EARLY STAGE DETECTION OF OVARIAN CANCER

Submitted for

Statistical Machine Learning CSET211

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Submitted to

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INDEX

1. Abstract:-

Ovarian cancer (OC), the *seventh* most prevalent cancer among women, poses a serious health threat due to its high mortality rate, driven by late-stage diagnosis and the lack of early symptoms. This study aims to address these challenges by advancing diagnostic precision through the integration of clinical data and biomarkers within a machine learning framework.

The significance of this work lies in its potential to revolutionize OC diagnostics, providing a scalable, non-invasive, and reliable tool for early detection. By addressing the limitations of current diagnostic strategies, this research offers a pathway to reduce mortality rates and improve patient outcomes, underscoring the critical role of biomarker-driven machine learning in modern oncology.

2. Introduction:-

Our goal is to provide comprehensive research of malignant epithelial ovarian tumours by integrating clinical data and biomarkers.

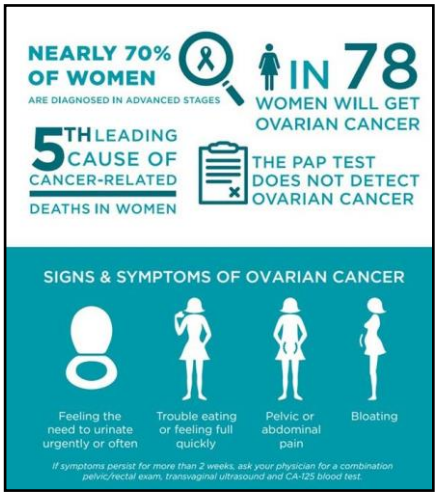
Crucial Biomarkers (RF Model)

-> CA125

-> HE4

-> NEU

These biomarkers represent the cutting edge of our research, each providing a distinct window into the complex molecular and clinical features of ovarian cancers. In addition to the well-known ovarian cancer marker CA125, HE4 and NEU complete a trio of biomarkers that together have the potential to improve the sensitivity and specificity of our diagnostic models.



3. Related Work:-

1. PAPER 1- Debaditya Chakroborty et.al

http://biorxiv.org/lookup/doi/10.1101/2023.07.24.550346

2. PAPER 2- Kristofer Linton-Reid et.al

https://www.medrxiv.org/content/10.1101/2023.04.26.23289155v1

3. PAPER 3- Haoxin Zhang et.al

https://www.sciencedirect.com/science/article/abs/pii/S0010482522011404?via=ihub

4. PAPER 4- Mingyang Lu et.al

https://linkinghub.elsevier.com/retrieve/pii/S1386505620302781

5. PAPER 5- Zhong Yu et.al

https://journals.lww.com/md-journal/Fulltext/2022/09090/Identification_of_prognosis_related_hub_genes_of.59.aspx?context=LatestArticles

4. Methodology:-

We have taken 3 different datasets of 350 women and integrated it into one such that it has a wide variety of attributes to analyse the data and make appropriate predictions. The attributes of datasets are as follows:

```
Dataset 1: OC_Markers.csv
Age: Age of the individual.
Menopause: Menopausal status (1: Yes, 0: No).
CA19-9: Carbohydrate antigen 19-9 biomarker.
CA72-4: Carbohydrate antigen 72-4 biomarker.
AFP: Alpha-fetoprotein biomarker.
CA125: Carbohydrate antigen 125 biomarker.
HE4: Human epididymis protein 4 biomarker.
CEA: Carcinoembryonic antigen biomarker.
TYPE: Target variable indicating the type of ovarian tumor (Binary classification).
```

```
Dataset 2: OC_General_Chem.csv
Age: Age of the individual.
AG: Alpha-1 globulin.
ALB: Albumin.
ALP: Alkaline phosphatase.
ALT: Alanine transaminase.
AST: Aspartate transaminase.
BUN: Blood urea nitrogen.
Ca: Calcium.
CL: Chloride.
CO2CP: Carbon dioxide content.
CREA: Creatinine.
DBIL: Direct bilirubin.
GGT: Gamma-glutamyl transferase.
GLO: Globulin.
GLU: Glucose.
IBIL: Indirect bilirubin.
K: Potassium.
Mg: Magnesium.
Na: Sodium.
PHOS: Phosphate.
TBIL: Total bilirubin.
TP: Total protein.
UA: Uric acid.
TYPE: Target variable indicating the type of ovarian tumor (Binary classification).
```

```
Dataset 3: OC_Blood_Routine.csv
Age: Age of the individual.
MPV: Mean platelet volume.
BASO#: Basophils count.
BASO%: Basophils percentage.
EO#: Eosinophils count.
EO%: Eosinophils percentage.
MCH: Mean corpuscular hemoglobin.
RDW: Red cell distribution width.
PDW: Platelet distribution width.
HGB: Hemoglobin.
LYM#: Lymphocytes count.
LYM%: Lymphocytes percentage.
MONO#: Monocytes count.
MONO%: Monocytes percentage.
PLT: Platelet count.
NEU: Neutrophils count.
RBC: Red blood cell count.
PCT: Plateletcrit.
HCT: Hematocrit.
MCV: Mean corpuscular volume.
TYPE: Target variable indicating the type of ovarian tumor (Binary classification).
```

DATA PRE-PROCESSING:

Data preparation is a crucial first step in preparing raw datasets for analysis and model construction. It employs multiple techniques to correct missing values, enhance the quality of the data, and ensure that machine learning algorithms can use it. The following are some essential steps in data preprocessing:

- Data Integration
- Handling Missing Data
- Dealing with Duplicates
- Handling Outliers
- Data Scaling

```
[ ]  combined_data = pd.concat([data1.set_index(['Age']),
                                oc_blood_routine.set_index(['Age']),
                                oc_general_chem.set_index(['Age'])],
                               axis=1).reset_index()

     # Print the resulting combined dataset
     print(combined_data)
```

1. This is how we have integrated 3 datasets, namely OC_Marker, OC_General_Chem and OC_Blood_Routine into 1 combined dataset and used this for the data analysis.
2. There are no NULL values in our final dataset.
3. Size of the combined_dataset:

```
[349 rows x 51 columns]
```

MODEL DEVELOPMENT:

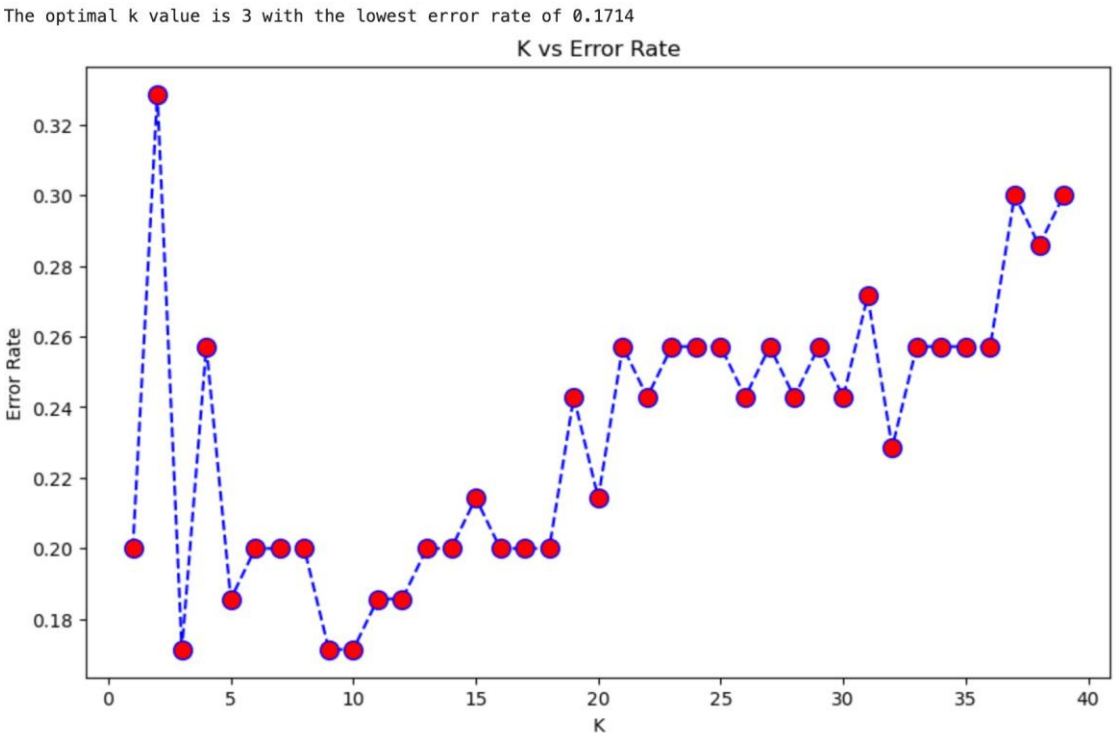
1) K-NEAREST NEIGHBORS(KNN) Classifier :

Implementation Steps

1. The implementation process began with training a basic KNN model using *n_neighbors=5* and using a test-train split (*test_size=0.2*).

2. To optimise the model, an analysis was conducted by iterating through k values from 1 to 40, with a plot of error rate versus k used to identify the optimal choice.

3. Following this, hyper-parameter tuning was performed using RandomizedSearchCV, exploring n_neighbors from 1 to 10 to further refine the model and select the best k value for improved performance.



2) RANDOM- FOREST:

- **Best RF Model-**

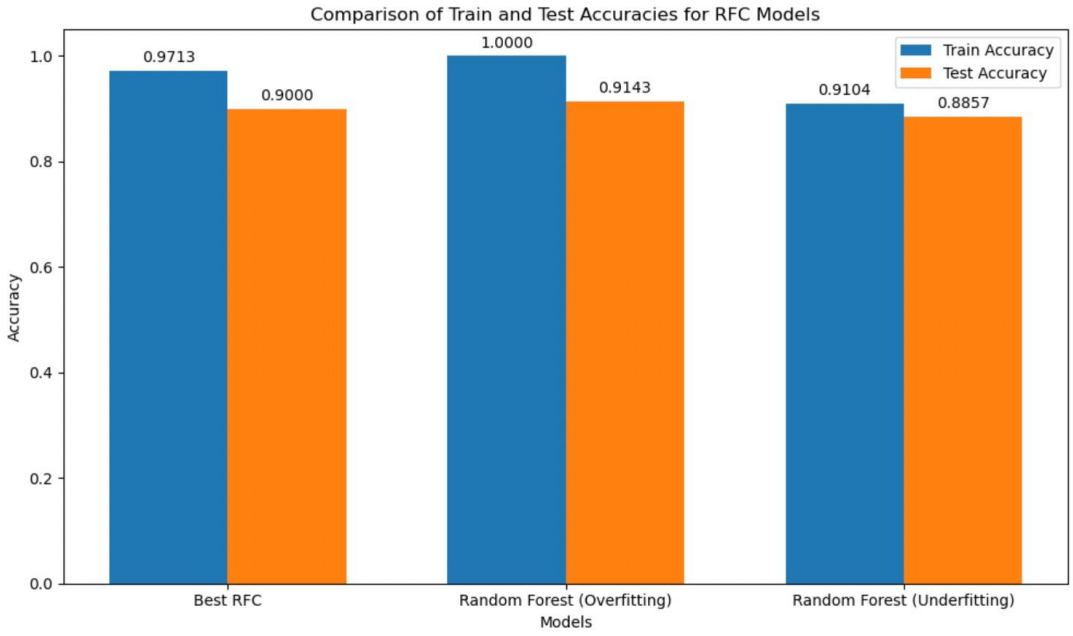
1. Initial Setup: A basic Random Forest Classifier was trained with default hyper-parameters and a train-test split of 80/20.
2. *Hyper-parameter Tuning*: GridSearchCV was used to optimize key hyper-parameters, such as n_estimators, max_depth, max_features, and criterion, through 5-fold cross-validation.
3. Model Evaluation: The best model was trained and evaluated on the test set using metrics like accuracy, precision, recall, F1 score, AUC, and log loss.

- **Overfitting-** The model showed a significant gap between training and testing accuracy, particularly when the training accuracy was much higher than the test accuracy.

```
Random Forest (Overfitting):
Train Accuracy: 1.0000
Test Accuracy: 0.9143
[[135   0]
 [  0 144]]
[[31  5]
 [ 1 33]]
```

- **Under-fitting-** In contrast, under-fitting was observed when the model's performance was poor both on the training and test data, indicating that the model was too simple to capture the underlying patterns of the data.

```
Random Forest (Underfitting):
Train Accuracy: 0.9104
Test Accuracy: 0.8857
[[115  20]
 [  5 139]]
[[29  7]
 [ 1 33]]
```



3) DECISION-TREE:

1. Initial Setup: A basic Decision Tree Classifier was trained with default hyper-parameters and a train-test split of 80/20.

2. *Hyper-parameter Tuning*: RandomizedSearchCV was used to explore a range of hyper-parameters, including criterion (gini /entropy), max_depth (with limits to prevent overfitting), min_samples_split (to control model complexity), min_samples_leaf (to avoid overfitting by reducing leaf nodes), class_weight (for imbalanced data), and max_features (to limit the number of features considered for each split). This approach employed 3-fold cross-validation to identify the optimal set of hyper-parameters.

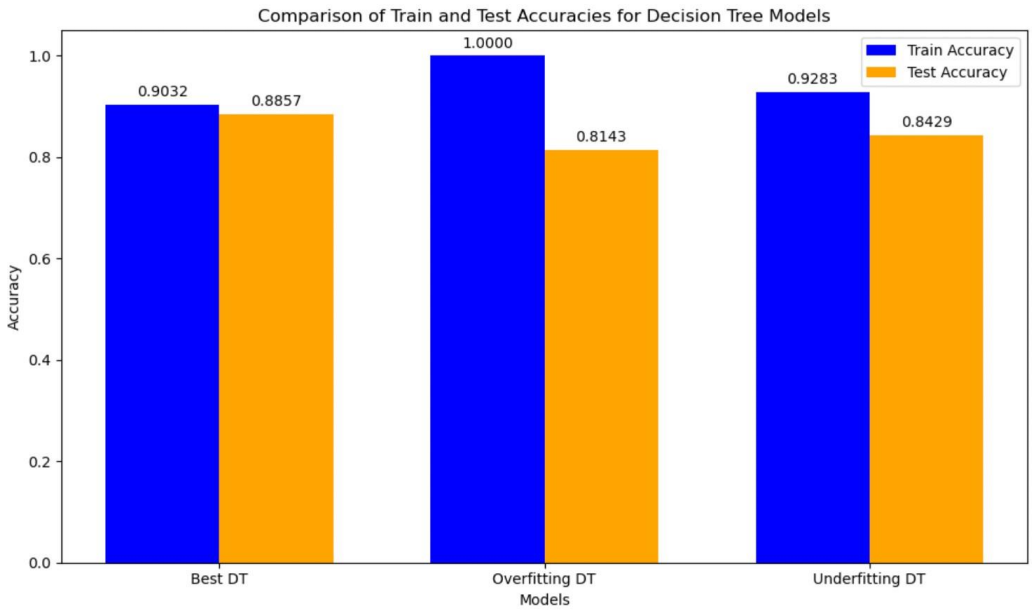
3. Model Evaluation: The best Decision Tree model was trained and evaluated on the test set using key performance metrics such as accuracy, precision, recall, F1 score, AUC, and log loss.

- **Overfitting**: The model showed a significant gap between training and testing accuracy, particularly when the training accuracy was much higher than the test accuracy.

```
Overfitting Decision Tree Model:
Train Accuracy: 1.0000
Test Accuracy: 0.7714
Training confusion matrix:
 [[135   0]
 [  0 144]]
Testing confusion matrix:
 [[28  8]
 [ 8 26]]
```

- **Under-fitting**: In contrast, under-fitting was observed when the model's performance was poor both on the training and test data, indicating that the model was too simple to capture the underlying patterns of the data.

```
Underfitting Decision Tree Model:
Train Accuracy: 0.8710
Test Accuracy:0.8143
Training confusion matrix:
 [[103  32]
 [  4 140]]
Testing confusion matrix:
 [[25 11]
 [ 2 32]]
```

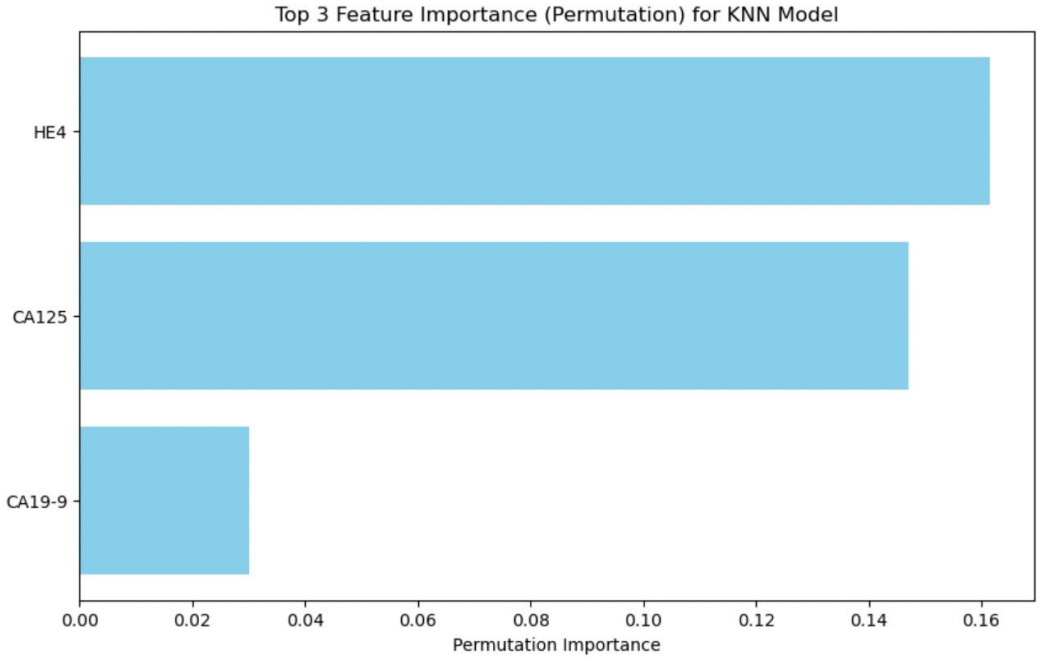


FEATURE IMPORTANCE ANALYSIS

Two key techniques were used to assess feature contributions:

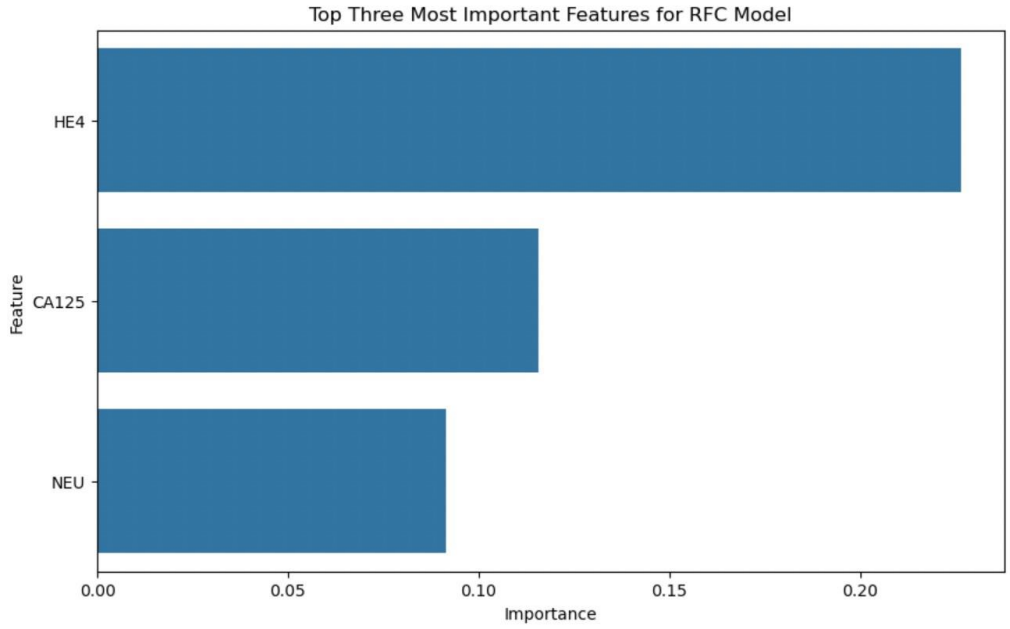
1. **Permutation Importance**: Identified the top features influencing model predictions, aiding in feature selection and ensuring interpretability.

- KNN Model :-



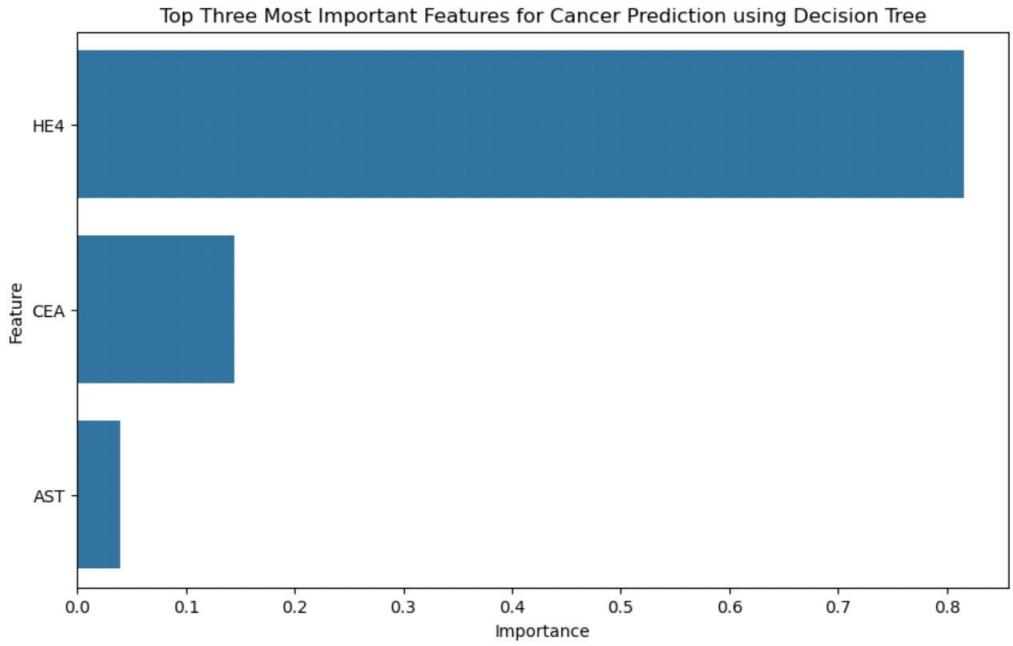
- RF Model :-

```
Top Three Important Features for RFC Model:
   Feature  Importance
6      HE4    0.226577
5    CA125    0.115553
22     NEU    0.091461
```



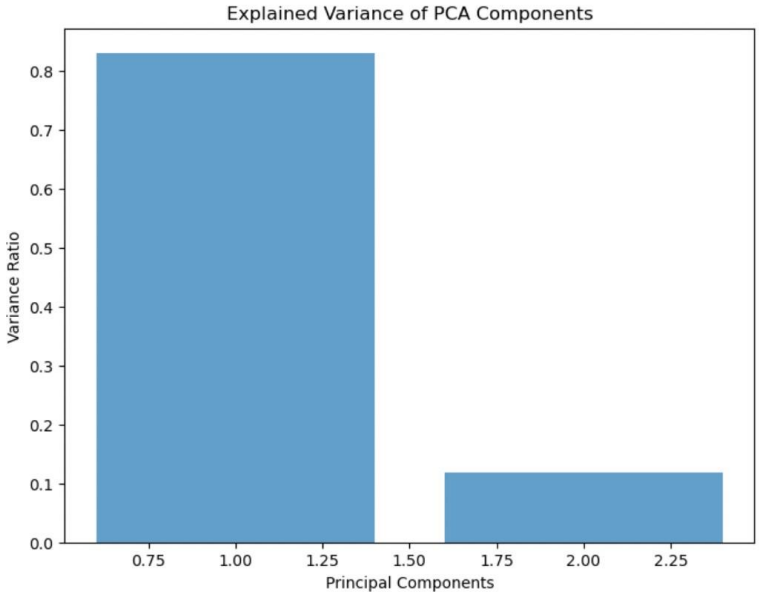
- DT Model :-

```
Top Three Important Features for DT Model:
   Feature  Importance
6      HE4    0.816087
7      CEA    0.144680
31     AST    0.039232
```

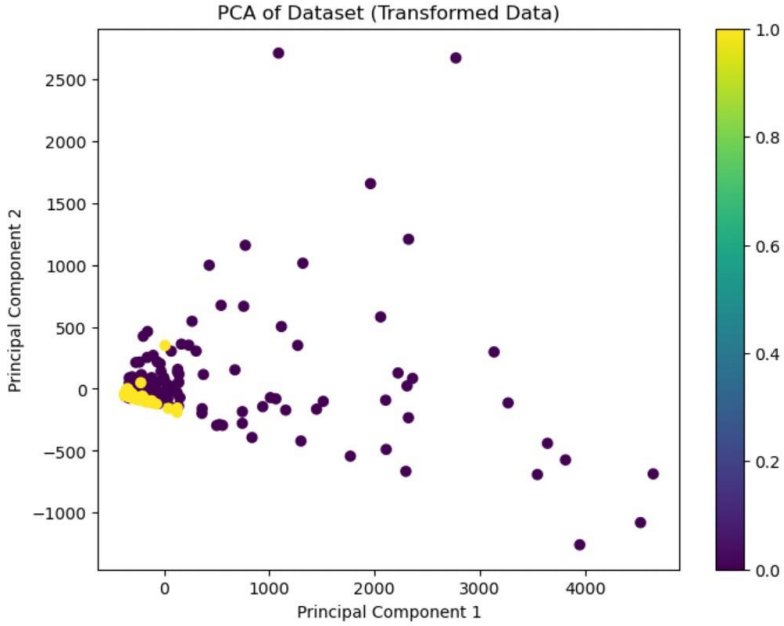


2. **Principal Component Analysis (PCA)**: Reduced dataset dimensionality, simplifying the data structure while retaining essential patterns for model training.

- KNN Model :-

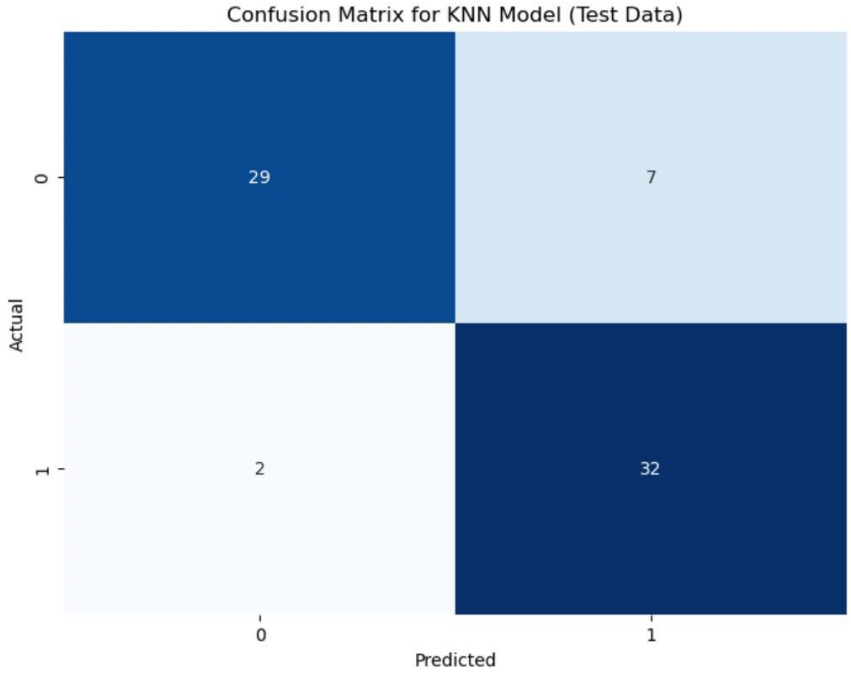


The explained variance ratio indicated that the first principal component (PC1) accounted for over 80% of the variance, highlighting its significant contribution to the dataset's structure.



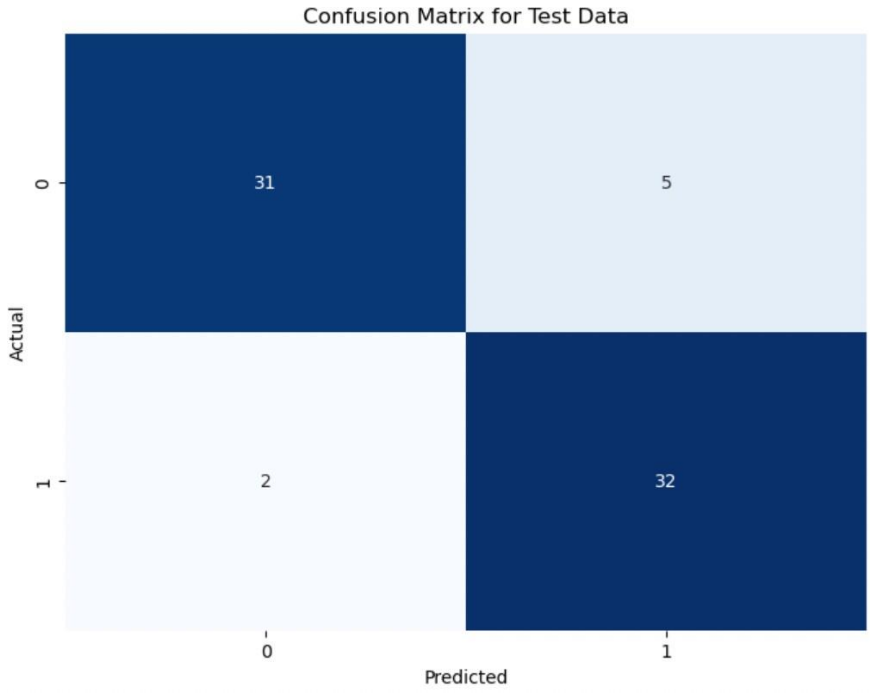
The PCA scatterplot showed a clear clustering of data points, which suggests the dataset's separability in the reduced-dimensional space.

```
Train Accuracy: 0.8746
Test Accuracy: 0.8714
Training Confusion Matrix:
[[108  27]
 [  8 136]]
Testing Confusion Matrix:
[[29  7]
 [ 2 32]]
```



- RF Model :-

```
Train Accuracy: 1.0000
Test Accuracy: 0.9000
Training Confusion Matrix:
[[135   0]
 [  0 144]]
Testing Confusion Matrix:
[[31  5]
 [ 2 32]]
```



5. Hardware/Software Required:-

Hardware Requirements

1. **Computing Device**
    a. A personal computer or laptop with adequate specifications.

Software Requirements

1. **Programming Environment**

    a. **Python**: The primary programming language for data analysis and machine learning, along with libraries like:
        i. `pandas` and `numpy` for data manipulation
        ii. `scikit-learn` for implementing the Random Forest model
        iii. `matplotlib` and `seaborn` for data visualization

2. **Integrated Development Environment (IDE)**

    a. Popular IDEs like:
        i. **Jupyter Notebook** (for interactive coding and visualization)
        ii. **PyCharm** or **VS Code** (for script-based development)

6. Experimental Results:-

The Best Accuracies of the models obtained are as follows:

- K-Nearest Neighbours:

  -> Basic KNN model

```
Basic KNN Model Evaluation:
[[27  5]
 [ 8 30]]
              precision    recall  f1-score   support

           0       0.77      0.84      0.81        32
           1       0.86      0.79      0.82        38

    accuracy                           0.81        70
   macro avg       0.81      0.82      0.81        70
weighted avg       0.82      0.81      0.81        70
```

-> Optimised KNN model (with tuned parameters and K=8)

```
The best k value is: 8

Evaluating KNN Model...
[[29  7]
 [ 3 31]]
Accuracy: 0.8571
Precision: 0.8623
Recall: 0.8571
F1 Score: 0.8569
AUC: 0.9105
Log Loss: 1.3167
```

- Random Forest:

```
Best RFC Model Evaluation:
Training confusion matrix:
[[127   8]
 [  0 144]]
Testing confusion matrix:
[[30  6]
 [ 1 33]]
Train Accuracy: 0.9713
Test Accuracy: 0.9000
Precision: 0.9087
Recall: 0.9000
F1 Score: 0.8997
AUC: 0.9412
Log Loss: 0.3424
```

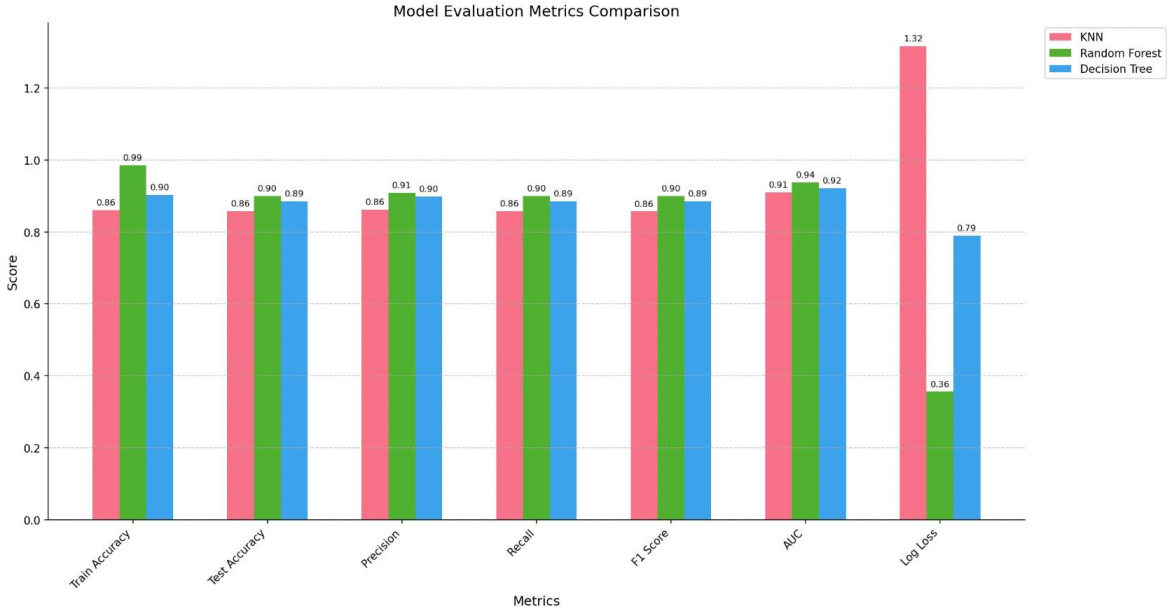
- Decision Tree:

```
Best Decision Tree Model Evaluation:
Training confusion matrix:
 [[115  20]
 [  5 139]]
Testing confusion matrix:
 [[28  8]
 [ 2 32]]
Train Accuracy: 0.9104
Test Accuracy: 0.8571
Precision: 0.8686
Recall: 0.8571
F1 Score: 0.8564
AUC: 0.7970
Log Loss: 3.8012
```

7. Conclusions:-

In conclusion, this study employs advanced data mining and machine learning techniques, including KNN, RF and DT, to uncover the relationship between biological/clinical data and cancer.

The Random Forest model outperforms the others with the highest accuracy (90%) and best metrics across precision, recall, F1 score, and AUC. The Decision Tree follows closely with accuracy of (88%), while KNN shows the lowest accuracy of (85.71%) and less effective precision and recall.
Overall, Random Forest is the most effective model for EARLY STAGE DETECTION OF OVARIAN CANCER.



8. Future Scope:-

1. **Integration with Advanced Machine Learning Models** - Utilise deep learning for better feature extraction and pattern recognition.

2. **Validation with Diverse Datasets** - Test the model on larger, diverse datasets to ensure reliability across populations.

3. **Integration with Healthcare Systems** - Incorporate the framework into EHR systems for automated diagnostics.

9. Github Link Of Our Project

Github Link