.0	80.0	1.010	3.0	2.0	1	0	1	1	157.0	...	16.0	11000.0	2.6	1	1	1	1
20	61.0	80.0	1.015	2.0	0.0	0	0	0	0	173.0	...	24.0	9200.0	3.2	1	1	1	1
22	48.0	80.0	1.025	4.0	0.0	1	0	0	0	95.0	...	32.0	6900.0	3.4	1	0	0	0
27	69.0	70.0	1.010	3.0	4.0	1	0	0	0	264.0	...	37.0	9600.0	4.1	1	1	1	0
48	73.0	70.0	1.005	0.0	0.0	1	1	0	0	70.0	...	29.0	18900.0	3.5	1	1	0	0
58	73.0	80.0	1.020	2.0	0.0	0	0	0	0	253.0	...	33.0	7200.0	4.3	1	1	1	0
71	46.0	60.0	1.010	1.0	0.0	1	1	0	0	163.0	...	28.0	14600.0	3.2	1	1	0	0

3

```
print(ckd.shape)
```

```
(400, 25)
```

```
ckd.dtypes
```

```
age       float64
bp        float64
sg        float64
al        float64
su        float64
rbc        object
pc         object
pcc        object
ba         object
bgr       float64
bu        float64
sc        float64
sod       float64
pot       float64
hemo      float64
pcv       float64
wbcc      float64
rbcc      float64
htn        object
dm         object
cad        object
appet      object
pe         object
ane        object
class      object
dtype: object
```

```
ckd.describe(include='all').transpose()
```

	count	unique	top	freq	mean	std	min	25%	50%	75%	max
age	391.0	NaN	NaN	NaN	51.483376	17.169714	2.0	42.0	55.0	64.5	90.0
bp	388.0	NaN	NaN	NaN	76.469072	13.683637	50.0	70.0	80.0	80.0	180.
sg	353.0	NaN	NaN	NaN	1.017408	0.005717	1.005	1.01	1.02	1.02	1.02
al	354.0	NaN	NaN	NaN	1.016949	1.352679	0.0	0.0	0.0	2.0	5.0
su	351.0	NaN	NaN	NaN	0.450142	1.099191	0.0	0.0	0.0	0.0	5.0
rbc	248	2	normal	201	NaN	NaN	NaN	NaN	NaN	NaN	NaN
pc	335	2	normal	259	NaN	NaN	NaN	NaN	NaN	NaN	NaN
pcc	396	2	notpresent	354	NaN	NaN	NaN	NaN	NaN	NaN	NaN
ba	396	2	notpresent	374	NaN	NaN	NaN	NaN	NaN	NaN	NaN
bgr	356.0	NaN	NaN	NaN	148.036517	79.281714	22.0	99.0	121.0	163.0	490.
bu	381.0	NaN	NaN	NaN	57.425722	50.503006	1.5	27.0	42.0	66.0	391.
sc	383.0	NaN	NaN	NaN	3.072454	5.741126	0.4	0.9	1.3	2.8	76.0
sod	313.0	NaN	NaN	NaN	137.528754	10.408752	4.5	135.0	138.0	142.0	163.
pot	312.0	NaN	NaN	NaN	4.627244	3.193904	2.5	3.8	4.4	4.9	47.0
hemo	348.0	NaN	NaN	NaN	12.526437	2.912587	3.1	10.3	12.65	15.0	17.8
pcv	329.0	NaN	NaN	NaN	38.884498	8.990105	9.0	32.0	40.0	45.0	54.0
wbcc	294.0	NaN	NaN	NaN	8406.122449	2944.47419	2200.0	6500.0	8000.0	9800.0	2640
rbcc	269.0	NaN	NaN	NaN	4.707435	1.025323	2.1	3.9	4.8	5.4	8.0
htn	398	2	no	251	NaN	NaN	NaN	NaN	NaN	NaN	NaN
dm	398	3	no	260	NaN	NaN	NaN	NaN	NaN	NaN	NaN
cad	398	2	no	364	NaN	NaN	NaN	NaN	NaN	NaN	NaN
appet	399	2	good	317	NaN	NaN	NaN	NaN	NaN	NaN	NaN
pe	399	2	no	323	NaN	NaN	NaN	NaN	NaN	NaN	NaN
ane	399	2	no	339	NaN	NaN	NaN	NaN	NaN	NaN	NaN
class	400	3	ckd	248	NaN	NaN	NaN	NaN	NaN	NaN	NaN

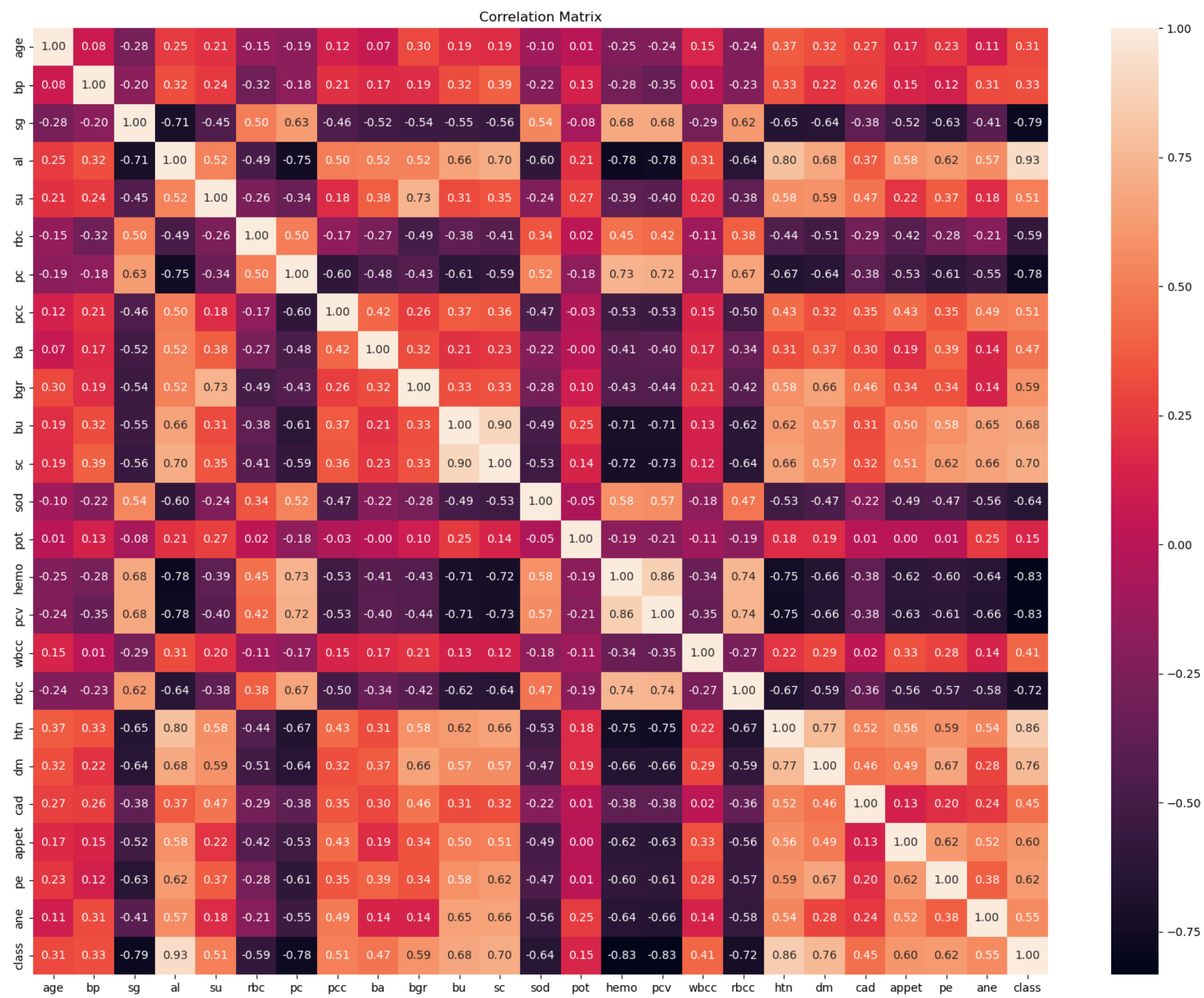
- Observation Count and Variables: The dataset contains 158 rows and 25 columns
- There are missing values (NaN) in many columns. For example, several key variables such as sg (specific gravity), al (albumin), and su (sugar) showed substantial missing data in

observations. This is critical because they are important for diagnosing kidney diseases.

- Data Types: Most variables related to medical measurements like blood pressure (bp), glucose levels (bgr), and others are floating point numbers. Variables like rbc (red blood cells) and pc (pus cell) are categorical, initially with text values which we converted to numerical codes.

4

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



Answer:

Hemoglobin and Packed Cell Volume (PCV): There is a very strong positive correlation between 'hemo' (hemoglobin) and 'pcv' (packed cell volume). Since both are indicators of the blood's ability to carry oxygen, they typically increase or decrease together.

Red Blood Cell Count (RBCC) and Hemoglobin (Hemo): A strong positive correlation exists between 'rbcc' and 'hemo'. These measures are linked to the blood's oxygen-carrying capacity, and typically, a lower hemoglobin level corresponds with a reduced red blood cell count.

Albumin (Al) and Blood Urea (Bu): A positive correlation is observed between these variables, suggesting that higher albumin levels in the urine, which may indicate reduced kidney function, are associated with increased blood urea levels due to the kidney's diminished ability to filter urea.

5

We should remove all the records that has missing values, instad of using imputed values, for the following reasons:

- Imputation introduces estimated values based on assumptions or patterns observed in other data. In health contexts, where every variable can be crucial and highly individual-specific, these estimates might not accurately represent the true state or condition of a patient. This could lead to incorrect conclusions or treatment decisions.
- Imputation methods themselves may introduce bias, particularly if the missing value is not random but related to certain unseen factors. If the method or the data used for imputation does not account for these factors accurately, it can skew the model's outputs.
- By removing incomplete records, it ensures that the model only learns from the most reliable, fully observed datasets. This is particularly important in clinical trials or scenarios where data quality is paramount for accurate predictions.

6

We should keep the outlier, because:

- Outliers might signify rare diseases or unique complications that are not common in the general population. Removing these outliers could prevent the model from learning how to identify and treat these rare conditions.

- A predictive model trained on a dataset that includes outliers might develop a more robust understanding of the full spectrum of possible medical scenarios.

7

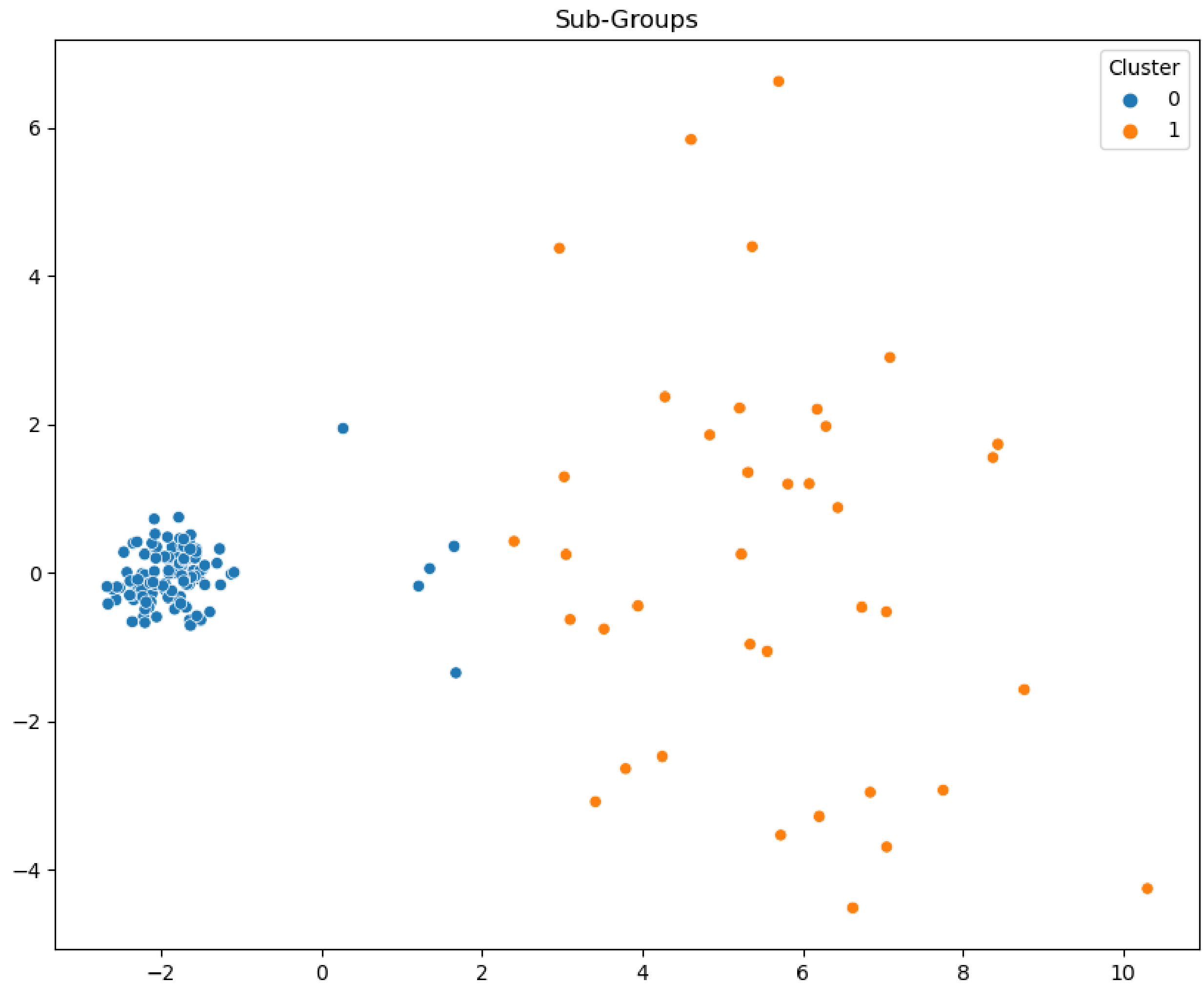
```
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans
from sklearn.decomposition import PCA

X = ckd_transform.drop(columns='class')
y = ckd_transform['class']
norm_transformer = StandardScaler()
X_normalized = norm_transformer.fit_transform(X)

# Configure and apply K-Means clustering
cluster_model = KMeans(n_clusters=2, random_state=1)
X_clusters = cluster_model.fit_predict(X_normalized)

# Setup and apply PCA
pca_transformer = PCA(n_components=2)
pca_results = pca_transformer.fit_transform(X_normalized)

# Plot the clustered data
plt.figure(figsize=(10, 8))
sns.scatterplot(x=pca_results[:, 0], y=pca_results[:, 1], hue=X_clusters)
plt.title('Sub-Groups')
plt.legend(title='Cluster')
plt.show()
```



Use the K-means and PCA, it can be seen that there are 1 clear subgroup of the data as labeled blue in the chart.

8

```
from sklearn.model_selection import train_test_split
X = ckd_transform.drop('class', axis=1)
y = ckd_transform['class']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=100, stra
```

9

- Logistic Regression: Logistic regression provides coefficients that can be directly interpreted in terms of odds ratios for understanding the impact of each feature.

- Random Forest: Random forests can capture complex interactions between features without the need for feature engineering, as they are non-linear models.

10

- AUC (Area Under the Receiver Operating Characteristic Curve): Measures the entire area under the ROC curve, which evaluates the trade-off between true positive rate and false positive rate across all classification thresholds, offering a robust assessment especially beneficial for imbalanced datasets.
- Accuracy Socre: Calculates the ratio of correct predictions (true positives and true negatives) to total observations, providing an easy-to-understand metric that's most effective for balanced datasets but can be misleading if the data is imbalanced.

11

We can normalize the numerical predictors.

12

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



# 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
acc_score_lr = accuracy_score(y_test, y_pred_lr)
acc_score_rf = accuracy_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 accuracy score: {acc_score_lr:.4f}')
print(f'Random Forest accuracy score: {acc_score_rf:.4f}')
```

```
Logistic Regression ROC score: 0.9978
Random Forest ROC score: 1.0000
Logistic Regression accuracy score: 0.9792
Random Forest accuracy score: 1.0000
```

Compare the result, Random Forest is better than logestic regression. However, given the 100% accurate rate, it indicatest that random forest could be over-fitted.

```
X
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	pcv	wbcc	rbcc	htn	dm
3	48.0	70.0	1.005	4.0	0.0	1	0	1	0	117.0	...	11.2	32.0	6700.0	3.9	1	0
9	53.0	90.0	1.020	2.0	0.0	0	0	1	0	70.0	...	9.5	29.0	12100.0	3.7	1	1

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	pcv	wbcc	rbcc	htn	dm
11	63.0	70.0	1.010	3.0	0.0	0	0	1	0	380.0	...	10.8	32.0	4500.0	3.8	1	1
14	68.0	80.0	1.010	3.0	2.0	1	0	1	1	157.0	...	5.6	16.0	11000.0	2.6	1	1
20	61.0	80.0	1.015	2.0	0.0	0	0	0	0	173.0	...	7.7	24.0	9200.0	3.2	1	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	55.0	80.0	1.020	0.0	0.0	1	1	0	0	140.0	...	15.7	47.0	6700.0	4.9	0	0
396	42.0	70.0	1.025	0.0	0.0	1	1	0	0	75.0	...	16.5	54.0	7800.0	6.2	0	0
397	12.0	80.0	1.020	0.0	0.0	1	1	0	0	100.0	...	15.8	49.0	6600.0	5.4	0	0
398	17.0	60.0	1.025	0.0	0.0	1	1	0	0	114.0	...	14.2	51.0	7200.0	5.9	0	0
399	58.0	80.0	1.025	0.0	0.0	1	1	0	0	131.0	...	15.8	53.0	6800.0	6.1	0	0

```python
# normalize X
norm_transformer = StandardScaler()
numerical_cols = X.select_dtypes(include='float64').columns
X_normalized = X.copy()
X_normalized[numerical_cols] = norm_transformer.fit_transform(X[numerical_cols])
X_train, X_test, y_train, y_test = train_test_split(X_normalized, y, test_size=0.3, random_sta

# redo logistic regression

# Initialize the two classifiers
log_reg = LogisticRegression()
log_reg.fit(X_train, y_train)
y_pred_lr = log_reg.predict(X_test)
y_pred_proba_lr = log_reg.predict_proba(X_test)[:, 1]

# Calculate ROC AUC
roc_auc_lr = roc_auc_score(y_test, y_pred_proba_lr)
# Calculate F1 Scores
acc_score_lr = accuracy_score(y_test, y_pred_lr)
```

```python
print(f'Logistic Regression ROC score: {roc_auc_lr:.4f}')
print(f'Logistic Regression accuracy score: {acc_score_lr:.4f}')
```

```
Logistic Regression ROC score: 1.0000
Logistic Regression accuracy score: 0.9792
```

Normalization improved the logistic regression.

13

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

```
       Coefficient
al        1.223405
wbcc      0.687336
bgr       0.510565
sc        0.440638
bu        0.400872
bp        0.308585
su        0.306532
htn       0.240473
age       0.232805
dm        0.125895
pcc       0.120178
cad       0.071545
pe        0.066590
ba        0.063082
appet     0.060222
ane       0.042827
pot       0.008539
pc       -0.237425
rbcc     -0.310068
```

```
rbc      -0.349323
sod      -0.466094
pcv      -0.520499
hemo     -0.587695
sg       -0.691706
```

From the coefficient parameters, we can observe that: * The negative coefficient for sodium levels (sod) suggests that higher serum sodium concentrations are associated with a lower likelihood of having CKD. This could indicate that lower sodium levels, possibly reflecting issues with the kidneys' ability to balance minerals and electrolytes, are a marker of kidney dysfunction.

- Similarly, a negative coefficient for packed cell volume (pcv) implies that lower pcv values are linked with a higher risk of CKD. This relationship might be due to anemia, which is common in kidney disease because of decreased erythropoietin production by the kidneys.
- The positive coefficient for blood glucose random levels (bgr) indicates that higher glucose levels are a predictor of CKD. This aligns with the understanding that diabetes, a leading cause of CKD, is characterized by high blood sugar levels, which over time, can damage the kidneys.

14

```python
from imblearn.over_sampling import SMOTE
from sklearn.datasets import make_classification
from collections import Counter

# Apply SMOTE
smote = SMOTE(random_state=42)
X_resampled, y_resampled = smote.fit_resample(X, y)
random_forest = RandomForestClassifier(random_state=1)
random_forest.fit(X_resampled, y_resampled)
y_pred_rf = random_forest.predict(X_test)
acc_score_lr = accuracy_score(y_test, y_pred_lr)
```

15

- Question 1-8: Zhen Ye
- Question 9-16: Jianghan Sun

16

https://github.com/zhenye4003/STATS3DA-A6