

Clustering Regression for Heart Disease Prediction

Machine Learning I
Final Project

Team 6
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1. **Research Objective**
2. **Data Description**
3. **Modeling Methodology**
4. **Results & Conclusion**

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Background

Heart Disease Affects Us All

- In 2022, 702,880 people died from heart disease. That's the equivalent of **1 in every 5 deaths**. ([Source](#))
- Heart disease remains the **leading cause of death** for men, women, and people of most racial and ethnic groups. ([Source](#))
- Heart disease **cost about \$252.2 billion** from 2019 to 2020. This includes the cost of healthcare services, medicines, and lost productivity due to death. ([Source](#))

Early Detection = Saving Lives & Saving Costs

- Early detection methods are not only cost-effective, but also reduces medical costs for treatment as opposed to no detection. ([Source](#))



Our goal is to:

**Produce interpretable profiles to
help physicians identify high-risk
individuals for further monitoring
and detection.**

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Heart Disease Dataset

Source: [University of California Irvine Machine Learning Repository](#)

13 Primary Features, 1 Target Variable:

- **age:** Age of patient in years
- **sex:** Sex of patient in years
- **cp:** chest pain type
- **trestbps:** resting blood pressure
- **chol:** serum cholesterol in mg/dl
- **fbs:** if fasting blood sugar > 120 mg/dl
- **restecg:** resting electrocardiographic results
- **thalach:** maximum heart rate achieved
- **exang:** exercise induced angina
- **oldpeak:** ST depression induced by exercise relative to rest (numeric)
- **slope:** slope of the peak exercise ST segment (3 attrib)
- **ca:** number of major vessels colored by fluoroscopy (numeric)
- **thal:** thallium stress test
- **num:** angiographic disease status (target v)

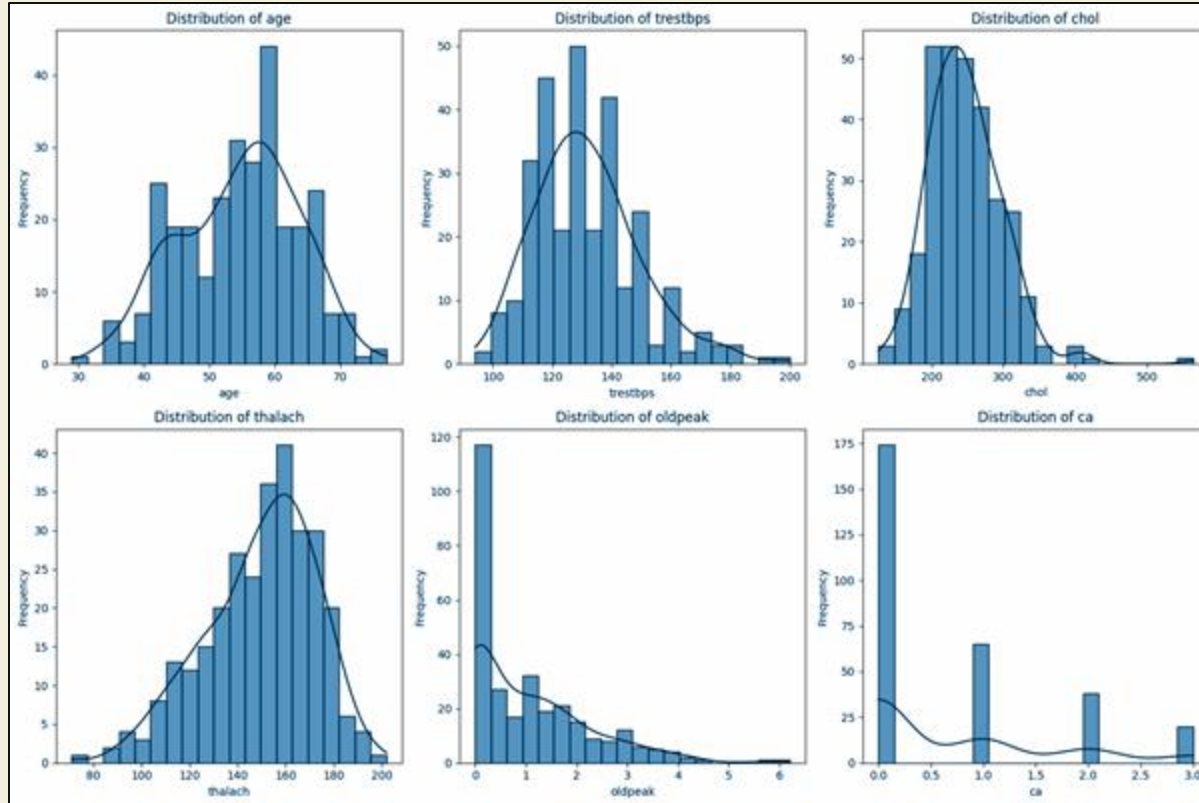
76 Attributes

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1 age: patient's age (years)
2 sex: patient's sex (male/female)
3 cp: chest pain type (0=normal, 1=atypical, 2=typical)
4 trestbps: resting blood pressure (mm Hg)
5 chol: serum cholesterol (mg/dl)
6 fbs: fasting blood sugar > 120 mg/dl (0=no, 1=yes)
7 restecg: resting electrocardiographic results (0=normal, 1=ST-T abnormal, 2=Q-wave abnormal)
8 thalach: maximum heart rate achieved
9 exang: exercise induced angina (0=no, 1=yes)
10 oldpeak: ST depression induced by exercise relative to rest
11 slope: slope of the peak exercise ST segment (0=uphill, 1=flat, 2=downhill)
12 ca: number of major vessels (0-3)
13 thal: thallium stress test (0=normal, 1=fixed defect, 2=reversible defect)
14 num: angiographic disease status (0=normal, 1=old-D, 2=new-D, 3=normal-vessel disease, 4=normal-vessel disease, 5=normal-vessel disease, 6=normal-vessel disease, 7=normal-vessel disease, 8=normal-vessel disease, 9=normal-vessel disease, 10=normal-vessel disease, 11=normal-vessel disease, 12=normal-vessel disease, 13=normal-vessel disease, 14=normal-vessel disease, 15=normal-vessel disease, 16=normal-vessel disease, 17=normal-vessel disease, 18=normal-vessel disease, 19=normal-vessel disease, 20=normal-vessel disease, 21=normal-vessel disease, 22=normal-vessel disease, 23=normal-vessel disease, 24=normal-vessel disease, 25=normal-vessel disease, 26=normal-vessel disease, 27=normal-vessel disease, 28=normal-vessel disease, 29=normal-vessel disease, 30=normal-vessel disease, 31=normal-vessel disease, 32=normal-vessel disease, 33=normal-vessel disease, 34=normal-vessel disease, 35=normal-vessel disease, 36=normal-vessel disease, 37=normal-vessel disease, 38=normal-vessel disease, 39=normal-vessel disease, 40=normal-vessel disease, 41=normal-vessel disease, 42=normal-vessel disease, 43=normal-vessel disease, 44=normal-vessel disease, 45=normal-vessel disease, 46=normal-vessel disease, 47=normal-vessel disease, 48=normal-vessel disease, 49=normal-vessel disease, 50=normal-vessel disease, 51=normal-vessel disease, 52=normal-vessel disease, 53=normal-vessel disease, 54=normal-vessel disease, 55=normal-vessel disease, 56=normal-vessel disease, 57=normal-vessel disease, 58=normal-vessel disease, 59=normal-vessel disease, 60=normal-vessel disease, 61=normal-vessel disease, 62=normal-vessel disease, 63=normal-vessel disease, 64=normal-vessel disease, 65=normal-vessel disease, 66=normal-vessel disease, 67=normal-vessel disease, 68=normal-vessel disease, 69=normal-vessel disease, 70=normal-vessel disease, 71=normal-vessel disease, 72=normal-vessel disease, 73=normal-vessel disease, 74=normal-vessel disease, 75=normal-vessel disease, 76=normal-vessel disease

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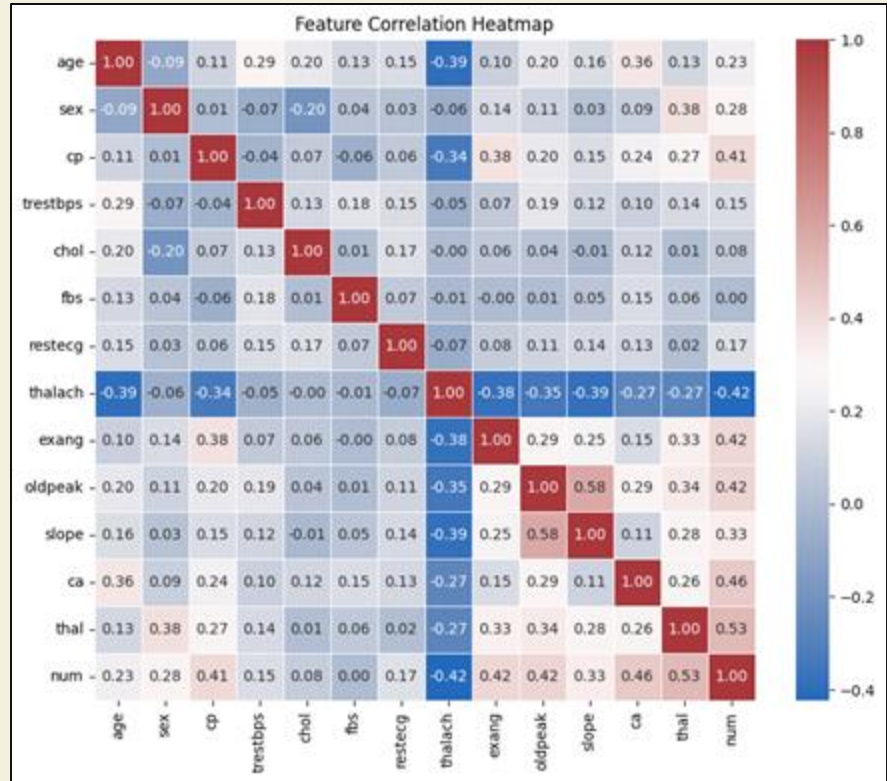
Numeric Feature Distributions



- Ranges of features vary on orders of magnitude implying **need to scale**
- Some features appear to be **non-normally distributed** (e.g. **oldpeak** exhibits heavy right-skew)
- The distribution of **ca** is integer-valued with few distinct values – it may make more sense to **treat it as categorical**

Correlation Analysis

- Strong potential linear predictors of **num**: **cp**, **thalach**, **exang**, **oldpeak**, **ca**, **thal**
- Concerns of potential multicollinearity in the data, particularly based on the correlations between **thalach** and other candidate predictors
- Some weakly correlated features such as **chol** and **fbs** might not be suitable for predicting heart disease on their own, but could yet interact with other variables or exhibit non-linear relationships with the target variable



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Methodology

Machine Learning Feature Selection



Using **Classification Trees**, we can derive the most important features for us to base our clustering methods on.



Clustering Model Selection



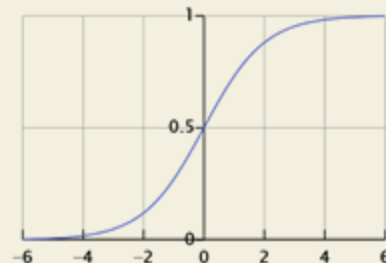
We trained multiple clustering models and compared to find the best clusters to cast on our regression.

We looked at three different methods:

Latent Class Analysis
Gaussian Mixture
K-Prototype Clustering

Within-Cluster Prediction

With our selected clustering method and its derived clusters, we can train a predictive model to help us determine what the probability of heart disease given a patient's cluster.



Feature Selection

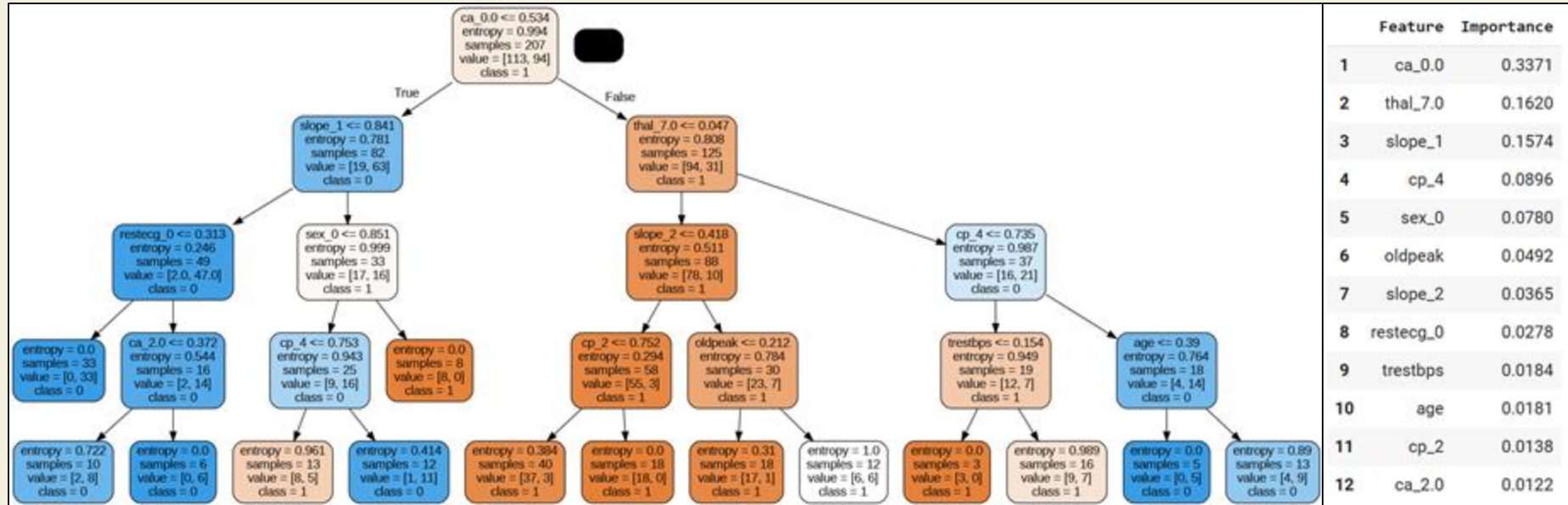
Why Feature Selection?

- Increase model interpretability as well as application generalizability by limiting the number of attributes a physician needs to analyze
- Reduces computational cost as well as noise in the data by focusing only on features which contribute meaningful information
- With the dummy-coding of many categorical variables, reduced feature set helps avoid the curse of dimensionality

Why Classification Tree?

- Captures non-linear relationships between features and the target variable, as well as naturally accounting for feature interactions
- Addresses the multicollinearity concerns from the correlation analysis by choosing additional features based on marginal information gain
- Clearly interpretable as well as less computationally expensive compared to wrapper methods

Feature Selection via Classification Tree



- GridSearchCV used to hyper-parameter tune this model
- Features with **non-zero importance** are selected for further model training
- Train Accuracy: 0.86, Test Accuracy: 0.86, Avg. Precision: 0.86, Avg. Recall: 0.86, Avg. F1: 0.86

Clustering via Gaussian Mixture (1/2)

1. Defined Number of Clusters (Unsupervised Learning)

2 (Positive vs Negative for heart disease)

1. Cluster Means Analysis (Strong differencing factors)

- 'Thal': Thallium Stress Test Result** (Indicates how well blood flows into your heart while exercising or at rest)
- 'cp': Chest pain type**
- 'ca': Number of major vessels (0-3)**



* Chest pain type ('cp')

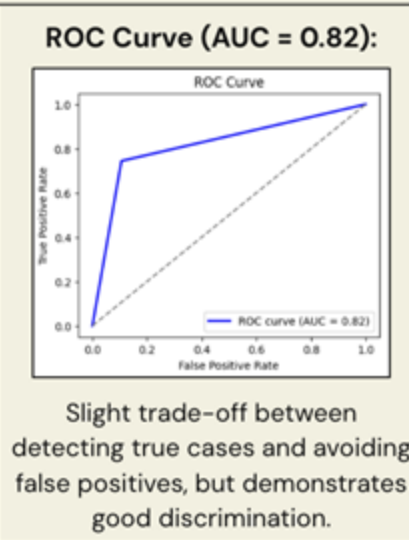
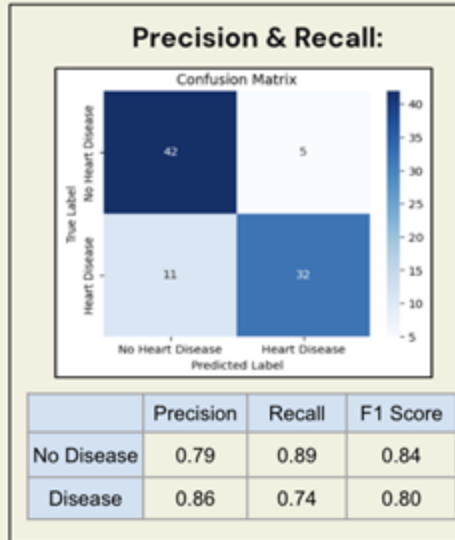
- 1: Typical angina
- 2: Atypical angina
- 3: Non-anginal pain
- 4: Asymptomatic

Clustering via Gaussian Mixture (2/2)

3. Mapping of cluster results to the actual data based on majority class

- a. **Cluster 0:** Negative on Heart Disease
- b. **Cluster 1:** Positive on Heart Disease

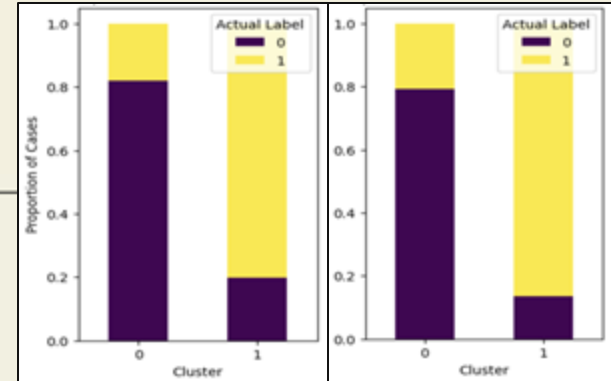
3. Evaluation:



Overall Accuracy:

- Train: 0.81
- Test: 0.82

Distribution of Actual Labels Across Clusters



Clustering via LCA

Method:

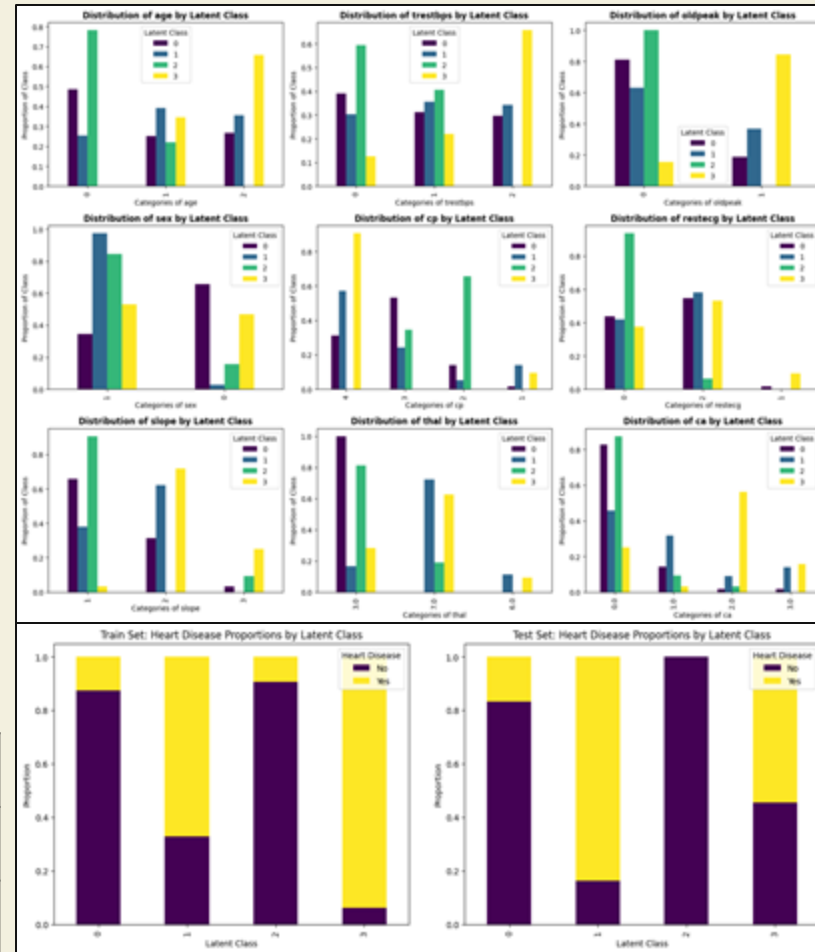
- Due to LCA requiring categorical variables, we processed the continuous variables into bins to “categorize” the variables
- By testing numerous class counts and measuring AIC and BIC, we found **4 classes to be the most optimal** using the elbow method

Cluster Profiles:

- Cluster 0 (**low risk**): majority female, mostly normal heart conditions
- Cluster 1 (**high risk**): mostly male, with some minimal to concerning heart conditions
- Cluster 2 (**low risk**): mostly male, with minimal conditions other than some atypical cardiac chest pain
- Cluster 3 (**high risk**): individuals with concerning heart conditions

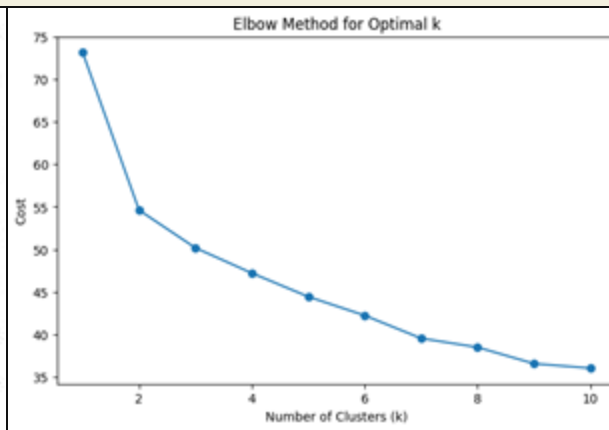
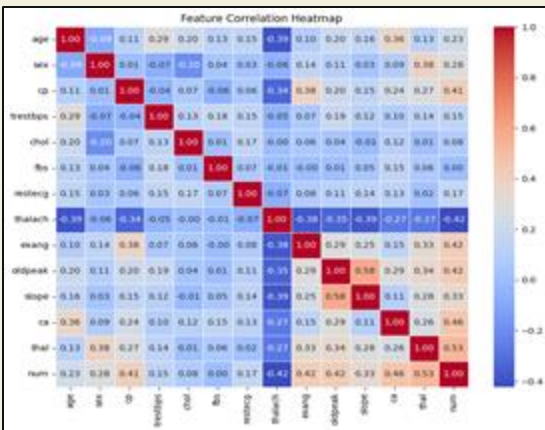
Performance Metrics:

	Precision	Recall	F1 Score
No Disease	0.89	0.75	0.81
Disease	0.75	0.88	0.81



Clustering via K-Prototype Clustering

1. Define the elbow value of 3
2. Fit the model and examine the clusters
 - K-prototype works well with both categorical and numerical variables
3. Assign majority class for prediction
4. Evaluation



Accuracy on Test Set: 0.8222

Confusion Matrix:

$$\begin{bmatrix} 43 & 4 \\ 12 & 31 \end{bmatrix}$$

Classification Report:

	precision	recall	f1-score	support
0	0.78	0.91	0.84	47
1	0.89	0.72	0.79	43
accuracy			0.82	90
macro avg	0.83	0.82	0.82	90
weighted avg	0.83	0.82	0.82	90

Within-Cluster Predictive Modeling

Classification Tree

- The Classification Tree used for feature selection performs with high accuracy, precision, recall, and F1 scores, suggesting it may model this dataset efficiently already
- Retains interpretability and readily captures non-linear relationships as well as interactions between different patient attributes

Logistic Regression

- Comparisons of baseline models in the literature on this dataset suggest Logistic Regression performs better than SVM, Random Forest, and Neural Net Classification models for this data on average
- A statistical model allows for probabilistic results interpretations and does not rely on heuristics

Model Comparison - Training Accuracy

Cluster Regression Combination	Latent Class Analysis	Gaussian Mixture	K-Prototype
Classification Tree	0.92	0.91	0.91
Logistic Regression	0.89	0.88	0.89

Model Comparison - Testing Accuracy

Cluster Regression Combination	Latent Class Analysis	Gaussian Mixture	K-Prototype
Classification Tree	0.82 -0.10	0.73 -0.18	0.80 -0.11
Logistic Regression	0.81 -0.08	<u>0.87</u> <u>-0.01</u>	0.81 -0.08

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Final Model Interpretation

Selected Clustering Method: Gaussian Mixture

- 2 clusters (High Risk, Low Risk): easy to profile and interpret
- Allows for calculating key metric: Relative Risk

Key Indicator: Relative Risk (RR)

$$\frac{\text{mean } \mathbb{P}(\text{num} = 1 | C_1)}{\text{mean } \mathbb{P}(\text{num} = 1 | C_0)} \approx \frac{\text{proportion of num} = 1 \text{ in } C_1}{\text{proportion of num} = 1 \text{ in } C_0} = RR = 4.43$$

- A patient classified in the “high-risk” cluster (C_1) is 4.4 times more likely to develop heart disease than a patient classified in the “low risk” cluster (C_0)
- Our logistic regression model’s predictive probabilities of heart disease converge to the empirical proportions, indicating model stability and well-separated clusters

```
Relative Risk (RR) Analysis
Heart Disease RR by Cluster
*****
LogReg Probabilities
  RR in Cluster 1: 4.4309
  RR in Cluster 0: 0.2257
  P(HD|Cluster 1): 0.8022
  P(HD|Cluster 0): 0.1810
*****
Frequentist Proportions
  RR in Cluster 1: 4.4312
  RR in Cluster 0: 0.2257
  P(HD|Cluster 1): 0.8022
  P(HD|Cluster 0): 0.1810
*****
```

Conclusion

With easy-to-interpret clusters with distinct risk levels for developing heart diseases, we believe **our model can be implemented as a “Red Flag” system to assist physicians in detecting patients who are at risk of developing heart diseases** based on their health condition.

Further development of the model include:

- Incorporating patients' lifestyle traits to further develop the model to recognize lifestyle patterns that might contribute towards risk levels
- Expanding the training dataset to further refine and validate our model



Moral of the Story:

The Machine Never Stops Learning

Thanks for listening!