DATA 101 Exam 2

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Due: Sunday, 11/29 at 11:59pm

Academic Honesty Statement (fill in your name)

I, Kamila Palys, hereby affirm that I have not communicated with or gained information in any way from my classmates or anyone other than the Professor during this exam, that I have not assisted anyone else with this exam, and that all work is my own.

Load packages and data

```
# load required packages here
library(tidyverse)
library(tidymodels)
library(janitor)
library(lubridate)
library(NHANES)
```

```
# read in the data here
nhanes <- NHANES %>%
  janitor::clean_names()
```

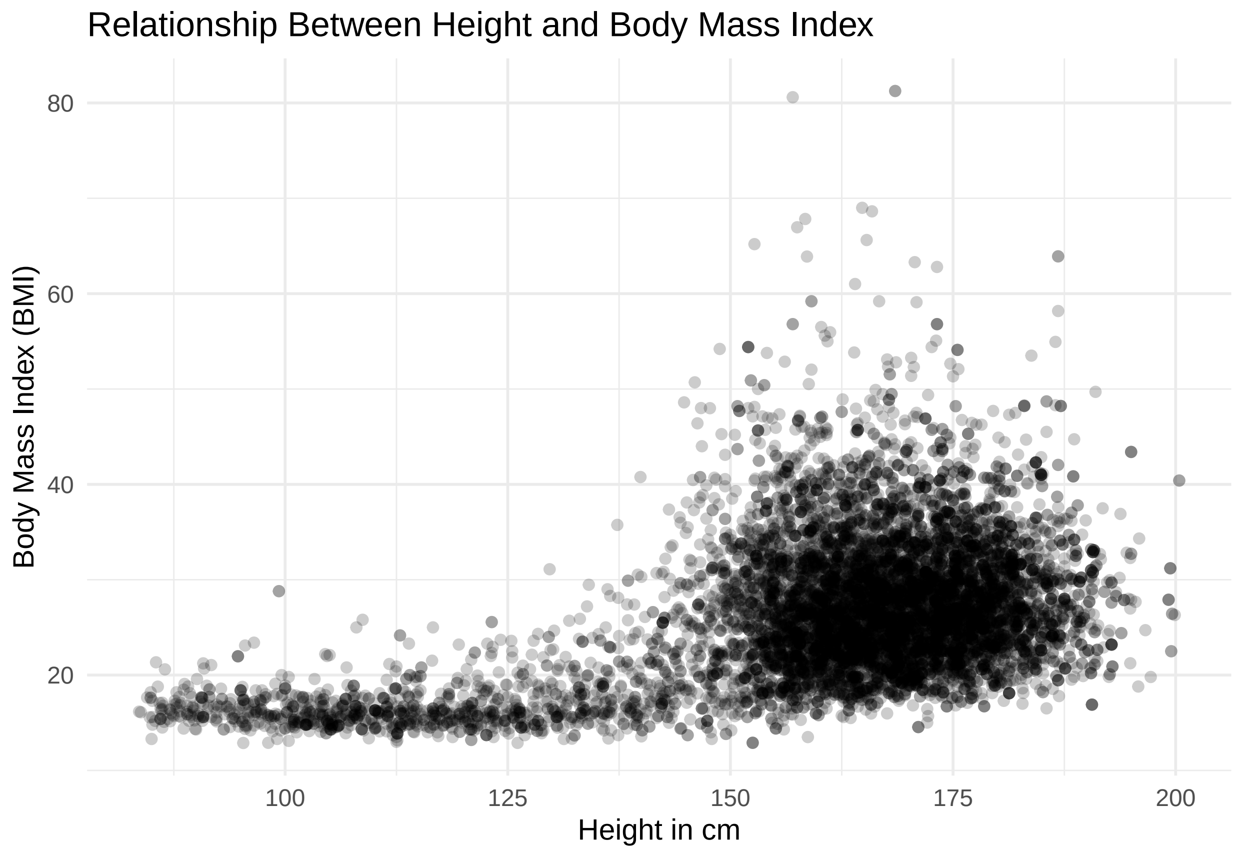
Questions

Question 1

Here we will show the relationship between the height and body mass index of a person using a scatterplot.

```
ggplot(data = nhanes, mapping = aes(x = height, y = bmi)) +
  geom_point(alpha = 0.2) +
  labs(x = "Height in cm",
       y = "Body Mass Index (BMI)",
       title = "Relationship Between Height and Body Mass Index") +
  theme_minimal()
```

```
## Warning: Removed 366 rows containing missing values (geom_point).
```

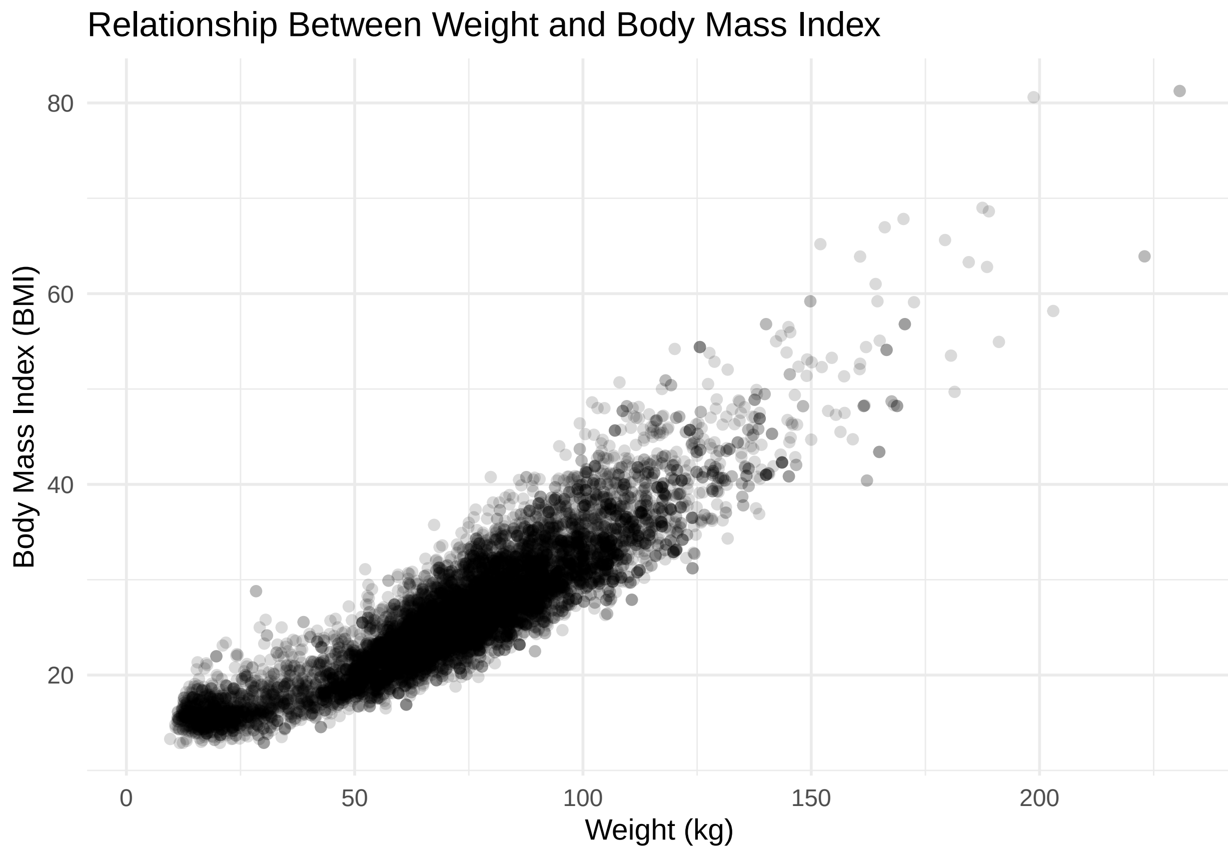


From this display, a slight upwards trend is seen. For heights of less than 150cm, not much of a slope is visible and body mass index stays relatively the same for various heights under 150cm. For heights above that amount, there are many more people whose body mass indexes are higher and there is a far greater range of them. In fact, most of the body mass indexes are higher than for people shorter than 150cm. One reason as to why this may be the case is because those shorter than 150cm are usually young children, whose parents have the main say in their diets. When the children grow up and therefore also get taller, they make more of their own decisions when it comes to their diet, which may not be good for their health and BMI.

Now we will show the relationship between the weight and body mass index of a person, also using a scatterplot.

```
ggplot(data = nhanes, mapping = aes(x = weight, y = bmi)) +
  geom_point(alpha = 0.15) +
  labs(x = "Weight (kg)",
       y = "Body Mass Index (BMI)",
       title = "Relationship Between Weight and Body Mass Index") +
  theme_minimal()
```

```
## Warning: Removed 366 rows containing missing values (geom_point).
```



Here, there is almost a perfectly linear positive slope between a person's weight and their body mass index. The positive relationship makes sense because as the weight of a person goes up, given a height, their body mass index will go up as well. Even though height is not a factor shown on this graph, it often increases along with weight, which may lead to little to no change in body mass index. However, weight can fluctuate a lot more and throughout a person's entire life, which is why this upward trend is seen, suggesting that a higher weight still generally leads to a higher body mass index.

Question 2

Now, a linear model will be created to predict bmi as a function of weight.

```
bmi_fit <- lm(bmi ~ weight, data = nhanes)
tidy(bmi_fit)
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic p.value
##   <chr>          <dbl>     <dbl>     <dbl>   <dbl>
## 1 (Intercept)    9.09    0.0915       99.4       0
## 2 weight         0.241   0.00118     205.        0
```

$\hat{bmi} = 9.09 + 0.24 weight$

The coefficient of weight in this equation is 0.24, rounded to the hundredths, meaning that for every additional kilogram of weight, a person's bmi is expected to go up by approximately 0.24.

Question 3

Now the coefficient of determination, or R-Squared, will be calculated.

```
glance(bmi_fit)$r.squared
```

```
## [1] 0.8139379
```

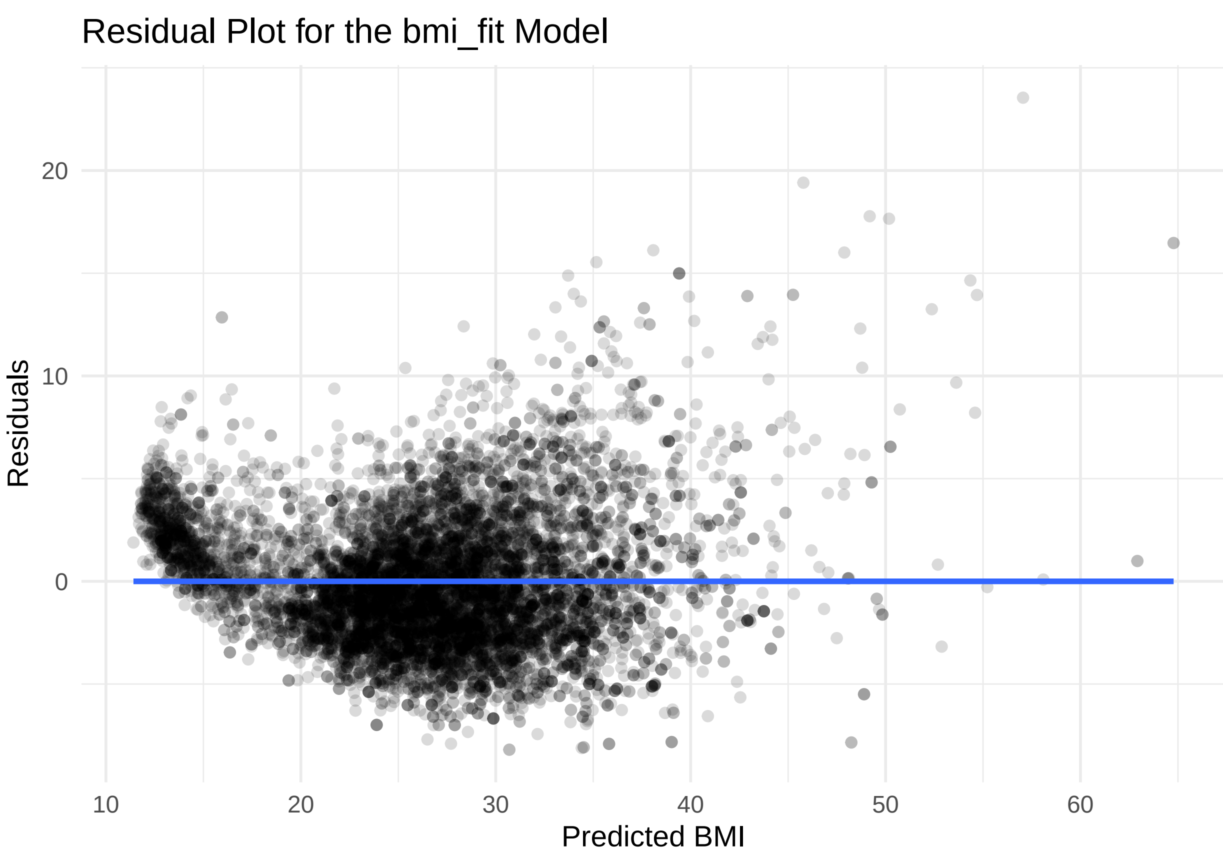
The coefficient of determination being approximately 0.81 tells us that 81% of the variability of the bmi can be explained by the weight from the linear model previously created. This high percentage suggests that the model created is a good fit for the data.

Question 4

A residual plot will now be created to represent the linear model.

```
augment(bmi_fit) %>%
  ggplot(mapping = aes(x = .fitted, y = .resid)) +
  geom_point(alpha = 0.15) +
  geom_smooth(method = "lm", se = FALSE) +
  labs(x = "Predicted BMI",
       y = "Residuals",
       title = "Residual Plot for the bmi_fit Model") +
  theme_minimal()
```

```
## `geom_smooth()` using formula 'y ~ x'
```



Looking at this residual plot, it can be concluded that the linear model is not a great fit for the data. The residuals spanning across the plot are inconsistent in their range and shape, and it is known that seeing any patterns on a residual plot is a sign that the model is not a great fit.

Question 5

A new linear model will be created to predict systolic blood pressure as a function of weight, age, and gender of a person.

```
bp_fit <- lm(bp_sys_ave ~ weight + age + gender, data = nhanes)

tidy(bp_fit)
```

```
## # A tibble: 4 x 5
##   term        estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)  92.3      0.580      159.   0.
## 2 weight        0.0937   0.00724     12.9  6.06e-38
## 3 age           0.414    0.00813     50.9  0.
## 4 gendermale    3.20     0.327        9.78 1.88e-22
```

The model equation for males: $\hat{bp} = 92.3 + 0.094weight + 0.414age + 3.20(1)$ The model equation for females: $\hat{bp} = 92.3 + 0.094weight + 0.414age + 3.20(0)$

As seen, the model equations for males and females differs only in that for the males, a 1 is substituted for the gender variable, meaning males here had a 3.20 higher systolic blood pressure on average than females.

```
predictbp <- tibble(age = 60, gender = "male", weight = 91)
predict(bp_fit, newdata = predictbp)
```

```
##        1
## 128.8575
```

With the code used after creating a new dataframe with the desire values, the predicted systolic blood pressure of a 60-year old man weighing 200 pounds, or 91 kilograms, shows to be approximately 128.86 mm Hg.

Question 6

Now a logistic model will be created to predict whether or not a patient has diabetes as a function of the patient's age, gender, and BMI.

```
diabetes_fit <- logistic_reg() %>%
  set_engine("glm") %>%
  fit(diabetes ~ age + gender + bmi, data = nhanes, family = "binomial")

tidy(diabetes_fit)
```

```
## # A tibble: 4 x 5
##   term        estimate std.error statistic   p.value
##   <chr>          <dbl>     <dbl>     <dbl>     <dbl>
## 1 (Intercept)  -8.38     0.258      -32.5  5.16e-231
## 2 age           0.0582   0.00252     23.1  3.60e-118
## 3 gendermale    0.365    0.0833       4.38 1.21e-  5
## 4 bmi           0.0965   0.00560     17.2  1.25e- 66
```

This model's equation is: $\log(p/(1-p)) = -8.38 + 0.058age + 0.365gendermale + 0.097bmi$

Question 7

Here a function will be written that outputs the inverse-logit of a number x.

```
inv_logit <- function(x) {
  exp(x)/(1 + exp(x))
}
```

This function could be useful if we wanted to find the probability of an event occurring, such as the probability of a patient having diabetes as a result of different factors from the logistic model from Question 6. In this case, we after substituting the conditions we wanted to test for, meaning a certain age, gender, and BMI, the result of that model would be substituted for the x in the inverse-logit to find the probability of the patient having diabetes.

Question 8

We will now make use of the logistic regression model, its answer, and the inverse-logit to obtain the predicted probability of a 55-year old woman who has a BMI of 24 of having diabetes.

-2.862

```
inv_logit(-2.862)
```

```
## [1] 0.05406433
```

The predicted probability of this patient having diabetes is approximately 0.054, or about 5.4% chance. This is a very small probability of this woman having diabetes, which is not entirely surprising because a BMI of 24 is not a very high one, and we might assume that people with a higher BMI have a higher chance of having diabetes. If we were to classify this result, we would classify the patient as not having diabetes.

Question 9

Five outputs from the diabetes_fit model will now be mapped to the inv_logit function.

```
outputs <- list(c(-2.20, 0.01, -0.35, 1.15, 0.83))

map(outputs, inv_logit)
```

```
## [[1]]
## [1] 0.09975049 0.50249998 0.41338242 0.75951092 0.69635493
```

The result for the third patient is approximately 0.41, as seen from the mapping results. This means that given the patient's age, gender, and BMI, he or she has a predicted probability of 0.41, or about a 41% chance, of having diabetes.

Question 10

[Enter code and/or narrative here.]

Question 11

[Enter code and/or narrative here.]

Question 12

[Enter code and/or narrative here.]

Question 13

[Enter code and/or narrative here.]