**Project Milestone 2**

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## 1. Dataset Description

The data is from the UCI Machine Learning Heart Disease Repository. It is publicly available on both Kaggle and the UCI website. This dataset is jointly collected by four hospitals to understand what factors could affect the severity of heart disease. It has 920 observations in total, and it contains 14 attributes, including age, sex, chest pain type, resting blood pressure etc. The target variable is `num`. It has 5 values, from 0 to 4, where 0 indicates no heart disease, and 4 indicates severe heart disease. Our task is to predict heart disease based on given features.

## 2. Potential Data Issues

### *2.1 Data missingness*

Figure 1 (in appendix) shows the distribution of missingness by variable. From the figure, we found that the missing patterns of `trestbps`, `thalch`, `exang`, `oldpeak` are similar with each other. We also found that `ca` and `thal` have a large proportion of missingness.

### *2.2 Data imbalance*

The distribution of outcomes is not balanced. According to Figure 2, the majority of the data is concentrated in classes 0 and 1, classes 2 and 3 have noticeably fewer samples, and class 4 is underrepresented.

### *2.3 Data scaling*

Table 1 presents the mean and standard deviation of the numerical features. While some features (e.g. cholesterol and thalach) have wider ranges, the standard deviations across features are relatively consistent, indicating no severe scaling imbalance. We also used pair plots to examine feature correlations, comparing the plots before and after scaling. Two pair plots (Figure 3 and Figure 4) are nearly identical, which confirms that scaling differences are unlikely to significantly impact analysis or model performance.

## 3. Ways to address the problem

### *3.1 Missingness*

To address missing data, we identified two variables— `ca` (the number of coronary arteries visualized by fluoroscopy during a coronary angiogram) and `thal` (results from a stress test)—that are likely missing not at random. Patients with mild symptoms or those perceived to have a lower risk of heart disease are often not referred for these tests by their physicians. Imputing these missing values as 'normal' could misrepresent the data, as these patients likely differ from those who underwent testing (even if the results were normal) due to higher perceived risk.

To accurately capture this clinical decision-making, we decided to incorporate an additional categorical value, `no_test_ordered`, for the `ca` and `thal` variables. This approach allows us to represent missingness directly through this new category, eliminating the need for a separate missingness indicator variable, which will ultimately be handled during one-hot encoding.

For the remaining missing variables, which we believe are missing at random, we opted to use multiple imputation. These values are standard clinical measurements that would typically be collected and are likely correlated with other variables (e.g., elevated cholesterol often correlates with elevated blood sugar). Multiple imputation (either using kNN or regression with cross validation using MSE as our loss function) will help us estimate these missing values in a statistically rigorous manner, preserving the relationships within the data.

### *3.2 Data imbalance*

We decided to combine outcome categories 1-4 into a single "heart disease" group. After combining, we have 509 samples with heart disease, and 411 samples without heart disease. This approach addresses the class imbalance issue and simplifies the model by focusing on the binary classification of heart disease risk. By grouping the less frequent categories into one, we also improve model interpretability and reduce complexity, allowing us to focus on predicting whether a patient is at risk of a heart disease rather than differentiating between levels of severity.

### *3.3 Data scaling*

Although the scaling issue in our data is not severe, we decided to scale the features to enhance model performance for distance-sensitive algorithms. Scaling ensures that all features contribute equally to distance calculations, preventing features with larger ranges from disproportionately influencing the results. This adjustment may improve the performance of models like k-nearest neighbors and support vector machines, which rely on distances between data points to make predictions.

## APPENDIX

**Figure 1.** Missing values by variable

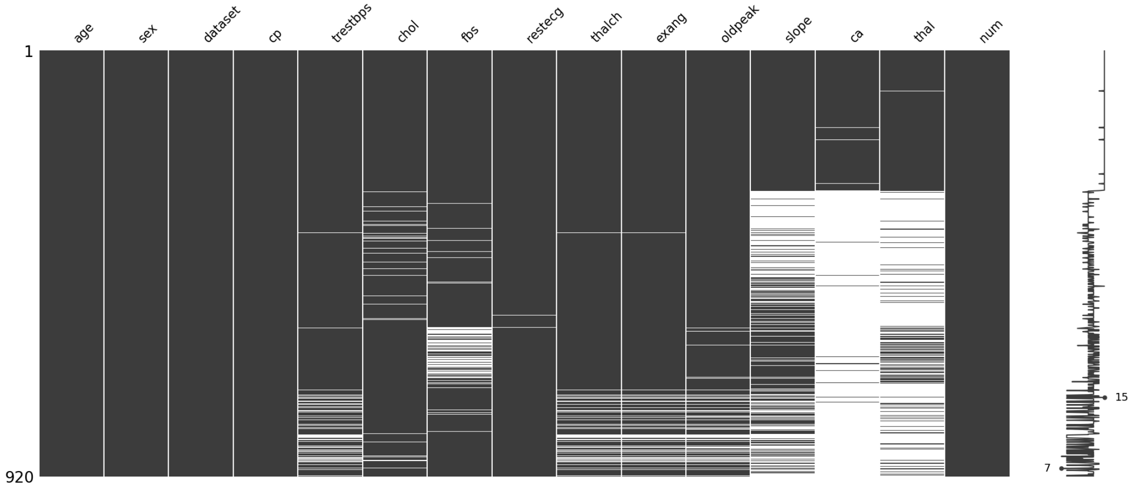


**Figure 2.** Distribution of outcome in the original dataset

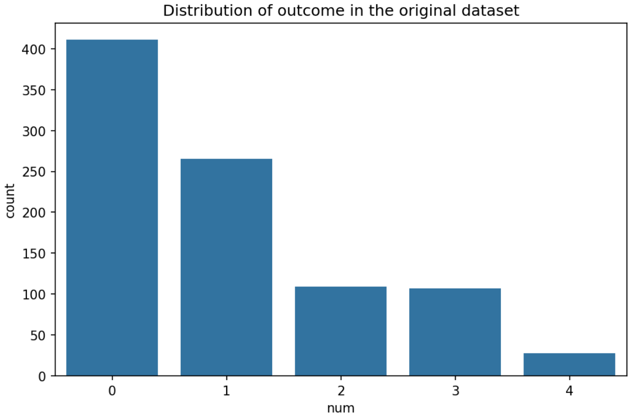
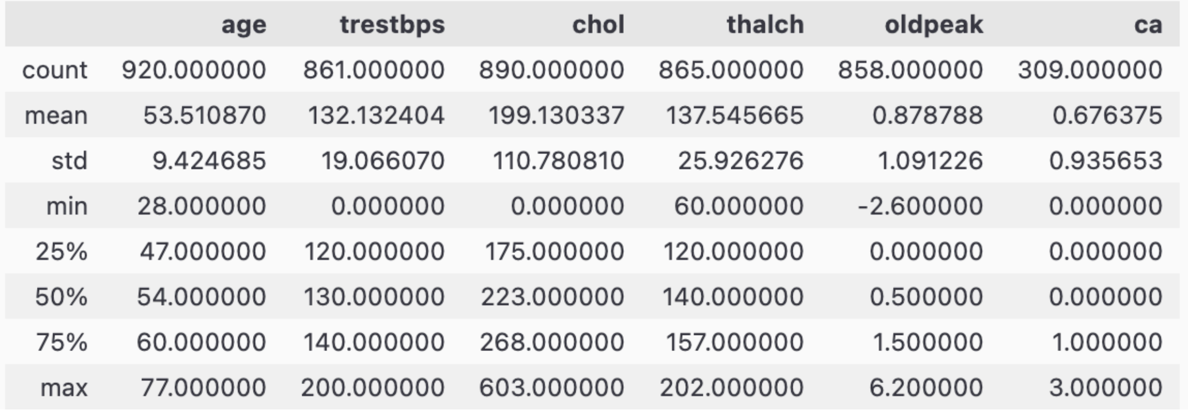


**Table 1.** Statistics for numerical features.



| | age | trestbps | chol | thalch | oldpeak | ca |
|---|---|---|---|---|---|---|
| count | 920.000000 | 861.000000 | 890.000000 | 865.000000 | 858.000000 | 309.000000 |
| mean | 53.510870 | 132.132404 | 199.130337 | 137.545665 | 0.878788 | 0.676375 |
| std | 9.424685 | 19.066070 | 110.780810 | 25.926276 | 1.091226 | 0.935653 |
| min | 28.000000 | 0.000000 | 0.000000 | 60.000000 | -2.600000 | 0.000000 |
| 25% | 47.000000 | 120.000000 | 175.000000 | 120.000000 | 0.000000 | 0.000000 |
| 50% | 54.000000 | 130.000000 | 223.000000 | 140.000000 | 0.500000 | 0.000000 |
| 75% | 60.000000 | 140.000000 | 268.000000 | 157.000000 | 1.500000 | 1.000000 |
| max | 77.000000 | 200.000000 | 603.000000 | 202.000000 | 6.200000 | 3.000000 |

**Figure 3**. Feature correlation (before scaling)

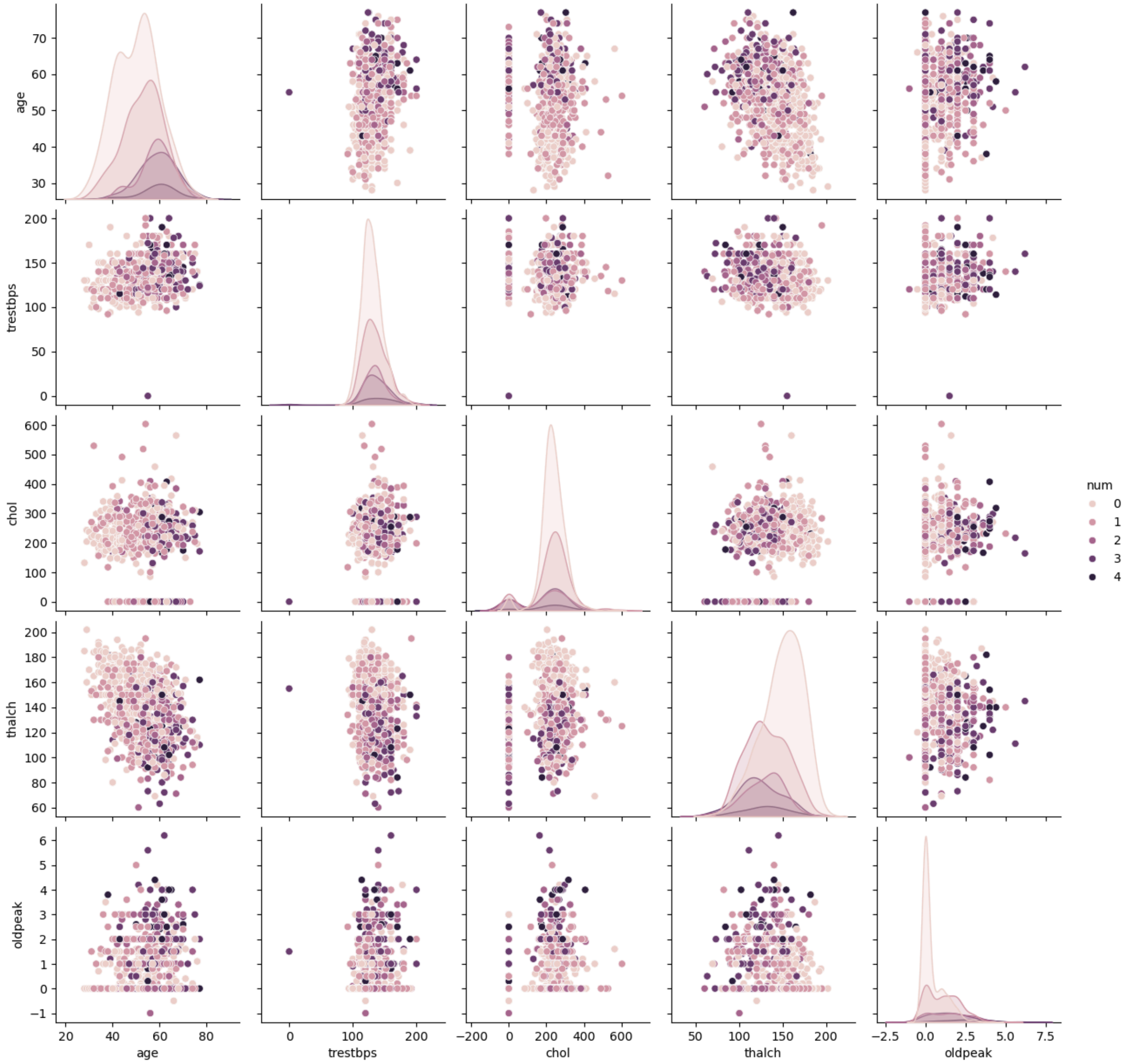


**Figure 4**. Feature correlation (after scaling)

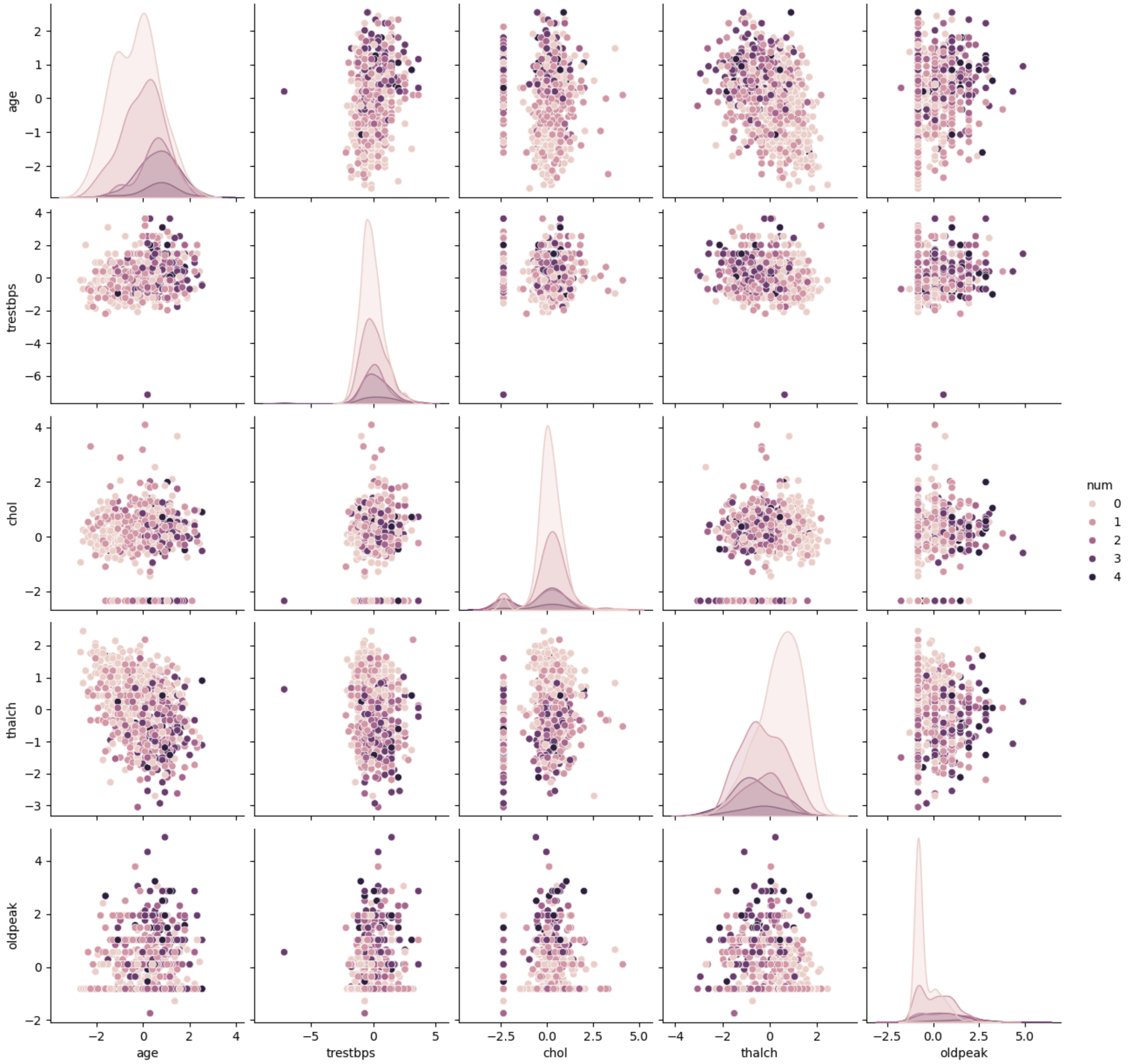
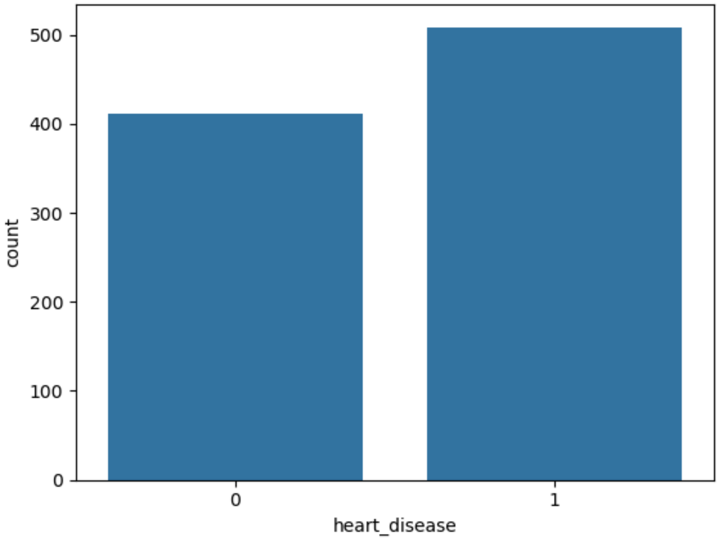


**Figure 5**. Outcome distribution after combining num 1-4.


count
heart_disease