

Machine Learning models interpretability using LIME: Multiple Cardio-Vascular Disease Dataset

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Abstract—Machine Learning (ML) techniques have become essential in improving healthcare systems by leveraging computers’ computational power and doctors’ diagnostic expertise. This paper presents a pipeline for heart disease classification using ML, specifically focusing on data exploration, preprocessing, model training, evaluation, and interpretation of individual predictions using Local Interpretable Model-Agnostic Explanations (LIME). We utilize the Heart Failure Prediction dataset, which contains clinical and demographic attributes of patients, to develop accurate prediction models. We employ Support Vector Machines (SVM) and Multiple Kernel Learning SVM with K-fold cross-validation as our classification models. The performance of these models is evaluated using metrics such as accuracy, sensitivity, and area under the curve (AUC). Furthermore, we utilize LIME to provide interpretable explanations for individual predictions made by the model, highlighting the essential features contributing to the decisions. Our results demonstrate the potential of ML techniques in improving heart failure prediction and emphasize the importance of model interpretability in building trust and understanding the behavior of ML models.

I. INTRODUCTION

Machine Learning (ML) has emerged as a critical component in improving healthcare systems, addressing the challenges faced by the healthcare system. The integration of ML leverages the computational power of computers and the diagnostic expertise of doctors to identify patterns and assist medical professionals in making accurate decisions. ML algorithms excel in detecting complex patterns and making informed decisions. These techniques can potentially reduce healthcare costs, enhance patient-clinician communication, and predict wait times in emergency departments. By employing various ML techniques such as Support Vector Machines, Naive Bayes Classification, Decision Trees, K-Nearest Neighbor, Fuzzy Logic, and CART, healthcare professionals can optimize diagnosis, treatment plans, and resource allocation [3].

Machine learning models have gained widespread adoption, but their lack of interpretability often poses challenges. Understanding the reasons behind predictions is crucial for assessing trust, especially when making decisions based on predictions or deploying new models. Fig. 1 illustrates the pipeline analysis of our work. In this work, we introduce LIME, a novel explanation technique that offers interpretable and faithful explanations for the predictions of any classifier.

LIME achieves this by locally approximating the prediction using an interpretable model [2] [8].

In this paper, we present a pipeline for heart disease classification, including data exploration, preprocessing, model training, evaluation, and interpretation of individual predictions using LIME. Then we provided a series of steps to analyze and classify heart disease using a machine learning approach. First, we imported the necessary libraries and loaded the heart disease dataset. Then we explored the dataset by visualizing its structure and checking for missing values. Categorical variables are selected and analyzed using count and box plots to understand their distribution and relationship with other variables. Next, the code preprocesses the data by encoding

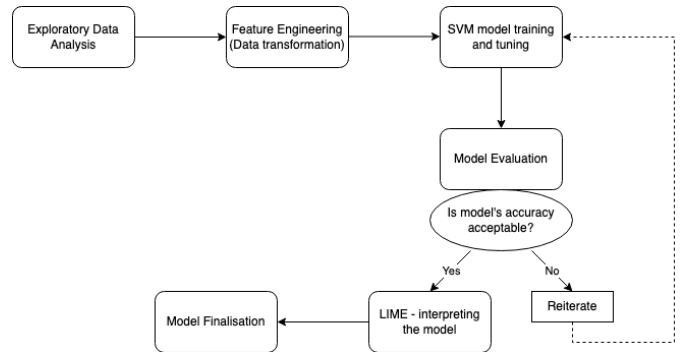


Fig. 1: Block Scheme of Pipeline Analysis

categorical variables using label encoding and standardizes the input features using feature scaling. The encoded data is split into training and testing sets. Then we build a support vector machine (SVM) model and evaluate its performance using accuracy as the metric. Additionally, we implemented a multiple-kernel learning (MKL) approach with SVM that performs K-fold cross-validation to optimize the model’s performance. The code calculates various metrics such as accuracy, sensitivity, and area under the curve (AUC) for evaluation. Finally, we utilized the LIME (Local Interpretable Model-Agnostic Explanations) to provide explanations for individual predictions made by the model. The explanations highlight the critical features contributing to the model’s decisions [9].

II. BACKGROUND AND RELATED WORK

Heart failure is a critical cardiovascular condition affecting millions of individuals worldwide. Early identification and prediction of heart failure can significantly improve patient outcomes and inform proactive healthcare interventions. The Heart Failure Prediction dataset offers a valuable resource to explore various risk factors associated with heart failure and build accurate prediction models. Heart failure prediction has gained significant attention from researchers and healthcare practitioners in recent years. Various studies have explored machine learning techniques to develop accurate prediction models. These studies highlight the potential of machine learning techniques in improving heart failure prediction and provide valuable insights into the key predictive factors associated with this cardiovascular condition [1].

Early examples like MYCIN and PXDES in medical knowledge systems emerged in the 1970s and 1980s, relying on expert input to provide decisions and predictions. More recently, the application of modern AI models has demonstrated promising results, including identifying COVID-19 from chest X-rays. Leveraging AI in the medical domain offers several advantages, such as the ability to predict future heart failure. Numerous AI models, including Logistic Regression, K-Nearest Neighbors (KNN), Support Vector Machines (SVM), Decision Trees, Forest Trees, and Artificial Neural Networks (ANN), have been employed for this purpose. However, a critical challenge arises from the need for more transparency in these models, as users are often unaware of the underlying reasons behind the generated decisions. To address this issue, Explainable Artificial Intelligence (X-AI) has emerged as a field that aims to provide explanations alongside AI model decisions. For models that lack inherent interpretability or are difficult to modify, ad-hoc explainer techniques like LIME (Local Interpretable Model-agnostic Explanations) and SHAP (Shapley Additive exPlanations) have been proposed. LIME provides explanations by training an interpretable model locally around the prediction, while SHAP calculates the contribution of each feature to the final decision [4] [11].

To provide interpretable and faithful explanations for the predictions made by any classifier or regressor, we are presented with LIME (Local Interpretable Model-agnostic Explanations). LIME approximates the local behavior of the classifier around a specific prediction using an interpretable model. We can also mention SP-LIME, a method for selecting representative instances with explanations to address the challenge of trusting the model. The utility of explanations is demonstrated through experiments, showing the impact of explanations on trust-related scenarios, such as deciding whether to trust a prediction, comparing models, improving an untrustworthy classifier, and identifying instances where a classifier should not be trusted. It is essential to highlight the importance of explanations in building trust and understanding the behavior of machine learning models, bridging the gap between black-box models and human interpretability [2].

III. MATERIALS AND METHODS

A. Dataset

The Heart Failure Prediction dataset, sourced from Kaggle, provides a rich collection of clinical and demographic factors, allowing researchers and healthcare professionals to investigate the potential predictors of heart failure and develop effective prediction models.

The Heart Failure Prediction dataset is a comprehensive collection of 13 clinical and demographic attributes for 299 patients with suspected heart failure. The data was compiled from patients admitted to a renowned cardiovascular institute, ensuring the reliability and relevance of the information. This dataset contains numerical, categorical, and binary features, providing a diverse set of variables for analysis. The dataset includes the following attributes, also reported in Table I:

- Age: The age of the patient (years).
- Anaemia: A binary variable indicating the presence of anemia (0: absence, 1: presence).
- High Blood Pressure: A binary variable indicating the presence of high blood pressure (0: absence, 1: presence).
- Creatinine Phosphokinase (CPK): The level of CPK enzyme in the blood (mcg/L).
- Diabetes: A binary variable indicating the presence of diabetes (0: absence, 1: presence).
- Ejection Fraction: The percentage of blood leaving the heart during contraction (%).
- Platelets: The platelet count in the blood (kilo platelets/mL).
- Sex: The gender of the patient (0: female, 1: male).
- Serum Creatinine: The creatinine level in the blood (mg/dL).
- Serum Sodium: The sodium level in the blood (mEq/L).
- Smoking: A binary variable indicating smoking habits (0: non-smoker, 1: smoker).
- Time: The follow-up period in days.
- Death Event: A binary variable indicating mortality within the follow-up period (0: survival, 1: deceased).

The generated visualizations of Figure 2 provide valuable insights into the relationship between different attributes, namely Resting Electrocardiographic Results (RestingECG), Exercise-induced Angina (ExerciseAngina), and Chest Pain Type (ChestPainType), and their association with heart disease, namely 0: survival and 1: deceased.

The Heart Failure Prediction dataset is highly significant in cardiovascular medicine research, offering opportunities to explore the relationships between clinical and demographic factors and heart failure occurrence, prognosis, and mortality. By applying advanced analytical techniques and machine learning algorithms, researchers can develop predictive models contributing to early detection and intervention strategies, ultimately improving patient care and outcomes. The dataset's diverse range of attributes allows for an in-depth investigation of the intricate interactions between factors and their influence on heart failure. By utilizing this resource, healthcare professionals can enhance their understanding of heart failure

TABLE I: Heart Failure Prediction Dataset Overview

ID	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	40	M	ATA	140	289	0	Normal	172	N	0.0	Up	0
1	49	F	NAP	160	180	0	Normal	156	N	1.0	Flat	1
2	37	M	ATA	130	283	0	ST	98	N	0.0	Up	0
3	48	F	ASY	138	214	0	Normal	108	Y	1.5	Flat	1
4	54	M	NAP	150	195	0	Normal	122	N	0.0	Up	0

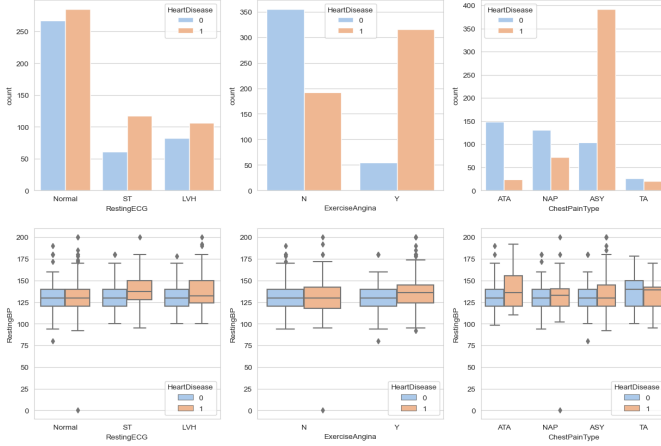


Fig. 2: Exploratory Data Analysis

and advance toward more personalized and effective treatment approaches.

B. Data preprocessing

We performed a data preprocessing step known as label encoding. The results are shown in Table II. It involves converting categorical variables in a dataset into numeric labels. In this case, the 'Sex', 'ChestPainType', 'RestingECG', 'ExerciseAngina', and 'ST_Slope' columns are encoded using a technique that assigns unique numerical values to each category, enabling subsequent analysis and modeling tasks that require numeric inputs.

Next, we calculated the Spearman correlation coefficients between the columns of the dataset, and we stored them in a correlation. Then, we computed the p-values for the correlations. The absolute values of the correlation coefficients are taken, and the data is converted to numeric types. This preprocessing step helps identify and remove highly correlated features, reducing multicollinearity and improving the performance of machine learning models.

Then we proceeded with the standardization of the input features. Standardization is transforming the features in a way that they have zero mean and unit variance. It helps in bringing the features to a similar scale. The features are extracted from the dataset and then transformed using a standardization technique. This step ensures that all features are on a comparable scale and ready for further analysis or modeling.

C. Machine Learning Models

In this section, we employ machine learning models to classify heart failure patients based on the available dataset.

We evaluate the performance of two models: Support Vector Machines (SVM) and Multiple Kernel Learning SVM with K-fold cross-validation.

- **Support Vector Machines (SVM)** We first train an SVM model with a linear kernel using K-fold cross-validation. We set the number of folds, k , to 10 and utilize the StratifiedKFold function for cross-validation. The dataset is split into training and validation sets for each fold. Within each fold, we instantiate an SVM classifier with a linear kernel and train it on the training set. We then make predictions on the validation set using the trained model. Additionally, we compute performance metrics such as accuracy, sensitivity, and area under the ROC curve (AUC) for the validation predictions. After iterating through all folds, we calculate the average accuracy, average sensitivity, and average AUC by taking the mean of the performance metrics obtained from each fold. These metrics provide an overall evaluation of the SVM model's performance. Next, we train the final SVM model on the entire training set and evaluate its performance on the test set. We make predictions on the test set and compute accuracy, sensitivity, and AUC metrics accordingly. The obtained metrics represent the performance of the SVM model on unseen data.

- **Multiple Kernel Learning SVM (MKL SVM)** with K-fold Cross-Validation

In addition to the SVM model, we employ the Multiple Kernel Learning (MKL) SVM technique, which combines different kernel functions to improve classification performance [6], [7]. Similar to the previous approach, we use K-fold cross-validation with $k = 10$ and the StratifiedKFold function. There have been studies exploiting Multiple Kernel SVM models in Heart Disease prediction as well [5]. We create three SVM classifiers within each fold with different kernel functions: linear, radial basis function (RBF), and polynomial. These classifiers are combined using the VotingClassifier with a "soft" voting scheme. We train this MKL SVM model on the training set and make predictions on the validation set. We compute accuracy, sensitivity, and AUC metrics for each fold and store them for further analysis. After completing all folds, we calculate the average accuracy, average sensitivity, and average AUC to assess the overall performance of the MKL SVM model. Like the SVM approach, we train the final MKL SVM model on the entire training set and evaluate its performance on the test set. We calculate the test predictions' accuracy, sensitivity, and AUC metrics, indicating the model's performance on unseen data.

TABLE II: Data Normalized

ID	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	40	1	1	140	289	0	1	172	0	0.0	2	0
1	49	0	2	160	180	0	1	156	0	1.0	1	1
2	37	1	1	130	283	0	2	98	0	0.0	2	0
3	48	0	0	138	214	0	1	108	1	1.5	1	1
4	54	1	2	150	195	0	1	122	0	0.0	2	0

D. LIME

Local Interpretable Model-Agnostic Explanations (LIME) is proposed to explain any classifier or regressor by approximating it locally with an interpretable model [2]. LIME conveys several desired characteristics as a method of Machine Learning Models explanation. In general, LIME aims to have a faithful and interpretable explainer. The explanation obtained by LIME is minimizing the following:

$$\xi(x) = \arg \min_{g \in G} \mathcal{L}(f, g, \pi_x) + \Omega(g)$$

where x are original features, f - a predictor, g - explanation model, π - a proximity measure between an instance z to x , so as to define locality around x , $\mathcal{L}(f, g, \pi_x)$ - a measure of unfaithfulness of g in approximating f in the locality defined by π_x , and $\Omega(g)$ - a measure of model complexity of explanation g [2].

The LIME model provides a possibility to explain individual predictions of the developed classifiers. In addition, it depicts how the features used for ML model training drive a specific decision - a so-called measure of the importance of each feature. Each possible class is explained separately for each prediction, so we can also explore the potential features that drive the classifier in the wrong direction in the probability of being assigned to each class.

In our study, we used the LIME technique to interpret the best-performing classifier to outline the essential features that predict heart failure in a subject. In order to generalize the results of LIME analysis, we performed LIME interpretation on all test subjects and averaged out the results for each feature. Before calculating an average, we first split the test predictions into four groups - True Positive (TP - heart failure was predicted correctly), True Negative (TN - the healthy subject was identified correctly), False Positive (FP - the model wrongly labeled the healthy subject to be a patient with heart disease), and False Negative (FN - a patient was wrongly labeled as a healthy subject). Based on this separation, we wanted to investigate how our model decides which class to assign a patient in cases the prediction is correct (TP, TN) and what drives our model to mispredict classes (FP, FN).

IV. RESULTS AND DISCUSSION

A. Statistical Analysis

In order to evaluate the possible relationship of the provided features with the target variable, we exploited the Spearman correlation as a primary measure. The Spearman correlation coefficient was calculated for each pair (f_i, f_j) , where f_i

and f_j are the dataset features. Each coefficient was evaluated using p-value, where H_0 hypothesis, correlation is not statistically significant, was rejected whenever $p_{(i,j)} \leq 0.1$ and accepted otherwise. Then, considering the acceptable correlation coefficient ($SCC_{(i,j)} > 0.2$), where $SCC_{(i,j)}$ is Spearman Correlation Coefficient for (f_i, f_j) , meaning at least weak correlation is present, and low p-value, were the deciding factors evaluating the features' association with the target.

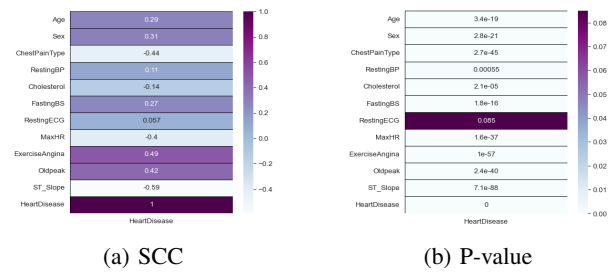


Fig. 3: Spearman Correlation matrix w.r.t. HeartDisease label.

Figure 3 shows the Spearman Correlation results concerning a group correspondence label. We may see that almost all of the features possess weak to moderate correlation measures with low p-values that prove the statistical significance of the calculations. At the same time, the 'RestingECG' feature has the highest p-value with the lowest correlation coefficient meaning that the coefficient itself does not have a meaningful contribution to the whole picture of the dataset. During the training and testing procedures, we discovered that getting rid of the 'Cholesterol' and 'RestingBP' is lowering our models' performance statistics by approximately 2% in terms of accuracy. Moreover, implementing LIME has shown a positive influence of these two features on the model's decision. Thus, at that point, we decided to move forward with classification utilizing the dataset with all the presented features.

B. Machine Learning Models

First, the SVM model was trained and evaluated using stratified K-fold cross-validation with ten folds. The average accuracy, sensitivity, and area under the curve (AUC) were calculated based on the validation sets. Comparing the SVM and MKL SVM models, both demonstrated high accuracy, sensitivity, and AUC values, indicating their effectiveness in classifying heart failure patients. Incorporating LIME into the analysis enhances our understanding of the SVM and MKL SVM models, providing insights into their decision-making processes for the classification of heart failure. These findings contribute to the interpretability and transparency of

the models, which are crucial factors for their adoption and trust in real-world applications. This knowledge contributes to the overall understanding and trustworthiness of the models, further enhancing their utility in aiding early detection and diagnosis of heart failure [2].

The performance comparison between the two models reveals that the MKL SVM model outperforms the SVM model in terms of average accuracy, sensitivity, and area under the curve (AUC) metrics. These results can be seen in Table III. The superior performance of the MKL SVM model can be attributed to its ability to leverage multiple kernels to capture diverse patterns and information present in the data. By combining different kernel functions, the MKL SVM model can effectively learn and integrate information from various aspects of the input features, resulting in improved classification accuracy and discriminatory power.

TABLE III: Performance Comparison: SVM vs. MKL SVM

Model	Avg. Acc.	Avg. Sens.	Avg. AUC	Test Acc.	Test Sens.	Test AUC
SVM	0.858	0.885	0.912	0.837	0.822	0.898
MKL SVM	0.852	0.880	0.919	0.864	0.850	0.921

C. LIME

In addition to the evaluation of the Support Vector Machine (SVM) and Multiple Kernel Learning (MKL) SVM models, the Local Interpretable Model-agnostic Explanations (LIME) technique was implemented to gain insights into the models' decision-making process. LIME provides interpretability by generating local explanations for individual predictions, allowing us to understand the factors influencing the models' classifications. LIME was applied to generate local explanations further to understand the best-performing model (MKL SVM). LIME analyzes individual instances and identifies the most influential features contributing to the model's decision. By visualizing the feature importance scores, we can gain insights into the specific factors the MKL SVM model considers when classifying heart failure patients.

Figure 4 depicts the averaged results of feature importance according to LIME analysis. We have decided to separate the TP, TN, FP, and FN because we would like to see the discriminative power of each feature independently for each class and understand why our classifier makes mistakes in predictions. There is a definite influence of the 'ST_Slope' feature on every subset, and it is visibly the most important one in driving the model to the correct class. Regarding heart failure disease, the 'ST_Slope', which represents the slope of the peak exercise ST segment, can provide valuable information about cardiac health and function. The ST segment is a portion of an electrocardiogram (ECG) waveform that reflects the time interval between ventricular depolarization (QRS complex) and repolarization (T wave). In clinical terms, the ST segment represents a period in which the myocardium maintains contraction to expel blood from the ventricles [10]. Multiple studies have shown that the ST segment slope deviation from

the norm can directly indicate heart disease like myocardial ischemia [12] or even a post-COVID-19 complication [13].

As for the LIME results for False Positives and False Negatives, we can observe that the most important features have not changed and the value of importance is even comparatively higher for FP than it is for TP. This can indicate a possibility of outliers in the general dataset, where we have the majority of patients with 'SP_Slope' equal to 'Down', but some of the patients may have a completely different behaviour in this variable. The same corresponds to the other two features we have outlined.

Figure 5 shows the relationship between the top three most significant features in terms of our model predictions. As we can see, most healthy subjects had a 'ST_Slope' parameter equal to 'Up', whereas the ones with a Heart Disease presented - 'Flat'. The 'ExerciseAngina', which represents exercise-induced angina, was prevalent in patients compared to healthy controls. Additionally, the distribution of these two variables was plotted w.r.t. 'Oldpeak' value representing ST segment measured in depression, showing the significant differences between the two groups in mean and deviation values. This supports the results of the LIME model depicting the differences between the groups picked up by the MKL SVM classifier.

V. CONCLUSIONS AND FUTURE WORK

Based on the results and discussion presented, the Spearman correlation analysis revealed weak to moderate correlations between the dataset features and the target variable, with most features showing statistically significant associations with heart failure disease.

Furthermore, the analysis of machine learning models showed that both the Support Vector Machine (SVM) and Multiple Kernel Learning (MKL) SVM models performed well in classifying heart failure patients. However, the MKL SVM model outperformed the SVM model regarding average accuracy, sensitivity, and area under the curve (AUC) metrics. This performance improvement can be attributed to the MKL SVM model's ability to leverage multiple kernels and capture diverse patterns and information from the input features.

Incorporating the Local Interpretable Model-agnostic Explanations (LIME), technique provided insights into the decision-making process of the MKL SVM model. LIME generated local explanations for individual predictions, highlighting the most influential features contributing to the models' classifications. The analysis revealed that the 'ST_Slope' feature played a crucial role in classifying heart failure patients, indicating its significance in assessing cardiac health and function. Additionally, features such as 'ExerciseAngina' and 'Oldpeak' were found to be informative in distinguishing between healthy subjects and those with heart disease.

Based on these findings, future work can focus on the following points. Further investigating the relationship between the 'ST_Slope' feature and heart disease could be beneficial by exploring its connection to heart failure diagnosis. This can provide a deeper understanding of the feature's role in

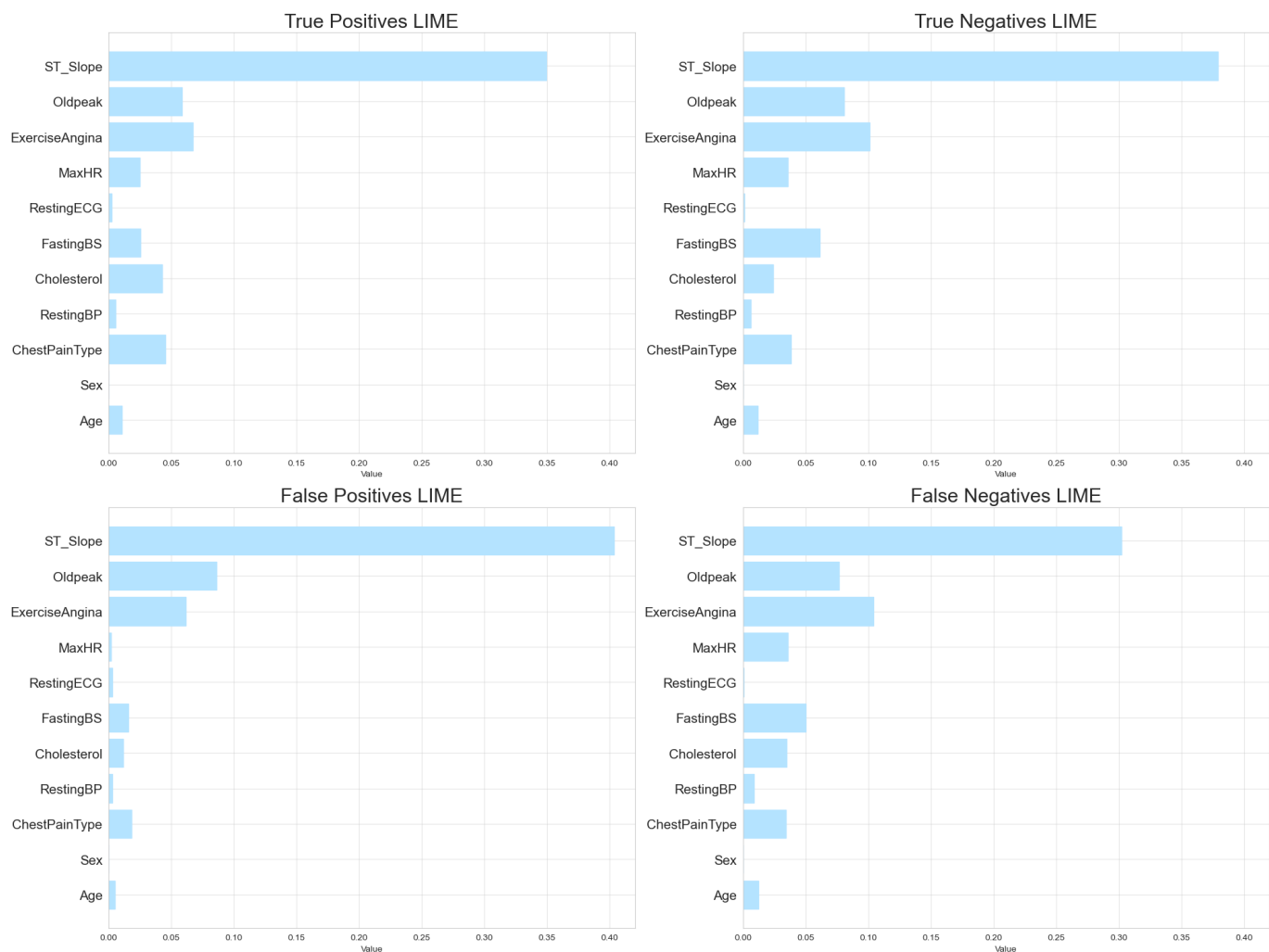


Fig. 4: LIME interpretability results averaged throughout the test dataset. The split on four subsets was performed based on comparison of a true label and a predicted label by MKL SVM model.

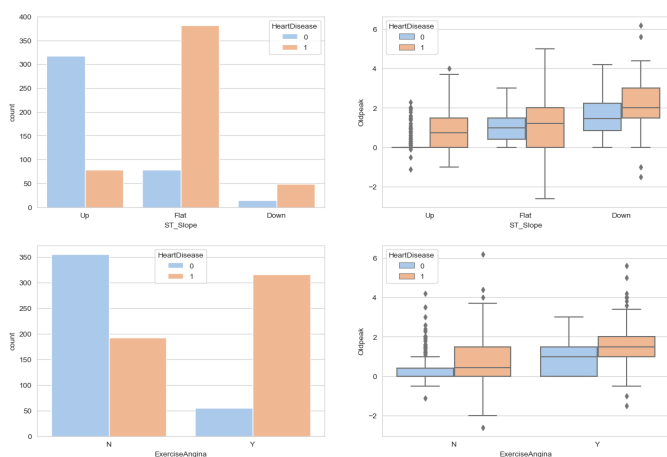


Fig. 5: Comparison of the top 3 most informative features - 'ST_Slope', 'Oldpeak' and 'ExerciseAngina' based on the LIME output (Figure 4)

diagnosing and assessing heart failure. This study results can also be used to conduct additional studies to validate the results obtained from the SVM and MKL SVM models using more extensive and diverse datasets. This can help assess the models' generalizability and performance across different populations. As we only used LIME to explain our model's performance, in the future, we could also explore other interpretability techniques and model-agnostic approaches to gain further insights into the decision-making processes of the SVM and MKL SVM models. This can enhance understanding of the model's predictions and improve their trustworthiness in real-world applications. Another practical step could be integrating clinical data and domain knowledge into the modeling process. Collaborations with medical experts can provide valuable insights and guidance in feature selection, model development, and interpretation of the results.

By addressing these future research directions, we can enhance the understanding, performance, and applicability of machine learning models in the early detection and diagnosis

of heart failure, ultimately benefiting patients and healthcare providers.

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Code available at: <https://github.com/AldaKola/E-Health-LIME-Homogeneous/tree/main>