

DATA583 Final Project Report

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Introduction

Heart disease is a leading cause of death worldwide. Due to the potential for heart disease to cause negative effects, such as death, it may be important to investigate ways to prevent heart disease.

One way to prevent heart disease is to examine the risk factors for heart disease. Understanding risk factors may help prevent heart disease development because, for example, it may allow medical practitioners to identify individuals who are susceptible to developing heart disease. After identification, early preventative interventions could be applied to this high-risk group, reducing the likelihood of heart disease.

Research Questions and Hypotheses

Therefore, the aim of the current investigation is to investigate the factors that contribute to the development of heart disease. More specifically, we investigate the three following questions:

1. What lifestyle variables are related to the diagnosis of heart disease?
2. What variables are most important to the diagnosis of heart disease?
3. What groups of people are most likely to develop heart disease?

To investigate the first two questions, we will conduct logistic regression analysis. To investigate the third question, we will use decision trees.

We hypothesize that, based on previous research (Ryo, Cho & Kim, 2012), that a number of variables (e.g. body mass index, smoking habits) will be related to heart disease. Furthermore, we will investigate the questions of identifying importance of coefficients, and identification of high risk groups for heart disease in an exploratory manner.

Methods and Dataset

To investigate our research questions, we obtain a dataset on Kaggle about heart disease (Pytlak, 2022), a subset of data collected by the Center for Disease Control and Prevention (CDC) in 2022. The CDC conducted telephone interviews for 401,958 residents of the United States across all 50 states. Participants were interviewed about a number of (that is, 279) general lifestyle factors (e.g. smoking habits) and chronic health diseases.

The dataset on Kaggle (Pytlak, 2022) was filtered to contain only variables related to heart disease, resulting in 18 heart-disease related factors, and cleaned (e.g. missing values were removed), resulting in 319,795 responses with no missing values. Amongst the dataset of 319,795 responses

we obtained on Kaggle, 18,078 duplicate responses were found and removed, resulting in a final sample size of 301,717 observations.

Table 1 provides a full description of variables in the dataset, including the questionnaire presented to interviewees, response type, observed distribution. In total, the dataset contains 17 lifestyle predictor factors (3 numeric, 14 categorical) to investigate on self-reported heart disease. Prior to data analysis, a number of variables were recoded (race turned into a binary variable, age category reduced into a four-group ordinal categorical variable) due to feedback received during exploratory data analysis.

Table 1: Table 1: Variables in the Dataset

Variable Name	Questionnaire	Data Type	Observed distribution
HeartDisease	Have you ever had coronary heart disease or myocardial infection in your life?	Binary (yes, no)	Imbalanced binary (9% yes, 91% no)
BMI	What is your body mass index?	Continuous	Normal (mean = 28.3, variance = 40)
Smoking	Have you smoked at least 100 cigarettes in your entire life?	Binary (Yes, no)	Binary (59% no, 41% yes)
AlcoholDrinking	Do you drink heavily? (Men: more than 14 drinks a week, women: more than 7 drinks a week)	Binary (Yes, no)	Imbalanced binary (7% yes, 93% no)
Stroke	Have you ever had a stroke?	Binary (Yes, no)	Imbalanced binary (4% yes, 96% no)
PhysicalHealth	Thinking about your physical health, which includes physical illness and injury, for how many days during the past 30 days was your physical health not good?	Discrete (0-30 days)	Poisson (lambda = 3.3)
MentalHealth	Thinking about your mental health, for how many days during the past 30 days was your mental health not good?	Discrete (0-30 days)	Poisson (lambda = 3.9)
DiffWalking	Do you have serious difficulty walking or climbing stairs?	Binary (Yes, no)	Imbalanced binary (14% yes, 86% no)
Sex	Are you male or female?	Binary (Yes, no)	Binary (48% Male, 52% Female)

Variable Name	Questionnaire	Data Type	Observed distribution
AgeCategory	What is your age group?	Ordinal categorical (e.g. less than 40, 40-59, 60-79, greater than 80)	Normal
Race	What is your race? (recoded to binary variable)	Binary (White, non-white)	Imbalanced binary (77% white, 23% non-white)
Diabetic	Have you ever had diabetes?	Nominal categorical (No, borderline diabetes, yes, yes (during pregnancy))	Positive skew (86% no, 14% non-no)
PhysicalActivity	Have you had physical activity or exercise during the past 30 days other than their regular job	Binary (Yes, no)	Imbalanced binary (78% yes, 22% no)
GenHealth	Would you say your health in general is	Ordinal categorical (Poor, fair, good, very good)	Negative skew (poor 4%, fair 10%)
SleepTime	On average, how many hours of sleep do you get in a 24-hour period?	Continuous	Normal (mean = 7, variance = 2)
Asthma	Have you ever had asthma?	Binary (Yes, no)	Imbalanced binary (14% yes, 86% no)
KidneyDisease	Have you ever had kidney disease (not including kidney stones, bladder infections)?	Binary (Yes, no)	Imbalanced binary (4% yes, 96% no)
SkinCancer	Have you ever had skin cancer?	Binary (Yes, no)	Imbalanced binary (9% yes, 91% no)

Logistic Regression Analysis

Logistic regression is a statistical method used to analyze and model relationships between a binary dependent variable (i.e., one that takes on only two values, such as 0 or 1) and one or more independent variables (also known as predictors or explanatory variables). It is a type of regression analysis that is used to predict the probability of an event occurring based on the values of the independent variables.

Model Fitting

Interaction term shows that one's effect on response variable depends on the other, with only one of the variable might not have predictive power, but combine them together, we can predict. Based on our EDA, we add interaction terms of *AgeCategory* * *Sex* and *AgeCategory* * *Race* as our full model.

The formula of our logistic models are:

Model1: Without interaction terms

```
## HeartDisease ~ BMI + Smoking + AlcoholDrinking + Stroke + PhysicalHealth +  
##      MentalHealth + DiffWalking + Sex + AgeCategory + Race + Diabetic +  
##      PhysicalActivity + GenHealth + SleepTime + Asthma + KidneyDisease +  
##      SkinCancer
```

Model2: With the interaction terms

```
## HeartDisease ~ BMI + Smoking + AlcoholDrinking + Stroke + PhysicalHealth +  
##      MentalHealth + DiffWalking + Sex + AgeCategory + Race + Diabetic +  
##      PhysicalActivity + GenHealth + SleepTime + Asthma + KidneyDisease +  
##      SkinCancer + Race * AgeCategory + Sex * AgeCategory
```

Goodness of Fit Tests

In logistic regression, we can perform an overall goodness-of-fit test using the likelihood ratio test, which compares the full model to a reduced model without the predictors of interest. The test is based on the difference in deviances between the full model and the reduced model, and it follows a chi-squared distribution with degrees of freedom equal to the difference in the number of parameters between the two models.

The null hypothesis of the likelihood ratio test is that the reduced model fits the data as well as the full model. And the alternative hypothesis is that the full model fits the data significantly better than the reduced model.

According to the goodness of fit test, we choose the model with interaction term.

```
## Analysis of Deviance Table  
##  
## Model 1: HeartDisease ~ BMI + Smoking + AlcoholDrinking + Stroke + PhysicalHealth +  
##      MentalHealth + DiffWalking + Sex + AgeCategory + Race + Diabetic +  
##      PhysicalActivity + GenHealth + SleepTime + Asthma + KidneyDisease +  
##      SkinCancer  
## Model 2: HeartDisease ~ BMI + Smoking + AlcoholDrinking + Stroke + PhysicalHealth +  
##      MentalHealth + DiffWalking + Sex + AgeCategory + Race + Diabetic +  
##      PhysicalActivity + GenHealth + SleepTime + Asthma + KidneyDisease +  
##      SkinCancer + Race * AgeCategory + Sex * AgeCategory  
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)  
## 1      301692      144564  
## 2      301686      144371   6    192.64 < 2.2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Variable Selection

To get a simpler model, we decided to perform the backward elimination stepwise selection based on the AIC. Stepwise selection is a statistical method to identify the best subset of predictors in a regression model. Backward elimination will remove the predictor one by one based on their contribution.

The models before and after are listed below:

Model_full:

```
## HeartDisease ~ BMI + Smoking + AlcoholDrinking + Stroke + PhysicalHealth +
##      MentalHealth + DiffWalking + Sex + AgeCategory + Race + Diabetic +
##      PhysicalActivity + GenHealth + SleepTime + Asthma + KidneyDisease +
##      SkinCancer + Race * AgeCategory + Sex * AgeCategory
```

Model_select:

```
## HeartDisease ~ BMI + Smoking + AlcoholDrinking + Stroke + DiffWalking +
##      Sex + AgeCategory + Race + Diabetic + GenHealth + SleepTime +
##      Asthma + KidneyDisease + SkinCancer + AgeCategory:Race +
##      Sex:AgeCategory
```

PhysicalHealth, *MentalHealth*, and *PhysicalActivity* are removed from the process.

Model Diagnosis

Cook's distance is a measure of the influence of each observation on the fitted values of a regression model. A large Cook's distance indicates that the corresponding observation has a significant impact on the regression results. As shown by Figure 1, there were a large number of influential points during model fit. Digging into what observations are considered highly influential, we found that these observations generally have response values that are outliers compared to the mean (e.g. BMI values of 40, when BMI is a normally distributed variable with mean of 28 and standard deviation of 6).

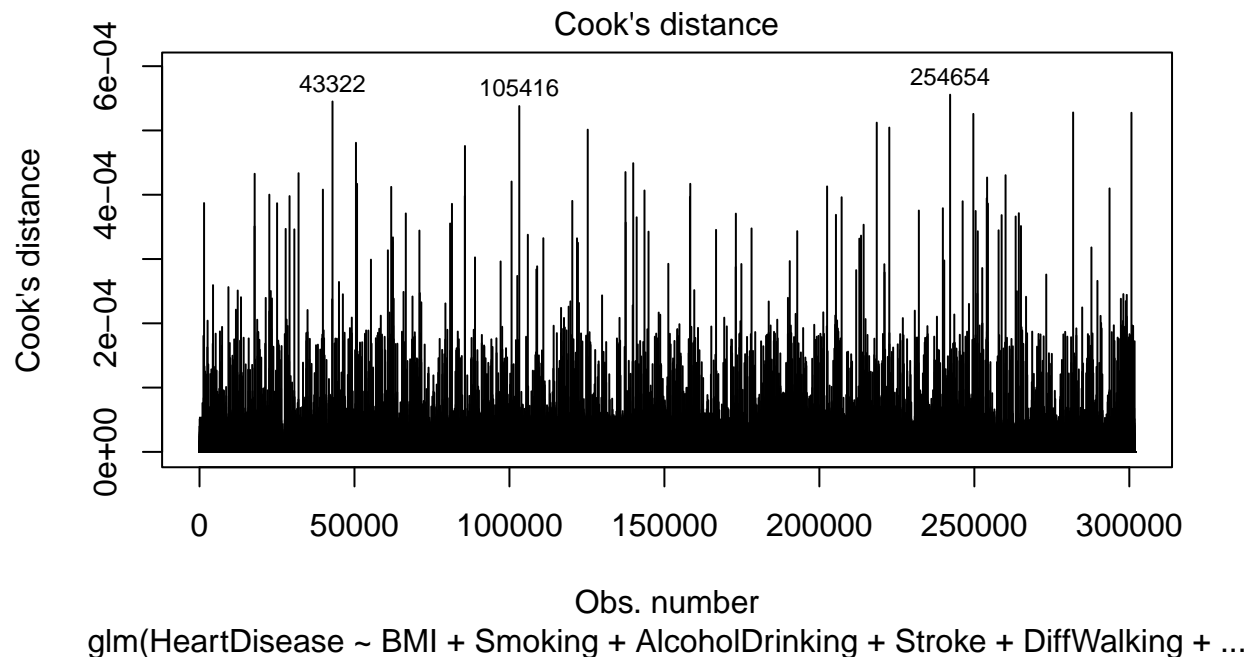


Figure 1: Figure 1: Cook's Distance

Research Questions 1

- Question 1: What lifestyle variables are related to heart disease?

According the final model we select in logistic regression analysis, except *PhysicalHealth*, *MentalHealth*, and *PhysicalActivity*, all the other variables are associated with heart disease.

```
##
## Call:
## glm(formula = HeartDisease ~ BMI + Smoking + AlcoholDrinking +
##      Stroke + DiffWalking + Sex + AgeCategory + Race + Diabetic +
##      GenHealth + SleepTime + Asthma + KidneyDisease + SkinCancer +
##      AgeCategory:Race + Sex:AgeCategory, family = "binomial",
##      data = heart_2020)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.2055  -0.4248  -0.2550  -0.1440   3.4318
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -5.497238    0.085564  -64.247  < 2e-16 ***
## BMI              0.004442    0.001122   3.958 7.57e-05 ***
## SmokingYes       0.355490    0.014350  24.773  < 2e-16 ***
## AlcoholDrinkingYes -0.301387    0.033386  -9.027  < 2e-16 ***
## StrokeYes        1.062048    0.022539  47.121  < 2e-16 ***
## DiffWalkingYes    0.258676    0.017407  14.860  < 2e-16 ***
## SexMale          0.168612    0.072421   2.328 0.019901 *
## AgeCategory40-59  0.955375    0.076802  12.439  < 2e-16 ***
## AgeCategory60-79  1.499783    0.073860  20.306  < 2e-16 ***
## AgeCategory80 or older 2.104839    0.088016  23.914  < 2e-16 ***
## RaceWhite        -0.109620    0.074063  -1.480 0.138848
## DiabeticNo, borderline diabetes 0.126777    0.041590   3.048 0.002302 **
## DiabeticYes       0.492763    0.016639  29.616  < 2e-16 ***
## DiabeticYes (during pregnancy) -0.002830    0.103909  -0.027 0.978275
## GenHealthFair     1.492174    0.031914  46.756  < 2e-16 ***
## GenHealthGood     1.001524    0.029545  33.898  < 2e-16 ***
## GenHealthPoor     1.924925    0.037098  51.888  < 2e-16 ***
## GenHealthVery good 0.470601    0.030477  15.441  < 2e-16 ***
## SleepTime        -0.016575    0.004278  -3.874 0.000107 ***
## AsthmaYes         0.240207    0.019076  12.592  < 2e-16 ***
## KidneyDiseaseYes  0.582908    0.024295  23.993  < 2e-16 ***
## SkinCancerYes     0.144511    0.019462   7.425 1.13e-13 ***
## AgeCategory40-59:RaceWhite 0.182002    0.081385   2.236 0.025331 *
## AgeCategory60-79:RaceWhite 0.449211    0.078116   5.751 8.89e-09 ***
## AgeCategory80 or older:RaceWhite 0.509895    0.092021   5.541 3.01e-08 ***
## SexMale:AgeCategory40-59 0.354893    0.078693   4.510 6.49e-06 ***
## SexMale:AgeCategory60-79 0.628598    0.074722   8.412  < 2e-16 ***
## SexMale:AgeCategory80 or older 0.443751    0.079873   5.556 2.77e-08 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 183054  on 301716  degrees of freedom
## Residual deviance: 144388  on 301689  degrees of freedom
## AIC: 144444
##
## Number of Fisher Scoring iterations: 7
```

Research Questions 2

- Question 2: What variables are most important to the development of heart disease?

In the logistic regression model, the estimated coefficients represent the change in the log-odds of the outcome associated with a one-unit increase in the predictor variable, holding other variables constant. Variables with larger coefficients (absolute value) are generally considered more important. But we should combine the p-value of them to see if the association is real or by chance (big p-value).

According to the summary of the stepwise model, *AgeCategory80 or older*, *GenHealthPoor*, *AgeCategory60-79*, and *GenHealthFair* are the most important variables indicators for heart disease (please refer to the coefficients and p-values in the following Table 2.)

Table 2: Table 2: Important Variables in the Logistic Regression Model

Variable	Coefficient	p-value
AgeCategory 80 or older	2.104838900	< 2e-16
GenHealth Poor	1.924924675	< 2e-16
AgeCategory 60-79	1.499782865	< 2e-16
GenHealth Fair	1.499782865	< 2e-16

Decision Tree Analysis

To examine what groups of people are most likely to develop heart disease, we ran a decision tree classifier model. We chose to run this model because decision trees provide easy and practical boundaries, allowing us to identify groups of patients that are most likely to develop heart disease.

Model Fitting

To examine high risk groups using decision trees, we followed these broad steps. First, we found the optimal decision tree for the dataset using 10-fold cross validation (cutting the tree at the optimal node size resulting from this process). Second, based off this tree, we distinguish between groups that have high risk of heart disease, and we filter the dataset to specifically examine group features that are at risk of developing heart disease. We repeat steps 1 and 2 until we find that the probability of a group having heart disease is above 50%. In total, the decision tree analysis process was repeated two times, described below.

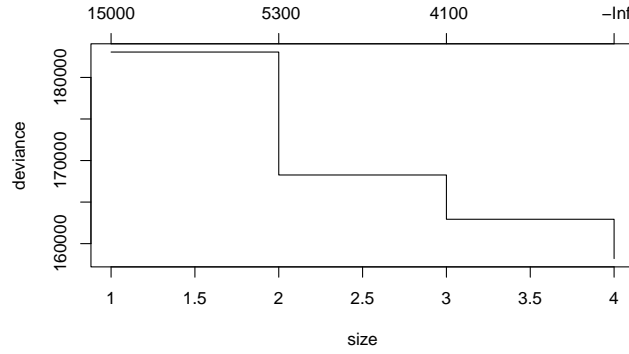


Figure 2: Figure 2.1: Cross Validated Mean Square Error versus Tree Size

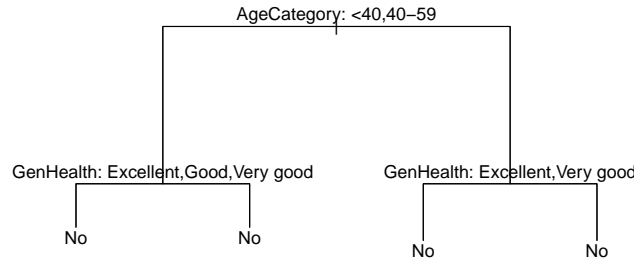


Figure 3: Figure 2.2: Decision Tree for Heart Disease on the Whole Dataset

In the first step of the process, 10 fold cross validation revealed that the optimal tree size was with 5 nodes (Figure 2.1) for the entire dataset. Plotting this tree (Figure 2.2), we can see from the results of the decision tree that if you are under 59 years of age and in good overall health, then the decision tree predicts the absence of heart disease (that is, you are in a low risk group). Furthermore, according to Figure 2.2, other factors such as mental health, race, physical activity, have little impact on the development of heart disease

In contrast, those who are older than 59 and report having health that is worse than good are at a higher risk of developing heart disease. If we examine this subset specifically, we select a total sample of 26,945 (8.93% of the total sample). These people are at a higher risk of getting heart disease, where the probability of having heart disease increases from 9.03% (whole dataset) to 31.30% (high risk group).

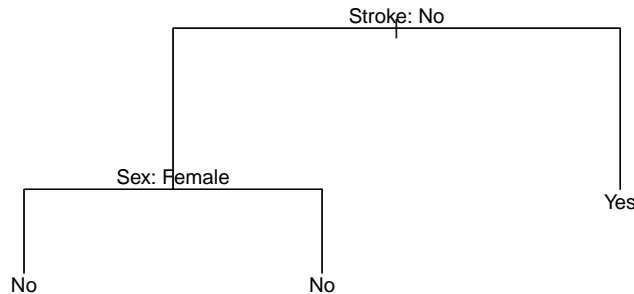


Figure 4: Figure 2.3: Decision Tree on Heart Disease for at risk Groups

In the second step of the process, we repeat fitting of the decision tree model to the high risk group. Plotting the optimal tree (Figure 2.3; node size determined by cross validation), we identify another

important feature of stroke history. In the high risk group, if there was no prior history of stroke, the decision tree predicts that the absence of a heart attack. In contrast, in the high risk group, if there was prior history of stroke, the risk of having heart disease increases from 31.10% to 50.67%.

Research Question 3

- Question 3 What groups of people are most likely to develop heart disease?

Based on the result of the decision tree analysis, Table 3 shows how our observations are categorized into different risk groups. People who are over the age of 60, have poor or fair health, and have past history of stroke were most likely to develop heart disease (50.67% of being diagnosed with heart disease).

Table 3: Table 3: Identifying High Risk Groups for Development of Heart Disease

Group	Condition	Probability of Having Heart Disease
Whole population benchmark	None	9.03%
Low risk group	Age below 59 or having health condition above good	6.85%
High risk group	Age above 60 or having health condition below good	31.10%
Extremely risk group	In high risk group and had stroke history	50.67%

Conclusion

```
##
## Call:
## glm(formula = HeartDisease ~ BMI + Smoking + AlcoholDrinking +
##      Stroke + DiffWalking + Sex + AgeCategory + Race + Diabetic +
##      GenHealth + SleepTime + Asthma + KidneyDisease + SkinCancer +
##      AgeCategory:Race + Sex:AgeCategory, family = "binomial",
##      data = heart_2020)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.2055  -0.4248  -0.2550  -0.1440   3.4318
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## Coefficients:
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## (Intercept)  -5.497238   0.085564 -64.247  < 2e-16 ***
## BMI           0.004442   0.001122   3.958 7.57e-05 ***
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## AlcoholDrinkingYes -0.301387   0.033386  -9.027  < 2e-16 ***
```

```

## StrokeYes          1.062048    0.022539   47.121 < 2e-16 ***
## DiffWalkingYes     0.258676    0.017407   14.860 < 2e-16 ***
## SexMale            0.168612    0.072421    2.328 0.019901 *
## AgeCategory40-59    0.955375    0.076802   12.439 < 2e-16 ***
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## RaceWhite          -0.109620    0.074063   -1.480 0.138848
## DiabeticNo, borderline diabetes 0.126777    0.041590    3.048 0.002302 **
## DiabeticYes         0.492763    0.016639   29.616 < 2e-16 ***
## DiabeticYes (during pregnancy) -0.002830    0.103909   -0.027 0.978275
## GenHealthFair       1.492174    0.031914   46.756 < 2e-16 ***
## GenHealthGood       1.001524    0.029545   33.898 < 2e-16 ***
## GenHealthPoor       1.924925    0.037098   51.888 < 2e-16 ***
## GenHealthVery good  0.470601    0.030477   15.441 < 2e-16 ***
## SleepTime          -0.016575    0.004278   -3.874 0.000107 ***
## AsthmaYes           0.240207    0.019076   12.592 < 2e-16 ***
## KidneyDiseaseYes    0.582908    0.024295   23.993 < 2e-16 ***
## SkinCancerYes       0.144511    0.019462    7.425 1.13e-13 ***
## AgeCategory40-59:RaceWhite 0.182002    0.081385    2.236 0.025331 *
## AgeCategory60-79:RaceWhite 0.449211    0.078116    5.751 8.89e-09 ***
## AgeCategory80 or older:RaceWhite 0.509895    0.092021    5.541 3.01e-08 ***
## SexMale:AgeCategory40-59 0.354893    0.078693    4.510 6.49e-06 ***
## SexMale:AgeCategory60-79 0.628598    0.074722    8.412 < 2e-16 ***
## SexMale:AgeCategory80 or older 0.443751    0.079873    5.556 2.77e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 183054 on 301716 degrees of freedom
## Residual deviance: 144388 on 301689 degrees of freedom
## AIC: 144444
##
## Number of Fisher Scoring iterations: 7

```

The present investigation aimed to develop a better understanding of risk factors that contribute to heart disease by asking three broad questions. First, we investigated what variables are related to the development of heart disease. Our final logistic regression model found the 15 variables of *BMI*, *Smoking*, *AlcoholDrinking*, *Stroke*, *DiffWalking*, *Sex*, *AgeCategory*, *Race*, *Diabetic*, *GenHealth*, *SleepTime*, *Asthma*, *KidneyDisease*, *SkinCancer* to be associated with the development of heart disease.

Second, we investigated what variables are most important to the development of heart disease. According to the rank of our final logistic regression model, *AgeCategory80 or older*, *GenHealthPoor*, *AgeCategory60-79*, and *GenHealthFair*, were the most important predictors of heart disease, with coefficients of above 1.5 (controlling for other variables).

Third, we investigated what groups were most at risk of developing heart disease. Our final decision tree model distinguished between different groups at risk for heart disease, from low risk groups

(e.g. 6.85% of heart disease) to high risk groups (e.g. 50.67% of heart disease), and identified the high risk group as people over the age of 45, in poor or fair general health, with past history of stroke.

Taken together, the findings from the current investigation identified, in a large-scale and representative sample of residents in the United States, risk factors that may contribute to the development of heart disease, findings of which may have implications for the real world, such as informing medical practitioners.

Limitations and Future Directions

While the present investigation yielded several insights into the risk factors related to heart disease, it should be noted that there were also a number of limitations.

One limitation is that, although our investigation yielded a large number of significant risk factors linked to heart disease, the factors within this investigation is only able to explain a weak proportion of the variation in heart disease, with an adjusted R-squared of **0.2** (though see Ryo et al., 2012 for similar R-squared values). In other words, though risk factors were identified, these risk factors may be less relevant because they may not be the main driving factors behind heart disease onset.

Why may there be a low R-squared value? There may be a variety of reasons. For one, it is possible that the methods of the current investigation may contribute to a low R-squared value. For example, it is possible that the current investigation fails to capture important predictor variables (e.g. biological or genetic markers) that are relevant to heart disease onset, to explain for the low variation explained in heart disease. Furthermore, it is also possible that the subjective nature of the methodology (e.g. telephone survey, self-reported heart disease, retrospective self-reports of exercise history) may hinder the extent to which explanatory variables can be related to response variables, compared to more objective measures of heart disease (e.g. biological measurements of heart disease). Future work could improve upon methodology (e.g., obtaining objective measurements of heart disease) when investigating risk factors for heart disease.

Second, it is also possible that the current modelling techniques may be the result of low R-squared values. For example, diagnostic plots during the fitting of logistic regression models showed that there were a high number of influential points (e.g. potentially due to a large number of imbalanced binary predictors), of which violates one of the assumptions of logistic regression models (that is, lack of influential points) and contributing to poor fit. Furthermore, another factor that may account for poor model fit of logistic regression models is imbalanced response variables. In the future, alternative modelling techniques should be considered, such as using models (e.g. generalized additive models) and methods (e.g. oversampling; Ustyannie & Suprpto, 2020) that are less susceptible to imbalanced predictors and response variables.

References

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