FINAL YEAR PROJECT REPORT

PROJECT - SUPERVISED MACHINE LEARNING APPROACHES FOR CANCER CLASSIFICATION USING GENE EXPRESSION DATA.

DATASET 1 **:-** Cancer gene expression datasets presented in the paper [leukemia (Golub et al.)]

FEATURES :- Number of genes: 5147
Number of samples: 72

DIAGNOSTIC CLASSES:

Acute lymphoblastic leukemia (ALL): 47 examples (65.3%)
Acute myeloid leukemia (AML): 25 examples (34.7%)

FEATURE SELECTION: Top 20 gene features having maximum cancerous cells based on PEARSON'S CORRELATION.

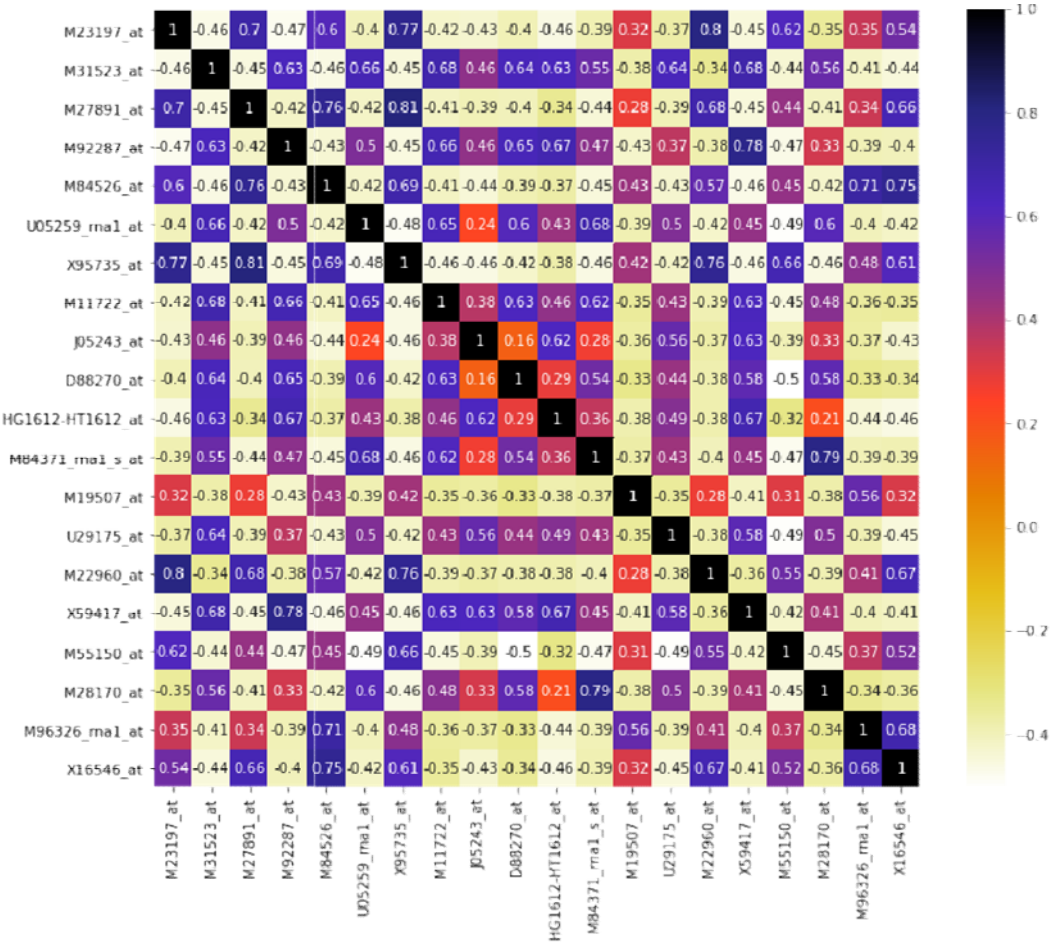


Diagram 1: Correlation diagram of 20 radviz visualizations with 8 attributes.

TRAINING DATA - TESTING DATA SPLIT:

1. Training Data : Testing Data = 1 : 1 i.e. 50-50 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	100%	100%	100%	100%
Support Vector Machine (SVM)	97.22%	100%	100%	100%	100%
Naive Bayes Classifier	100%	100%	100%	100%	100%
eXtreme Gradient Boosting	100%	94.44%	90.91%	90.91%	90.91%
Random Forest Classifier	100%	100%	100%	100%	100%

2. Training Data : Testing Data = 7 : 3 i.e. 70-30 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	100%	100%	100%	100%
Support Vector Machine (SVM)	96%	100%	100%	100%	100%
Naive Bayes Classifier	100%	100%	100%	100%	100%
eXtreme Gradient Boosting	100%	100%	100%	100%	100%
Random Forest Classifier	100%	95.45%	85.71%	100%	92.31%

3. Training Data : Testing Data = (8:2) 4 : 1 i.e. 80-20 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	100%	100%	100%	100%
Support Vector Machine (SVM)	96.49%	100%	100%	100%	100%
Naive Bayes Classifier	100%	100%	100%	100%	100%
eXtreme Gradient Boosting	100%	100%	100%	100%	100%
Random Forest Classifier	100%	93.33%	80%	100%	88.89%

➧ Conclusion Table :- Average Accuarcy Score for all ML Algorithms

Machine Learning Algorithms	Logistic Regression	Support Vector Machine (SVM)	Naive Bayes Classifier	eXtreme Gradient Boosting	Random Forest Classifier
Average Accuracy	100%	100%	100%	98.1466666667%	96.26%

➧ **Mini Conclusion for Dataset 1**:- In accordance with the above mentioned data, we can conclude that **Logistic Regression, Support Vector Machine (SVM)** & **Naive Bias Classifier** are the best classification algorithms to predict cancer for Leukemia gene samples.

DATASET 2 :- Cancer gene expression datasets presented in the paper
SRBCT (Khan et al.)

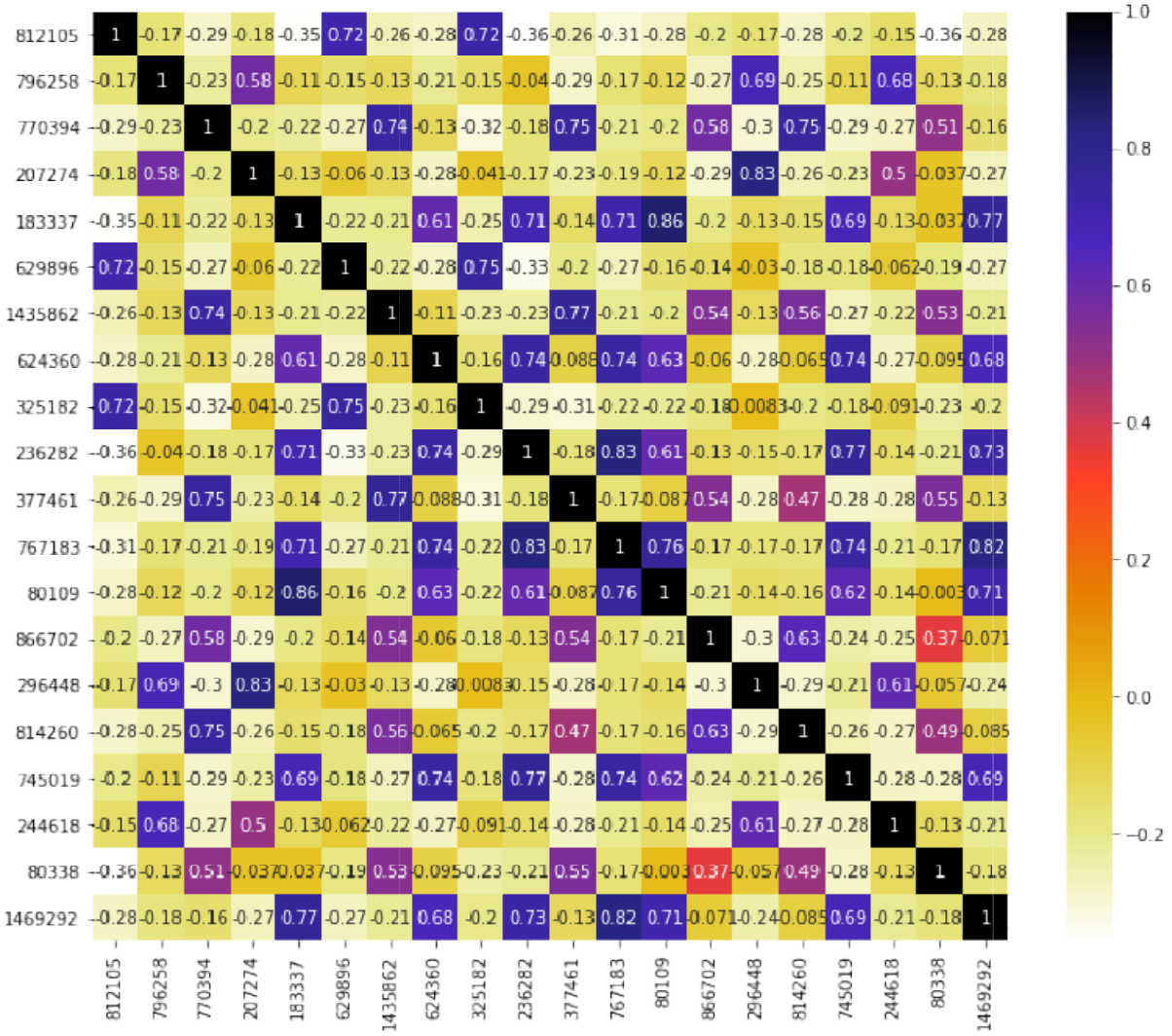
FEATURE :- Number of genes: 2308
Number of samples: 83

DIAGNOSTIC CLASSES:

Ewing's sarcoma (**EWS**): **29** examples (34.9%)
Burkitt's lymphoma (**BL**): **11** examples (13.3%)
Neuroblastoma (**NB**): **18** examples (21.7%)
Rhabdomyosarcoma (**RMS**): **25** examples (30.1%)

FEATURE SELECTION: Top 20 gene features having maximum cancerous cells based on PEARSON'S CORRELATION.

Diagram 2 : Correlation diagram of 20 radviz visualizations with 8 attributes.



TRAINING DATA - TESTING DATA SPLIT:

1. Training Data : Testing Data = 1 : 1 i.e. 50-50 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	97.56%	97.56%	97.56%	97.56%
Support Vector Machine (SVM)	100%	92.68%	94%	93%	93%
Naive Bayes Classifier	100%	100%	100%	100%	100%
eXtreme Gradient Boosting	100%	87.8%	91.01%	87.8%	87.56%
Random Forest Classifier	100%	100%	100%	100%	100%

2. Training Data : Testing Data = 7 : 3 i.e. 70-30 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	96%	96%	96%	96%
Support Vector Machine (SVM)	100%	96%	96.44%	96%	95.9%
Naive Bayes Classifier	100%	100%	100%	100%	100%
eXtreme Gradient Boosting	100%	100%	100%	100%	100%
Random Forest Classifier	100%	100%	100%	100%	100%

3. Training Data : Testing Data = (8:2) 4 : 1 i.e. 80-20 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	94.12%	95.29%	94.12%	93.86%
Support Vector Machine (SVM)	100%	94.12%	95.29%	94.12%	93.86%
Naive Bayes Classifier	100%	94.12%	95.29%	94.12%	93.86%
eXtreme Gradient Boosting	100%	100%	100%	100%	100%
Random Forest Classifier	100%	100%	100%	100%	100%

➡ Conclusion Table :- Average Accuarcy Score for all ML Algorithms

Machine Learning Algorithms	Logistic Regression	Support Vector Machine (SVM)	Naive Bayes Classifier	eXtreme Gradient Boosting	Random Forest Classifier
Average Accuracy	95.8933%	94.266667%	98.04%	95.9333333 %	100%

➡ **Mini Conclusion for Dataset 2** :- In accordance with the above mentioned data, we can conclude that **Random Forest Classifier** is the best classification algorithms to predict cancer for SRBCT gene samples.

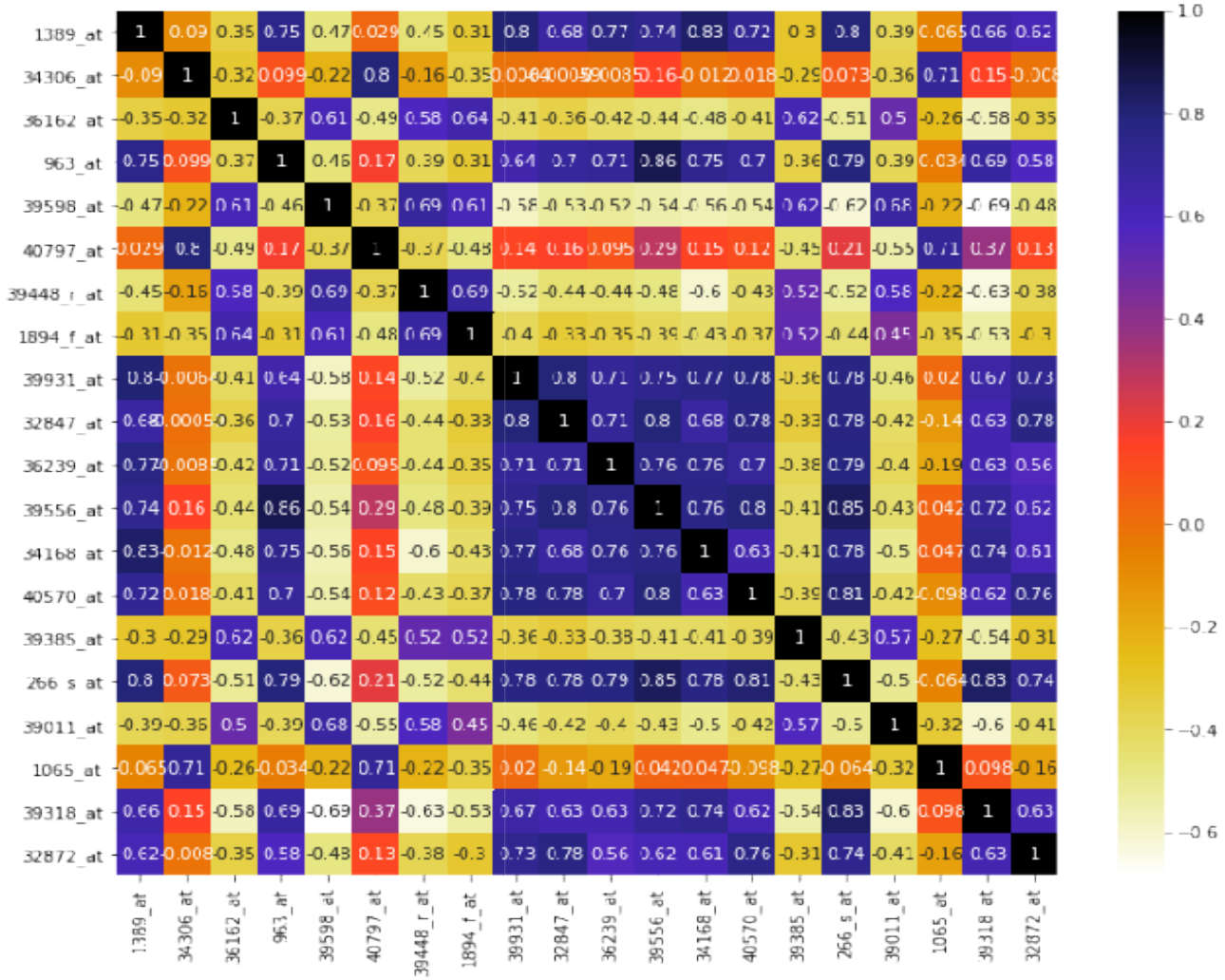
DATASET 3 :- Cancer gene expression datasets presented in the paper
[MLL (Armstrong et al.)]

FEATURES :- Number of genes: 12533
Number of samples: 72

DIAGNOSTIC CLASSES:
Acute lymphoblastic leukemia (**ALL**): **24** examples (33.3%)
Mixed-lineage leukemia (**MLL**): **20** examples (27.8%)
Acute myeloid leukemia (**AML**): **28** examples (38.9%)

FEATURE SELECTION: Top 20 gene features having maximum cancerous cells based on PEARSON'S CORRELATION.

Diagram 3 :- Correlation diagram of 20 radviz visualizations with 8 attributes.
(Contd….)



TRAINING DATA - TESTING DATA SPLIT:

1. Training Data : Testing Data = 1 : 1 i.e. 50-50 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	97.22%	97.47%	97.22%	97.23%
Support Vector Machine (SVM)	100%	94.44%	95%	94.44%	94.44%
Naive Bayes Classifier	100%	86.11%	86.11%	86.11%	86.11%
eXtreme Gradient Boosting	100%	88.89%	89.24%	88.89%	88.64%
Random Forest Classifier	100%	91.67%	91.67%	91.67%	91.67%

2. Training Data : Testing Data = 7 : 3 i.e. 70-30 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	95.45%	96%	95.45%	96%
Support Vector Machine (SVM)	98%	95.45%	96.21%	95.45%	95.53%
Naive Bayes Classifier	100%	95.45%	96.21%	95.45%	95.51%
eXtreme Gradient Boosting	100%	95.45%	95.96%	95.45%	95.34%
Random Forest Classifier	100%	95.45%	96.21%	95.45%	95.51%

3. Training Data : Testing Data = (8:2) 4 : 1 i.e. 80-20 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	93.33%	95%	93.33%	93.55%
Support Vector Machine (SVM)	98.25%	93.33%	95%	93.33%	93.55%
Naive Bayes Classifier	100%	93.33%	95%	93.33%	93.44%
eXtreme Gradient Boosting	100%	100%	100%	100%	100%
Random Forest Classifier	100%	93.33%	95%	93.33%	93.44%

➡ Conclusion Table :- Average Accuarcy Score for all ML Algorithms

Machine Learning Algorithms	Logistic Regression	Support Vector Machine (SVM)	Naive Bayes Classifier	eXtreme Gradient Boosting	Random Forest Classifier
Average Accuracy	95.3333%	94.406667%	91.63%	94.78%	93.483333%

➡ **Mini Conclusion for Dataset 3** :- In accordance with the above mentioned data, we can conclude that **Logistic Regression** is the best classification algorithms to predict cancer for ALL, MLL & AML gene samples.

DATASET 4 :- Cancer gene expression datasets presented in the paper
DLBCL (Shipp et al.)

FEATURES :- Number of genes: 7070
Number of samples: 77

DIAGNOSTIC CLASSES:

Diffuse large B-cell lymphoma (**DLBCL**): **58** examples (75.3%)
Follicular lymphoma (**FL**): **19** examples (24.7%)

FEATURE SELECTION: Top 20 gene features having maximum cancerous cells based on PEARSON'S CORRELATION.

List of top 20 genes :
['X16983_at', 'X02152_at', 'M94880_f_at', 'Z21966_at', 'J03909_at', 'D87119_at', 'HG417-HT417_s_at', 'M22382_at', 'L17131_rna1_at', 'L42324_at', 'X56494_at', 'M63138_at', 'Z11793_at', 'D82348_at', 'AB002409_at', 'HG1980-HT2023_at', 'M14328_s_at', 'J04173_at', 'X03689_s_at', 'D78134_at']

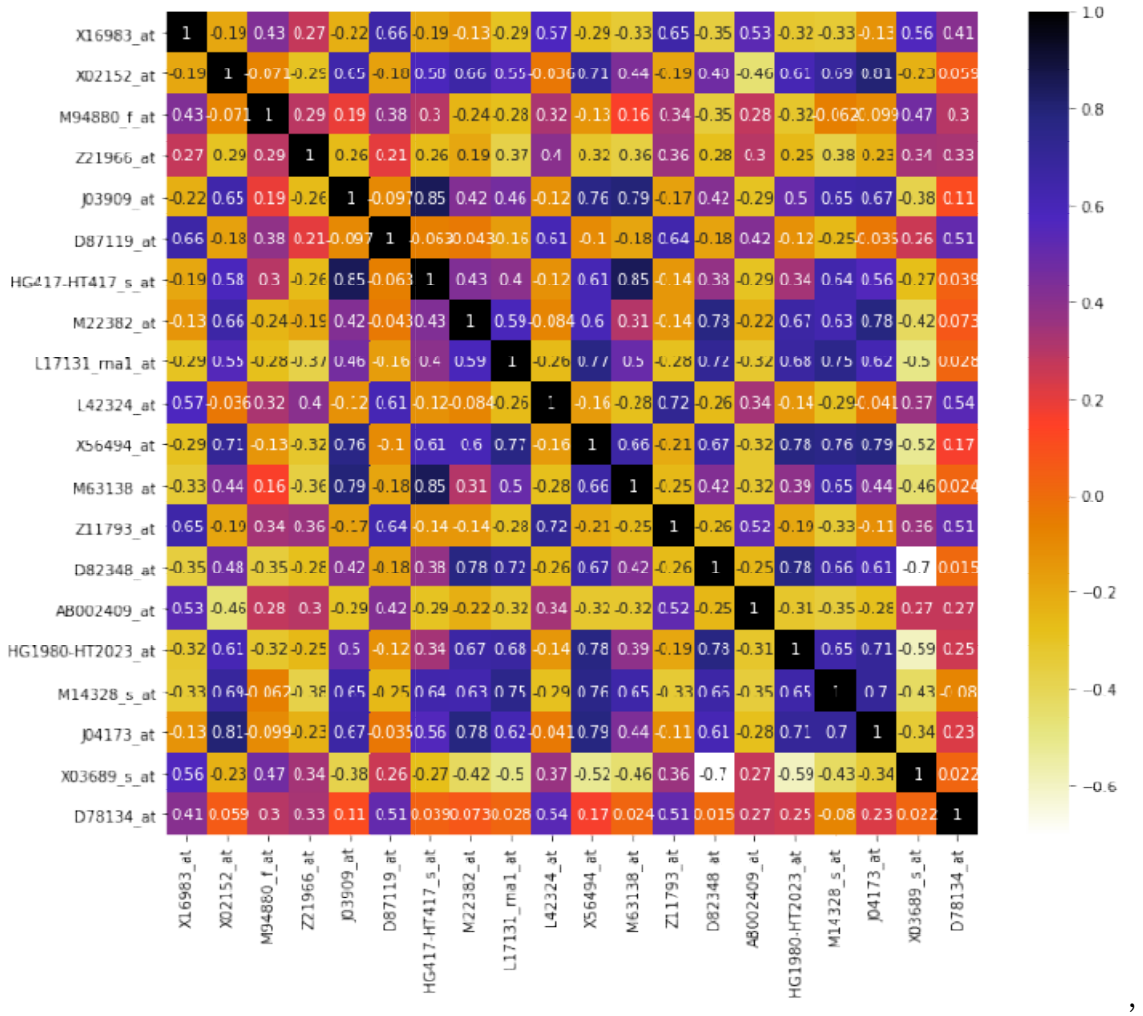


Diagram 4 :- Correlation diagram of 20 radviz visualizations with 8 attributes.

TRAINING DATA - TESTING DATA SPLIT:

1. Training Data : Testing Data = 1 : 1 i.e. 50-50 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	92.11%	75%	100%	85.71%
Support Vector Machine (SVM)	94.87%	94.74%	81.82%	100%	90%
Naive Bayes Classifier	97.44%	94.74%	81.82%	100%	90%
eXtreme Gradient Boosting	100%	78.95%	57.14%	44.44%	50%
Random Forest Classifier	100%	92.11%	80%	88.89%	84.21%

2. Training Data : Testing Data = 7 : 3 i.e. 70-30 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	95.83%	80%	100%	88.89%
Support Vector Machine (SVM)	94.34%	95.83%	80%	100%	88.89%
Naive Bayes Classifier	96.23%	95.83%	80%	100%	88.89%
eXtreme Gradient Boosting	100%	83.33%	50%	25%	33.33%
Random Forest Classifier	100%	87.5%	66.67%	50%	57.14%

3. Training Data : Testing Data = (8:2) 4 : 1 i.e. 80-20 split

Machine Learning Algorithms	Model Score	Accuracy	Precision	Recall	F1 Score
Logistic Regression	100%	93.75%	80%	100%	88.89%
Support Vector Machine (SVM)	98.36%	93.75%	80%	100%	88.89%
Naive Bayes Classifier	96.72%	93.75%	80%	100%	88.89%
eXtreme Gradient Boosting	100%	81.25%	66.67%	50%	57.14%
Random Forest Classifier	100%	81.25%	66.67%	50%	57.14%

➧ Conclusion Table :- Average Accuarcy Score for all ML Algorithms

Machine Learning Algorithms	Logistic Regression	Support Vector Machine (SVM)	Naive Bayes Classifier	eXtreme Gradient Boosting	Random Forest Classifier
Average Accuracy	93.8967%	94.773333%	94.773333%	81.1766667%	86.9533333%

➧ **Mini Conclusion for Dataset 4** :- In accordance with the above mentioned data, we can conclude that **Support Vector Machine (SVM)** & **Naive Bias Classifier** are the best classification algorithms to predict cancer for DLBCL and FL gene samples.

FINAL CONCLUSION :-

Let us find out the average accuracy for a particular Machine Learning Algorithm for all the datasets considered, so that we can come into a final conclusion about the best ML algorithm to work with in each and every case.

Final Accuracy = (Sum of all average accuracies for a particular ML algorithm) / 4

Machine Learning Algorithms	Logistic Regression	Support Vector Machine (SVM)	Naive Bayes Classifier	eXtreme Gradient Boosting	Random Forest Classifier
Final Accuracy	96.2808%	95.8616668%	96.110833%	92.5091668%	95.1091665%

We can see from the above table, that all the Machine Learning Algorithms have very close accuracies. However, the most accurate Machine Learning Algorithm for correctly predicting the cancerous cells via the given gene expression datasets is **LOGISTIC REGRESSION**.

So we can infer that if we consider Logistic Regression as the classification algorithm for all the above mentioned datasets, it will give us **96.2808%** accuracy for prediction, which is perhaps the highest.

References:-

Datasets for Cancerous Gene Classification(Orange Dataset):
https://file.biolab.si/biolab/supp/bi-cancer/projections/info/SRBCT.html