Epi207-Assignment 3

The final written assignment will include clean and well-documented SAS code, the student's reproduction of tables/figures, and a reflection (maximum 1 page double-spaced) on whether you were able to reproduce the results; if not, describe what information was missing and any other insights about your attempts to replicate the results. •In your reflection, please note whether found the code necessary to understand precisely what was done.

https://github.com████████████████████████

Objective: Reproduce results from the Kim group assignment 2. Specifically, to describe the association between appendicular skeletal muscle mass (ASM) per body weight and hypertension (HT) among Korean adults aged 25 to 60 years?

Replicated Tables/Figures:

Table 1

Table 1. Study participants	
	mean ± SD or number (%) Total (n=10,759)
Appendicular skeletal muscle mass (ASM)	20.2 ± 4.90
ASM (%)	30.22±3.47
Age (years)	44.1± 9.62
BMI (kg/m^2)	23.69± 3.50
Waist circumference (cm)	83.23± 9.93
Female	4846 (45.0)
Obesity status according to BMI	
Under weight (BMI <18.5 kg/m^2)	444 (4.1)
Normal (BMI 18.5-22.9 kg/m^2)	4469 (41.5)
Overweight (BMI 23-24.9 kg/m^2)	2334 (21.7)
Obesity (BMI >=25 kg/m^2)	3512 (32.6)
Dyslipidemia	3682 (34.2)
Diabetes	651 (6.1)
History of smoking	2064 (19.2)
History of alcohol intake	6098 (56.7)
Hypertension	2826 (26.3)

Table 2a

| Table 2a. Association between appendicular skeletal mass per body weight (%) and hypertension		
	OR (95% CI)	E-value
Crude	1.0 (0.99, 1.01)	N/A
Model 1	0.80 (0.78, 0.81)	1.46
Model 2	0.81 (0.79, 0.83)	1.46

Model 1 adjusted for age, sex
Model 2 adjusted for age, sex, history of smoking, history of alcohol intake

Table 2b

Table 2b. Average change in MAP per 10% increase in appendicular skeletal mass per body weight	
	β (95% CI)
Crude	2.4 (1.7, 3.0)
Model 1	-11.2 (-12.0, -10.5)
Model 2	-11.3 (-12.0, -10.5)

Model 1 adjusted for age, sex
Model 2 adjusted for age, sex, history of smoking, history of alcohol intake

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Supplemental Figure

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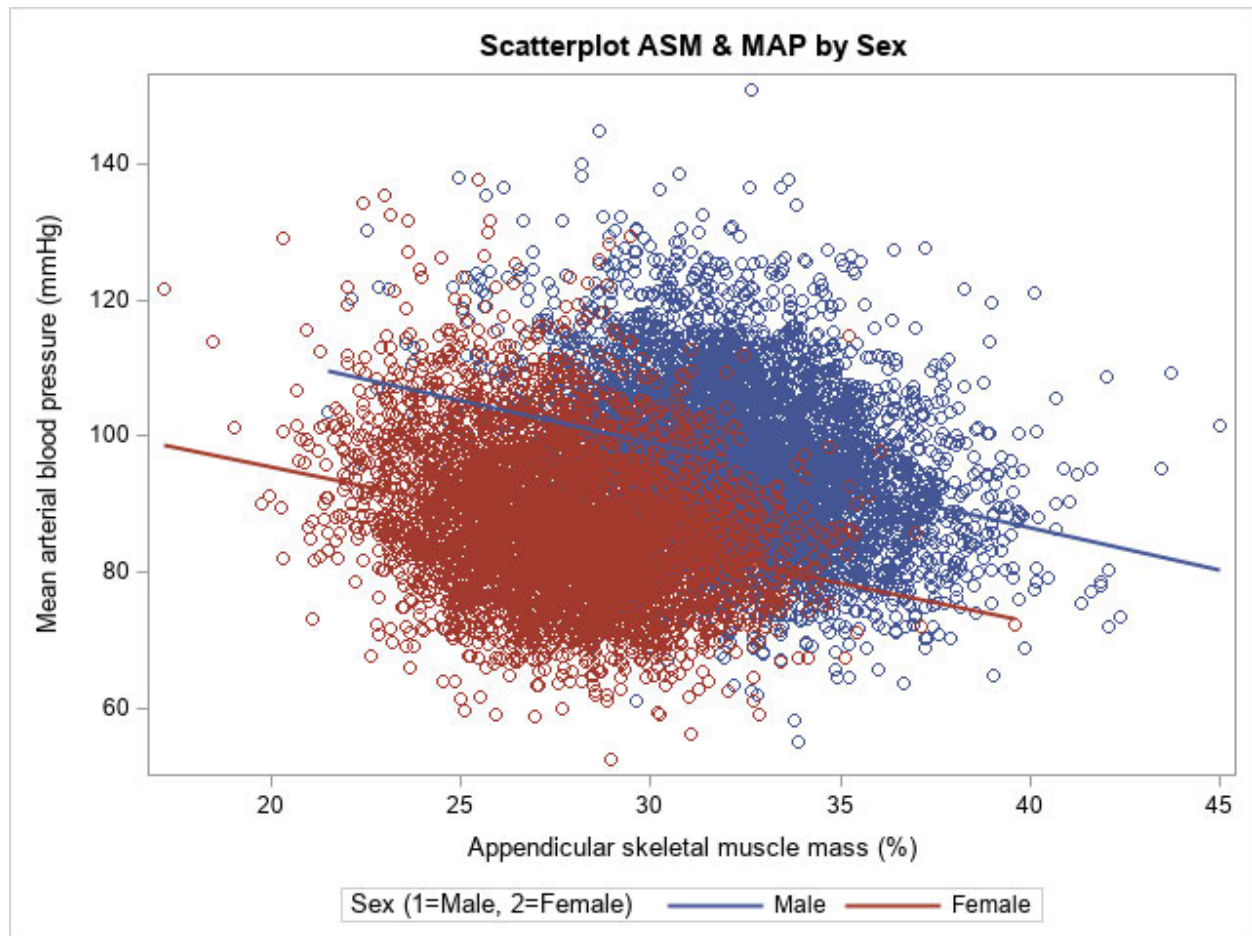
Reflection:

 I was able to reproduce the main results of this analysis, including table 1, table 2, and the supplementary figure. I could reproduce the results of the supplemental table if relying on the authors' code but had a difficult time doing it on my own by only reading the text. This could be more a reflection of my programming skills in SAS, however.

I was unable to reproduce the data cleaning, data and variable transformation and variable recoding that the authors did because the raw data was not provided in the github repository. Ideally with a repository, the folder could be downloaded or pulled and the scripts could be run with very little adjustment and the data transformations and results would be reproduced. I also noted that there is no readme in the assignment 2 repo which would be nice for reproducibility, just for guidance and description.

One small thing I noted is that in table 1 there is a row for sex and another for Female. The sex row is empty that I did not include in my table 1 because Female is listed with a value.

I did find their code sufficient to reproduce precisely what was done for the analytic component but not the data cleaning. While their code was sufficient for the analytic component on its own, I had a hard time following the sensitivity analysis from the write up methods and I wasn't sure how to generate that code on my own while reproducing the results.

This was an interesting project and I appreciated having the github repo. It demonstrated to me that for reproducibility, the repositories are really helpful. That said, it's still important to try to recreate/recode the analytic steps to make sure.

CODE:

3/1/2022
;

```
*RF: adjust location;
libname epi207 "C:\Users\e655411\Downloads\EPIDEM207-2022-winter-
main\EPIDEM207-2022-winter-main\Assignment 2";



/************************************************************************
/
/********* The section of the code that is cleaning raw data
**********/
/*********** not reproducible, raw data not provided in repo
**********/
/************************************************************************
/

*RF, starting here pulling in the saved clean dataset from the
repository folder;
data outdata_label;
set epi207.outdata_label;
run;


*Load Formats;

PROC FORMAT;
     value Sex    1='Male'
                       2='Female';
     value YN     0='No'
                       1='Yes';
     value BMIgr low-<18.5 = '0'
                       18.5-22.9 = '1'
                       23-24.9        = '2'
                       25-high    = '3';
     value BMItx 0 = 'Under weight (BMI <18.5 kg/m^2)'
                       1 = 'Normal (BMI 18.5-22.9 kg/m^2)'
```

```
                                       2 = 'Overweight (BMI 23-24.9 kg/m^2)'
                                       3 = 'Obesity (BMI >=25 kg/m^2)';
RUN;


*Descriptive stats (means + SDs or Freqs + Percents) for table 1 in
order of how they appear in the table;


title "Table 1 Means";
proc means data = outdata_label n mean std nmiss;
var ASM_Wt_
        ASM_10
        age
        bexam_BMI
        bexam_wc;
run;


title "Table 1 Freqs";
proc freq data=outdata_label;
tables sex
            BMIgr
            DysL_
            DM
            shx_smoke_yn
            shx_alcohol_yn
            HT /missing;
run;


** Regressions for Table 2;


*Logistic regression for Table 2;
title "HTN: ASM Crude Model";
proc logistic data=outdata_label;
model HT (event='Yes') = ASM_Wt_;
run;


title "HTN: ASM Model 1";
proc logistic data=outdata_label;
model HT (event='Yes') = ASM_Wt_ sex age;
run;


title "HTN: ASM Model 2";
proc logistic data=outdata_label;
model HT (event='Yes') = ASM_Wt_ sex age shx_smoke_yn shx_alcohol_yn;
```

```
run;

*Not sure how they did the sensitivity analysis;

*plot;

proc sgplot data=outdata_label;
title "Plot of ASM by Map Stratified by Age";
  reg x=ASM_Wt_ y=MAP / group=sex;
run;
title;
```