Unveiling Heart Attack Risk:

A Comprehensive Analysis of BMI and its Implications

STAT 344

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Introduction

Myocardial infarctions, more commonly known as heart attacks, continue to pose a significant global health challenge. Recent research has highlighted the role of higher Body Mass Index (BMI) values as a robust predictor of heart attack risk, contributing to the multifaceted challenge of cardiovascular disease (Adams, 2020). These events, not only a leading cause of mortality but also a substantial contributor to the global burden of disease, underscore the need for a comprehensive understanding of factors contributing to heart attack risk, with specific attention to BMI.

The Heart Attack Risk Prediction Dataset is a valuable repository, housing a wealth of patient-specific data that spans demographic information, lifestyle choices, medical history, and socio-economic factors. It represents the culmination of extensive efforts to unravel the intricate dynamics of heart health, with a primary focus on the factors influencing it, most notably BMI. The dataset holds immense potential to transform heart disease prevention and management, placing a pronounced emphasis on the significance of BMI in predicting heart attacks.

Cardiovascular diseases, particularly heart attacks, are often preventable through lifestyle adjustments and early interventions (Renninger, M., 2018). Through a meticulous analysis of the dataset, with a specific focus on BMI values, we aim to take a substantial step toward practical strategies for heart disease prevention. The primary aim of this research project is to harness the Heart Attack Risk Prediction Dataset, constructing a robust predictive model that accurately assesses an individual's heart attack risk based on the diverse attributes within the dataset. This model places a strong emphasis on BMI values as a key predictor of heart attack risk, enabling the timely identification of individuals at higher risk, particularly those with elevated BMI values, and facilitating proactive interventions and preventive measures. Addressing heart attack risk, specifically focusing on BMI management, is crucial for enhancing public health and reducing escalating healthcare costs. Furthermore, the identification of heart attack risk factors, particularly higher BMI values, empowers individuals to make informed lifestyle choices and seek medical assistance when necessary. Thus, this research project has the potential to promote preventive healthcare globally, with a pronounced emphasis on BMI-related interventions. The analysis of this dataset, with a specific focus on BMI, fosters collaboration between the fields of medicine, data science, and public health. This project aims to generate actionable recommendations and strategies for individuals and healthcare providers to mitigate heart attack risk, with a strong emphasis on addressing higher BMI as a significant predictor of heart attacks.

Method

We used the Heart Attack Risk Prediction dataset from the internet. To answer the question of how BMI values are affected by the risk of having a heart attack, the population of our interest is the people at risk of heart attack. The parameter of interest is BMI values. To better answer our question, we treated our targeted population as either a continuous or binary population. For the continuous population, we were interested in estimating the mean BMI values from our population, patients who are at risk of having a heart attack. For the binary population, we set a threshold of BMI > 30 kg/m^2 to split our population into whether patients had a high BMI value or not since studies have reported that individuals who have a BMI value greater than 30 kg/m^2 are considered obese. Carbone et al. (2019) found that obesity and being overweight are major risk factors for developing heart diseases and conditions, such as heart attacks.

Further, two different sampling methods, Simple Random Sampling (SRS) and Stratification Sampling were selected for comparison and form the basis of our research. For SRS, we found the recommended sample size by assuming the worst-case proportion equals 0.5. With a 95% confidence interval and the Finite Population Correction (FPC) ignored, since we assume the population total is large enough to ignore FPC, we found the recommended sample size to be 385 [1]. However, since we know the population total, considering FPC will yield a more accurate result than without it. Hence, we needed a sample size of 343 [2] with FPC, given a 95% confidence interval. Further, CLT is assumed to construct the confidence interval for the binary population, we must check the conditions $np \geq 10$ and $n(1-p) \geq 10$ be satisfied with our recommended sample size and worst-case proportion. Since we found that both conditions are met, we can apply CLT in our calculations. For stratification sampling, it is critical to determine the stratified variables because different stratified variables give us different estimations and different standard errors. For an accurate estimate of the mean BMI value, its standard error should be small. Since each stratum is formed based on differences between the individuals' shared characteristics, we found that sex, diet, obesity, and whether the patient has diabetes or has a family history of heart-related problems are shared attributes within our population. To compare the five study designs, we computed the within-strata variances for each of our stratified variables and found that stratifying by sex resulted in the lowest variance, 39.09994 [3]. Since the stratification study design performs best when the within-strata variance is the smallest, hence the between-strata variance is the largest, we decided to stratify by sex. By optimal allocation, the resulting sample sizes chosen for the two strata, male and female, are 235 and 108 [4], respectively.

Result and Data Analysis

For the continuous population, with a sample size of 343 using SRS, we estimated the mean BMI value to be 29.09 kg/m^2 [5] with a standard error of 0.324 [7], where its respective 95% confidence interval was (28.46, 29.73) [9]. Hence, we can conclude from the result of the SRS method that we are 95% confident that the true mean BMI of people at risk of heart attack is between 28.46 kg/m^2 and 29.73 kg/m^2. On the other hand, with a sample size of 235 for the stratum male and 108 for the stratum female using stratified sampling, we estimated the mean BMI value for each stratum and then took the sum of their weighted BMI means. We found the stratified estimator for means to be 29.14 kg/m^2 [6] with a standard error of 0.31 [8], where its respective 95% confidence interval was (28.52, 29.75) [9]. Thus, we can conclude from the result of the stratified sampling method that we are 95% confident that the true mean BMI of people at risk of heart attack is between 28.52 kg/m^2 and 29.75 kg/m^2. It is known that a BMI value of 25 kg/m^2 is considered overweight (Body Mass Index (BMI) Calculator, n.d.). As both the 95% confidence interval using SRS and stratification sampling methods capture BMI values greater than 25 kg/m^2, this suggests that our population of interest, patients at risk of heart attack, are identified as being overweight.

For the binary population, with a sample size of 343 using SRS, we estimated the proportion of patients with high BMI (BMI greater than 30 kg/m^2) to be 0.458 [10] with a standard error of 0.027 [11]. Following a 95% confidence interval of this estimator, we computed (0.405, 0.510) [12]. Therefore, we are 95% confident that the true proportion of patients with high BMI (BMI values greater than 30 kg/m^2) is between 0.405 and 0.510. Conversely, with a sample size of 235 for the stratum male and 108 for the stratum female using stratified sampling, we calculated the sum of the weighted stratified proportions of patients with high BMI, given by the overall stratified proportion estimate of 0.457 [13], with a standard error of 0.025 [8]. Thus, its 95% confidence interval yielded the interval (0.407, 0.506) [12]. So, we can say that we are 95% confident that the true proportion of patients with high BMI (BMI values greater than 30 kg/m^2) is between 0.407 and 0.506. Since both the 95% confidence interval of the SRS and Stratification sampling methods cover 0.5, we cannot conclude that less than half the population who are at risk of heart attacks have high BMI.

The stratified sampling method may provide more coverage of our population, being more easily administered and less costly than SRS. Such an idea aligns with our findings as we computed a lower standard error of our stratification estimates than the SRS estimates for both our continuous and binary population, implying higher accuracy and efficiency of our estimates.

Final Conclusion and Discussion

In conclusion, our investigation utilized Simple Random Sampling (SRS) and Stratified Sampling to assess parameters of the population at risk of heart attacks, focusing specifically on Body Mass Index (BMI) and the proportion of individuals with elevated BMI. The comparative analysis of sampling methods revealed that Stratified Sampling exhibited superior performance, as evidenced by lower standard errors and increased accuracy in both continuous and binary population estimations. This emphasizes the effectiveness of gender-based stratification in enhancing result reliability. The confidence intervals for mean BMI generated by both sampling methods encompassed values exceeding 25 kg/m^2, indicative of elevated BMI, while simultaneously refuting the proposition that less than half the population is at risk of heart attacks due to high BMI.

Despite the insightful contributions of our study, several limitations merit consideration. Foremost among these is the reliance on a dataset not procured by our research team, raising concerns regarding data quality, accuracy, and potential biases inherent in the original data source. Moreover, our study failed to account for other factors that may influence BMI and heart attack risk like high blood pressure, physical inactivity, and smoking history of patients, necessitating future research endeavours to incorporate a more comprehensive set of variables. and heart attack risk, necessitating future research endeavours to incorporate a more comprehensive set of variables. The use of an AI-generated dataset introduces uncertainties in real-world applicability. Additionally, the absence of a reference from a prior study to inform our determination of an appropriate sample size poses implications for the precision of our continuous estimates.

In terms of generalizability, our findings are restricted by the specific nature of our dataset and the characteristics of the population under study. Consequently, we assert that our dataset and results are not entirely applicable for extrapolation to broader or dissimilar populations. While our research methodology endeavours to bolster the robustness of our conclusions, caution is warranted when extending the implications of our findings. Our results find optimal relevance within populations sharing characteristics akin to those in our study. To enhance the broader applicability of our conclusions, future research initiatives should scrutinize a more expansive array of features and execute validation studies across diverse datasets. In summary, our study aspires to strike a judicious balance between methodological rigour and pragmatic constraints, with findings most aptly suited for populations resembling the group under investigation. Consequently, caution is advised, particularly when applying our conclusions to a markedly distinct population.

Appendix

Calculating worst case variance sample size and determining whether CLT applicable for our binary population

Find recommended sample size for this study

```r
# calculate min sample size needed
pop_size <- nrow(heartattack) # 3139

# using 95% CI, find n for worst case scenario: p = 0.5
MOE <- 0.05
z <- 1.96
p_guess <- 0.5

# if N is large enough to ignore FPC
n_0 = ceiling( (z^2*(0.5)*(0.5)) / (MOE^2)) # 385
# since we know N = 3139, using FPC
n = ceiling( n_0 / (1 + (n_0/pop_size)) ) # 343

# to use CLT for our binary population, must check 1. np >= 10 and n(1-p) >= 10
(n*p_guess >= 10) & (n*(1-p_guess) >= 10)
```

```
## [1] TRUE
```

Calculating weighted sample size for Sex stratums and overall stratified variance

```r
#Calculate within variance of each sex: Male, Female
variance_within_strata <- aggregate(BMI ~ Sex, heartattack, var)
colnames(variance_within_strata) <- c("Sex","Within Variance Sex")
print(variance_within_strata)
```

Method 1: stratify by sex

```
##      Sex Within Variance Sex
## 1 Female            38.33507
## 2   Male            40.77213
```

```r
#Get stratum sizes
male_stratum_size <- nrow(heartattack[heartattack$Sex == "Male",])
female_stratum_size <- nrow(heartattack[heartattack$Sex == "Female",])


#Sample size n_h proportional to N_h*S_pw^2/sqrt(cost)
#Ignore costs

#total is used to normalize N_h*S_pw^2/sqrt(cost) to equal 1
total <- sum(male_stratum_size*variance_within_strata$`Within Variance Sex`[1],
            female_stratum_size*variance_within_strata$`Within Variance Sex`[2])
```

```r
male_size_proportion <-
  male_stratum_size*variance_within_strata$`Within Variance Sex`[1]/total

female_size_proportion <-
  female_stratum_size*variance_within_strata$`Within Variance Sex`[2]/total

#total sample size * strata proportion = strata sample size
male_sample_size <- round(male_size_proportion*n)
female_sample_size <- round(female_size_proportion*n)

#Overall stratified variance
var.strata <- c(variance_within_strata$`Within Variance Sex`[1],
                variance_within_strata$`Within Variance Sex`[2])
wt.strata <- c(male_size_proportion, female_size_proportion)

overall.sex.var <- sum(wt.strata*var.strata)
data.frame(`Overall Sex Variation` = c(overall.sex.var))
```

```
##   Overall.Sex.Variation
## 1              39.09994
```

Overall Variance results from stratifying using different variables calculated using a similar method from above

```
##   Overall Sex Var. Overall Diet Var. Overall Diabetes Var. Overall History Var.
## 1         39.09994          40.07295              39.65881              39.7444
##   Overall Obesity Var.
## 1             40.06844
```

Sample Selection using SRS and stratified sampling by Sex stratums

Selecting Samples through SRS and Stratification by sex

```
# set seed
set.seed(2)

# take SRS of n = 343
SRS.index <- sample.int(pop_size, n, replace=F)
SRS_sample <- heartattack[SRS.index, ]
head(SRS_sample)
```

```
##         Sex Diabetes Family.History Obesity      Diet      BMI
## 2772   Male        1              0       1   Healthy 29.65312
## 2043 Female        1              0       1   Average 36.52504
## 7828   Male        0              0       0 Unhealthy 21.60942
## 1224   Male        1              1       0   Healthy 22.68139
## 1152 Female        1              1       1   Healthy 24.21819
## 831    Male        1              0       1 Unhealthy 26.88142
```

```
#Stratify male and female stratums to take samples from
male_stratum <- heartattack[heartattack$Sex == "Male",]
female_stratum <- heartattack[heartattack$Sex == "Female",]

#Take Stratified samples of males (n = 708) and females (n = 324)
stratified_male.index <- sample.int(male_stratum_size, male_sample_size, replace = F)
male_sample <- male_stratum[stratified_male.index,]
head(male_sample)
```

```
##       Sex Diabetes Family.History Obesity      Diet      BMI
## 2621 Male        1              1       0 Unhealthy 36.16253
## 1338 Male        1              1       1   Average 21.84712
## 3776 Male        1              1       0 Unhealthy 28.15095
## 6685 Male        1              0       1   Average 37.04400
## 4694 Male        0              1       1 Unhealthy 36.39712
## 3791 Male        0              0       0   Healthy 39.47205
```

```
stratified_female.index <- sample.int(female_stratum_size, female_sample_size, replace = F)
female_sample <- female_stratum[stratified_female.index,]
head(female_sample)
```

```
##         Sex Diabetes Family.History Obesity      Diet      BMI
## 462  Female        1              1       0   Healthy 36.98066
## 3659 Female        1              1       1 Unhealthy 25.21583
## 3933 Female        1              0       0 Unhealthy 23.69793
## 2407 Female        1              1       0   Average 24.88832
## 316  Female        1              0       0   Healthy 22.86218
## 3004 Female        1              0       1   Healthy 21.31734
```

Calculations for mean BMI estimation for SRS and stratified samples

Continuous Population

```r
#Calculate mean BMI from SRS

SRS_BMI_mean <- mean(SRS_sample$BMI)

#Calculate mean BMI from male sample and female sample

male_BMI_mean <- mean(male_sample$BMI)
female_BMI_mean <- mean(female_sample$BMI)
#Calculate stratified estimator for BMI mean (sum of weighted BMI means)

strata_estimator_BMI_mean <- (male_stratum_size/pop_size)*male_BMI_mean +
                                 (female_stratum_size/pop_size)*female_BMI_mean


data.frame(`Sampling Method` = c("SRS","Stratified Estimate"),
           `BMI Mean` = c(SRS_BMI_mean,strata_estimator_BMI_mean))
```

Estimate Mean

```
##       Sampling.Method BMI.Mean
## 1                 SRS 29.09488
## 2 Stratified Estimate 29.13750
```

Calculations for SE of mean BMI for SRS and stratified samples

```r
#Calculate SE for SRS and Stratified

#SRS SE calculation
SRS_variance <- sum((SRS_sample$BMI - SRS_BMI_mean)^2)/(n-1)
SRS_FPC <- (1- n/pop_size)
SRS_SE <- sqrt(SRS_FPC * SRS_variance/n)

#Stratified SE calculation

#First calculate male and female strata variances
#and the strata FPC and proportions relative to population size squared
male_strata_variance <- sum((male_sample$BMI - male_BMI_mean)^2)/(male_sample_size-1)
male_strata_FPC <- (1 - male_sample_size/male_stratum_size)
male_proportion_squared <- (male_stratum_size/pop_size)^2

female_strata_variance <-
  sum((female_sample$BMI - female_BMI_mean)^2)/(female_sample_size-1)
female_strata_FPC <- (1 - female_sample_size/female_stratum_size)
female_proportion_squared <- (female_stratum_size/pop_size)^2

# SE = sqrt(sum ((N_h/N)^2 * Strata_H_FPC * Strata Variance / strata sample size))
stratified_SE <- sqrt(
  (male_proportion_squared*male_strata_FPC*male_strata_variance/male_sample_size)+
(female_proportion_squared*female_strata_FPC*female_strata_variance/female_sample_size))

data.frame(`Sampling Method` = c("SRS","Stratification"),
           `Continuous SE` = c(SRS_SE,stratified_SE))
```

Calculate Standard Error

```
##   Sampling.Method Continuous.SE
## 1             SRS     0.3240470
## 2  Stratification     0.3136828
```

Calculations for 95% confidence interval for BMI mean of SRS and stratified samples

```r
# Construct 95% CI for mean BMI for SRS
SRS_cont_moe <- 1.96*SRS_SE
SRS_cont_ci <- c(SRS_BMI_mean - SRS_cont_moe,
                 SRS_BMI_mean + SRS_cont_moe)


# Construct 95% CI for mean BMI for Stratified
stratified_cont_moe <- 1.96*stratified_SE
stratified_cont_ci <- c(strata_estimator_BMI_mean - stratified_cont_moe,
                        strata_estimator_BMI_mean + stratified_cont_moe)

data.frame(`Sampling Method` = c("SRS","Stratification"),
           `CI Lower Bound` = c(SRS_cont_ci[1], stratified_cont_ci[1]),
           `CI Upper Bound` = c(SRS_cont_ci[2], stratified_cont_ci[2]))
```

Construct 95% Confidence Interval

```
##   Sampling.Method CI.Lower.Bound CI.Upper.Bound
## 1             SRS       28.45975       29.73001
## 2  Stratification       28.52268       29.75232
```

Calculations for estimated proportion of BMI > 30 kg/m^2 for SRS and stratified samples

Binary Population

```r
#We use the previous samples

#SRS
#Find number of observations where BMI > 30 from SRS sample
num_obs_BMI_over_30 <- nrow(SRS_sample[SRS_sample$BMI > 30,])

#Find estimated proportion of BMI over 30 by dividing observed BMI > 30 by sample size
SRS_proportion_obs_BMI_over_30 <- num_obs_BMI_over_30/n

#STRATIFIED
#male estimated proportion of BMI over 30
male_num_obs_BMI_over_30 <- nrow(male_sample[male_sample$BMI > 30,])
male_proportion_BMI_over_30 <- male_num_obs_BMI_over_30/male_sample_size

#female estimated proportion of BMI over 30
female_num_obs_BMI_over_30 <- nrow(female_sample[female_sample$BMI > 30,])
female_proportion_BMI_over_30 <- female_num_obs_BMI_over_30/female_sample_size

#Sum weighted stratified proportions to get overall stratified proportion estimate
stratified_overall_proportion <-
  (male_stratum_size/pop_size)*male_proportion_BMI_over_30 +
  (female_stratum_size/pop_size)*female_proportion_BMI_over_30

data.frame(`Sampling Method` = c("SRS","Stratification"),
           `Proportion of BMI Greater Than 30 Estimate` =
             c(SRS_proportion_obs_BMI_over_30,stratified_overall_proportion))
```

Estimate Proportion

```
##   Sampling.Method Proportion.of.BMI.Greater.Than.30.Estimate
## 1             SRS                                  0.4577259
## 2  Stratification                                  0.4566627
```

Calculations for SE of proportion of BMI > 30 kg/m^2 for SRS and stratified samples

```r
#SRS

#variance = sqrt[p(1-p)/n]
SRS_proportion_SE <-
  sqrt(SRS_proportion_obs_BMI_over_30*(1-SRS_proportion_obs_BMI_over_30)/n)


# square root(sum(StratumProportion^2 * stratumFPC * variance/stratum_sample_size))

#Male proportions Variance
male_proportion_BMI_over_30_variance <-
  male_proportion_BMI_over_30 * (1 - male_proportion_BMI_over_30)
#Female proportions Variance
```

```r
female_proportion_BMI_over_30_variance <-
  female_proportion_BMI_over_30 * (1 - female_proportion_BMI_over_30)

#   FPC used is same as the one used from calculated continuous SE:
#   male_strata_FPC, female_strata_FPC

#   Male and Female stratum proportions squared
#   is same as one used to calculate continuous SE:
#   male_proportion_squared, female_proportion_squared

stratified_proportion_SE <-
  sqrt( (male_proportion_squared * male_strata_FPC *
  male_proportion_BMI_over_30_variance/male_sample_size) +

  (female_proportion_squared * female_strata_FPC *
  female_proportion_BMI_over_30_variance/female_sample_size) )

data.frame(`Sampling Method` = c("SRS","Stratification"),
           `Proportion of BMI greater than 30 SE` =
             c(SRS_proportion_SE,stratified_proportion_SE))
```

Calculate Standard Error

```
##   Sampling.Method Proportion.of.BMI.greater.than.30.SE
## 1             SRS                           0.02690080
## 2  Stratification                           0.02533275
```

Calculations for constructing 95% confidence interval for estimated proportions of SRS and stratified samples

```r
# Construct 95% CI for proportion of observations with BMI > 30 for SRS
SRS_binary_moe <- 1.96*SRS_proportion_SE
SRS_binary_ci <- c(SRS_proportion_obs_BMI_over_30 - SRS_binary_moe,
                   SRS_proportion_obs_BMI_over_30 + SRS_binary_moe)


# Construct 95% CI for proportion of observations with BMI > 30 for Stratified
stratified_binary_moe <- 1.96*stratified_proportion_SE
stratified_binary_ci <- c(stratified_overall_proportion - stratified_binary_moe,
                          stratified_overall_proportion + stratified_binary_moe)

data.frame(`Sampling Method` = c("SRS","Stratification"),
           `CI Lower Bound` = c(SRS_binary_ci[1], stratified_binary_ci[1]),
           `CI Upper Bound` = c(SRS_binary_ci[2], stratified_binary_ci[2]))
```

Construct 95% confidence interval

```
##   Sampling.Method CI.Lower.Bound CI.Upper.Bound
## 1             SRS      0.4050004      0.5104515
## 2  Stratification      0.4070105      0.5063149
```

Formulas

$$\frac{z^2 p_{guess}(1-p_{guess})}{\delta^2} = n_0 \quad [1]$$

$$\frac{n_0}{1+\frac{n_0}{N}} = n \quad [2]$$

$$\frac{\Sigma y_i - \hat{y_i}}{n-1} = variance_{within} \quad [3]$$

$$n_h \ \alpha \ \frac{N_h S^2{}_{sh}}{\sqrt{c_h}} \quad [4]$$

$$\frac{\Sigma y_i}{n} = \underline{y} \quad [5]$$

$$\Sigma(\frac{N_h}{N})\underline{y}_{sh} = \underline{y}_{str} \quad [6]$$

$$\sqrt{(1-\frac{n}{N})\frac{S_s{}^2}{n}} = SE \quad [7]$$

$$\sqrt{\Sigma(\frac{N_h}{N})^2 (1-\frac{n_h}{N_h})^2 \frac{S_{sh}{}^2}{n_h}} = SE_{str} \quad [8]$$

$$\underline{y} \pm 1.96 * SE = CI \quad [9]$$

$$\frac{n_i}{n} = \hat{p}\ ;\ n_i = \#\, obs\ BMI > 30 \quad [10]$$

$$\sqrt{\frac{p(1-p)}{n}} = SE \ [11]$$

$$\hat{p} \pm 1.96\, SE = CI \quad [12]$$

$$\Sigma \frac{N_h}{N} \widehat{p_h} = \hat{p}_{str} \ [13]$$

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