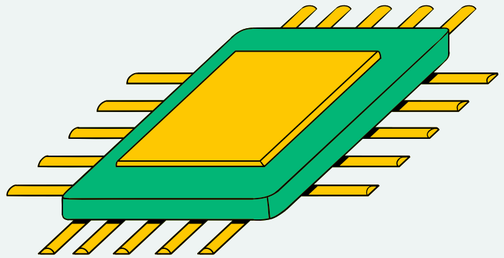
PREDICTION OF AML SUBTYPES THROUGH SUPERVISED MACHINE LEARNING

PRESENTED BY: GROUP H

Contributers: Keerthana Kathavarayan, Tao Shengmin



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INTRODUCTION

ACUTE MYELOID LEUKAEMIA (AML)

- Cancer of **blood** and **bone marrow**.
- Overproduction of immature white blood cells (**myeloblasts**).
- Various subtypes–> critical for treatment plans.

FAB CLASSIFICATION

- **French–American–British Classification:** 8 subtypes (**MO–M7**) based on cell morphology.
- M2, M3, and M4 most common.

FAB subtype	Name
M0	Undifferentiated acute myeloblastic leukemia
M1	Acute myeloblastic leukemia with minimal maturation
M2	Acute myeloblastic leukemia with maturation
M3	Acute promyelocytic leukemia (APL)
M4	Acute myelomonocytic leukemia
M4	Acute myelomonocytic leukemia with eosinophilia
M5	Acute monocytic leukemia
M6	Acute erythroid leukemia
M7	Acute megakaryoblastic leukemia

GENETIC COMPLEXITY

- **Known Mutations:** Includes fusion genes RUNX1/CBFA2T1, CEBPA mutations, etc.
- **Research Challenges:** High heterogeneity complicates marker identification.
- **Importance of Genetics:** Essential for targeted therapies and understanding disease mechanisms.

DIAGNOSTIC METHODS

- **Current Approaches:** Imaging (X-rays), Microscopy, Cytogenetics, and PCR-based genetic tests.
- **Limitations:** Labour intensive, insufficient genetic markers, for precise subtype classification and developing treatment plans.

PROJECT BASIS

Objective:

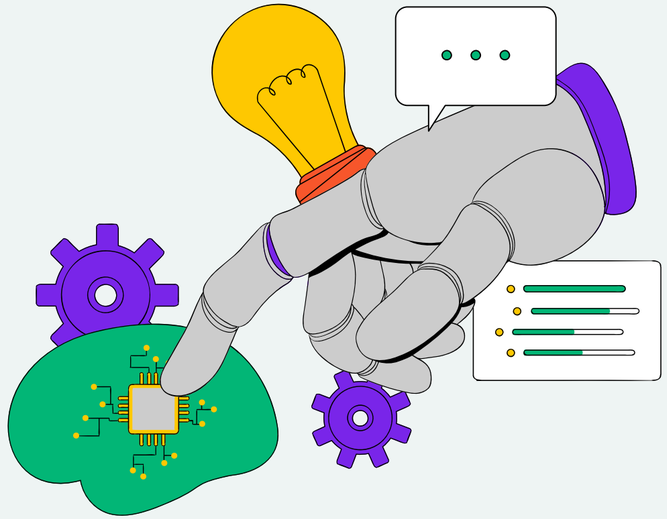
To enhance FAB classification with gene expression data for precise subtype identification.

Method:

Gene expression patterns analyzed as features for prediction of AML subtypes through Machine Learning models.

Future Impact:

- Improve diagnostic accuracy
- Enable efficient prognosis & treatment
- Advance precision oncology



DATASET OVERVIEW

Database:

- Gene Expression Omnibus (GEO)

Microarray data:

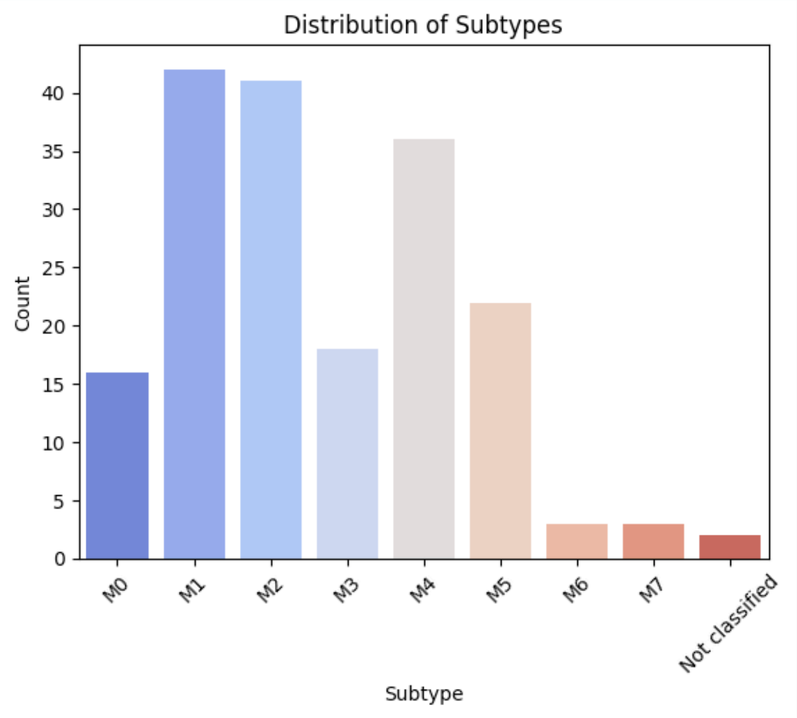
- Affymetrix HG-U133 Plus 2.0
- 16384 Probe IDs
- M0 – M7 AML Subtypes + Not Classified

Samples:

- Whole Blood Tissue
- 183 AML Patients

Gene Expression Omnibus

183 x 16384



METHODOLOGY

DATA PRE-PROCESSING

- Cleaning
- Annotation
- Normalization
- Feature selection

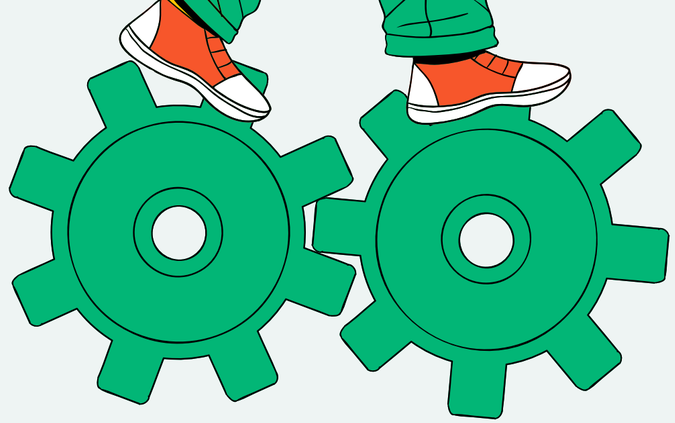
MODEL DEVELOPMENT

- Classification Model
- Best-K hyper-parameter fine-tuning
  - Gridsearch
  - Cross Validation
  - Kfold
- CNNs model architecture to further explore

MODEL EVALUATION

- Metrics
  - Accuracy
  - Weighted-Average F1 score
- Visualisation
  - Confusion Matrix
  - Accuracy Barchart
  - Validation lineplot

DATA PRE-PROCESSING



10k+ features

TRANSFORMATION

- Annotated Gene symbols
- Removed Probe IDs with no match
- Dropped Classes outside of FAB framework.

NORMALISATION

- Log-Transformations

4k+ features

STATS

- Anova threshold p-value<0.05

FEATURE SELECTION

Fold change

- Threshold –> optimal features for downstream

Random-Forest

- n_estimators –> no. of trees in the forest

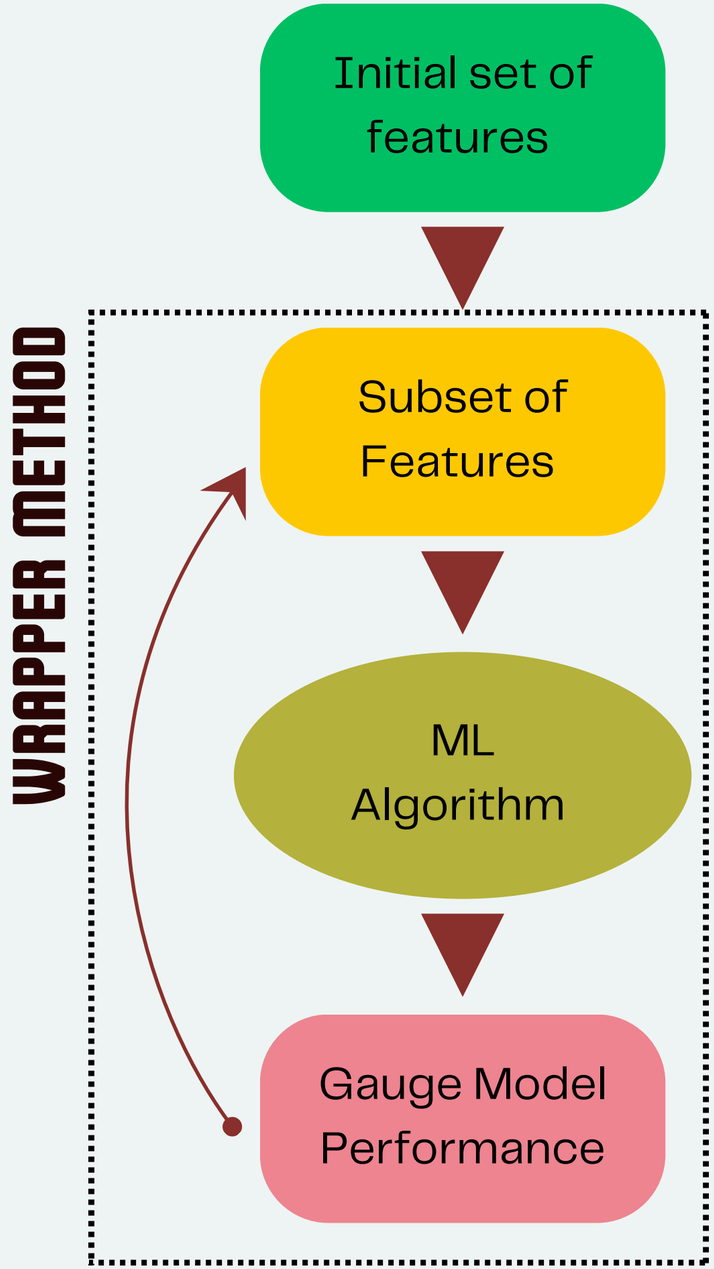
Ridge Regularisation (L2)

- ‘penalty’ –> penalise the λ coefficient

Recursive Feature Elimination with Cross-Validation

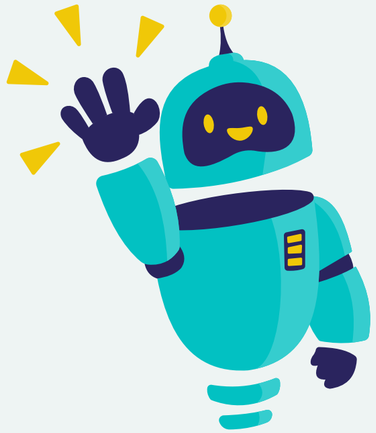
- ‘step’ –> no. of features to remove at each iteration till min. features is achieved.

330 gene features

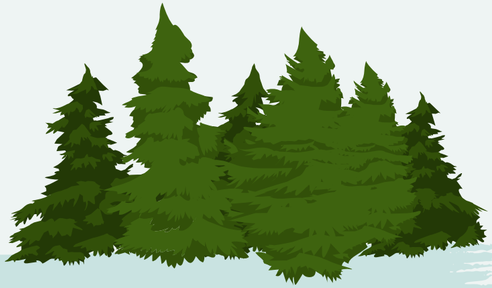


MODELING: OVERVIEW

- **Methods defining:** Multi-class (9 classes) prediction -> handling multi-label classification task
- **Model selection:**
  - Random Forest
  - Supportive Vector Machine
  - Ensemble Model
  - Convolutional Neural Networks
- **Best model fine-tuning:** Finding the Best-K Hyper-parameter
  - GridSearch
  - KFold + Cross Validation
- **Evaluation metrics:**
  - Accuracy, ROC score, F1 recall score
  - confusion matrix
- **Visualisation**

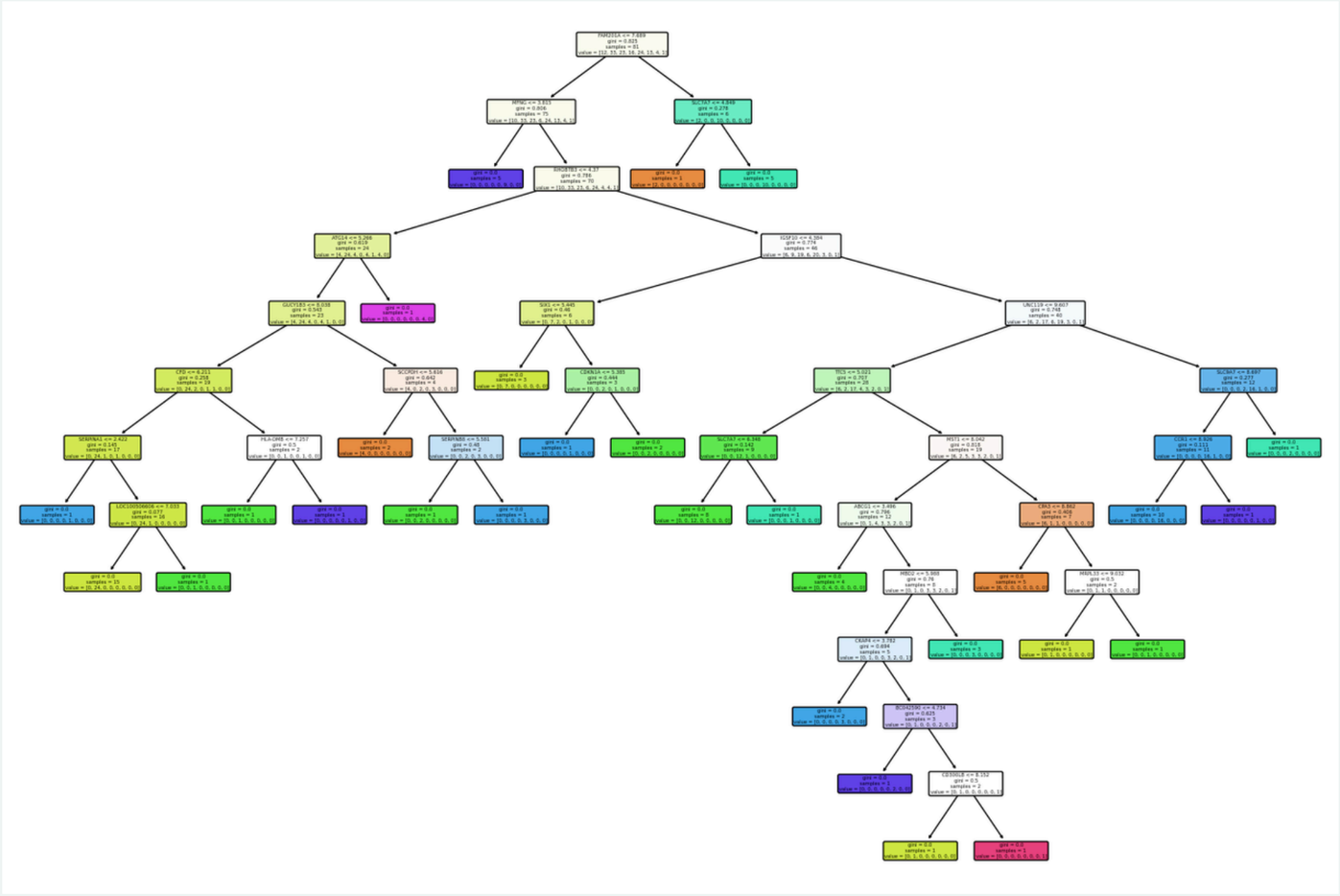


MODELING: RANDOM FOREST

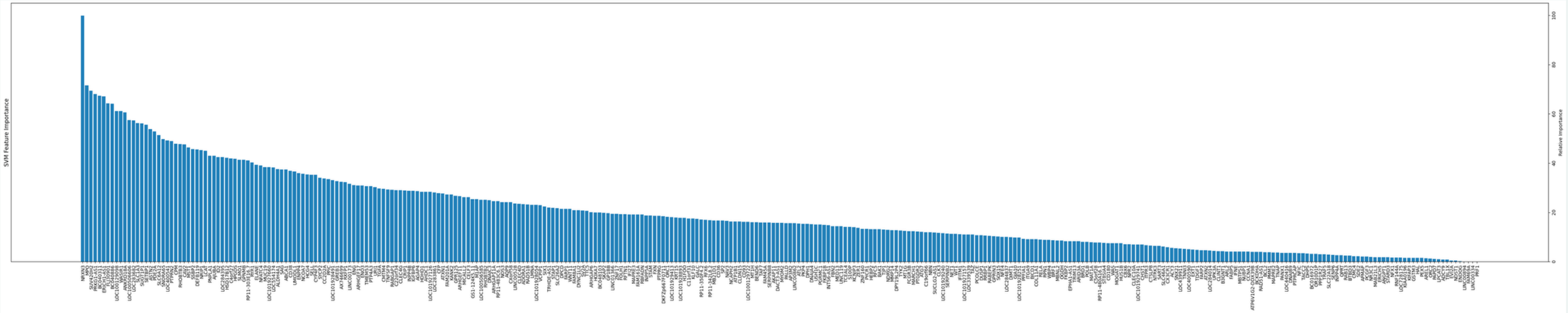


RESULT

- Accuracy: 0.61
- Weighted-Average F1 Score: 0.57



MODELING: SVM

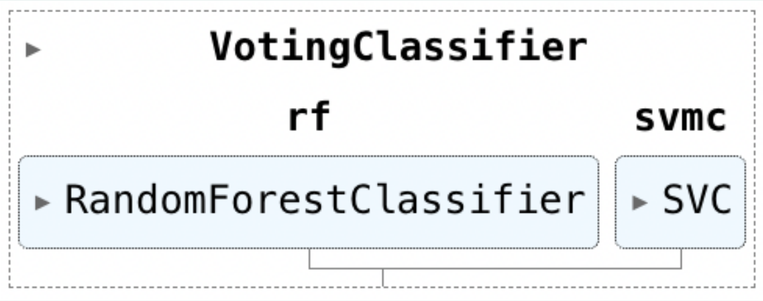


RESULT

- Accuracy: 0.75
- Weighted-Average F1 Score: 0.73

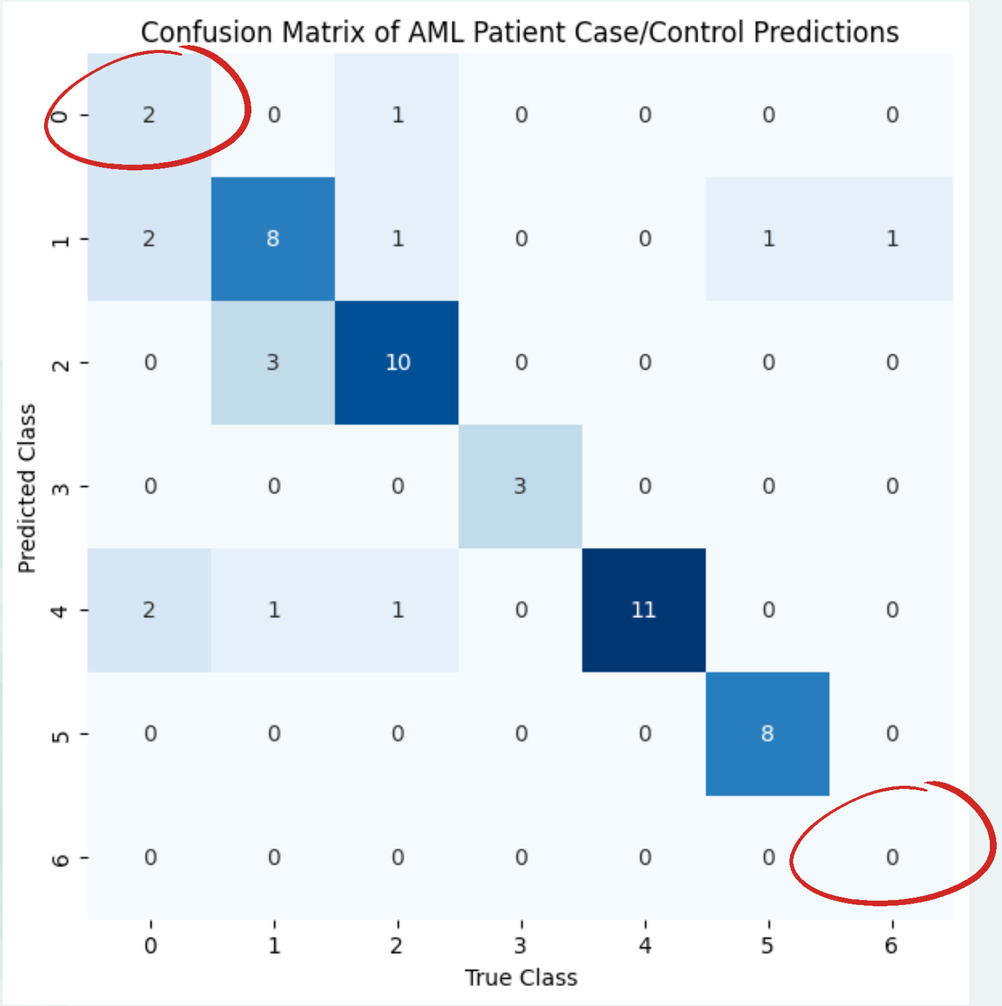
- Can make further improvement on feature cutting based on the ` Feature Importance Bar chart`

MODELING: ENSEMBLE SOFT-VOTING



- Address overfitting, bias and variance
- Improve accuracy: > +4%
- Improve single model generalisation

Classes imbalance



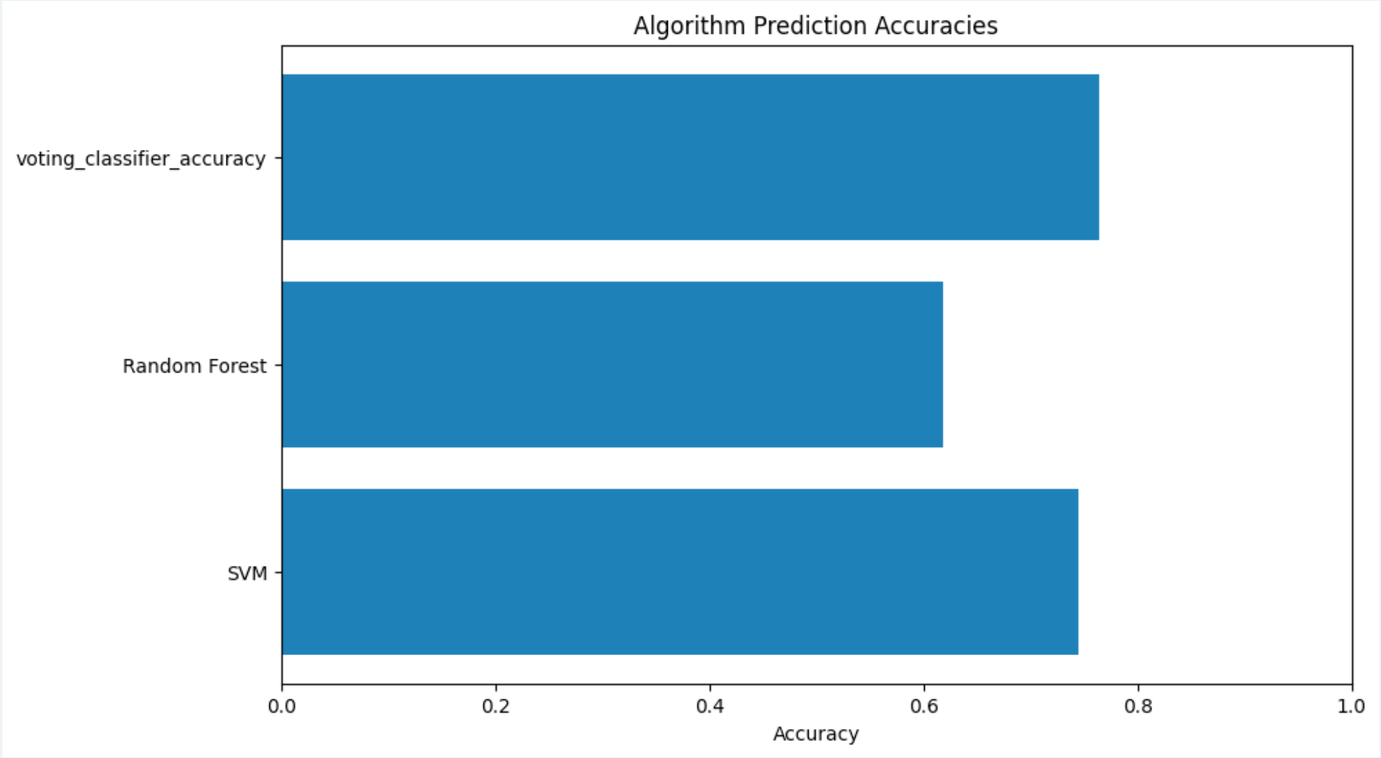
RESULT

- Accuracy: 0.76

MACHINE LEARNING ACCURACY COMPARISON

Strength

- **Random Forest:**
  - Feature identification
  - Dimension reduction
- **SVM:**
  - Nonlinear data
  - Optimal hyperplane

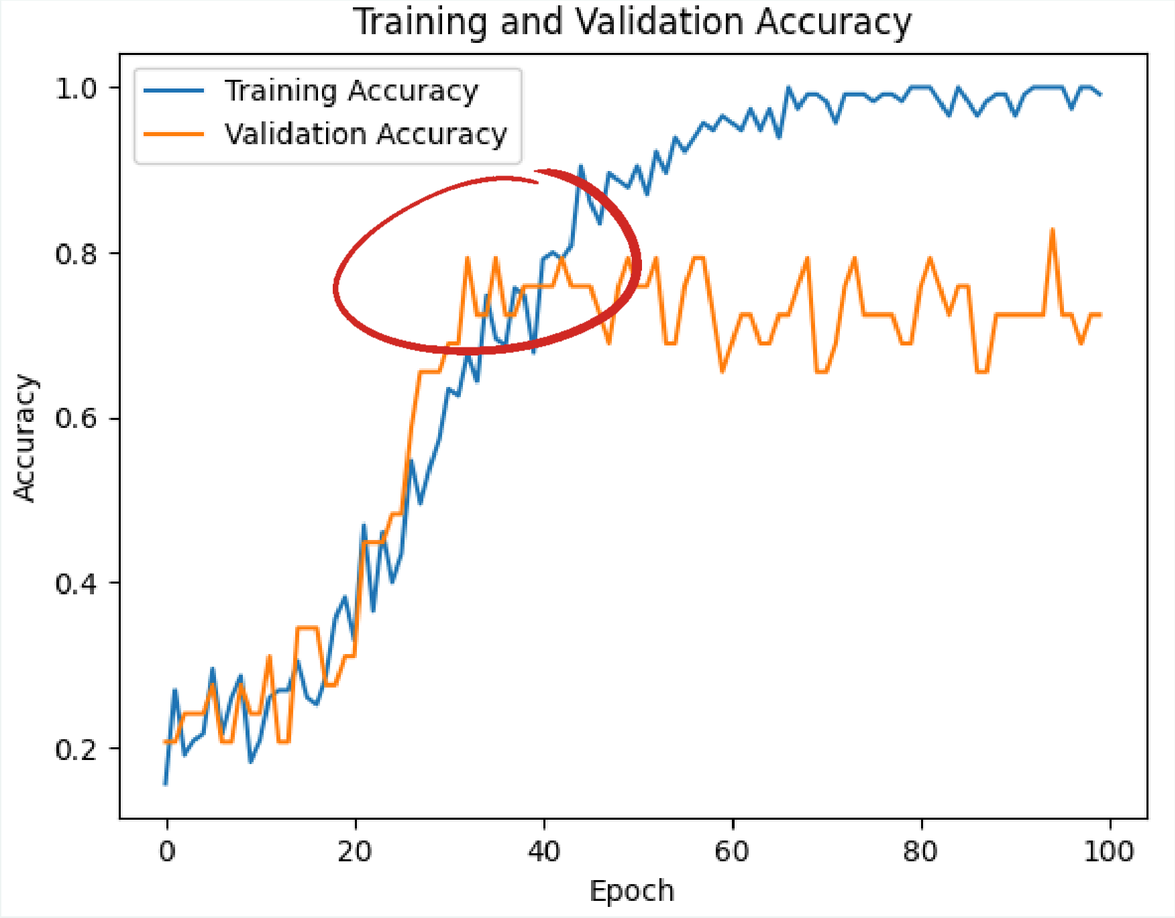


RESULT

- Relatively stable accuracy
- Overall: +16%

MODELING APPENDIX: CNN

- CNN converges at 40ish epochs.
- Over-fitting: Validation not always increasing & aligned with training.



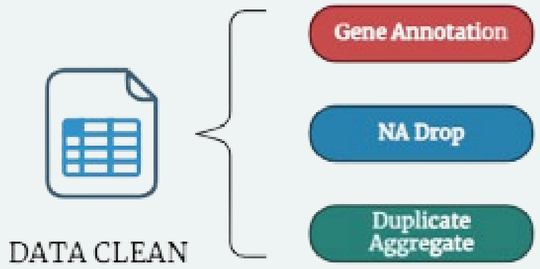
Input
Reshape
Conv1D (64, kernel 3, ReLU)
MaxPooling1D (pool size 2)
Conv1D (128, kernel 3, ReLU)
MaxPooling1D (pool 2)
Conv1D (256, kernel 3, ReLU)
MaxPooling1D (pool 2)
Flatten
Dense (256, ReLU)
Dropout (rate 0.5)
Dense (9, softmax)
Output (9 classes)

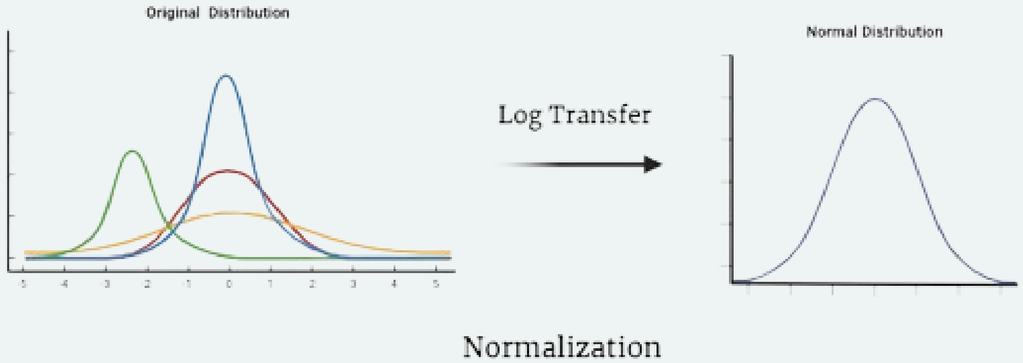
RESULT

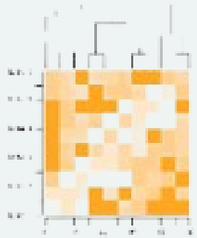
- Accuracy differs each time, but within range of (0.65, 0.70)

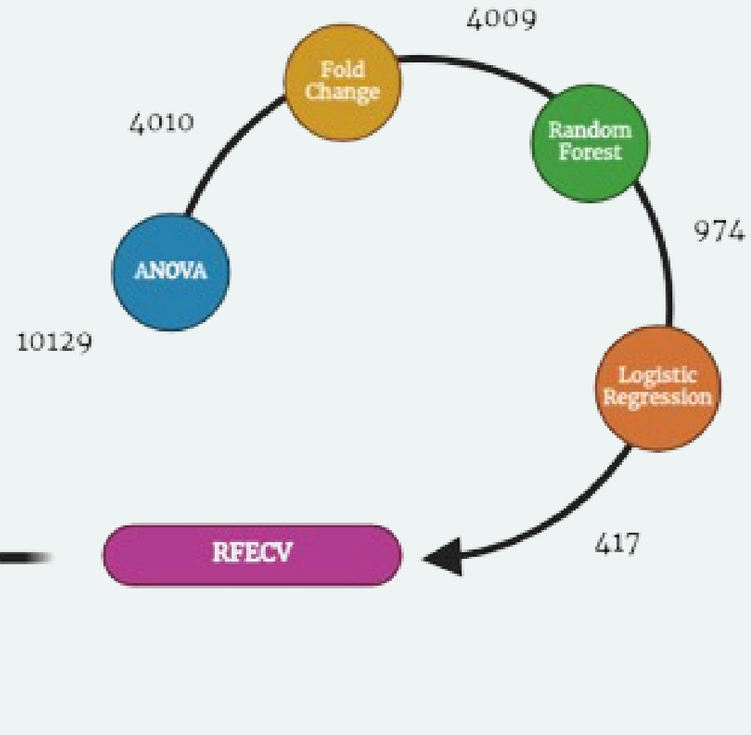
STRENGTHS

Comprehensive Preprocessing and Feature Selection



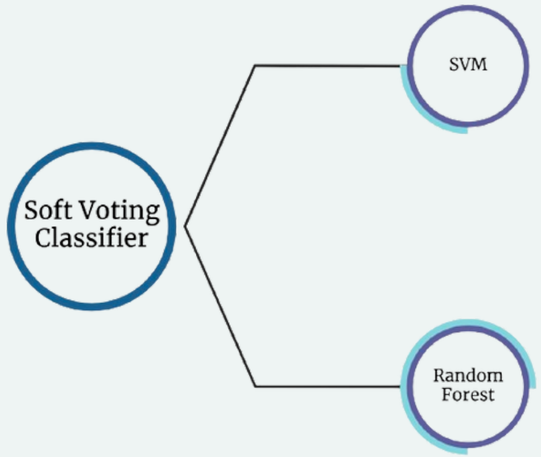


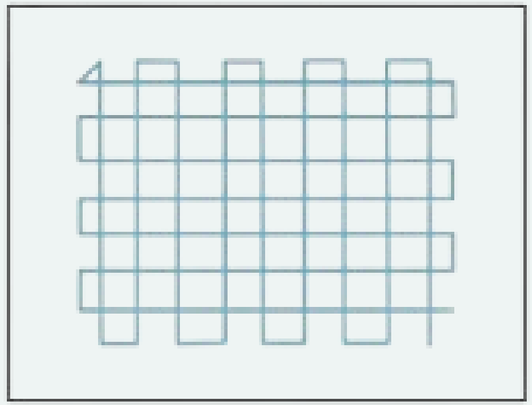


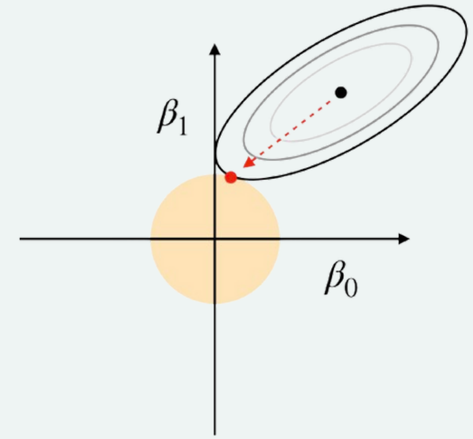


STRENGTHS

- Use of Multiple Models and Ensemble Method
- Hyperparameter Tuning and Regularization
- Comparative Analysis
- Integrate results from different models
- Crucial for optimizing model performance
- L2 regularization help in feature selection and combating overfitting







Multiple Models

Ensemble Method

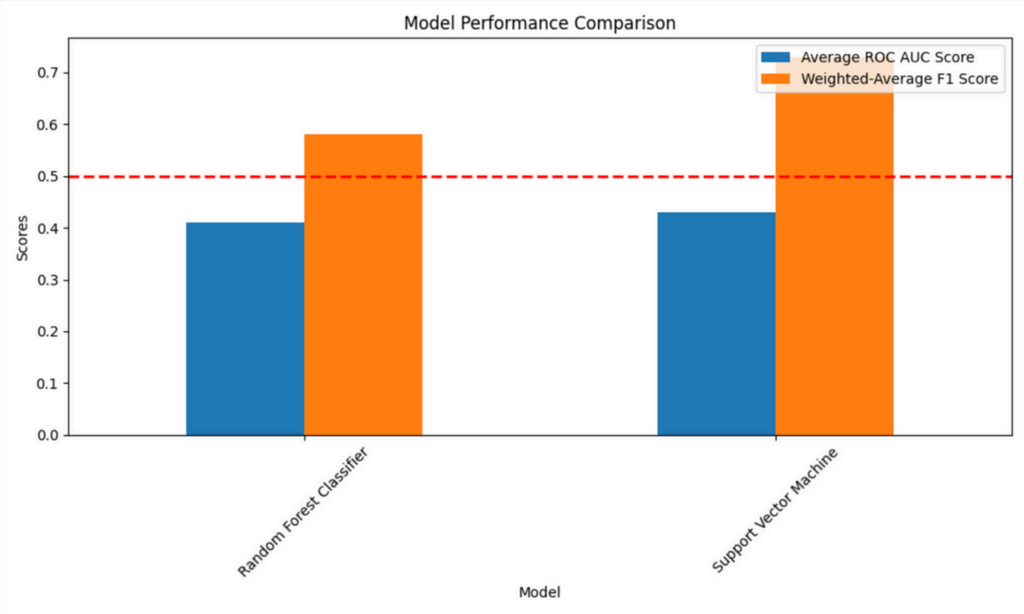
Hyperparameter Space Search

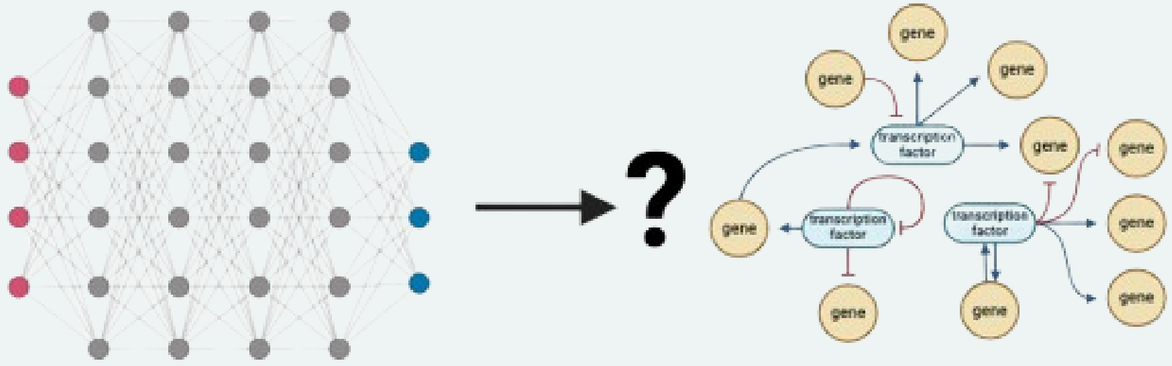
L2 Regularization

LIMITATIONS

- **Moderate Model Performance**
- **Model Complexity and Interpretability**

- **The accuracy and average ROC AUC across the model indicate a significant room for improvement**
- **The use of ensemble methods and multiple layers of feature selection increase model complexity**





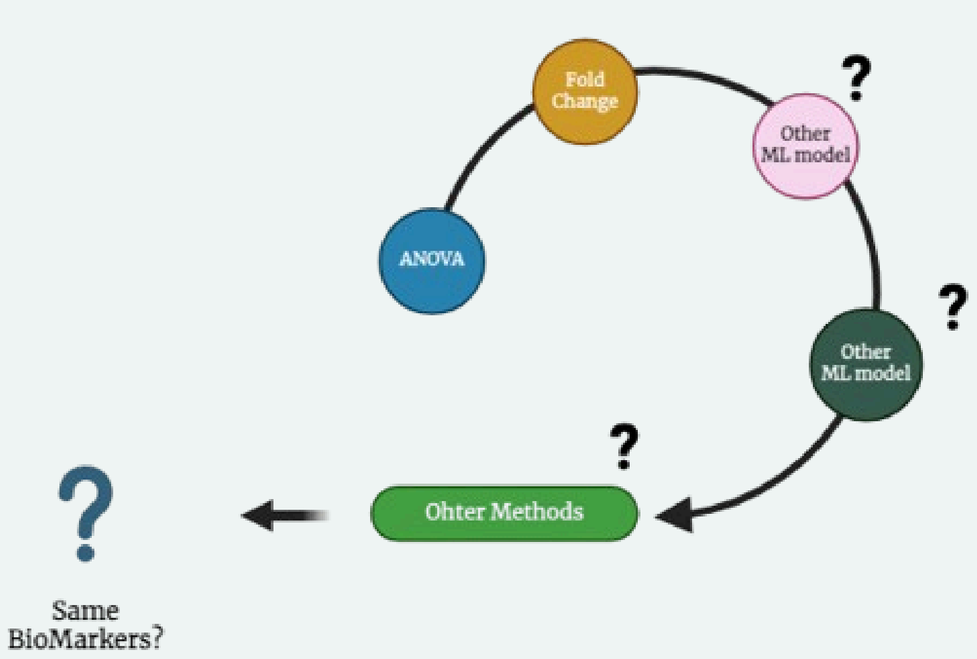
Machine Learning Model

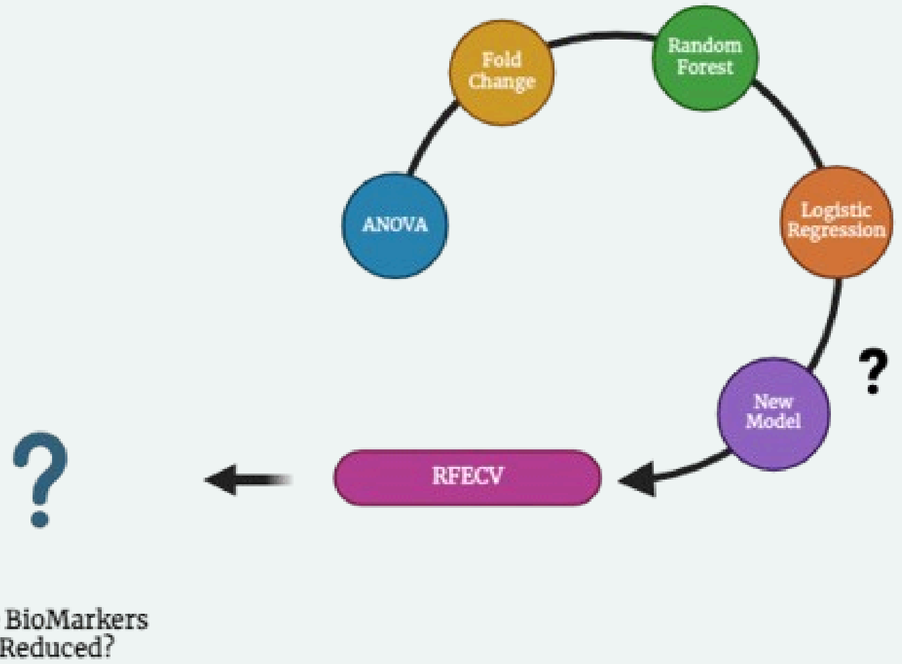
Biological Meaning

LIMITATIONS

Feature Selection

- **The threshold set for Fold Change is empirical, may result in the exclusion of potentially informative genes**
- **The convergency of features selected by our workflow do not evaluated**





FUTURE DIRECTIONS

- **Combine other biological information for predicting**
  - Blood routine examination
  - Microscope image data
- **Use Biological field knowledge to help feature selection**
  - Conduct GO and KEGG pathway enrichment analysis
  - Conduct a GSEA analysis to focus on the feature selection in a significant gene set
- **Find a convergence feature set using different methods**
- **Use a larger dataset to do feature selection and model training**
- **Apply other Machine Learning Methods to improve the prediction**
  - LSTM, Neuron Network, Transformer

REFLECTIONS

Technical Learning:

- Struggled with coding and dataset comprehension, but improved through hands-on experience and learning data-preprocessing and feature selection techniques.

Coding Insights:

- Found joy in coding, seeing it as a puzzle-solving activity despite no background.

Methodology Focus:

- Emphasize the importance of data cleaning, preprocessing, and feature engineering over hyper-parameter tuning.
- Realized traditional machine learning is often more practical than deep learning for real-world scenarios.

Project Management:

- Faced challenges with back-to-back deadlines, highlighting the need for better time management.

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CHATGPT HISTORY

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- https://copilot.microsoft.com/sl/cJJiGYEtrWu
- https://chat.openai.com/share/c2c3f278-5b28-4d7b-971b-3743a04ddb31

Thank you!