Project Prototype

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All code in the report has been hidden, but the full markdown can be accessed at the following team Github repository (https://github.com/connerbyrd/CS-216-Final-Project).

I. Introduction

According to the Center for Disease Control, heart disease is one of the leading causes of death for people of most races in the United States. About half of all Americans half at least one of three key risk factors for heart disease defined by the CDC (high blood pressure, high cholesterol, and smoking), and detecting and preventing the factors that have the greatest impact on heart disease is very important to healthcare, as heart disease is treatable if there is quick access to equipped hospitals and early diagnosis, as well as key predictive screening to analyze the risk factors of patients. To prevent individuals from having heart disease, it is first necessary to be able to determine risk factors which can be used to create actionable prevention plans. Currently, there are several different ways for physicians to diagnose patients that they believe to be at risk for heart disease, which often include measuring blood pressure, cholesterol level, and conducting further tests such as exercise stress tests and electrocardiograms. However, there are many issues with current diagnostic methods. A study of 500 patients found a false positive reading between 77 and 82 percent in patients in patients at risk of heart disease screened by ECG, and a false negative reading between 6 to 7 percent in the same patient population. To more successfully prevent diagnose individuals that are at risk for heart disease, it is first necessary to be able to determine other strong risk factors which can be used to create actionable prevention plans.

In that aim, our research has two main questions. Our first question is what demographic and health factors tend to be the best at predicting the occurrence of heart disease? To answer this question, we plan on creating predictive models to assess the likelihood of a heart disease diagnostic for potential at-risk patients based on a number of factors. Our second question is what health and demographic factors tend to affect the risk of having heart disease? We plan on creating models for the purpose of interpretation to answer this question and provide a greater understanding of signs that patients can analyze to check their risk for heart disease. Overall, nothing has changed from our research question in the proposal.

Answering these questions requires an in-depth and substantial analysis of patient data. Examining health-related statistics and lifestyle choices that impact those numbers may reveal what increases the chance of heart disease and how to alleviate the risk. This necessitates resolving what health factors correlate with a greater percentage of patients that have heart disease. Following those results, we will need to determine an algorithm to optimize health factors related to heart disease prevalence and subsequently develop an action plan to achieve the optimized attributes. With readily-available patient datasets pertaining to heart disease prevalence, answering these questions is a feasible goal for our team within the six week timeframe. With adequate contribution, time-management, and communication by each team member, we will be able to reach conclusive answers. Doing so is positively relevant to the scientific community given the scope of the disease globally and within the United States. With the current metric of nearly half of Americans at risk of heart disease according to the CDC, diagnosing this issue and proposing a solution has the potential to save the lives and prosperity of countless millions around the world.

Overall, we made no significant changes to the introduction.

II. Data Sources

The dataset we utilize to answer our research questions is the 2020 CDC survey as part of the Behavioral Risk Factor Surveillance System, which conducts telephone surveys to gather data on the health status of US residents in all 50 states as well as the District of Columbia and three US territories, asking questions about the respondents' health status and demographic information (please see Works Cited for link to data). The original dataset of nearly 402,000 observations nearly 300 variables was reduced to 18 variables relating to various demographic health conditions, such as BMI, whether the respondent was a smoker, as well as the sex and race of the respondent. The categorical variable of whether the respondent has ever had heart disease is also included in the dataset. We acquired the dataset from Kaggle, and the dataset has already been pre-processed and cleaned by both the CDC and Kaggle, with only observations where all 18 variables have been recorded kept in the cleaned data (Please see the Appendix for a description of the variables).

The dataset utilized for our project is relevant and appropriate for addressing our research question as the dataset is one of the largest datasets available on the health status of individuals that includes information on the prevalence of heart disease. The dataset, collected and curated by the CDC, also has a wide reach across the United States geographically. The datasets size and geographic breadth will allow us to generalize our findings across the United States with fewer issues and also has the potential to provide more predictive power and better data to train our models on than smaller datasets curated elsewhere.

Overall, nothing has changed in terms of our data source.

Data Pre-Processing

The data was already pre-processed by both the CDC and the uploader to Kagle, and had no missing variables. Due to the size of the dataset and the high runtime with fitting models using such a large dataset, we trim down the dataset to 50,000 observations by sampling 10,000 observations randomly in the dataset, and split the sampled dataset into both a testing and a training set. The 18 variables included include 17 predictor variables as well as the dependent variable, `HeartDisease`. Some of the variables, such as `PhysicalHealth`, `MentalHealth`, and `SleepTime`, make more sense being a proportion of the number of days in the month or number of hours in the day, as `PhysicalHealth` and `MentalHealth` are limited to the number of days in a month and `SleepTime` is limited to 24 hours. Thus, we scale them to be in-between 0 and 1. Furthermore, `BMI` is transformed into a categorical variable defined to conventional medical norms (BMI of under 18.5 is underweight, 18.5 to 25 is considered normal, 25 to 30 is considered overweight, and over 30 is considered obese) as medically, there are very few differences in changes in BMI within a category, and most medical professionals utilize BMI as a categorical variable.

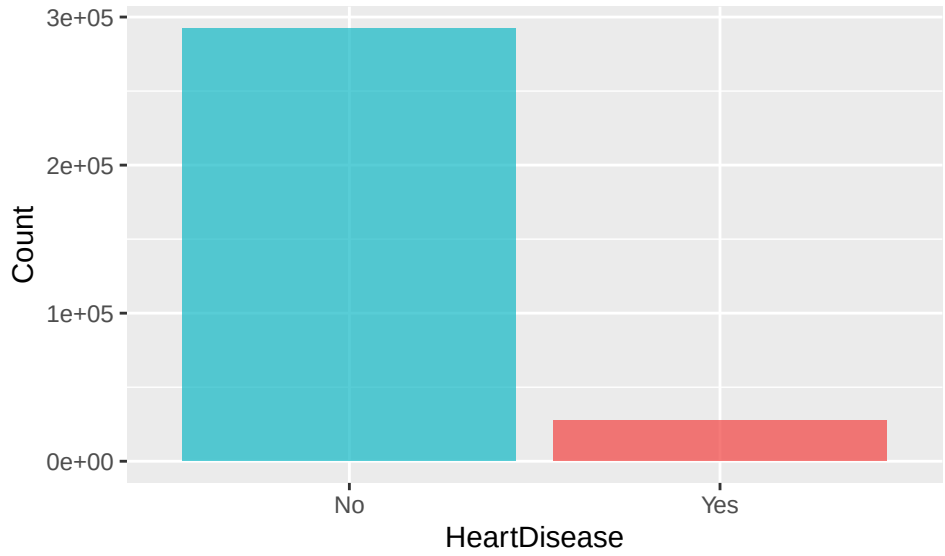
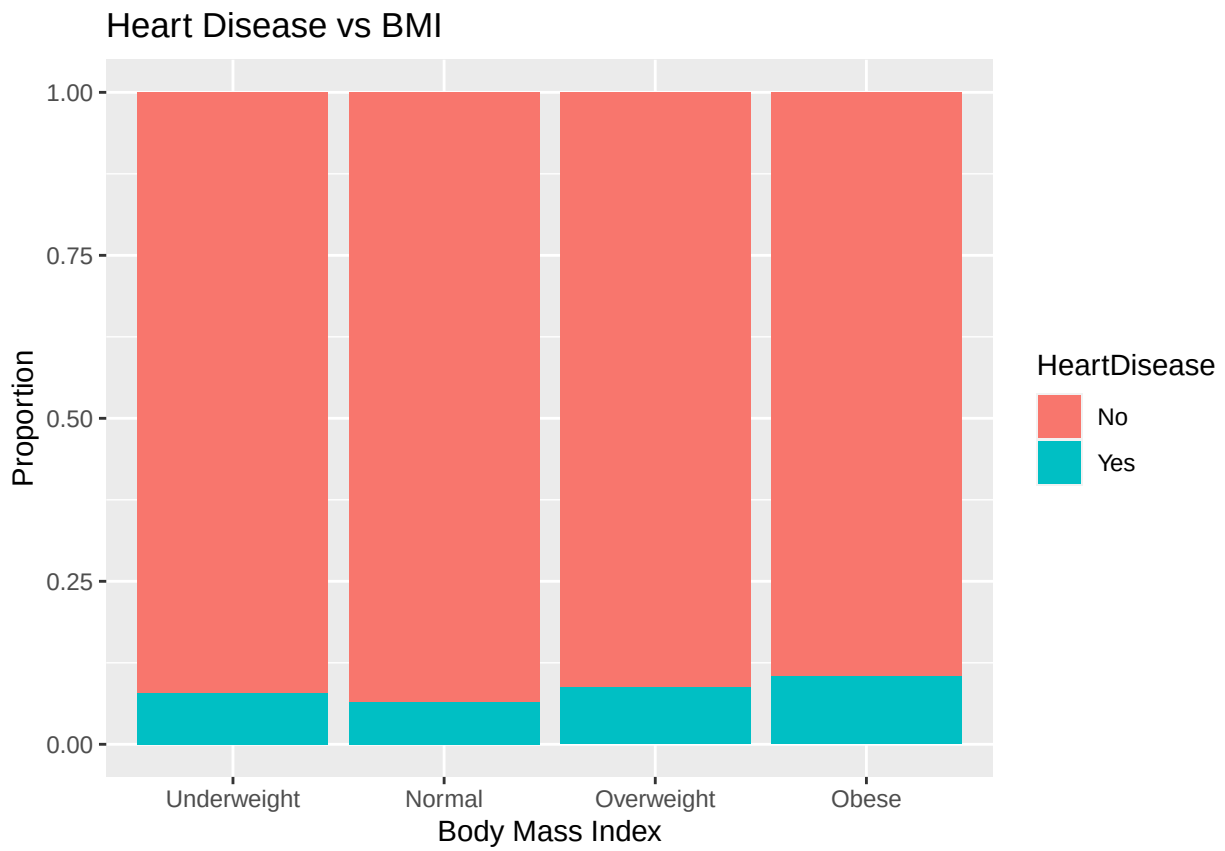


Figure 1: Counts of Individuals with and without Heart Disease

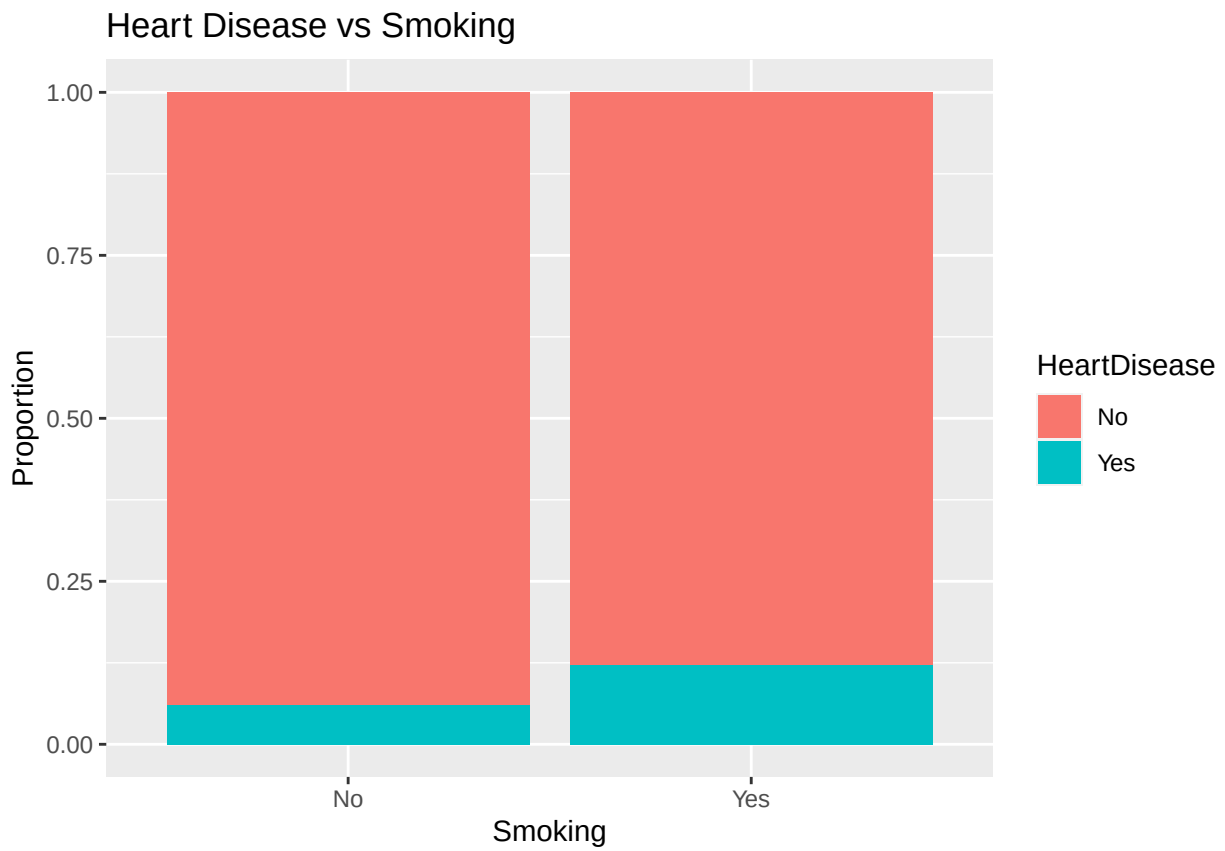
As shown above, the data is heavily imbalanced, with far more observations where heart disease was not observed than where it was observed. Imbalanced data poses a problem, as the model being trained would be dominated by the majority class, which in this case is where the patient does not have heart disease. The model would predict the majority class more effectively than the minority class, which is undesirable in this case as we want to ensure a high sensitivity rate as it is far more important to be able to correctly identify individuals with heart disease. A technique to reduce the negative impact of imbalanced datasetes is by subsampling the data. Thus, we upsample the minority class by sampling with replacement so the two classes have the same size to create an upsampled training dataset.

Exploratory Data Analysis

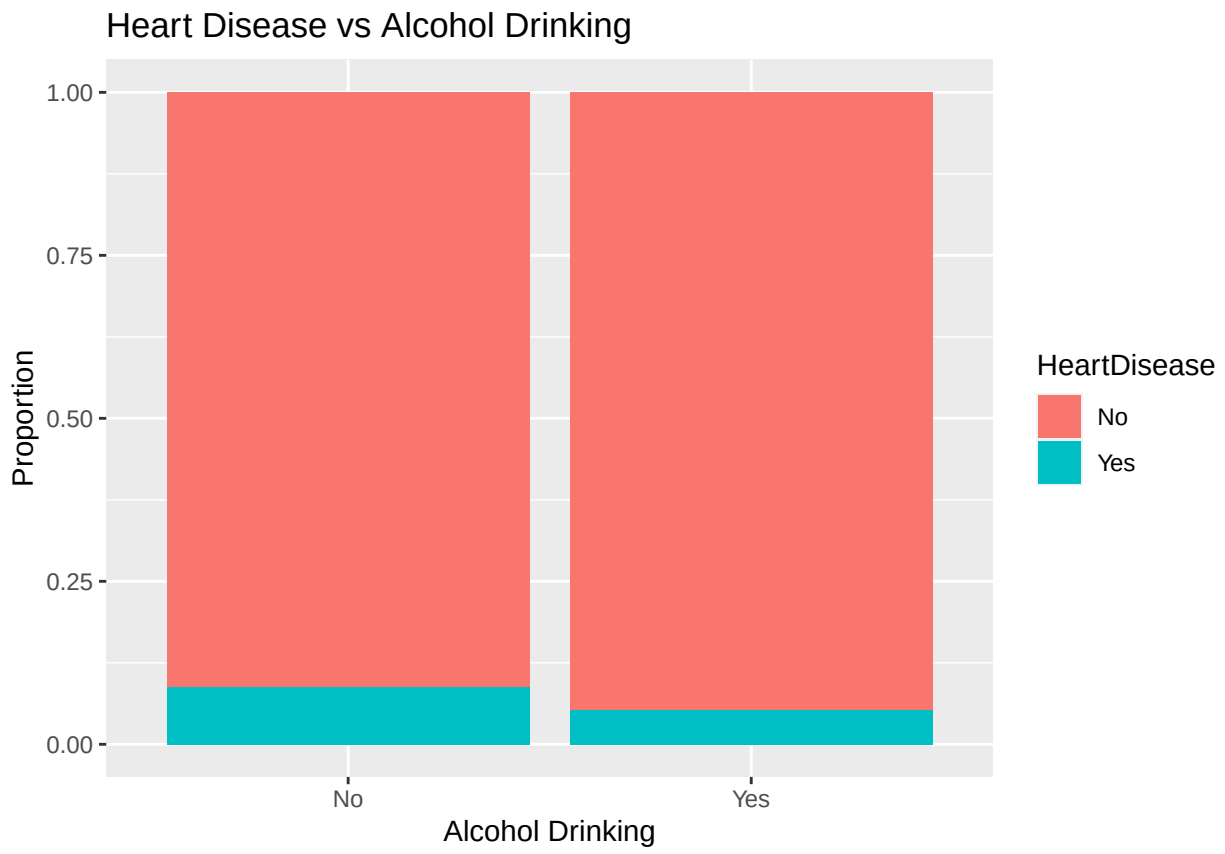
We first explore a few potential interesting relationships between the prevalence of heart disease and some general lifestyle and health factors that may be of interest, such as BMI and whether a person smokes or drinks. We first decided to explore any potential relationship between BMI and the prevalence of Heart Disease, as although the usage of BMI is controversial, BMI is still popular in its medical usage in regards to association with heart disease.



The plot above displays the prevalence of heart disease by BMI classification. From the visual analysis, it appears that higher body mass may be correlated with a higher chance of heart disease.



The plot above displays the prevalence of heart disease by whether or not the respondent is a smoker (defined as having smoked at least 100 cigarettes in the study). From the visual analysis, it appears that whether an individual is smoking may be positively correlated with a higher chance of heart disease.



The plot above displays the prevalence of heart disease by whether or not the respondent is a heavy drinker. From the visual analysis, it appears that heavy drinking may be associated with a lower chance of heart disease, interestingly.

III. Modules Used

Being that our project will involve locating relevant predictors and using them to make inferences, Modules 3, 5, and 9 are all very applicable.

Module 3 - Probability

Probability is a foundational aspect of statistics and is used heavily when running experiments, making predictions or estimations, using distributions, and much more. Throughout the course of our project, we expect to use probability for numerous applications. The vast majority of these applications will come during the data investigation, data analysis, and final report portions of the project. When looking for significant predictors, probability is used in the form of p-values and is compared against a set alpha level in order to determine statistical significance. We will use probability in this manner to determine which patient variables lead to an increased risk of heart disease. Probability is also an important aspect of statistical distributions, which we expect to use substantially throughout our project. Noting which distributions to use based on the relationships between the response (heart disease indicator) and the various dependent variables will determine useful probabilities that can then be analyzed. Other probabilistic values such as the mean, variance, and standard deviation will also be useful for prediction, estimation, and even data imputation for certain patient lifestyle variables.

Module 5 - Statistical Inference

Much like probability, statistical inference is highly important for making conclusions about data. In our project, the majority of statistical inference will come in the form of hypothesis testing. Using hypothesis testing, we will be able to test certain variables for their significance when it comes to heart disease occurrence. From there, we can use the techniques described in Module 3 to determine exactly which health and body attributes most prominently lead to an increased risk in heart disease. Much like with probability, we expect to use statistical inference in the data investigation, analysis, and final report sections of the project.

Module 9 - Prediction & Supervised Machine Learning

Seeing as one of our research questions revolves entirely around prediction, we will be using concepts from Module 9 liberally throughout our project. Linear and Logistic Regression will be very useful to help us construct models of both numerical and categorical data and aid us in our predictive efforts. Other concepts learned in Module 9 will be helpful with checking for correlation between variables, performing stepwise regression, constructing a decision tree or support vector machine, and more. These techniques will allow us to further our understanding of the relationship between predictors and heart disease occurrence and to construct accurate models that we can then make sensible interpretations from. We will also likely end up splitting the data into training and testing cohorts in order to perform further analysis of variable selection and model fit. Prediction will be used in the data analysis and final report portions of the project.

IV. Preliminary Results and Methods

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Model for Inference

We decided to utilize a logistic regression model, with whether the person has heart disease (`HeartDisease`) as the response variable, to examine the relationship between the log-odds of heart disease and various predictors. Using logistic regression lends itself well to both inference and prediction. For the purposes of inference, we decided to fit a model including all variables, as we are interesting in exploring the relationship between the predictors and the response variable. We do not utilize any automated variable selection method for our inference exploration, as variable selection methods such as stepwise selection may drop variables based on its criteria that we are still interested in examining the relationship with the response variable. We utilize the training split from the 100,000-large sample as the data to train the model on, as mentioned in section II. The results are displayed below.

	estimate	std_error	z_value	pr_z
(Intercept)	-5.2663	0.6028	-8.7367	<0.001
BMIObese	-0.0027	0.1251	-0.0217	0.9827
BMIOverweight	0.1151	0.1173	0.9807	0.3268
BMIUnderweight	0.5892	0.3123	1.8868	0.0592
SmokingYes	0.1901	0.0924	2.0585	0.0396
AlcoholDrinkingYes	-0.5441	0.2357	-2.3083	0.021
StrokeYes	1.0265	0.1514	6.7805	<0.001
PhysicalHealth	-0.0694	0.1666	-0.4165	0.6771
MentalHealth	0.1042	0.1657	0.6287	0.5296
DiffWalkingYes	0.3737	0.1175	3.1800	<0.001
SexMale	0.7575	0.0942	8.0454	<0.001
AgeCategory25-29	-0.0191	0.6134	-0.0311	0.9752
AgeCategory30-34	0.8651	0.5040	1.7165	0.0861
AgeCategory35-39	0.5108	0.5186	0.9849	0.3247
AgeCategory40-44	0.4127	0.5132	0.8041	0.4214
AgeCategory45-49	0.9686	0.4730	2.0477	0.0406
AgeCategory50-54	1.1084	0.4625	2.3964	0.0166
AgeCategory55-59	1.6651	0.4418	3.7687	<0.001
AgeCategory60-64	1.7017	0.4386	3.8795	<0.001
AgeCategory65-69	1.8873	0.4361	4.3281	<0.001
AgeCategory70-74	2.1638	0.4358	4.9654	<0.001
AgeCategory75-79	2.2684	0.4406	5.1484	<0.001
AgeCategory80 or older	2.3623	0.4395	5.3743	<0.001
RaceAsian	-0.2517	0.5153	-0.4884	0.6253
RaceBlack	-0.1795	0.3951	-0.4543	0.6497
RaceHispanic	-0.2742	0.4018	-0.6824	0.495
RaceOther	0.0436	0.4355	0.1001	0.9203
RaceWhite	-0.0619	0.3612	-0.1715	0.8639
DiabeticNo, borderline diabetes	0.1267	0.2787	0.4547	0.6493
DiabeticYes	0.4200	0.1113	3.7751	<0.001
DiabeticYes (during pregnancy)	0.4535	0.5569	0.8143	0.4155
PhysicalActivityYes	-0.0226	0.1043	-0.2170	0.8282
GenHealthFair	1.6020	0.2061	7.7744	<0.001
GenHealthGood	0.8673	0.1871	4.6343	<0.001
GenHealthPoor	1.6418	0.2621	6.2650	<0.001
GenHealthVery good	0.5173	0.1880	2.7521	<0.001
SleepTime	-1.1975	0.7968	-1.5029	0.1329
AsthmaYes	0.2555	0.1223	2.0888	0.0368
KidneyDiseaseYes	0.7999	0.1566	5.1091	<0.001
SkinCancerYes	0.0803	0.1309	0.6131	0.5398

Model for Prediction

Whereas we utilize the full model for inference, we are interested in model performance for prediction. To select for models, we utilize stepwise selection, which consists of iteratively adding and removing predictors, in the predictive model, to find the subset of variables resulting in the best performing model with the lowest prediction error. To select for variables, we began by performing both forwards and backwards selection on the full model. These forms of stepwise regression allow us to select for variables that result in the model lowest possible AIC value. AIC itself is an estimator of the predictive error of a model, allowing us to directly assess our model's performance. Rather than utilizing

Performing forwards and backwards selection resulted in the dropping of 6 variables from our model: BMI, $PhysicalHealth$, $MentalHealth$, $Race$, $PhysicalActivity$, and $SkinCancer$.

	estimate	std_error	z_value	pr_z
(Intercept)	-5.3188	0.4822	-11.0294	<0.001
SmokingYes	0.1989	0.0916	2.1724	0.0299
AlcoholDrinkingYes	-0.5131	0.2345	-2.1878	0.0287
StrokeYes	1.0436	0.1507	6.9247	<0.001
DiffWalkingYes	0.3568	0.1115	3.1993	<0.001
SexMale	0.7537	0.0929	8.1125	<0.001
AgeCategory25-29	-0.0344	0.6128	-0.0562	0.9552
AgeCategory30-34	0.8367	0.5025	1.6651	0.0959
AgeCategory35-39	0.4905	0.5169	0.9489	0.3427
AgeCategory40-44	0.3904	0.5115	0.7631	0.4455
AgeCategory45-49	0.9759	0.4707	2.0733	0.0382
AgeCategory50-54	1.1053	0.4601	2.4026	0.0163
AgeCategory55-59	1.6716	0.4390	3.8080	<0.001
AgeCategory60-64	1.7229	0.4355	3.9566	<0.001
AgeCategory65-69	1.9007	0.4325	4.3943	<0.001
AgeCategory70-74	2.2025	0.4315	5.1041	<0.001
AgeCategory75-79	2.3048	0.4358	5.2884	<0.001
AgeCategory80 or older	2.4112	0.4338	5.5579	<0.001
DiabeticNo, borderline diabetes	0.1036	0.2769	0.3742	0.7083
DiabeticYes	0.3857	0.1082	3.5637	<0.001
DiabeticYes (during pregnancy)	0.4411	0.5563	0.7929	0.4279
GenHealthFair	1.5950	0.1989	8.0201	<0.001
GenHealthGood	0.8674	0.1855	4.6754	<0.001
GenHealthPoor	1.6536	0.2374	6.9667	<0.001
GenHealthVery good	0.5264	0.1872	2.8116	<0.001
SleepTime	-1.1752	0.7954	-1.4775	0.1396
AsthmaYes	0.2588	0.1218	2.1248	0.0337
KidneyDiseaseYes	0.8061	0.1554	5.1855	<0.001

Discussion of Results

Full Model for Inference

We plan on adding the interpretation of the significant coefficients in our final project. As we have not finalized certain aspects of our model, such as whether or not we will utilize a larger sample of the data once we figure out runtime constraints, we have held off on interpreting our model output as the output and coefficients are subject to change.

Predictive Model

To observe our model's initial predictive performance, we performed k-fold cross validation. K-fold cross validation starts by splitting the dataset into k equally sized "folds". Then, for each unique group, 1 fold is held out as the test dataset whereas the other remaining folds combine to form the training dataset. We found that for values $1 < k < 21$, $k = 5$ (5-fold cross validation) produced the highest model accuracy, at 91.56%.

```
## Generalized Linear Model
##
## 10000 samples
##    11 predictor
##     2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 8000, 8001, 7999, 7999, 8001
## Resampling results:
##
##   Accuracy   Kappa
##   0.9127996  0.1339602
```

For further interpretation and analysis of our model, we fit a random forest. A random forest combines multiple decision trees (in this case, 20) in order to yield the most common prediction class for certain values of the predictor variables. The out-of-bag error from this model (the black line) is 0.1%, meaning we expect this model to classify patients incorrectly around 0.1% of the time. We can also see the false positive rate (green) and false negative rate (red) that comprise this out-of-bag error.

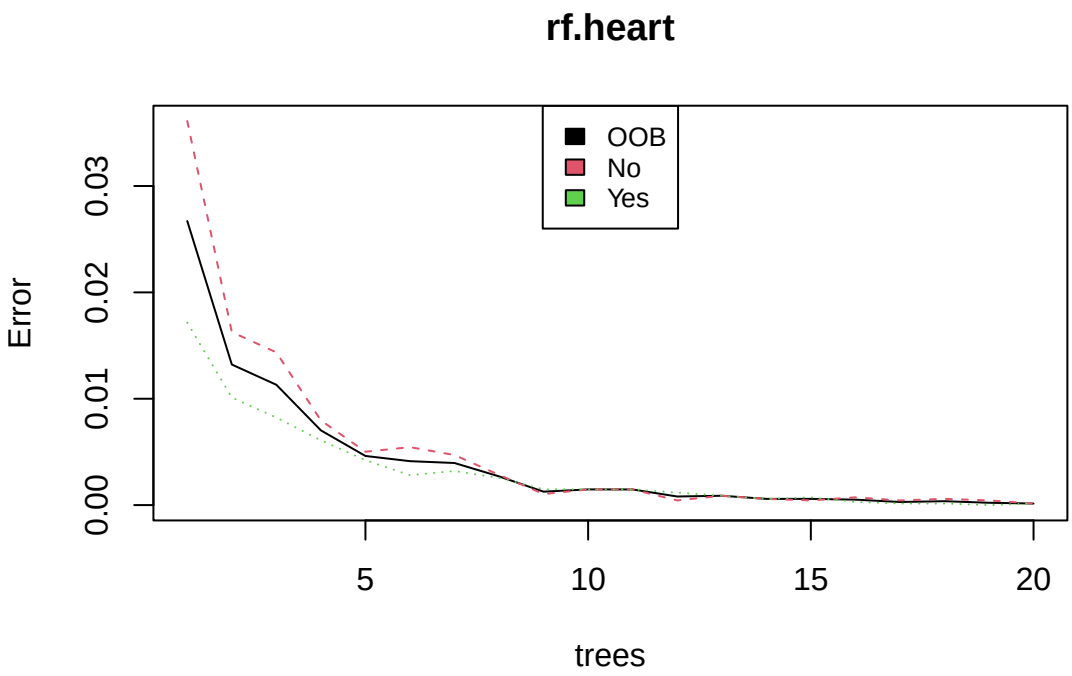

Figure 2: Error Lines for Random Forest

Table 1: Output of the optimal Random Forest model in the first MICE Chain

Out-of-bag Error	**0.1%**		
Confusion Matrix			
	Predicted as 0	Predicted as 1	Class Error
Actually 0	6848	1	1e-04
Actually 1	1	6848	1e-04

V. Reflection and Next Steps

Successes

Overall, we have made significant progress on the project. We believe that our introduction is essentially complete, as we have provided significant context as well as our research questions. Our data pre-processing is also essentially complete. We believe that our modelling is essentially complete, and our methodology for our models is good. Much of the technical lift has been finished in terms of the actual code. Furthermore, we have made substantial progress

Challenges

Overall, we still need to decide on what further visuals to use for the exploratory data analysis. For the purposes of the prototype, in the interest of report length, we only included a few variables to visually examine their relationships in the exploratory data analysis section. In the full report, we'll likely add more variables and utilize better visualizations. Furthermore, we'll likely dive deeper in our conclusion and further discuss our results in terms of our predictive model and our inference model. We'll add more diagnostics to examine model performance, as discussed in the Next Steps section. Furthermore, we are also interested in doing model assumption checks for the logistic regression model, but we were struggling with the code and decided to remove it for the time being from the prototype.

Another challenge is the runtime. We plan on trying to solve the long runtime with fitting the models in the future to be able to utilize a larger sample of data.

Collaboration Plan Reflection

The project has been going smoothly for all members and the collaboration plan has been effective in its approach. Despite our busy, conflicting schedules and time commitments, we have been able to meet on Zoom, in-person, and even in-class in order to discuss and work on our project. We have spent roughly 3-4 hours each per week on the project, contributing and communicating with each other effectively. During Zoom meetings, we are able to quickly chat about progress updates and work together to identify and solve problems. During in-person meetings, we are generally able to work more collaboratively on parts of the project that are a bit more tedious or intensive for one individual to complete. After each meeting, we agree on our next steps and split up the work so that the load is roughly even for each group member. We plan on continuing this collaboration plan for the remainder of the project with the only thing changing being a slight uptick in the amount of weekly hours we each expect to put in.

Next Steps

The primary goal of our next steps will be to focus on the conclusions and interpretations of our models. An ROC curve and measure of specificity sensitivity will be added to allow us to interpret our k-fold cross validation model and get a better understanding of our primary model's predictability. This will give us a better diagnostic and visual to assess model performance. With these ROC curves, we can then analyze the area under the curve in order determine concrete classification rates for our model. In addition, the random forest model and its accompanying confusion matrix will continue to be tidied up and there will be more substantial dialogue on the meaning of the output in the context of our data. We will also have a comprehensive results and conclusions section added in order to more formally answer our research questions and present the figures obtained by our models in a more interpretable manner. We'll also add more visuals for the exploratory data analysis section. Once we have finalized our sample size and thus our model results, we will also provide interpretations of the model coefficients. Finally, certain figures and tables will need additional tidying in order to make their output look more presentable for our final report.

Appendix

Full Description of Variables

`HeartDisease`: An indicator variable that equals 1 if respondents indicate they have had coronary heart disease (CHD) or myocardial infarction (MI).

`BMI`: Body Mass Index (BMI)

`Smoking`: Indicator variable that indicates if the respondent has smoked at least 100 cigarettes, equal to 5 packs, in their life

`AlcoholDrinking`: Indicator variable that indicates if the respondent identifies as a heavy drinker (defined as having more than 14 drinks per week for adult men and more than 7 drinks per week for adult women).

`Stroke`: Indicator variable that indicates whether or not the respondent has had a stroke.

`PhysicalHealth`: The number of days over the past 30 days the respondent has had physical illness or industry.

`MentalHealth`: The number of days over the past 30 days the respondent has had poor mental health.

`DiffWalking`: Indicator variable that indicates if the respondent has had serious difficulty walking or climbing stairs.

`Sex`: Indicator variable that indicates the sex of the respondent as male or female.

`AgeCategory`: The age of the respondent, split into 14 levels.

`Race`: The imputed race/ethnicity of the respondent

`Diabetic`: Whether or not the respondent has had diabetes.

`PhysicalActivity`: Indicator variable indicating whether or not the respondent has done physical activity or exercise during the past 30 days other than their regular job.

`GenHealth`: The respondent's self-identification of their general health, split into five different levels, from "poor" to "excellent".

`SleepTime`: The average amount of sleep the respondent gets in a 24-hour period.

`Asthma`: Indicator variable indicating whether or not the respondent has had asthma.

`KidneyDisease`: Indicator variable indicating whether or not the respondent has had kidney disease, not including bladder infection or kidney stones.

`SkinCancer`: Indicator variable indicating whether or not the respondent has had skin cancer.

Citations

Kaggle. (n.d.). Personal Key Indicators of Heart Disease. Kaggle. Retrieved October 15, 2022, from https://www.kaggle.com/datasets/kamilpytlak/personal-key-indicators-of-heart-disease