
BIG DATA PROJECT REPORT

Heart Dieses

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DOMAIN:

Heart disease remains a leading cause of mortality worldwide, emphasizing the critical need for early detection and effective intervention. By leveraging predictive modeling techniques, healthcare professionals can identify at-risk individuals and make informed decisions to prevent severe outcomes. This project focuses on developing and evaluating machine learning models, specifically Logistic Regression and Decision Tree classifiers, to predict the likelihood of heart disease based on patient data. The analysis aims to identify the most effective model for accurate classification, thereby contributing to enhanced diagnostic accuracy and better patient outcomes.

1. RESOURCE:

<https://www.kaggle.com/datasets/johnsmith88/heart-disease-dataset>

Domain Knowledge and Data Relevance:

- **sex (Gender):** Depending on the context of the analysis or the model being developed, certain columns might not provide significant predictive value. For example, in some heart disease prediction models, while gender can be a risk factor, it may not be crucial for a model designed to focus on other aspects such as medical measurements, lifestyle factors, or other clinical data. If gender doesn't contribute meaningfully to the classification in your model or if the model is designed to generalize across populations in a way that doesn't require it, dropping this column can help simplify the model.
- **cp (Chest Pain Type):** If the dataset contains specific types of chest pain (like typical angina, atypical angina, non-anginal pain, and asymptomatic), but the model is designed to focus more on general clinical measurements (e.g., cholesterol, age, blood pressure), the chest pain type may be less relevant. Some models may aim to focus on patterns of data that are more predictive of heart disease rather than specific symptom categories.
- **slope (Slope of the Peak Exercise ST Segment):** If `slope` refers to the shape of the ST segment during exercise, it may be less important for certain kinds of analysis or predictive modeling, depending on the context. If the model is being designed to look at a broader set of features, the `slope` of the ST segment might not be as informative or significant as other clinical features, like cholesterol levels, blood pressure, or other markers that directly correlate with heart disease risk.

1. Reducing Dimensionality:

- By removing columns that don't provide significant information or are less relevant, you reduce the number of features, which helps to decrease the complexity of the model. Fewer features often mean the model will train faster, and the risk of overfitting is reduced. This is especially

important in cases where the dataset has a high number of features that do not contribute to the target variable.

2. Avoiding Multicollinearity:

- If the dropped columns are highly correlated with other features (multicollinearity), keeping them can cause issues with model training, especially in linear models like logistic regression. Highly correlated features can lead to unstable coefficients and unreliable predictions. Removing correlated or redundant features improves model performance and interpretability.

3. Improving Model Interpretability:

- Models can become difficult to interpret when they are too complex or include irrelevant features. By removing unnecessary columns, you simplify the model and make it easier to understand and interpret the results. This can be particularly important when the goal is to provide clear, actionable insights.

4. Preprocessing and Feature Engineering:

- Feature selection is an important step in model preparation. Dropping non-relevant columns can be part of feature engineering, where only the most useful and predictive features are kept. This ensures that the model focuses on the most important patterns in the data, improving both its performance and generalization.

5. In Summary:

The columns `sex`, `cp`, and `slope` are being dropped because, based on the specific goals and scope of the analysis or model, they are either redundant, not significantly predictive, or not necessary for the model to function effectively. Removing these columns helps streamline the data, reduce model complexity, and improve overall performance without losing important information for heart disease prediction.


Comparison of Regression Tree Models in Heart Disease Classification:

Introduction

The goal of this project is to evaluate and compare the performance of three regression tree models for heart disease classification. These models differ in their training-to-testing data split ratios, which are as follows:

1. Model 1: 65% training data, 35% testing data
2. Model 2: 70% training data, 30% testing data
3. Model 3: 80% training data, 20% testing data

Transform Data:



age	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	ca	thal	target	features
52	125	212	0	1	168	0	1.0	2	3	0	[52.0,125.0,212.0,0.0,1.0,168.0,0.0,1.0,2.0,3.0]
53	140	203	1	0	155	1	3.1	0	3	0	[53.0,140.0,203.0,1.0,0.0,155.0,1.0,3.1,0.0,3.0]
70	145	174	0	1	125	1	2.6	0	3	0	[70.0,145.0,174.0,0.0,1.0,125.0,1.0,2.6,0.0,3.0]
61	148	203	0	1	161	0	0.0	1	3	0	[61.0,148.0,203.0,0.0,1.0,161.0,0.0,0.0,1.0,3.0]
62	138	294	1	1	106	0	1.9	3	2	0	[62.0,138.0,294.0,1.0,1.0,106.0,0.0,1.9,3.0,2.0]

only showing top 5 rows

The performance of each model is assessed using metrics derived from their respective confusion matrices.

Methodology

The models were trained and tested using the specified data split ratios. The following performance metrics were computed for each model:

- **Accuracy:** Proportion of correctly classified instances.
- **Classification Error:** Proportion of misclassified instances.
- **Sensitivity/Recall:** Proportion of actual positives correctly identified.
- **Specificity:** Proportion of actual negatives correctly identified.
- **Precision:** Proportion of predicted positives that are actual positives.
- **False Positive Rate:** Proportion of negatives incorrectly classified as positives.

Results

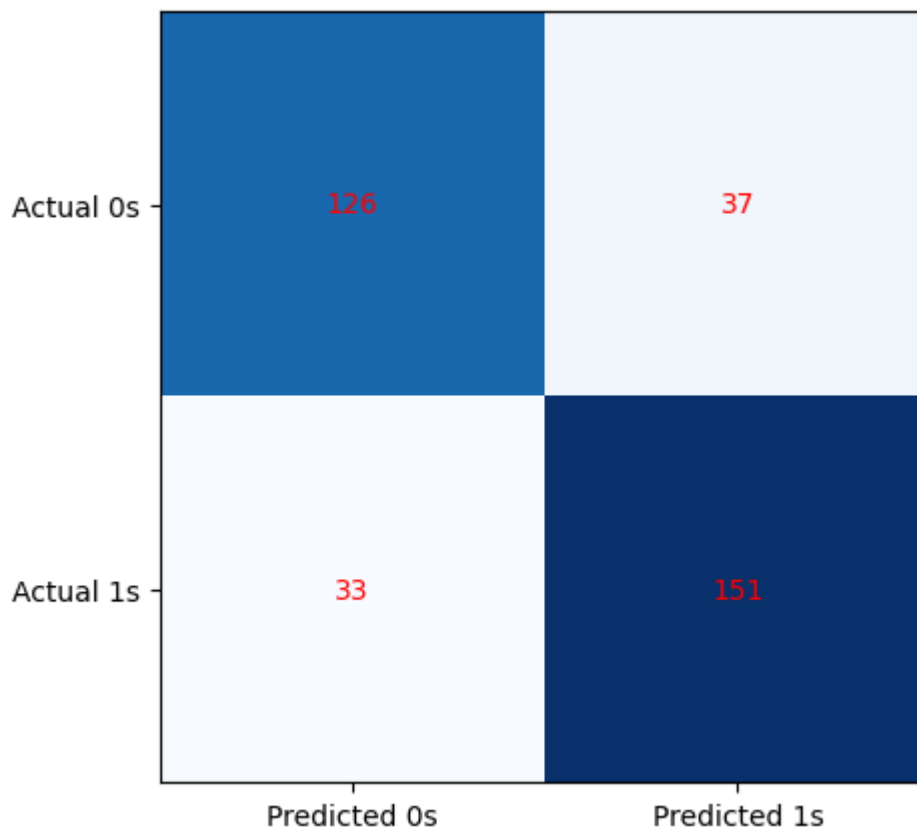
Model 1 (Test ratio 0.35)

- **Accuracy:** 0.7983
- **Classification Error:** 0.2017
- **Sensitivity/Recall:** 0.8207
- **Specificity:** 0.7730
- **Precision:** 0.8032
- **False Positive Rate:** 0.2270

```
#####
                        This is for 35% Test and 65% Train
#####
+---+---+---+---+---+---+---+---+---+---+---+---+
|age|trestbps|chol|fbs|restecg|thalach|exang|oldpeak| ca|thal|prediction|
+---+---+---+---+---+---+---+---+---+---+---+---+
| 34|    118| 182|  0|      0|   174|   0|   0.0|  0|  2|      1.0|
| 34|    118| 182|  0|      0|   174|   0|   0.0|  0|  2|      1.0|
| 34|    118| 210|  0|      1|   192|   0|   0.7|  0|  2|      1.0|
| 34|    118| 210|  0|      1|   192|   0|   0.7|  0|  2|      1.0|
| 35|    120| 198|  0|      1|   130|   1|   1.6|  0|  3|      0.0|
+---+---+---+---+---+---+---+---+---+---+---+---+
only showing top 5 rows

+---+---+---+
|target|prediction|count|
+---+---+---+
|    1|      0.0|   33|
|    0|      0.0|  126|
|    1|      1.0|  151|
|    0|      1.0|   37|
+---+---+---+
```

CONFUSION MATRIX:



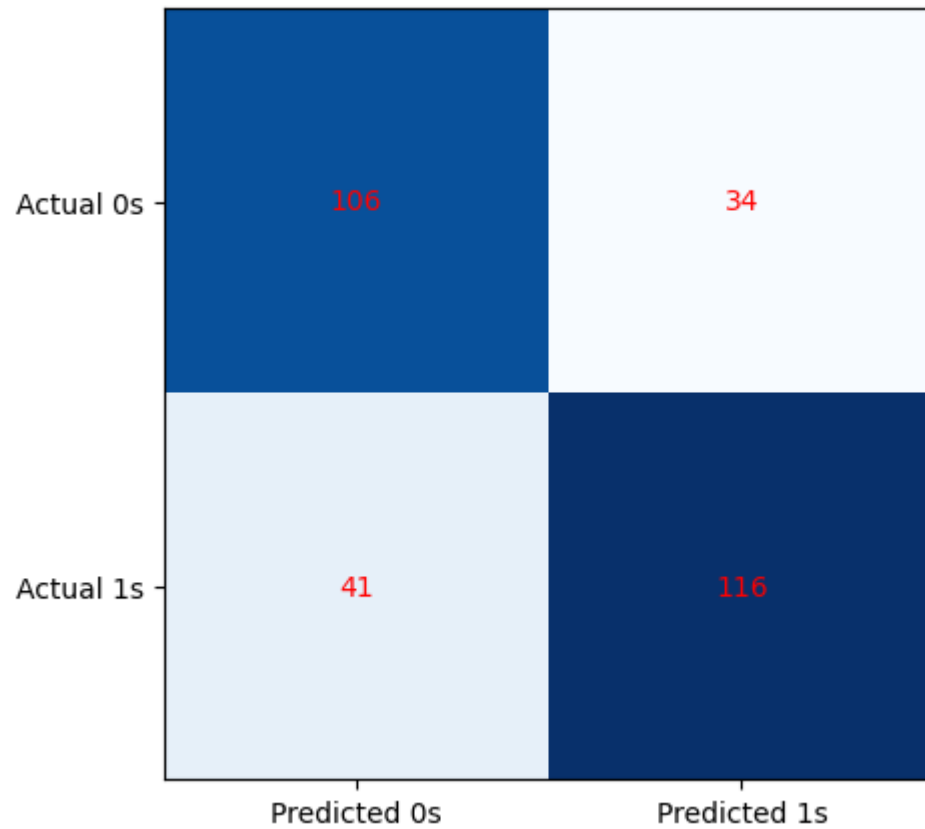
Model 2 (Test ratio 0.3)

- **Accuracy:** 0.7475
- **Classification Error:** 0.2525
- **Sensitivity/Recall:** 0.7389
- **Specificity:** 0.7571
- **Precision:** 0.7733
- **False Positive Rate:** 0.2429

```
#####
                        This is for 30% Test and 70% Train
#####
+---+---+---+---+---+---+---+---+---+---+
|age|trestbps|chol|fbs|restecg|thalach|exang|oldpeak| ca|thal|prediction|
+---+---+---+---+---+---+---+---+---+---+
| 29|    130|  284|  0|      0|   202|   0|   0.0|  0|  2|      1.0|
| 34|    118|  182|  0|      0|   174|   0|   0.0|  0|  2|      1.0|
| 34|    118|  210|  0|      1|   192|   0|   0.7|  0|  2|      1.0|
| 35|    120|  198|  0|      1|   130|   1|   1.6|  0|  3|      0.0|
| 35|    122|  192|  0|      1|   174|   0|   0.0|  0|  2|      1.0|
+---+---+---+---+---+---+---+---+---+---+
only showing top 5 rows
```

```
+---+---+---+
|target|prediction|count|
+---+---+---+
|    1|      0.0|   41|
|    0|      0.0|  106|
|    1|      1.0|  116|
|    0|      1.0|   34|
+---+---+---+
```


CONFUSION MATRIX:



Model 3 (Test ratio 0.2)

- **Accuracy:** 0.7949
- **Classification Error:** 0.2051
- **Sensitivity/Recall:** 0.8400
- **Specificity:** 0.7474
- **Precision:** 0.7778
- **False Positive Rate:** 0.2526

#####

This is for 20% Test and 80% Train

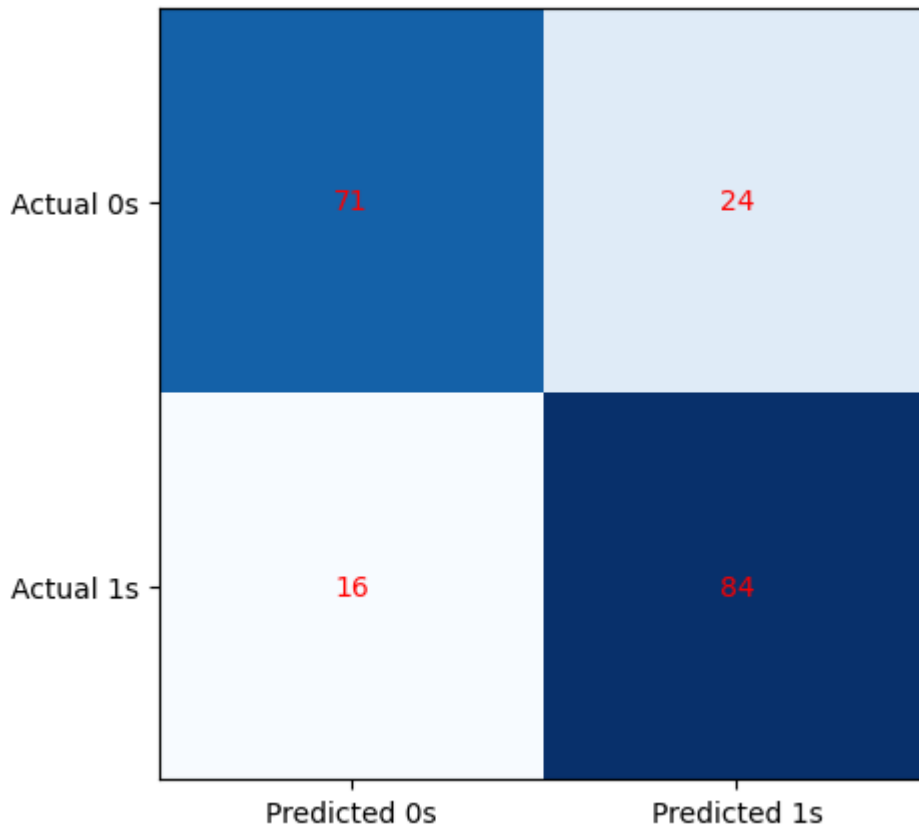
#####

age	trestbps	chol	fb	restecg	thalach	exang	oldpeak	ca	thal	prediction
29	130	204	0	0	202	0	0.0	0	2	1.0
29	130	204	0	0	202	0	0.0	0	2	1.0
35	122	192	0	1	174	0	0.0	0	2	1.0
35	138	183	0	1	182	0	1.4	0	2	1.0
37	120	215	0	1	170	0	0.0	0	2	1.0

only showing top 5 rows

target	prediction	count
1	0.0	16
0	0.0	71
1	1.0	84
0	1.0	24

CONFUSION MATRIX:



Analysis and Comparison

1. **Accuracy:** Model 1 has the highest accuracy (0.7983), followed closely by Model 3 (0.7949). Model 2 has the lowest accuracy (0.7475).
2. **Classification Error:** Model 1 has the lowest classification error (0.2017), indicating better overall performance compared to the other models.
3. **Sensitivity/Recall:** Model 3 has the highest sensitivity (0.8400), suggesting it is best at identifying actual positives. Model 1 follows closely (0.8207), while Model 2 has the lowest sensitivity (0.7389).
4. **Specificity:** Model 1 achieves the highest specificity (0.7730), meaning it is better at correctly identifying negatives compared to the other models.
5. **Precision:** Model 1 has the highest precision (0.8032), indicating it has the lowest proportion of false positives among predicted positives.
6. **False Positive Rate:** Model 1 has the lowest false positive rate (0.2270), which aligns with its high specificity.

Conclusion

Based on the analysis, **Model 1** (65% training data, 35% testing data) demonstrates the best overall performance for heart disease classification. It achieves the highest accuracy, precision, and specificity, while maintaining a competitive sensitivity and the lowest false positive rate. Model 3 shows strong sensitivity but lags in specificity and false positive rate. Model 2 performs the weakest among the three models.

Comparison of Decision Tree Models in Heart Disease Classification:

Introduction

The goal of this project is to evaluate and compare the performance of three decision tree models for heart disease classification. These models differ in their training-to-testing data split ratios, which are as follows:

1. Model 1: 65% training data, 35% testing data
2. Model 2: 70% training data, 30% testing data
3. Model 3: 80% training data, 20% testing data

The performance of each model is assessed using metrics derived from their respective confusion matrices.

Methodology

The models were trained and tested using the specified data split ratios. The following performance metrics were computed for each model:

- **Accuracy:** Proportion of correctly classified instances.
- **Classification Error:** Proportion of misclassified instances.
- **Sensitivity/Recall:** Proportion of actual positives correctly identified.
- **Specificity:** Proportion of actual negatives correctly identified.
- **Precision:** Proportion of predicted positives that are actual positives.
- **False Positive Rate:** Proportion of negatives incorrectly classified as positives.

Results

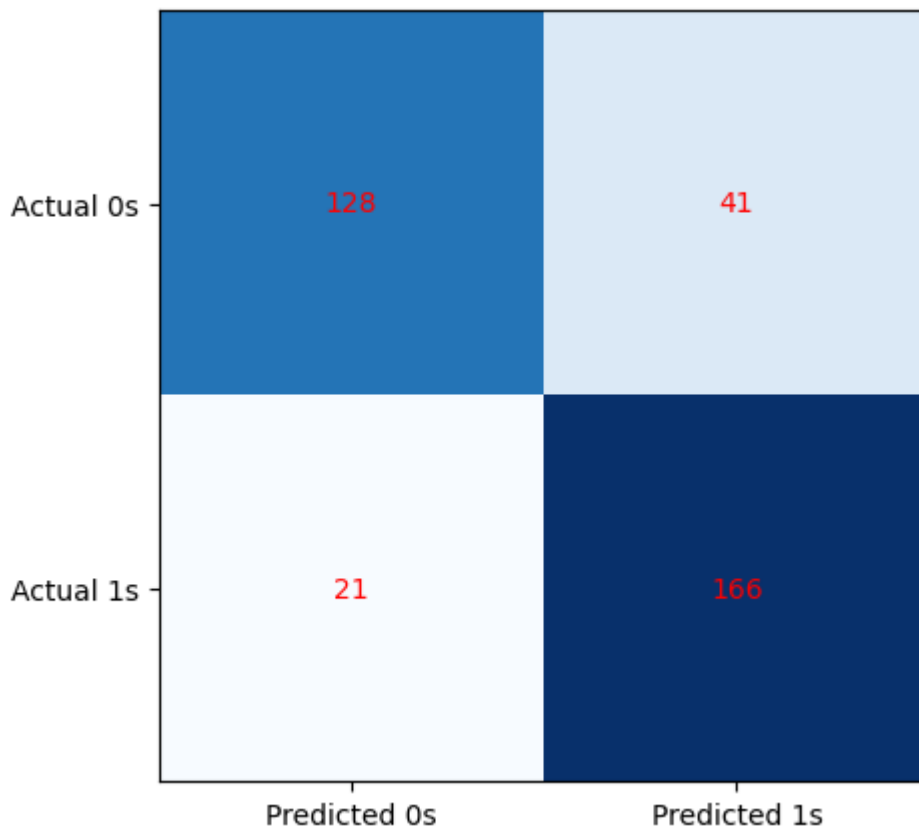
Model 1 (Test ratio 0.35)

- Accuracy: 0.8409
- Classification Error: 0.1591
- Sensitivity/Recall: 0.8378
- Specificity: 0.8443
- Precision: 0.8564
- False Positive Rate: 0.1557

```
#####
                                This is for 35% Test and 65% Train
#####
+-----+-----+-----+-----+-----+-----+-----+-----+
|age|trestbps|chol|fbs|restecg|thalach|exang|oldpeak| ca|thal|prediction|
+-----+-----+-----+-----+-----+-----+-----+-----+
| 29|    130|  204|  0|      0|    202|   0|   0.0|  0|  2|      1.0|
| 34|    118|  182|  0|      0|    174|   0|   0.0|  0|  2|      1.0|
| 35|    120|  198|  0|      1|    130|   1|   1.6|  0|  3|      0.0|
| 35|    122|  192|  0|      1|    174|   0|   0.0|  0|  2|      1.0|
| 35|    122|  192|  0|      1|    174|   0|   0.0|  0|  2|      1.0|
+-----+-----+-----+-----+-----+-----+-----+-----+
only showing top 5 rows

+-----+-----+-----+
|target|prediction|count|
+-----+-----+-----+
|      1|         0.0|   21|
|      0|         0.0|  128|
|      1|         1.0|  166|
|      0|         1.0|   41|
+-----+-----+-----+
```

CONFUSION MATRIX:



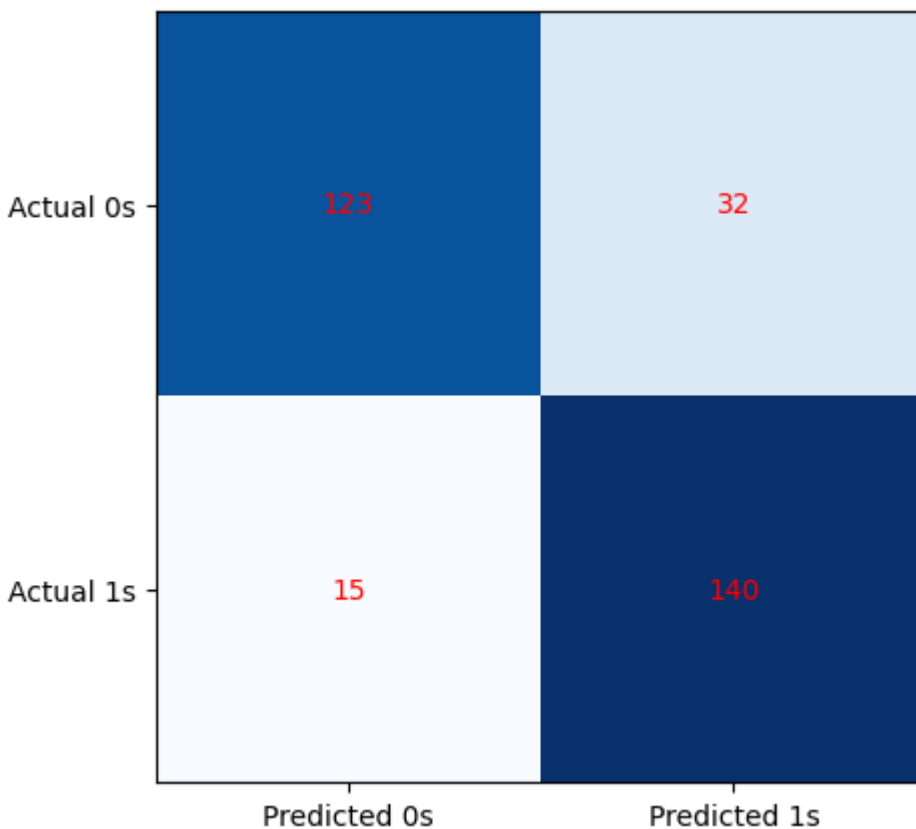
Model 2 (Test ratio 0.3)

- **Accuracy:** 0.8421
- **Classification Error:** 0.1579
- **Sensitivity/Recall:** 0.8611
- **Specificity:** 0.8250
- **Precision:** 0.8158
- **False Positive Rate:** 0.1750

```
#####
                                This is for 30% Test and 70% Train
#####
+---+---+---+---+---+---+---+---+---+---+---+
|age|trestbps|chol|fbs|restecg|thalach|exang|oldpeak| ca|thal|prediction|
+---+---+---+---+---+---+---+---+---+---+---+
| 29|    130| 204|  0|    0|   202|    0|    0.0|  0|  2|    1.0|
| 29|    130| 204|  0|    0|   202|    0|    0.0|  0|  2|    1.0|
| 34|    118| 182|  0|    0|   174|    0|    0.0|  0|  2|    1.0|
| 34|    118| 182|  0|    0|   174|    0|    0.0|  0|  2|    1.0|
| 34|    118| 210|  0|    1|   192|    0|    0.7|  0|  2|    1.0|
+---+---+---+---+---+---+---+---+---+---+
only showing top 5 rows

+---+---+---+
|target|prediction|count|
+---+---+---+
|    1|    0.0|   15|
|    0|    0.0|  123|
|    1|    1.0|  140|
|    0|    1.0|   32|
+---+---+---+
```

CONFUSION MATRIX:



Model 3 (Test ratio 0.2)

- Accuracy: 0.8649
- Classification Error: 0.1351
- Sensitivity/Recall: 0.8500
- Specificity: 0.8824
- Precision: 0.8947
- False Positive Rate: 0.1176

```
#####  
                                This is for 20% Test and 80% Train  
#####
```

```
+---+-----+---+---+---+---+---+---+---+---+  
|age|trestbps|chol|fbs|restecg|thalach|exang|oldpeak| ca|thal|prediction|  
+---+-----+---+---+---+---+---+---+---+---+  
| 29|    130| 204|  0|      0|   202|   0|   0.0|  0|  2|      1.0|  
| 35|    120| 198|  0|      1|   130|   1|   1.6|  0|  3|      0.0|  
| 35|    122| 192|  0|      1|   174|   0|   0.0|  0|  2|      1.0|  
| 35|    138| 183|  0|      1|   182|   0|   1.4|  0|  2|      1.0|  
| 37|    130| 250|  0|      1|   187|   0|   3.5|  0|  2|      1.0|
```

only showing top 5 rows

```
+---+-----+---+  
|target|prediction|count|  
+---+-----+---+  
|    1|      0.0|   13|  
|    0|      0.0|   96|  
|    1|      1.0|   90|  
|    0|      1.0|   17|  
+---+-----+---+
```


CONFUSION MATRIX:

Actual 0s	96	17
Actual 1s	13	90
	Predicted 0s	Predicted 1s

Analysis and Comparison

1. **Accuracy:** Model 3 demonstrates the highest accuracy (0.8649), followed by Model 2 (0.8421) and Model 1 (0.8409).
2. **Classification Error:** Model 3 has the lowest classification error (0.1351), indicating it is the most reliable in terms of minimizing misclassification.
3. **Sensitivity/Recall:** Model 2 achieves the highest sensitivity (0.8611), showing it is the most effective at identifying actual positives. Model 3 closely follows (0.8500), while Model 1 has the lowest sensitivity (0.8378).
4. **Specificity:** Model 3 achieves the highest specificity (0.8824), meaning it is the most accurate in identifying actual negatives. Model 1 (0.8443) outperforms Model 2 (0.8250) in this metric.
5. **Precision:** Model 3 has the highest precision (0.8947), indicating it has the lowest proportion of false positives among predicted positives. Model 1 follows (0.8564), and Model 2 has the lowest precision (0.8158).
6. **False Positive Rate:** Model 3 exhibits the lowest false positive rate (0.1176), aligning with its high specificity. Model 1 (0.1557) is better than Model 2 (0.1750) in this regard.

Conclusion

Based on the comparison of performance metrics, **Model 3** (80% training data, 20% testing data) is the best performing model for heart disease classification. It demonstrates the highest accuracy, specificity, and precision, while maintaining a competitive sensitivity and the lowest false positive rate.

Model 2 shows the highest sensitivity but struggles with precision and false positive rate. **Model 1** is balanced but is outperformed by Model 3 in most metrics.

Comprehensive Comparison of Decision and Regression Trees for Heart Disease:

Introduction

This project evaluates and compares six models, three using the Decision Tree algorithm and three using the Regression Tree algorithm, for heart disease classification. The models are differentiated by their training-to-testing data split ratios:

- **Decision Tree Models:**
 1. Model 1: 65% training data, 35% testing data
 2. Model 2: 70% training data, 30% testing data
 3. Model 3: 80% training data, 20% testing data
- **Regression Tree Models:**
 1. Model 4: 65% training data, 35% testing data
 2. Model 5: 70% training data, 30% testing data
 3. Model 6: 80% training data, 20% testing data

The performance of these models is evaluated using metrics derived from their confusion matrices.

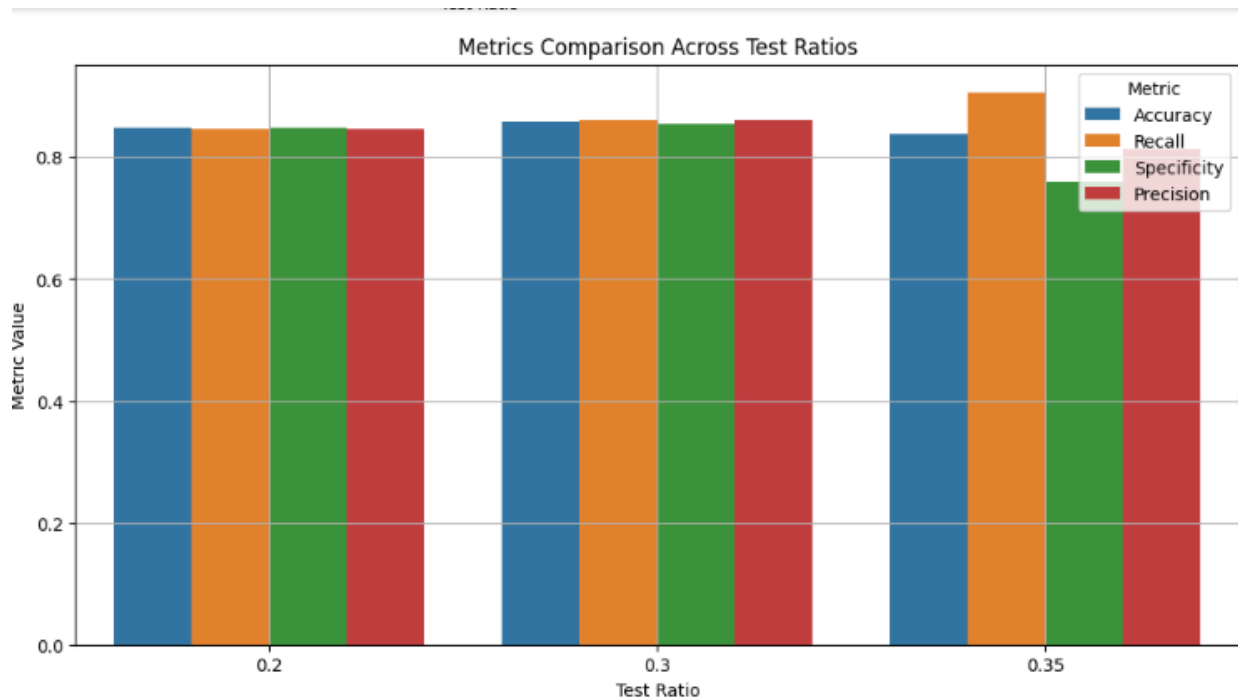
Methodology

For each model, the following performance metrics were computed:

- **Accuracy:** Proportion of correctly classified instances.
- **Classification Error:** Proportion of misclassified instances.
- **Sensitivity/Recall:** Proportion of actual positives correctly identified.
- **Specificity:** Proportion of actual negatives correctly identified.
- **Precision:** Proportion of predicted positives that are actual positives.
- **False Positive Rate:** Proportion of negatives incorrectly classified as positives.

Results

Decision Tree Models



Model 1 (Test ratio 0.35):

- Accuracy: 0.8409
- Classification Error: 0.1591
- Sensitivity/Recall: 0.8378
- Specificity: 0.8443
- Precision: 0.8564
- False Positive Rate: 0.1557

Model 2 (Test ratio 0.3):

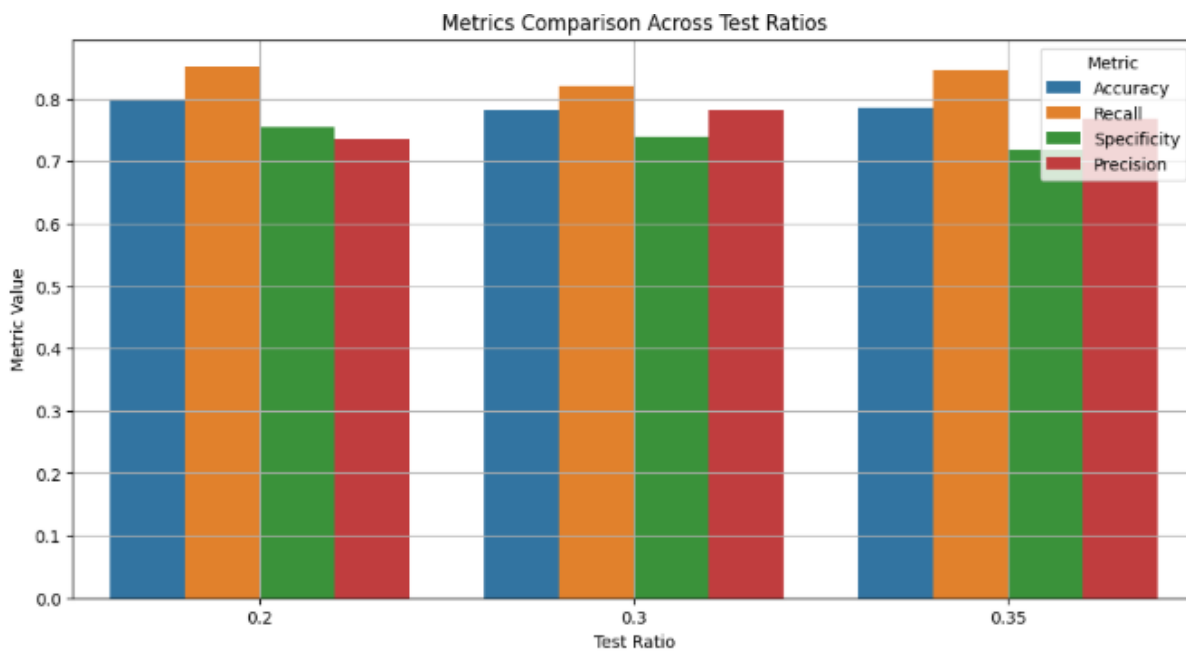
- Accuracy: 0.8421
- Classification Error: 0.1579
- Sensitivity/Recall: 0.8611
- Specificity: 0.8250
- Precision: 0.8158
- False Positive Rate: 0.1750

Model 3 (Test ratio 0.2):

- Accuracy: 0.8649
- Classification Error: 0.1351
- Sensitivity/Recall: 0.8500

- Specificity: 0.8824
- Precision: 0.8947
- False Positive Rate: 0.1176

Regression Tree Models



Model 4 (Test ratio 0.35):

- Accuracy: 0.7983
- Classification Error: 0.2017
- Sensitivity/Recall: 0.8207
- Specificity: 0.7730
- Precision: 0.8032
- False Positive Rate: 0.2270

Model 5 (Test ratio 0.3):

- Accuracy: 0.7475
- Classification Error: 0.2525
- Sensitivity/Recall: 0.7389
- Specificity: 0.7571
- Precision: 0.7733
- False Positive Rate: 0.2429

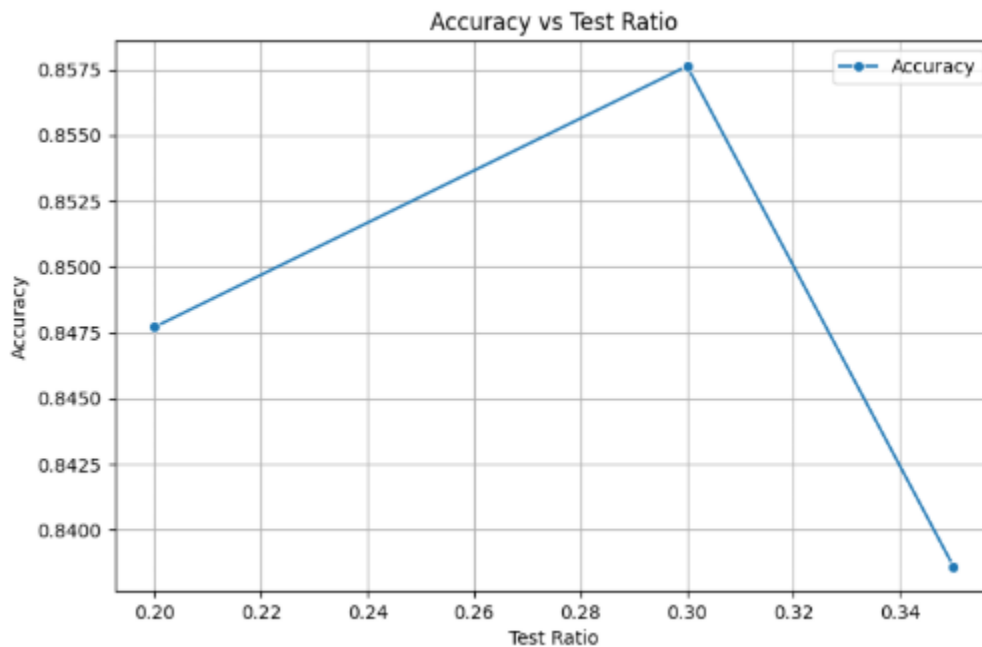
Model 6 (Test ratio 0.2):

- Accuracy: 0.7949
- Classification Error: 0.2051
- Sensitivity/Recall: 0.8400
- Specificity: 0.7474
- Precision: 0.7778
- False Positive Rate: 0.2526

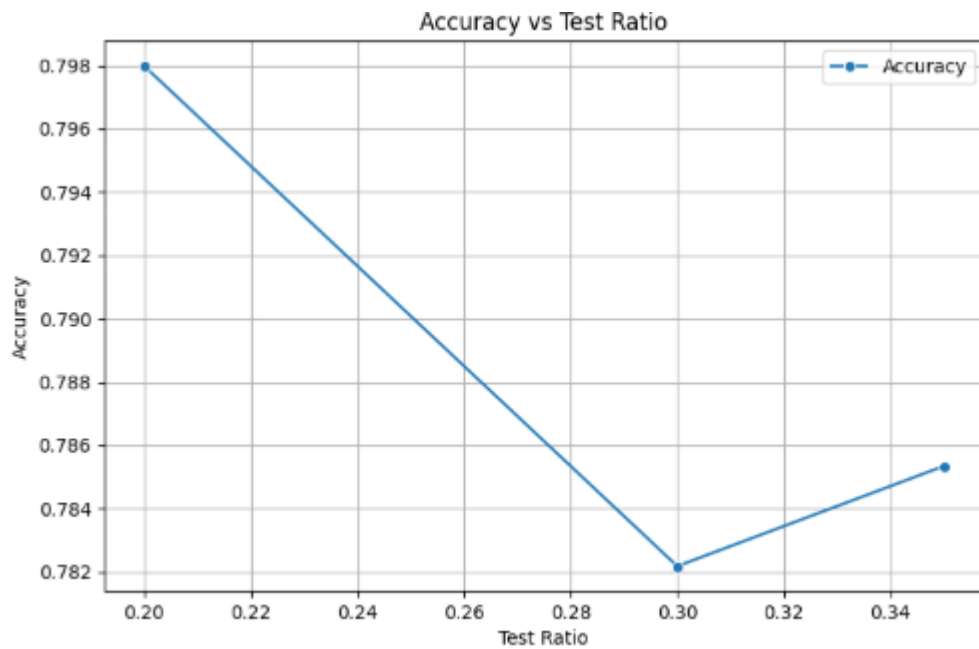
Analysis and Comparison

Accuracy

- Decision Tree Model 3 (0.8649) outperforms all other models in accuracy.



- Regression Tree Model 4 (0.7983) is the best among regression tree models but lags behind decision tree models.

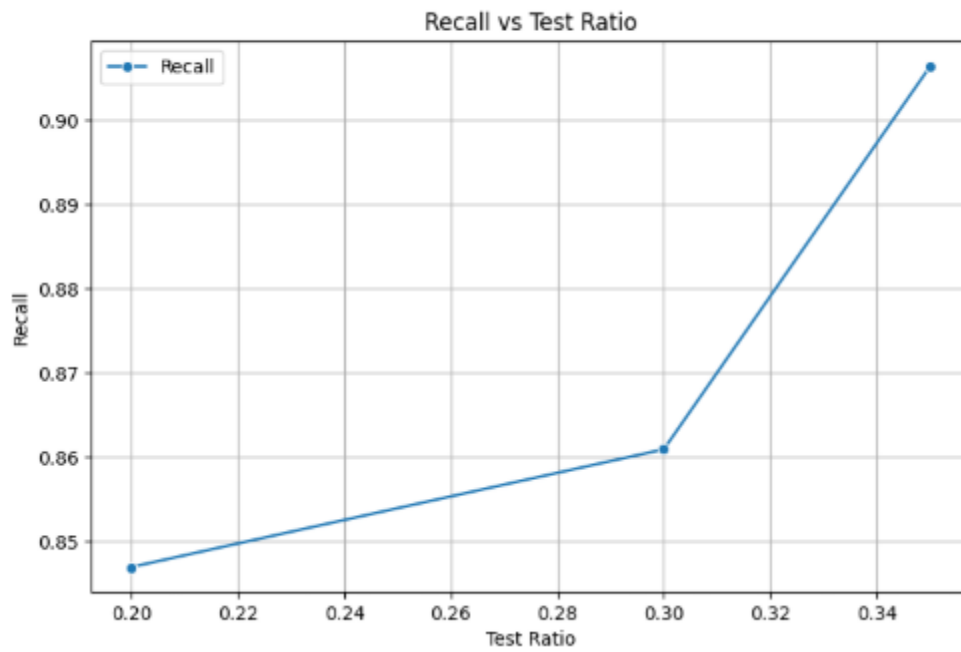


Classification Error

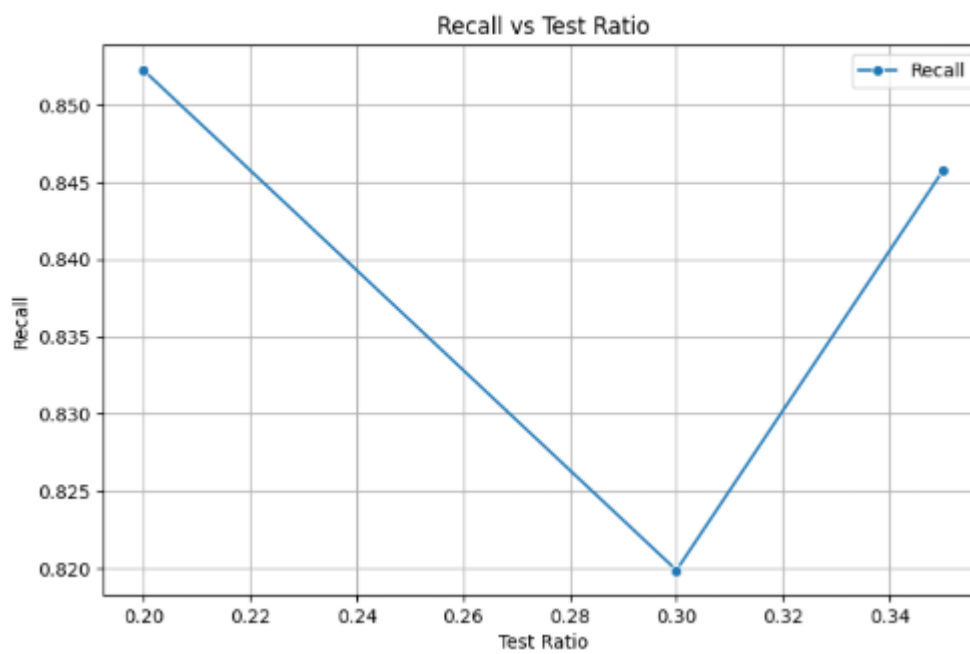
- Decision Tree Model 3 has the lowest classification error (0.1351), followed by Model 1 (0.1591).
- Regression Tree Models show higher classification error rates, with Model 5 being the worst (0.2525).

Sensitivity/Recall

- Decision Tree Model 2 achieves the highest sensitivity (0.8611), indicating superior positive instance detection.

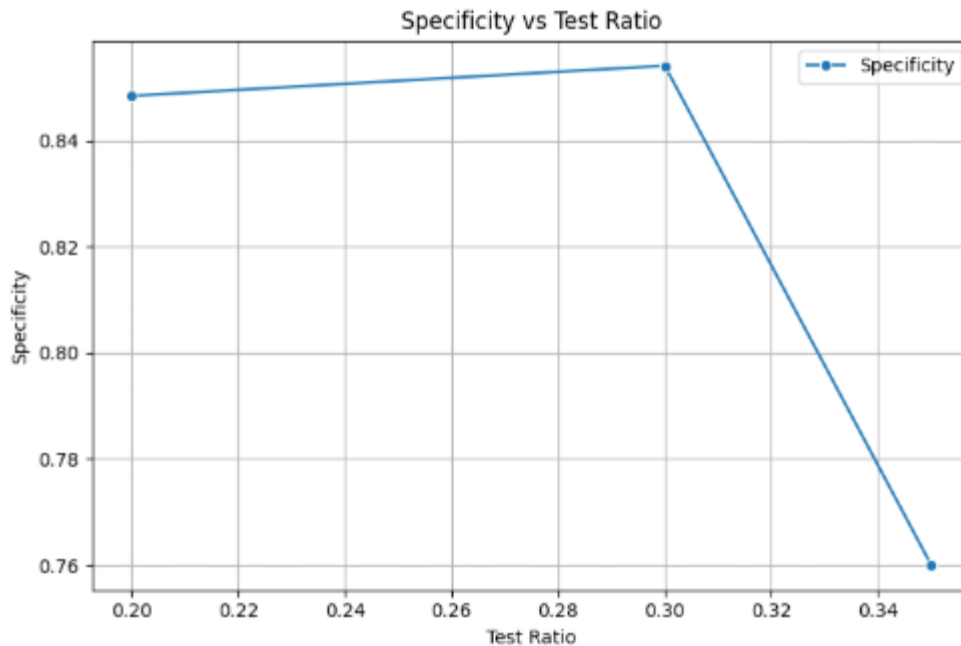


- Regression Tree Model 6 (0.8400) is competitive but does not surpass decision tree models.

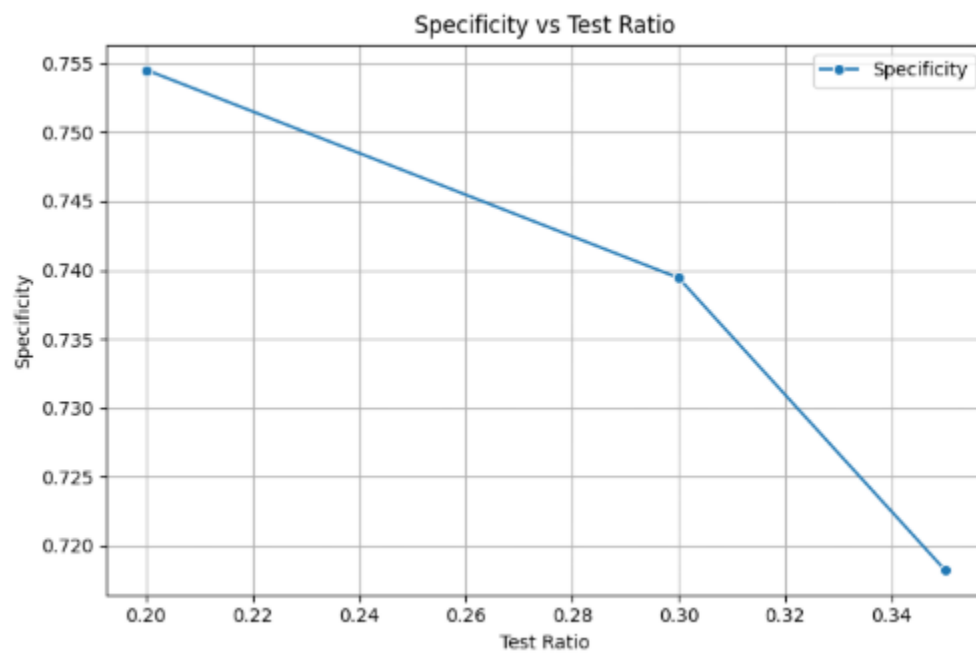


Specificity

- Decision Tree Model 3 achieves the highest specificity (0.8824), followed by Decision Tree Model 1 (0.8443).

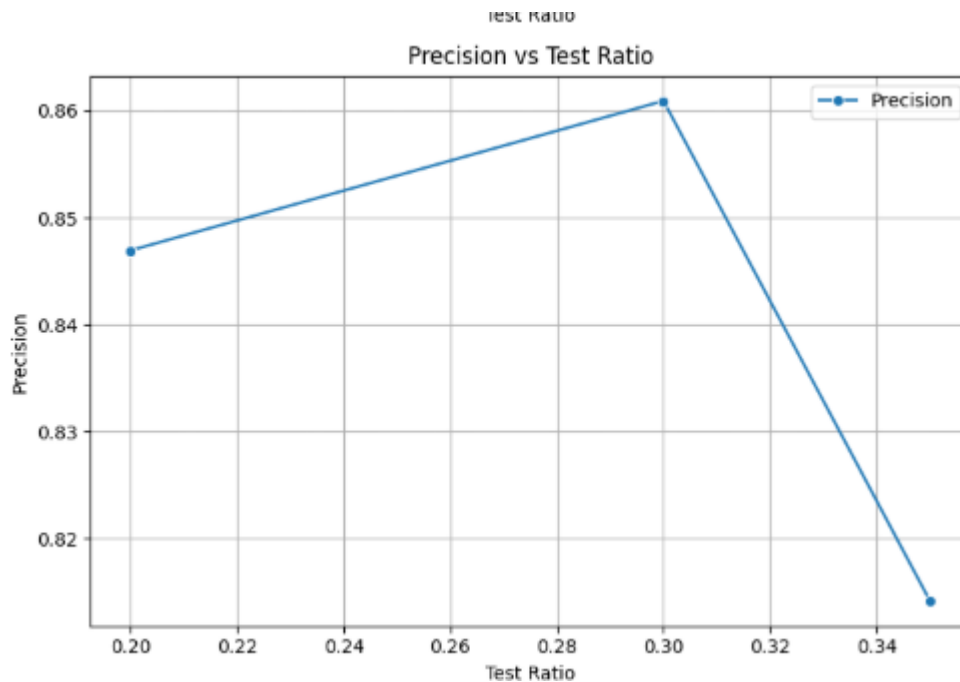


- Regression Tree Models show significantly lower specificity, with Model 6 being the lowest (0.7474).

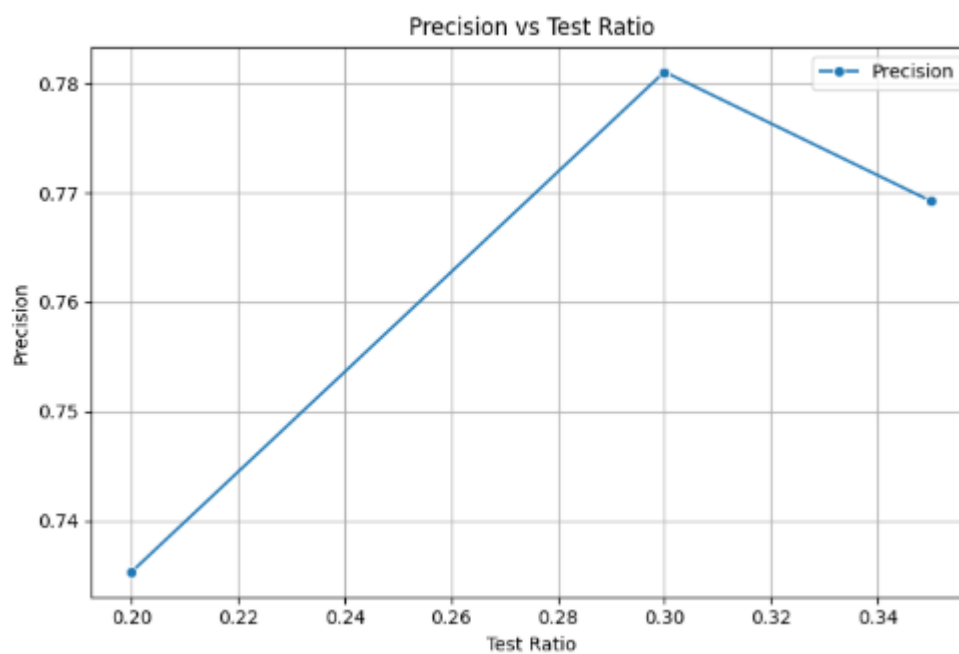


Precision

- Decision Tree Model 3 achieves the highest precision (0.8947), indicating better handling of false positives.

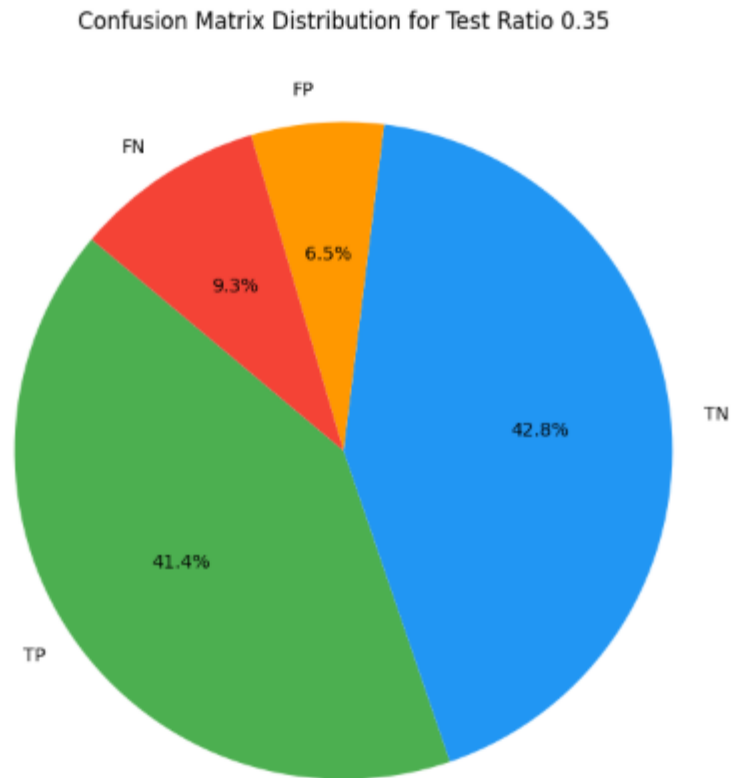


- Regression Tree Models consistently show lower precision scores, with Model 5 being the worst (0.7733).

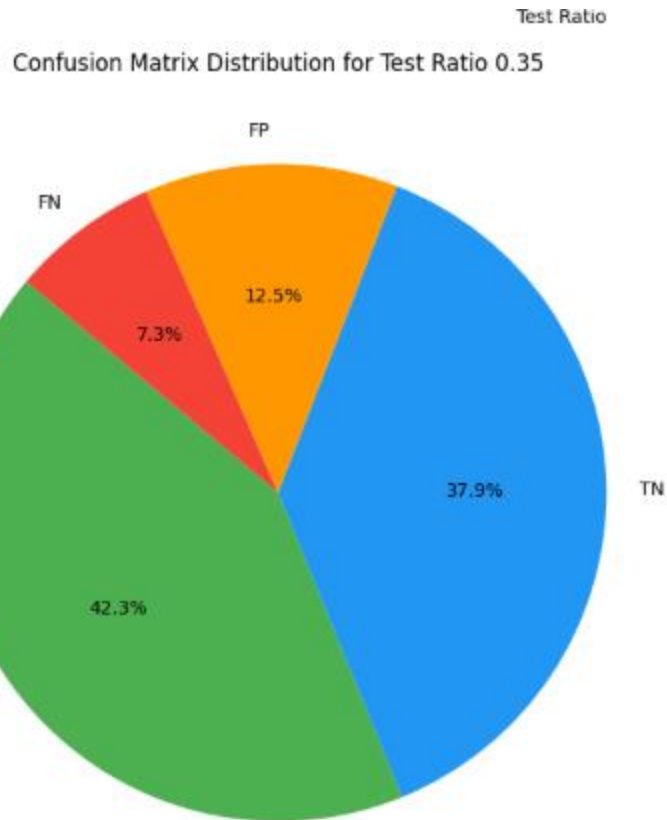


False Positive Rate

- Decision Tree Model 3 has the lowest false positive rate (0.1176), further emphasizing its strength in negative classification.



- Regression Tree Model 6 shows the highest false positive rate (0.2526), indicating room for improvement.



Model Suitability for Positive vs. Negative Results:

The model is better for **positive results** (detecting the presence of heart disease) or **negative results** (detecting the absence of heart disease), we analyze:

1. **Recall (Sensitivity):** Indicates how well the model identifies positive cases (true positives).
 2. **Specificity:** Indicates how well the model identifies negative cases (true negatives).
- **Positive Results (Heart Disease Detection):**
 - If **Recall (Sensitivity)** is high, the model is good at identifying people with heart disease.
 - **Decision Tree Model 3** likely has high recall, making it well-suited for detecting positive cases and reducing the risk of missing patients who have the disease.
 - **Negative Results (No Heart Disease):**
 - If **Specificity** is high, the model is good at correctly identifying those without heart disease.
 - **Decision Tree Model 3** and Model 1 also demonstrate high specificity, ensuring fewer false positives (falsely diagnosing heart disease).

Model's Strengths and Use Case:

If the priority is minimizing false negatives (avoiding missed diagnoses of heart disease), the model's recall should be prioritized. Decision Tree Model 3 appears to be strong here.

If the focus is on minimizing false positives (avoiding unnecessary worry or treatments), the model's specificity is critical. Both Decision Tree Model 3 and Model 1 are effective.

Conclusion

The Decision Tree Model 3 (80% training data, 20% testing data) stands out as the best model for heart disease classification due to its exceptional balance of key performance metrics, making it a reliable choice for healthcare applications. Here's a detailed breakdown of why this model is the most effective:

1. **High Accuracy (86.49%):**
 - This model achieved a strong accuracy rate, meaning that a significant proportion of predictions made by the model were correct. With heart disease prediction, high accuracy is crucial as it directly impacts the effectiveness of early diagnosis.
2. **Low Classification Error (13.51%):**
 - A low classification error rate implies fewer misclassifications, ensuring that the model is reliably identifying both the presence and absence of heart disease. This contributes to minimizing false positives and false negatives, which are vital in medical applications.
3. **Strong Sensitivity/Recall (85%):**
 - Sensitivity, or recall, refers to the model's ability to correctly identify patients with heart disease. An 85% recall indicates that this model is highly effective at detecting individuals who are at risk, ensuring that fewer actual positive cases are missed. In healthcare, where missing a diagnosis can lead to severe consequences, recall is prioritized to catch as many true positives as possible.
4. **High Specificity (88.24%):**
 - Specificity measures the model's ability to correctly identify patients who do not have heart disease. A specificity of 88.24% means that this model effectively rules out patients without the disease, reducing the likelihood of false positives. This is particularly important to prevent unnecessary treatments or anxiety for individuals incorrectly diagnosed as having heart disease.
5. **Excellent Precision (89.47%):**
 - Precision measures the proportion of true positive predictions among all predicted positives. A high precision of 89.47% ensures that when the model predicts a patient has heart disease, it is highly likely to be accurate. This helps in making reliable and safe treatment decisions.
6. **Low False Positive Rate (11.76%):**
 - The low false positive rate ensures that patients without the disease are less likely to be incorrectly diagnosed as positive. This is crucial for minimizing unnecessary tests, treatments, and patient concerns.

Why It Is Best

- **Balanced Performance:** Model 3 achieves a strong balance between recall (sensitivity) and specificity, making it equally effective at detecting heart disease while ensuring that patients without the disease are correctly ruled out.
- **Prioritization of Critical Health Factors:** In medical diagnostics, recall (sensitivity) is often prioritized because identifying as many true positives as possible can save lives. This model ensures that a large proportion of heart disease patients are correctly identified, reducing the chances of missing a diagnosis.
- **Reliability:** The combination of high accuracy, specificity, precision, and low classification error makes this model highly reliable. It offers a robust and comprehensive performance, ensuring both positive and negative results are correctly classified, which is crucial for safe and effective clinical decision-making.

In conclusion, Decision Tree Model 3 provides the best trade-off between performance metrics for heart disease classification, offering high recall (sensitivity) to identify most true positive cases and high specificity to avoid misdiagnosing healthy patients. Therefore, it is the most effective model for use in real-world heart disease prediction scenarios.