

```
In [1]: # importing libraries

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

matplotlib.inline
```

Performing EDA

```
In [5]: data=pd.read_csv("C:\\Users\\User\\Desktop\\lymphography.csv")

In [3]: data

Out[3]:
```

	3	4	2	1	1.1	1.2	1.3	1.4	2.1	1.5	2.2	2.3	2.4	4.1	8	1.6	1.7	2.5	2.6
0	2	3	2	1	1	2	2	1	2	1	3	3	2	3	4	2	2	2	2
1	1	3	3	2	2	2	2	2	2	1	4	3	3	4	8	3	2	2	7
2	3	3	1	1	1	1	2	1	2	1	1	3	3	4	4	4	3	1	2
3	2	3	1	1	1	1	1	1	1	1	2	2	4	3	5	1	2	2	1
4	2	2	1	1	1	1	1	1	2	1	3	3	3	6	3	1	2	4	
...
142	3	3	2	1	1	2	2	1	2	1	2	2	4	3	5	2	2	2	4
143	2	2	1	1	1	1	1	1	1	1	1	1	1	3	3	1	2	2	1
144	3	2	2	1	1	1	2	1	2	1	3	3	3	8	3	2	2	4	
145	2	2	1	1	1	1	1	1	2	2	4	2	2	1	2	2	2	1	
146	2	2	2	1	2	2	1	2	1	3	3	4	3	4	3	2	2	6	

147 rows × 19 columns

```
In [6]: # In above data set column names are not given,we are trying to add column names to dataset
data.columns=['class', 'lymphatics', 'block of affere', 'bl. of lymph. c', 'bl. of lymph. s', 'by pass',
'extravasates', 'regeneration of', 'early uptake in', 'lym.nodes dimin', 'lym.nodes enlar', 'changes in lym.', 'defect in node', 'changes in node', 'changes in stru', 'special forms', 'dislocation of', 'exclusion of no', 'no. of nodes in']

In [7]: data

Out[7]:
```

	class	lymphatics	block of affere	bl. of lymph. c	bl. of lymph. s	by pass	extravasates	regeneration of	early uptake in	lym.nodes dimin	lym.nodes enlar	changes in lym.	defect in node	changes in node	changes in stru	special forms	dislocation of	exclusion of no	no. of nodes in
0	2	3	2	1	1	2		2	1	2		3	3	2	3	4	2	2	2
1	3	3	2	2	2	2		2	2	2	1	4	3	3	4	8	3	2	7
2	3	3	1	1	1	1		2	1	2	1	3	3	4	4	4	3	1	2
3	2	3	3	1	1	1		1	1	1	2	2	2	4	3	5	1	2	2
4	2	2	1	1	1	1		1	1	2	1	3	3	3	6	3			
...
142	3	3	2	1	1	2		2	1	2	1	2	2	4	3	5	2	2	4
143	2	2	2	1	1	1		1	1	1	1	1	1	1	3	1	2	2	1
144	3	2	2	2	1	1		2	1	2	1	3	3	3	8	3	2	2	4
145	2	2	1	1	1	1		1	1	2	1	2	2	4	2	2	1	2	1
146	2	2	2	2	2	1		2	2	1	2	3	3	4	3	4	3	2	6

147 rows × 19 columns

```
In [8]: data.head()

Out[8]:
```

	class	lymphatics	block of affere	bl. of lymph. c	bl. of lymph. s	by pass	extravasates	regeneration of	early uptake in	lym.nodes dimin	lym.nodes enlar	changes in lym.	defect in node	changes in node	changes in stru	special forms	dislocation of	exclusion of no	no. of nodes in
0	2	3	2	1	1	2		2	1	2		3	3	2	3	4	2	2	2
1	3	3	2	2	2	2		2	2	2	1	4	3	3	4	8	3	2	7
2	3	3	1	1	1	1		2	1	2	1	3	3	4	4	4	3	1	2
3	2	3	3	1	1	1		1	1	1	2	2	2	4	3	5	1	2	2
4	2	2	1	1	1	1		1	1	2	1	3	3	3	6	3			

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

Out[10]:
```

	class	lymphatics	block of affere	bl. of lymph. c	bl. of lymph. s	by pass	extravasates	regeneration of	early uptake in	lym.nodes dimin	lym.nodes enlar	changes in lym.	defect in node	changes in node	changes in stru	special forms	dislocation of	exclusion of no	no. of nodes in
0	2	3	2	1	1	2		2	1	2		3	3	2	3	4	2	2	2
1	3	3	2	2	2	2		2	2	2	1	4	3	3	4	8	3	2	7
2	3	3	1	1	1	1		2	1	2	1	3	3	4	4	4	3	1	2
3	2	3	3	1	1	1		1	1	1	2	2	2	4	3	5	1	2	2
4	2	2	1	1	1	1		1	1	2	1	3	3	3	6	3	1	2	4

```
In [11]: data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 147 entries, 0 to 146
Data columns (total 19 columns):
#   Column                Non-Null Count  Dtype
---  ---
0   class                 147 non-null    int64
1   lymphatics            147 non-null    int64
2   block of affere       147 non-null    int64
3   bl. of lymph. c       147 non-null    int64
4   bl. of lymph. s       147 non-null    int64
5   by pass               147 non-null    int64
6   extravasates         147 non-null    int64
7   regeneration of       147 non-null    int64
8   early uptake in      147 non-null    int64
9   lym.nodes dimin       147 non-null    int64
10  lym.nodes enlar       147 non-null    int64
11  changes in lym.       147 non-null    int64
12  defect in node        147 non-null    int64
13  changes in node       147 non-null    int64
14  changes in stru       147 non-null    int64
15  special forms         147 non-null    int64
16  dislocation of        147 non-null    int64
17  exclusion of no       147 non-null    int64
18  no. of nodes in      147 non-null    int64
dtypes: int64(19)
memory usage: 21.9 KB

In [12]: data.describe()

Out[12]:
```

	class	lymphatics	block of affere	bl. of lymph. c	bl. of lymph. s	by pass	extravasates	regeneration of	early uptake in	lym.nodes dimin	lym.nodes enlar	changes in lym.	defect in node	changes in node	changes in stru	special forms	dislocation of	exclusion of no	no. of nodes in
count	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000	147.000000
mean	2.448980	2.734694	1.551020	1.176871	1.047619	1.244898		1.510204	1.068027	1.700680	1.061224	2.476190	2.401361	2.972789	2.795918	5.197279	2.795918	2.16493	2.34
std	0.575572	0.813638	0.499091	0.382864	0.213687	0.431497		0.501605	0.252653	0.495626	0.314588	0.839568	0.569305	0.867571	0.757960	2.16493	0.757960	0.757960	0.77
min	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000		1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.00
25%	2.000000	2.000000	1.000000	1.000000	1.000000	1.000000		1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	2.000000	2.000000	2.000000	2.000000	4.000000	2.00
50%	2.000000	3.000000	2.000000	1.000000	1.000000	1.000000		1.000000	2.000000	1.000000	2.000000	1.000000	2.000000	2.000000	3.000000	3.000000	3.000000	5.000000	3.00
75%	3.000000	3.000000	2.000000	1.000000	1.000000	1.000000		2.000000	1.000000	2.000000	1.000000	2.000000	1.000000	3.000000	4.000000	4.000000	3.000000	8.000000	3.00
max	4.000000	4.000000	2.000000	2.000000	2.000000	2.000000		2.000000	2.000000	2.000000	3.000000	4.000000	3.000000	4.000000	4.000000	4.000000	4.000000	8.000000	3.00

```
In [14]: data['class'].value_counts()

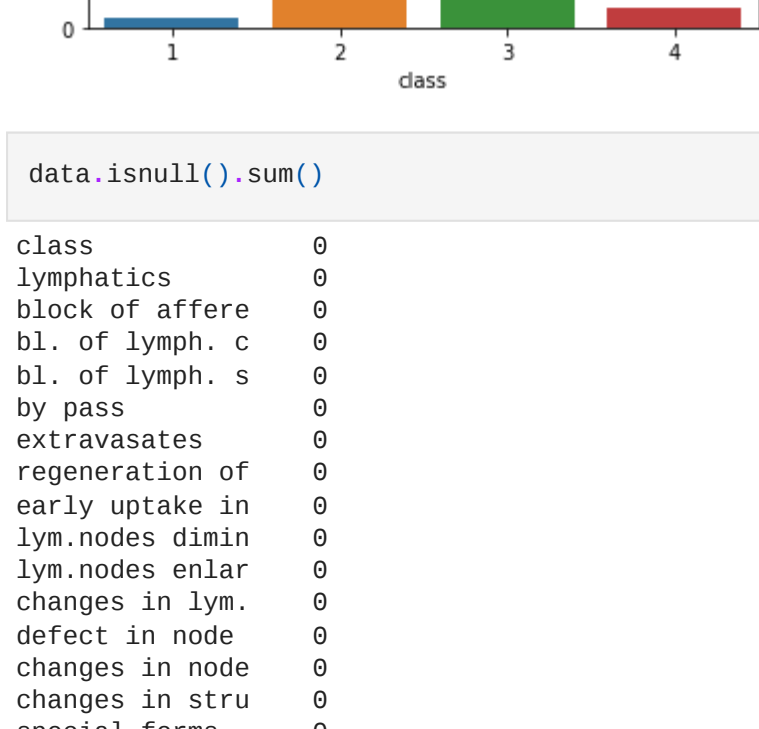
Out[14]:
```

class	count
1	81
2	60
3	4
4	2

Name: class, dtype: int64

```
In [25]: def count_plot(col):
sns.countplot(x=data[col])
plt.title(col+" "+count")
plt.show()

count_plot("class")
```



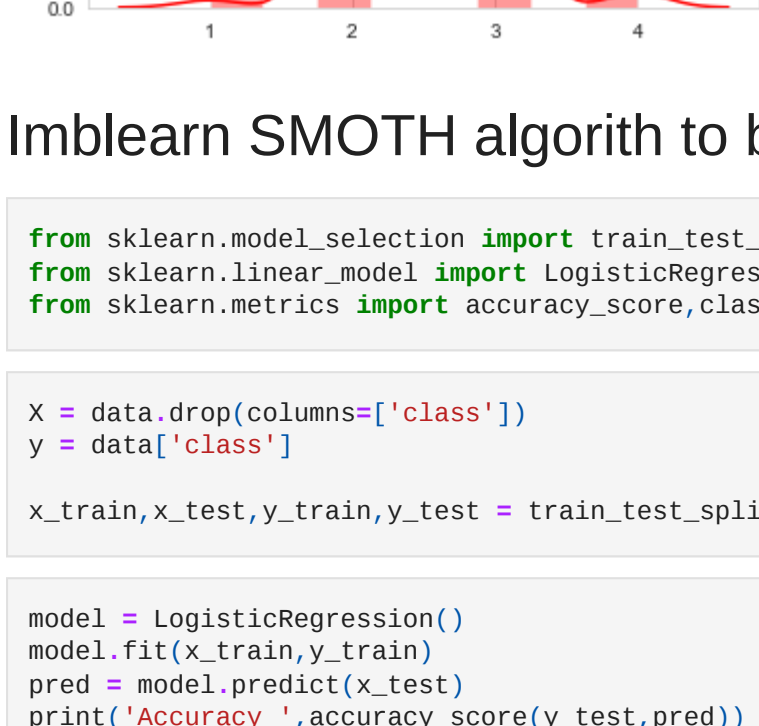
```
In [19]: data.isnull().sum()

Out[19]:
```

class	0
lymphatics	0
block of affere	0
bl. of lymph. c	0
bl. of lymph. s	0
by pass	0
extravasates	0
regeneration of	0
early uptake in	0
lym.nodes dimin	0
lym.nodes enlar	0
changes in lym.	0
defect in node	0
changes in node	0
changes in stru	0
special forms	0
dislocation of	0
exclusion of no	0
no. of nodes in	0
dtype:	int64

```
In [31]: sns.set_style('whitegrid')
sns.distplot(x=data['class'],kde=True,color='red')
plt.show()

C:\Users\User\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: 'distplot' is a deprecated function and will be removed in a future version. Please adapt your code to use either 'displot' (a Figure-level function with similar flexibility) or 'histplot' (an axes-level function for histogram s).
warnings.warn(msg, FutureWarning)
```



Imblearn SMOTH algorithm to balance the classes

```
In [32]: from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score,classification_report,confusion_matrix
```

```
In [34]: X = data.drop(columns=['class'])
y = data['class']

X_train,X_test,y_train,y_test = train_test_split(X,y,random_state=100,test_size=0.3,stratify=y)
```

```
In [35]: model = LogisticRegression()
model.fit(X_train,y_train)
pred = model.predict(X_test)
print('Accuracy ',accuracy_score(y_test,pred))
print(classification_report(y_test,pred))
sns.heatmap(confusion_matrix(y_test,pred),annot=True,fmt='.2g')
```

```
Accuracy 0.9111111111111111
precision recall f1-score support
1 1.00 1.00 1.00 1
2 0.92 0.92 0.92 25
3 0.89 0.89 0.89 18
4 1.00 1.00 1.00 1
accuracy 0.91 45
macro avg 0.95 0.95 0.95 45
weighted avg 0.91 0.91 0.91 45
```

```
C:\Users\User\anaconda3\lib\site-packages\sklearn\linear_model\_logistic.py:763: 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-regression
n_iter_ = 1
_check_optimize_result()
AxesSubplot: =
```

```
Out[35]:
```



```
In [46]: np.bincount(y_train)

Out[46]: array([ 0, 1, 56, 42, 3], dtype=int64)
```

```
In [49]: !pip install imblearn

Collecting imblearn
  Downloading imblearn-0.0-py2.py3-none-any.whl (1.9 kB)
Collecting imbalanced-learn
  Downloading imbalanced-learn-0.9.1-py3-none-any.whl (199 kB)
Requirement already satisfied: threadpoolctl>=2.0.0 in c:\users\User\anaconda3\lib\site-packages (from imbalanced-learn->imblearn) (2.2.0)
Collecting scikit-learn>=1.1.0
  Downloading scikit-learn-1.1.1-cp39-cp39-win_amd64.whl (7.4 MB)
Requirement already satisfied: joblib>=1.0.0 in c:\users\User\anaconda3\lib\site-packages (from imbalanced-learn->imblearn) (1.2.0.3)
Requirement already satisfied: scipy>=1.3.2 in c:\users\User\anaconda3\lib\site-packages (from imbalanced-learn->imblearn) (1.1.0)
Installing collected packages: scikit-learn, imbalanced-learn, imblearn
Attempting uninstall: scikit-learn
  Found existing installation: scikit-learn 0.24.2
  Successfully uninstalled scikit-learn-0.24.2
ERROR: Could not install packages due to an OSError: [WinError 5] Access is denied: 'C:\Users\User\anaconda3\lib\site-packages\sklearn\linear_model\c_fast_csp39-win_amd64.pyd'
Consider using the '--user' option or check the permissions.
```

```
In [50]: from tensorflow.keras.layers import Dense ##W
from tensorflow.keras.models import Sequential
from tensorflow.keras.utils import to_categorical
```

```
In [52]: features = data.drop(columns=['class'])
target = data['class']
from sklearn.model_selection import train_test_split

X_train,X_test,y_train,y_test = train_test_split(features,target)
X_train,X_val,y_train,X_val = train_test_split(X_train,y_train)
```

```
In [53]: model = Sequential()

model.add(Dense(100, input_shape=(features.shape[1],)))
model.add(Dense(30, activation='relu'))
# model.add(Dense(45, activation='relu'))
# model.add(Dense(32, activation='relu'))
# model.add(Dense(23, activation='relu'))
model.add(Dense(3, activation='softmax'))
```

```
In [54]: model.summary()

Model: "sequential"

Layer (type) Output Shape Param #
=====
dense (Dense) (None, 100) 1900
dense_1 (Dense) (None, 30) 3080
dense_2 (Dense) (None, 3) 93
=====
Total params: 5,023
Trainable params: 5,023
Non-trainable params: 0
```

```
In [55]: import tensorflow

model.compile(optimizer='sgd',
loss=tensorflow.keras.losses.CategoricalCrossentropy(),
metrics=['accuracy'])
```

```
In [56]: X_train.shape

Out[56]: (82, 18)
```

```
In [57]: y_train.shape

Out[57]: (82,)
```

```
In [58]: y_pred = model.predict(X_test)

2/2 [=====] - 3s 38ms/step
```

```
In [59]: y_pred

Out[59]: array([[0.2842906, 0.39191616, 0.3279392 ],
[0.9058309, 0.53342235, 0.3907468 ],
[0.14020651, 0.6940643, 0.1657952 ],
[0.13786979, 0.35841462, 0.5037156 ],
[0.31172487, 0.52495, 0.16332507],
[0.33757296, 0.58763136, 0.1547957 ],
[0.2311017, 0.4343732, 0.3275166 ],
[0.21250094, 0.5462308, 0.24120823],
[0.09637376, 0.5041701, 0.39945014],
[0.1452966, 0.5433517, 0.2113517 ],
[0.2030861, 0.48162958, 0.31528425],
[0.04732128, 0.6502925, 0.3023802 ],
[0.12813976, 0.72519976, 0.14675044],
[0.21660917, 0.3919136, 0.2914772 ],
[0.15910102, 0.37537763, 0.49552134],
[0.25856593, 0.4954762, 0.24595793],
[0.24793877, 0.60022056, 0.15173265],
[0.17327465, 0.46261495, 0.3641194 ],
[0.1420327, 0.43413, 0.42383733],
[0.11997617, 0.556118, 0.32391182],
[0.1613808, 0.3311738, 0.50744545],
[0.1121099, 0.45640546, 0.43142453],
[0.15353942, 0.35260624, 0.49376434],
[0.06045634, 0.5630878, 0.37593585],
[0.13262907, 0.65843407, 0.20939611],
[0.10264533, 0.74369925, 0.1536554 ],
[0.14297211, 0.5973466, 0.25968134],
[0.17489491, 0.5985232, 0.22658183],
[0.31535045, 0.33349165, 0.35097793],
[0.10302313, 0.58925277, 0.3077241 ],
[0.14801906, 0.52372354, 0.32825732],
[0.19771169, 0.5736271, 0.22866118],
[0.14669308, 0.5348587, 0.21944022],
[0.15222462, 0.5957431, 0.25203216],
[0.10941499, 0.45927483, 0.43131012],
[0.2210852, 0.5139864, 0.26590842],
[0.08093782, 0.7728947, 0.14706749]], dtype=float32)
```

Tune the Model using GridSearchCv

```
In [63]: !pip install pipeline

Collecting pipeline
  Downloading pipeline-0.1.0-py3-none-any.whl (2.6 kB)
Installing collected packages: pipeline
Successfully installed pipeline-0.1.0
```

```
In [70]: from sklearn.model_selection import GridSearchCV
```

```
In [72]: parameters={'learning_rate':[0.1,0.15,0.20,0.25,0.3],
'gamma':[0,0.1,0.2,0.3,0.4]}
```

```
In [1]: #gridsearch=GridSearchCV(model, param_grid=parameters, scoring='neg_log_loss',cv=10, n_jobs=-1)
#gridsearch.fit(X_train,y_train)
```

Plot the Accuracy and Loss graph

```
In [69]: X = data.drop(columns=['class'])
y = data['class']
model.compile(optimizer='adam',
loss='mse',
metrics=['accuracy'])
```