

BVRIT HYDERABAD College of Engineering for Women

Department of Information Technology

BREAST CANCER PROGNOSIS USING MACHINE LEARNING

Under the guidance of

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Agenda

- Summary of Stage 1
- Implementation of Experimental Design
- Execution video
- Analysis of Results, Discussion
- Conclusion & Future scope



Summary of Stage 1

On the Wisconsin Breast Cancer Diagnostic dataset (WBCD) we applied five main algorithms which are: SVC, Random Forests, Logistic Regression, Decision Tree, K -NN, to calculate, compare and evaluate different results obtained based on confusion matrix, accuracy, sensitivity, precision, AUC to identify the best machine learning algorithm that are precise, reliable and find the higher accuracy. All algorithms have been programmed in Python using scikit-learn library in Jupyter notebook environment. After an accurate comparison between our models, we found that Support Vector Classifier achieved a higher Accuracy of 96.49%, efficiency of 97.2%, Precision of 97.5%, AUC of 96.6% and outperforms all other algorithms.

Implementation of Experimental Design

```
In [2]: import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import plotly.express as px
import plotly.graph_objects as go
%matplotlib inline
```

```
In [3]: dataset = pd.read_csv('data.csv')
```

```
In [4]: X = dataset.iloc[:, 1:31].values
Y = dataset.iloc[:, 31].values
```

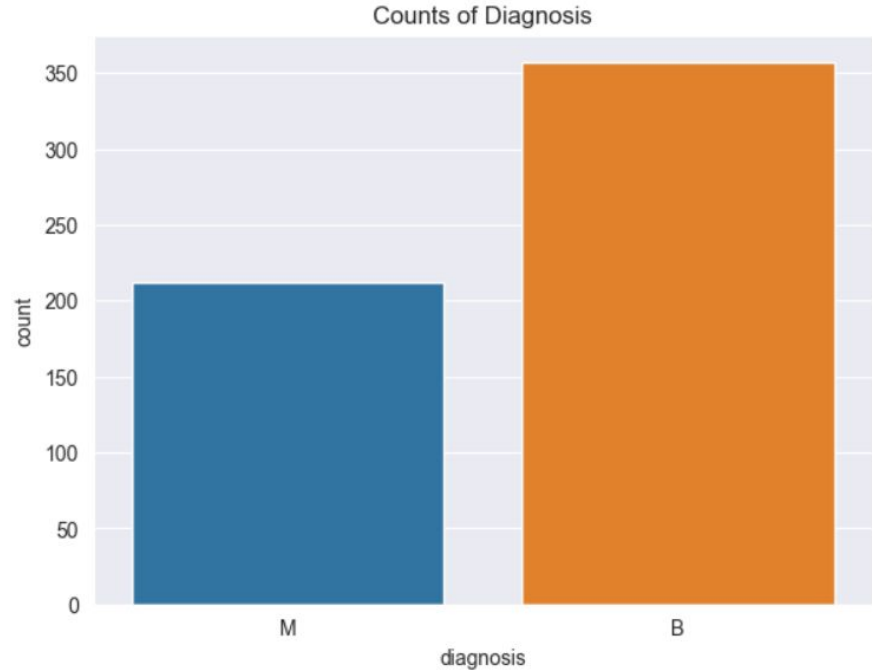
```
In [5]: dataset.head()
```

Out[5]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...	t
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	...	
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	...	
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	...	
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	...	

Implementation of Experimental Design

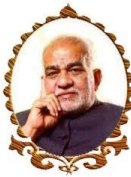
```
In [10]: sns.set_style('darkgrid')  
plt.figure(figsize=(15, 5))  
plt.xlabel("Diagnosis")  
plt.subplot(1, 2, 2)  
plt.title("Counts of Diagnosis")  
sns.countplot(x='diagnosis', data=dataset)
```





Implementation of Experimental Design

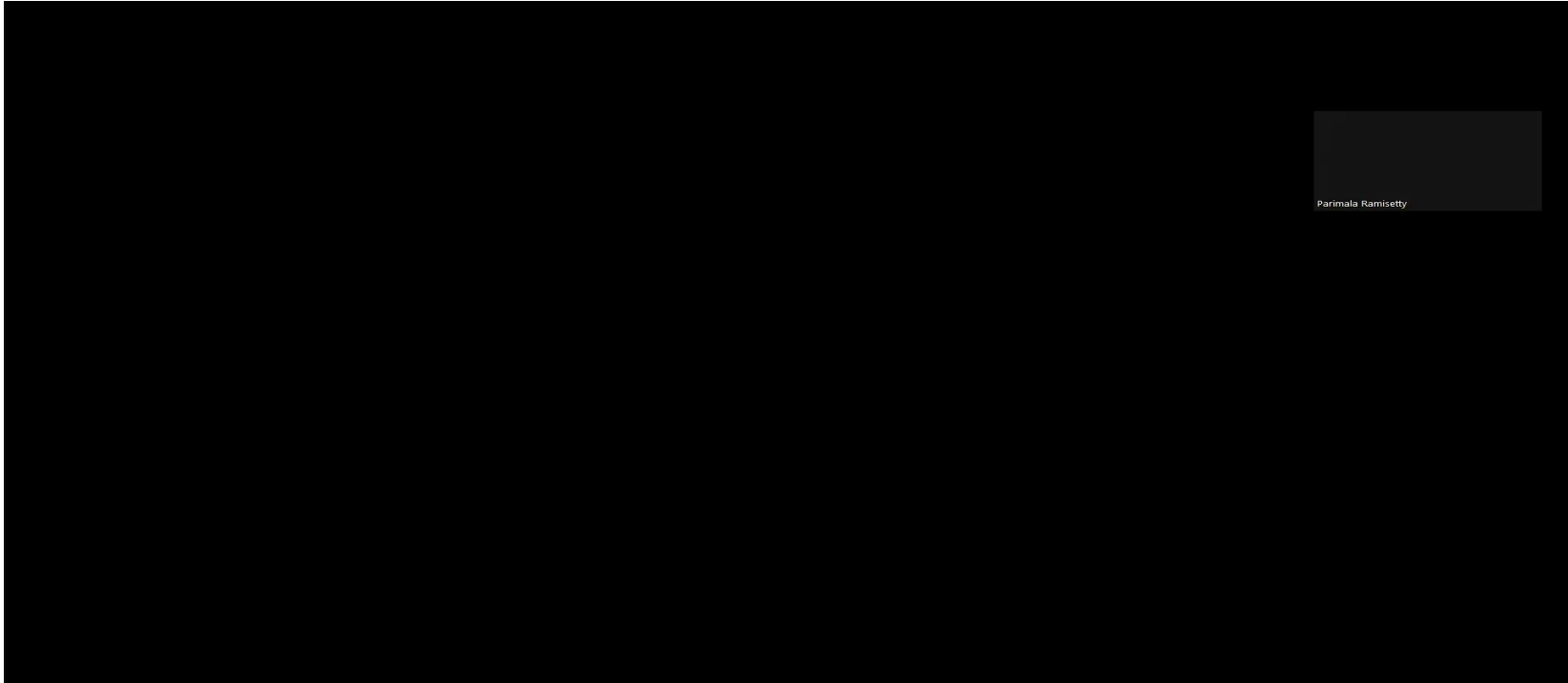
```
models_list = {  
    "LogisticRegression" : LogisticRegression(random_state=0),  
    "K-NearestNeighbor" : KNeighborsClassifier(n_neighbors = 5, metric = 'minkowski', p = 2),  
    "SVC" : SVC(kernel = 'rbf', random_state = 2,C = 2),  
    "SVM" : SVC(kernel = 'linear', random_state = 0),  
    "NaiveBayes" : GaussianNB(),  
    "DecisionTreeClassifier" : DecisionTreeClassifier(criterion='entropy', random_state=0),  
    "RandomForestClassifier" : RandomForestClassifier(n_estimators=10, criterion='entropy', random_state=0),  
}
```



Implementation of Experimental Design

```
: #train test splitting
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score, confusion_matrix, f1_score
from sklearn.metrics import classification_report
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_validate, cross_val_score
from sklearn.svm import SVC
from sklearn import metrics
```

Execution video



Analysis of Results

The accuracies of different algorithms are as follows:

	model_name	score	accuracy_score	accuracy_percentage
5	DecisionTreeClassifier	1.000000	0.883041	88.30%
6	RandomForestClassifier	0.994975	0.918129	91.81%
2	SVC	0.962312	0.964912	96.49%
1	K-NearestNeighbor	0.937186	0.964912	96.49%
0	LogisticRegression	0.934673	0.959064	95.91%
3	SVM	0.932161	0.959064	95.91%
4	NaiveBayes	0.912060	0.929825	92.98%



Analysis of Results

On comparing the accuracies of different algorithms, we observe that SVC (Support Vector Classifier) and KNN (k-nearest neighbors) shows best accuracy percentage, but we choose SVC because KNN is easier to interpret but can identify only a limited set of patterns.



Analysis of Results

```
import random
a = random.random()
meanR=round(random.uniform(0,30),3)
meanT=round(random.uniform(0,50),3)
meanS=round(random.uniform(0,1),5)
meanC=round(random.uniform(0,1),5)
meanSy=round(random.uniform(0,1),4)
meanF=round(random.uniform(0,1),5)
seR=round(random.uniform(0,2),4)
seT=round(random.uniform(0,3),4)
seS=round(random.uniform(0,1),6)
seC=round(random.uniform(0,1),6)
seSy=round(random.uniform(0,1),6)
seF=round(random.uniform(0,1),6)
input_1=[]
lst = map(lambda x : x[1], filter(lambda x : x[0].startswith('mean'), globals().items()))
for i in lst:
    input_1.append(i)
lst1 = map(lambda x : x[1], filter(lambda x : x[0].startswith('se'), globals().items()))
for i in lst1:
    input_1.append(i)
input_array = np.asarray(input_1)
input_resaped = input_array.reshape(1,-1)
predict = model.predict(input_resaped)
if (predict[0] < 0.5):
    print("breast cancer is malignant")
else:
    print("breast cancer is benign")
```

breast cancer is benign

The result of the data given is that the cancer is benign .

Analysis of Results, Discussion

```
a = random.random()
meanR=round(random.uniform(0,30),3)
meanT=round(random.uniform(0,50),3)
meanS=round(random.uniform(0,1),5)
meanC=round(random.uniform(0,1),5)
meanSy=round(random.uniform(0,1),4)
meanF=round(random.uniform(0,1),5)
seR=round(random.uniform(0,2),4)
seT=round(random.uniform(0,3),4)
seS=round(random.uniform(0,1),6)
seC=round(random.uniform(0,1),6)
seSy=round(random.uniform(0,1),6)
seF=round(random.uniform(0,1),6)
input_2=[]
lst = map(lambda x : x[1], filter(lambda x : x[0].startswith('mean'), globals().items()))
for i in lst:
    input_2.append(i)
lst1 = map(lambda x : x[1], filter(lambda x : x[0].startswith('se'), globals().items()))
for i in lst1:
    input_2.append(i)
input_array = np.asarray(input_2)
input_resaped = input_array.reshape(1,-1)
predict = model.predict(input_resaped)
if (predict[0] == 1):
    print("breast cancer is malignant and more chances to occur")
else:
    print("breast cancer is benign and more chances to occur")
```

breast cancer is malignant and more chances to occur

Prediction of
Recurrence module

The recurrence is
predicted on dataset
based on diagnosis and
tumour size.

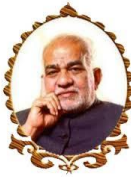


Conclusion

- We have explored different prediction models and various evaluation methods.
- We measuring the performance of the models using real data.
- 5 popular classification algorithms have been used and after comparing these algorithms with different performance metrics we concluded that SVC is the best machine learning algorithm to predict breast cancer.

Future Scope

We discovered that SVC and KNN provide the most accurate results for predicting breast cancer. The accuracy of this work can be improved in the future by altering the currently used machine learning approaches or by creating new algorithms. The future of breast cancer prediction is machine learning, and machine learning models are improving daily thanks to the tremendous research being done in this area by researchers. Artificial intelligence and machine learning will revolutionise the medical sector in the next decades. The prediction of breast cancer will perform better than conventional pathology testing with the addition of cutting-edge technology like convolutional neural networks.



References

- [1] Usman Naseem, Junaid Rashid, "An Automatic Detection of Breast Cancer Diagnosis and Prognosis Based on Machine Learning Using Ensemble of Classifiers" 12 May 2022
- [2] Sharma, A. & Mishra, P. K. Performance analysis of machine learning based optimized feature selection approaches for breast cancer diagnosis. *Int. J. Inf. Technol.* 14, 1949–1960. (2022).
- [3] Ahmad, S. *et al.* A novel hybrid deep learning model for metastatic cancer detection. *Comput. Intell. Neurosci* (2022).
- [4] L Yang, B Fu, Y Li, Y Liu, W Huang, S Feng et al., "Prediction model of the response to neoadjuvant chemotherapy in cancers by a Naive Bayes algorithm", *Computer methods and programs in biomedicine*, vol. 192, pp. 105458, 2020.

THANK YOU