

# Final Project

Jenna Orvitz, Noah Ripstein, Viransh Shah

2024-04-18

```
from ucimlrepo import fetch_ucirepo
import pandas as pd
import numpy as np
from sklearn.preprocessing import StandardScaler
import seaborn as sns
```

```
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

# metadata
print(chronic_kidney_disease.metadata)

# variable information
print(chronic_kidney_disease.variables)

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

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

|    | 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  |

|   | age  | bp   | sg    | al  | su  | rbc    | pc       | pcc        | ba         | bgr   | ... | pcv  | wbcc   | rbc |
|---|------|------|-------|-----|-----|--------|----------|------------|------------|-------|-----|------|--------|-----|
| 0 | 48.0 | 80.0 | 1.020 | 1.0 | 0.0 | NaN    | normal   | notpresent | notpresent | 121.0 | ... | 44.0 | 7800.0 | 5.2 |
| 1 | 7.0  | 50.0 | 1.020 | 4.0 | 0.0 | NaN    | normal   | notpresent | notpresent | NaN   | ... | 38.0 | 6000.0 | Na  |
| 2 | 62.0 | 80.0 | 1.010 | 2.0 | 3.0 | normal | normal   | notpresent | notpresent | 423.0 | ... | 31.0 | 7500.0 | Na  |
| 3 | 48.0 | 70.0 | 1.005 | 4.0 | 0.0 | normal | abnormal | present    | notpresent | 117.0 | ... | 32.0 | 6700.0 | 3.9 |
| 4 | 51.0 | 80.0 | 1.010 | 2.0 | 0.0 | normal | normal   | notpresent | notpresent | 106.0 | ... | 35.0 | 7300.0 | 4.6 |

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

Using different variables does a person have Chronic Kidney Disease.

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

```
df.describe()
```

|       | age        | bp         | sg         | al         | su         | bgr        | bu         | sc         |
|-------|------------|------------|------------|------------|------------|------------|------------|------------|
| count | 391.000000 | 388.000000 | 353.000000 | 354.000000 | 351.000000 | 356.000000 | 381.000000 | 383.000000 |
| mean  | 51.483376  | 76.469072  | 1.017408   | 1.016949   | 0.450142   | 148.036517 | 57.425722  | 3.072454   |
| std   | 17.169714  | 13.683637  | 0.005717   | 1.352679   | 1.099191   | 79.281714  | 50.503006  | 5.741126   |
| min   | 2.000000   | 50.000000  | 1.005000   | 0.000000   | 0.000000   | 22.000000  | 1.500000   | 0.400000   |
| 25%   | 42.000000  | 70.000000  | 1.010000   | 0.000000   | 0.000000   | 99.000000  | 27.000000  | 0.900000   |
| 50%   | 55.000000  | 80.000000  | 1.020000   | 0.000000   | 0.000000   | 121.000000 | 42.000000  | 1.300000   |
| 75%   | 64.500000  | 80.000000  | 1.020000   | 2.000000   | 0.000000   | 163.000000 | 66.000000  | 2.800000   |
| max   | 90.000000  | 180.000000 | 1.025000   | 5.000000   | 5.000000   | 490.000000 | 391.000000 | 76.000000  |

```
float64_columns = df.select_dtypes(
    include=['float64']
).columns
float64_columns
scaler = StandardScaler()
df[float64_columns] = scaler.fit_transform(df[float64_columns])
```

```
cat_columns = df.select_dtypes(
    include=['object']
).columns

for col in cat_columns:
    print(df[col].value_counts(normalize=True))
```

rbc

```

normal      0.810484
abnormal    0.189516
Name: proportion, dtype: float64

pc
normal      0.773134
abnormal    0.226866
Name: proportion, dtype: float64

pcc
notpresent  0.893939
present     0.106061
Name: proportion, dtype: float64

ba
notpresent  0.944444
present     0.055556
Name: proportion, dtype: float64

htn
no          0.630653
yes         0.369347
Name: proportion, dtype: float64

dm
no          0.653266
yes         0.344221
\tno       0.002513
Name: proportion, dtype: float64

cad
no          0.914573
yes         0.085427
Name: proportion, dtype: float64

appet
good        0.794486
poor        0.205514
Name: proportion, dtype: float64

```

```

pe
no      0.809524
yes     0.190476
Name: proportion, dtype: float64
ane
no      0.849624
yes     0.150376
Name: proportion, dtype: float64
class
ckd      0.620
notckd   0.375
ckd\t    0.005
Name: proportion, dtype: float64

```

```

for col in cat_columns:
    df[col] = df[col].astype('category').cat.codes
df.head(5)

```

|   | age       | bp        | sg        | al        | su        | rbc | pc | pcc | ba | bgr       | ... | pcv       | v |
|---|-----------|-----------|-----------|-----------|-----------|-----|----|-----|----|-----------|-----|-----------|---|
| 0 | -0.203139 | 0.258373  | 0.454071  | -0.012548 | -0.410106 | -1  | 1  | 0   | 0  | -0.341498 | ... | 0.569881  | - |
| 1 | -2.594124 | -1.936857 | 0.454071  | 2.208413  | -0.410106 | -1  | 1  | 0   | 0  | NaN       | ... | -0.098536 | - |
| 2 | 0.613295  | 0.258373  | -1.297699 | 0.727772  | 2.323069  | 1   | 1  | 0   | 0  | 3.473064  | ... | -0.878356 | - |
| 3 | -0.203139 | -0.473370 | -2.173584 | 2.208413  | -0.410106 | 1   | 0  | 1   | 0  | -0.392022 | ... | -0.766953 | - |
| 4 | -0.028189 | 0.258373  | -1.297699 | 0.727772  | -0.410106 | 1   | 1  | 0   | 0  | -0.530963 | ... | -0.432744 | - |

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

```
df.info()
```

```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399

```

Data columns (total 25 columns):

| #  | Column | Non-Null Count | Dtype   |
|----|--------|----------------|---------|
| 0  | age    | 391 non-null   | float64 |
| 1  | bp     | 388 non-null   | float64 |
| 2  | sg     | 353 non-null   | float64 |
| 3  | al     | 354 non-null   | float64 |
| 4  | su     | 351 non-null   | float64 |
| 5  | rbc    | 400 non-null   | int8    |
| 6  | pc     | 400 non-null   | int8    |
| 7  | pcc    | 400 non-null   | int8    |
| 8  | ba     | 400 non-null   | int8    |
| 9  | bgr    | 356 non-null   | float64 |
| 10 | bu     | 381 non-null   | float64 |
| 11 | sc     | 383 non-null   | float64 |
| 12 | sod    | 313 non-null   | float64 |
| 13 | pot    | 312 non-null   | float64 |
| 14 | hemo   | 348 non-null   | float64 |
| 15 | pcv    | 329 non-null   | float64 |
| 16 | wbcc   | 294 non-null   | float64 |
| 17 | rbcc   | 269 non-null   | float64 |
| 18 | htn    | 400 non-null   | int8    |
| 19 | dm     | 400 non-null   | int8    |
| 20 | cad    | 400 non-null   | int8    |
| 21 | appet  | 400 non-null   | int8    |
| 22 | pe     | 400 non-null   | int8    |
| 23 | ane    | 400 non-null   | int8    |
| 24 | class  | 400 non-null   | int8    |

dtypes: float64(14), int8(11)

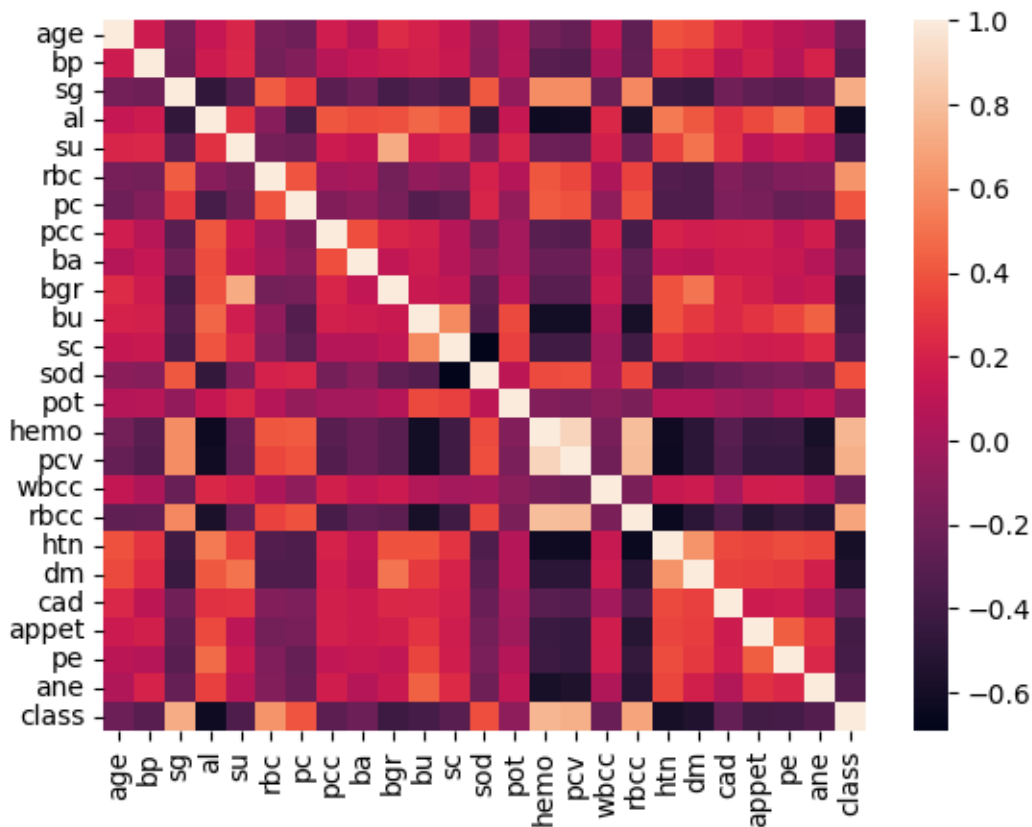
memory usage: 48.2 KB

```
df.describe()
```

|       | age           | bp            | sg            | al         | su         | rbc        | pc         | po         |
|-------|---------------|---------------|---------------|------------|------------|------------|------------|------------|
| count | 3.910000e+02  | 3.880000e+02  | 3.530000e+02  | 354.000000 | 351.000000 | 400.000000 | 400.000000 | 400.000000 |
| mean  | 9.994847e-17  | -2.380684e-16 | 2.415443e-15  | 0.000000   | 0.000000   | 0.12250    | 0.485000   | 0.000000   |
| std   | 1.001281e+00  | 1.001291e+00  | 1.001419e+00  | 1.001415   | 1.001428   | 0.93256    | 0.759089   | 0.000000   |
| min   | -2.885708e+00 | -1.936857e+00 | -2.173584e+00 | -0.752868  | -0.410106  | -1.00000   | -1.000000  | -1.000000  |
| 25%   | -5.530393e-01 | -4.733701e-01 | -1.297699e+00 | -0.752868  | -0.410106  | -1.00000   | 0.000000   | 0.000000   |
| 50%   | 2.050779e-01  | 2.583733e-01  | 4.540705e-01  | -0.752868  | -0.410106  | 1.00000    | 1.000000   | 0.000000   |
| 75%   | 7.590867e-01  | 2.583733e-01  | 4.540705e-01  | 0.727772   | -0.410106  | 1.00000    | 1.000000   | 0.000000   |
| max   | 2.246163e+00  | 7.575807e+00  | 1.329955e+00  | 2.948733   | 4.145186   | 1.00000    | 1.000000   | 1.000000   |

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

```
sns.heatmap(df.corr())
```





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.
6. Outlier Analysis: Implement your approach for identifying and managing outliers, or provide reasons for not addressing them.
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).
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.
9. Classifier Choices: Identify the two classifiers you have chosen and justify your selections.
10. Performance Metrics: Outline the two metrics for comparing the performance of the classifiers.
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).
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).
14. Sub-group Improvement Strategy: If sub-groups were identified, propose and implement a method to improve one classifier performance further. Compare the performance of the new classifier with the results in (12).

## Contributions

Jenna: Created/set up repository and jupyter notebook, started working on questions 1-4

## Github Link

[Github link](https://github.com/JennaOrvitz/Stats3DA3FinalProject/tree/main) (https://github.com/JennaOrvitz/Stats3DA3FinalProject/tree/main)

## References

Rubini, Soundarapandian, L., and P. Eswaran. 2015. “Chronic Kidney Disease.” UCI Machine Learning Repository.

Sanmarchi, Francesco, Claudio Fanconi, Davide Golinelli, Davide Gori, Tina Hernandez-Boussard, and Angelo Capodici. 2023. “Predict, Diagnose, and Treat Chronic Kidney Disease with Machine Learning: A Systematic Literature Review - Journal of Nephrology.” *SpringerLink*. Springer International Publishing. <https://link.springer.com/article/10.1007/s40620-023-01573-4>.