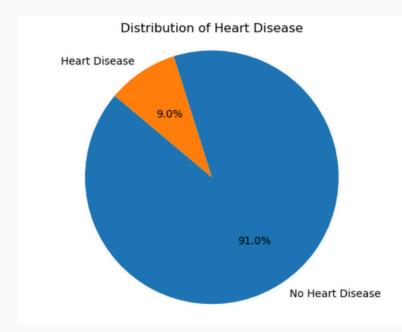


## Feature selection and EDA

#### **Dataset Overview**

- Heart Disease dataset with 301,717 samples and 18 features.
- Balanced dataset using Random Undersampling (27,261 instances per class).



#### **Feature Selection**

#### **Encoding:**

- One-Hot Encoding applied to categorical features.
- K-1 Dummy Encoding used for binary features to reduce dimensionality.

#### **Correlation Analysis:**

- Point-Biserial Correlation for continuous features (e.g., BMI, PhysicalHealth).
- Cramer's V for categorical features (e.g., Smoking, Diabetic).
- Features ranked by correlation with the target variable (HeartDisease).

#### **Feature Sets:**

- Created datasets with Top 10, Top 20, and All Features for experimentation.
- We saved separate datasets for original and under sampled data.

#### **Key Findings**

### Top Correlated Features with Target Class:

• GenHealth (0.38), DiffWalking (0.28), Diabetic (0.25), PhysicalHealth (0.23), Stroke (0.23).

# Image Pre-Processing

#### **Image Dataset Overview**

- Abnormal Heartbeat (HB): 240
- ·Myocardial Infraction (MI): 233
- ·Normal Patient: 172
- Patients with a history of Myocardial Infraction (PMI): 284

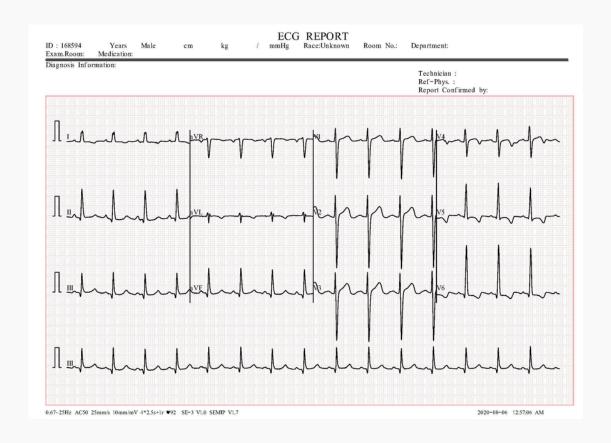
#### Image dataset after processing

- Abnormal Heartbeat HB: 2796
- ·Myocardial Infraction MI: 2868
- Normal Patient: 3408
- Patients with a history of Myocardial Infraction: 2064

#### Image dataset after preprocessing

Entire image consists of 12 signals (leads) for a single patient. The leads were extracted, the dataset became each instance is a lead.

The data was processed through performing the following actions: Cropping, Grayscale, Conversion, Smoothing, Thresholding and resizing





## CLASSIFICATION

#### **Objective**

• Address class imbalance and assess the effect of feature selection and undersampling.

#### Our Approach:

#### Primary classifier: **Decision Trees**

Key Metrics Before Undersampling:

- High Accuracy: 91%
- Poor Recall: Only 7-25% of heart disease cases detected
- F1-Score: 0.12
- AUC: 0.74 (with 10 features)

#### After Undersampling:

- Balanced Accuracy: 70%
- Improved Recall: 66% heart disease detection
- F1-Score: 0.69
- More reliable predictions overall

#### GridSearch Results:

- Parameter Testing:
  - max\_depth: [None, 10, 20, 30, 40, 50]
  - min\_samples\_split: [2, 5, 10, 20]
  - min\_samples\_leaf: [1, 2, 5, 10]
  - criterion: ['gini', 'entropy']
- Key Finding: Simpler trees (depth=10) with gini criterion performed best, achieving 0.91 crossvalidation accuracy while avoiding overfitting

#### **Additional Classifiers**

#### **Random Forest:**

- Accuracy: 0.90 -> 0.73
- F1-Score: 0.18 -> 0.74
- AUC: 0.78 -> 0.80
- Precision: 0.38 -> 0.72
- Recall: 0.12 -> 0.77

#### **Logistic Regression:**

- Accuracy: 0.91 -> 0.76
- F1-Score: 0.17 -> 0.76
- AUC: 0.83 -> 0.83
- Precision: 0.54 -> 0.75
- Recall: 0.10 -> 0.78

#### KNN:

- Accuracy: 0.90 -> 0.71
- F1-Score: 0.19 -> 0.72
- AUC: 0.70 -> 0.77
- Precision: 0.36 -> 0.71
- Recall: 0.13 -> 0.74

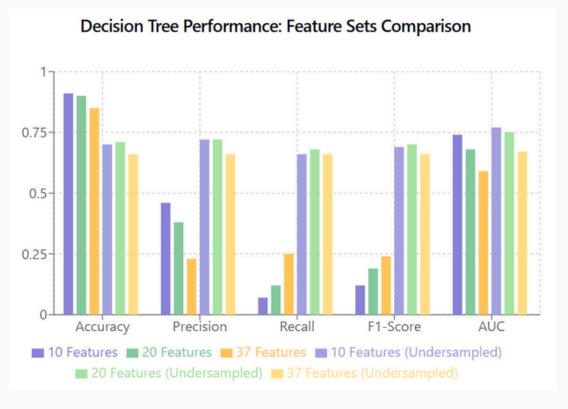
#### **Key Cross-Model Findings:**

#### 1. Feature Selection Impact

- 10 Features: Often insufficient information
- 20 Features: Optimal for most models
- 37 Features: Diminishing returns/overfitting

#### 2. Undersampling Effects

- All models showed significant improvement
- Recall improved by 50-60% across models
- F1-scores improved from ~0.15 to ~0.70



## CLUSTERING

#### **Objective**

• The objective of clustering was to group patients or data points into two distinct clusters—those with heart disease ("Yes Heart Disease") and those without heart disease ("No Heart Disease")—based on shared characteristics within the dataset.

#### Our Approach:

Primary algorithm: K-Means

Dimensionality reduction with PCA - to simplify visualization and reduce computational complexity for clustering Evaluation Metrics: Silhouette Analysis, Elbow Method

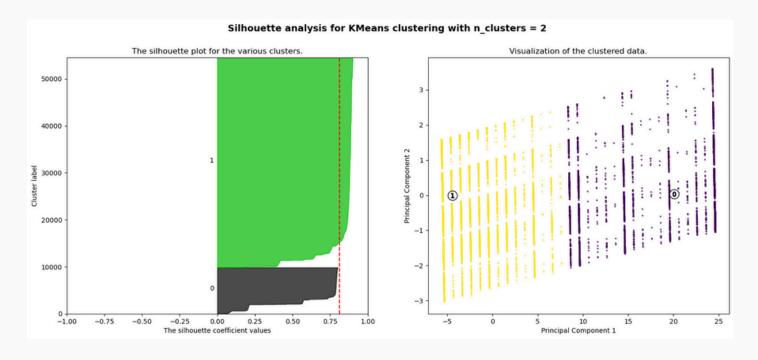
#### **Results**

Best Silhouette Score: 0.811 for k=2.

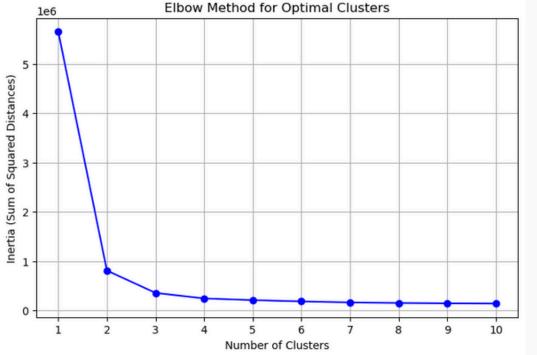
Cluster A (No Heart Disease): 90% purity.

Cluster B (Yes Heart Disease): 26% purity (due to overlap).

Overall Clustering Accuracy: 82%.



Silhouette Plot: Optimal k=2 clusters



Elbow Method Plot for the optimal no. of clusters

#### **Additional Algorithms**

#### Gaussian Mixture Models (GMM):

- Explored soft clustering but increased overlap.
- Using BIC (Bayesian Information Criterion) and Silhouette Scores, the optimal number of clusters was determined to be 2.

### MLP

#### MLP configuration:

Input Layer: Flattening 2D array

Hidden Layers: 200, 100, 32 Dropout Rate: 0.7, 0.6, 0.6

Output Layer: 4

#### **Observation:**

#### Detecting an Abnormal Heartbeat (HB)

 Had a high rate of false positives with PMI and Normal and misses 33% of cases with abnormal heartbeat

#### **Detecting Myocardial Infarction (MI)**

 Very low false positive rate and correctly identifies all instances of MI

### Detecting Patients with a History of Myocardial Infarction (PMI)

• High rate of false positives for HB, a few for HB and misses 29% of PMI

### Detecting Patients with Normal Heart Health (Normal)

• High rate of false positives, misses fewer cases of normal cases

#### **Performance:**

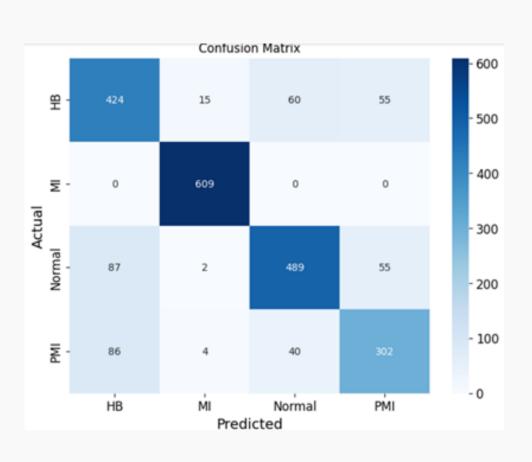
The model struggled with overfitting, as can be seen with the results between the training, validation and test accuracy.

Training Accuracy: 96.3%
·Validation Accuracy: 87.2%

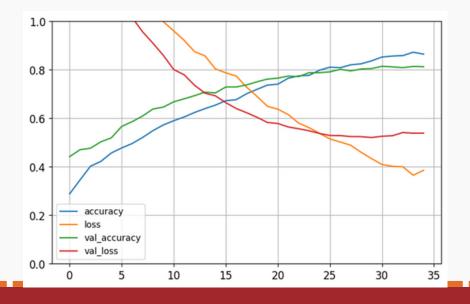
·Test Accuracy: 85.4%

#### **Conclusion:**

The model excels at identifying cases of Myocardial Infarction; however, it misses quite a high number of Abnormal Heartbeats, and Patients with a history of MI. There is confusion between PMI and HB, but also a high rate of false positives for normal ECGs. Therefore, the model is good at identifying heart attacks but, has an issue identifying patients with heart problems.



Class	Precision	Recall	F1-score	Support
НВ	0.78	0.67	0.72	554
MI	0.97	1	0.99	609
Normal	0.76	0.84	0.79	633
PMI	0.71	0.71	0.71	432
Accuracy			0.81	2228
macro avg	0.81	0.8	0.8	2228
weighted avg	0.81	0.81	0.81	2228



### CNN

#### **CNN** configuration:

Convolutional layers: 3

Filter sizes: **(32, 64, 128)** 

Dense layer: **128 neurons** 

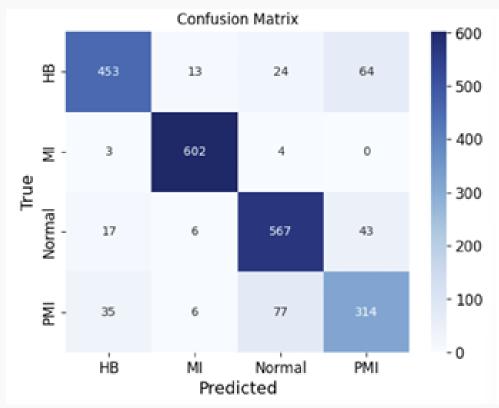
Activation function: ReLU

Dropout rate: 0.5

Output layer: **Softmax** 

Train and Validation split: 80%

Training and 20% validation



#### **Optimizations made:**

- Increased dropout rate: 0.3 and 0.4 for Convolutional layers, 0.5 for dense layer
- Data Augmentation: Rotation, Zoom, Horizontal flipping.
- Reduced learning rate: 1×10<sup>-4</sup>.

Metric	MLP Baseline	CNN Baseline	Optimized CNN
Training Accuracy	96.3%	99.9%	99.9%
Validation Accuracy	87.2%	90.2%	87.6%
Test Accuracy	85.4%	87.0%	TBD

