Module 4 - Data Finding and Wrangling

Gender and Nicotine Dependence

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The below data was retrieved from the Global Adult Tobacco Survey website (link: ). The data was collected in 2018 in Botswana among adults 15 years and older. Both smokers and non smokers participated in the survey. a total of 4643 participated in this survey, a subset of 463 participants are used in this analysis. The below are unweighted calculations as I dont know yet how to weight the data. The codebook is located in the datanalysis folder.

The objective of this analysis is to see if Gender predicts nicotine dependence. Only smokers were included in this analysis. Heavy Smoking Indeix(HSI) re:nicotine dependence was calculated as a score by adding B01+B07 variables.The scores were categorized as low addicition if score is between 0 and 2, and medium/high addiction if between 3 and 6.

This uses MS Word as output format. [See here](https://quarto.org/docs/output-formats/ms-word.html) for more information. You can switch to other formats, like html or pdf. See [the Quarto documentation](https://quarto.org/) for other formats.

Warning: package 'skimr' was built under R version 4.2.2

Warning: package 'memisc' was built under R version 4.2.2

Warning: package 'ggplot2' was built under R version 4.2.2

Botsdata<-read\_sav("data\_analysis\_exercise/Data/Botswana.sav")

class(Botsdata)

[1] "tbl\_df" "tbl" "data.frame"

#subsetting for variables of interest see bodebook. #A01 Gender, B01 smoking status, B04 age of smoking initiation, B07 smoking how soonafter awaking up, B06A number of cigarettes smoked

Bselect<- Botsdata[,c("A01","B01","B04","B07","B06A")]

#checking my variables names of interest are selected and their strucutre

names(Bselect)

[1] "A01" "B01" "B04" "B07" "B06A"

str(Bselect)

tibble [4,643 × 5] (S3: tbl\_df/tbl/data.frame)  
 $ A01 : dbl+lbl [1:4643] 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,...  
 ..@ label : chr "A01. [RECORD GENDER FROM OBSERVATION. ASK IF NECESSARY.]"  
 ..@ format.spss: chr "F8.0"  
 ..@ labels : Named num [1:2] 1 2  
 .. ..- attr(\*, "names")= chr [1:2] "MALE" "FEMALE"  
 $ B01 : dbl+lbl [1:4643] 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 1, 2, 3,...  
 ..@ label : chr "B01. Do you currently smoke tobacco on a daily basis, less than daily, or not at all?"  
 ..@ format.spss: chr "F8.0"  
 ..@ labels : Named num [1:5] 1 2 3 7 9  
 .. ..- attr(\*, "names")= chr [1:5] "DAILY" "LESS THAN DAILY" "NOT AT ALL" "DON'T KNOW" ...  
 $ B04 : num [1:4643] NA NA NA NA NA NA NA NA NA NA ...  
 ..- attr(\*, "label")= chr "B04. How old were you when you first started smoking tobacco daily? [IF DON'T KNOW OR REFUSED, ENTER 99]"  
 ..- attr(\*, "format.spss")= chr "F10.0"  
 $ B07 : dbl+lbl [1:4643] NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N...  
 ..@ label : chr "B07. How soon after you wake up do you usually have your first smoke? Would you say within 5 minutes, 6 to 30 minutes,"  
 ..@ format.spss: chr "F8.0"  
 ..@ labels : Named num [1:5] 1 2 3 4 9  
 .. ..- attr(\*, "names")= chr [1:5] "WITHIN 5 MINUTES" "6 TO 30 MINUTES" "31 TO 60 MINUTES" "MORE THAN 60 MINUTES" ...  
 $ B06A: num [1:4643] NA NA NA NA NA NA NA NA NA NA ...  
 ..- attr(\*, "label")= chr "B06A. On average, how many of the following products do you currently smoke each day? Also, let me know if you smoke t"  
 ..- attr(\*, "format.spss")= chr "F10.0"

summary(Bselect$B01)

Found more than one class "haven\_labelled" in cache; using the first, from namespace 'haven'

Also defined by 'memisc'

Found more than one class "haven\_labelled" in cache; using the first, from namespace 'haven'

Also defined by 'memisc'

Min. 1st Qu. Median Mean 3rd Qu. Max.   
 1.000 3.000 3.000 2.764 3.000 3.000

#creating a subset for smokers only based on B01 Do you currently smoke? only interested in responses 1,2 only (for daily and less than daily)

subset(Bselect, B01<=2)

# A tibble: 631 × 5  
 A01 B01 B04 B07 B06A  
 <dbl+lbl> <dbl+lbl> <dbl> <dbl+lbl> <dbl>  
 1 1 [MALE] 1 [DAILY] 16 2 [6 TO 30 MINUTES] 5  
 2 1 [MALE] 2 [LESS THAN DAILY] NA NA NA  
 3 1 [MALE] 1 [DAILY] 18 2 [6 TO 30 MINUTES] 5  
 4 1 [MALE] 1 [DAILY] 14 2 [6 TO 30 MINUTES] 4  
 5 1 [MALE] 1 [DAILY] 17 1 [WITHIN 5 MINUTES] 1  
 6 1 [MALE] 2 [LESS THAN DAILY] NA NA NA  
 7 1 [MALE] 2 [LESS THAN DAILY] NA NA NA  
 8 1 [MALE] 2 [LESS THAN DAILY] NA NA NA  
 9 1 [MALE] 1 [DAILY] 19 2 [6 TO 30 MINUTES] 15  
10 1 [MALE] 1 [DAILY] 20 3 [31 TO 60 MINUTES] 2  
# … with 621 more rows  
# ℹ Use `print(n = ...)` to see more rows

#saving the above as your dataset

Bselect2=subset(Bselect, B01<=2)

summary(Bselect2)

A01 B01 B04 B07   
 Min. :1.000 Min. :1.00 Min. : 1.00 Min. :1.000   
 1st Qu.:1.000 1st Qu.:1.00 1st Qu.:17.50 1st Qu.:1.000   
 Median :1.000 Median :1.00 Median :20.00 Median :2.000   
 Mean :1.165 Mean :1.26 Mean :28.83 Mean :2.456   
 3rd Qu.:1.000 3rd Qu.:2.00 3rd Qu.:25.50 3rd Qu.:4.000   
 Max. :2.000 Max. :2.00 Max. :99.00 Max. :9.000   
 NA's :164 NA's :164   
 B06A   
 Min. : 0.00   
 1st Qu.: 1.00   
 Median : 4.00   
 Mean : 27.85   
 3rd Qu.: 6.00   
 Max. :999.00   
 NA's :164

#creting the HSI variable by adding B01 and B07,

Bselect2$HSI<-Bselect2$B01 + Bselect2$B07

#check if your variable has been calculated/ added

dim(Bselect2)

[1] 631 6

names(Bselect2)

[1] "A01" "B01" "B04" "B07" "B06A" "HSI"

str(Bselect2)

tibble [631 × 6] (S3: tbl\_df/tbl/data.frame)  
 $ A01 : dbl+lbl [1:631] 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ...  
 ..@ label : chr "A01. [RECORD GENDER FROM OBSERVATION. ASK IF NECESSARY.]"  
 ..@ format.spss: chr "F8.0"  
 ..@ labels : Named num [1:2] 1 2  
 .. ..- attr(\*, "names")= chr [1:2] "MALE" "FEMALE"  
 $ B01 : dbl+lbl [1:631] 1, 2, 1, 1, 1, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, ...  
 ..@ label : chr "B01. Do you currently smoke tobacco on a daily basis, less than daily, or not at all?"  
 ..@ format.spss: chr "F8.0"  
 ..@ labels : Named num [1:5] 1 2 3 7 9  
 .. ..- attr(\*, "names")= chr [1:5] "DAILY" "LESS THAN DAILY" "NOT AT ALL" "DON'T KNOW" ...  
 $ B04 : num [1:631] 16 NA 18 14 17 NA NA NA 19 20 ...  
 ..- attr(\*, "label")= chr "B04. How old were you when you first started smoking tobacco daily? [IF DON'T KNOW OR REFUSED, ENTER 99]"  
 ..- attr(\*, "format.spss")= chr "F10.0"  
 $ B07 : dbl+lbl [1:631] 2, NA, 2, 2, 1, NA, NA, NA, 2, 3, 1, 4, 4, 4...  
 ..@ label : chr "B07. How soon after you wake up do you usually have your first smoke? Would you say within 5 minutes, 6 to 30 minutes,"  
 ..@ format.spss: chr "F8.0"  
 ..@ labels : Named num [1:5] 1 2 3 4 9  
 .. ..- attr(\*, "names")= chr [1:5] "WITHIN 5 MINUTES" "6 TO 30 MINUTES" "31 TO 60 MINUTES" "MORE THAN 60 MINUTES" ...  
 $ B06A: num [1:631] 5 NA 5 4 1 NA NA NA 15 2 ...  
 ..- attr(\*, "label")= chr "B06A. On average, how many of the following products do you currently smoke each day? Also, let me know if you smoke t"  
 ..- attr(\*, "format.spss")= chr "F10.0"  
 $ HSI : num [1:631] 3 NA 3 3 2 NA NA NA 3 4 ...

#check your new variable

Bselect2[1:500, ]

# A tibble: 500 × 6  
 A01 B01 B04 B07 B06A HSI  
 <dbl+lbl> <dbl+lbl> <dbl> <dbl+lbl> <dbl> <dbl>  
 1 1 [MALE] 1 [DAILY] 16 2 [6 TO 30 MINUTES] 5 3  
 2 1 [MALE] 2 [LESS THAN DAILY] NA NA NA NA  
 3 1 [MALE] 1 [DAILY] 18 2 [6 TO 30 MINUTES] 5 3  
 4 1 [MALE] 1 [DAILY] 14 2 [6 TO 30 MINUTES] 4 3  
 5 1 [MALE] 1 [DAILY] 17 1 [WITHIN 5 MINUTES] 1 2  
 6 1 [MALE] 2 [LESS THAN DAILY] NA NA NA NA  
 7 1 [MALE] 2 [LESS THAN DAILY] NA NA NA NA  
 8 1 [MALE] 2 [LESS THAN DAILY] NA NA NA NA  
 9 1 [MALE] 1 [DAILY] 19 2 [6 TO 30 MINUTES] 15 3  
10 1 [MALE] 1 [DAILY] 20 3 [31 TO 60 MINUTES] 2 4  
# … with 490 more rows  
# ℹ Use `print(n = ...)` to see more rows

summary(Bselect2$HSI)

Min. 1st Qu. Median Mean 3rd Qu. Max. NA's   
 2.000 2.000 3.000 3.456 5.000 10.000 164

#remove missing by removig rows if HSI value is N/A

complete.cases(Bselect2$HSI)

[1] TRUE FALSE TRUE TRUE TRUE FALSE FALSE FALSE TRUE TRUE TRUE TRUE  
 [13] TRUE TRUE TRUE TRUE FALSE TRUE FALSE TRUE FALSE FALSE TRUE TRUE  
 [25] FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE  
 [37] TRUE TRUE TRUE FALSE TRUE TRUE FALSE TRUE FALSE TRUE FALSE TRUE  
 [49] TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE FALSE TRUE TRUE TRUE  
 [61] TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE  
 [73] FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE  
 [85] TRUE TRUE FALSE TRUE FALSE TRUE TRUE TRUE FALSE TRUE TRUE TRUE  
 [97] TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE FALSE TRUE FALSE  
[109] TRUE TRUE FALSE TRUE TRUE FALSE TRUE FALSE TRUE TRUE TRUE TRUE  
[121] TRUE TRUE TRUE FALSE FALSE TRUE TRUE FALSE TRUE TRUE TRUE TRUE  
[133] FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE  
[145] TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE FALSE TRUE TRUE  
[157] TRUE TRUE FALSE TRUE TRUE TRUE TRUE FALSE FALSE FALSE TRUE TRUE  
[169] TRUE FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE  
[181] FALSE TRUE TRUE FALSE TRUE TRUE TRUE TRUE FALSE TRUE FALSE TRUE  
[193] TRUE FALSE TRUE TRUE TRUE TRUE FALSE TRUE FALSE FALSE TRUE TRUE  
[205] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE FALSE  
[217] TRUE TRUE FALSE TRUE TRUE FALSE TRUE TRUE TRUE FALSE FALSE TRUE  
[229] TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE FALSE  
[241] TRUE TRUE FALSE FALSE TRUE FALSE TRUE FALSE TRUE FALSE FALSE TRUE  
[253] TRUE TRUE FALSE FALSE TRUE TRUE FALSE TRUE FALSE FALSE FALSE TRUE  
[265] FALSE TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE FALSE TRUE  
[277] TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE  
[289] TRUE FALSE TRUE FALSE FALSE TRUE TRUE TRUE TRUE FALSE TRUE TRUE  
[301] FALSE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE FALSE TRUE FALSE  
[313] TRUE FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE  
[325] TRUE TRUE FALSE FALSE TRUE TRUE TRUE TRUE FALSE FALSE TRUE TRUE  
[337] TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE  
[349] TRUE FALSE FALSE TRUE FALSE TRUE TRUE TRUE TRUE TRUE FALSE FALSE  
[361] TRUE TRUE TRUE TRUE TRUE FALSE FALSE TRUE TRUE TRUE TRUE TRUE  
[373] TRUE TRUE TRUE TRUE TRUE FALSE TRUE FALSE TRUE TRUE FALSE TRUE  
[385] TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE  
[397] FALSE FALSE TRUE FALSE TRUE TRUE TRUE TRUE FALSE FALSE TRUE TRUE  
[409] TRUE TRUE TRUE FALSE FALSE TRUE TRUE TRUE FALSE FALSE FALSE TRUE  
[421] TRUE FALSE TRUE FALSE TRUE FALSE TRUE TRUE FALSE TRUE TRUE FALSE  
[433] TRUE FALSE TRUE FALSE TRUE TRUE TRUE FALSE FALSE FALSE TRUE TRUE  
[445] FALSE FALSE FALSE FALSE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE  
[457] FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE  
[469] TRUE TRUE TRUE FALSE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE  
[481] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE  
[493] TRUE TRUE TRUE TRUE TRUE FALSE TRUE FALSE TRUE TRUE TRUE TRUE  
[505] TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE FALSE  
[517] TRUE FALSE TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE  
[529] TRUE FALSE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE  
[541] TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE  
[553] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE  
[565] TRUE TRUE FALSE FALSE FALSE TRUE TRUE TRUE TRUE FALSE TRUE TRUE  
[577] TRUE TRUE FALSE TRUE TRUE FALSE TRUE FALSE TRUE FALSE TRUE TRUE  
[589] TRUE TRUE FALSE TRUE FALSE TRUE TRUE TRUE FALSE TRUE TRUE FALSE  
[601] TRUE TRUE TRUE FALSE FALSE TRUE TRUE FALSE TRUE TRUE TRUE FALSE  
[613] FALSE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE  
[625] TRUE TRUE TRUE TRUE TRUE TRUE TRUE

df\_Bselect2<-Bselect2[complete.cases(Bselect2$HSI),]

#check if NA is removed

df\_Bselect2[1:500, ]

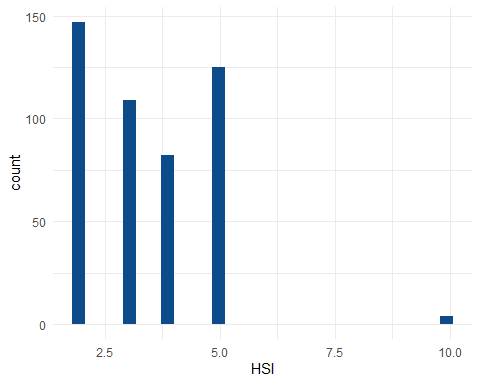
# A tibble: 500 × 6  
 A01 B01 B04 B07 B06A HSI  
 <dbl+lbl> <dbl+lbl> <dbl> <dbl+lbl> <dbl> <dbl>  
 1 1 [MALE] 1 [DAILY] 16 2 [6 TO 30 MINUTES] 5 3  
 2 1 [MALE] 1 [DAILY] 18 2 [6 TO 30 MINUTES] 5 3  
 3 1 [MALE] 1 [DAILY] 14 2 [6 TO 30 MINUTES] 4 3  
 4 1 [MALE] 1 [DAILY] 17 1 [WITHIN 5 MINUTES] 1 2  
 5 1 [MALE] 1 [DAILY] 19 2 [6 TO 30 MINUTES] 15 3  
 6 1 [MALE] 1 [DAILY] 20 3 [31 TO 60 MINUTES] 2 4  
 7 1 [MALE] 1 [DAILY] 16 1 [WITHIN 5 MINUTES] 6 2  
 8 1 [MALE] 1 [DAILY] 16 4 [MORE THAN 60 MINUTES] 6 5  
 9 1 [MALE] 1 [DAILY] 18 4 [MORE THAN 60 MINUTES] 2 5  
10 1 [MALE] 1 [DAILY] 18 4 [MORE THAN 60 MINUTES] 10 5  
# … with 490 more rows  
# ℹ Use `print(n = ...)` to see more rows

summary(df\_Bselect2$HSI)

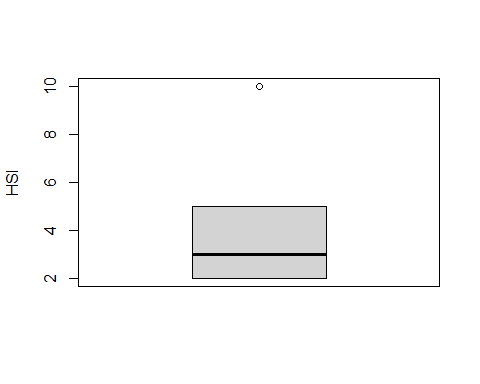
Min. 1st Qu. Median Mean 3rd Qu. Max.   
 2.000 2.000 3.000 3.456 5.000 10.000

#NA is removed but there is an outlier as the max should only be 6, so removing the oulier. plotting a historgram and boxplot to see how many outliers there are

ggplot(df\_Bselect2)+  
 aes(x=HSI)+ geom\_histogram(bins=30L,fill="#0c4c8a")+  
 theme\_minimal()



boxplot(df\_Bselect2$HSI, ylab="HSI")



#identify the outlier

boxplot.stats(df\_Bselect2$HSI)$out

[1] 10 10 10 10

#Identify the rows correpding to the outlier

out<-boxplot.stats(df\_Bselect2$HSI)$out  
out\_ind<-which(df\_Bselect2$HSI %in% c(out))  
out\_ind

[1] 22 28 86 142

#subsetting to remove rows with 10 from the df

df\_BSelect3<-subset(df\_Bselect2, HSI!=10)

#check if outlier removed

summary(df\_BSelect3$HSI)

Min. 1st Qu. Median Mean 3rd Qu. Max.   
 2.0 2.0 3.0 3.4 5.0 5.0

#catagorize HSI scores by 0 for scores 0-2 and 1 for scores 3 to 6, female(2) recoded to 0 keep male as is 1

df\_BSelect3$HSI[df\_BSelect3$HSI>=0 & df\_BSelect3$HSI<=2] <- 0  
  
df\_BSelect3$HSI[df\_BSelect3$HSI>=3 & df\_BSelect3$HSI<=6] <- 1

df\_BSelect3$A01[df\_BSelect3$A01>=2] <- 0

summary(df\_BSelect3)

A01 B01 B04 B07 B06A   
 Min. :0.0000 Min. :1 Min. : 1.00 Min. :1.0 Min. : 0.00   
 1st Qu.:1.0000 1st Qu.:1 1st Qu.:17.00 1st Qu.:1.0 1st Qu.: 1.00   
 Median :1.0000 Median :1 Median :20.00 Median :2.0 Median : 4.00   
 Mean :0.8467 Mean :1 Mean :28.56 Mean :2.4 Mean : 26.16   
 3rd Qu.:1.0000 3rd Qu.:1 3rd Qu.:25.00 3rd Qu.:4.0 3rd Qu.: 6.00   
 Max. :1.0000 Max. :1 Max. :99.00 Max. :4.0 Max. :999.00   
 HSI   
 Min. :0.0000   
 1st Qu.:0.0000   
 Median :1.0000   
 Mean :0.6825   
 3rd Qu.:1.0000   
 Max. :1.0000

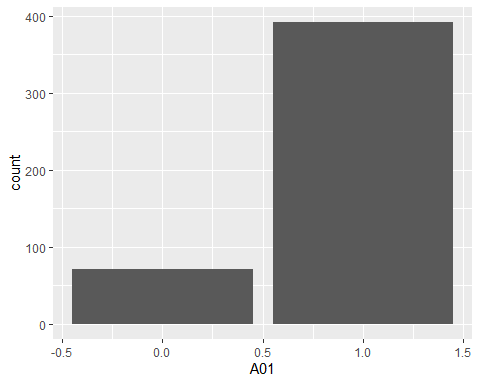
#tried to label the column names here but it didnt work #labels(df\_BSelect3[[“HSI”]])<-“Nicotine Dependnece” #labels(df\_BSelect3[[“A01”]])<-“Gender” #labels(df\_BSelect3) #tables(df\_BSelect3HSI)

#plot

ggplot(df\_BSelect3)+geom\_bar(aes(x=A01, fill=HSI))

Don't know how to automatically pick scale for object of type  
<haven\_labelled/vctrs\_vctr/double>. Defaulting to continuous.

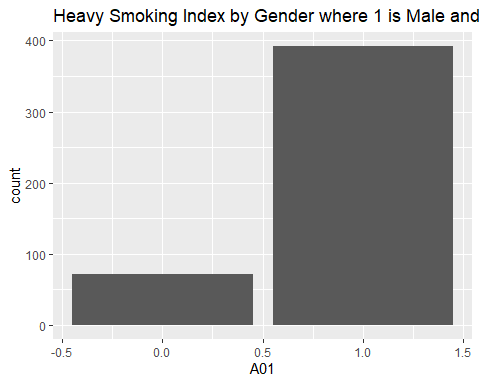
Warning: The following aesthetics were dropped during statistical transformation: fill  
ℹ This can happen when ggplot fails to infer the correct grouping structure in  
 the data.  
ℹ Did you forget to specify a `group` aesthetic or to convert a numerical  
 variable into a factor?



ggplot(df\_BSelect3)+geom\_bar(aes(x=A01, fill=HSI))+ggtitle(label="Heavy Smoking Index by Gender where 1 is Male and 0 is Female")

Don't know how to automatically pick scale for object of type  
<haven\_labelled/vctrs\_vctr/double>. Defaulting to continuous.

Warning: The following aesthetics were dropped during statistical transformation: fill  
ℹ This can happen when ggplot fails to infer the correct grouping structure in  
 the data.  
ℹ Did you forget to specify a `group` aesthetic or to convert a numerical  
 variable into a factor?



#regression y~x

fit1<-glm(HSI~A01,family=binomial(link="logit"),data=df\_BSelect3)

summary(fit1)

Call:  
glm(formula = HSI ~ A01, family = binomial(link = "logit"), data = df\_BSelect3)  
  
Deviance Residuals:   
 Min 1Q Median 3Q Max   
-1.5226 -1.5226 0.8678 0.8678 0.9083   
  
Coefficients:  
 Estimate Std. Error z value Pr(>|z|)   
(Intercept) 0.6721 0.2509 2.679 0.00739 \*\*  
A01 0.1104 0.2735 0.404 0.68635   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for binomial family taken to be 1)  
  
 Null deviance: 578.72 on 462 degrees of freedom  
Residual deviance: 578.56 on 461 degrees of freedom  
AIC: 582.56  
  
Number of Fisher Scoring iterations: 4

#The coeffecient of HSI is .11. The log of odds of being Male(1) is .11 times higher for those with medium addiction compared to those with low addiction.

print(fit1)

Call: glm(formula = HSI ~ A01, family = binomial(link = "logit"), data = df\_BSelect3)  
  
Coefficients:  
(Intercept) A01   
 0.6721 0.1104   
  
Degrees of Freedom: 462 Total (i.e. Null); 461 Residual  
Null Deviance: 578.7   
Residual Deviance: 578.6 AIC: 582.6

#save cleanted dataset as RDS

save(df\_BSelect3,file="df\_BSelect3.RDS")

To cite other work (important everywhere, but likely happens first in introduction), make sure your references are in the bibtex file specified in the YAML header above (here dataanalysis\_template\_references.bib) and have the right bibtex key. Then you can include like this:

Examples of reproducible research projects can for instance be found in [@mckay2020; @mckay2020a]

# 1. Methods

*Describe your methods. That should describe the data, the cleaning processes, and the analysis approaches. You might want to provide a shorter description here and all the details in the supplement.*

## 1.1 Data aquisition

*As applicable, explain where and how you got the data. If you directly import the data from an online source, you can combine this section with the next.*

## 1.2 Data import and cleaning

*Write code that reads in the file and cleans it so it’s ready for analysis. Since this will be fairly long code for most datasets, it might be a good idea to have it in one or several R scripts. If that is the case, explain here briefly what kind of cleaning/processing you do, and provide more details and well documented code somewhere (e.g. as supplement in a paper). All materials, including files that contain code, should be commented well so everyone can follow along.*

## 1.3 Statistical analysis

*Explain anything related to your statistical analyses.*

# 2. Results

## 2.1 Exploratory/Descriptive analysis

*Use a combination of text/tables/figures to explore and describe your data. Show the most important descriptive results here. Additional ones should go in the supplement. Even more can be in the R and Quarto files that are part of your project.*

Note the loading of the data providing a **relative** path using the ../../ notation. (Two dots means a folder up). You never want to specify an **absolute** path like C:\ahandel\myproject\results\ because if you share this with someone, it won’t work for them since they don’t have that path. You can also use the here R package to create paths. See examples of that below.

## 2.2 Basic statistical analysis

*To get some further insight into your data, if reasonable you could compute simple statistics (e.g. simple models with 1 predictor) to look for associations between your outcome(s) and each individual predictor variable. Though note that unless you pre-specified the outcome and main exposure, any “p<0.05 means statistical significance” interpretation is not valid.*

## 2.3 Full analysis

*Use one or several suitable statistical/machine learning methods to analyze your data and to produce meaningful figures, tables, etc. This might again be code that is best placed in one or several separate R scripts that need to be well documented. You want the code to produce figures and data ready for display as tables, and save those. Then you load them here.*

getwd()

# 3. Discussion

## 3.1 Summary and Interpretation

*Summarize what you did, what you found and what it means.*

## 3.2 Strengths and Limitations

*Discuss what you perceive as strengths and limitations of your analysis.*

## 3.3 Conclusions

*What are the main take-home messages?*

*Include citations in your Rmd file using bibtex, the list of references will automatically be placed at the end*

This paper [@leek2015] discusses types of analyses.

These papers [@mckay2020; @mckay2020a] are good examples of papers published using a fully reproducible setup similar to the one shown in this template.

Note that this cited reference will show up at the end of the document, the reference formatting is determined by the CSL file specified in the YAML header. Many more style files for almost any journal [are available](https://www.zotero.org/styles). You also specify the location of your bibtex reference file in the YAML. You can call your reference file anything you like, I just used the generic word references.bib but giving it a more descriptive name is probably better.

library(pandoc)