Group 3 Progress Report:
Heart Disease Prediction using Machine Learning

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1 Introduction

This project aims to use ML method to predict the likelihood of heart disease based on eleven clinical and demographic features. Heart disease continues to be a major global health concern, and early detection is crucial for reducing severe outcomes. As outlined in our project proposal, the goal of this work is to develop a reliable classification model that can identify high-risk patients using routinely collected medical measurements.

In this progress report, we will discuss the steps completed so far, including dataset preprocessing, feature encoding, and the development of a Chi-Square + PCA feature-engineering pipeline. We also present initial results from models such as SVM, Logistic Regression, and Random Forest, and outline feedback from the TA along with our planned next steps.

Building on these prior studies, our project adopts a supervised learning pipeline that combines Chi-square feature selection and Principal Component Analysis (PCA) with an RBF-kernel SVM classifier. We first apply a column transformer with median imputation and standardization for numerical features, and most-frequent imputation with one-hot encoding for categorical features; Then we use a MinMaxScaler followed by `SelectKBest` with the Chi-square statistic to keep the top-k informative features, and apply PCA with the number of components chosen using the Kaiser criterion [5, 6]. The low-dimensional representation is fed into an RBF-SVM, and the full pipeline is evaluated on the Kaggle Heart Failure Prediction dataset [4] using stratified k-fold cross validation, reporting accuracy, precision, recall, F1-score, and AUC as in previous work.

2 Related Work

Our progress in this project builds directly on the foundation built in Milestone01, where we considered both the clinical motivation and the technical approaches. In that proposal, we discussed the limitations of traditional diagnostic methods and highlighted the importance of ML models that can identify multi-feature interactions such as age, cholesterol level, chest pain type, and ECG-related measurements, which observations align with prior work showing that heart disease prediction is well suited to ML due to its multivariate and non-linear nature.

As we talked about in M1, several existing studies have explored this predictive task using classical and modern machine learning techniques. Logistic regression remains a common baseline method, as demonstrated by Awan [3], who achieved approximately 85% accuracy on the Kaggle using minimal feature engineering. More advanced pipelines integrate supervised feature selection and dimensionality reduction. The Chi-Square + PCA framework proposed by Gárate-Escamila et al. [5] achieved up to 99% accuracy on multiple UCI heart disease datasets, motivating our decision in Milestone 1 to incorporate both Chi-Square filtering and PCA into our own preprocessing pipeline.

Moreover, foundational statistic work such as Kaiser factor analysis criterion [6] provides justification for retaining only principal components with eigenvalues greater than one, a rule we apply in our dimensionality reduction stage. Other work has examined optimization strategies for medical classification models, including scalable L1-regularized training [2] and multi-task predictive structure learning [1], which highlight broader approaches to improving generalization when datasets are small—one of the challenges noted in our proposal.

3 Dataset and Preprocessing

This section will introduce the raw dataset we used, and how we clean and process it.

3.1 Dataset Description

The dataset we used in this project is the *Heart Failure Prediction Dataset* published by Fedesoriano on Kaggle [4]. It contains **918 patient observations** and **12 attributes**, including 11 clinical predictor variables and one binary target label indicating the presence of heart disease. This dataset was designed to support research on early detection of cardiovascular risks, particularly heart failure, which remains one of the leading causes of global mortality.

The dataset includes a mixture of demographic features (Age, Sex), physiological measurements (like RestingBP, Cholesterol, MaxHR), and exercise-induced ECG-related metrics (ExerciseAngina, Oldpeak, ST_Slope). Those attributes show common risk factors used in medical diagnostics for cardiovascular disease and have been widely adopted in machine learning models for clinical prediction tasks.

A complete list of raw features and their corresponding descriptions is provided in Table 2.

Feature	**Description**
Age	Age of patient (years)
Sex	Biological sex (M/F)
ChestPainType	Chest pain type (ATA, NAP, ASY, TA)
RestingBP	Resting blood pressure (mm Hg)
Cholesterol	Serum cholesterol (mg/dL)
FastingBS	Fasting blood sugar (0/1)
RestingECG	Resting ECG results (Normal, ST, LVH)
MaxHR	Maximum heart rate achieved
ExerciseAngina	Exercise-induced angina (Y/N)
Oldpeak	ST depression value induced by exercise
ST_Slope	Slope of ST segment (Up, Flat, Down)
HeartDisease	Target label (1 = disease, 0 = healthy)

Table 1: Raw dataset features.

Originally, the dataset contains:

$$\textbf{918 samples} \quad \times \quad \textbf{11 features}.$$

3.2 Feature Preprocessing

The feature matrix X was constructed by removing the target column and retaining the remaining 18 input attributes. Since the dataset includes both numerical and categorical variables, several preprocessing steps were required to convert all values into a machine-learning- ready numeric form.

Binary Encoding Three features, namely Sex, ExerciseAngina, and FastingBS contain only two possible values and were mapped directly to 0/1 following our preprocessing script:

- **Sex:** `M` $\rightarrow 1$, `F` $\rightarrow 0$
- **ExerciseAngina:** `Y` $\rightarrow 1$, `N` $\rightarrow 0$
- **FastingBS:** preserved as integer `0/1`

Ordinal Mapping of Multi-Class Features Three categorical features contain more than two categories. In the stored processed dataset (`X_encoded.csv`), they were converted to integer codes according to predefined mappings:

$$\text{ChestPainType: } \{\texttt{ATA}, \texttt{NAP}, \texttt{ASY}, \texttt{TA}\} \rightarrow \{0, 1, 2, 3\},$$

$$\text{RestingECG: } \{\texttt{Normal}, \texttt{ST}, \texttt{LVH}\} \rightarrow \{0, 1, 2\},$$

$$\text{ST\_Slope: } \{\texttt{Up}, \texttt{Flat}, \texttt{Down}\} \rightarrow \{0, 1, 2\}.$$

These mappings avoid string-based ambiguity and ensure that all feature columns are numeric at the preprocessing stage.

In contrast from progress report, we adopted feedback from TA to change our way of presenting One-Hot Encoding, instead of present them in one single column to split them across the columns for every single category.

Therefore, after spliting them into one-hot encoding, the final dataset shape changes to 918 x 18.

Feature	Description
Age	Age of patient (years)
Sex	Biological sex (M/F)
ChestPainType_0	ATA
ChestPainType_1	NAP
ChestPainType_2	ASY
ChestPainType_3	TA
RestingBP	Resting blood pressure (mm Hg)
Cholesterol	Serum cholesterol (mg/dL)
FastingBS	Fasting blood sugar (0/1)
RestingECG_0	Normal
RestingECG_1	ST
RestingECG_2	LVH
MaxHR	Maximum heart rate achieved
ExerciseAngina	Exercise-induced angina (Y/N)
Oldpeak	ST depression value induced by exercise
ST_Slope_0	Up
ST_Slope_1	Flat
ST_Slope_2	Down
HeartDisease	Target label (1 = disease, 0 = healthy)

Table 2: One-Hot Encoding Table.

3.3 Target Label Extraction

The target label `HeartDisease` is a binary indicator representing whether a patient shows signs of heart disease. We extract this column and converted it to integer form using:

$$y = \texttt{df['HeartDisease'].astype(int).}$$

The resulting is a one-dimensional vector , which was saved as `processed/y.csv` for all downstream training and evaluation.

The cleaned dataset was saved to `processed/X_encoded.csv`, and the corresponding feature names were exported to `processed/feature_names.txt` for reproducibility.

4 Model Inputs (Features)

During our data preprocessing phase, we utilize `scikit-learn` built-in function `pipeline` to transform our data before feeding into Machine Learning Model The dataset has both numerical and categorical features,

in the previous part we mentioned that for each numerical part we standardized them, while for categorical part we used one-hot encoding to transform them into vectors. In result, we have total 18 features after

preprocessing, including 8 numerical features and 10 categorical features "(One-Hot Encoding)". Something

different from progress report, as we realize our dataset is way too easy compare to the heart diease dataset from the paper. So, this time we decided to only use PCA method as our feature engineering method, instead of using Chi-square + PCA method [5].

- **PCA:** After feature selection, we then applied Principal Component Analysis (PCA) to reduce the dimensionality of the selected features. PCA works by identifying the directions (principal components) in which the data varies the most, and projecting the data onto these directions.

  To determine the number of principal components to retain, we adopt the **Kaiser criterion** [6]. This rule suggests keeping only components with eigenvalues greater than 1.0.

  After doing a experiments of calculating eigenvalues for every single increase of principal components, we found that the first five components have eigenvalues greater than 1.0. Thus, we decided to retain five principal components for our final feature representation.

Hence, each patient sample is represented as a compact (data, 5) feature vector summarizing the most informative physiological and categorical characteristics. This final feature set is then used as input to our machine learning model.

5 Model Implementation

We have implemented a supervised learning pipeline for binary classification of heart disease presence. Our main model is a **Support Vector Machine (SVM)** with a **Radial Basis Function (RBF)** kernel, implemented using the `scikit-learn` library. This kernel choice allows the decision boundary to be nonlinear, which is important given the heterogeneous mixture of categorical and numerical medical features in the dataset.

Loss Function:

$$\min_{\mathbf{w},b} \frac{1}{2}\|\mathbf{w}\|^2 + C\sum_{i=1}^{n} \max(0, 1 - y_i(\mathbf{w}^\top \phi(\mathbf{x}_i) + b))$$

where C is the penalty parameter controlling the trade-off between the margin size and misclassification tolerance, and $\phi(\cdot)$ denotes the nonlinear mapping induced by the **RBF Kernel:**

$$K(\mathbf{x}_i, \mathbf{x}_j) = \exp(-\gamma \|\mathbf{x}_i - \mathbf{x}_j\|^2)$$

The model was optimized using the `libsvm` implementation, which employs a coordinate descent solver with kernel caching for efficiency.

To evaluate our implementation, we compared SVM–RBF against two baseline models:

- **Logistic Regression:** This baseline model was chosen from kaggle [3], where the author didn't use features selection or dimensionality reduction, and he was able to achieve 85% accuracy.
- **Random Forest:** From this paper [5], the author has 98% accuracy by using Random Forest with Chi-PCA method. However, he used a 74 features and around 1000 datapoint of heartdiease dataset from UCL.

With SVM-RBF, we evaluate it's accuracy by using cross-validation, and we was only able to achieve 86% of accuracy.

We then use Random Forest and Logistic Regression as our model, Randomforest was able to achieve 87% accuracy, while Logistic Regression was able to achieve 85% accuracy.

Varies reason can be introduces in here, such as different dataset, the quality of dataset, or minor changes in the preprocessing phase that effect the data values meaning.

In future iterations, we plan to explore a **neural network architecture** (e.g., a multi-layer perceptron) to capture more complex feature interactions and potentially improve generalization performance. We also intent to change the detail in our preprocessing phase, such as using different order, or different preprocessing tools to present the data in a better way.

6 Evaluation Strategy and Results

In turns of method evalution, we first split the dataset into training and validaion. Training dataset with 80% of the data, while validation dataset with 20% of the data.

6.1 Evaluation Method

In our evaluation stage, we use stratified K-fold cross-validation. The reason for this choice is that our dataset contains only 918 patient records, and using a fixed train/validation/test split may lead to overfitting due to the small number of data points.

6.2 Metrics

SVM with RBF Kernel Model Performance :

Same as progress report, we have in total six metrics to evaluate our model performance. The metrics used in this project include **accuracy, recall, precision, F1-score, and AUC–ROC and Confusion Matrix**. Our rationale for choosing these metrics is as follows. First, in disease prediction, precision (closely related to Type II error) is especially important. Hospitals cannot afford to misclassify a patient with the disease as healthy. Therefore, minimizing false negatives is crucial. In addition, we use the AUC–ROC curve because it is an effective way to evaluate the overall performance of a binary classifier.

6.3 Results

The figures are listed in the last page, please check them out

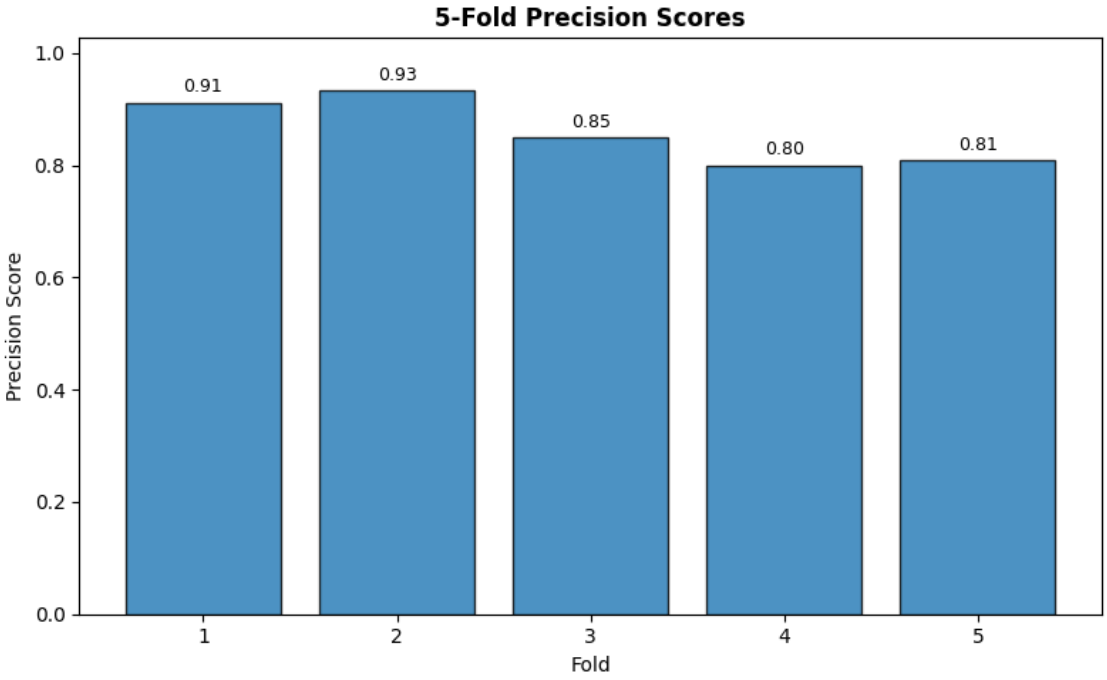

Figure 1: 5-fold precision scores.

```
===== K-Fold Cross Validation Results =====
Accuracy : 0.8627
Recall   : 0.9001
Precision: 0.8610
F1-score : 0.8785
============================================
```

Figure 2: Summary metrics across folds.

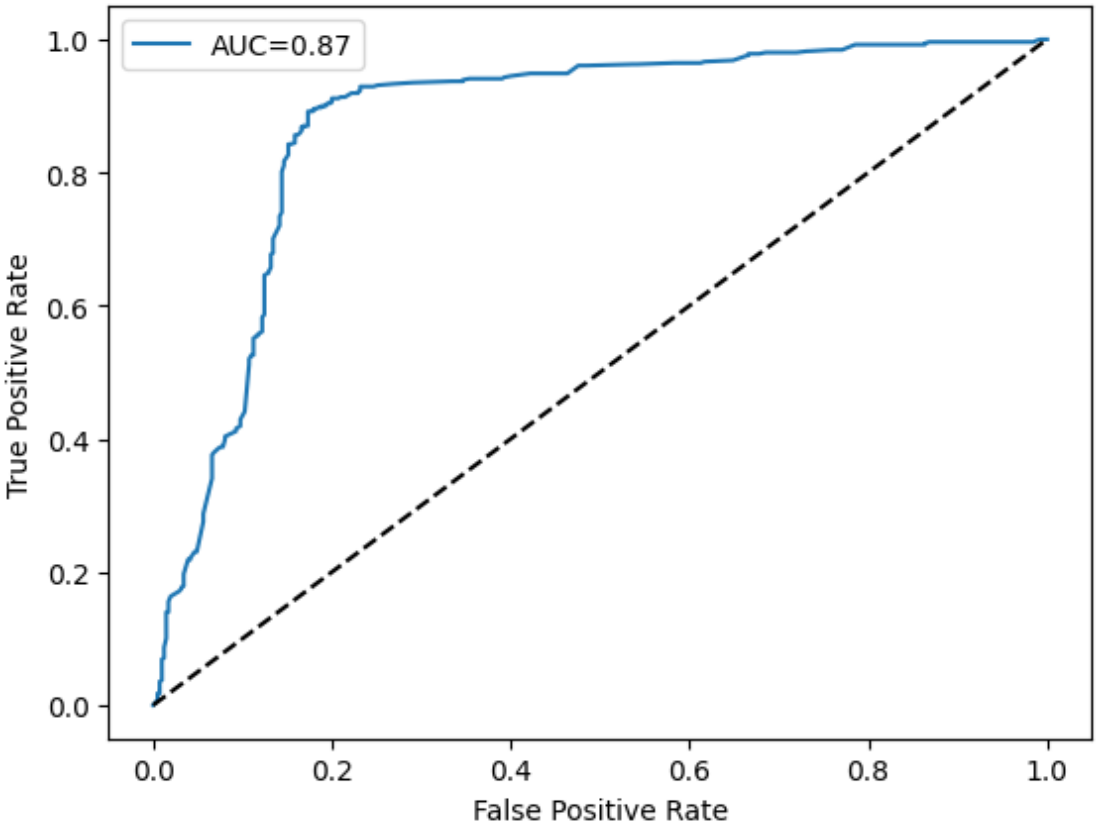

Figure 3: AUC–ROC curves.

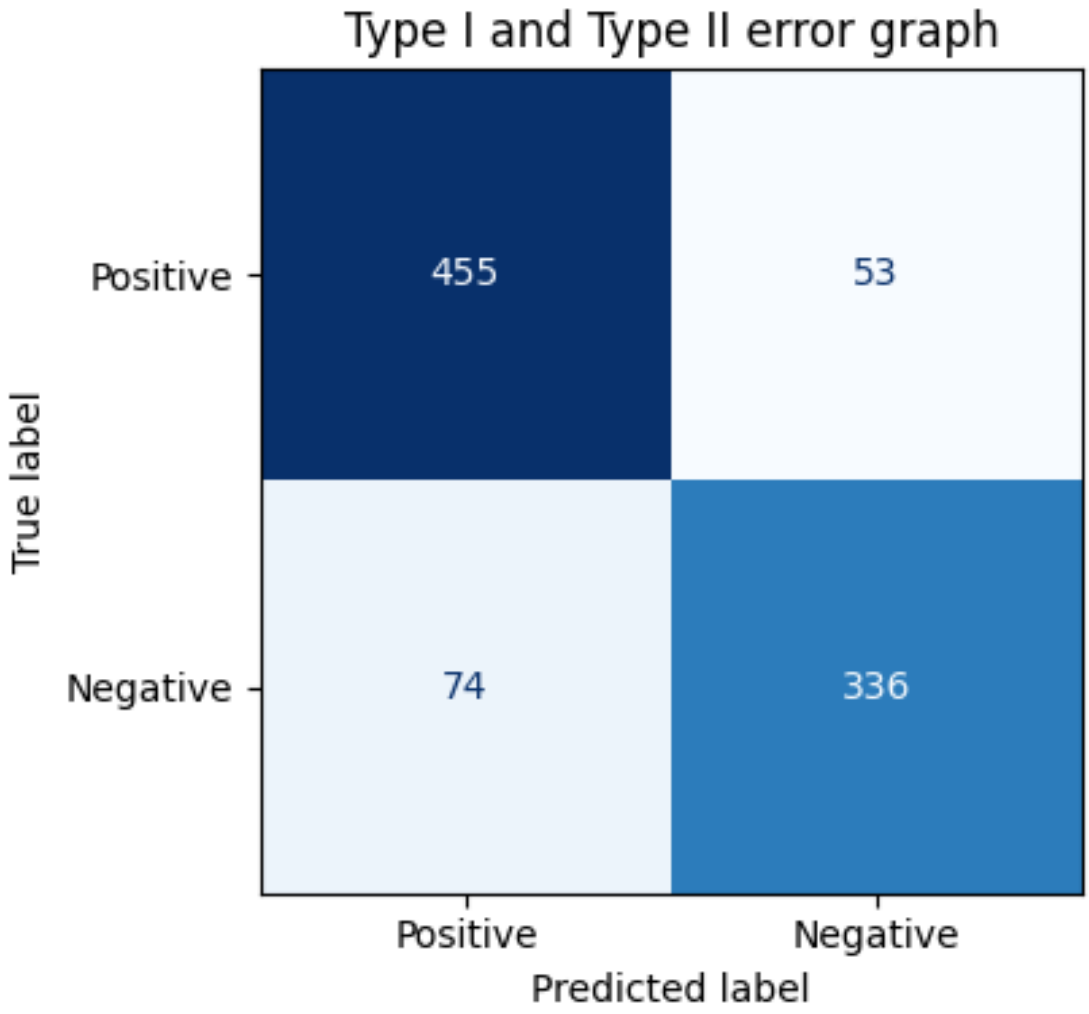

Figure 4: Confusion matrices.

Team Contributions

Jeffrey Lin: Section 4 to 5 and implementation of model
ZiDi Yao: Section 1 to 3 and raw data introduction and processing
Ke Ma: Section 6 to 7 and data validation and clean

References

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