Chronic kidney disease prediction & Data Analysis

Abstract

The goal of a chronic kidney disease prediction project would be to develop a model or algorithm that can identify individuals at risk for CKD based on their medical history, lifestyle factors, and other relevant information. This could help healthcare providers identify and intervene with at-risk individuals earlier, potentially improving their health outcomes and reducing the burden of CKD on the healthcare system

1.Introduction

Chronic kidney disease (CKD) is a serious health condition that affects millions of people worldwide. It is important to understand the risk factors for CKD and to develop effective interventions for preventing and managing the disease.

In our project we use logistic regression since we have binary outcome and it not complicated to fit liear seperable line or plane.Logistic regression is a statistical method that can be used to predict the likelihood of an event occurring, given a set of independent variables. In the context of chronic kidney disease (CKD) prediction, logistic regression could be used to predict the likelihood of an individual developing CKD, based on various risk factors such as age, blood pressure, diabetes status, and other variables.
We used various methods to improve the output of logistic regression, selecting the best number of features and PCA with optimum number of features

2. Methodology

1. First step in for statistical analysis is normality tese, here I performed univariate normality check using shapiro test & multi_variate normality check :

The Shapiro test, also known as the Shapiro-Wilk test, is a statistical test used to determine whether a sample of data comes from a normally distributed population. It is often used to assess the normality of data before conducting statistical tests that assume the data are normally distributed, such as t-tests and ANOVA.

2. For comparing two means The Mann-Whitney Test :

   The Mann-Whitney test, also known as the Wilcoxon rank-sum test, is a nonparametric statistical test used to compare the medians of two independent samples. It is often used as an alternative to the t-test when the data are not normally distributed or when the variances of the two samples are not equal.
   H0: The two populations are equal versus

   H1: The two populations are not equal.

3. One-way Anove :

   The Kruskal-Wallis test, also known as the one-way analysis of variance (ANOVA) on ranks, is a nonparametric statistical test used to compare the medians of two or more independent samples. It is often used as an alternative to the one-way ANOVA when the data are not normally distributed or when the variances of the samples are not equal.

   H0: $\mu1 =\mu2 =\cdots=\mu I$
   H1: at least two means differ

4. Nemenyi Test:

   The Friedman Test is used to find whether there exists a significant difference between the means of more than two groups. In such groups, the same subjects show up in each group. If the p-value of the Friedman test turns out to be statistically significant then we can conduct the Nemenyi test to find exactly which groups are different. This test is also known as Nemenyi post-hoc test.

5.Logistic regression :

To evaluate the performance of the logistic regression model, you can use various metrics such as accuracy, precision, and recall. These metrics can help you understand how well the model is able to predict the likelihood of an individual developing CKD, and whether there is room for improvement.

Overall, logistic regression can be a useful tool for predicting the likelihood of an individual developing CKD, and it can help healthcare providers identify individuals at risk of the disease so that preventive measures can be taken.

6.PCA :

Principal component analysis (PCA) is a statistical technique used to reduce the dimensionality of a dataset by projecting the data onto a lower-dimensional space. It is often used as a data preprocessing step to reduce the complexity of the data and make it more amenable to analysis.

3. Data descrption

1.Data is taken from: https://archive.ics.uci.edu/ml/datasets/chronic_kidney_disease

2.Original data is having many rows with missing values, I have cleaned such that there are no missing values.

3. Data set has total size has 158 Rows X 25 Columns , each column is renamed with appropriate medical name.

4. 10 columns are categorical with 2 categories each and 15 are numrical.

5. There are some columns with more than 0.8 correlation between them.

6. Categorical columns are mapped with appropriate numbers as per code given below

7.From distibution graphs we can observe that data in non-normal.

In [1]:
```
#importig required libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import scikit_posthocs as sp
from scipy.stats import shapiro
import scipy.stats as stats
from scipy.stats import kruskal
from statsmodels.stats.multicomp import MultiComparison
from scipy.stats import mannwhitneyu


from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

import statsmodels.api as sm
from sklearn.decomposition import PCA

from pingouin import multivariate_normality
```

In [2]:
```
data = pd.read_csv('ckd_clean.csv')
```

In [3]:
```
df = data.copy()
```

In [4]:
```
df.head()
```

Out[4]:

	Age	Blood Pressure	Specific Gravity	Albumin	Sugar	Red Blood Cells	Pus Cell	Pus Cell clumps	Bacteria	Bloc Glucos Rando
0	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117
1	53.0	90.0	1.020	2.0	0.0	abnormal	abnormal	present	notpresent	70
2	63.0	70.0	1.010	3.0	0.0	abnormal	abnormal	present	notpresent	380
3	68.0	80.0	1.010	3.0	2.0	normal	abnormal	present	present	157
4	61.0	80.0	1.015	2.0	0.0	abnormal	abnormal	notpresent	notpresent	173

5 rows × 25 columns

In [5]:
```
cat_df = df.select_dtypes(['object'])
cat_df.columns,len(cat_df.columns)
```

Out[5]:
```
(Index(['Red Blood Cells', 'Pus Cell', 'Pus Cell clumps', 'Bacteria',
        'Hypertension', 'Diabetes Mellitus', 'Coronary Artery Disease',
        'Appetite', 'Pedal Edema', 'Anemia'],
       dtype='object'),
 10)
```

In [6]:
```
num_df = df.select_dtypes(['float','int'])
num_df.columns , len(num_df.columns)
```

Out[6]:
```
(Index(['Age', 'Blood Pressure', 'Specific Gravity', 'Albumin', 'Sugar',
        'Blood Glucose Random', 'Blood Urea', 'Serum Creatinine', 'Sodium',
        'Potassium', 'Hemoglobin', 'Packed Cell Volume',
        'White Blood Cell Count', 'Red Blood Cell Count', 'Class'],
       dtype='object'),
 15)
```

In [7]:
```
mapping = {"normal": 0, "abnormal": 1, "present": 1,"notpresent":0,'yes':1,'n
```

In [8]:
```
cat_cols = df.select_dtypes(include=['object'])

cat_cols = cat_cols.applymap(lambda x: mapping[x]).astype('float')
cat_df.update(cat_cols)
df.update(cat_cols)
df = df.astype(float)
```

```
/opt/anaconda3/lib/python3.9/site-packages/pandas/core/frame.py:7511: SettingW
ithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/st
able/user_guide/indexing.html#returning-a-view-versus-a-copy
  self[col] = expressions.where(mask, this, that)
```

In [9]:
```
cat_df.update(cat_cols)
```

In [10]:
```
df.head()
```

Out[10]:

	Age	Blood Pressure	Specific Gravity	Albumin	Sugar	Red Blood Cells	Pus Cell	Pus Cell clumps	Bacteria	Blood Glucose Random	...	Pack C Volu
0	48.0	70.0	1.005	4.0	0.0	0.0	1.0	1.0	0.0	117.0	...	3
1	53.0	90.0	1.020	2.0	0.0	1.0	1.0	1.0	0.0	70.0	...	2
2	63.0	70.0	1.010	3.0	0.0	1.0	1.0	1.0	0.0	380.0	...	3
3	68.0	80.0	1.010	3.0	2.0	0.0	1.0	1.0	1.0	157.0	...	1
4	61.0	80.0	1.015	2.0	0.0	1.0	1.0	0.0	0.0	173.0	...	2

5 rows × 25 columns

In [11]:

```
df.describe().transpose()
```

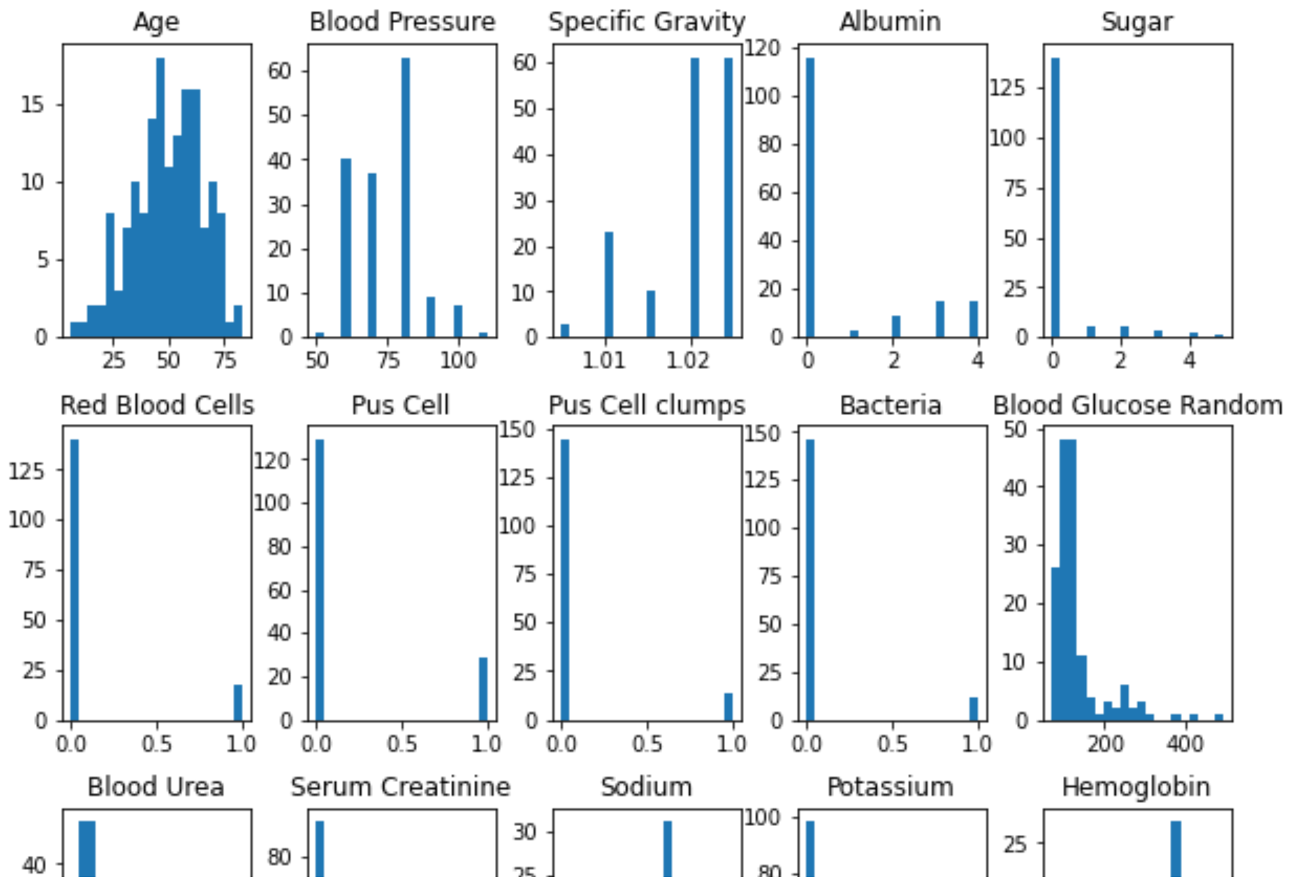
Out[11]:

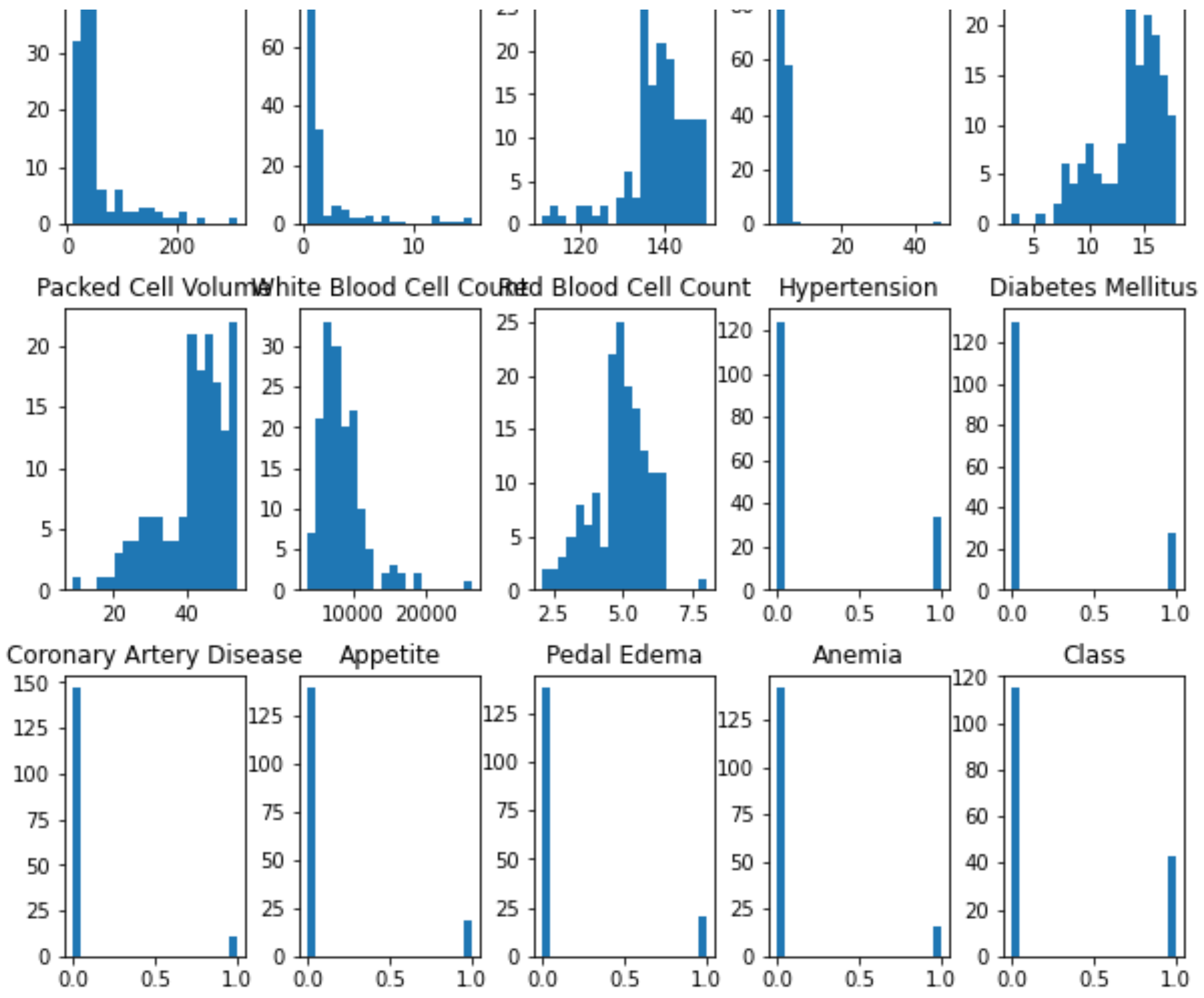
	count	mean	std	min	25%	50%	75%	r
Age	158.0	49.563291	15.512244	6.000	39.25	50.50	60.000	83.
Blood Pressure	158.0	74.050633	11.175381	50.000	60.00	80.00	80.000	110.
Specific Gravity	158.0	1.019873	0.005499	1.005	1.02	1.02	1.025	1.
Albumin	158.0	0.797468	1.413130	0.000	0.00	0.00	1.000	4.
Sugar	158.0	0.253165	0.813397	0.000	0.00	0.00	0.000	5.
Red Blood Cells	158.0	0.113924	0.318729	0.000	0.00	0.00	0.000	1.
Pus Cell	158.0	0.183544	0.388343	0.000	0.00	0.00	0.000	1.
Pus Cell clumps	158.0	0.088608	0.285080	0.000	0.00	0.00	0.000	1.
Bacteria	158.0	0.075949	0.265759	0.000	0.00	0.00	0.000	1.
Blood Glucose Random	158.0	131.341772	64.939832	70.000	97.00	115.50	131.750	490.
Blood Urea	158.0	52.575949	47.395382	10.000	26.00	39.50	49.750	309.
Serum Creatinine	158.0	2.188608	3.077615	0.400	0.70	1.10	1.600	15.
Sodium	158.0	138.848101	7.489421	111.000	135.00	139.00	144.000	150.
Potassium	158.0	4.636709	3.476351	2.500	3.70	4.50	4.900	47.
Hemoglobin	158.0	13.687342	2.882204	3.100	12.60	14.25	15.775	17.

Packed Cell Volume	158.0	41.917722	9.105164	9.000	37.50	44.00	48.000	54.
White Blood Cell Count	158.0	8475.949367	3126.880181	3800.000	6525.00	7800.00	9775.000	26400.
Red Blood Cell Count	158.0	4.891772	1.019364	2.100	4.50	4.95	5.600	8.
Hypertension	158.0	0.215190	0.412261	0.000	0.00	0.00	0.000	1.
Diabetes Mellitus	158.0	0.177215	0.383065	0.000	0.00	0.00	0.000	1.
Coronary Artery Disease	158.0	0.069620	0.255315	0.000	0.00	0.00	0.000	1.
Appetite	158.0	0.120253	0.326292	0.000	0.00	0.00	0.000	1.
Pedal Edema	158.0	0.126582	0.333562	0.000	0.00	0.00	0.000	1.
Anemia	158.0	0.101266	0.302640	0.000	0.00	0.00	0.000	1.
Class	158.0	0.272152	0.446483	0.000	0.00	0.00	1.000	1.

In [12]:

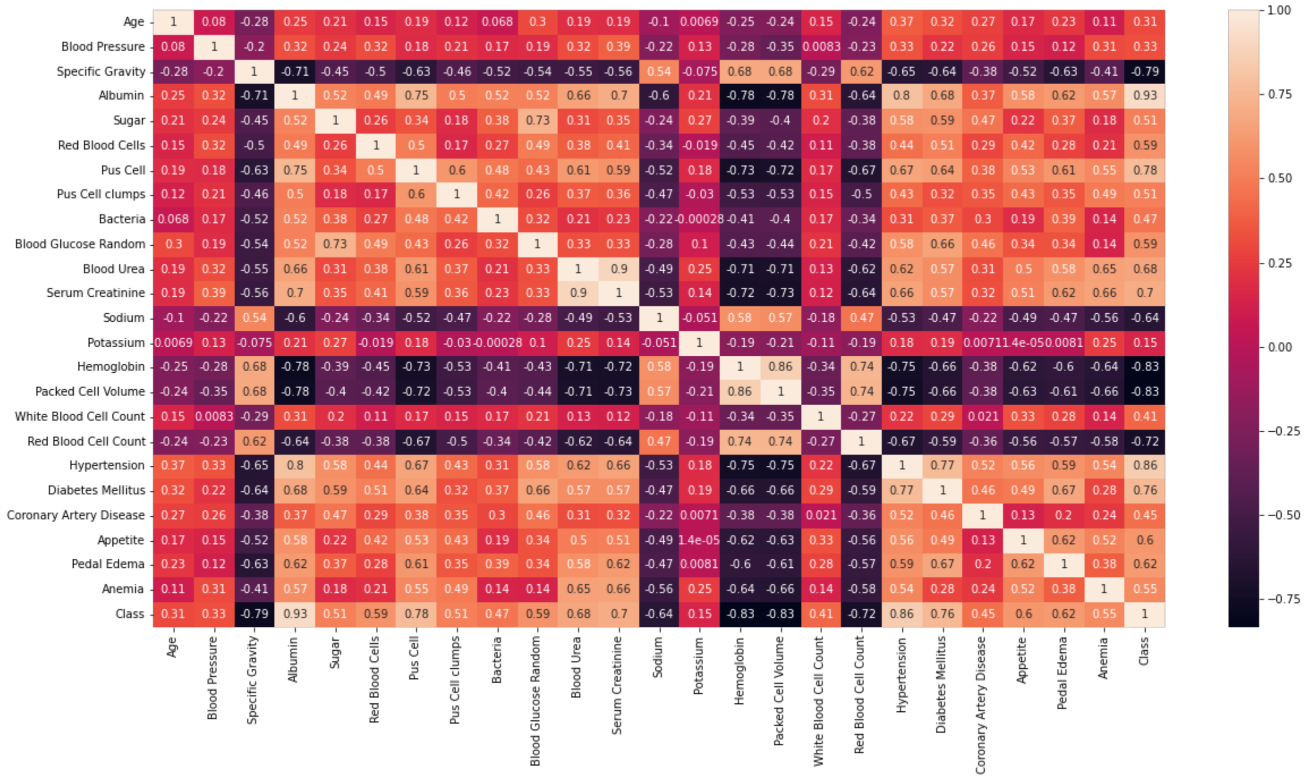
```
df.hist(figsize=(10,16),bins=20,grid = False)
plt.show()
```





In [13]:
```
corr_matrix = df.corr()
```

In [14]:
```
plt.figure(figsize = (20,10))
sns.heatmap(corr_matrix,annot = True)
plt.show()
```



4.1 Comparing Two samples

Checking normality :

In [15]:

```
results = {}
for col in num_df.columns[:-1]:
    w, p = shapiro(num_df[col])
    results[col] = (w, p)

normal_columns = []
non_normal_columns = []
for i, (w, p) in results.items():
    if p > 0.05:
        normal_columns.append(i)
    else:
        non_normal_columns.append(i)

print('Normal columns:',normal_columns,',(W & P Values):',results[normal_colu
```

```
Normal columns: ['Age'] ,(W & P Values): (0.9849788546562195, 0.08524563908576
965)
```

In [16]:

```
print(normal_columns)
```

```
['Age']
```

There is only one feature which is normal among the numerical value from the results of above of sapiro test.We fail to reject Ho for age since p_value is more than 0.05

In [17]:
```
multivariate_normality(num_df, alpha=.05)
```

Out[17]:
```
HZResults(hz=1.5756432383932815, pval=0.0, normal=False)
```

From multivariate normality check we observe p_values is very small, we reject Ho

In [18]:
```
num_df
for i,col1 in enumerate(num_df.columns):
    for col2 in num_df.columns[i+1:]:
        statistic,p_value = stats.mannwhitneyu(num_df[col1], num_df[col2])
        if p_value > 0.05:
            print(col1,'&',col2,':',"{:.3f}".format(statistic),'&',"{:.3f}".f
```

```
Specific Gravity & Serum Creatinine : 12166.000 & 0.695
Albumin & Class : 13241.500 & 0.230
Blood Urea & Packed Cell Volume : 10903.500 & 0.052
```

There are only three pairs with same population distribution among all the numerical features, we can observed from above result for Specific Gravity & Serum Creatinine ,Albumin & Class and Blood Urea & Packed Cell Volume we fail to reject H0. For remaining all pairs we reject Ho since p_value is less than 0.05

4.2 The Analysis of Variance:

In [19]:
```
columns = num_df.columns
statistic, p_value = stats.kruskal(num_df[columns[0]],num_df[columns[1]],num_
if p_value > 0.05:
    print("{:.3f}".format(statistic), "{:.3f}".format(p_value))
    print('All means are same')
else:
    print("{:.3f}".format(statistic), "{:.3f}".format(p_value))
    print('Atleast one pair of means is not same')
```

```
2106.394 0.000
Atleast one pair of means is not same
```

Mann-whitney test result and k-w test results are implied to each other

4.3 The Analysis of Categorical Data:

In [20]:
```python
import scikit_posthocs as sp
```

In [21]:
```python
nemenyi = sp.posthoc_nemenyi(num_df.T.values)
```

In [22]:
```python
nemenyi
```

Out[22]:

	1	2	3	4	5	6
1	1.000000e+00	8.690782e-01	1.161290e-27	3.585449e-46	7.438681e-55	8.439494e-03
2	8.690782e-01	1.000000e+00	1.623283e-44	3.617188e-67	1.712019e-77	9.514256e-01
3	1.161290e-27	1.623283e-44	1.000000e+00	7.694778e-01	1.494673e-01	1.441087e-62
4	3.585449e-46	3.617188e-67	7.694778e-01	1.000000e+00	9.999801e-01	7.848536e-89
5	7.438681e-55	1.712019e-77	1.494673e-01	9.999801e-01	1.000000e+00	1.357423e-100
6	8.439494e-03	9.514256e-01	1.441087e-62	7.848536e-89	1.357423e-100	1.000000e+00
7	1.000000e+00	5.939949e-01	1.098393e-24	2.445514e-42	1.107147e-50	8.801753e-04
8	1.995193e-25	1.081672e-41	1.000000e+00	5.362053e-01	5.240970e-02	3.115608e-59
9	1.904340e-05	3.311640e-01	8.753502e-74	4.989765e-102	1.401888e-114	9.999202e-01
10	2.034251e-10	1.118386e-21	2.568070e-01	2.037675e-06	6.136897e-10	6.540785e-35
11	4.474129e-02	8.294402e-08	4.563040e-08	2.659075e-19	3.887017e-25	1.912341e-16
12	9.999982e-01	3.439277e-01	1.594334e-22	1.615080e-39	1.329018e-47	1.163477e-04
13	4.082466e-13	7.510615e-05	5.312383e-97	6.548411e-129	6.341610e-143	2.989452e-01
14	3.253715e-08	1.924275e-18	5.153751e-02	2.279214e-08	2.352381e-12	8.433485e-31
15	8.557120e-53	4.691089e-75	2.588595e-01	9.999993e-01	1.000000e+00	7.955041e-98

In [23]:
```python
nemenyi > 0.05
```

Out[23]:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	
1	True	True	False	False	False	False	True	False	False	False	False	True	False	False	F
2	True	True	False	False	False	True	True	False	True	False	False	True	False	False	F
3	False	False	True	True	True	False	False	True	False	True	False	False	False	True	
4	False	False	True	True	True	False	False	True	False	False	False	False	False	False	
5	False	False	True	True	True	False	False	True	False	False	False	False	False	False	
6	False	True	False	False	False	True	False	False	True	False	False	False	True	False	F
7	True	True	False	False	False	False	True	False	False	False	True	True	False	False	F
8	False	False	True	True	True	False	False	True	False	True	False	False	False	True	
9	False	True	False	False	False	True	False	False	True	False	False	False	True	False	F
10	False	False	True	False	False	False	False	True	False	True	True	False	False	True	F
11	False	False	False	False	False	False	True	False	False	True	True	True	False	True	F
12	True	True	False	False	False	False	True	False	False	False	True	True	False	False	F
13	False	False	False	False	False	True	False	False	True	False	False	False	True	False	F
14	False	False	True	False	False	False	False	True	False	True	True	False	False	True	F
15	False	False	True	True	True	False	False	True	False	False	False	False	False	False	

In [24]:

```python
columns = cat_df.columns[:-1]

from scipy.stats import chi2_contingency
from scipy.stats import chisquare, chi2_contingency, chi2


results = []
for i,col1 in enumerate(columns):
    for col2 in cat_df.columns[i+1:]:

        contingencyTable = pd.crosstab(cat_df[col1],cat_df[col2])
        stat, p, dof, expected = chi2_contingency(contingencyTable)

        prob = 0.95
        critical = chi2.ppf(prob, dof)

        if abs(stat) >= critical:
            print(col1,'&',col2,':Dependent (reject H0)')
        else:
            print(col1,'&',col2,'Independent (fail to reject H0)')
```

```
Red Blood Cells & Pus Cell :Dependent (reject H0)
Red Blood Cells & Pus Cell clumps Independent (fail to reject H0)
Red Blood Cells & Bacteria :Dependent (reject H0)
Red Blood Cells & Hypertension :Dependent (reject H0)
Red Blood Cells & Diabetes Mellitus :Dependent (reject H0)
Red Blood Cells & Coronary Artery Disease :Dependent (reject H0)
Red Blood Cells & Appetite :Dependent (reject H0)
Red Blood Cells & Pedal Edema :Dependent (reject H0)
Red Blood Cells & Anemia :Dependent (reject H0)
Pus Cell & Pus Cell clumps :Dependent (reject H0)
Pus Cell & Bacteria :Dependent (reject H0)
Pus Cell & Hypertension :Dependent (reject H0)
Pus Cell & Diabetes Mellitus :Dependent (reject H0)
Pus Cell & Coronary Artery Disease :Dependent (reject H0)
Pus Cell & Appetite :Dependent (reject H0)
Pus Cell & Pedal Edema :Dependent (reject H0)
Pus Cell & Anemia :Dependent (reject H0)
Pus Cell clumps & Bacteria :Dependent (reject H0)
Pus Cell clumps & Hypertension :Dependent (reject H0)
Pus Cell clumps & Diabetes Mellitus :Dependent (reject H0)
Pus Cell clumps & Coronary Artery Disease :Dependent (reject H0)
Pus Cell clumps & Appetite :Dependent (reject H0)
Pus Cell clumps & Pedal Edema :Dependent (reject H0)
Pus Cell clumps & Anemia :Dependent (reject H0)
Bacteria & Hypertension :Dependent (reject H0)
Bacteria & Diabetes Mellitus :Dependent (reject H0)
Bacteria & Coronary Artery Disease :Dependent (reject H0)
Bacteria & Appetite Independent (fail to reject H0)
Bacteria & Pedal Edema :Dependent (reject H0)
Bacteria & Anemia Independent (fail to reject H0)
Hypertension & Diabetes Mellitus :Dependent (reject H0)
Hypertension & Coronary Artery Disease :Dependent (reject H0)
Hypertension & Appetite :Dependent (reject H0)
Hypertension & Pedal Edema :Dependent (reject H0)
Hypertension & Anemia :Dependent (reject H0)
Diabetes Mellitus & Coronary Artery Disease :Dependent (reject H0)
Diabetes Mellitus & Appetite :Dependent (reject H0)
Diabetes Mellitus & Pedal Edema :Dependent (reject H0)
Diabetes Mellitus & Anemia :Dependent (reject H0)
Coronary Artery Disease & Appetite Independent (fail to reject H0)
Coronary Artery Disease & Pedal Edema :Dependent (reject H0)
Coronary Artery Disease & Anemia :Dependent (reject H0)
Appetite & Pedal Edema :Dependent (reject H0)
Appetite & Anemia :Dependent (reject H0)
Pedal Edema & Anemia :Dependent (reject H0)
```

4.4 Logistic regression

In [25]:
```
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.metrics import confusion_matrix
from sklearn.metrics import roc_auc_score
from sklearn.metrics import precision_recall_curve
from sklearn.metrics import accuracy_score as acc
```

In [26]:
```
 df1 = df.copy()
```

In [27]:
```
target = df1.pop('Class')
features = df1
```

In [28]:
```
X_train, X_test, y_train, y_test = train_test_split(features, target, test_si
```

In [29]:
```
model = LogisticRegression(solver='lbfgs',max_iter = 500)
model.fit(X_train, y_train)
test_score = model.score(X_test, y_test)
train_score = model.score(X_train, y_train)
```

In [30]:
```
test_score,train_score
```

Out[30]:
```
(0.96875, 1.0)
```

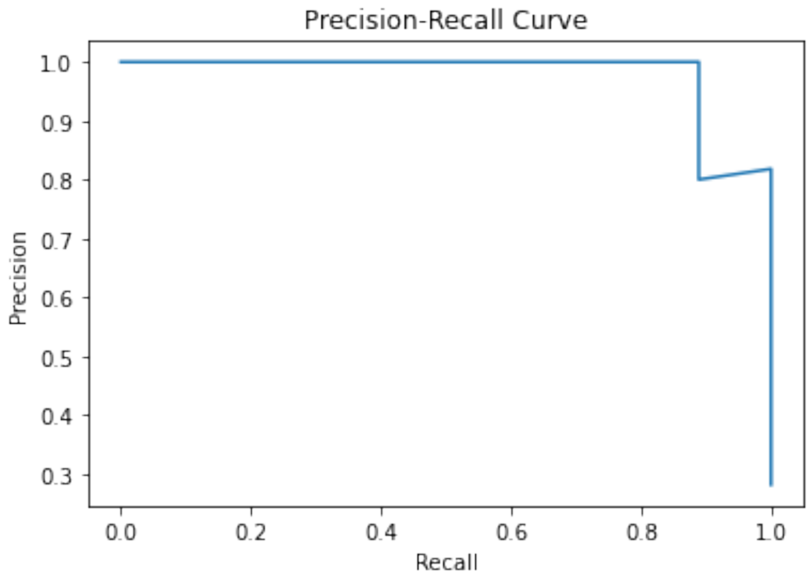
In [31]:
```
y_pred_test = model.predict(X_test)
y_pred_train = model.predict(X_train)
```

In [32]:
```
confusion_mat_test = confusion_matrix(y_test, y_pred_test)
confusion_mat_train = confusion_matrix(y_train, y_pred_train)

print(confusion_mat_test)
print(confusion_mat_train)
```

```
[[23  0]
 [ 1  8]]
[[92  0]
 [ 0 34]]
```

In [33]:
```
y_pr = model.predict_proba(X_test)[:,1]

auc = roc_auc_score(y_test, y_pr)

print(auc)

precision, recall, thresholds = precision_recall_curve(y_test, y_pr)
plt.plot(recall, precision)
plt.xlabel("Recall")
plt.ylabel("Precision")
plt.title("Precision-Recall Curve")
plt.show()
```

```
0.9903381642512078
```



4.5 Resampling Methods

In [34]:
```
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import chi2

x_new_test = []
x_new_train = []

for i in range(2,10):
    k = i
    selector = SelectKBest(chi2, k=k)
    X_new_train = selector.fit_transform(X_train, y_train)
    X_new_test = selector.fit_transform(X_test, y_test)
    x_new_test.append(X_new_test)
    x_new_train.append(X_new_train)
```

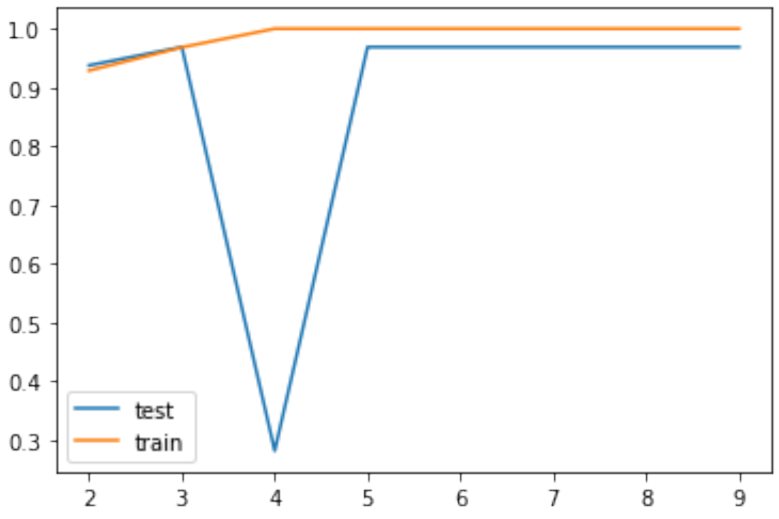
In [35]:
```
test_scores = []
train_scores = []
for i in range(8):

    model = LogisticRegression(solver='lbfgs',max_iter = 500)
    model.fit(x_new_train[i], y_train)
    test_score = model.score(x_new_test[i], y_test)
    train_score = model.score(x_new_train[i], y_train)
    test_scores.append(test_score)
    train_scores.append(train_score)
```

In [36]:
```
test_scores
```

Out[36]:
```
[0.9375, 0.96875, 0.28125, 0.96875, 0.96875, 0.96875, 0.96875, 0.96875]
```

In [37]:
```
x = [i for i in range(2,10)]
plt.plot(x,test_scores,label = 'test')
plt.plot(x,train_scores,label = 'train')
plt.legend()
```

Out[37]:
```
<matplotlib.legend.Legend at 0x7f83f9726940>
```



In [38]:
```
from mlxtend.feature_selection import SequentialFeatureSelector as sfs
```

In [39]:
```
clf = model = LogisticRegression(solver='lbfgs',max_iter = 500)
sfs1 = sfs(clf,
           k_features=5,
           forward=True,
           floating=False,
           verbose=2,
           scoring='accuracy',
           cv=5)

# Perform SFFS
sfs1 = sfs1.fit(X_train, y_train)
```

```
[Parallel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent worker
s.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  24 out of  24 | elapsed:    0.3s finished

[2022-12-16 23:56:06] Features: 1/5 -- score: 0.984[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  23 out of  23 | elapsed:    0.4s finished

[2022-12-16 23:56:06] Features: 2/5 -- score: 0.992[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  22 out of  22 | elapsed:    0.5s finished

[2022-12-16 23:56:07] Features: 3/5 -- score: 0.992[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  21 out of  21 | elapsed:    0.5s finished

[2022-12-16 23:56:07] Features: 4/5 -- score: 0.992[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  20 out of  20 | elapsed:    0.6s finished

[2022-12-16 23:56:08] Features: 5/5 -- score: 0.992
```

In [40]:
```
feat_cols = list(sfs1.k_feature_idx_)
feat_cols
```

Out[40]:
```
[0, 1, 2, 3, 15]
```

In [41]:
```
clf  = LogisticRegression(solver='lbfgs',max_iter = 500)
sfs1 = sfs(clf,
           k_features=5,
           forward=False,
           floating=False,
           verbose=2,
           scoring='accuracy',
           cv=5)

# Perform SFFS
sfs1 = sfs1.fit(X_train, y_train)
```

```
[Parallel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent worker
s.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  24 out of  24 | elapsed:    1.5s finished

[2022-12-16 23:56:09] Features: 23/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  23 out of  23 | elapsed:    1.5s finished

[2022-12-16 23:56:11] Features: 22/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  22 out of  22 | elapsed:    1.5s finished

[2022-12-16 23:56:12] Features: 21/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
[Parallel(n_jobs=1)]: Done  21 out of  21 | elapsed:    1.4s finished

[2022-12-16 23:56:14] Features: 20/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  20 out of  20 | elapsed:    1.3s finished
```

```
[2022-12-16 23:56:15] Features: 19/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  19 out of  19 | elapsed:    1.3s finished

[2022-12-16 23:56:16] Features: 18/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  18 out of  18 | elapsed:    1.2s finished

[2022-12-16 23:56:18] Features: 17/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  17 out of  17 | elapsed:    1.1s finished

[2022-12-16 23:56:19] Features: 16/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done  16 out of  16 | elapsed:    1.0s finished

[2022-12-16 23:56:20] Features: 15/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
[Parallel(n_jobs=1)]: Done  15 out of  15 | elapsed:    1.0s finished

[2022-12-16 23:56:21] Features: 14/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
```

```
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
[Parallel(n_jobs=1)]: Done  14 out of  14 | elapsed:    1.0s finished
```

```
[2022-12-16 23:56:22] Features: 13/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
[Parallel(n_jobs=1)]: Done  13 out of  13 | elapsed:    0.8s finished

[2022-12-16 23:56:22] Features: 12/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
```

```
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
[Parallel(n_jobs=1)]: Done  12 out of  12 | elapsed:    0.8s finished

[2022-12-16 23:56:23] Features: 11/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
```

```
  n_iter_i = _check_optimize_result(
[Parallel(n_jobs=1)]: Done  11 out of  11 | elapsed:    0.7s finished

[2022-12-16 23:56:24] Features: 10/5 -- score: 1.0[Parallel(n_jobs=1)]: Using
backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
[Parallel(n_jobs=1)]: Done  10 out of  10 | elapsed:    0.7s finished

[2022-12-16 23:56:25] Features: 9/5 -- score: 1.0[Parallel(n_jobs=1)]: Using b
ackend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
[Parallel(n_jobs=1)]: Done   9 out of   9 | elapsed:    0.6s finished

[2022-12-16 23:56:25] Features: 8/5 -- score: 1.0[Parallel(n_jobs=1)]: Using b
ackend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0
s
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
/opt/anaconda3/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:4
58: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
ion
  n_iter_i = _check_optimize_result(
[Parallel(n_jobs=1)]: Done   8 out of   8 | elapsed:    0.5s finished

[2022-12-16 23:56:26] Features: 7/5 -- score: 1.0[Parallel(n_jobs=1)]: Using b
ackend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.1s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done   7 out of   7 | elapsed:    0.3s finished

[2022-12-16 23:56:26] Features: 6/5 -- score: 1.0[Parallel(n_jobs=1)]: Using b
ackend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0
s
[Parallel(n_jobs=1)]: Done   6 out of   6 | elapsed:    0.2s finished

[2022-12-16 23:56:26] Features: 5/5 -- score: 1.0
```

In [42]:

```
feat_cols = list(sfs1.k_feature_idx_)
feat_cols
```

Out[42]:

```
[1, 9, 10, 12, 16]
```

In [43]:

```
X_train.iloc[:, feat_cols].head()
```

Out[43]:

	Blood Pressure	Blood Glucose Random	Blood Urea	Sodium	White Blood Cell Count
137	70.0	97.0	27.0	145.0	6400.0
55	80.0	118.0	18.0	135.0	7200.0
126	80.0	81.0	15.0	141.0	10500.0
84	60.0	137.0	17.0	150.0	7900.0
154	70.0	75.0	31.0	141.0	7800.0

In [44]:
```
clf  = LogisticRegression(solver='lbfgs',max_iter = 500)
clf.fit(X_train.iloc[:, feat_cols], y_train)

y_train_pred = clf.predict(X_train.iloc[:, feat_cols])
print('Training accuracy on selected features: %.3f' % acc(y_train, y_train_p

y_test_pred = clf.predict(X_test.iloc[:, feat_cols])
print('Testing accuracy on selected features: %.3f' % acc(y_test, y_test_pred
```

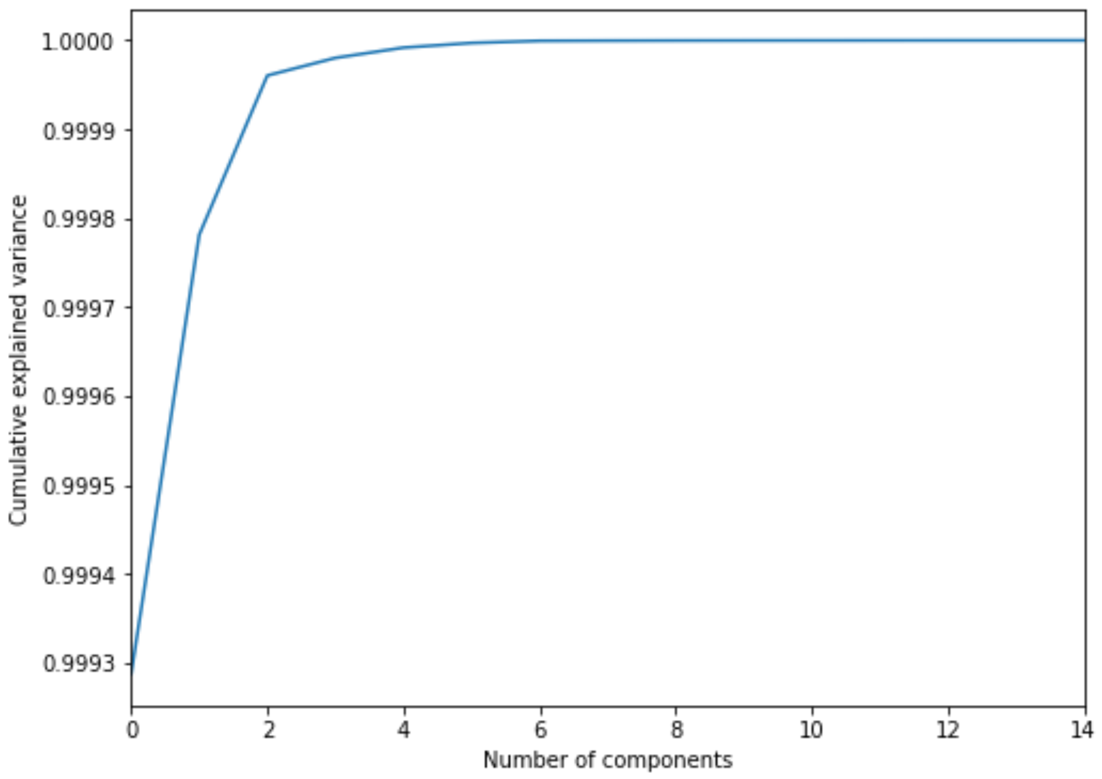
```
Training accuracy on selected features: 1.000
Testing accuracy on selected features: 0.969
```

4.6 PCA

In [45]:
```
X = df.drop(['Class'], axis=1)
y = df['Class']

X_train = pd.DataFrame(X_train, columns = X.columns)


pca= PCA()
pca.fit(X_train)
cumsum = np.cumsum(pca.explained_variance_ratio_)
dim = np.argmax(cumsum >= 0.99995) + 1
print('The number of dimensions required to preserve 99.99% of variance is',d
```

```
The number of dimensions required to preserve 99.99% of variance is 3
```

In [46]:
```
plt.figure(figsize=(8,6))
plt.plot(np.cumsum(pca.explained_variance_ratio_))
plt.xlim(0,14,1)
plt.xlabel('Number of components')
plt.ylabel('Cumulative explained variance')
plt.show()
```


Cumulative explained variance
1.0000
0.9999
0.9998
0.9997
0.9996
0.9995
0.9994
0.9993
0
2
4
6
8
10
12
14
Number of components

```
In [ ]:
```