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Predicting Risk of Cardiovascular Disease

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INTRODUCTION

Cardiovascular diseases, such as coronary artery disease, are the leading cause of death worldwide for both men and women. In the United States, 1 in every 4 deaths is caused by cardiovascular disease (CVD, otherwise known as heart disease). Every year, roughly 790,000 Americans suffer from a heart attack - that's one heart attack every 40 seconds. However, it is estimated that up to 90% of heart disease cases are preventable. Known risk factors for heart disease include high cholesterol, high blood pressure, inactivity, poor diet, and smoking. Early identification of those at higher risk of developing heart disease is critical so that preventative interventions such as lifestyle changes and medication can be implemented.

The goal of this project is to use a large cardiovascular dataset to examine trends between the presence of cardiovascular disease and different health data such as gender, blood pressure, BMI, and cholesterol level. I will then build predictive models that use the most relevant features to classify patients with heart disease and predict risk of heart disease based on the combination of risk factors.

DATA OVERVIEW

The data used for this project was obtained during medical examinations and includes objective data such as height, weight, and blood pressure that was taken at the time of the examination as well as subjective data such as alcohol intake and physical activity level that was reported by the patient. There are a total of 70,000 observations (i.e. patient records) in the dataset and 11 features in addition to the target variable.

Features:

1. Age | Objective Feature | age | int (days)
2. Height | Objective Feature | height | int (cm) |
3. Weight | Objective Feature | weight | float (kg) |

4. Gender | Objective Feature | gender | categorical code |1: female, 2: male
5. Systolic blood pressure | Examination Feature | ap_hi | int |
6. Diastolic blood pressure | Examination Feature | ap_lo | int |
7. Cholesterol | Examination Feature | cholesterol | 1: normal, 2: above normal, 3: well above normal |
8. Glucose | Examination Feature | gluc | 1: normal, 2: above normal, 3: well above normal |
9. Smoking | Subjective Feature | smoke | binary | 0: no, 1: yes
10. Alcohol intake | Subjective Feature | alco | binary |
11. Physical activity | Subjective Feature | active | binary |
12. Presence or absence of cardiovascular disease | Target Variable | cardio | binary |

The dataset for this project is available from Kaggle: https://www.kaggle.com/sulianova/cardiovascular-disease-dataset

DATA CLEANING

The dataset was relatively clean overall, and a first examination of the dataset revealed that there were no null entries for any of the features. Before analyzing the data further, I first converted the units of age from days to years and of height from centimeters to meters to be more easily interpretable. Additionally, I converted the gender feature from a numerical to a categorical data type and renamed the categories ‘F’ and ‘M,’ also for easy readability. I also added a new column that calculated the body mass index (BMI) for each individual. The BMI is a useful measure for this dataset as it uses an individual’s weight in relation to their height as a rough estimate of body fat; BMIs are used to categorize individuals as underweight, normal weight, overweight, or obese.

Next, I plotted histograms of the continuous features to examine their distributions and identify outliers (Figure 1). The height distribution immediately jumps out, as there are a number of individuals that are either very short (52 individuals under 3.9 ft) or very tall (1 over 8 ft). A number of different medical conditions that may result in either a very short or very tall stature could also disproportionately affect cardiovascular health and thus complicate analysis of the dataset; I have therefore removed any individuals whose height is less than 1.2 m (~4 ft) or more than 2.1 m (~6.9 ft) from the dataset. There were also many blood pressure values that did not make sense, such as a systolic blood pressure of 16020 or -150. Such values are most likely the cause of transcription errors such as dropped decimal points (i.e. 160.20, not 16020) or incorrect negative signs (i.e. 150, not -150), but as I cannot be sure, all such values were dropped from the dataset.

Finally, I also dropped the observations with the five lowest BMIs, as they were unrealistic and likely the result of a transcription error (for example, a 5’8” tall man who weighed only 24 pounds). I then re-plotted the histograms to check the distributions after removing these outliers (Figure 2). As you can see, the height distribution in particular looks much better, though the data is still heavily skewed towards larger weights and BMIs. However, this is also true of the global population these days, so the filtered dataset is likely a reasonable representation of modern human populations.

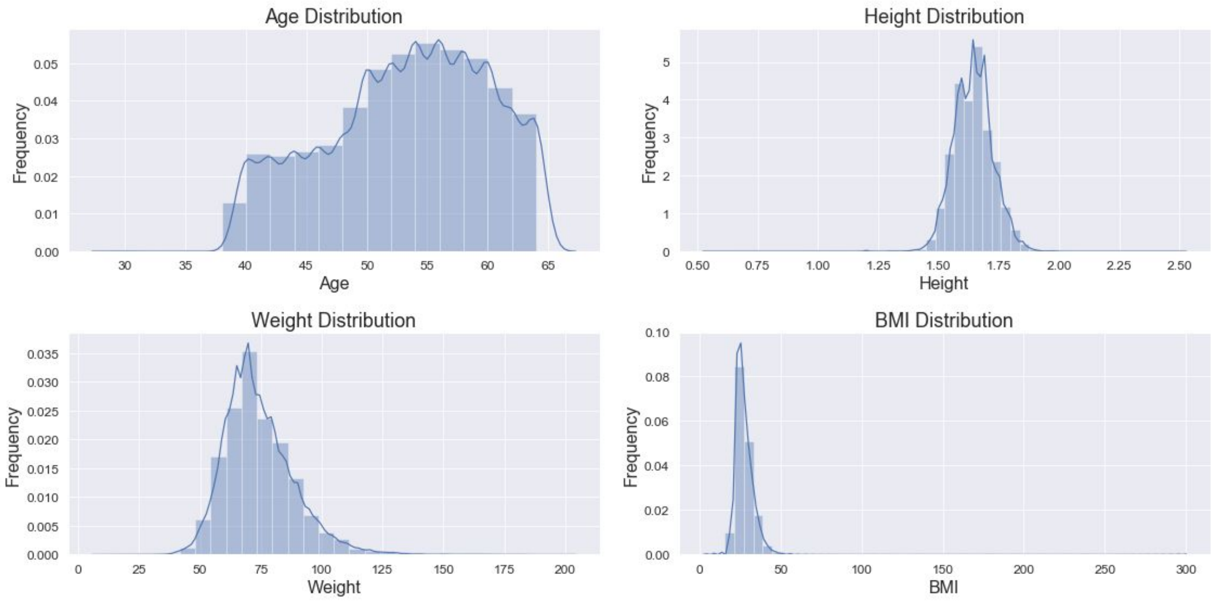
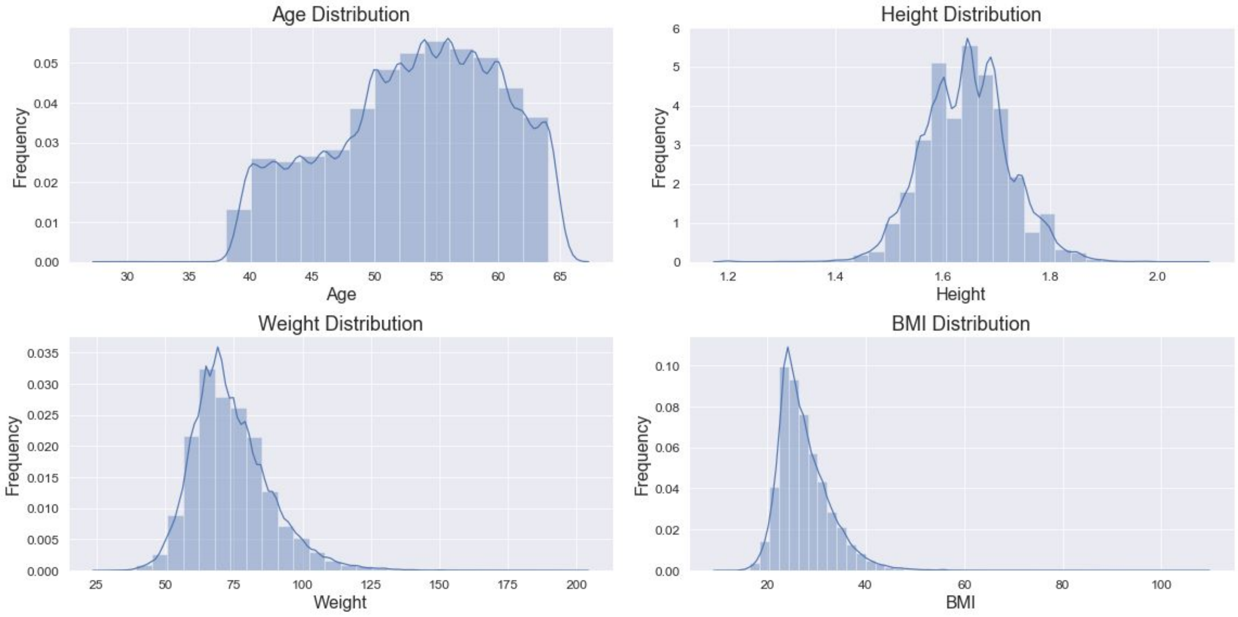


Figure 1: Histograms of age, height, weight, and BMI using full dataset.



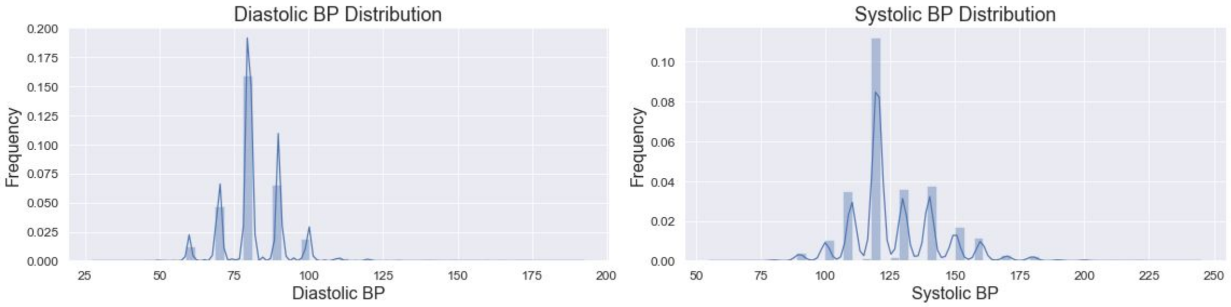


Figure 2: Histograms of age, height, weight, BMI, and blood pressure (BP) using filtered dataset with outliers removed.

A total of 1,274 outlier observations were removed from the dataset, leaving 68,726 observations for subsequent data analysis and model building.

EXPLORATORY DATA ANALYSIS

The next several sections explore the dataset by groups of related features. First, I will explore connections between age, gender, and cardiovascular disease, then move on to look at the effects of height, weight, and BMI, followed by measures of cholesterol and glucose levels in the blood. Finally, I will wrap up with a discussion of the self-reported features around smoking, alcohol consumption, and physical activity.

I. Age, Gender, and Cardiovascular Disease

I began by first examining the number of men and women in the dataset and found that women comprise 65% of the dataset, while men only comprise 35% - in other words, women outnumber men by nearly 2:1 (Figure 3, plot 1). This is interesting in itself - are

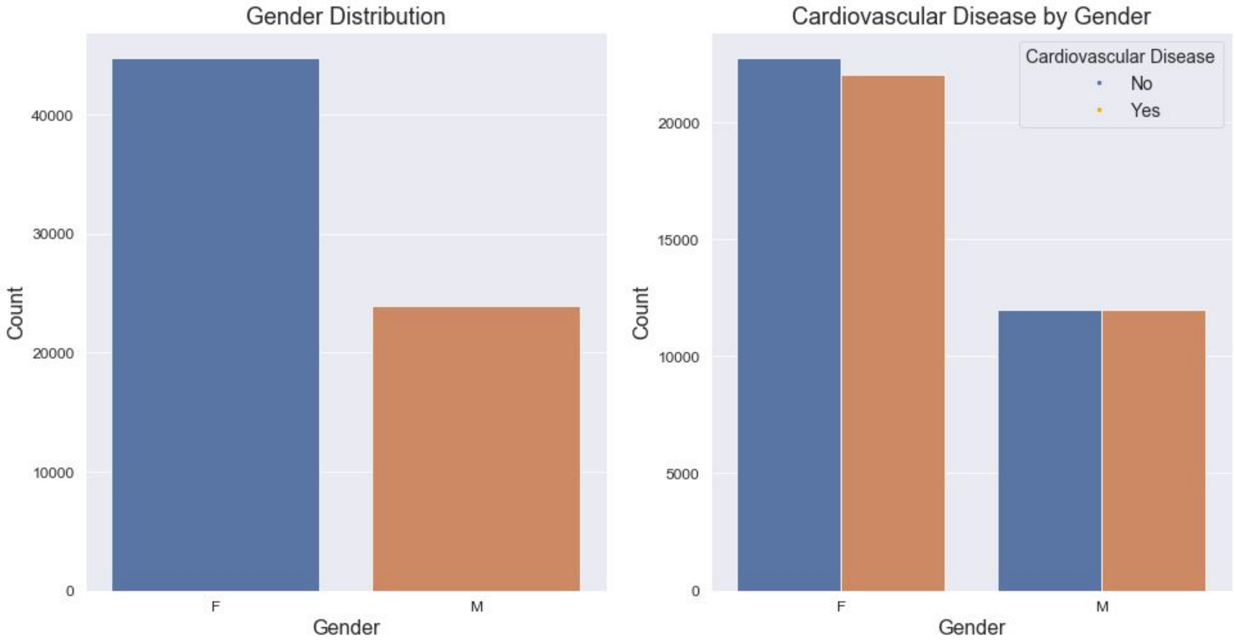


Figure 3: Left - Overall gender distribution. Right - Gender distribution by cardiovascular disease.

women more likely to visit the doctor than men? As the source of the dataset was not given, this question must remain unanswered. By dividing gender further into those with cardiovascular disease and those without, however, we can see that women may have a slightly lower risk of cardiovascular disease than men (Figure 3, plot 2). A chi-square test was then performed to assess whether gender and cardiovascular disease are independent, yielding a chi-square value of 3.62 and a p-value of 0.057, just above the 95% threshold for significance. Therefore, gender is not correlated with cardiovascular disease (i.e. gender and cardiovascular disease are independent).

Moving on to age, we can see from Figure 2 that the dataset is heavily biased towards older individuals. There are only 4 individuals out of over 68,000 who are 30 years old or younger; the next youngest age in the dataset is 39 years old. The oldest person in the dataset is just under 65 years old, so the dataset is only representative of adults from middle-age through to retirement age. Plotting the empirical cumulative distribution functions (ECDFs) for age by cardiovascular disease shows a definite age shift from those without cardiovascular disease and to those with it, indicating that the risk of cardiovascular disease increases with age (Figure 4). The significance of this age shift can be assessed using Student’s t-test:

H_O: The mean age of those with or without cardiovascular disease is the same.

H_A: The mean age of those with or without cardiovascular disease is different.

T-statistic: -64.68 p-value: 0.0

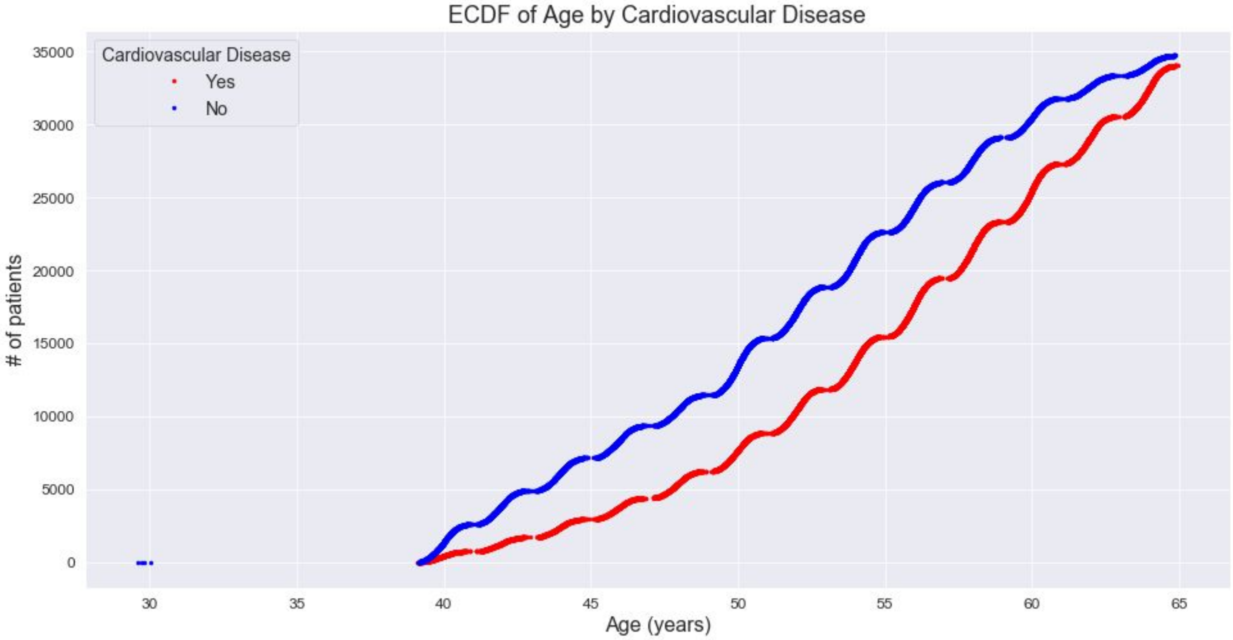


Figure 4: ECDF of age by presence or absence of cardiovascular disease.

As the p-value is well below the 95% significance threshold (0.05), we reject the null hypothesis. Thus, the average age of those with heart disease is higher than for those without heart disease.

The age distribution for those with or without cardiovascular disease can be further visualized using boxen plots. Boxen plots, also known as letter-value plots, are ideal for visualizing the distributions of large datasets, as they afford more precise estimates of quantiles beyond quartiles. A boxen plot is more useful than a normal box plot in this situation because the increased number of quantiles provide more detailed information about the shape of the distribution, especially in the tails. From this plot, we can see not only that older individuals are more likely to have cardiovascular disease on average, but also that the entire age distribution is heavily shifted to the higher age ranges (Figure 5, left plot). We can further subdivide the age distribution by gender, revealing that women tend to develop cardiovascular disease later than men (Figure 5, right plot).

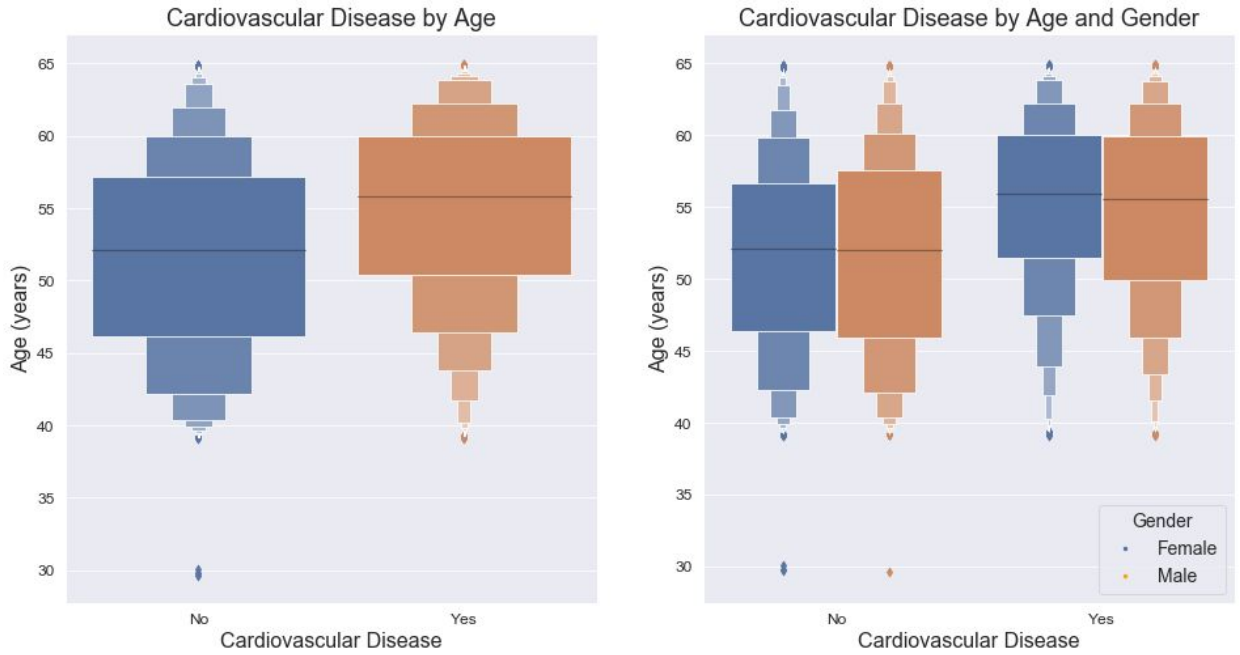


Figure 5: Left - Boxen plot distribution of age by cardiovascular disease. Right - Boxen plot distribution of age by gender and cardiovascular disease.

A t-test can again be used to assess the hypothesis that the average age of women with heart disease is higher than the average age of men with heart disease, yielding a t-statistic of 8.42 with a p-value of 0.0 (or more precisely, 3.9 x 10^{-17}). Therefore, women with heart disease do have a higher average age than men with cardiovascular disease. Performing the analogous t-test for men and women without heart disease results in a t-statistic of 1.37 and a p-value of 0.17, demonstrating that men and women *without* heart disease have the same average age, statistically speaking.

II. Effect of Height, Weight, and BMI on Cardiovascular Disease

Next, I examined the relationships between height, weight, BMI, and cardiovascular disease. A scatterplot of height vs. weight, colored by cardiovascular disease, shows that heart disease is more prevalent at higher weights, which is perhaps unsurprising (Figure 5). The linear regression lines were also determined and have been overlaid on the scatterplot. The equations for these lines are as follows:

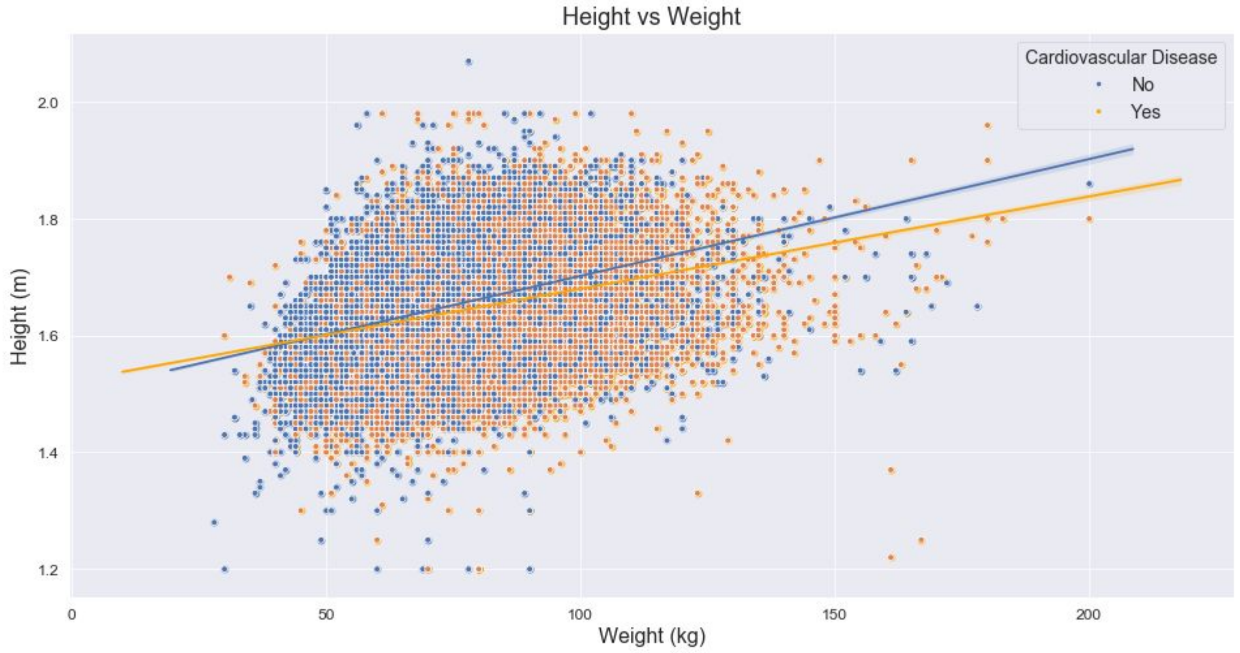


Figure 6: Scatterplot of height vs weight overlaid with linear regression lines; blue: no heart disease, orange: heart disease.

No Heart Disease: $y = 0.0020x + 1.50$

Heart Disease: $y = 0.0016x + 1.52$

The slopes of the lines also seem to indicate that weight has more of an effect on cardiovascular disease than height.

ECDFs can be used to further explore potential differences in height and weight by cardiovascular disease. First, the ECDFs for height by cardiovascular disease look fairly similar, indicating that height might not be an important factor in cardiovascular disease (Figure 7). The ECDFs for weight, however, show a definite shift to higher weight for those with cardiovascular disease (Figure 8). As BMI is a function of both height and weight, it is not surprising to see that the ECDF for those with cardiovascular disease also show a shift to higher BMIs compared to the ECDF for those without cardiovascular disease (Figure 9).

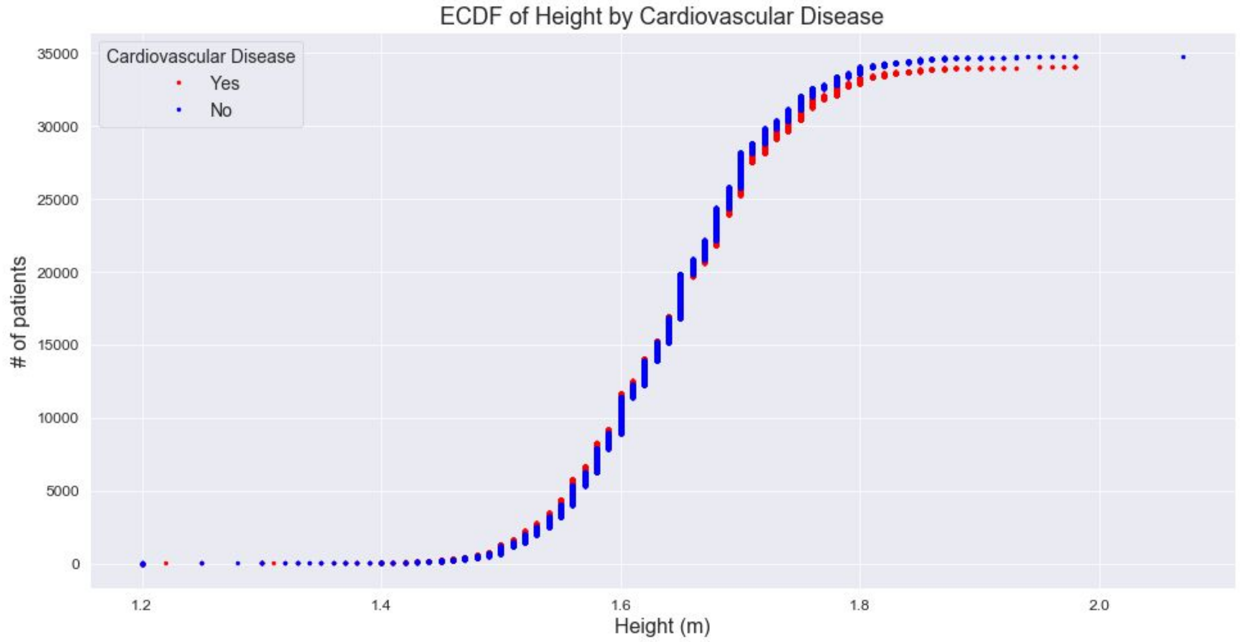


Figure 7: ECDF for height by cardiovascular disease.

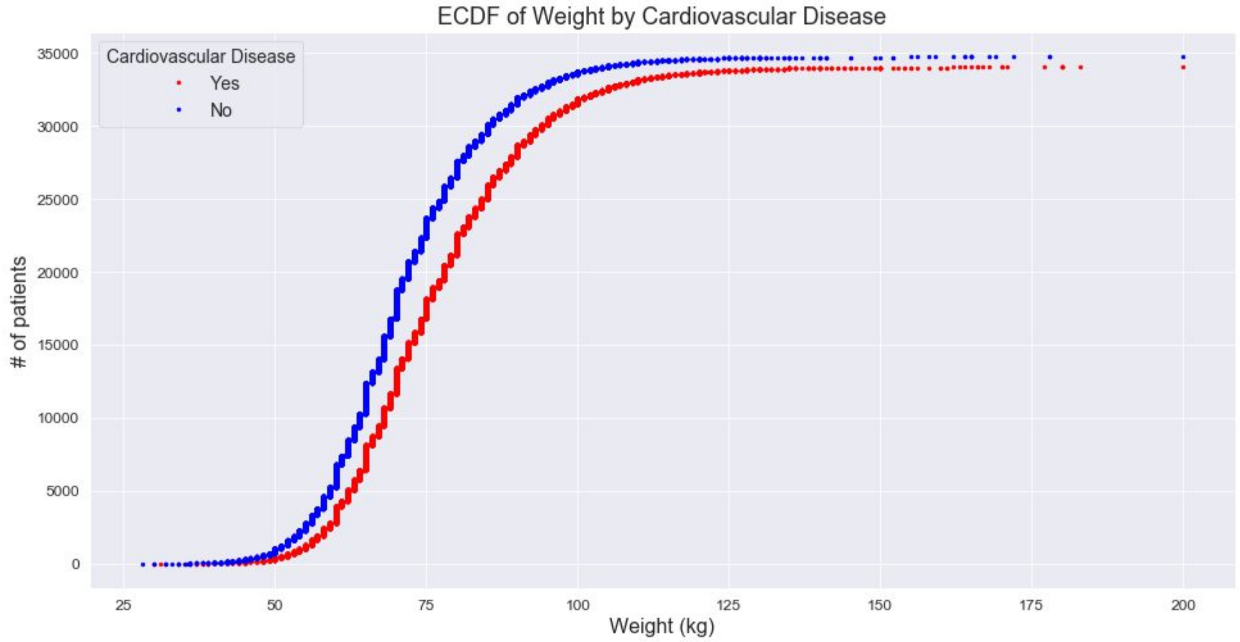


Figure 8: ECDF for weight by cardiovascular disease.

One of the main advantages of working with such a large sample size, increased precision, can also be a disadvantage by enabling detection of differences that are so small as to be meaningless in a practical sense. In this case, the mean height of those without cardiovascular disease is 1.645 m, while the mean height of those with cardiovascular disease is 1.643 m. While a t-test indicates that the mean height is statistically different between those with cardiovascular disease and those without (t-statistic: 3.10 ; p-value: 0.0019), the difference, at only 2 cm, is not *practically* significant. In addition, the boxen plots for height by cardiovascular disease are nearly

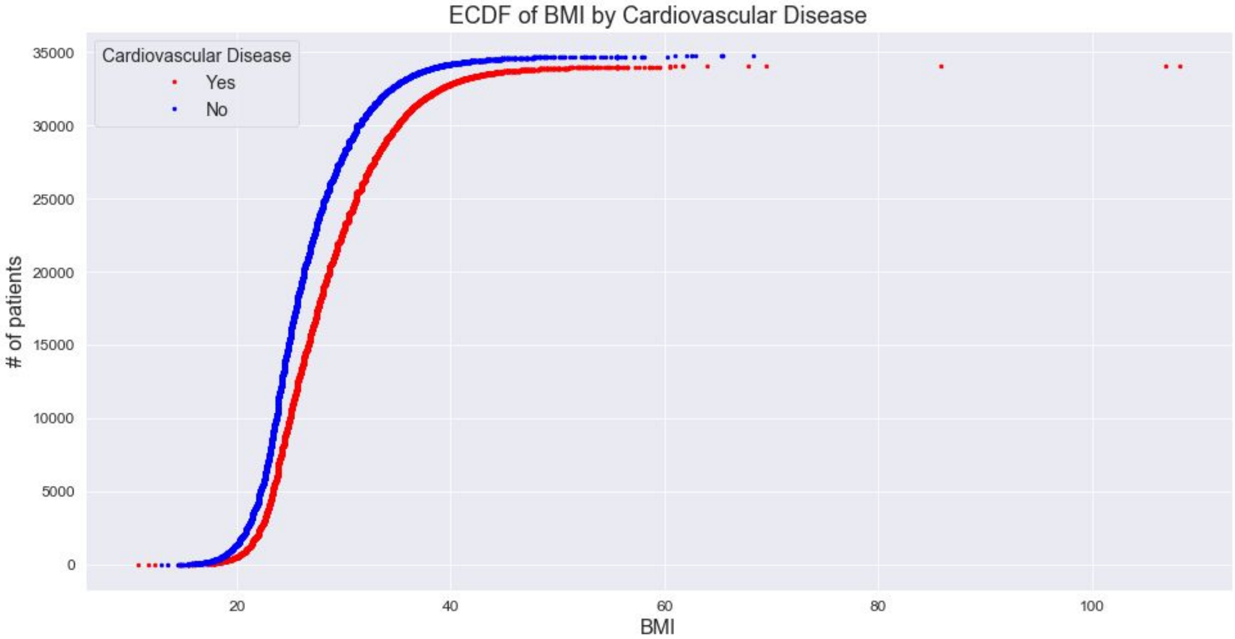


Figure 9: ECDF for BMI by cardiovascular disease.

indistinguishable, further emphasizing that the height distributions are not different in a meaningful sense (Figure 10, plot 1). In contrast, the boxen plots for both weight and BMI segregated by cardiovascular disease show clear shifts in both the mean values and the overall distributions between those with or without cardiovascular disease (Figure 10, plots 2 and 3). Performing t-tests confirms that the shifts in the average weight (t-statistic: 47.99; p-value: 0.0) and average BMI (t-statistic: 50.61; p-value: 0.0) are statistically significant, and both p-values are far smaller than the p-value for height.

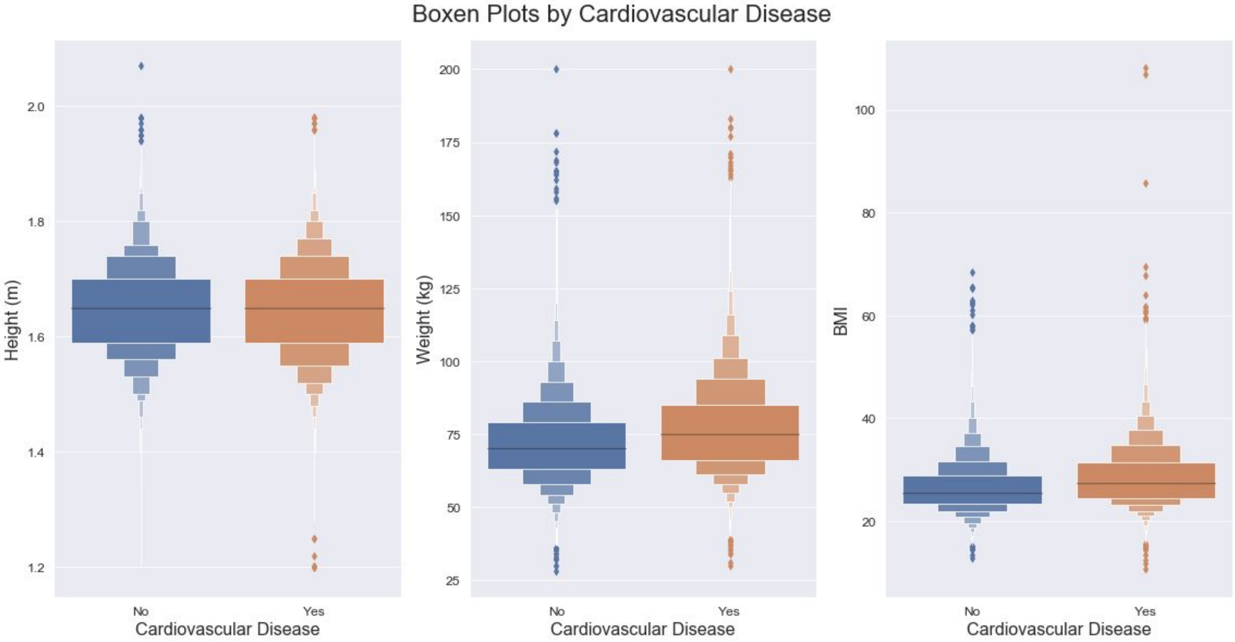


Figure 10: Boxen plots of height (plot 1), weight (plot 2), and BMI (plot 3) by cardiovascular disease.

III. High Blood Pressure Increases Risk of Cardiovascular Disease

Blood pressure is a measure of how much pressure your blood exerts on the walls of your arteries. Systolic blood pressure indicates the amount of pressure when your heart beats, while diastolic blood pressure indicates the amount of pressure when your heart is resting between beats. As expected, a scatterplot of systolic vs diastolic blood pressure shows a clear positive correlation (Figure 11), which can be confirmed by calculating the Pearson correlation coefficient (0.697, p-value = 0.0).

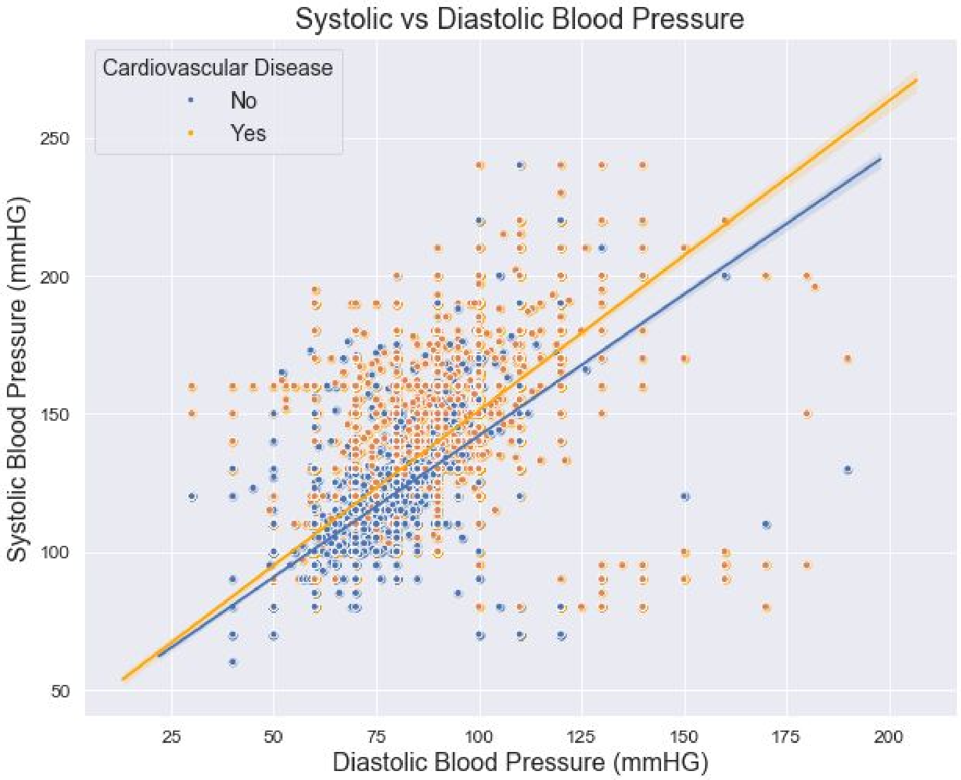


Figure 11: Scatterplot of systolic vs diastolic blood pressure overlaid with linear regression lines; blue: no heart disease, orange: heart disease.

The linear regression lines for the patients with cardiovascular disease (in orange) and those without it (in blue) were also determined and overlaid on the scatterplot (without CVD: y = 1.0233x + 39.57; with CVD: y = 1.1215x + 38.87). While patients with cardiovascular disease have higher systolic blood pressure on average, there is an interesting subset that have high diastolic blood pressure higher and low systolic blood pressure (Figure 11, bottom left). As it is unlikely that blood pressure would be *higher* when the heart is resting than when it is beating, the data points may indicate transcription errors in the dataset.

The ECDFs for systolic (Figure 12) and diastolic (Figure 13) blood pressure for those with cardiovascular disease are both shifted to the left (higher blood pressure) than the

ECDFs for those without cardiovascular disease; however, the shift to higher blood pressure is particularly pronounced for systolic blood pressure.

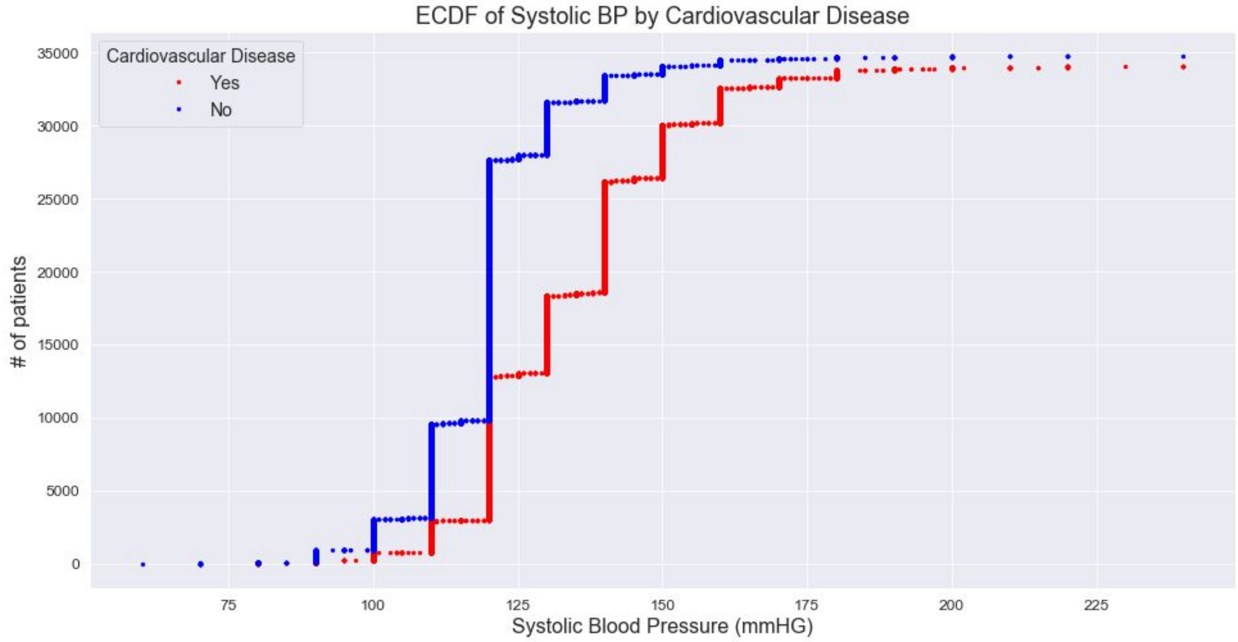


Figure 12: ECDF of systolic blood pressure for patients with or without CVD.

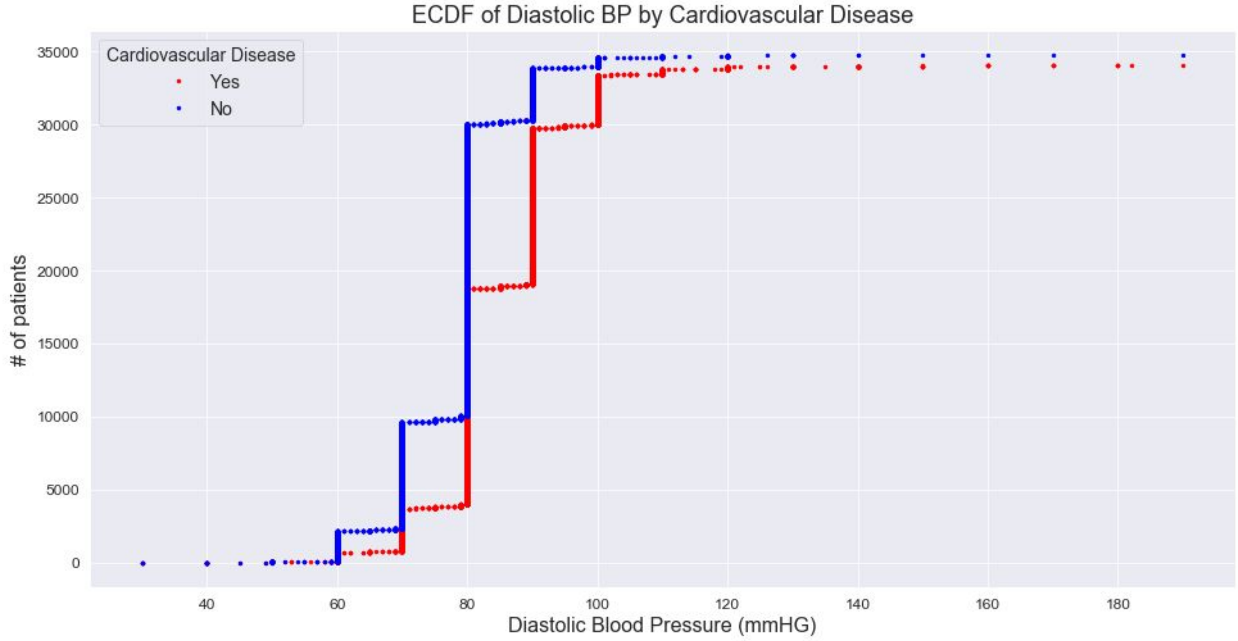


Figure 13: ECDF of diastolic blood pressure for patients with or without CVD.

The shift in mean blood pressure observed in patients with cardiovascular disease is even more apparent in boxen plots of the diastolic and systolic blood pressure (Figure 14). Student’s t-tests confirmed that the mean shifts are statistically significant for both diastolic and systolic blood pressure (Table 1). The strength of the correlation

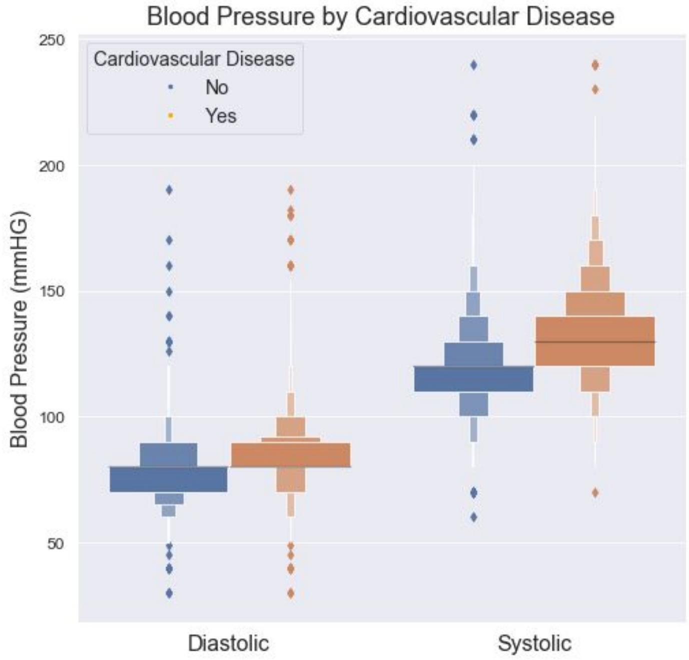


Figure 14: Boxen plots of diastolic and systolic blood pressure by cardiovascular disease.

between blood pressure and cardiovascular disease can also be measured using the point biserial correlation coefficient, which measures the relationship between a binary variable (i.e. cardiovascular disease) and a continuous variable (i.e. blood pressure). The point biserial correlation coefficients show that both systolic and diastolic blood pressure are strongly correlated with cardiovascular disease (Table 1). The point biserial correlation coefficients for the continuous features discussed previously (age, height, weight, and BMI) were also calculated and compared to those for systolic and diastolic

	Mean without CVD	Mean with CVD	T-statistic	p-value	Point Biserial Correlation	p-value
Age	51.72	54.96	64.68	0.0	0.425	0.0
Height (m)	1.645	1.643	3.1	0.0019	-0.012	0.0019
Weight (kg)	71.57	76.72	47.99	0.0	0.18	0.0
BMI	26.47	28.46	50.61	0.0	0.19	0.0
Systolic BP (mmHG)	119.56	133.82	123.14	0.0	0.425	0.0
Diastolic BP (mmHG)	78.17	84.65	93.11	0.0	0.335	0.0

Table 1: Summary statistics for continuous features for patients with and without cardiovascular disease.

blood pressure. Of the continuous features, age and systolic blood pressure are most strongly correlated with cardiovascular disease, followed by diastolic blood pressure.

IV. Cholesterol and Glucose Levels

Cholesterol and glucose levels have been categorized in the dataset as either ‘normal,’ ‘above normal,’ or ‘well above normal’ instead of reporting the exact values. While having the data in this form is slightly less useful than the raw values would be, analysis of the data can still yield valuable insights. Count plots for both the cholesterol and glucose data were used to examine the distribution across the three levels for patients with or without cardiovascular disease, revealing that the proportion of patients with CVD increases as either the cholesterol or glucose levels increase (Figure 15). The relationship between cholesterol or glucose level and cardiovascular disease is even more apparent if we instead plot the percentage of patients with cardiovascular disease at each level (Figure 16). Among individuals with normal cholesterol levels, 43.56% also have cardiovascular disease. However, this number drastically increases to 76.28% among individuals with the highest cholesterol levels (Table 2). A similar, though less dramatic, increase is observed between individuals with normal glucose levels (47.57%)

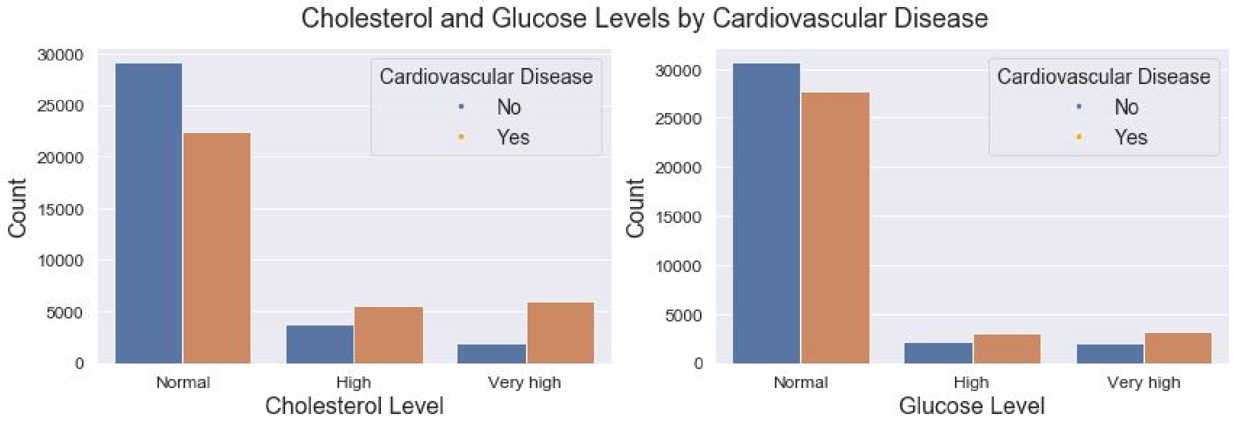


Figure 15: Count plots of individuals with or without CVD by cholesterol or glucose level.

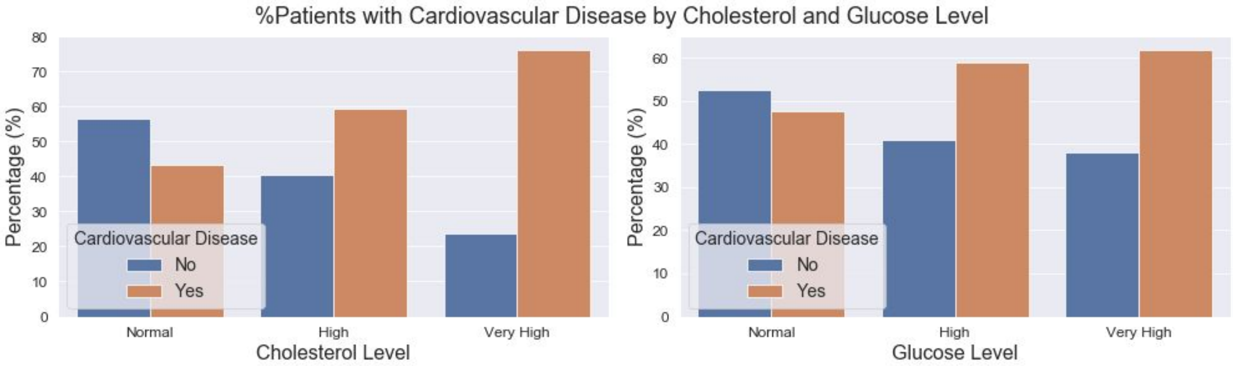


Figure 16: Percentage of patients with or without CVD at different cholesterol and glucose levels.

and those with very high levels (61.88%). Chi-square tests for independence can be used to confirm the statistical significance of the observed increases in cardiovascular disease between cholesterol and glucose levels. The p-values for both chi-square tests were essentially 0, providing strong evidence that cardiovascular disease is linked to both cholesterol and glucose level (Table 2). Additionally, the chi-square values were used to calculate the contingency coefficient, which is another measure of the strength of an association between two variables, similar to Pearson's correlation coefficient or the point biserial correlation coefficient. The disadvantage of the contingency coefficient is that it does not reach a maximum value of 1, and cannot therefore be directly compared to other correlation coefficients. However, we can see from the contingency coefficients that cholesterol level and cardiovascular disease are more strongly associated than glucose level and cardiovascular disease.

	Cholesterol Level			Glucose Level		
	Normal	**High**	**Very High**	**Normal**	**High**	**Very High**
% with CVD	43.56%	59.63%	76.28%	47.57%	58.87%	61.88%
% without CVD	56.44%	40.37%	23.72%	52.43%	41.13%	38.12%
χ^2	3372.1			586.33		
p-value	0.0			0.0		
χ^2 **correlation**	0.2163			0.092		

Table 2: Percentage of patients with or without CVD at different cholesterol and glucose levels and results of chi-square tests.

V. Trends in Self-Reported Features: Smoking, Alcohol Intake, and Physical Activity

The last few features of the dataset were self-reported by the patients and are therefore inherently subjective, making them much less reliable than the objective physical and medical features analyzed previously. In addition, the dataset does not include the questions that the patients were responding to. Take smoking as an example: we might assume that 'No' means that the patient did not consider themselves to be a smoker when the data was collected. However, it is possible that the patient had been a smoker in the past, or perhaps just smokes occasionally. For alcohol intake, it is unknown whether a negative response indicates that the patient never drinks, or is instead a measure of the level of alcohol intake (i.e. 'light' or 'moderate' vs. 'heavy'). There is also no guarantee that the respondents were truthful in their responses. For example, if we examine the count plot for alcohol intake, split into those with CVD and those without, only a small proportion of the patients responded positively, but it seems highly unlikely that only this small fraction of the patients drink alcohol (Figure 17, plot 1). In general, the distributions across the three features give the impression that most people exercise regularly and don't drink or smoke (Figure 17), but the reliability of these data is questionable. Despite all of these complicating factors, we might still be able to glean some useful information from analyzing this data.

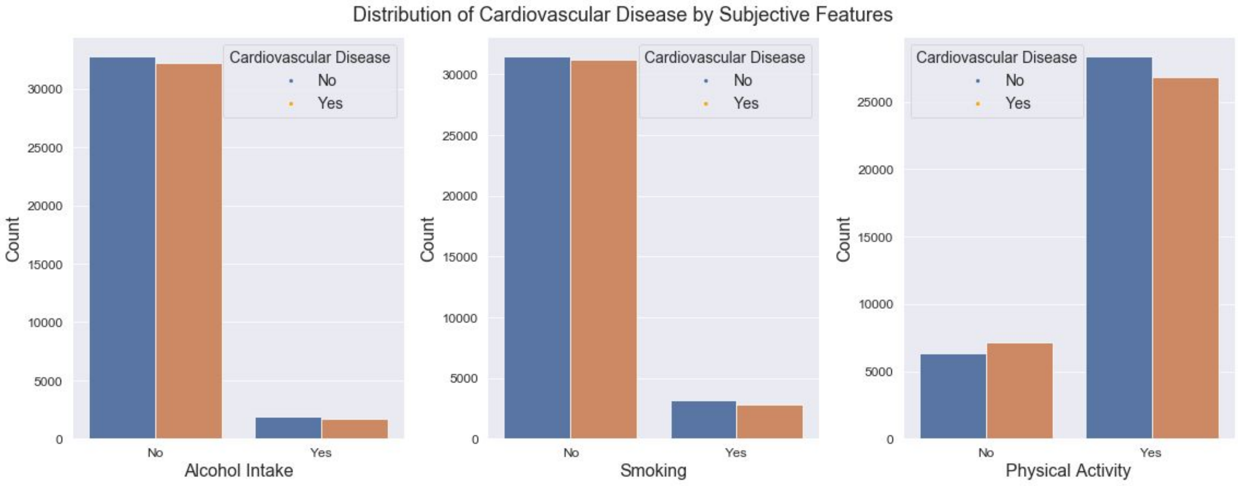


Figure 17: Count plots for smoking, alcohol intake, and physical activity by cardiovascular disease.

Chi-square tests for independence between the subjective features and cardiovascular disease all indicate that cardiovascular disease is in fact associated with all of these features (Table 3). However, the correlations are not necessarily in the expected direction. Plotting the percentage of patients with or without CVD rather than simply the number of patients normalizes the data between the positive and negative categories for each feature so that the differences between those with CVD and those without are much easier to see (Figure 18). From these plots, it appears that patients who reported

	Smoking		Alcohol Intake		Physical Activity	
	No	Yes	No	Yes	No	Yes
% with CVD	49.74%	46.86%	49.58%	47.80%	53.27%	48.56%
% without CVD	50.26%	53.14%	50.42%	52.20%	46.73%	51.44%
χ^2	18.25		4.36		96.22	
p-value	1.9×10^{-5}		0.037		1.0×10^{-22}	
χ^2 correlation	0.0163		0.008		0.0374	

Table 3: Effects of smoking, alcohol intake, and physical activity on cardiovascular disease.

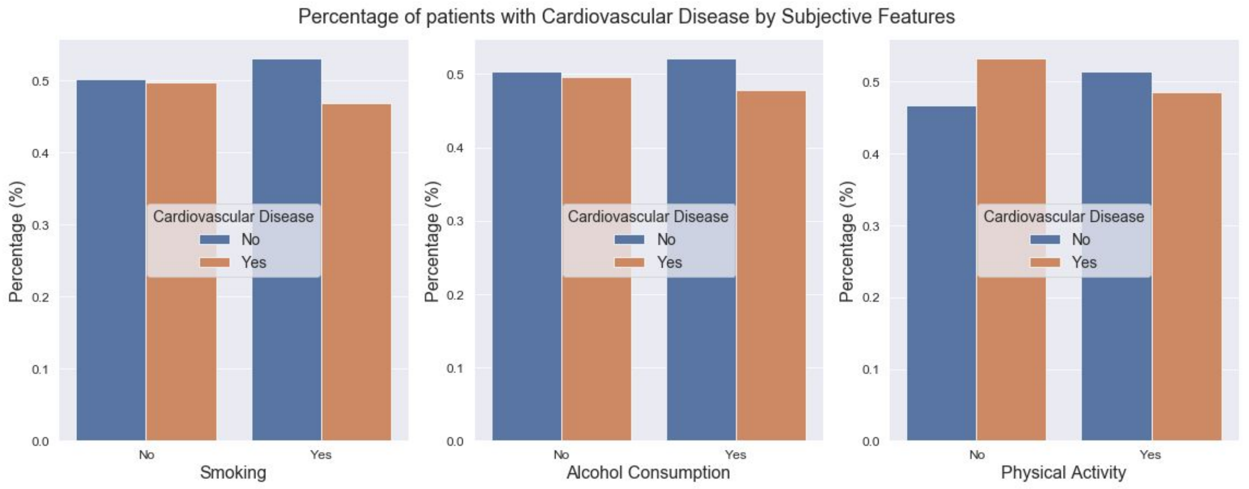


Figure 18: Percentage of patients with or without CVD by smoking, alcohol intake, and physical activity.

'yes' to either smoking or alcohol intake are slightly *less* likely to have cardiovascular disease than patients who responded 'No' to smoking and alcohol intake. Physical activity, on the other hand, shows the opposite effect - patients who reported no physical activity are more likely to have heart disease than those who do exercise. Although the chi-square tests indicate that these differences are statistically significant, the real-world practical significance of these results is much lower when you consider both the magnitude of the difference - only a few percentage points in either direction - and the reliability of the data used in the analysis.

VI. EDA Summary

Overall, this initial analysis of the dataset indicate that age, weight, BMI, systolic and diastolic blood pressure, and cholesterol and glucose levels are all influential factors when it comes to cardiovascular health. Although there is a statistical difference in average height between healthy individuals and those with cardiovascular disease, the effect is too small to have any meaningful applications on its own. However, it might be advantageous to simply include BMI in place of height and weight as a feature during model building, as BMI is derived from both. As both BMI and weight were correlated with cardiovascular disease to a similar degree, including both would be redundant. While gender on its own does not have a strong association with cardiovascular disease, it may have an effect in combination with other factors such as age. Finally, the data around smoking, alcohol intake, and physical activity were self-reported, which leaves a lot of room for interpretation, misunderstanding, or even intentional misinformation, especially as the exact questions put to the participants was not included in the dataset. Therefore, these features should potentially be given less weight or removed altogether when building predictive models.

IN-DEPTH ANALYSIS AND MACHINE LEARNING

Several preprocessing steps were necessary before the dataset could be fed into the different machine learning algorithms to train predictive classifiers. First, as many scikit-learn estimators cannot directly handle categorical data, several of the dataset features needed to be encoded into binary features. Gender, which is encoded as either ‘1’ for female or ‘2’ for male, was trivial to recode as ‘0’ for ‘not male’ and ‘1’ for ‘male’. Both the cholesterol and glucose features were also encoded such that each of the three categorical levels were split into individual binary features, resulting in six features from the original two. The features for alcohol intake, smoking, and physical activity, already being binary, needed no further encoding. The second necessary preprocessing step was to standardize the features by scaling them to have a zero mean and unit variance. In order to apply the same scaling to both the train and test data, I used the transformer StandardScaler as part of a pipeline to first scale the data before passing it to the classifier.

With a dataset of this size, splitting the dataset into training and test sets also required some trial-and-error based optimization. At nearly 70,000 observations, it is both unfeasible and unnecessary to use more than 10-20% of the dataset for training predictive models. Including a larger fraction of the observations in the training dataset increased the computational time needed for model training and prediction, but did not significantly affect model accuracy. Therefore, the classifiers discussed in this section were all trained using just 10% of the dataset; the remaining 90% of the data were reserved for testing the classifiers’ performance.

I. Feature Selection

Although the feature set is not very large, the large number of observations nevertheless makes it worthwhile to trim the feature set as much as possible to decrease the computational power required to fit and predict the data. First, as height and weight were highly collinear, I removed them from the dataset and instead used BMI in their place. Both weight and BMI were similarly correlated with cardiovascular disease in my preliminary analyses, and keeping just one feature removes redundancy from the feature set. I then used several different methods to rank the features and identify the most important features in the dataset. First, I tried two tree-based methods for feature selection; one using the random forest algorithm and the other using the extra-trees method (extremely randomized trees). Both algorithms were trained using the training dataset only (10% of total dataset), then the feature importances were extracted and plotted (Figure 19). Both of the models identified age, BMI, systolic blood pressure, and diastolic blood pressure as the most informative features, and placed alcohol intake, smoking, and the three glucose levels as the least important features. I also performed a similar analysis using a gradient boosting classifier, which yielded a similar ranking, though the feature importance scores were quite different (Figure 20). While age is ranked as the most important feature by all three classifiers, the importance score goes

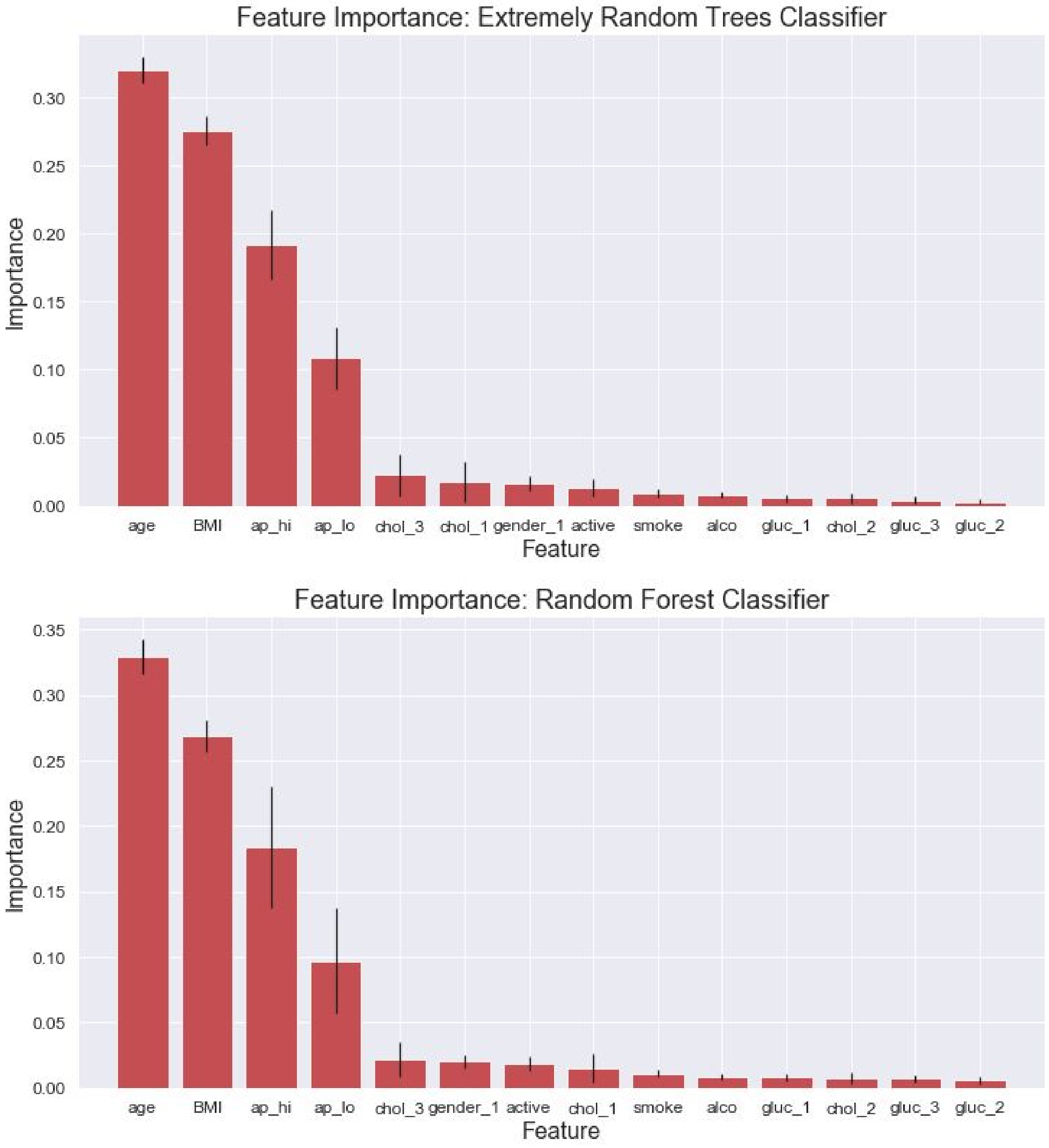


Figure 19: Top - bar chart of feature importance using an Extra-Trees Classifier. Bottom - bar chart of feature importance using a Random Forest Classifier.

from roughly 0.32/0.33 for the tree-based classifiers to ~0.54 for the gradient boosting classifier. Finally, I also used recursive feature elimination with a logistic regression classifier to identify the top-ranked features. When set to select the top five features, the estimator returned age, systolic blood pressure, BMI, normal-level cholesterol and very high cholesterol as the top features. I further used cross validation with recursive feature elimination to identify the optimal number of features to include when training machine learning classifiers. While this varies slightly for different values of the C parameter passed to the logistic regression estimator, the cross validation score increases up to 3-4 features, then fluctuates around the same score as more features are added to the analysis (Figure 21). Using these combine results, I created a smaller

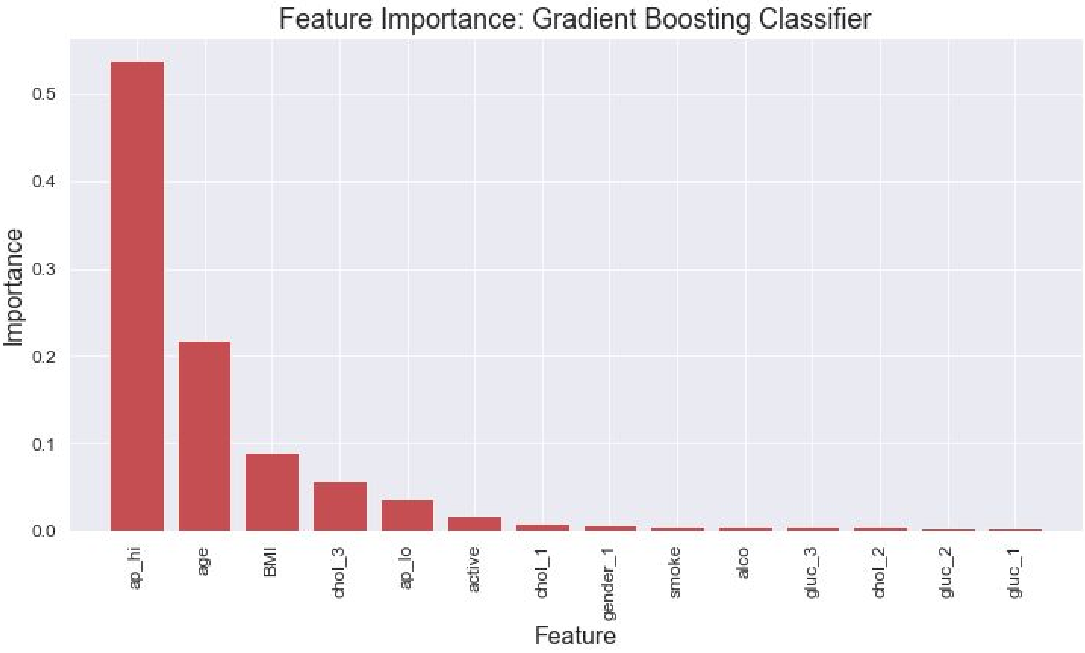


Figure 20: Bar chart of feature importance using a Gradient Boosting Classifier.

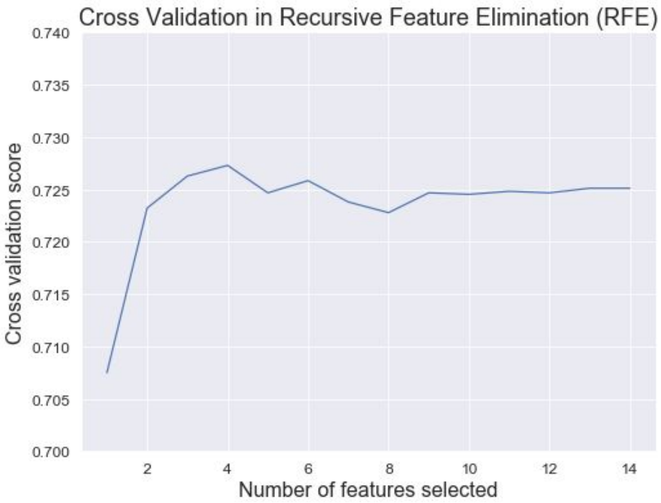
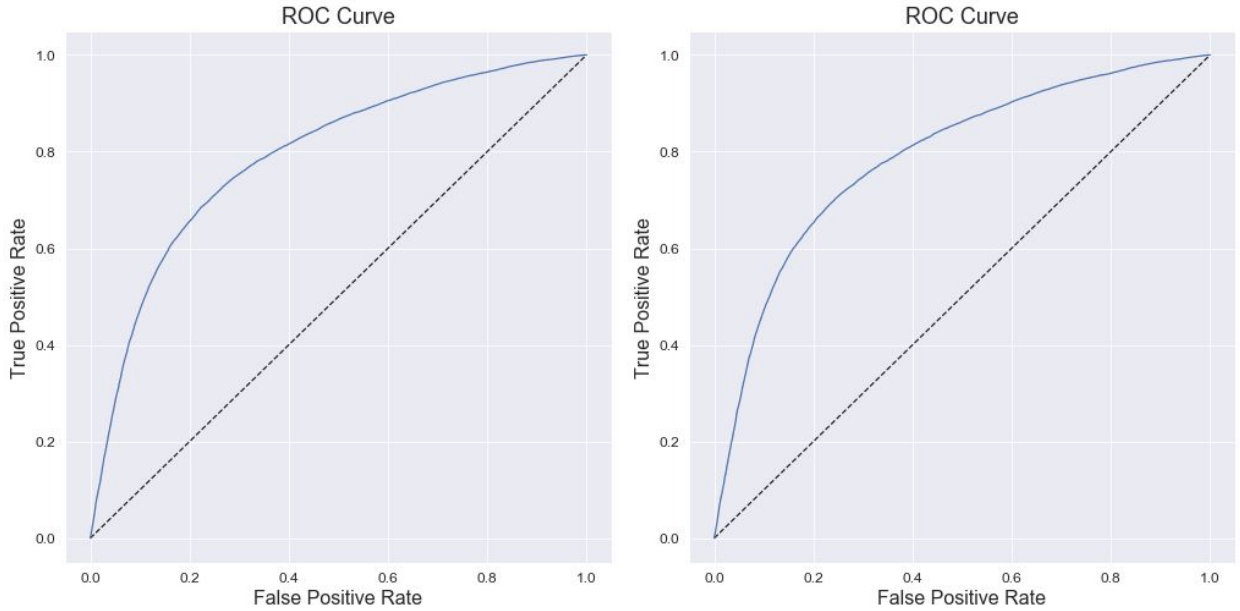


Figure 21: Cross-validation scores for # of features selected in recursive feature elimination.

feature set containing age, BMI, systolic blood pressure, diastolic blood pressure, and the very high cholesterol features to use for classifier training. In the next sections, I compare the performance of classifiers trained using this reduced feature set to that of classifiers trained using the full feature set (excluding height and weight).

II. Logistic Regression

Logistic regression is one of the best models to predict a binary outcome such as presence or absence of cardiovascular disease. I used five-fold cross validation combined with grid search to tune the ‘C’ parameter, which determines the strength of the regularization (smaller C values specify stronger regularization). The classifier trained using the full feature set, excluding height and weight, performed quite well, yielding 73.02% accuracy and an AUC of 0.79. The classifier trained using the reduced feature set also performed quite well, with a slightly lower accuracy of 72.85% (Figure 22). Both models also had similar precision, recall, and F1 scores, as shown in Table 4.



AUC = 0.79, Accuracy = 73.02% **AUC = 0.79, Accuracy = 72.85%**

Figure 22: Comparison of ROC curves for Logistic Regression classifiers trained using either the full feature set (left) or the reduced feature set (right).

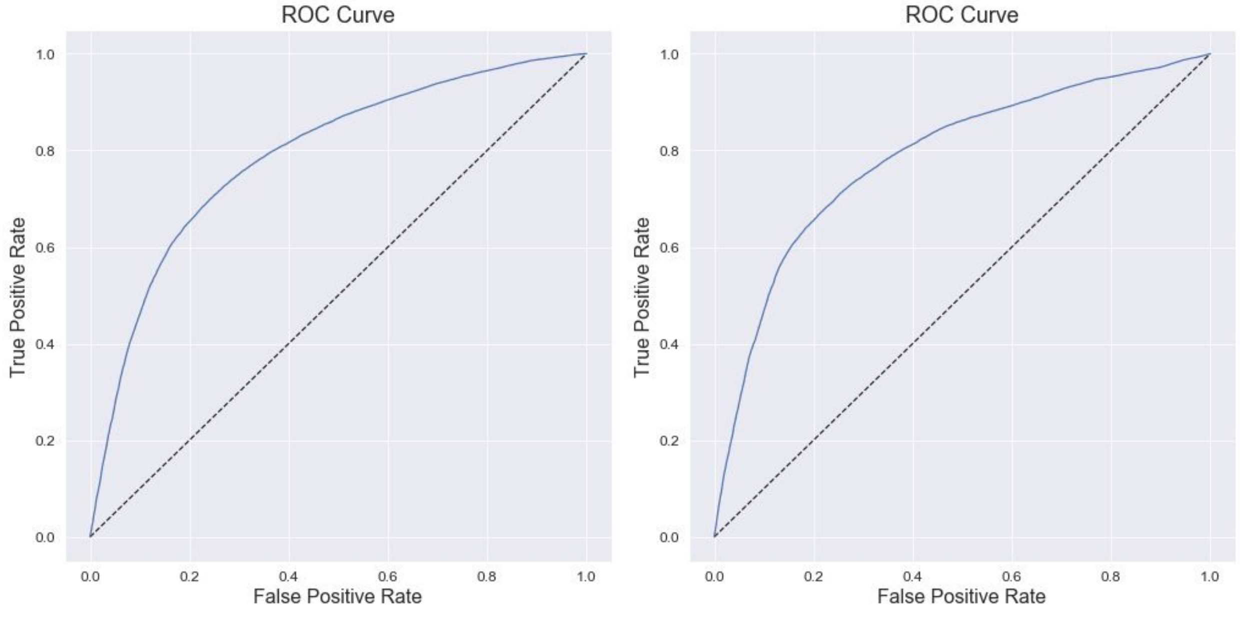
	Full Feature Set		Reduced Feature Set	
	Without CVD	**With CVD**	**Without CVD**	**With CVD**
Precision	0.71	0.75	0.71	0.76
Recall	0.78	0.67	0.79	0.67
F1-score	0.75	0.71	0.75	0.71

Table 4: Evaluation metrics for logistic regression classifiers.

Fitting and predicting using a logistic regression classifier was quite quick with this dataset, so I was also able to assess model performance when using different combinations of the features. I was able to remove height, weight, smoking, and the normal glucose category from the feature set without decreasing the accuracy of the logistic regression model (73.02%).

III. Support Vector Classifier

I next fit a model using the scikit learn's implementation of a Support Vector Classification (SVC) method. I used randomized search cross-validation to assess different values for the penalty parameter C and the kernel coefficient gamma. As the fit time for an SVC scales quadratically with the number of samples, it is not the most practical model for such a large dataset; the SVC classifiers took the longest time by far to complete the fit and prediction steps than the other classifiers I tested. Both the classifier trained with the full feature set (72.48% accuracy) and the one trained with the reduced feature set (72.81% accuracy) were slightly less accurate than the logistic regression classifiers, though in this case the reduced model was the more accurate of the two (Figure 23). The precision, recall, and F1-scores were also similar to those obtained from the logistic regression models (data not shown). I also assessed scikit-learn's Linear SVC model, which is similar to the SVC model using a linear kernel, but which scales better for datasets with large numbers of samples. Using the full



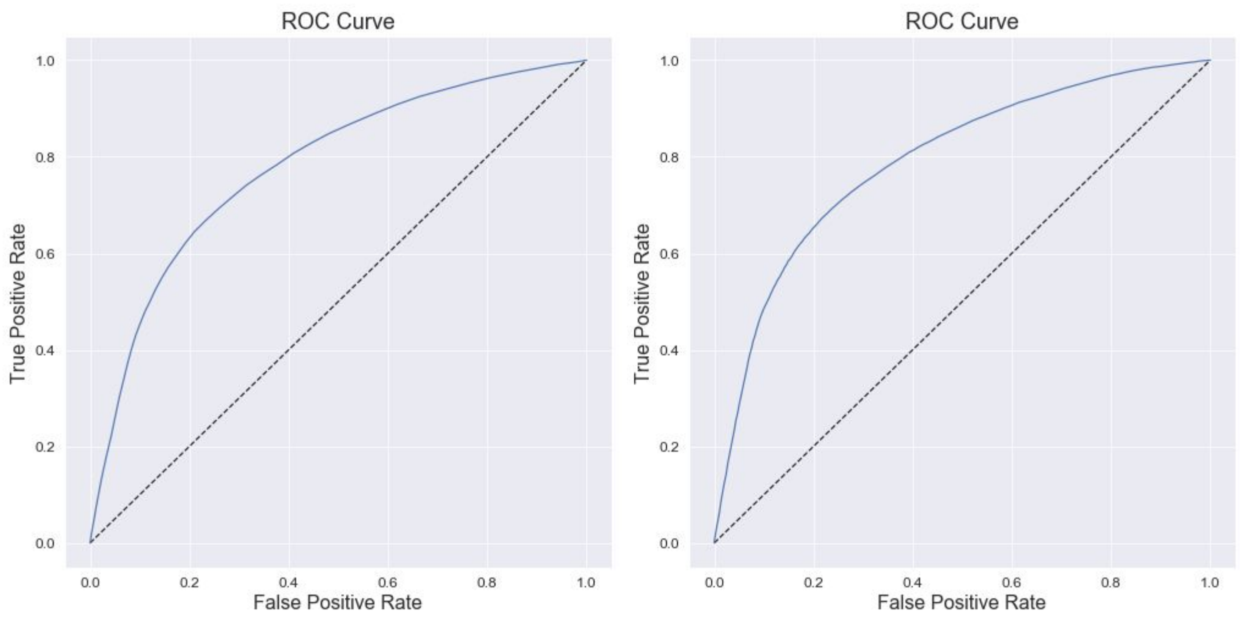
AUC = 0.79, Accuracy = 72.48% **AUC = 0.78, Accuracy = 72.81%**

Figure 23: Comparison of ROC curves for Support Vector Classification models trained using either the full feature set (left) or the reduced feature set (right).

feature set with a linear SVC yielded an accuracy of 72.85%, while the reduced feature set yielded an accuracy of 72.72%. The faster performance of the Linear SVCs over the normal SVCs The Linear SVC models were significantly faster to train than the SVC models (a few seconds vs. 30-40 minutes) and were roughly equally accurate. All in all, support vector classification, while accurate, is simply not efficient at handling a large dataset without further computational power.

IV. K Nearest Neighbors

The k nearest neighbor (kNN) algorithm predicts the class of a new data point by majority vote of its k-nearest neighbors. Fitting a kNN classifier is very quick because the training data is simply stored for later. All computation work is deferred until classification of a new set of data, at which point distances between the new data and the training data are determined to identify the k-nearest neighbors for each new data point. Grid search cross-validation identified k-nearest neighbors between 100-200 as optimal, depending on which feature set I began with. Overall, the reduced feature set classifier, with an accuracy score of 72.59%, performed slightly better than the full feature set classifier at 71.80% accuracy. However, the logistic regression classifier still performed slightly better and was much faster at fitting and prediction.

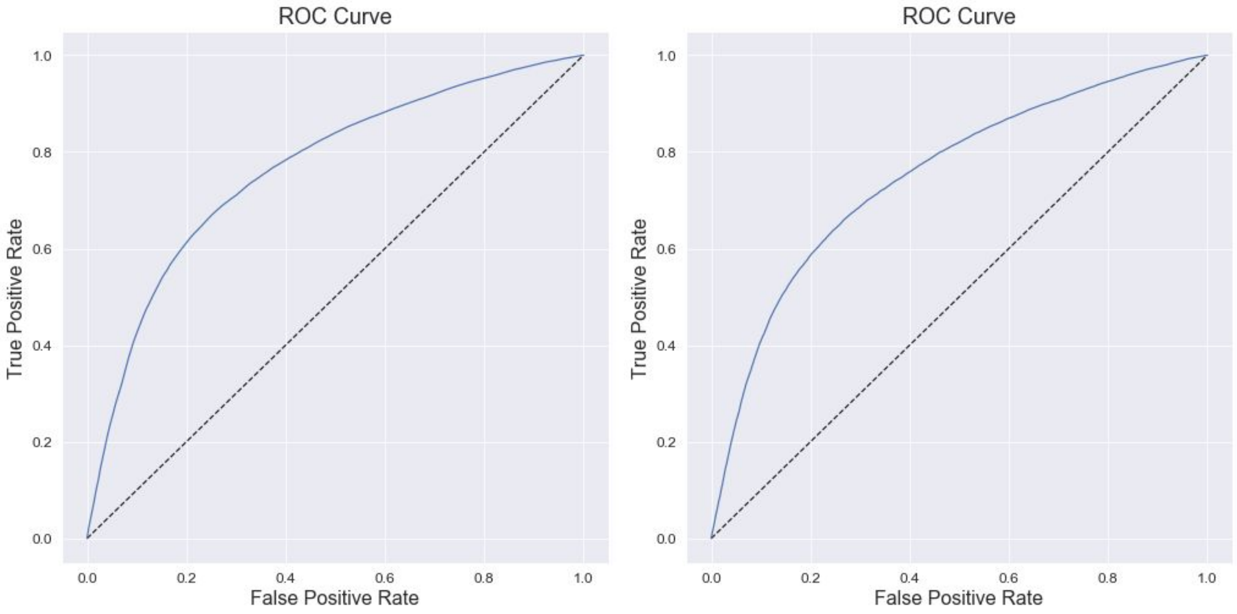


AUC = 0.78, Accuracy = 71.80% **AUC = 0.78, Accuracy = 72.59%**

Figure 24: Comparison of ROC curves for k-Nearest Neighbors classification models trained using either the full feature set (left) or the reduced feature set (right).

V. Random Forest

The random forest classifiers performed the worst out of all the classifiers that I trained, though the margin between the best and worst classifier was still only 3.6%. The number of features and the number of estimators used in the classifiers were selected using grid search cross-validation. The full feature classifier had an accuracy of 70.75% and the reduced feature classifier had an accuracy of 69.38%. However, all of the other classifiers assessed outperformed the random forest classifiers.



AUC = 0.77, Accuracy = 70.75% **AUC = 0.75, Accuracy = 69.38%**

Figure 25: Comparison of ROC curves for Random Forest Classification models trained using either the full feature set (left) or the reduced feature set (right).

VI. Machine Learning Summary

In the end, the first classifier I tested turned out to be the best. The logistic regression classifier trained using the full feature set except for height and weight yielded the highest accuracy, 73.02%, in predicting the labels of the test samples. In addition, the classifier trained using the reduced set of features displayed only a slight drop in accuracy down to 72.85%, indicating that many of the features could potentially be dropped if a predictive model were to be deployed for use by healthcare practitioners. However, as most, if not all, of the features are data that would normally be gathered during a routine physical examination, it may be worthwhile to keep all features in the model for the slight increase in accuracy. On the other hand, as the veracity of the subjective features cannot be determined, my inclination would be to leave them out of the predictive model entirely despite the slight accuracy gain they provide.

CONCLUSION

In conclusion, I have successfully trained a predictive model that can classify patients with heart disease based on information collected during routine medical examinations. While a simple binary classification outcome of ‘heart disease’ or ‘no heart disease’ may not be as useful for identifying patients who are at risk for developing heart disease, similar datasets that contained more nuanced outcomes, such as rankings of cardiovascular health or stages of cardiovascular disease, could easily be used to develop a more sophisticated predictive model using the same techniques. However, the current model could still be useful as a routine screening tool for healthcare providers to identify patients who should be referred for further assessment of their cardiovascular health. Analysis of the dataset also revealed the top risk factors for cardiovascular disease to be increased age, weight, systolic & diastolic blood pressure, and cholesterol level. This information could be used by doctors and health advocates to design and promote awareness and prevention campaigns and to encourage the general public, especially those in their 50s and up, to routinely monitor their weight, blood pressure, and cholesterol.

Future ideas I would like to implement to further improve the predictive power of the model include testing several other machine learning algorithms such as AdaBoost or Naive Bayes. Additionally, I would like to make use of a framework such as Apache Spark to increase the computational power using computing clusters and decrease the time required to train classifiers so that more of the dataset could be used for training.