

Heart Failure Survival Analysis

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Summary

We built a classification model using the logistic regression algorithm to predict survival outcomes for patients with heart failure. Using patient test results, the final classifier achieves an accuracy of 0.82. The model's precision of 0.7 suggests it is moderately conservative in predicting the positive class (death), minimizing false alarms. More importantly, the recall of 0.74 ensures the model identifies the majority of high-risk patients, reducing the likelihood of missing true positive cases, which could have serious consequences. The F1-score of 0.72 reflects a good balance between precision and recall, highlighting the model's robustness in survival prediction, see Table 7.

From the confusion matrix, the model correctly identified 14 patients who passed away (true positives) and 35 patients who survived (true negatives). However, it also predicted 6 false positives, incorrectly classifying some survivors as deceased, and missed 5 actual cases of death (false negatives). While these errors warrant consideration, the model's performance demonstrates strong predictive capabilities for both positive and negative outcomes, see Table 6.

Overall, the logistic regression classifier effectively leverages patient test results to support survival prediction, providing a valuable tool to aid clinical decision-making in heart failure management.

Introduction

Cardiovascular diseases are responsible for approximately 17 million deaths globally each year, with heart failure and myocardial infarctions being the leading contributors to this staggering toll (Chicco and Jurman 2020). Electronic medical records from patients with heart failure, collected during follow-up care, provide a wealth of data on symptoms, test results, and clinical outcomes. Leveraging this data, our team applies machine learning algorithms to predict patient survival after heart failure. This approach uncovers critical patterns and insights that might otherwise remain hidden from traditional clinical assessments, offering valuable tools to support medical decision-making and improve patient outcomes.

Data

We analyzed a dataset containing the medical records of 299 heart failure patients (Dua and Graff 2017). The patients consisted of 105 women and 194 men, and their ages range between 40 and 95 years old. The dataset contains 13 features shown in Table 1, which report clinical, body, and lifestyle information (“Heart Failure Clinical Records [Dataset]” 2020). The **death event** was used as the target variable in our binary classification study. It states whether the patient died or survived before the end of the follow-up period, which lasted 130 days on average. Our dataset has a class imbalance where the number of survived patients (death event = 0) is 203 (67.89%) and the number of dead patients (death event = 1) is 96 (32.11%), see Table 3.

Explanatory Data Analysis and Visualizations

Table 1: Description of the columns in the heart failure dataset.

Table 1

	Column Name	Description
0	age	Patient's age
1	anaemia	Decrease of red blood cells or hemoglobin
2	creatinine_phosphokinase	Level of the CPK enzyme in the blood
3	diabetes	If the patient has diabetes
4	ejection_fraction	Percentage of blood leaving the heart at each contraction
5	high_blood_pressure	If the patient has hypertension
6	platelets	Platelets in the blood
7	serum_creatinine	Level of serum creatinine in the blood
8	serum_sodium	Level of serum sodium in the blood
9	sex	Woman or man
10	smoking	If the patient smokes or not
11	time	Follow-up period
12	DEATH_EVENT	Whether the patient died or not (target variable)

Based on the correlation matrix graph Figure 1, all features have relatively low correlations between each other, the correlations are below 0.5, so there is no strong evidence to drop additional features.

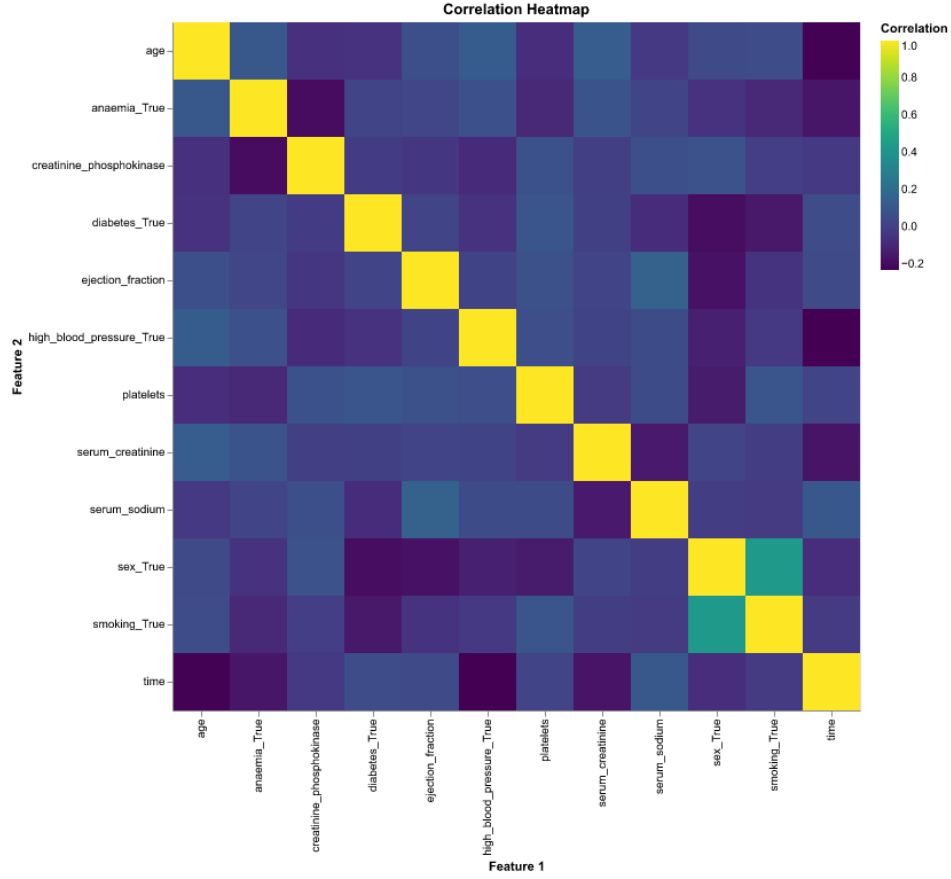


Figure 1: Correlation heatmap

Table 2: Number of missing values in each column of the heart failure dataset.

Table 2

	Column	Missing Values
0	age	0
1	anaemia	0
2	creatinine_phosphokinase	0
3	diabetes	0
4	ejection_fraction	0
5	high_blood_pressure	0
6	platelets	0
7	serum_creatinine	0
8	serum_sodium	0
9	sex	0

	Column	Missing Values
10	smoking	0
11	time	0
12	DEATH_EVENT	0

No missing values, no imputation or filling Nulls required

Table 3: Distribution of the target variable DEATH_EVENT in the heart failure dataset.

	DEATH_EVENT	Count
0	0	203
1	1	96

Dataset Size: The dataset is relatively small, with only 300 rows.

Class Imbalance: The target variable, DEATH_EVENT, has few examples in the “True” class (i.e., the event occurred), which might affect the model’s ability to learn and generalize well. This class imbalance will be taken into consideration during analysis and model evaluation.

Model

We compared Decision Tree, KNN, Logistic Regression, and selected Logistic Regression due to its interpretability, and ability to handle both linear and non-linear relationships between features. Logistic Regression performed better than the other two models as it works well with fewer features and is less prone to overfitting compared to more complex models like Decision Trees or KNN, especially when the data is relatively small.

Hyperparameter tuning to find the best Logistic Regression model:

Table 4: Logistic Regression Scores

	param_logisticregression__C	mean_test_score	mean_train_score
1	0.0001	0.832428	0.834022
2	0.001	0.828261	0.833096
3	0.01	0.819928	0.825187
4	0.1	0.815761	0.824731
5	1.0	0.799275	0.823807

The model is performing well with $C = 0.0001$ with a CV score of 0.83 and is close to train score, indicating that model is generalising well.

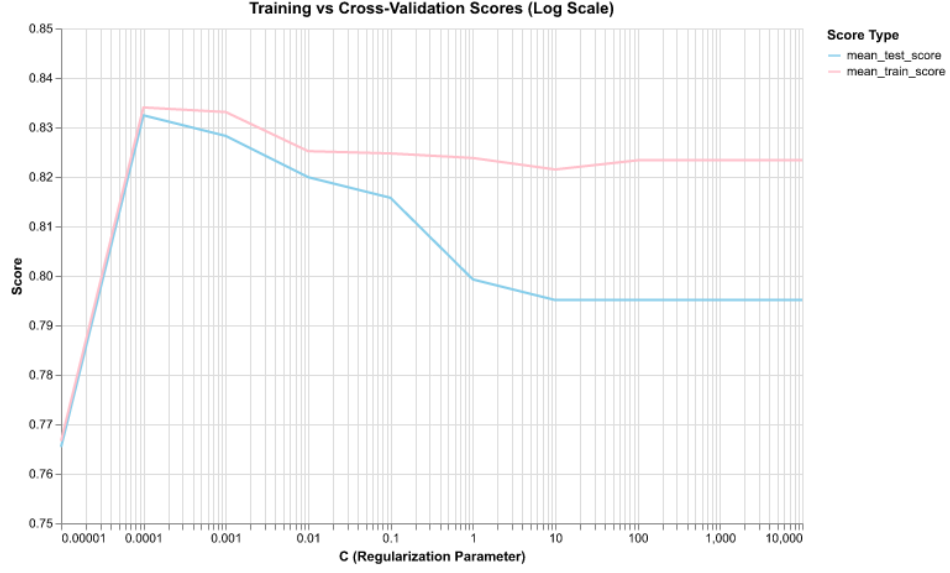


Figure 2: Cross-validation scores for Logistic Regression

Logistic regression performs better than Decision tree and KNN on the cross validation data, hence, we selected it as our final model.

The best features to train our model are show in Table 5:

Table 5: Top features for trainig the model.

	Feature	Coefficient	Absolute_Coefficient
6	platelets	-0.006702	0.006702
4	ejection_fraction	0.004108	0.004108
2	creatinine_phosphokinase	-0.003465	0.003465
0	age	0.002880	0.002880
5	high_blood_pressure	-0.002383	0.002383
1	anaemia	0.001004	0.001004
9	sex	0.000714	0.000714
7	serum_creatinine	0.000431	0.000431
3	diabetes	-0.000375	0.000375
11	time	-0.000208	0.000208
10	smoking	-0.000106	0.000106
8	serum_sodium	-0.000064	0.000064

Model Evaluation

Confusion Matrix

Table 6: Confusion matrix for the final model on the test dataset.

Table 6

Predicted	0	1
Actual		
0	35	6
1	5	14

Table 7: Evaluation metrics for the final model.

	Metric	Value
0	Accuracy	0.82
1	Precision	0.70
2	Recall	0.74
3	F1 Score	0.72

Results and Conclusion

The analysis revealed that `platelets` and `ejection_fraction` are the most important features (see Table 5) in predicting the risk of patient mortality. These features significantly impact the model’s ability to assess patient risk, which is crucial for early intervention. Our model achieved a recall score of 0.74 (see Table 7), which is a good start, but there is room for improvement, particularly in reducing the number of high risk patients the model might miss, i.e., maximising recall by minimising False Negatives.

The main challenges in this project stem from class imbalance and limited data availability. With more diverse and comprehensive datasets, performance could be further enhanced. We would also like to explore other machine learning models to improve the overall accuracy.

In conclusion, while the current model shows potential, there is significant opportunity to enhance its effectiveness. With improvements in data quality and model optimization, this tool could become a crucial asset in predicting patient risk and saving lives.

References

- Chicco, D., and G. Jurman. 2020. “Machine Learning Can Predict Survival of Patients with Heart Failure from Serum Creatinine and Ejection Fraction Alone.” *BMC Medical Informatics and Decision Making* 20 (16). <https://doi.org/10.1186/s12911-020-1023-5>.
- Dua, Dheeru, and Casey Graff. 2017. “UCI Machine Learning Repository.” University of California, Irvine, School of Information; Computer Sciences. <http://archive.ics.uci.edu/ml>.
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