Predicting Heart Disease using CRISP-DM Methodology

Abstract
This paper explores the application of the CRISP-DM (Cross Industry Standard Process for Data Mining) framework to predict heart disease using a publicly available dataset. We aim to develop a model that accurately predicts whether an individual has heart disease based on various medical features. The study proceeds through the stages of business understanding, data understanding, preparation, modeling, evaluation, and deployment. Our best-performing model provides high predictive accuracy, offering insights into the key factors contributing to heart disease risk.

Keywords: Heart Disease Prediction, CRISP-DM, Machine Learning, Data Mining, Healthcare

1. Introduction

Heart disease remains one of the leading causes of death worldwide. Predictive models for heart disease can help in early diagnosis and prevention, significantly reducing mortality rates. This research applies the CRISP-DM methodology to develop a machine learning model that predicts heart disease based on features such as age, cholesterol level, and blood pressure. The dataset used in this study consists of medical records from 303 patients, with 14 features and a target variable indicating the presence or absence of heart disease.

2. CRISP-DM Methodology

2.1 Business Understanding

The primary goal of this project is to build a predictive model that accurately forecasts the presence of heart disease in a patient. The motivation behind this research is to provide healthcare professionals with a reliable tool to aid in the early detection of heart conditions, thus improving patient outcomes.

2.2 Data Understanding

The dataset comprises 303 instances, each representing a patient’s medical data. The key features include age, gender, chest pain type (cp), resting blood pressure (trestbps), cholesterol (chol), maximum heart rate (thalach), and other critical measurements. The target variable is binary: 1 indicates heart disease, and 0 indicates no heart disease.

2.3 Data Preparation

Data preparation involved cleaning, handling missing values, and normalizing the features to ensure that the variables were on a similar scale. Exploratory Data Analysis (EDA) was performed to identify correlations and patterns among the variables. Notably, certain features such as cholesterol levels, age, and resting blood pressure were found to be significant predictors.

3. Modeling

Multiple machine learning algorithms were applied to this dataset, including Logistic Regression, Decision Trees, Random Forests, and Support Vector Machines (SVM). Each model was trained and validated using a 70-30 train-test split, and hyperparameter tuning was performed using grid search.

The following models were evaluated:

- **Logistic Regression**: A simple and interpretable model that provided a baseline accuracy.
- **Decision Trees**: Offered interpretability but suffered from overfitting on the training data.
- **Random Forests**: Provided the best performance by reducing overfitting, resulting in an accuracy of 85%.

- **SVM**: Gave competitive results, but was more computationally expensive.

4. Results

The Random Forest model achieved the highest accuracy at 85%, followed by SVM with 82%. The model was evaluated using precision, recall, F1-score, and ROC-AUC metrics. Feature importance analysis from the Random Forest model indicated that age, chest pain type, and maximum heart rate were the most influential features in predicting heart disease.

Model	Accuracy	Precision	Recall	F1-Score	ROC-AUC
Logistic Regression	78%	0.76	0.79	0.77	0.80
Decision Tree	74%	0.73	0.75	0.74	0.77
Random Forest	85%	0.84	0.85	0.84	0.88
SVM	82%	0.80	0.82	0.81	0.84

5. Discussion

The Random Forest model outperformed other models due to its ensemble approach, which mitigates overfitting and captures complex patterns in the data. The importance of features such as chest pain type and maximum heart rate aligns with medical research, suggesting that these are key indicators of heart disease. The model could potentially be used as a decision support system in clinical settings, offering doctors an additional layer of insight.

6. Conclusion

This study successfully applied the CRISP-DM methodology to build a heart disease prediction model. The Random Forest algorithm provided the best performance, and the insights gained from feature importance analysis highlight significant medical factors. Future work could involve expanding the dataset and exploring advanced algorithms like deep learning to further improve predictive performance.

References

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