Heart Failure Prediction

高自在	曾駿馳	顏永明	王柏鈞
N26102131	F74089046	P76101136	N26102050

1. Introduction

> Cardiovascular diseases (CVDs) are the number 1 cause of death globally, taking an estimated 17.9 million lives each year, which accounts for 31% of all deaths worldwide. Four out of 5CVD deaths are due to heart attacks and strokes, and one-third of these deaths occur prematurely in people under 70 years of age. Heart failure is a common event caused by CVDs and this dataset contains 11 features that can be used to predict a possible heart disease.
>
> People with cardiovascular disease or who are at high cardiovascular risk (due to the presence of one or more risk factors such as hypertension, diabetes, hyperlipidaemia or already established disease) need early detection and management wherein a machine learning model can be of great help. [1]

The motivation for starting this project is to demonstrate knowledge of artificial learning and data analysis and expound upon model building and training skills that we have learned throughout the course. The main obstacle is data preprocessing which includes missing data imputation, feature selection, and feature scaling.

2. System framework

In this project, our task is to create a model to assess the likelihood of a possible heart disease event. It is a binary classification task in supervised learning. Some common classification models such as decision trees and support vector machines can be applied. In addition to the common models, there are advanced models such as gradient boosting classifiers and deep neural networks. We will construct some of these models and analyze the differences between them.

There are three problems for data preprocessing, as we mentioned above: missing data imputation, feature selection, and feature scaling.

For missing data imputation, Mean/Median/Mode imputation is a common technique to deal with it. KNN imputation is also a considerable option [2].

For feature selection, we will evaluate the correlation between each feature with heatmap and drop unnecessary features if there are any. Besides feature selection, feature extraction is also a technique used for dimensionality reduction, which can be considered as another solution [2].

For feature scaling, standard mean/std scaler and min;max normalization are two standard methods. In addition, Gauss rank transformation, a novel standardization technique with better performance in deep neural networks training, is worth trying in this project [3].

3. Expected results

We expect our model's prediction will have over 60% recall score, which is a best score to look at, since false negatives are unacceptable in medical applications.

Table 1 is the detail of the dataset features [1].

Feature	Description	Value
Age	age of the patient	years
Sex	sex of the patient	M:Male, F:Female
ChestPainType	chest pain type	TA: Typical Angina, ATA: Atypical Angina, NAP: Non-Anginal Pain, ASY: Asymptomatic
RestingBP	resting blood pressure	mm Hg
Cholesterol	serum cholesterol	mm/dl
FastinBS	fasting blood sugar	1: if FastingBS > 120 mg/dl, 0: otherwise
RestingECG	resting electrocardiogram results	Normal: Normal, ST: having ST-T wave abnormality, LVH: showing probable or definite left ventricular hypertrophy by Estes' criteria
MaxHR	maximum heart rate achieved	Numeric value between 60 and 202
ExerciseAngina	exercise-induced angina	Y: Yes, N: No
Oldpeak	oldpeak=ST	Numeric value measured in depression
ST_Slope	the slope of the peak exercise ST segment	Up: upsloping, Flat: flat, Down: downsloping
HeartDisease	output class	1: heart disease, 0: Normal

Table 1. Dataset features [1]

4. Exploratory Data Analysis

4.1. Data Features

We can separate data features into numeric features, categorical features and the target for our task :

Numeric Features

- Age
- RestingBP
- Cholesterol
- MaxHR
- Oldpeak

Categorical Features

- Sex
- ChestPainType
- FastingBS
- RestingECG
- ExerciseAngin
- ST_Slope

Target

- HeartDisease

4.2. Check Missing Values

First, let's take a glimpse of the dataset. It shows that there is no null value in the dataset. However, we find that the minimum values of RestingBP and Cholesterol are 0, which is not normal. We assume that they are missing the values filled with 0s incorrectly.

Age	0
Sex	0
ChestPainType	0
RestingBP	0
Cholesterol	0
FastingBS	0
RestingECG	0
MaxHR	0
ExerciseAngina	0
Oldpeak	0
ST_Slope	0
HeartDisease	0

Table 2. Missing values

There is only 1 row missing value at RestingBP. We can simply remove this row.

	Age	Sex	ChestPainType	RestingBP
449	55	M	NAP	0

Table 3. Missing values

It seems that there are so many missing values at Cholesterol. We replace 0s with NaN by now, will deal with them later.

	Age	Sex	ChestPainType	RestingBP	Cholesterol
293	65	M	ASY	115	0
294	32	M	TA	95	0
295	61	M	ASY	105	0
296	50	M	ASY	145	0
297	57	M	ASY	110	0
...	...	...	...	...	...
514	43	M	ASY	122	0
515	63	M	NAP	130	0
518	48	M	NAP	102	0
535	56	M	ASY	130	0
536	62	M	NAP	133	0

Figure 1. Cholesterol with 0

4.3. Duplicated Data

Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS

Figure 2. No duplicated data

There is no duplicated data.

4.4. Categorical Features Encoding

For further analysis, we want to encode the categorical features. Before encoding, we need to separate categorical features into nominal and ordinal features. Nominal variable comprises a finite set of discrete values with no relationship between values. Ordinal variable comprises a finite set of discrete values with a ranked ordering between values.

4.4.1 Nominal Features

- Sex
- ExerciseAngina

Nominal features in this dataset are both binary, so we can simply assign 0 and 1.

Sex		
M	$\longrightarrow$	0
F	$\longrightarrow$	1
ExerciseAngina		
N	$\longrightarrow$	0
Y	$\longrightarrow$	1

Table 4. Encoding Nominal Features

4.4.2 Ordinal Features

- ChestPainType
- RestingECG
- ST_Slope

Fortunately, ordinal features are introduced in sequence of order. We assign values according to the information given above

ChestPainType		
ASY	$\longrightarrow$	0
NAP	$\longrightarrow$	1
ATA	$\longrightarrow$	2
TA	$\longrightarrow$	3
RestingECG		
Normal	$\longrightarrow$	0
ST	$\longrightarrow$	1
LVH	$\longrightarrow$	2
ST_Slope		
Down	$\longrightarrow$	0
Flat	$\longrightarrow$	1
Up	$\longrightarrow$	2

Table 5. Encoding Nominal Features

4.5. Relation Observation

After encoding, now we can show the relation between each feature.

Numeric features

Now we want to see the correlation between each numerical features

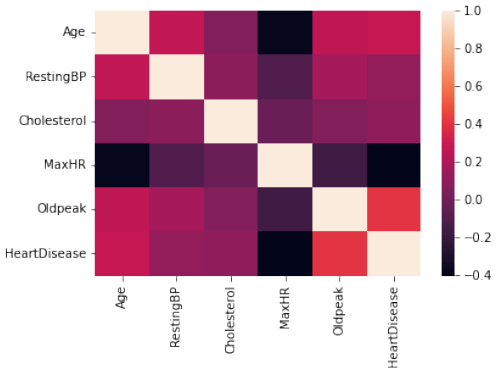


Figure 3. Heat map

As shown above, the correlation between each features are not high, so we don't have to worry about multicollinearity. We can see that OldPeak and MaxHR have relatively high correlation with HeartDisease

Categorical Features

	name1	name2	chi_value	chi_p	chi_DF	chi_LLP
0	ST_Slope	HeartDisease	35.988984	1.531410e-08	2	17.994492
0	ChestPainType	HeartDisease	32.254736	4.624851e-07	3	14.586651
0	ExerciseAngina	HeartDisease	15.593001	7.854479e-05	1	9.451841
0	Sex	HeartDisease	7.688718	5.556708e-03	1	5.192749
0	FastingBS	HeartDisease	4.966882	2.583719e-02	1	3.655941
0	RestingECG	HeartDisease	2.990942	2.241430e-01	2	1.495471

Figure 4. Chi-Square test

To see the relation between categorical features and heartdisease, we randomly choose 100 samples from dataset to have a Pearson Chi-Square Independent Test. We can say ST_Slope, ChestPainType and ExerciseAngina are related to HeartDisease.

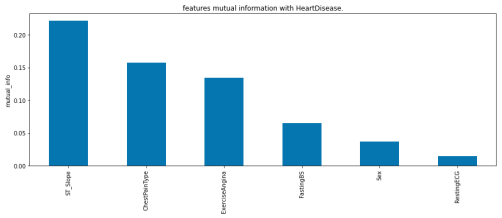


Figure 5. Feature mutual information

Here, we use features mutual information to enhance our conjecture.

5. Preprocessing

5.1. Encoding Categorical Features

We encode the categorical features same as we did in EDA.

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	40	0	2	140	289.0	0	0	172	0	0.0	2	0
1	49	1	1	160	180.0	0	0	156	0	1.0	1	1
2	37	0	2	130	283.0	0	1	98	0	0.0	2	0
3	48	1	0	138	214.0	0	0	108	1	1.5	1	1
4	54	0	1	150	195.0	0	0	122	0	0.0	2	0

Figure 6. Encode categorical feature

5.2. Spliting Data

First of all, we need to split our dataset before further preprocessing. Here, we split dataset into train-set:test-set to 9:1

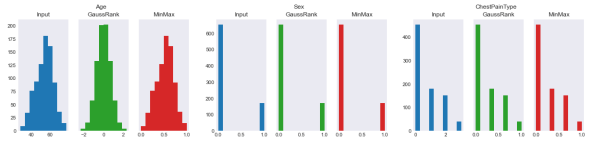
5.3. Missing Data Imputation

After splitting, we can now study how to imput missing values of Cholesterol. We perform the imputation only on the training set to avoid any data leakage. Here we choose KNNImputer as our imputer. It is an imputation for completing missing values using k-Nearest Neighbors.

5.4. Feature Scaling

Standard mean/std scalar and min-max normalization are two common methods for feature scaling. However, there is a new technique called Gauss rank transformation. It is believed that Gauss rank transformation has better performance in deep neural networks training. It should be noted that Gauss rank transformation can only be performed on numeric features

Transformation Comparison



(a) Numeric (b) Nominal (c) Ordinal

6. Model

Inspired by residual neural network, we stack 4 fully connection layers that stay same dimension and add previous input every 2 layers. Then we reduce dimension with 2 fully connection layers.

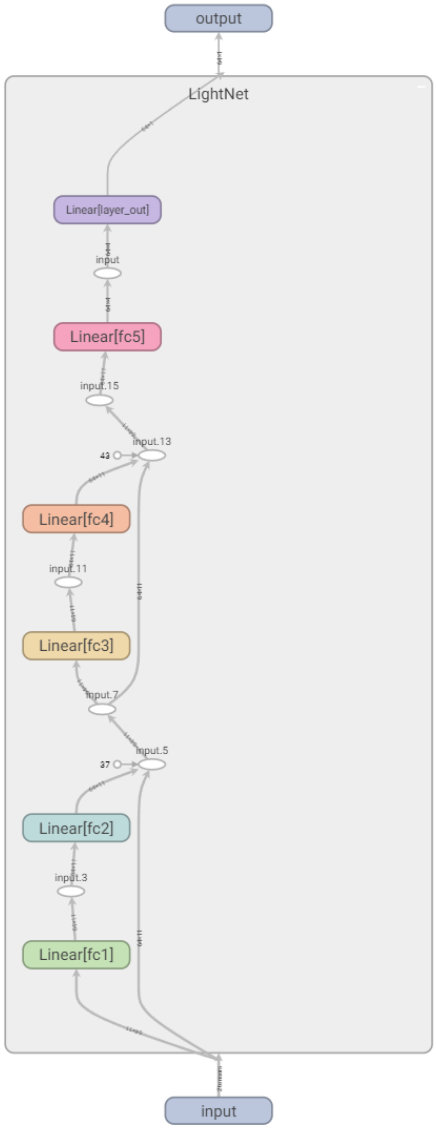


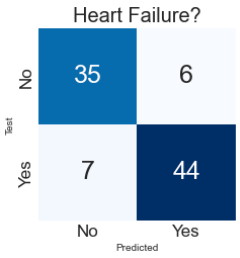
Figure 8. Model

Model Training

We use Adam(adaptive moment estimation) optimizer to train our model. Since our task is a binary classification problem, binary cross-entropy with logits is the first loss function that comes up with our minds.

Model Performance

Our classification model reaches 89% F1 score with 90% Recall score and 88% Accuracy score.



(a) Confusion matrix

Accuracy	0.88
Precision	0.88
Recall	0.90
F1	0.89
ROC AUC	0.88

(b) Result

Figure 9

Model Explanation

By SHAP(SHapley Additive exPlanations), we calculate shapl values to analyze the importance of each features. We can see that Oldpeak and ST_Slope are top 2 contributors to the prediction, which matches our conjecture in EDA.

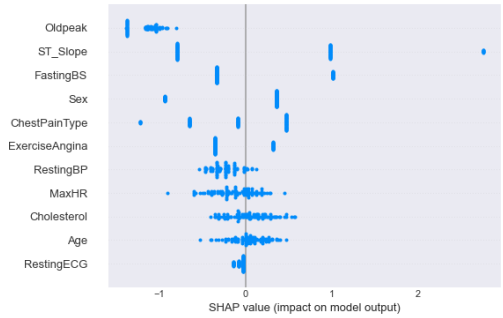


Figure 10. Shap values

7. Compare To Different Methods

Also, we compare different classification models with our model. It turns out that our model is slightly better than other models except KNN classifier, which has lower Recall score than ours. It is worth noting that Recall score is the best score to look at since false negative is unacceptable in medical applications.

	ours	Logistic Regression	Random Forest	SVC	KNN	Ada Boost
Accuracy	0.88	0.86	0.86	0.88	0.90	0.88
Precision	0.88	0.90	0.91	0.92	0.96	0.93
Recall	0.90	0.84	0.82	0.86	0.86	0.84
F1	0.89	0.87	0.87	0.89	0.91	0.89
ROC AUC	0.88	0.86	0.86	0.88	0.91	0.88

Table 6. Compare to different models

References

[1] fedesoriano. Heart failure prediction dataset. https://www.kaggle.com/fedesoriano/heart-failure-prediction, Sept. 2021. Accessed: 2021-12-16. 1, 2

[2] JacksonKwong. Hf prediction(98% rec 85% acc 89% f1) with lgbm. https://www.kaggle.com/jacksonkwong/hf-prediction-98-rec-85-acc-89-f1-with-lgbm#3.-Data-Modeling, Dec. 2021. Accessed: 2021-12-16. 1

[3] Jiwei Liu. Gauss rank transformation is 100x faster with rapids and cupy. https://developer.nvidia.com/blog/gauss-rank-transformation-is-100x-faster-with-rapids-and-cupy/, June 2021. Accessed: 2021-12-16. 1