chronic_diseases_forecasting

December 8, 2022

1 Chronic diseases forecasting

[3]:
```
import warnings

import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import plotly.express as px
import seaborn as sns

warnings.filterwarnings("ignore")

plt.style.use("fivethirtyeight")
%matplotlib inline
pd.set_option("display.max_columns", 26)
```

1.1 Data Loading

[7]:
```
df = pd.read_csv("kidney_disease.csv").drop("id", axis=1)
df.columns = [
    "age",
    "blood_pressure",
    "specific_gravity",
    "albumin",
    "sugar",
    "red_blood_cells",
    "pus_cell",
    "pus_cell_clumps",
    "bacteria",
    "blood_glucose_random",
    "blood_urea",
    "serum_creatinine",
    "sodium",
    "potassium",
    "haemoglobin",
    "packed_cell_volume",
    "white_blood_cell_count",
    "red_blood_cell_count",
    "hypertension",
    "diabetes_mellitus",
    "coronary_artery_disease",
    "appetite",
    "peda_edema",
    "aanemia",
    "class",
]
df.head()
```

[7]:
```
    age  blood_pressure  specific_gravity  albumin  sugar red_blood_cells  \
0  48.0            80.0             1.020      1.0    0.0             NaN
1   7.0            50.0             1.020      4.0    0.0             NaN
2  62.0            80.0             1.010      2.0    3.0          normal
3  48.0            70.0             1.005      4.0    0.0          normal
4  51.0            80.0             1.010      2.0    0.0          normal

   pus_cell pus_cell_clumps    bacteria  blood_glucose_random  blood_urea  \
0    normal      notpresent  notpresent                 121.0        36.0
1    normal      notpresent  notpresent                   NaN        18.0
2    normal      notpresent  notpresent                 423.0        53.0
3  abnormal         present  notpresent                 117.0        56.0
4    normal      notpresent  notpresent                 106.0        26.0

   serum_creatinine  sodium  potassium  haemoglobin packed_cell_volume  \
0               1.2     NaN        NaN         15.4                 44
1               0.8     NaN        NaN         11.3                 38
2               1.8     NaN        NaN          9.6                 31
3               3.8   111.0        2.5         11.2                 32
4               1.4     NaN        NaN         11.6                 35

  white_blood_cell_count red_blood_cell_count hypertension diabetes_mellitus  \
0                   7800                  5.2          yes               yes
1                   6000                  NaN           no                no
2                   7500                  NaN           no               yes
3                   6700                  3.9          yes                no
4                   7300                  4.6           no                no

  coronary_artery_disease appetite peda_edema aanemia class
0                      no     good         no      no   ckd
1                      no     good         no      no   ckd
2                      no     poor         no     yes   ckd
3                      no     poor        yes     yes   ckd
4                      no     good         no      no   ckd
```

[8]:
```
df.describe()
```

```
[8]:               age  blood_pressure  specific_gravity     albumin       sugar  \
count  391.000000      388.000000        353.000000  354.000000  351.000000
mean    51.483376       76.469072          1.017408    1.016949    0.450142
std     17.169714       13.683637          0.005717    1.352679    1.099191
min      2.000000       50.000000          1.005000    0.000000    0.000000
25%     42.000000       70.000000          1.010000    0.000000    0.000000
50%     55.000000       80.000000          1.020000    0.000000    0.000000
75%     64.500000       80.000000          1.020000    2.000000    0.000000
max     90.000000      180.000000          1.025000    5.000000    5.000000

       blood_glucose_random  blood_urea  serum_creatinine      sodium  \
count            356.000000  381.000000        383.000000  313.000000
mean             148.036517   57.425722          3.072454  137.528754
std               79.281714   50.503006          5.741126   10.408752
min               22.000000    1.500000          0.400000    4.500000
25%               99.000000   27.000000          0.900000  135.000000
50%              121.000000   42.000000          1.300000  138.000000
75%              163.000000   66.000000          2.800000  142.000000
max              490.000000  391.000000         76.000000  163.000000

        potassium  haemoglobin
count  312.000000   348.000000
mean     4.627244    12.526437
std      3.193904     2.912587
min      2.500000     3.100000
25%      3.800000    10.300000
50%      4.400000    12.650000
75%      4.900000    15.000000
max     47.000000    17.800000
```

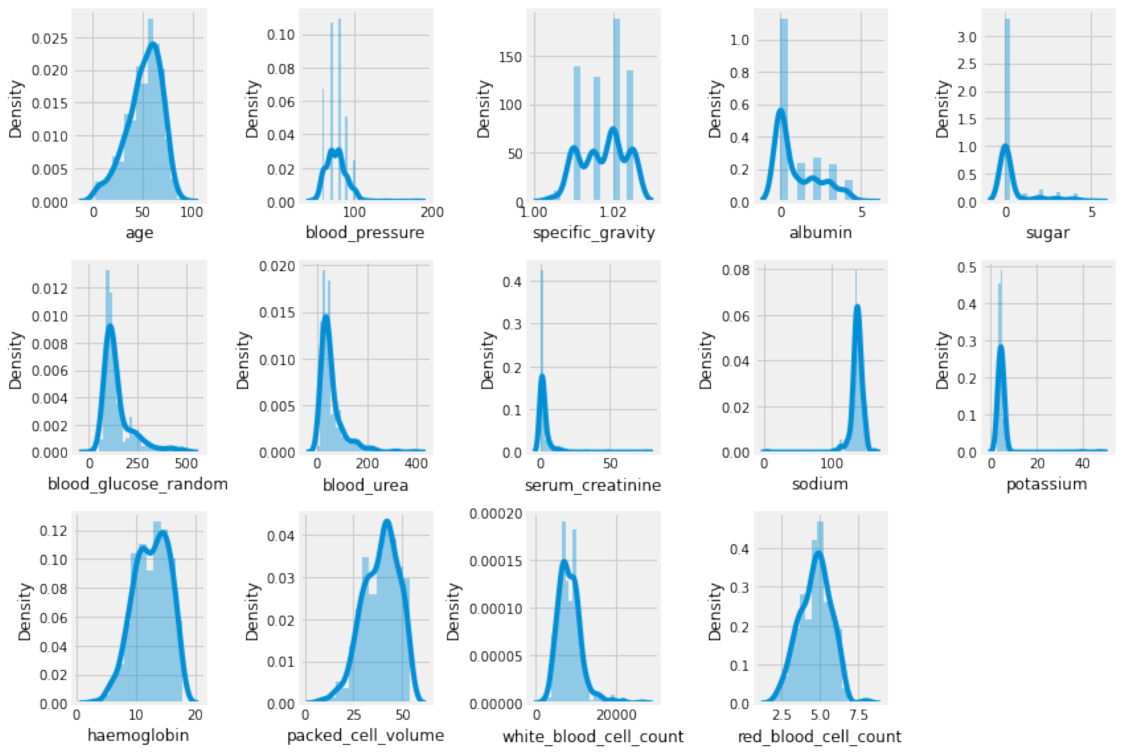
```
[9]: df.info()
```

```
<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   blood_pressure           388 non-null    float64
 2   specific_gravity         353 non-null    float64
 3   albumin                  354 non-null    float64
 4   sugar                    351 non-null    float64
 5   red_blood_cells          248 non-null    object
 6   pus_cell                 335 non-null    object
 7   pus_cell_clumps          396 non-null    object
 8   bacteria                 396 non-null    object
 9   blood_glucose_random     356 non-null    float64
 10  blood_urea               381 non-null    float64
 11   serum_creatinine         383 non-null    float64
 12   sodium                   313 non-null    float64
 13   potassium                312 non-null    float64
 14   haemoglobin              348 non-null    float64
 15   packed_cell_volume       330 non-null    object
 16   white_blood_cell_count   295 non-null    object
 17   red_blood_cell_count     270 non-null    object
 18   hypertension             398 non-null    object
 19   diabetes_mellitus        398 non-null    object
 20   coronary_artery_disease  398 non-null    object
 21   appetite                 399 non-null    object
 22   peda_edema               399 non-null    object
 23   aanemia                  399 non-null    object
 24   class                    400 non-null    object
dtypes: float64(11), object(14)
memory usage: 78.2+ KB
```

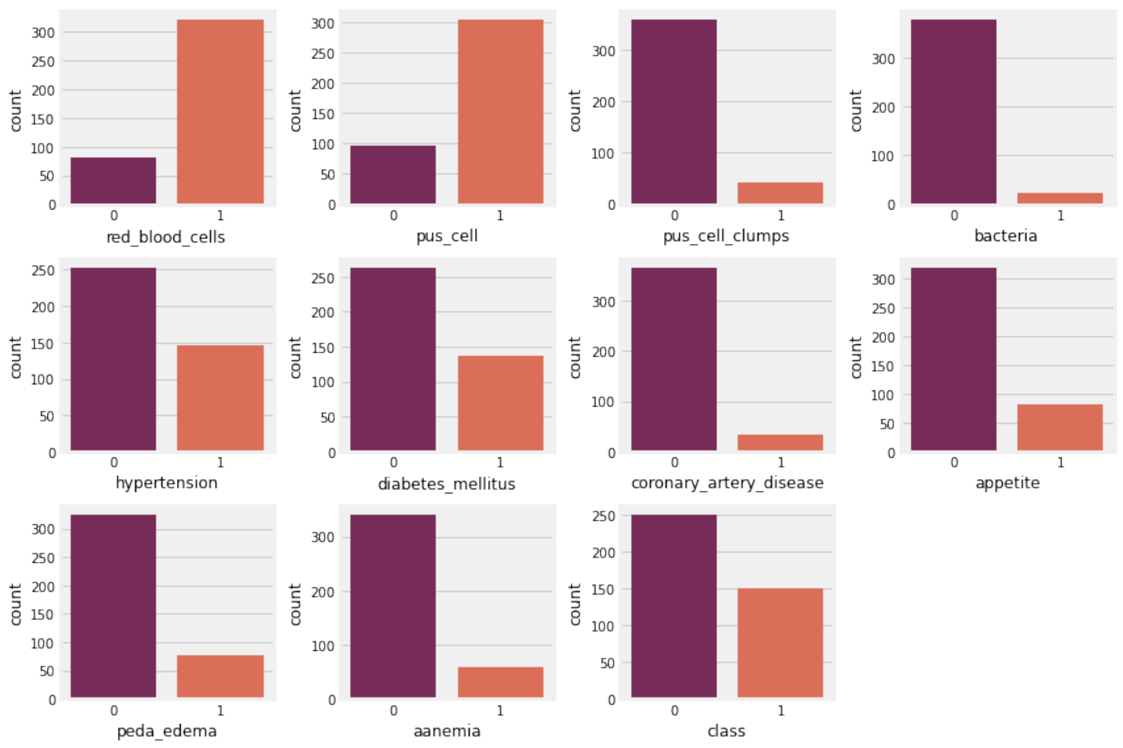
[10]:
```
df["packed_cell_volume"] = pd.to_numeric(df["packed_cell_volume"],␣
 ↪errors="coerce")
df["white_blood_cell_count"] = pd.to_numeric(df["white_blood_cell_count"],␣
 ↪errors="coerce")
df["red_blood_cell_count"] = pd.to_numeric(df["red_blood_cell_count"],␣
 ↪errors="coerce")

cat_cols = [col for col in df.columns if df[col].dtype == "object"]
num_cols = [col for col in df.columns if df[col].dtype != "object"]

df["diabetes_mellitus"].replace(to_replace={"\tno": "no", "\tyes": "yes", "␣
 ↪yes": "yes"}, inplace=True)

df["coronary_artery_disease"] = df["coronary_artery_disease"].
 ↪replace(to_replace="\tno", value="no")

df["class"] = df["class"].replace(to_replace={"ckd\t": "ckd", "notckd": "not␣
 ↪ckd"})


df["class"] = df["class"].map({"ckd": 0, "not ckd": 1})
df["class"] = pd.to_numeric(df["class"], errors="coerce")
```

1.2 Data Exploration

[25]:
```
plt.figure(figsize = (12, 8))
plotnumber = 1

for column in num_cols:
    if plotnumber <= 14:
        ax = plt.subplot(3, 5, plotnumber)
        sns.distplot(df[column])
        plt.xlabel(column)

    plotnumber += 1

plt.tight_layout()
plt.show()
```



[24]:
```
plt.figure(figsize = (12, 8))
plotnumber = 1

for column in cat_cols:
    if plotnumber <= 11:
        ax = plt.subplot(3, 4, plotnumber)
        sns.countplot(df[column], palette = 'rocket')
        plt.xlabel(column)

    plotnumber += 1

plt.tight_layout()
plt.show()
```



1.3 Missing Values

[13]:
```
# filling null values, we will use two methods, random sampling for higher null␣
↪values and
# mean/mode sampling for lower null values

def random_value_imputation(feature):
    random_sample = df[feature].dropna().sample(df[feature].isna().sum())
    random_sample.index = df[df[feature].isnull()].index
    df.loc[df[feature].isnull(), feature] = random_sample

def impute_mode(feature):
    mode = df[feature].mode()[0]
    df[feature] = df[feature].fillna(mode)

# filling num_cols null values using random sampling method

for col in num_cols:
    random_value_imputation(col)

# filling "red_blood_cells" and "pus_cell" using random sampling method and␣
↪rest of cat_cols using mode imputation
```

```
random_value_imputation('red_blood_cells')
random_value_imputation('pus_cell')

for col in cat_cols:
    impute_mode(col)
```

1.4 Data Spliting

[14]:
```
from sklearn.preprocessing import LabelEncoder

le = LabelEncoder()

for col in cat_cols:
    df[col] = le.fit_transform(df[col])

ind_col = [col for col in df.columns if col != 'class']
dep_col = 'class'

X = df[ind_col]
y = df[dep_col]

from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.30,␣
 ↪random_state = 0)
```

1.5 KNN Predictor

[15]:
```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score, confusion_matrix,␣
 ↪classification_report

knn = KNeighborsClassifier()
knn.fit(X_train, y_train)

# accuracy score, confusion matrix and classification report of knn

knn_acc = accuracy_score(y_test, knn.predict(X_test))

print(f"Training Accuracy of KNN is {accuracy_score(y_train, knn.
 ↪predict(X_train))}")
print(f"Test Accuracy of KNN is {knn_acc} \n")

print(f"Confusion Matrix :- \n{confusion_matrix(y_test, knn.
 ↪predict(X_test))}\n")
print(f"Classification Report :- \n {classification_report(y_test, knn.
 ↪predict(X_test))}")
```

```
Training Accuracy of KNN is 0.8178571428571428
Test Accuracy of KNN is 0.6583333333333333

Confusion Matrix :-
[[51 21]
 [20 28]]

Classification Report :-
               precision    recall  f1-score   support

           0       0.72      0.71      0.71        72
           1       0.57      0.58      0.58        48

    accuracy                           0.66       120
   macro avg       0.64      0.65      0.65       120
weighted avg       0.66      0.66      0.66       120
```

1.6 Randomforest Predictor

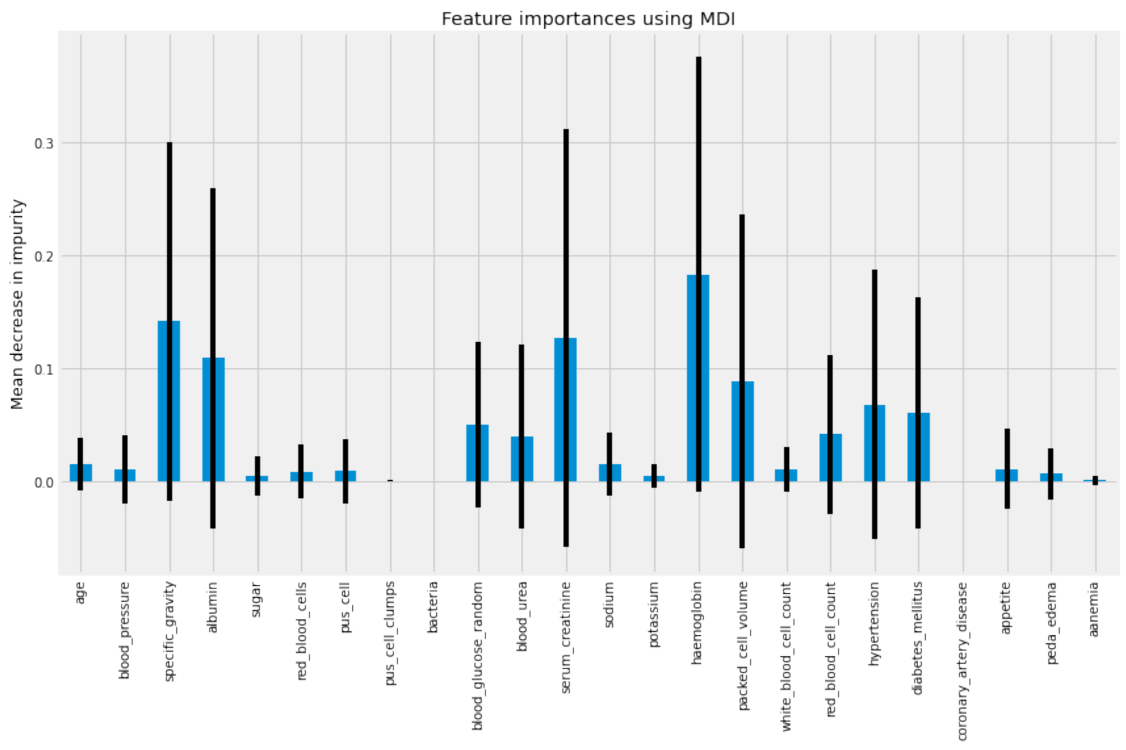
[29]:
```python
from sklearn.ensemble import RandomForestClassifier

rd_clf = RandomForestClassifier(criterion = 'entropy', max_depth = 11,␣
 ↪max_features = 'auto', min_samples_leaf = 2, min_samples_split = 3,␣
 ↪n_estimators = 130)
rd_clf.fit(X_train, y_train)

# accuracy score, confusion matrix and classification report of random forest

rd_clf_acc = accuracy_score(y_test, rd_clf.predict(X_test))

print(f"Training Accuracy of Random Forest Classifier is␣
 ↪{accuracy_score(y_train, rd_clf.predict(X_train))}")
print(f"Test Accuracy of Random Forest Classifier is {rd_clf_acc} \n")

print(f"Confusion Matrix :- \n{confusion_matrix(y_test, rd_clf.
 ↪predict(X_test))}\n")
print(f"Classification Report :- \n {classification_report(y_test, rd_clf.
 ↪predict(X_test))}")
```

```
Training Accuracy of Random Forest Classifier is 0.9964285714285714
Test Accuracy of Random Forest Classifier is 0.9916666666666667

Confusion Matrix :-
[[72  0]
 [ 1 47]]

Classification Report :-
```

```
              precision    recall  f1-score   support

           0       0.99      1.00      0.99        72
           1       1.00      0.98      0.99        48

    accuracy                           0.99       120
   macro avg       0.99      0.99      0.99       120
weighted avg       0.99      0.99      0.99       120
```

1.7 Feature Importances

[30]:
```python
importances = rd_clf.feature_importances_
std = np.std([tree.feature_importances_ for tree in rd_clf.estimators_], axis=0)


forest_importances = pd.Series(importances, index=X_train.columns)


fig, ax = plt.subplots(figsize = (12, 8))
forest_importances.plot.bar(yerr=std, ax=ax)
ax.set_title("Feature importances using MDI")
ax.set_ylabel("Mean decrease in impurity")
fig.tight_layout()
```


Feature importances using MDI
Mean decrease in impurity
age
blood_pressure
specific_gravity
albumin
sugar
red_blood_cells
pus_cell
pus_cell_clumps
bacteria
blood_glucose_random
blood_urea
serum_creatinine
sodium
potassium
haemoglobin
packed_cell_volume
white_blood_cell_count
red_blood_cell_count
hypertension
diabetes_mellitus
coronary_artery_disease
appetite
peda_edema
aanemia