STATS 3DA3

Homework Assignment 6

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```python
# we start import our dataset from the project discription
from ucimlrepo import fetch_ucirepo

# we set up the variables for the upcoming questions
# fetch dataset
chronic_kidney_disease = fetch_ucirepo(id=336)

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

# metadata
print(chronic_kidney_disease.metadata)

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

```
{'uci_id': 336, 'name': 'Chronic Kidney Disease', 'repository_url': 'https://archive.ics.uci.ec
     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
```

```
# we put most of the import codes here for the simplicity of the code
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
import random
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
from sklearn.cluster import KMeans
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, roc_auc_score
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
```

Question 1

Based on the above dataset, our classification problem is to predict whether an individual has chronic kidney disease (CKD) by comparing 24 features such as age, blood pressure, glucose, and red blood cells. The prediction result of the model can help doctors to make early intervention.

Question 2

```
# display the data type in the ckd dataset
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
dtype: object
```

```
# select the columns by data type(float64 and object), and print first 10 observations
float_columns = ckd.select_dtypes(include=['float64']).columns
object_columns = ckd.select_dtypes(include=['object']).columns
```

```
print(ckd[object_columns].head(10))
```

```
        rbc        pc         pcc          ba  htn   dm cad appet   pe  ane
0       NaN    normal  notpresent  notpresent  yes  yes  no  good   no   no
1       NaN    normal  notpresent  notpresent   no   no  no  good   no   no
2    normal    normal  notpresent  notpresent   no  yes  no  poor   no  yes
3    normal  abnormal     present  notpresent  yes   no  no  poor  yes  yes
4    normal    normal  notpresent  notpresent   no   no  no  good   no   no
5       NaN       NaN  notpresent  notpresent  yes  yes  no  good  yes   no
6       NaN    normal  notpresent  notpresent   no   no  no  good   no   no
7    normal  abnormal  notpresent  notpresent   no  yes  no  good  yes   no
8    normal  abnormal     present  notpresent  yes  yes  no  good   no  yes
9  abnormal  abnormal     present  notpresent  yes  yes  no  poor   no  yes
```

```
#mapping the object columns to the numercial values
transfer = {
    'rbc': {'abnormal':0, 'normal':1},
    'pc': {'abnormal':0, 'normal':1},
    'pcc': {'notpresent':0, 'present':1},
    'ba': {'notpresent':0, 'present':1},
    'htn': {'no':0, 'yes':1},
    'dm': {'no':0, 'yes':1},
    'cad': {'no':0, 'yes':1},
    'appet': {'poor':0, 'good':1},
    'pe': {'no':0, 'yes':1},
    'ane': {'no':0, 'yes':1},
}
```

```
# apply the mappings defined in the previous code.
ckd_transformed = pd.DataFrame(ckd)


for column, mapping in transfer.items():
```

```
    if column in ckd_transformed.columns:
        ckd_transformed[column] = ckd_transformed[column].map(mapping)
```

```
# print the summary of the dataset after mapping.
ckd_transformed.describe()
```

	age	bp	sg	al	su	rbc	pc	pcc
count	391.000000	388.000000	353.000000	354.000000	351.000000	248.000000	335.000000	396.000000
mean	51.483376	76.469072	1.017408	1.016949	0.450142	0.810484	0.773134	0.106061
std	17.169714	13.683637	0.005717	1.352679	1.099191	0.392711	0.419431	0.308305
min	2.000000	50.000000	1.005000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	42.000000	70.000000	1.010000	0.000000	0.000000	1.000000	1.000000	0.000000
50%	55.000000	80.000000	1.020000	0.000000	0.000000	1.000000	1.000000	0.000000
75%	64.500000	80.000000	1.020000	2.000000	0.000000	1.000000	1.000000	0.000000
max	90.000000	180.000000	1.025000	5.000000	5.000000	1.000000	1.000000	1.000000

```
# normalize the float columns, scale the float type column using standardScaler
scaler = StandardScaler()
ckd_transformed[float_columns] = scaler.fit_transform(ckd_transformed[float_columns])
```

```
#print the summary of our dataset after mapping and normalization.
ckd_transformed[float_columns].describe()
```

	age	bp	sg	al	su	bgr	bu
count	3.910000e+02	3.880000e+02	3.530000e+02	354.000000	351.000000	3.560000e+02	3.810000e-
mean	9.994847e-17	-2.380684e-16	2.415443e-15	0.000000	0.000000	-1.796316e-16	-3.729883e
std	1.001281e+00	1.001291e+00	1.001419e+00	1.001415	1.001428	1.001407e+00	1.001315e-
min	-2.885708e+00	-1.936857e+00	-2.173584e+00	-0.752868	-0.410106	-1.591967e+00	-1.108830e
25%	-5.530393e-01	-4.733701e-01	-1.297699e+00	-0.752868	-0.410106	-6.193803e-01	-6.032459e
50%	2.050779e-01	2.583733e-01	4.540705e-01	-0.752868	-0.410106	-3.414983e-01	-3.058433e
75%	7.590867e-01	2.583733e-01	4.540705e-01	0.727772	-0.410106	1.890038e-01	1.700008e-

	age	bp	sg	al	su	bgr	bu
max	2.246163e+00	7.575807e+00	1.329955e+00	2.948733	4.145186	4.319341e+00	6.613723e-

Question 3

```
#let's show the detatypes of transformed dataset
ckd_transformed.dtypes
```

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

```
ane      float64
dtype: object
```

```
# show the summary of transformed dataset
ckd_transformed.describe()
```

	age	bp	sg	al	su	rbc	pc	
count	3.910000e+02	3.880000e+02	3.530000e+02	354.000000	351.000000	248.000000	335.000000	3
mean	9.994847e-17	-2.380684e-16	2.415443e-15	0.000000	0.000000	0.810484	0.773134	0
std	1.001281e+00	1.001291e+00	1.001419e+00	1.001415	1.001428	0.392711	0.419431	0
min	-2.885708e+00	-1.936857e+00	-2.173584e+00	-0.752868	-0.410106	0.000000	0.000000	0
25%	-5.530393e-01	-4.733701e-01	-1.297699e+00	-0.752868	-0.410106	1.000000	1.000000	0
50%	2.050779e-01	2.583733e-01	4.540705e-01	-0.752868	-0.410106	1.000000	1.000000	0
75%	7.590867e-01	2.583733e-01	4.540705e-01	0.727772	-0.410106	1.000000	1.000000	0
max	2.246163e+00	7.575807e+00	1.329955e+00	2.948733	4.145186	1.000000	1.000000	1

From the dataset, we can see that numerical variables such as “age”, “blood pressure” and “specific gravity” have been standardized. Categorical variables such as “erythrocytes”, “pus cells”, and “hypertension” have been coded as binary values.

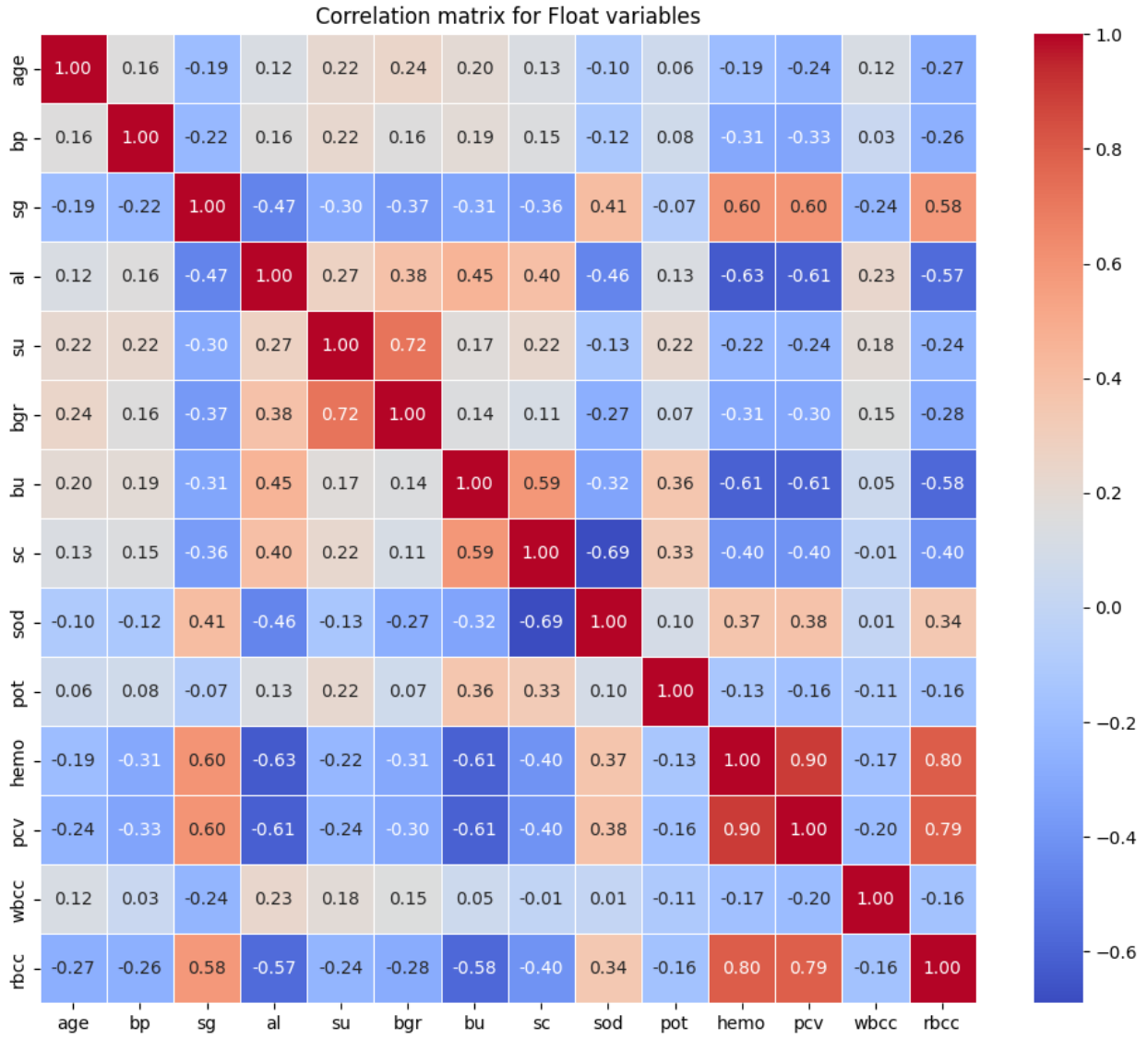
The dataset has 400 observations. The number of non-null values varies from variable to variable, indicating that there is missing data in multiple columns, which needs to be addressed in subsequent data processing steps.

Standardized numerical variables now have a mean close to 0 and a standard deviation of 1. This standardization helps keep the model inputs consistent.

Question 4

```
# calculate and show the heatmap of the correlation matrix
correlation_matrix = ckd_transformed[float_columns].corr()
```

```
plt.figure(figsize=(12, 10))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', fmt=".2f", linewidths=.5)
plt.title('Correlation matrix for Float variables')
plt.show()
```



from the plot, we can see that 'hemo'(homoglobin) and 'pcv'(packed cells volumn) show a very strong positive correlation, which means they might have redunant informations.

The variable 'pot'(potassium) has relatively low correlations with all other variables. This may suggest that this variable will plays an important role in prediction.

from the plot, we can see that 'sod'(sodium) and 'sc'(serum creatinine) have a strong negative correlation, which is -0.69. This means if sod increase will cause a decrease in sc.

Question 5

```
#let's find all the missing values
missing_value = ckd_transformed.isnull().sum()
missing_value
```

```
age        9
bp        12
sg        47
al        46
su        49
rbc      152
pc        65
pcc        4
ba         4
bgr       44
bu        19
sc        17
sod       87
pot       88
hemo      52
pcv       71
wbcc     106
rbcc     131
htn        2
dm         3
cad        2
appet      1
pe         1
```

```
ane        1
dtype: int64
```

```
#next, let's handling all the missing values
ckd_mean = ckd_transformed.mean()
ckd_filled = ckd_transformed.fillna(ckd_mean)


ckd_filled.head()
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	h
0	-0.203139	0.258373	0.454071	-0.012548	-0.410106	0.810484	1.0	0.0	0.0	-3.414983e-01	...	0.
1	-2.594124	-1.936857	0.454071	2.208413	-0.410106	0.810484	1.0	0.0	0.0	-1.796316e-16	...	-0
2	0.613295	0.258373	-1.297699	0.727772	2.323069	1.000000	1.0	0.0	0.0	3.473064e+00	...	-1
3	-0.203139	-0.473370	-2.173584	2.208413	-0.410106	1.000000	0.0	1.0	0.0	-3.920223e-01	...	-0
4	-0.028189	0.258373	-1.297699	0.727772	-0.410106	1.000000	1.0	0.0	0.0	-5.309633e-01	...	-0

Question 6

1. There are some outliers on the Blood Pressure hiigher end. Given that high blood pressure is a significant clinical indicator, those outliers can be examined further, not removed.
2. Some outliers in Serum Creatinine and Blood Urea Nitrogen may relevant to the study on chronic kidney disease. So, it is better to keep those outliers.

In the context of medical data, the outliers may represent the special cases for diagnosis. Therefore, we should keep them in the dataset instead of remove them.

Question 7

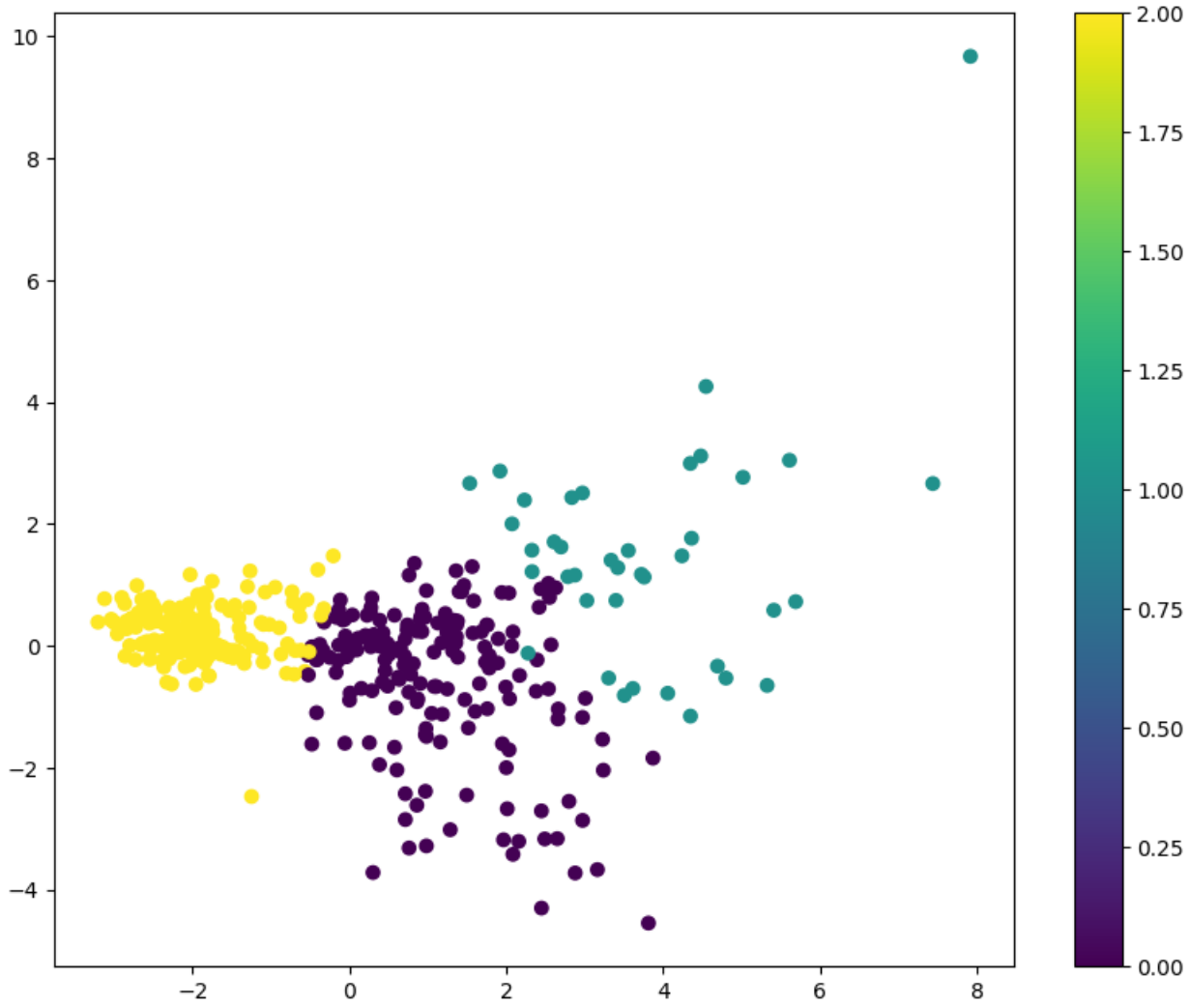
```
# let's use PCA and K-means clustering and show the figure.
ckd_cluster = pd.concat([ckd_filled], axis=1)


pca = PCA(n_components=2)
```

```
pca_data = pca.fit_transform(ckd_cluster)


kmeans = KMeans(n_clusters=3, random_state=17)
cluster_labels = kmeans.fit_predict(ckd_cluster)


plt.figure(figsize=(10, 8))
plt.scatter(pca_data[:, 0], pca_data[:, 1], c=cluster_labels, cmap='viridis', marker='o')
plt.colorbar()
plt.show()
```



Question 8

```
#split the data for model training
X_train, X_test, y_train, y_test = train_test_split(
    ckd_filled,
    y,
    test_size=0.3,
    random_state=1
)
(X_train.shape, X_test.shape, y_train.shape, y_test.shape)
```

```
((280, 24), (120, 24), (280, 1), (120, 1))
```

Question 9

1. We can choose Random Forest Classifier. Random forests don't suffer too much from outliers and it can handle unbalanced datasets. This is useful for the healthcare industry, especially for collecting special case scenarios.
2. We also can use Logistic Regression in our model. Our model is a classical binary classification model, and logistic regression is very effective for dealing with binary classification models. It can provide insight into the role of different features in preventing CKD.

Question 10

1. Accuracy:

Accuracy measures the proportion of total correct predictions amony the total number of cases examined.It enables us to evaluate the effectiveness of various classifiers in the simplest way possible. But it may not be very informative on its own when the data is unbalanced. It may be more misleading when the model needs to predict majority class.

2. Area Under the ROC Curve(AUC-ROC)

This metric assesses the ability of the classifier to distinguish between classes. When AUC is higher, it indicates the better ability to distinguish between CKD and not CKD. Compare with Accuracy metric, when the classes are imbalance, ROC will more useful than Accuracy because it considers both the true postive rate and the false positive rate.

Question 11

```
# let's train the random forest classifier and show the importance of each feature
rf = RandomForestClassifier(random_state=1)
rf.fit(X_train, y_train)

fi = rf.feature_importances_
ckd_fi = pd.DataFrame({'Feature': X_train.columns, 'Importance': fi})
sorted_ckd_fi = ckd_fi.sort_values(by='Importance', ascending=False)

sorted_ckd_fi
```

```
/Library/Frameworks/Python.framework/Versions/3.11/lib/python3.11/site-packages/sklearn/base.py
  return fit_method(estimator, *args, **kwargs)
```

	Feature	Importance
15	pcv	0.183065
14	hemo	0.149958
2	sg	0.135327
11	sc	0.092571
3	al	0.077848
5	rbc	0.075599
17	rbcc	0.068890
18	htn	0.038598
19	dm	0.034299
12	sod	0.026322

	Feature	Importance
9	bgr	0.025741
10	bu	0.025468
0	age	0.013358
4	su	0.012915
1	bp	0.009555
16	wbcc	0.007720
6	pc	0.006608
13	pot	0.005260
21	appet	0.005227
22	pe	0.003003
7	pcc	0.001677
23	ane	0.000685
20	cad	0.000186
8	ba	0.000120

Question 12

```
# We build the model with only the important features and evaluates them on accuracy and metri
top_features = sorted_ckd_fi[sorted_ckd_fi['Importance'] > 0.05]['Feature']
rf_top_features = RandomForestClassifier(random_state=1)
rf_top_features.fit(X_train[top_features], y_train)

logreg = LogisticRegression(max_iter=1000, random_state=1)
logreg.fit(X_train[top_features], y_train)

y_pred_rf = rf_top_features.predict(X_test[top_features])
y_pred_logreg = logreg.predict(X_test[top_features])

accuracy_rf = accuracy_score(y_test, y_pred_rf)
```

```
accuracy_logreg = accuracy_score(y_test, y_pred_logreg)
auc_roc_rf = roc_auc_score(y_test, rf_top_features.predict_proba(X_test[top_features])[:, 1])
auc_roc_logreg = roc_auc_score(y_test, logreg.predict_proba(X_test[top_features])[:, 1])

(accuracy_rf, accuracy_logreg, auc_roc_rf, auc_roc_logreg)
```

```
/Library/Frameworks/Python.framework/Versions/3.11/lib/python3.11/site-packages/sklearn/base.py
  return fit_method(estimator, *args, **kwargs)
/Library/Frameworks/Python.framework/Versions/3.11/lib/python3.11/site-packages/sklearn/utils/v
  y = column_or_1d(y, warn=True)

(0.9916666666666667, 0.9833333333333333, 0.37142857142857144, 0.09)
```

1. We can see from the result, The accuracy has significantly higher ratio in both Random Forest and Logistic Regression than AUC-ROC. accuracy have 99.16% in Random Forest and 98.33% in Logistic Regression. But AUC-ROC only have 37.14% in Random Forest and 9% in Logistic Regression.
2. From the result, we also can make the decision that Random Froest is more suitable in our model than Logistic Regression. Both Accuracy and AUC-ROC have higher ratio in Random Froest. Random Forest is highly accurate and robust against overfitting.

Question 13

```
# we train a logistic regression model on the whole dataset using the selected features.
# and calculate the coefficents
rf_full = LogisticRegression(max_iter=1000, random_state=1)
rf_full.fit(ckd_filled[top_features],y)

coef = rf_full.coef_[0]
ckd_coef = pd.DataFrame({'Feature': top_features, 'Coefficient': coef})
```

```
sorted_ckd_coef = ckd_coef.sort_values(by='Coefficient', key=abs, ascending=False)
sorted_ckd_coef
```

```
/Library/Frameworks/Python.framework/Versions/3.11/lib/python3.11/site-packages/sklearn/utils/v
  y = column_or_1d(y, warn=True)
```

	Feature	Coefficient
5	rbc	-1.332504
3	al	0.876320
2	sg	-0.861387
14	hemo	-0.819001
11	sc	0.791152
15	pcv	-0.712005
17	rbcc	0.155859

1. rbc have the most significant negative coefficient (-1.33). Represent that this feature has the highest impact on predicting CKD.
2. al have a significant positive coefficient (0.87), also have a lagre impact on predicting CKD.

Question 14

Team contribution

Question 1:Xianmiao Zhao

Question 2:Haochen Wei

Question 3:Xianmiao Zhao

Question 4:Haochen Wei

Question 5:Xianmiao Zhao

Question 6:Haochen Wei

Question 7:Xianmiao Zhao

Question 8:Haochen Wei

Question 9:Xianmiao Zhao

Question 10:Haochen Wei

Question 11:Haochen Wei, Xianmiao Zhao

Question 12:Haochen Wei, Xianmiao Zhao

Question 13:Haochen Wei, Xianmiao Zhao

link to public GitHub repository

https://github.com/ShoterMK2/Assignment_6.git