Heart_failure

AUTHOR
Amir A. Seid

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1 Building a Prediction Model for Coronary Artery Disease

1.1 Abstract

Methodology: This study uses the UCI Heart Disease repository to develop a predictive framework for Coronary Artery Disease (CAD). Python 3.14 was used for data preparation and R 4.5.2for the analysis. Partial Proportional Odds (PPO) model was used to respect ordinal disease severity (Classes 0–4) after variables failed the parallel lines assumption. Missing values were addressed via MICE with specialized logistic regressions, and coefficients were pooled using Rubin's Rules. A Bayesian-inspired weighting strategy was applied to minimize systemic bias and prioritize clinical safety over raw accuracy.

Results: The binary model demonstrated clinical viability with an accuracy of 56% and a balanced accuracy of 84.2% . While the unweighted model achieved a sensitivity of 85% and specificity of 83%, the multinomial version struggled with rare severity stages (Classes 2 and 4). The weighting strategy achieved a 51.5% (from 0.33 to 0.17) reduction in systemic bias, successfully trading absolute success rate for the higher sensitivity required in diagnostic screening.

1.2 Introduction:

Coronary Artery Disease (CAD) remains the leading cause of global mortality, accounting for an estimated 17.8 million deaths annually. Epidemiological trends indicate a shifting burden; while mortality rates have stabilized in high-income countries due to advanced interventions, the prevalence of CAD is surging in developing regions and among younger populations. This "epidemiological transition" presents a critical challenge: the sheer volume of patients at risk is outpacing the availability of specialized diagnostic resources, such as coronary angiography.

Traditional clinical risk scores often struggle with the non-linear complexity of biological data. Machine Learning models have been tuned for accuracy and have extended to include the nuanced and unpredictable nature of medicine. By using the famous data sets, the UCI Cleveland Heart Disease repository, we developed an ML model that can identify patterns hard to check with standard diagnostic methods. Many traditional models collapse the target variable into a binary. In contrary, we respected the ordinal nature of our target variable to consider the nuances. Since three of our variables (age, sex, and exercise-induced angina) couldn't meet parallel line assumptions, Partial Proportional Odds (PPO) was preferred in the model. The model achieved a binary accuracy of 85% (Healthy vs Sick) and a mean predictive difference of 0.59, showing the model errors tend to fall to the most correct value. While the UCI Heart Disease data is the benchmark in the application of machine learning in healthcare, we believe this report sheds light on a predictive framework to provide actionable diagnostic foresight to clinicians.

1.3 Methods

The infamous UCI Heart Disease data, usually considered a benchmark for applying data science in healthcare, was used for the analysis. The four databases are Cleveland, Switzerland, VA, and Hungarian data sets. These data sets were pooled and merged using Python 3.

1.3.1 Presented Variables:

The merged csv data had 14 variables (13 features and 1 target variable)

Variables	datatypes	feature/target	explanation	Missing Value (in%)
ca	numeric	feature	Number of major vessels (0-3) colored by flourosopy	66%
thal	numeric	feature	Thalassemia (3 = normal; 6 = fixed defect; 7 = reversable defect)	53%
slope	ordered, factor	feature	The slope of the peak exercise ST segment	34%
fbs	factor	feature	Fasting blood sugar > 120 mg/dl (1 = true; 0 = false)	10%
oldpeak	numeric	feature	ST depression induced by exercise relative to rest	7%
trestbps	numeric	feature	Resting blood pressure (in mm Hg on admission)	6%
thalach	numeric	feature	Maximum heart rate achieved	6%
exang	factor	feature	Exercise induced angina (1 = yes; 0 = no)	6%
chol	numeric	feature	Serum cholestoral in mg/dl	3%
age	numeric	feature	Age in years	0%
sex	factor	feature	Sex (1 = male; 0 = female)	0%
cp	factor	feature	Chest pain type (1: typical, 2: atypical, 3: non-anginal, 4: asymptomatic)	0%
restecg	factor	feature	Resting electrocardiographic results	0%
num	ordered, factor	target	Diagnosis of heart disease (angiographic disease status)	0%

1.3.2 Data Cleaning

After skimming for the soundness of the values in our data, we converted our features from characters to their intended types of variables: Nominal, Ordinal, and Numerical. NA value representation was then handled according to the dataset description (-9 and ?). We also assumed "0" as missing data in cholesterol.

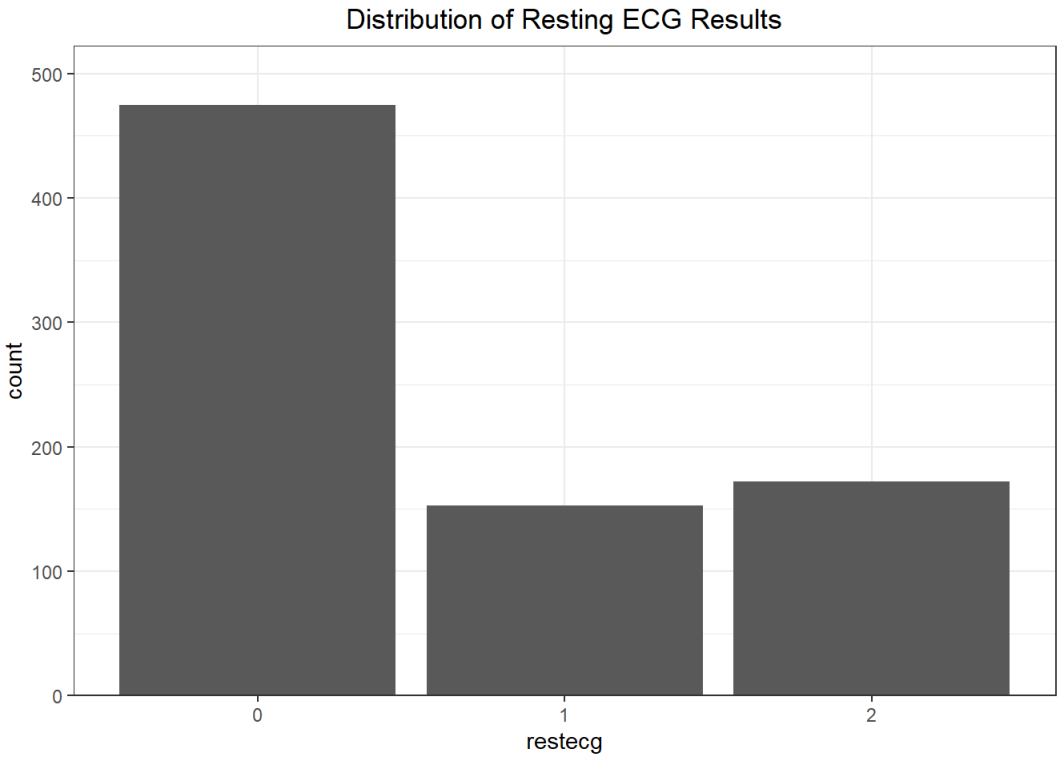
Four variables,

1. thalassemia type
2. number of major blood vessels as seen by coronary angiography, an expensive process that can be difficult to apply to every patient.
3. Slope of the peak exercise ST segment
4. Cholesterol – there is an unbalanced lack of data in "Switzerland.data".

These variables were excluded due to the significant amount of missing data they contained.
120 observations for the test set and 800 observations for the training set were then selected randomly.

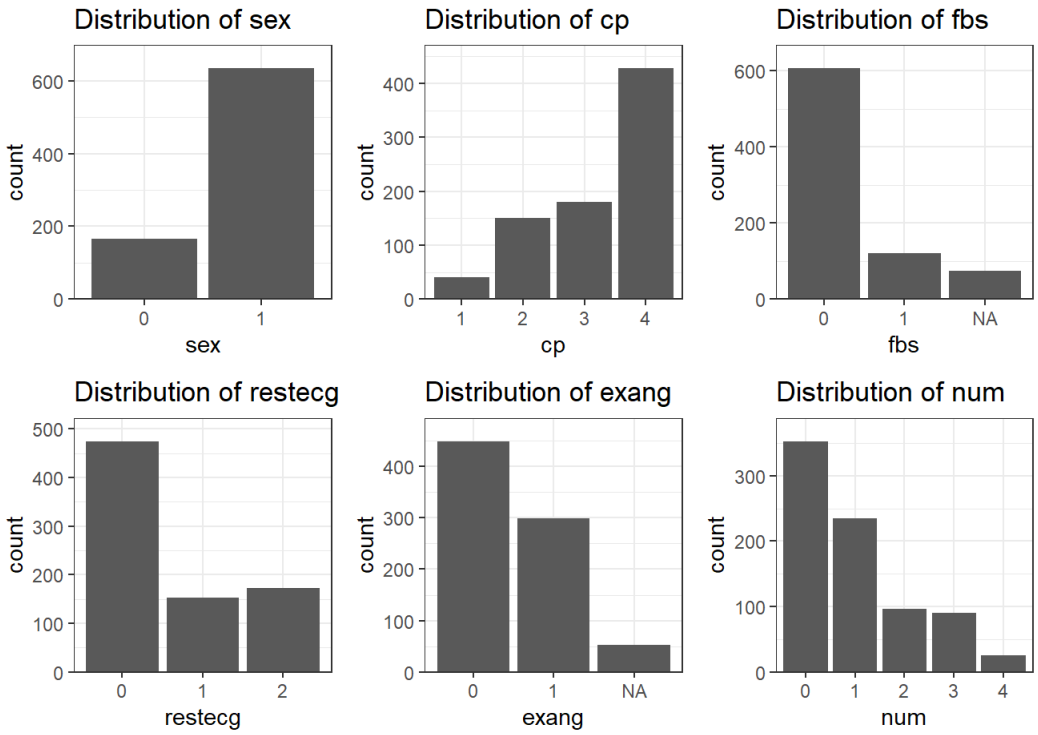
1.3.3 Handling Missing Values.

For restecg (Resting ECG), missing values were negligible (XX%), so we imputed the mode 0.

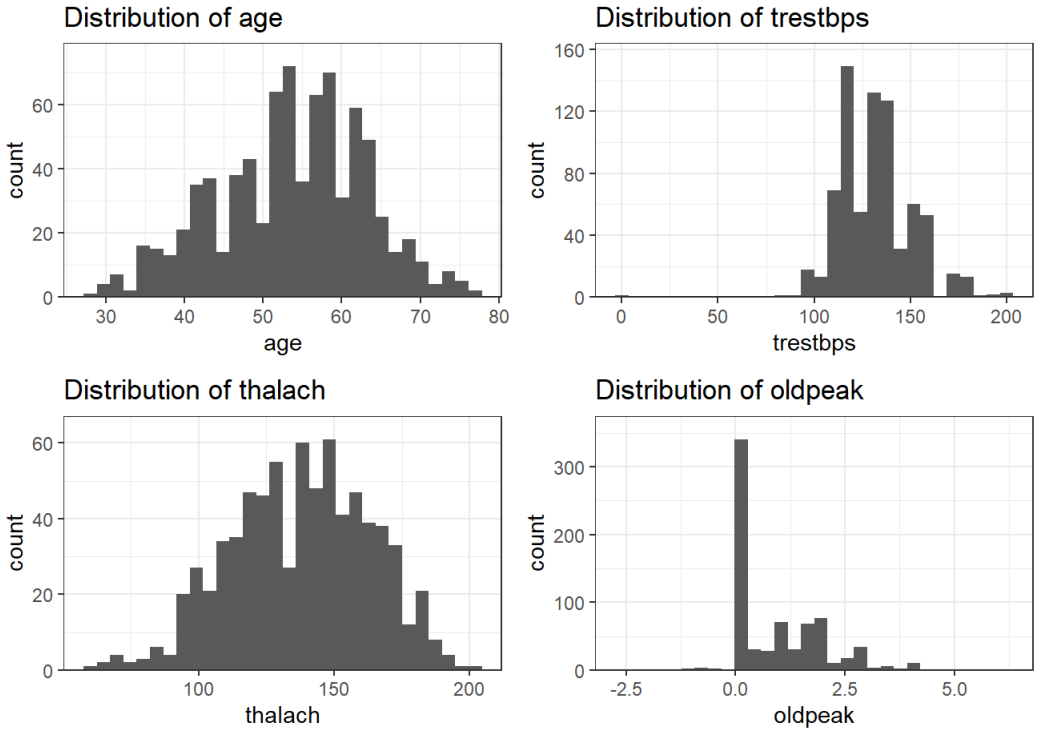


The other feature variables undergo MICE (Multivariate Imputation Chain Equation) after we checked for a sensibly balanced distribution of all our remaining categorical and numerical features using plots, and confirmed that we can use all remaining columns.

Categorical Variables



Numerical Variables

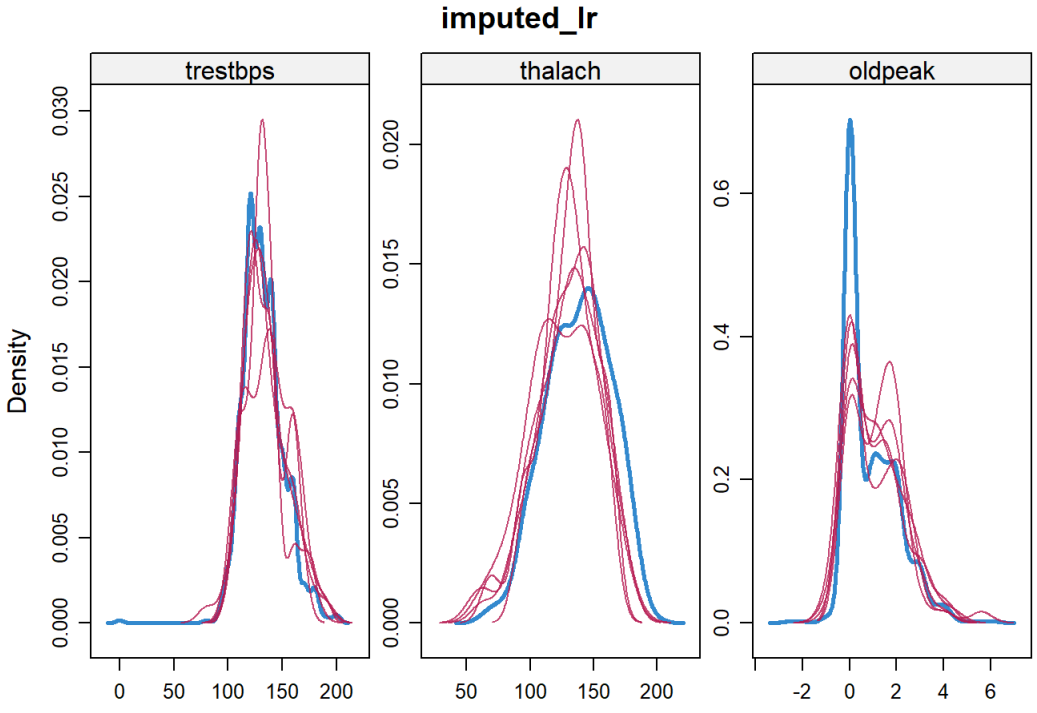


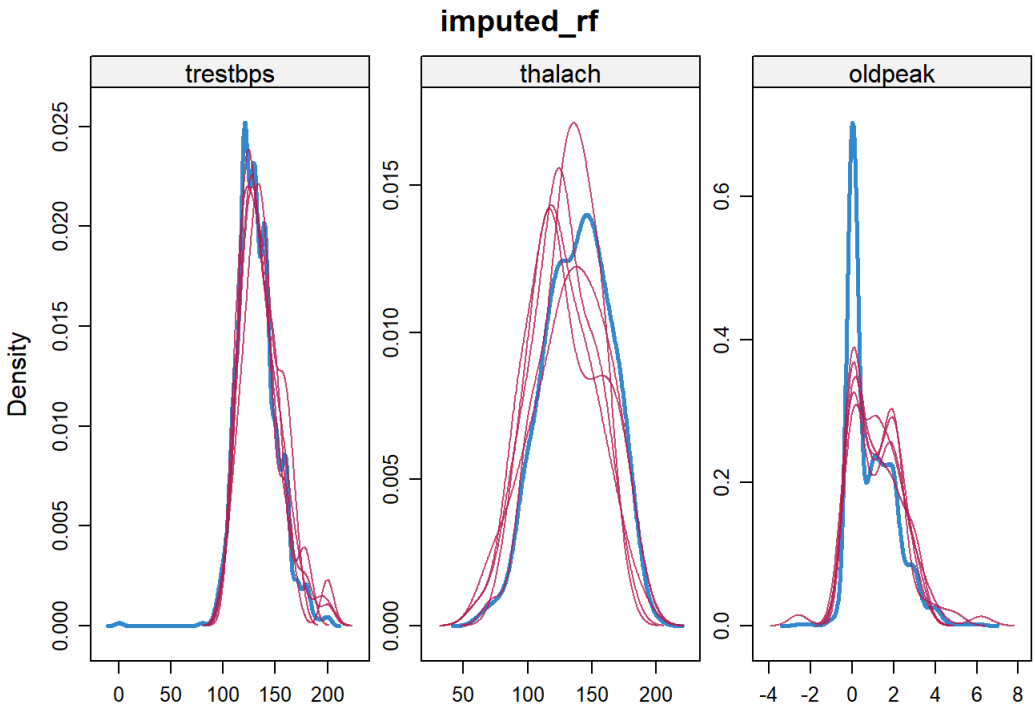
We did two MICE imputations: one using PMM - Predictive Mean Matching and Random Forests when fitting, and the other using PMM and specialized Logistic Regressions: Logistic regression (for binary), POLR (for ordinal features), and POLYREG (for categorical features).

We compared two imputation methods using:

1. Density plot: to check similarity in the distribution of our five imputations,
2. Strip plots: to test if it gives a valid output.
3. Trace plots: to analyze the difference in mean and standard deviation for each loopXX.
4. Selected columns: we take the difference between the real value and the imputed value for two selected columns.

And we chose the MICE model which uses specialized logistic regressions.



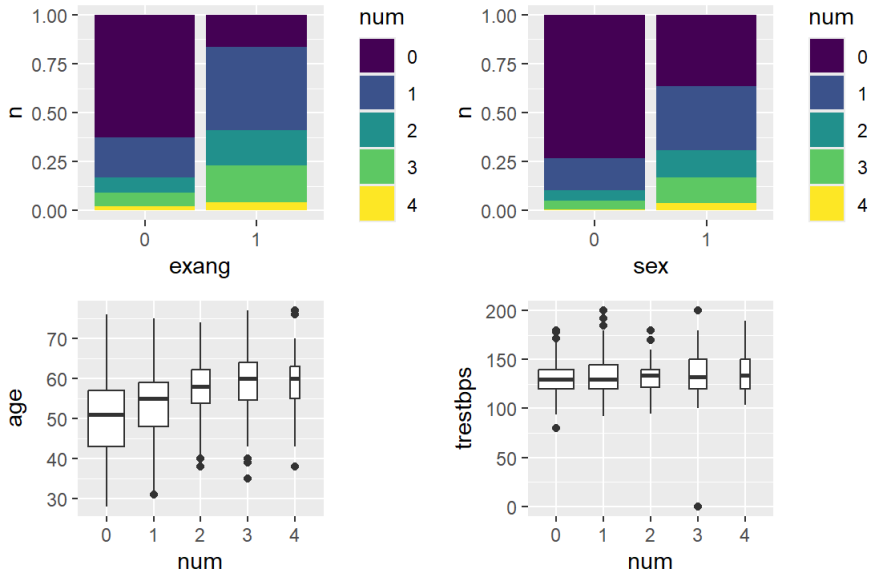


1.3.4 Building a Regression Model

While we planned to use a proportional odds logistic regression model (POLR), three of our feature variables, age, sex and exang, failed to meet the Brant test for the Parallel Lines Assumption to proceed with POLR.

	X2	df	probability
Omnibus	79.9423104	36	0.00
age	6.5843225	3	0.09
sex1	2.7320300	3	0.43
cp2	0.3413144	3	0.95
cp3	0.8620800	3	0.83
cp4	1.4067443	3	0.70
trestbps	2.6273437	3	0.45
fbs1	1.9471604	3	0.58
restecg1	3.5628397	3	0.31
restecg2	7.0017508	3	0.07
thalach	5.3177306	3	0.15
exang1	14.2963833	3	0.00
oldpeak	4.1961999	3	0.24

The plots …



Therefore, we chose the Partial Proportional Logistic regression model. This model doesn't assume for homoscedacity or Parallel assumption tests, and is one of the most flexible regression models. However, feature variables that fit many of the statistical assumptions yield better accuracy than their counterparts.

We build our model by fitting all our imputed datasets. We also used Rubin's Rule to pool our test model and check if our model is not just random noise using the total variance and the Z-score

```
(Intercept):1 (Intercept):2 (Intercept):3 (Intercept):4         age:1
  1.093778948   3.980227324   4.085424440   3.344427211  -2.425581054
        age:2         age:3         age:4         sex1           cp2
 -4.678326843  -3.335065648  -1.282744966  -5.385122343   2.442607369
          cp3           cp4     trestbps         fbs1    restecg1:1
  0.128781368  -2.836136622   0.357001993  -1.935239808  -1.155086961
   restecg1:2    restecg1:3    restecg1:4    restecg2:1    restecg2:2
 -3.098745954  -2.087068948  -0.973779131   0.093265018  -1.893010113
   restecg2:3    restecg2:4       thalach      exang1:1      exang1:2
 -2.764923900  -2.354069551   3.590211333  -4.024988280   0.005065197
     exang1:3      exang1:4       oldpeak
  0.015017842   0.852190139  -6.891312462
```

Parameters	Total Variance	degree of freedom	Margin of Error
(Intercept):1	1.2982422	171	2.2491089
(Intercept):2	1.3717221	202	2.3093563
(Intercept):3	1.6631494	167	2.5460820
(Intercept):4	3.5240047	468	3.6888494
age:1	0.0001217	681	0.0216648
age:2	0.0001450	732	0.0236375
age:3	0.0002120	686	0.0285881
age:4	0.0007335	771	0.0531645
sex1	0.0477894	762	0.4291450
cp2	0.1731850	723	0.8170165
cp3	0.1396490	502	0.7342016
cp4	0.1280772	514	0.7030850
trestbps	0.0000162	611	0.0079084
fbs1	0.0384195	711	0.3848253
restecg1:1	0.0653273	757	0.5017535
restecg1:2	0.0564539	730	0.4664616
restecg1:3	0.0777318	666	0.5474413
restecg1:4	0.2986341	760	1.0727783
restecg2:1	0.0539111	771	0.4557951
restecg2:2	0.0564092	753	0.4662532
restecg2:3	0.0761729	725	0.5418435
restecg2:4	0.2528393	762	0.9870990
thalach	0.0000144	86	0.0075362
exang1:1	0.0491118	245	0.4365076
exang1:2	0.0441734	483	0.4129697
exang1:3	0.0682185	137	0.5164788
exang1:4	0.2073441	232	0.8971507
oldpeak	0.0060177	135	0.1534168

1.3.5 Tools

Python 3.14 was used for primary data preparation, and R 4.5.2 was used for the analysis.

1.4 Results

Our unweighted model achieved a binary success rate of 83%. Moreover, our model has an absolute success rate of 62.5%. Considering the mean absolute error is 0.6, our model is providing a valuable prediction. However, our data is under predicting. Medicine is known for its inherent nature of caution.

Confusion matrix for our unweighted model (Multinomial prediction)

	Sensitivity	Specificity	Pos Pred Value	Neg Pred Value	Precision	Recall	F1	Prevalence	Detection Rate	Detection Prevalence	Balanced Accuracy
Class: 0	0.80	0.88	0.88	0.79	0.88	0.80	0.84	0.53	0.42	0.48	0.84
Class: 1	0.45	0.87	0.67	0.73	0.67	0.45	0.54	0.37	0.17	0.25	0.66
Class: 2	0.25	0.90	0.08	0.97	0.08	0.25	0.12	0.03	0.01	0.11	0.57
Class: 3	0.25	0.88	0.12	0.94	0.12	0.25	0.17	0.07	0.02	0.13	0.56
Class: 4	NA	0.98	NA	NA	0.00	NA	NA	0.00	0.00	0.03	NA

Confusion matrix for our unweighted model Binomial Prediction(Healthy and Sick)

Sensitivity	Specificity	Pos Pred Value	Neg Pred Value	Precision	Recall	F1	Prevalence	Detection Rate	Detection Prevalence	Balanced Accuracy
0.8	0.88	0.88	0.79	0.88	0.8	0.84	0.53	0.42	0.48	0.84

We applied a Bayesian-method-inspired weighting strategy. By considering the cost of missing a diagnosis and the prevalence of rare cases, we aligned our model closer to clinical safety. By applying a cube-root inverse prevalence factor, we achieved a 49% reduction in systemic bias (from -0.33 to -0.17) and a binary accuracy rate of 84.2%, while this resulted in an 8% decrease in the absolute success rate. This trade-off enhances our model's sensitivity.

Confusion matrix for our weighted model (Multinomial prediction)

	Sensitivity	Specificity	Pos Pred Value	Neg Pred Value	Precision	Recall	F1	Prevalence	Detection Rate	Detection Prevalence	Balanced Accuracy
Class: 0	0.83	0.85	0.84	0.84	0.84	0.83	0.84	0.49	0.41	0.48	0.84
Class: 1	0.38	0.81	0.50	0.73	0.50	0.38	0.43	0.32	0.12	0.25	0.60
Class: 2	0.10	0.89	0.08	0.92	0.08	0.10	0.09	0.08	0.01	0.11	0.50
Class: 3	0.18	0.87	0.12	0.91	0.12	0.18	0.15	0.09	0.02	0.13	0.53
Class: 4	0.00	0.97	0.00	0.99	0.00	0.00	NaN	0.01	0.00	0.03	0.49

Confusion matrix for our weighted model Binomial Prediction(Healthy and Sick)

Sensitivity	Specificity	Pos Pred Value	Neg Pred Value	Precision	Recall	F1	Prevalence	Detection Rate	Detection Prevalence	Balanced Accuracy
0.83	0.85	0.84	0.84	0.84	0.83	0.84	0.49	0.41	0.48	0.84

1.5 Discussion

This results show us that our model was poor at detecting Class 2 and Class 4 because we had too limited observations for our model to generalize the pattern.

The results of this study shows the inherent challenge of predicting disease severity in imbalanced medical datasets. While the model demonstrated high proficiency in binary classification, performance significantly declined when identifying specific severity stages. Specifically, the model struggled to detect Class 2 and Class 4 cases. This is primarily attributed to the limited number of observations for these categories in the test set, which restricted the model's ability to generalize patterns for end-stage CAD.

These findings suggest that Partial Proportional Odds (PPO) modeling provides a flexible and statistically sound framework for CAD screening, particularly when standard assumptions like parallel lines are violated. Future refinements should focus on larger, multi-center datasets to bolster the representation of rare severity classes and further enhance the model's predictive foresight.

1.6 Reference: