<Automation Lab> <Fall 2024>

Heart Failure Data Set

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<Step 1> <Problem Definition>

Objective:

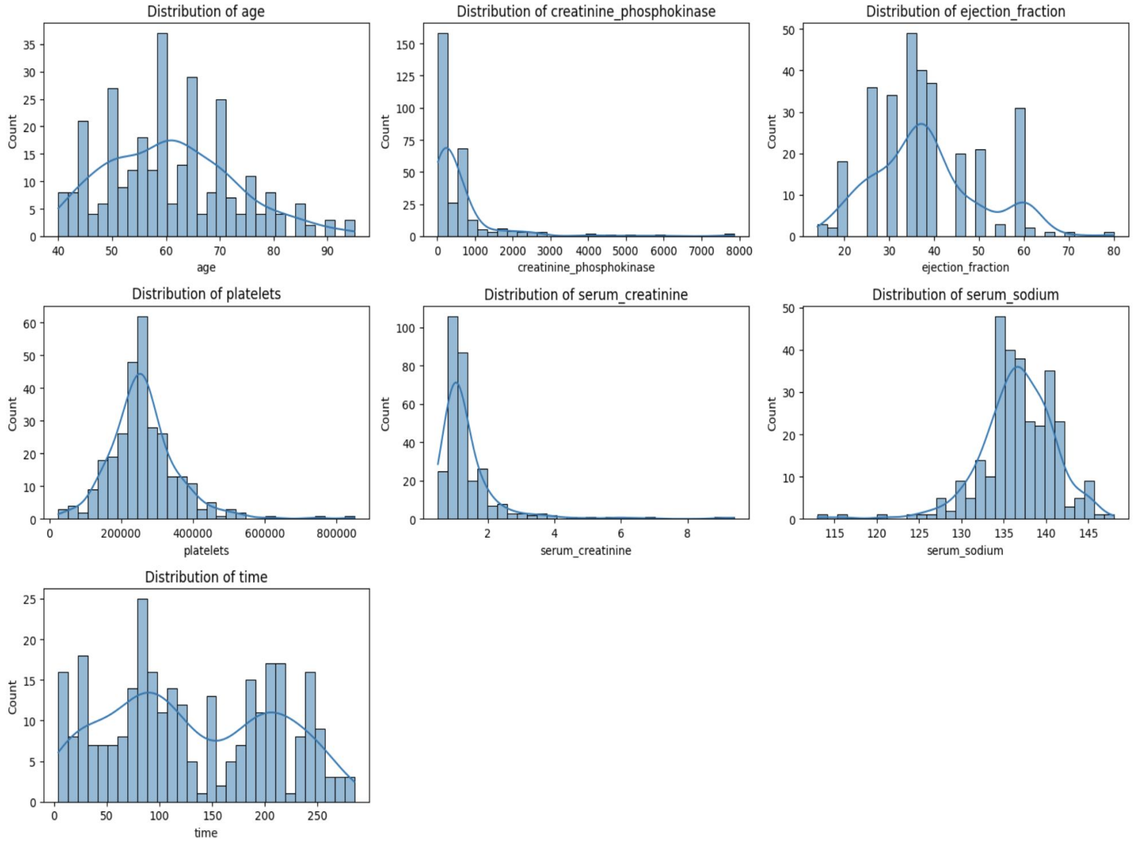
To understand what is causing a Death Event. By understanding what causes a Death Event it may help put a focus and emphasis on that specific issue. Understanding what causes Death Events can ultimately help reduce the number of Death Events.

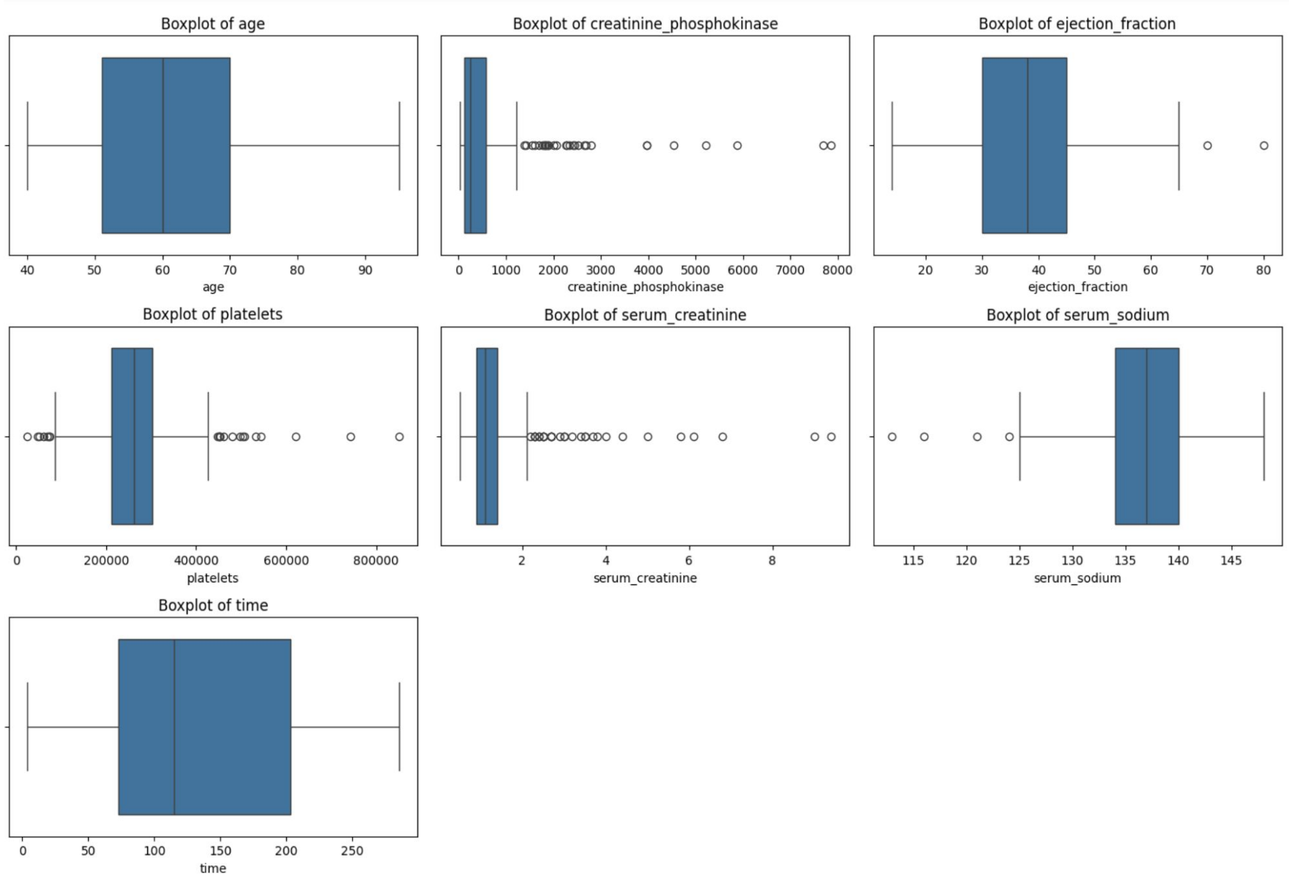
Task:

We will perform a classification analysis to determine how the independent variables impact the dependent variable Death Event. We are doing this to determine what events determine the change of a death event.

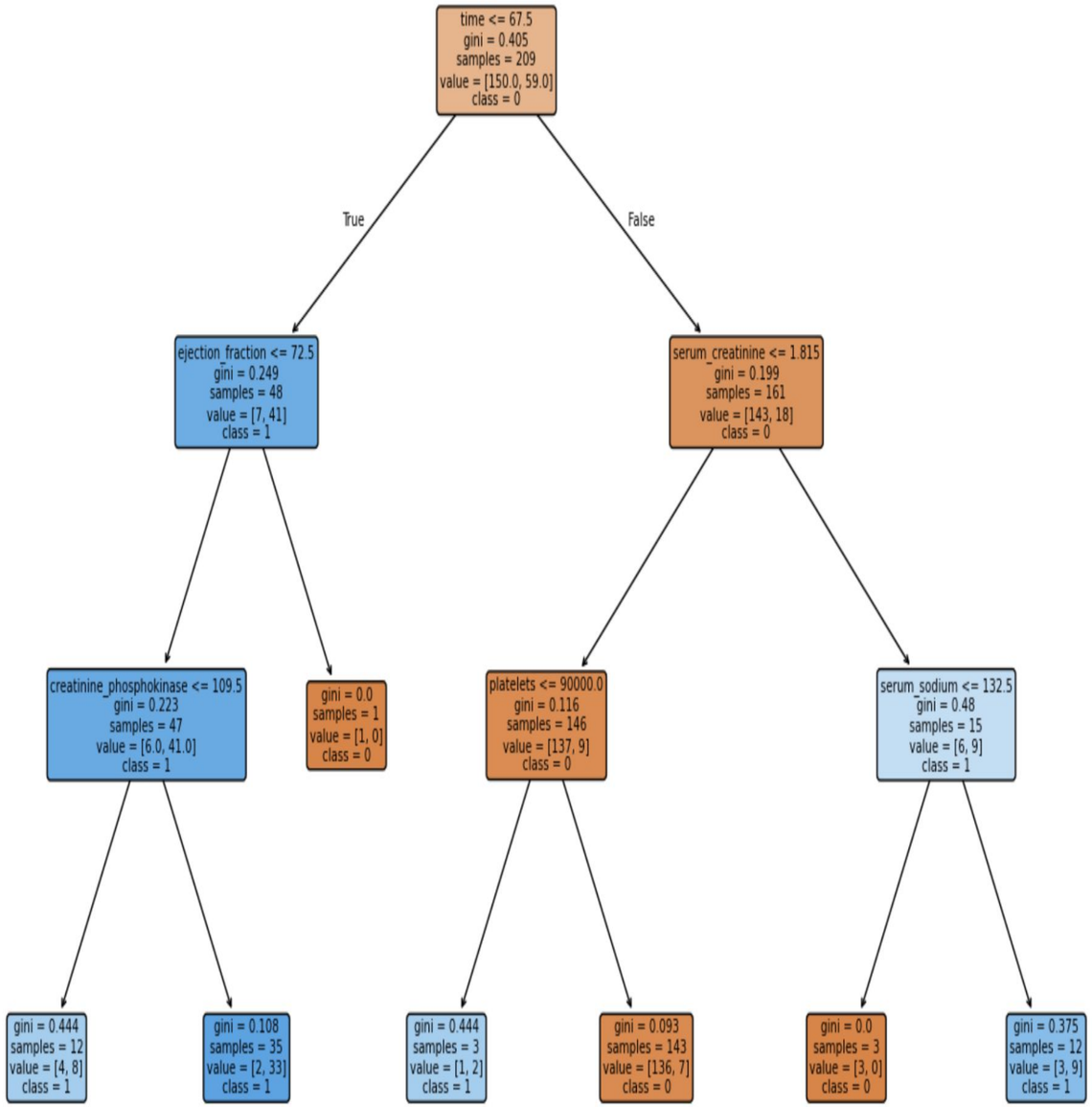
<Step 2> <Exploratory Data Analysis (EDA)>

- Zero missing values detected
- Creatinine Phosphokinase and Serum Creatinine have the most outliers and have a right skewed graph
- Null Hypothesis (H_0): There is no significant relationship between the categories (features such as age, anaemia, creatinine phosphokinase, diabetes, etc.) and the likelihood of a Death Event.
- Alternative Hypothesis (H_1): At least one of the categories (features) significantly impacts the likelihood of a Death Event.





<Step 2> <Exploratory Data Analysis (EDA)>



If time ≤ 67.5, the samples are sent to the left branch.
If time > 67.5, the samples are sent to the right branch.

Left branch 1:
If ejection fraction ≤ 72.5, the samples are further split into the next level.
If ejection fraction > 72.5, only one patient is classified, with no death event (class 0).

Left branch 2:
If creatinine phosphokinase ≤ 109.5, the samples are split further.
If creatinine phosphokinase > 109.5, there is a strong majority of no death events (class 0)

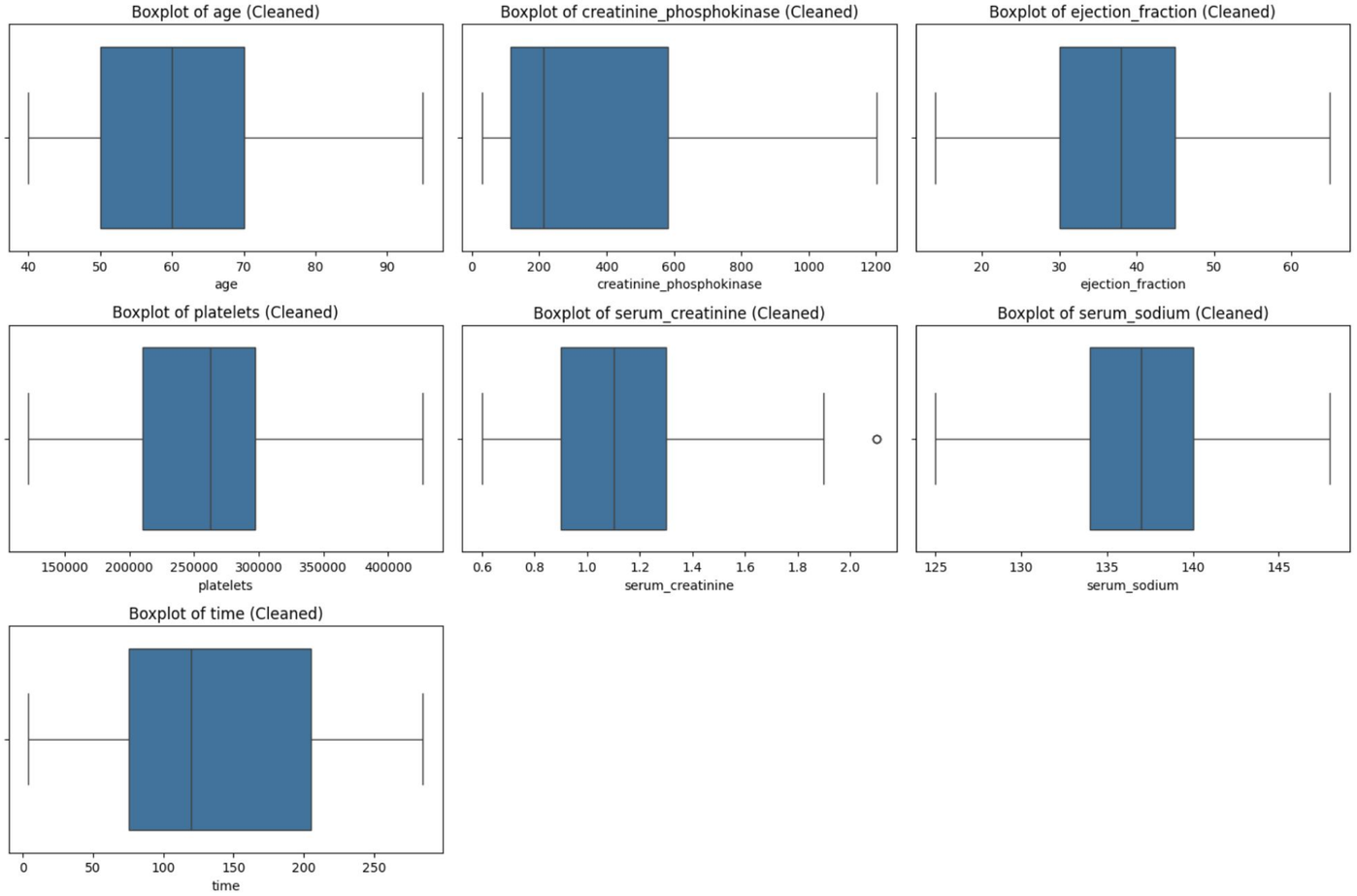
Right branch 1:
If serum creatinine ≤ 1.815, the majority of patients experience no death events (class 0).
If serum creatinine > 1.815, there's a higher proportion of death events, leading to further splits.

Right branch 2:
If platelets ≤ 90,000, the data splits again based on serum sodium.
If platelets > 90,000, the model predicts no death events (class 0) with very high confidence (low Gini index of 0.093).

Right branch 3:
If serum sodium ≤ 132.5, the risk of a death event (class 1) is high.
If serum sodium > 132.5, the risk of a death event is lower.

<Step 3> <Data Preprocessing>

- Dropped any duplicates
- Detected and handled outliers by removing them front the dataset
  - 29 from creatinine_phosphokinase
  - 2 from ejection_fraction
  - 18 from platelets
  - 23 from serum_creatinine
  - 3 from serum_sodium
- Check for Erroneous Data (negative values where not applicable)
- Create a feature for age group



<Step 4> <Feature Selection>

```
X = data.drop(['DEATH_EVENT'],axis=1)
y = data['DEATH_EVENT']
```

```
X_train shape: (209, 12), y_train shape: (209,)
X_test shape: (90, 12), y_test shape: (90,)
```

Split Data into Features and Target

- Features (**X**): All columns except DEATH_EVENT.
- Target (**y**): The DEATH_EVENT column.

Dropped the Target Variable (DEATH_EVENT) from Features to avoid data leakage.
Used the **train_test_split Function** from sklearn.model_selection to separate data into training and testing sets.

<Step 5> <Modeling>

Data Splitting:

- Divided the dataset into **70% training** and **30% testing** using train_test_split.
- Maintained reproducibility with random_state=42.

Model Training:

- Used a **Decision Tree Classifier** with a maximum depth of 3 to avoid overfitting.
- Trained the model on the **training set (X_train, y_train)**.

Model Visualization:

- Plotted and visualized the **Decision Tree**, showing key splits and decision paths.

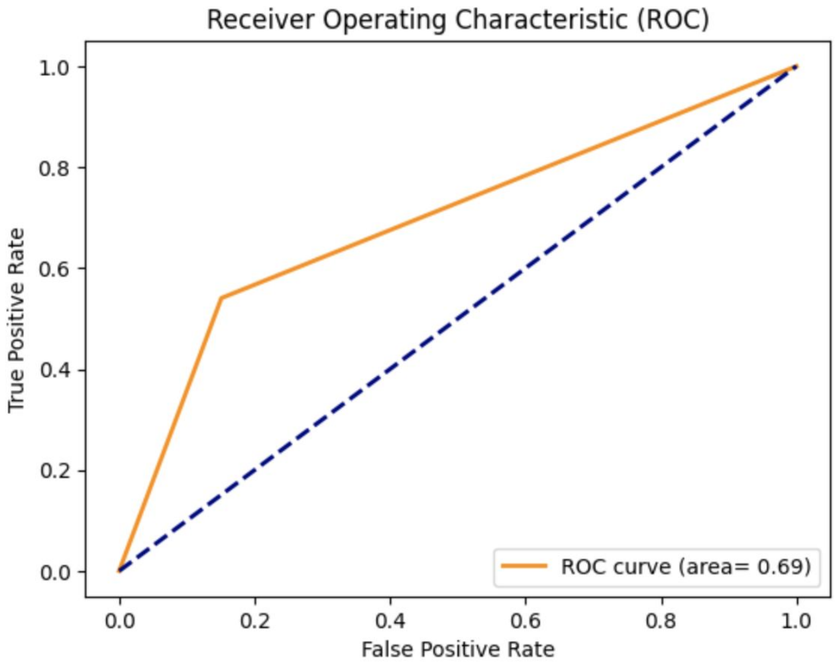
Prediction:

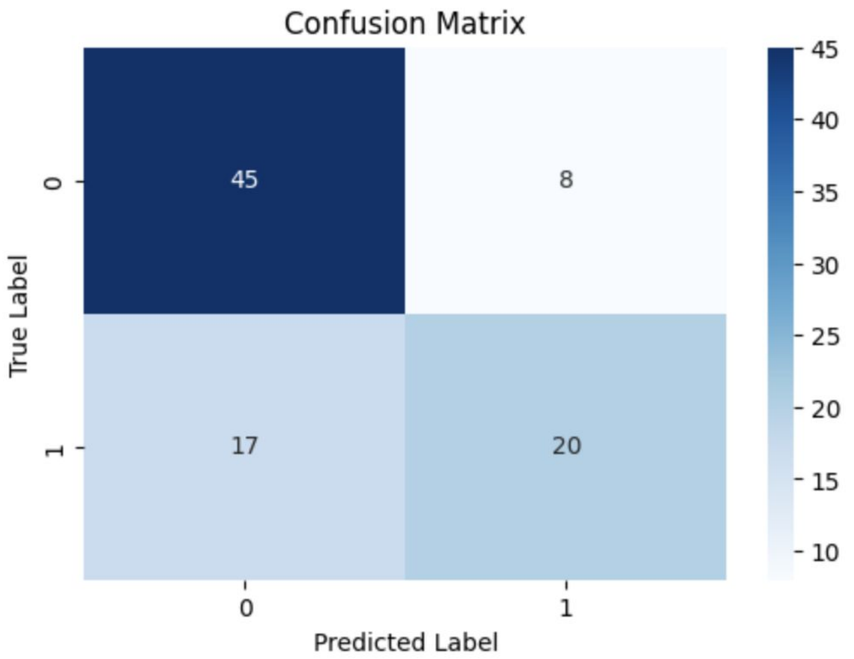
- Predicted outcomes (y_pred) on the **test set (X_test)**.

Model Evaluation:

- Calculated model accuracy: **{accuracy:.2f}** (replace with the printed accuracy).
- Generated a **classification report** to evaluate precision, recall, F1-score, and support for each class.

<Step 6> <Model Evaluation>





- An ROC curve (area) of 0.69 indicates that the model is better than random guessing but still leaves room for improvement
- For the confusion matrix:
  - **False Negatives**: The model misses 17 "Death" cases, highlighting low recall (54.1%) for the positive class, which is critical in high-stakes contexts.
  - **False Positives**: There are 8 incorrect "Death" predictions; while less critical, they could lead to unnecessary actions.
  - **Class Imbalance**: Likely skewed towards "No Death," affecting the model's ability to detect minority cases.
  - **Model Simplicity**: A max depth of 3 limits the model's complexity, potentially causing misclassifications.

<Step 7> <Model Interpretation and Insights>

ROC AUC Score (0.69):

- Moderate ability to discriminate between death and survival events.
- Not sufficient for reliable predictions in high-stakes healthcare settings.

Confusion Matrix Insights:

- 17 false negatives, indicating missed death events.
- Risks of not identifying patients needing critical intervention.

Key Features:

- **Serum creatinine** and **ejection fraction** align with medical knowledge of heart failure.
- Model captures some high-risk patterns but shows variability in **platelets** and **serum sodium** predictions.

Model Context:

- False negatives are critical in healthcare; missing death events can have severe consequences.
- Model conservatively identifies survival cases but risks overlooking critical patients.

Next Steps:

- Focus on reducing false negatives for better detection.
- Explore resampling or cost-sensitive methods to handle class imbalance.

<Thank You!>

Any Questions?