

▼ KDDM Lab8

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```
# import libraries
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
# Importing Data file
data = pd.read_csv('bc2.csv')
dataset = pd.DataFrame(data)
dataset.columns
```

```
Index(['ID', 'ClumpThickness', 'Cell Size', 'Cell Shape', 'Marginal Adhesion',
       'Single Epithelial Cell Size', 'Bare Nuclei', 'Normal Nucleoli',
       'Bland Chromatin', 'Mitoses', 'Class'],
      dtype='object')
```

```
dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 699 entries, 0 to 698
Data columns (total 11 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   ID                                    699 non-null    int64
1   ClumpThickness                       699 non-null    int64
2   Cell Size                           699 non-null    int64
3   Cell Shape                          699 non-null    int64
4   Marginal Adhesion                   699 non-null    int64
5   Single Epithelial Cell Size         699 non-null    int64
6   Bare Nuclei                         699 non-null    object
7   Normal Nucleoli                     699 non-null    int64
8   Bland Chromatin                     699 non-null    int64
9   Mitoses                             699 non-null    int64
10  Class                               699 non-null    int64
dtypes: int64(10), object(1)
memory usage: 60.2+ KB
```

```
dataset.describe().transpose()
```

	count	mean	std	min	25%	50%	75%	max
ID	699.0	1.071704e+06	617095.729819	61634.0	870688.5	1171710.0	1239999.0	1239999.0
ClumpThickness	699.0	4.417740e+00	2.815741	1.0	2.0	4.0	4.0	10.0
Cell Size	699.0	3.134478e+00	3.051459	1.0	1.0	1.0	1.0	10.0
Cell Shape	699.0	3.207439e+00	2.971913	1.0	1.0	1.0	1.0	10.0
Marginal Adhesion	699.0	2.806867e+00	2.855379	1.0	1.0	1.0	1.0	10.0
Single Epithelial Cell Size	699.0	3.216023e+00	2.214300	1.0	2.0	2.0	2.0	10.0

```
dataset = dataset.replace('?', np.nan)
```

```
dataset = dataset.apply(lambda x: x.fillna(x.median()),axis=0)
```

```
# converting the hp column from object 'Bare Nuclei'/ string type to float
```

```
dataset['Bare Nuclei'] = dataset['Bare Nuclei'].astype('float64')
```

```
dataset.isnull().sum()
```

```
ID          0
ClumpThickness  0
Cell Size      0
Cell Shape     0
Marginal Adhesion  0
Single Epithelial Cell Size  0
Bare Nuclei    0
Normal Nucleoli  0
Bland Chromatin  0
Mitoses        0
Class          0
dtype: int64
```

```
from sklearn.model_selection import train_test_split
```

```
# To calculate the accuracy score of the model
```

```
from sklearn.metrics import accuracy_score, confusion_matrix
```

```
target = dataset["Class"]
```

```
features = dataset.drop(["ID","Class"], axis=1)
```

```
X_train, X_test, y_train, y_test = train_test_split(features,target, test_size = 0.2, random_state=0)
```

```
from sklearn.svm import SVC
```

```
# Building a Support Vector Machine on train data
```

```
svc_model = SVC(C= .1, kernel='linear', gamma= 1)
```

```
svc_model.fit(X_train, y_train)
```

```
prediction = svc_model .predict(X_test)
```

```
# check the accuracy on the training set
```

```
print(svc_model.score(X_train, y_train))
```

```
print(svc_model.score(X_test, y_test))
```

```
0.9749552772808586
```

```
0.9642857142857143
```

```
print("Confusion Matrix:\n",confusion_matrix(prediction,y_test))
```

```
Confusion Matrix:
```

```
[[95  2]
```

```
[ 3 40]]
```

```
# Building a Support Vector Machine on train data
```

```
svc_model = SVC(kernel='rbf')
```

```
svc_model.fit(X_train, y_train)
```

```
SVC()
```

```
print(svc_model.score(X_train, y_train))
```

```
print(svc_model.score(X_test, y_test))
```

```
0.9785330948121646
```

```
0.9642857142857143
```

```
#Building a Support Vector Machine on train data(changing the kernel)
```

```
svc_model = SVC(kernel='poly')
```

```
svc_model.fit(X_train, y_train)
```

```
prediction = svc_model.predict(X_test)
```

```
print(svc_model.score(X_train, y_train))
```

```
print(svc_model.score(X_test, y_test))
```

```
0.9785330948121646
```

```
0.9571428571428572
```

```
svc_model = SVC(kernel='sigmoid')
```

```
svc_model.fit(X_train, y_train)
```

```
prediction = svc_model.predict(X_test)
```

```
print(svc_model.score(X_train, y_train))
```

```
print(svc_model.score(X_test, y_test))
```

```
0.3953488372093023
```

```
0.44285714285714284
```

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