

STATS 3DA3

Project Chronic Kidney Disease Classification Challenge

Group 3

Xiangdong Wang (400335790)

Lingyun Huang (Student ID)

Jingyang Li (Student ID)

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```
pip install ucimlrepo
```

Requirement already satisfied: ucimlrepo in /Library/Frameworks/Python.framework/Versions/3.11.

Note: you may need to restart the kernel to use updated packages.

```
from ucimlrepo import fetch_ucirepo
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
```

1. Classification Problem Identification

Dataset is used from the [Early Stage of Indians Chronic Kidney Disease \(CKD\)](#) project, which comprises data on 250 early-stage CKD patients and 150 healthy controls.

In this assignment, machine learning (ML) techniques have been deployed to predict, diagnose, and treat chronic kidney disease (CKD).

```
## Load Dataset
data_url = 'https://archive.ics.uci.edu/static/public/336/data.csv'
df = pd.read_csv(data_url)
df.head(2)
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc	rbcc	ht
0	48.0	80.0	1.02	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	...	44.0	7800.0	5.2	ye
1	7.0	50.0	1.02	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	38.0	6000.0	NaN	no

```
# fetch dataset
chronic_kidney_disease = fetch_ucirepo(id=336)
# metadata
print(chronic_kidney_disease.metadata)
```

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

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

```
# Features
X.head(2)
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	pcv	wbcc	r
0	48.0	80.0	1.02	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	...	15.4	44.0	7800.0	5
1	7.0	50.0	1.02	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	11.3	38.0	6000.0	N

```
# Target
y.head(2)
```

	class
0	ckd
1	ckd

The classification problem is determining whether a patient has early-stage CKD based on various medical measurements included in the dataset. There are two classes here: Early-stage Indian CKD patients and Healthy patients.

2. Variable Transformation

```
df.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

```

From the dictionary `sg`, `al`, `su` are Categorical variables. `age`, `bp`, `bgr`, `bu`, `sod`, `pcv`, `wbcc` are Integer variable. `rbc`, `pc`, `pcc`, `ba`, `htn`, `dm`, `cad`, `appet`, `pe`, `ane`, `class` are Binary variables. `sc`, `pot`, `hemo`, and `rbcc` are continuous variables. Then, we need to transform the data type.

In general, we do not need to convert categorical and binary variables. Since the classification algorithm is sensitive to the scale of the data, we choose to standardize those data under integer and continuous variable.

```

from sklearn.preprocessing import StandardScaler

#df_scale = df.select_dtypes(include=['int64', 'float64']).columns.tolist()
#df_scale

scale = ['age', 'bp', 'bgr', 'bu', 'sod', 'pcv', 'wbcc', 'sc', 'pot', 'hemo', 'rbcc']
scaler = StandardScaler()
df[scale] = scaler.fit_transform(df[scale])
df.head(2)

```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv
0	-0.203139	0.258373	1.02	1.0	0.0	NaN	normal	notpresent	notpresent	-0.341498	...	0.569881
1	-2.594124	-1.936857	1.02	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	-0.098536

3. Dataset Overview

```
df.describe
```

```

<bound method NDFrame.describe of
0    -0.203139  0.258373  1.020  1.0  0.0    NaN    normal  notpresent
1    -2.594124 -1.936857  1.020  4.0  0.0    NaN    normal  notpresent
2     0.613295  0.258373  1.010  2.0  3.0  normal    normal  notpresent
3    -0.203139 -0.473370  1.005  4.0  0.0  normal  abnormal    present
4    -0.028189  0.258373  1.010  2.0  0.0  normal    normal  notpresent
..         ...         ...    ...    ...    ...         ...         ...
395   0.205078  0.258373  1.020  0.0  0.0  normal    normal  notpresent
396  -0.553039 -0.473370  1.025  0.0  0.0  normal    normal  notpresent
397  -2.302541  0.258373  1.020  0.0  0.0  normal    normal  notpresent
398  -2.010957 -1.205114  1.025  0.0  0.0  normal    normal  notpresent
399   0.380028  0.258373  1.025  0.0  0.0  normal    normal  notpresent

```

		ba	bgr	...	pcv	wbcc	rbcc	htn	dm	cad	\
0	notpresent	-0.341498	...	0.569881	-0.206202	0.481295	yes	yes	no		
1	notpresent	NaN	...	-0.098536	-0.818559	NaN	no	no	no		
2	notpresent	3.473064	...	-0.878356	-0.308261	NaN	no	yes	no		
3	notpresent	-0.392022	...	-0.766953	-0.580420	-0.788961	yes	no	no		
4	notpresent	-0.530963	...	-0.432744	-0.376301	-0.104977	no	no	no		
..		
395	notpresent	-0.101509	...	0.904090	-0.580420	0.188159	no	no	no		
396	notpresent	-0.922524	...	1.683910	-0.206202	1.458415	no	no	no		
397	notpresent	-0.606749	...	1.126896	-0.614440	0.676719	no	no	no		
398	notpresent	-0.429915	...	1.349701	-0.410321	1.165279	no	no	no		
399	notpresent	-0.215188	...	1.572507	-0.546400	1.360703	no	no	no		

	appet	pe	ane	class
0	good	no	no	ckd
1	good	no	no	ckd
2	poor	no	yes	ckd
3	poor	yes	yes	ckd
4	good	no	no	ckd
..
395	good	no	no	notckd
396	good	no	no	notckd
397	good	no	no	notckd
398	good	no	no	notckd
399	good	no	no	notckd

[400 rows x 25 columns]>

```
# Observations count
print(df.shape)

# type check
df.dtypes
```

(400, 25)

```
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
```

```
## Check the distribution of each variable
df.hist(xlabelsize=6,ylabelsize=6,figsize=(6,8))
```

```
array([[<Axes: title={'center': 'age'}>, <Axes: title={'center': 'bp'}>],
```

```

    <Axes: title={'center': 'sg'}>, <Axes: title={'center': 'al'}>],
    [<Axes: title={'center': 'su'}>, <Axes: title={'center': 'bgr'}>,
     <Axes: title={'center': 'bu'}>, <Axes: title={'center': 'sc'}>],
    [<Axes: title={'center': 'sod'}>, <Axes: title={'center': 'pot'}>,
     <Axes: title={'center': 'hemo'}>,
     <Axes: title={'center': 'pcv'}>],
    [<Axes: title={'center': 'wbcc'}>,
     <Axes: title={'center': 'rbcc'}>, <Axes: >, <Axes: >]],
    dtype=object)

```


