Data Science for Biological, Medical and Health Research: Notes for 431

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Contents

Introduction

These Notes provide a series of examples using R to work through issues that are likely to come up in PQHS/CRSP/MPHP 431.

While these Notes share some of the features of a textbook, they are neither comprehensive nor completely original. The main purpose is to give 431 students a set of common materials on which to draw during the course. In class, we will sometimes:

- reiterate points made in this document,
- amplify what is here,
- simplify the presentation of things done here,
- use new examples to show some of the same techniques,
- refer to issues not mentioned in this document

but what we don't do is follow these notes very precisely. We assume instead that you will read the materials and try to learn from them, just as you will attend classes and try to learn from them. We welcome feedback of all kinds on this document or anything else. Just email us at 431-help at case dot edu, or submit a pull request.

What you will mostly find are brief explanations of a key idea or summary, accompanied (most of the time) by R code and a demonstration of the results of applying that code.

Everything you see here is available to you as HTML or PDF. You will also have access to the R Markdown files, which contain the code which generates everything in the document, including all of the R results. We will demonstrate the use of R Markdown (this document is generated with the additional help of an R package called `bookdown`) and R Studio (the "program" which we use to interface with the R language) in class.

Structure

The Notes, like the 431 course, are split into three main parts.

Part A is about **visualizing data and exploratory data analyses**. These Notes focus on using R to work through issues that arise in the process of exploring data, managing (cleaning and manipulating) data into a tidy format to facilitate useful work downstream, and describing those data effectively with visualizations, numerical summaries, and some simple models.

Part B is about **making comparisons** with data. The Notes discuss the use of R to address comparisons of means and of rates/proportions, primarily. The main ideas include confidence intervals, the bootstrap and parametric and non-parametric tests of hypotheses. Key ideas from Part A that have an impact here include visualizations to check the assumptions behind our inferences, and cleaning/manipulating data to facilitate our comparisons.

Part C is about **building models** with data. The Notes are primarily concerned (in 431) with linear regression models for continuous quantitative outcomes, using one or more predictors. We'll see how to use

models to accomplish many of the comparisons discussed in Part B, and make heavy use of visualization and data management tools developed in Part A to assess our models.

Course Philosophy

In developing this course, we adopt a modern approach that places data at the center of our work. Our goal is to teach you how to do truly reproducible research with modern tools. We want you to be able to answer real questions using data and equip you with the tools you need in order to answer those questions well (Cetinkaya-Rundel (2017) has more on a related teaching philosophy.)

The curriculum includes more on several topics than you might expect from a standard graduate introduction to statistics.

- data gathering
- data wrangling
- exploratory data analysis and visualization
- multivariate modeling
- communication

It also nearly completely avoids formalism and is extremely applied - this is most definitely **not** a course in theoretical or mathematical statistics.

The 431 course is about **getting things done**. It's not a statistics course, nor is it a computer science course. It is instead a course in **data science**.

Chapter 1

Data Science

The definition of **data science** can be a little slippery. One current view of data science, is exemplified by Steven Geringer's 2014 Venn diagram.

- The field encompasses ideas from mathematics and statistics and from computer science, but with a heavy reliance on subject-matter knowledge. In our case, this includes clinical, health-related, medical or biological knowledge.
- As Gelman and Nolan (2017) suggest, the experience and intuition necessary for good statistical practice are hard to obtain, and teaching data science provides an excellent opportunity to reinforce statistical thinking skills across the full cycle of a data analysis project.
- The principal form in which computer science (coding/programming) play a role in this course is to provide a form of communication. You'll need to learn how to express your ideas not just orally and in writing, but also through your code.

1.1 Why a unicorn?

Data Science is a **team** activity. Everyone working in data science brings some part of the necessary skillset, but no one person can cover all three areas alone for excellent projects.

> [The individual who is truly expert in all three key areas (mathematics/statistics, computer science and subject-matter knowledge) is] a mythical beast with magical powers who's rumored to exist but is never actually seen in the wild.
>
> http://www.kdnuggets.com/2016/10/battle-data-science-venn-diagrams.html

1.2 Data Science Project Cycle

A typical data science project can be modeled as follows, which comes from the introduction to the amazing book **R for Data Science**, by Garrett Grolemund and Hadley Wickham, which is a key text for this course (Grolemund and Wickham 2017).

This diagram is sometimes referred to as the Krebs Cycle of Data Science. For more on the steps of a data science project, we encourage you to read the Introduction of Grolemund and Wickham (2017).

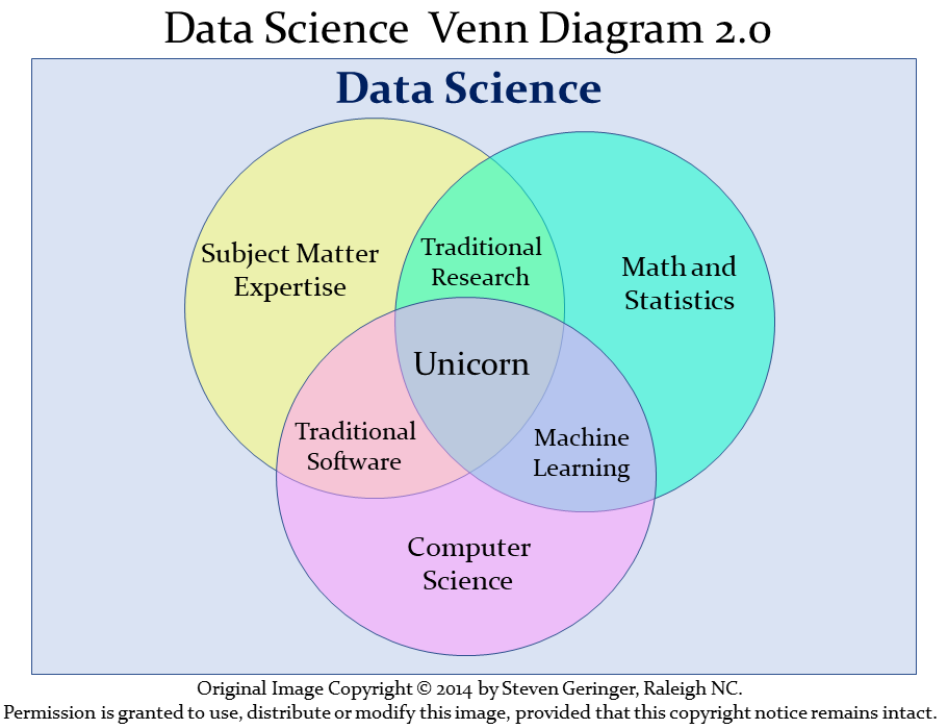


Figure 1.1: Data Science Venn Diagram from Steven Geringer

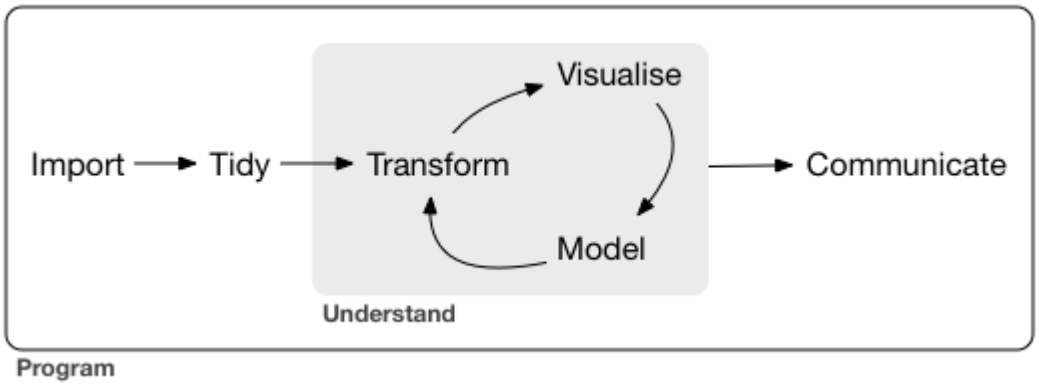


Figure 1.2: Source: R for Data Science: Introduction

1.3 What Will We Discuss in 431?

We'll discuss each of these elements in the 431 course, focusing at the start on understanding our data through transformation, modeling and (especially in the early stages) visualization. In 431, we learn how to get things done.

- We get people working with R and R Studio and R Markdown, even if they are completely new to coding. A gentle introduction is provided at Ismay and Kim (2017)
- We learn how to use the `tidyverse` (http://www.tidyverse.org/), an array of tools in R (mostly developed by Hadley Wickham and his colleagues at R Studio) which share an underlying philosophy to make data science faster, easier, more reproducible and more fun. A critical text for understanding the tidyverse is Grolemund and Wickham (2017). Tidyverse tools facilitate:
  - **importing** data into R, which can be the source of intense pain for some things, but is really quite easy 95% of the time with the right tool.
  - **tidying** data, that is, storing it in a format that includes one row per observation and one column per variable. This is harder, and more important, than you might think.
  - **transforming** data, perhaps by identifying specific subgroups of interest, creating new variables based on existing ones, or calculating summaries.
  - **visualizing** data to generate actual knowledge and identify questions about the data - this is an area where R really shines, and we'll start with it in class.
  - **modeling** data, taking the approach that modeling is complementary to visualization, and allows us to answer questions that visualization helps us identify.
  - and last, but definitely not least, **communicating** results, models and visualizations to others, in a way that is reproducible and effective.
- Some programming/coding is an inevitable requirement to accomplish all of these aims. If you are leery of coding, you'll need to get past that, with the help of this course and our stellar teaching assistants. Getting started is always the most challenging part, but our experience is that most of the pain of developing these new skills evaporates by early October.
- Having completed some fundamental work in Part A of the course, we then learn how to use a variety of R packages and statistical methods to accomplish specific inferential tasks (in Part B, mostly) and modeling tasks (in Part C, mostly.)

Chapter 2

Setting Up R

These Notes make extensive use of

- the statistical software language R, and
- the development environment R Studio

both of which are free, and you'll need to install them on your machine. Instructions for doing so are in found in the course syllabus.

If you need an even gentler introduction, or if you're just new to R and RStudio and need to learn about them, we encourage you to take a look at http://moderndive.com/, which provides an introduction to statistical and data sciences via R at Ismay and Kim (2017).

2.1 R Markdown

These notes were written using R Markdown. R Markdown, like R and R Studio, is free and open source.

R Markdown is described as an *authoring framework* for data science, which lets you

- save and execute R code
- generate high-quality reports that can be shared with an audience

This description comes from http://rmarkdown.rstudio.com/lesson-1.html which you can visit to get an overview and quick tour of what's possible with R Markdown.

Another excellent resource to learn more about R Markdown tools is the Communicate section (especially the R Markdown chapter) of Grolemund and Wickham (2017).

2.2 R Packages

To start, I'll present a series of commands I run at the beginning of these Notes. These particular commands set up the output so it will look nice as either an HTML or PDF file, and also set up R to use several packages (libraries) of functions that expand its capabilities. A chunk of code like this will occur near the top of any R Markdown work.

```
knitr::opts_chunk$set(comment = NA)

library(boot); library(devtools); library(forcats)
library(grid); library(knitr); library(pander)
```

```
library(pwr); library(viridis); library(NHANES)
library(tidyverse)
```

I have deliberately set up this list of loaded packages/libraries to be relatively small, and will add some other packages later, as needed. You only need to install a package once, but you need to reload it every time you start a new session.

2.3 Other Packages

I will also make use of functions in the following packages/libraries, but when I do so, I will explicitly specify the package name, using a command like `Hmisc::describe(x)`, rather than just `describe(x)`, so as to specify that I want the Hmisc package's version of `describe` applied to whatever `x` is. Those packages are:

- `aplpack` which provides `stem.leaf` and `stem.leaf.backback` for building fancier stem-and-leaf displays
- `arm` which provides a set of functions for model building and checking that are used in Gelman and Hill (2007)
- `car` which provides some tools for building scatterplot matrices, but also many other functions described in Fox and Weisberg (2011)
- `Epi` for 2x2 table analyses and materials for classical epidemiology: http://BendixCarstensen.com/Epi/
- `GGally` for scatterplot and correlation matrix visualizations: http://ggobi.github.io/ggally/
- `gridExtra` which includes a variety of functions for manipulating graphs: https://github.com/baptiste/gridextra
- `Hmisc` from Frank Harrell at Vanderbilt U., for its version of `describe` and for many regression modeling functions we'll use in 432. Details on Hmisc are at http://biostat.mc.vanderbilt.edu/wiki/Main/Hmisc. Frank has written several books - the most useful of which for 431 students is probably Harrell and Slaughter (2017)
- `mice`, which we'll use (a little) in 431 for multiple imputation to deal with missing data: http://www.stefvanbuuren.nl/mi/
- `mosaic`, mostly for its `favstats` summary, but Project MOSAIC is a community of educators you might be interested in: http://mosaic-web.org/
- `psych` for its own version of `describe`, but other features are described at http://personality-project.org/r/psych/

We also will use a package called `xda` for two functions called `numSummary` and `charSummary`, but that package gets loaded via `devtools` and GitHub by the code in these Notes.

When compiling the Notes from the original code files, these packages will need to be installed (but not loaded) in R, or an error will be thrown when compiling this document. To install all of the packages used within these Notes, type in (or copy and paste) the following commands and run them in the R Console. Again, you only need to install a package once, but you need to reload it every time you start a new session.

```
pkgs <- c("aplpack", "arm", "boot", "car", "devtools", "Epi", "forcats", "GGally",
          "gridExtra", "Hmisc", "knitr", "mice", "mosaic", "NHANES", "pander",
          "psych", "pwr", "tidyverse", "viridis")
install.packages(pkgs)
```

Part A. Exploring Data

Chapter 3

Visualizing Data

Part A of these Notes is designed to ease your transition into working effectively with data, so that you can better understand it. We'll start by visualizing some data from the US National Health and Nutrition Examination Survey, or NHANES. We'll display R code as we go, but we'll return to all of the key coding ideas involved later in the Notes.

3.1 The NHANES data: Collecting a Sample

To begin, we'll gather a random sample of 1,000 subjects participating in NHANES, and then identify several variables of interest about those subjects[1]. The motivation for this example came from a Figure in Baumer, Kaplan, and Horton (2017).

```
library(NHANES) # load the NHANES package/library of functions, data

set.seed(431001)
# use set.seed to ensure that we all get the same random sample
# of 1,000 NHANES subjects in our nh_data collection

nh_data <- sample_n(NHANES, size = 1000) %>%
    select(ID, Gender, Age, Height, Weight, BMI, Pulse, Race1, HealthGen, Diabetes)

nh_data
```

```
# A tibble: 1,000 x 10
      ID Gender   Age Height Weight   BMI Pulse    Race1 HealthGen
   <int> <fctr> <int>  <dbl>  <dbl> <dbl> <int>   <fctr>    <fctr>
 1 59640   male    54  175.7  129.0 41.79    74    White      Good
 2 59826 female    67  156.5   50.2 20.50    66    White     Vgood
 3 56340   male     9  128.3   23.3 14.15    86    Black        NA
 4 56747   male    33  194.2  105.1 27.87    68    White     Vgood
 5 51754 female    58  167.2  106.0 37.92    70    White        NA
 6 52712   male     6  108.6   16.9 14.33    NA    White        NA
 7 63908   male    55  168.6   90.6 31.90    62 Mexican     Vgood
 8 60865 female    25  155.5   55.0 22.75    58    Other     Vgood
 9 66642   male    41  177.9   89.3 28.20    72    White     Vgood
10 59880 female    45  163.2   98.3 36.91    80 Hispanic      Good
```

[1]For more on the NHANES data available in the NHANES package, type ?NHANES in the Console in R Studio.

```
# ... with 990 more rows, and 1 more variables: Diabetes <fctr>
```

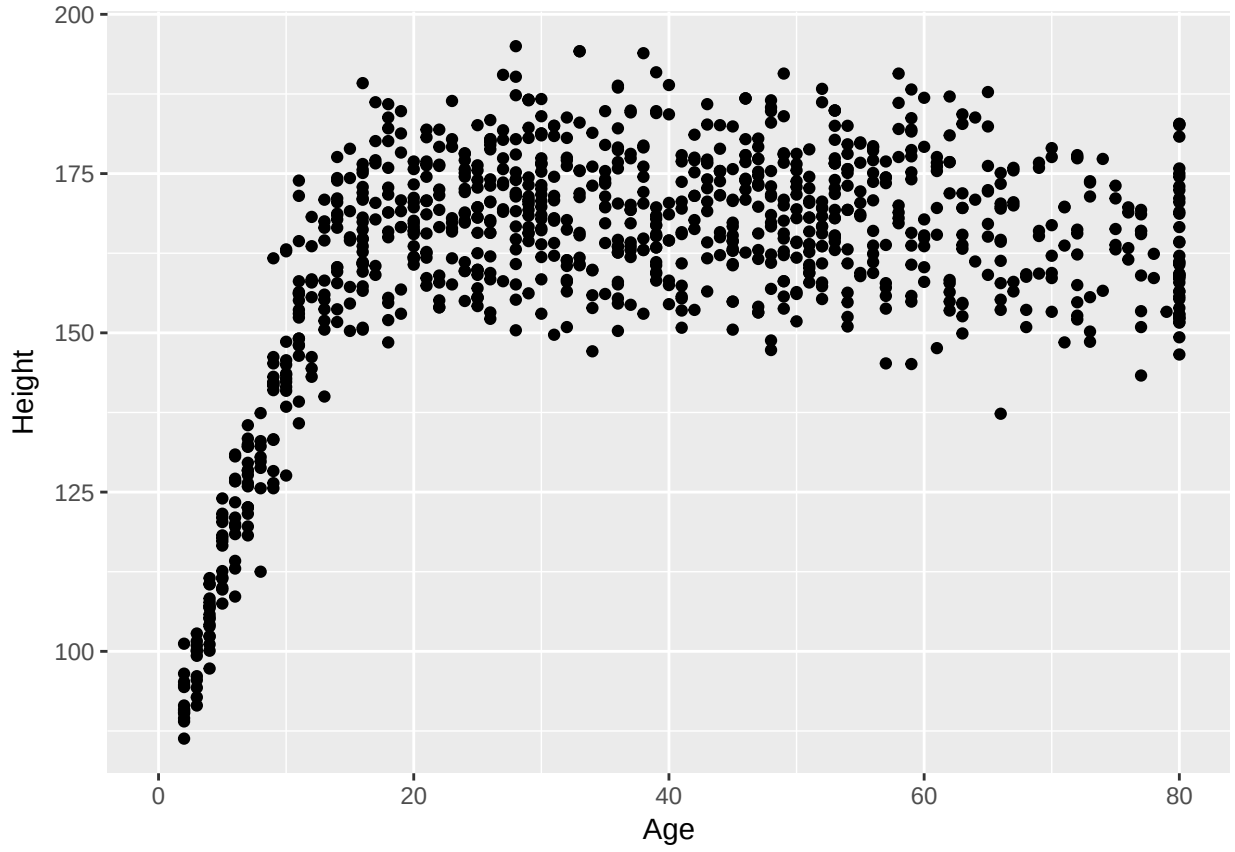
We have 1000 rows (observations) and 10 columns (variables) that describe the subjects listed in the rows.

3.2 Age and Height

Suppose we want to visualize the relationship of Height and Age in our 1,000 NHANES observations. The best choice is likely to be a scatterplot.

```
ggplot(data = nh_data, aes(x = Age, y = Height)) +
    geom_point()
```

```
Warning: Removed 25 rows containing missing values (geom_point).
```



We note several interesting results here.

1. As a warning, R tells us that it has "Removed 25 rows containing missing values (geom_point)." Only 975 subjects plotted here, because the remaining 25 people have missing (NA) values for either Height, Age or both.
2. Unsurprisingly, the measured Heights of subjects grow from Age 0 to Age 20 or so, and we see that a typical Height increases rapidly across these Ages. The middle of the distribution at later Ages is pretty consistentat at a Height somewhere between 150 and 175. The units aren't specified, but we expect they must be centimeters. The Ages are clearly reported in Years.
3. No Age is reported over 80, and it appears that there is a large cluster of Ages at 80. This may be due to a requirement that Ages 80 and above be reported at 80 so as to help mask the identity of those

individuals.[2]

As in this case, we're going to build most of our visualizations using tools from the `ggplot2` package, which is part of the `tidyverse` series of packages. You'll see similar coding structures throughout this Chapter, most of which are covered as well in Chapter 3 of Grolemund and Wickham (2017).

3.3 Subset of Subjects with Known Age and Height

Before we move on, let's manipulate the data set a bit, to focus on only those subjects who have complete data on both Age and Height. This will help us avoid that warning message.

```
nh_dat2 <- nh_data %>%
    filter(complete.cases(Age, Height))

summary(nh_dat2)
```

```
       ID           Gender         Age             Height
 Min.   :51654   female:498   Min.   : 2.00   Min.   : 86.3
 1st Qu.:56753   male  :477   1st Qu.:20.00   1st Qu.:156.4
 Median :61453                Median :36.00   Median :165.8
 Mean   :61602                Mean   :37.27   Mean   :161.7
 3rd Qu.:66484                3rd Qu.:53.00   3rd Qu.:174.1
 Max.   :71826                Max.   :80.00   Max.   :195.0

     Weight            BMI             Pulse            Race1
 Min.   : 12.50   Min.   :13.17   Min.   : 42.00   Black   :112
 1st Qu.: 57.60   1st Qu.:21.60   1st Qu.: 66.00   Hispanic: 69
 Median : 73.40   Median :26.10   Median : 72.00   Mexican :104
 Mean   : 73.41   Mean   :26.96   Mean   : 73.75   White   :607
 3rd Qu.: 90.20   3rd Qu.:31.10   3rd Qu.: 82.00   Other   : 83
 Max.   :198.70   Max.   :80.60   Max.   :124.00
 NA's   :2        NA's   :2       NA's   :120
     HealthGen   Diabetes
 Excellent: 87   No  :910
 Vgood    :276   Yes : 64
 Good     :276   NA's:  1
 Fair     :103
 Poor     : 15
 NA's     :218
```

Note that the units and explanations for these variables are contained in the NHANES help file, available via ?NHANES in the Console of R Studio.

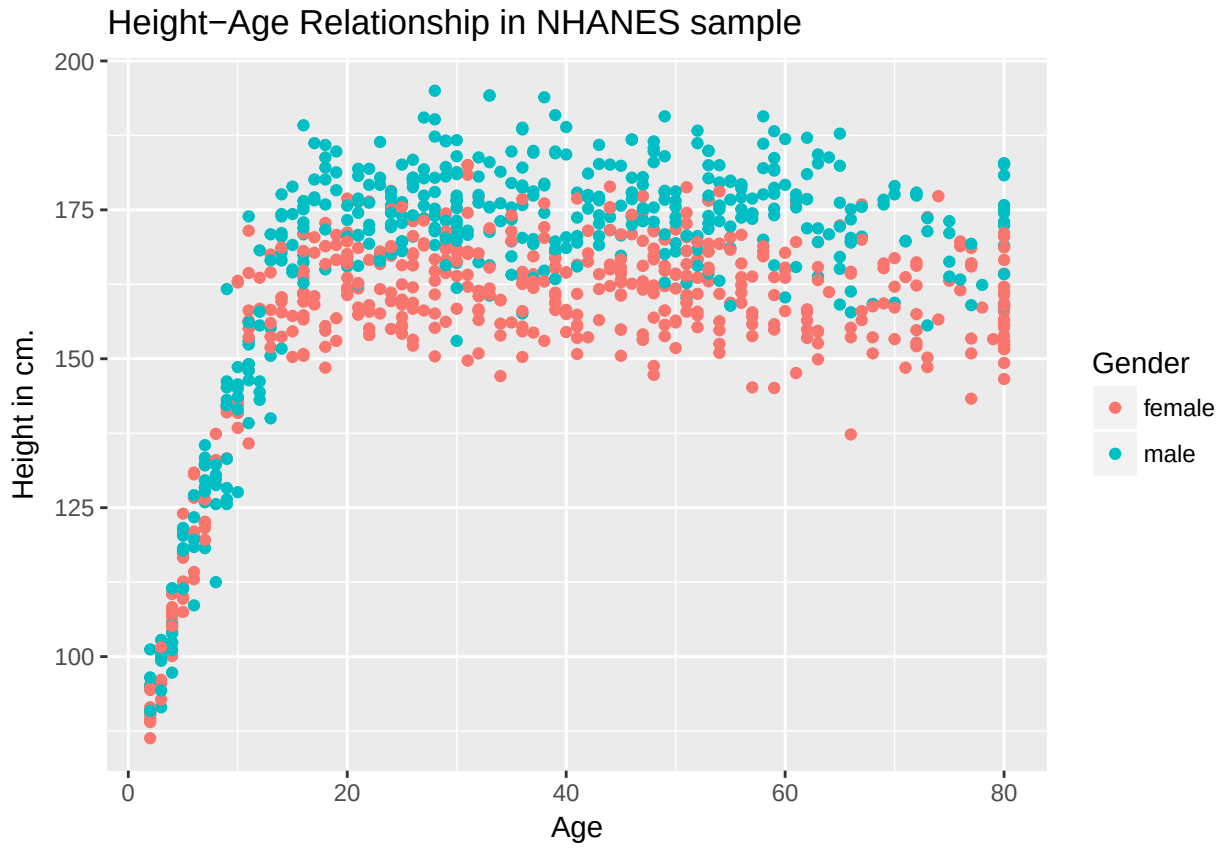
3.4 Age-Height and Gender?

Let's add Gender to the plot using color, and also adjust the y axis label to incorporate the units of measurement.

```
ggplot(data = nh_dat2, aes(x = Age, y = Height, color = Gender)) +
    geom_point() +
```

[2] If you visit the NHANES help file with ?NHANES, you will see that subjects 80 years or older were indeed recorded as 80.

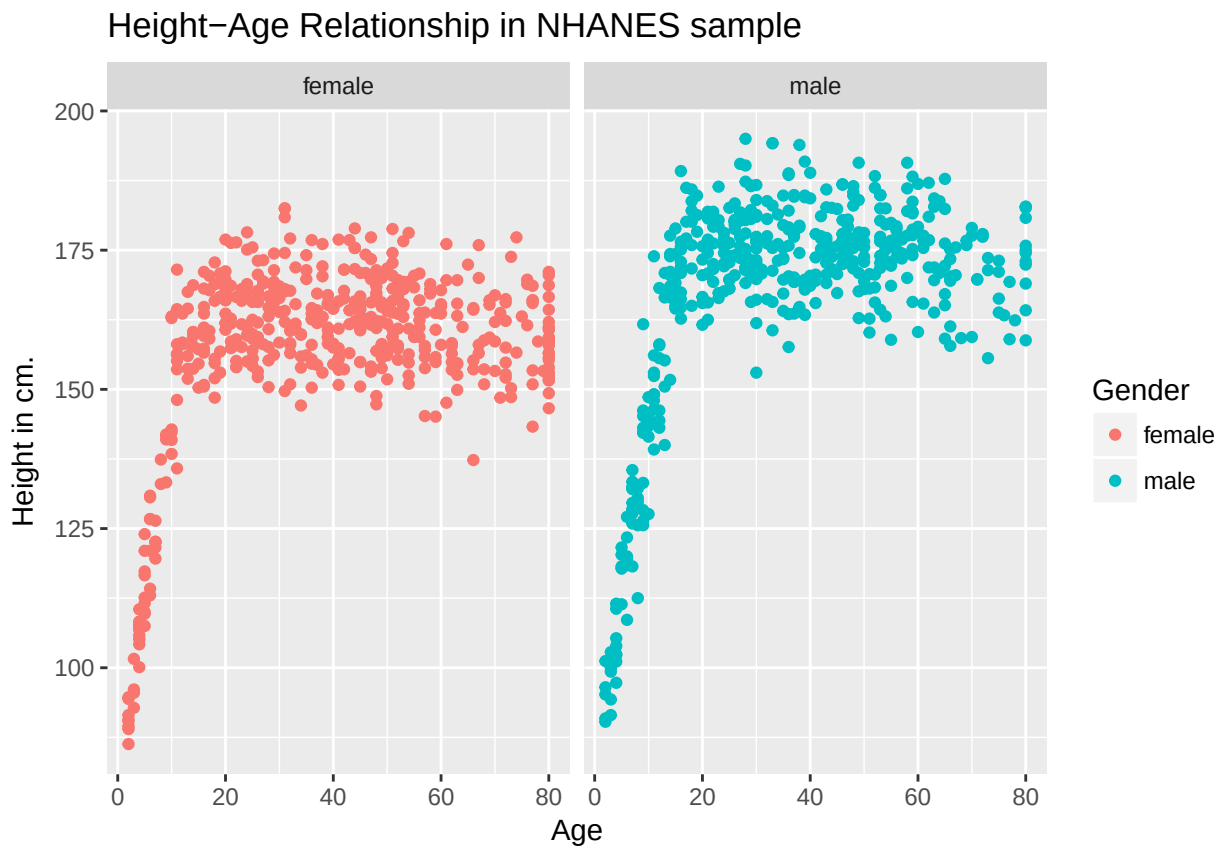
```
    labs(title = "Height-Age Relationship in NHANES sample",
         y = "Height in cm.")
```



3.4.1 Can we show the Female and Male relationships in separate panels?

Sure.

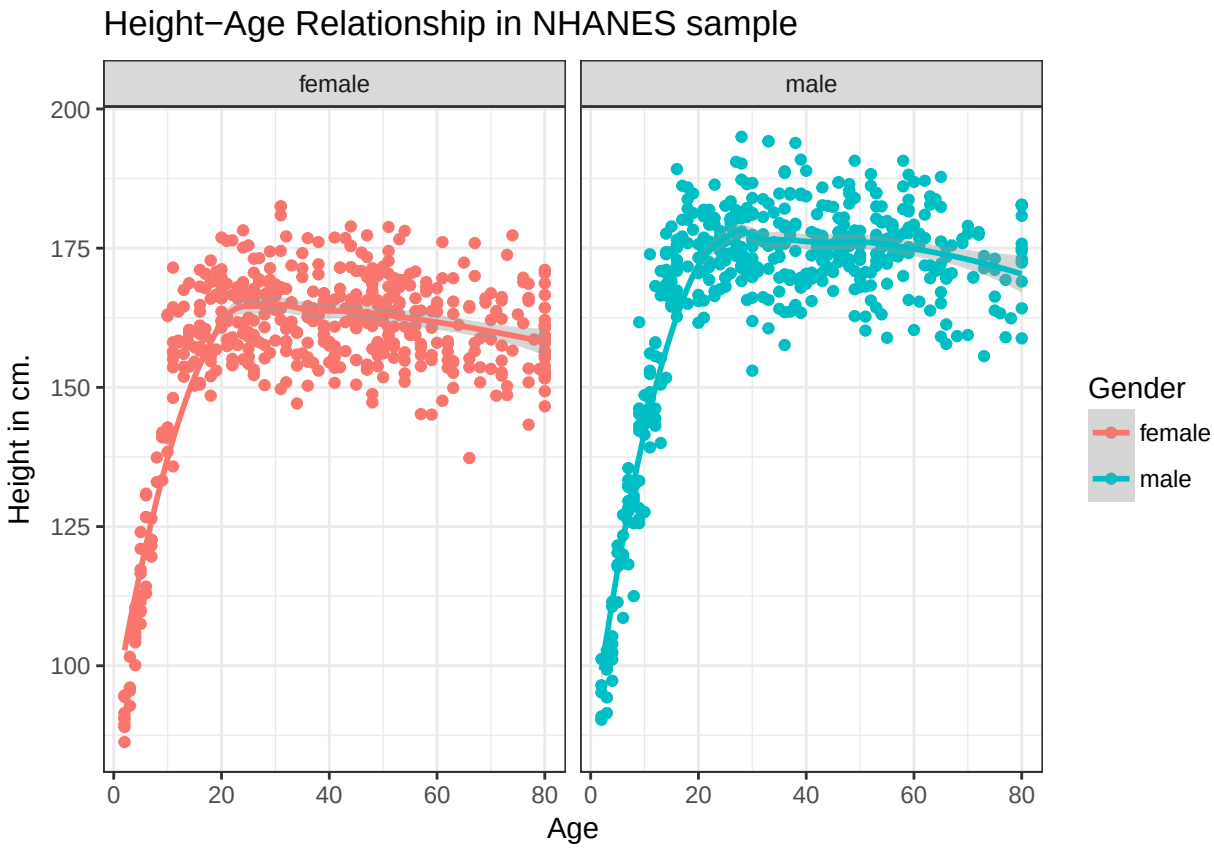
```
ggplot(data = nh_dat2, aes(x = Age, y = Height, color = Gender)) +
    geom_point() +
    labs(title = "Height-Age Relationship in NHANES sample",
         y = "Height in cm.") +
    facet_wrap(~ Gender)
```



3.4.2 Can we add a smooth curve to show the relationship in each plot?

Yep, and let's change the theme of the graph to remove the gray background, too.

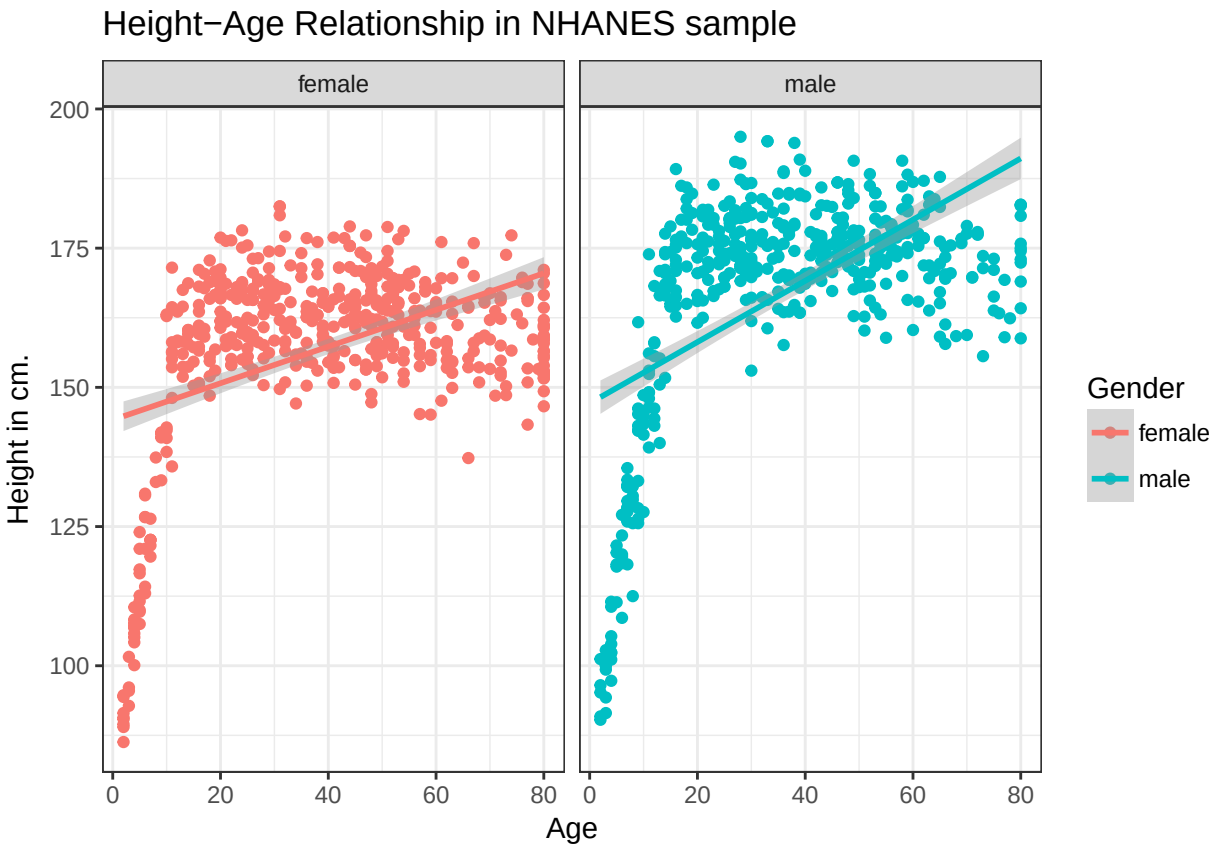
```
ggplot(data = nh_dat2, aes(x = Age, y = Height, color = Gender)) +
    geom_point() +
    geom_smooth(method = "loess") +
    labs(title = "Height-Age Relationship in NHANES sample",
         y = "Height in cm.") +
    theme_bw() +
    facet_wrap(~ Gender)
```



3.4.3 What if we want to assume straight line relationships?

We could look at a linear model in the plot. Does this make sense here?

```
ggplot(data = nh_dat2, aes(x = Age, y = Height, color = Gender)) +
    geom_point() +
    geom_smooth(method = "lm") +
    labs(title = "Height-Age Relationship in NHANES sample",
         y = "Height in cm.") +
    theme_bw() +
    facet_wrap(~ Gender)
```



3.5 A Subset: Ages 21-79

Suppose we wanted to look at a subset of our sample - those observations (subjects) whose Age is at least 21 and at most 79. We'll create that sample below, and also subset the variables to include nine of particular interest, and remove any observations with any missingness on *any* of the nine variables we're including here.

```
nh_data_2179 <- nh_data %>%
    filter(Age > 20 & Age < 80) %>%
    select(ID, Gender, Age, Height, Weight, BMI, Pulse, Race1, HealthGen, Diabetes) %>%
    na.omit

nh_data_2179
```

```
# A tibble: 594 x 10
      ID Gender   Age Height Weight   BMI Pulse    Race1 HealthGen
   <int> <fctr> <int>  <dbl>  <dbl> <dbl> <int>   <fctr>    <fctr>
 1 59640   male    54  175.7  129.0 41.79    74    White      Good
 2 59826 female    67  156.5   50.2 20.50    66    White     Vgood
 3 56747   male    33  194.2  105.1 27.87    68    White     Vgood
 4 63908   male    55  168.6   90.6 31.90    62  Mexican     Vgood
 5 60865 female    25  155.5   55.0 22.75    58    Other     Vgood
 6 66642   male    41  177.9   89.3 28.20    72    White     Vgood
 7 59880 female    45  163.2   98.3 36.91    80 Hispanic      Good
 8 71784 female    24  161.1   50.2 19.30    72    White     Vgood
 9 67616   male    63  184.3   70.0 20.60    82    White     Vgood
```

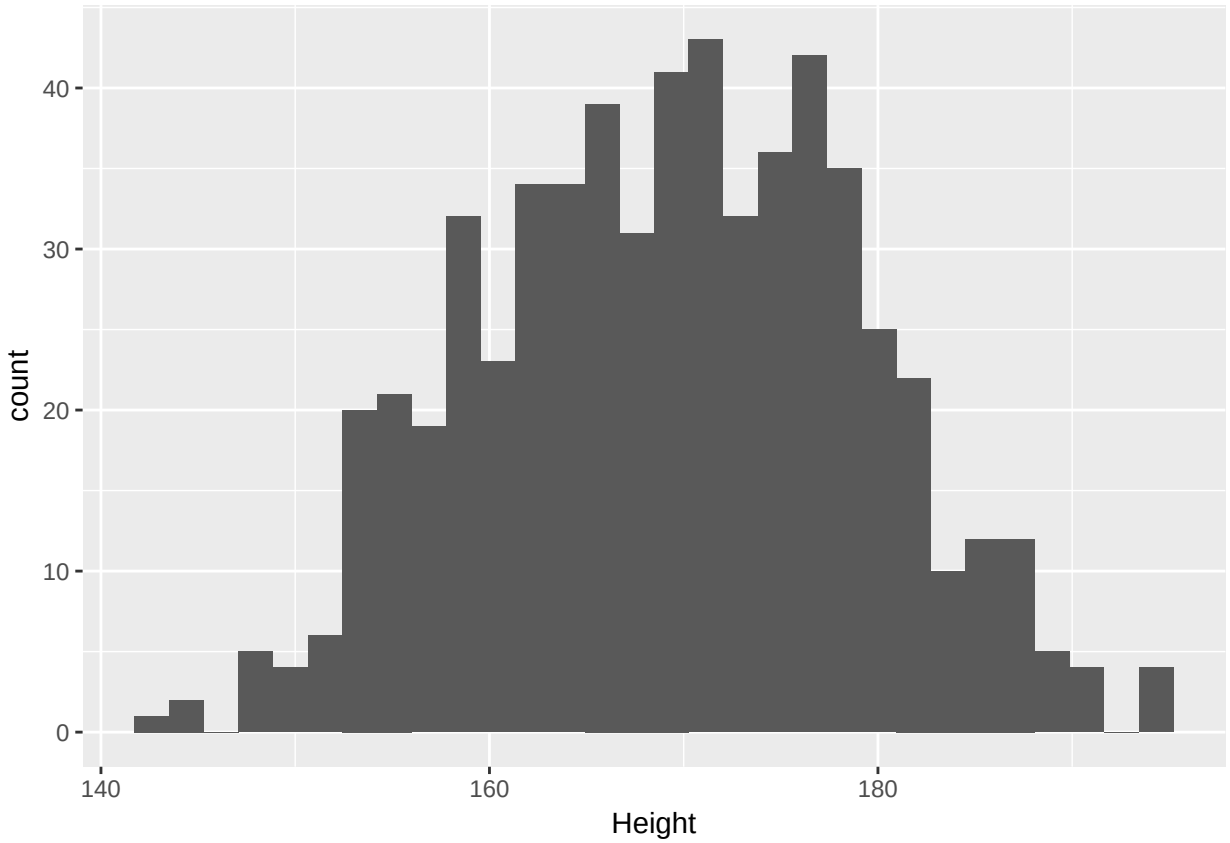
```
10 55391 female    32  161.4   69.2 26.56   114    Other      Good
# ... with 584 more rows, and 1 more variables: Diabetes <fctr>
```

3.6 Distribution of Heights

What is the distribution of height in this new sample?

```
ggplot(data = nh_data_2179, aes(x = Height)) +
    geom_histogram()
```

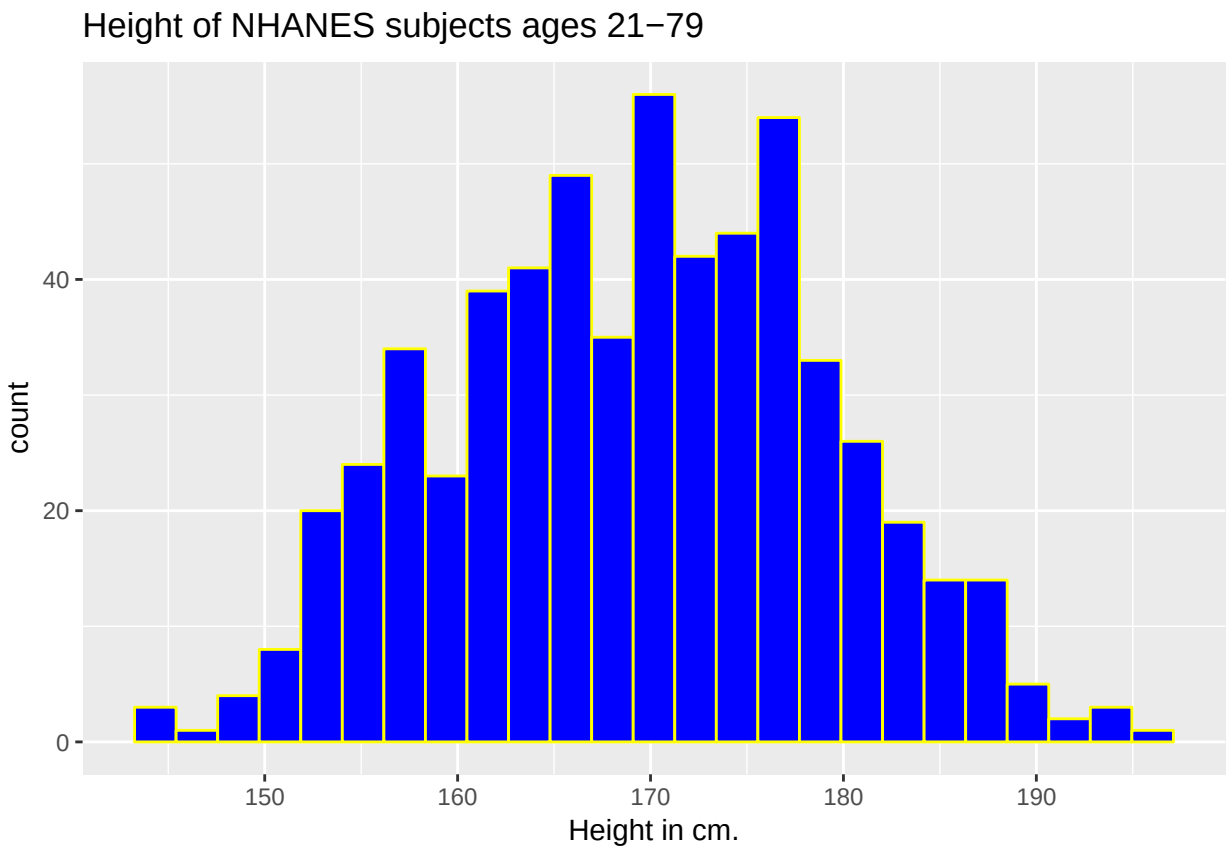
```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



We can do several things to clean this up.

1. We'll change the color of the lines for each bar of the histogram.
2. We'll change the fill inside each bar to make them stand out a bit more.
3. We'll add a title and relabel the horizontal (x) axis to include the units of measurement.
4. We'll avoid the warning by selecting a number of bins (we'll use 25 here) into which we'll group the heights before drawing the histogram.

```
ggplot(data = nh_data_2179, aes(x = Height)) +
    geom_histogram(bins = 25, col = "yellow", fill = "blue") +
    labs(title = "Height of NHANES subjects ages 21-79",
         x = "Height in cm.")
```

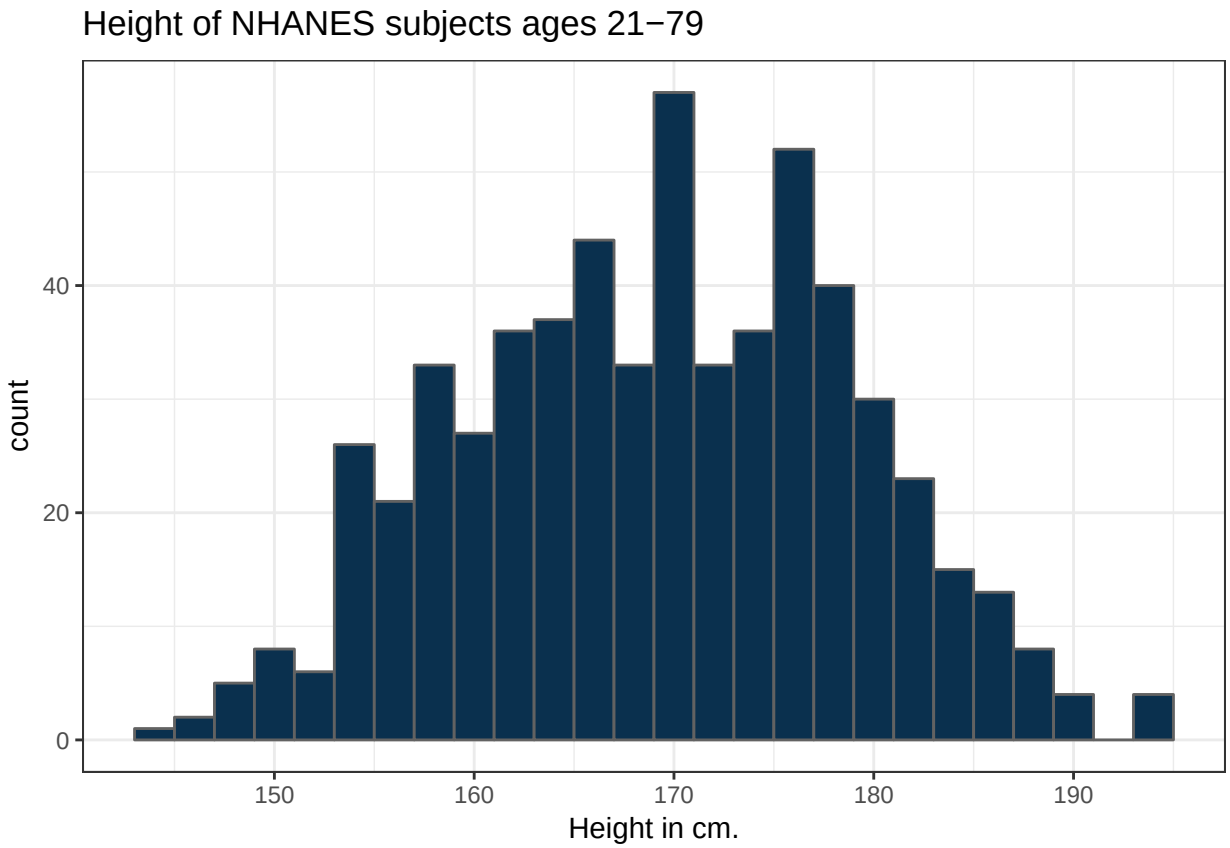


3.6.1 Changing a Histogram's Fill and Color

The CWRU color guide (https://case.edu/umc/our-brand/visual-guidelines/) lists the HTML color schemes for CWRU blue and CWRU gray. Let's match that color scheme.

```
cwru.blue <- '#0a304e'
cwru.gray <- '#626262'

ggplot(data = nh_data_2179, aes(x = Height)) +
    geom_histogram(binwidth = 2, col = cwru.gray, fill = cwru.blue) +
    labs(title = "Height of NHANES subjects ages 21-79",
         x = "Height in cm.") +
    theme_bw()
```

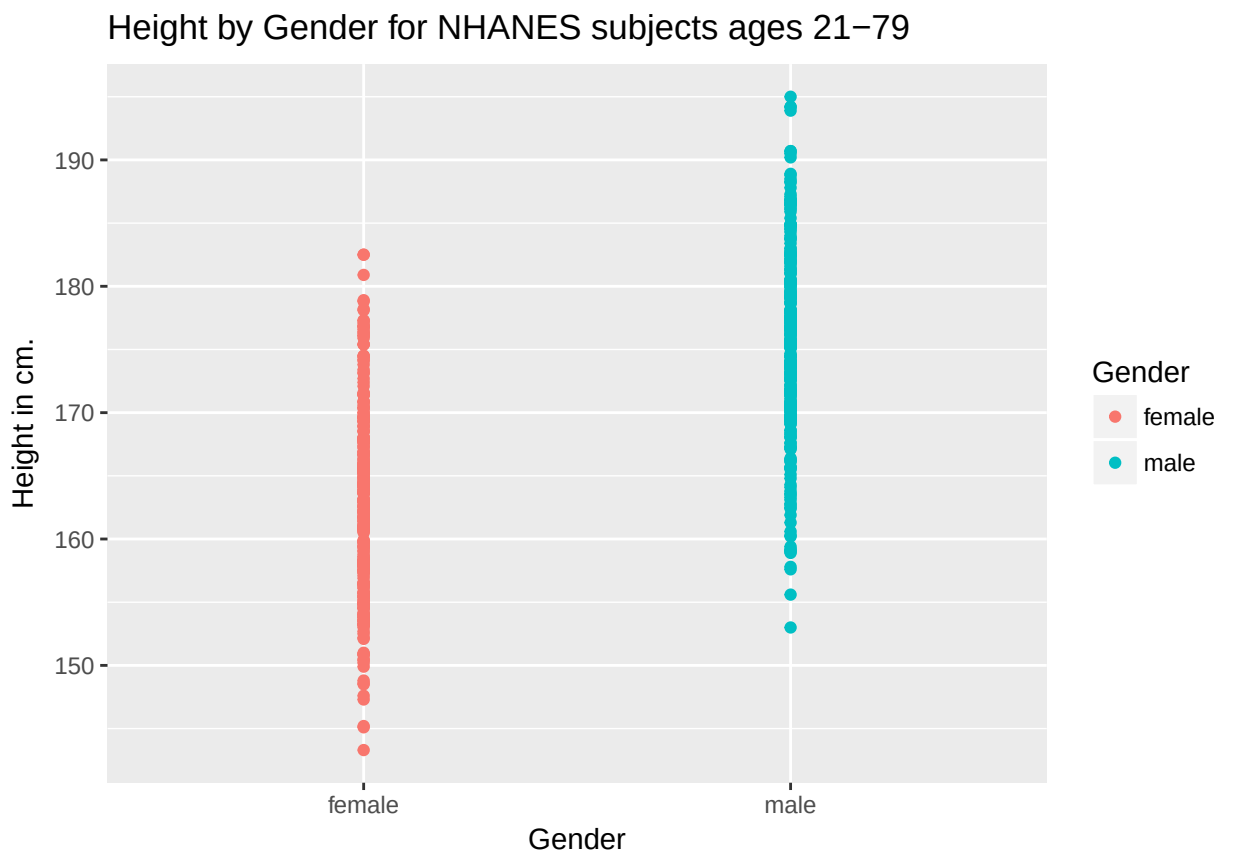


Note the other changes to the graph above.

1. We changed the theme to replace the gray background.
2. We changed the bins for the histogram, to gather observations into groups of 2 cm. each.

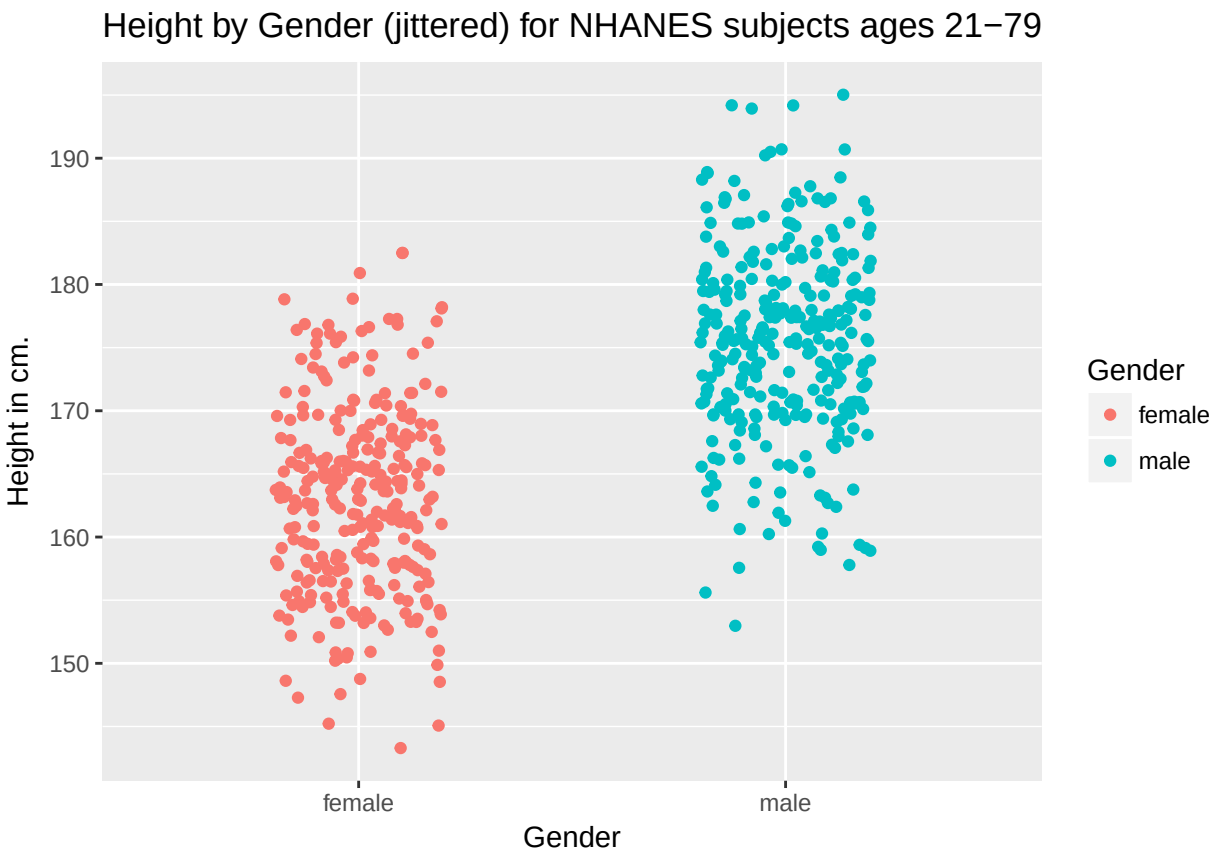
3.7 Height and Gender

```
ggplot(data = nh_data_2179, aes(x = Gender, y = Height, color = Gender)) +
    geom_point() +
    labs(title = "Height by Gender for NHANES subjects ages 21-79",
         y = "Height in cm.")
```



This plot isn't so useful. We can improve things a little by jittering the points horizontally, so that the overlap is reduced.

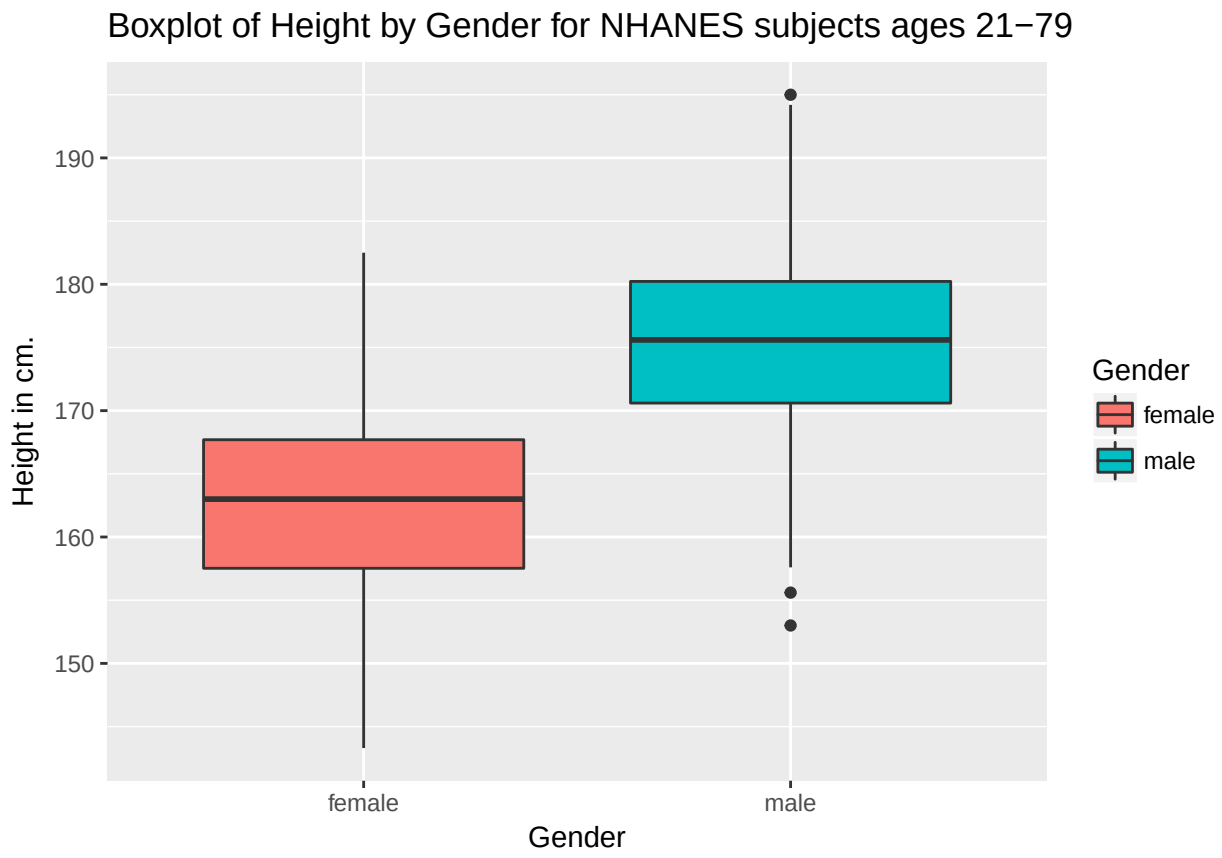
```
ggplot(data = nh_data_2179, aes(x = Gender, y = Height, color = Gender)) +
    geom_jitter(width = 0.2) +
    labs(title = "Height by Gender (jittered) for NHANES subjects ages 21-79",
         y = "Height in cm.")
```



Perhaps it might be better to summarize the distribution in a different way. We might consider a boxplot of the data.

3.7.1 A Boxplot of Height by Gender

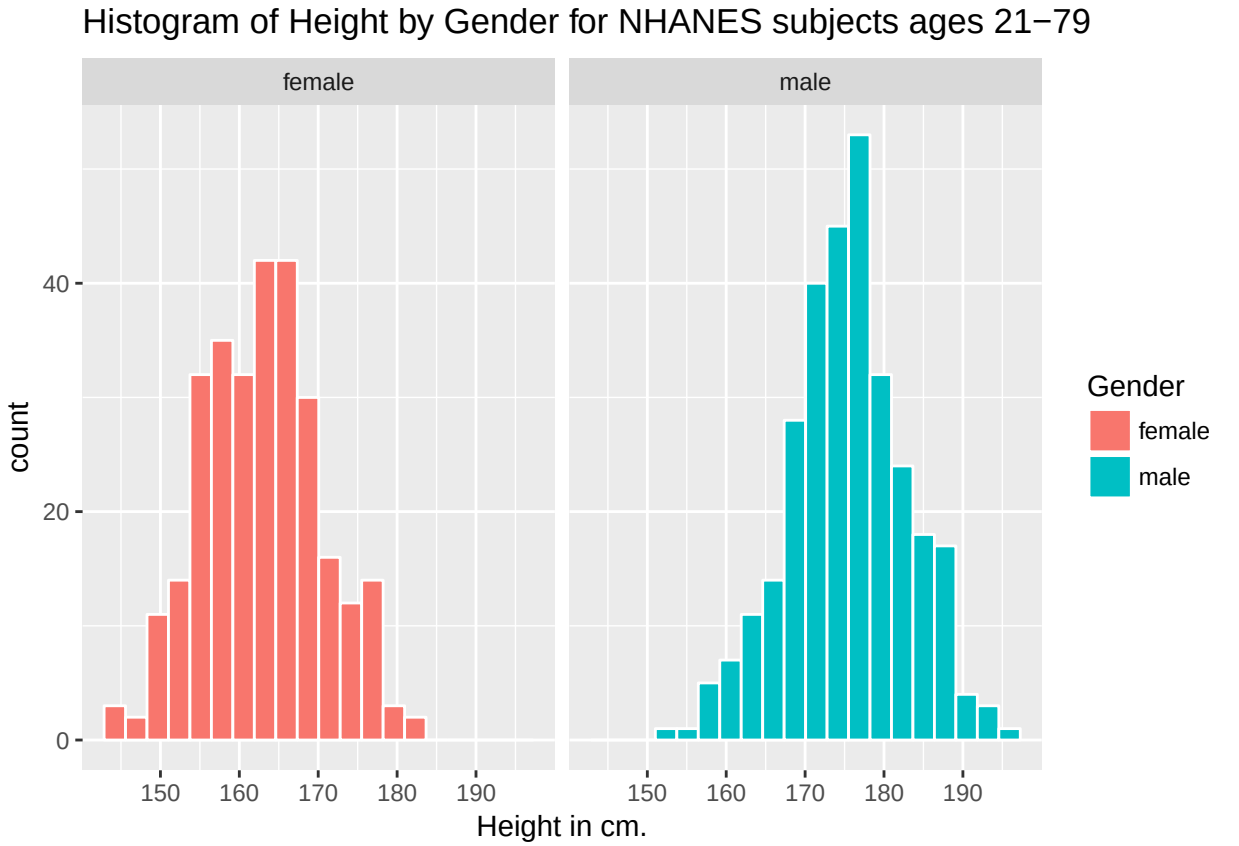
```
ggplot(data = nh_data_2179, aes(x = Gender, y = Height, fill = Gender)) +
    geom_boxplot() +
    labs(title = "Boxplot of Height by Gender for NHANES subjects ages 21-79",
         y = "Height in cm.")
```



Or perhaps we'd like to see a pair of histograms?

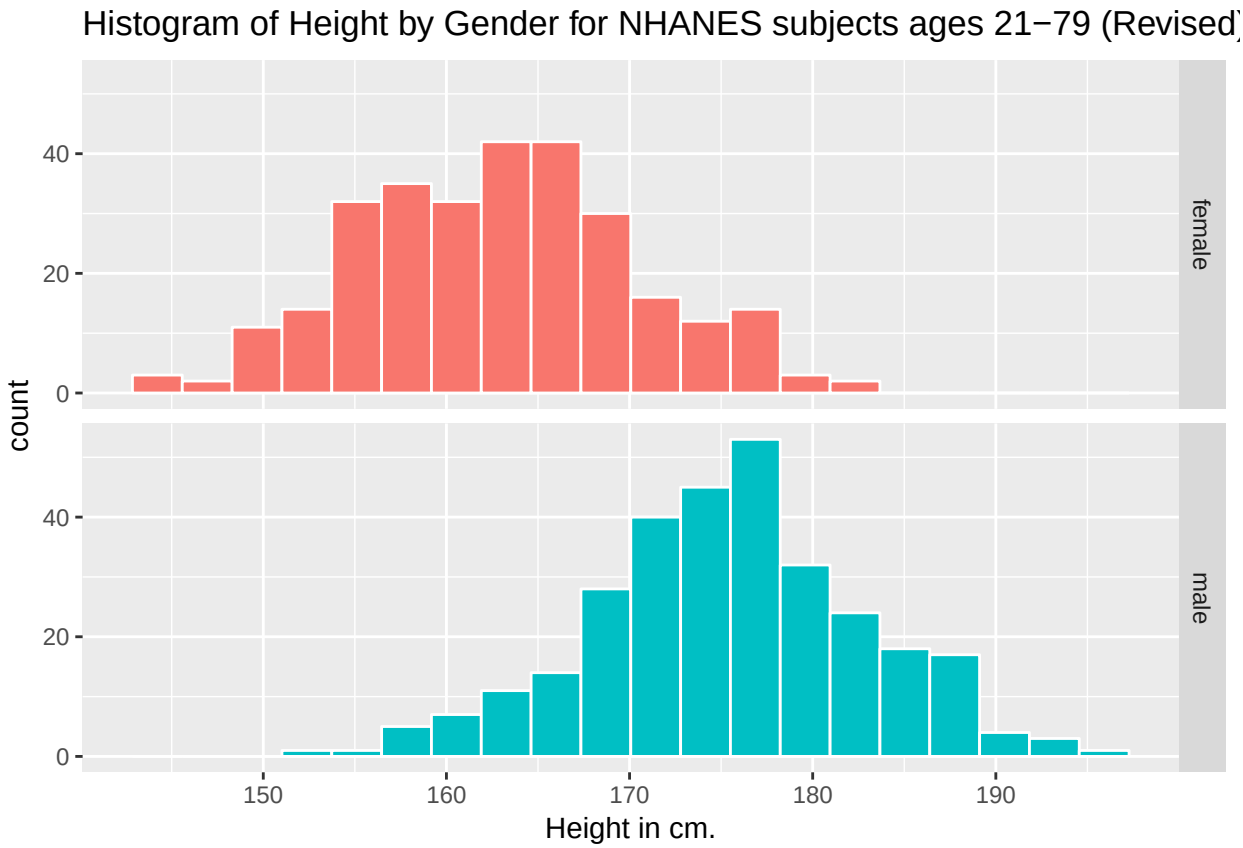
3.7.2 Histograms of Height by Gender

```
ggplot(data = nh_data_2179, aes(x = Height, fill = Gender)) +
    geom_histogram(color = "white", bins = 20) +
    labs(title = "Histogram of Height by Gender for NHANES subjects ages 21-79",
         x = "Height in cm.") +
    facet_wrap(~ Gender)
```



Can we redraw these histograms so that they are a little more comparable, and to get rid of the unnecessary legend?

```
ggplot(data = nh_data_2179, aes(x = Height, fill = Gender)) +
    geom_histogram(color = "white", bins = 20) +
    labs(title = "Histogram of Height by Gender for NHANES subjects ages 21-79 (Revised)",
         x = "Height in cm.") +
    guides(fill = FALSE) +
    facet_grid(Gender ~ .)
```



3.8 A Look at Body-Mass Index

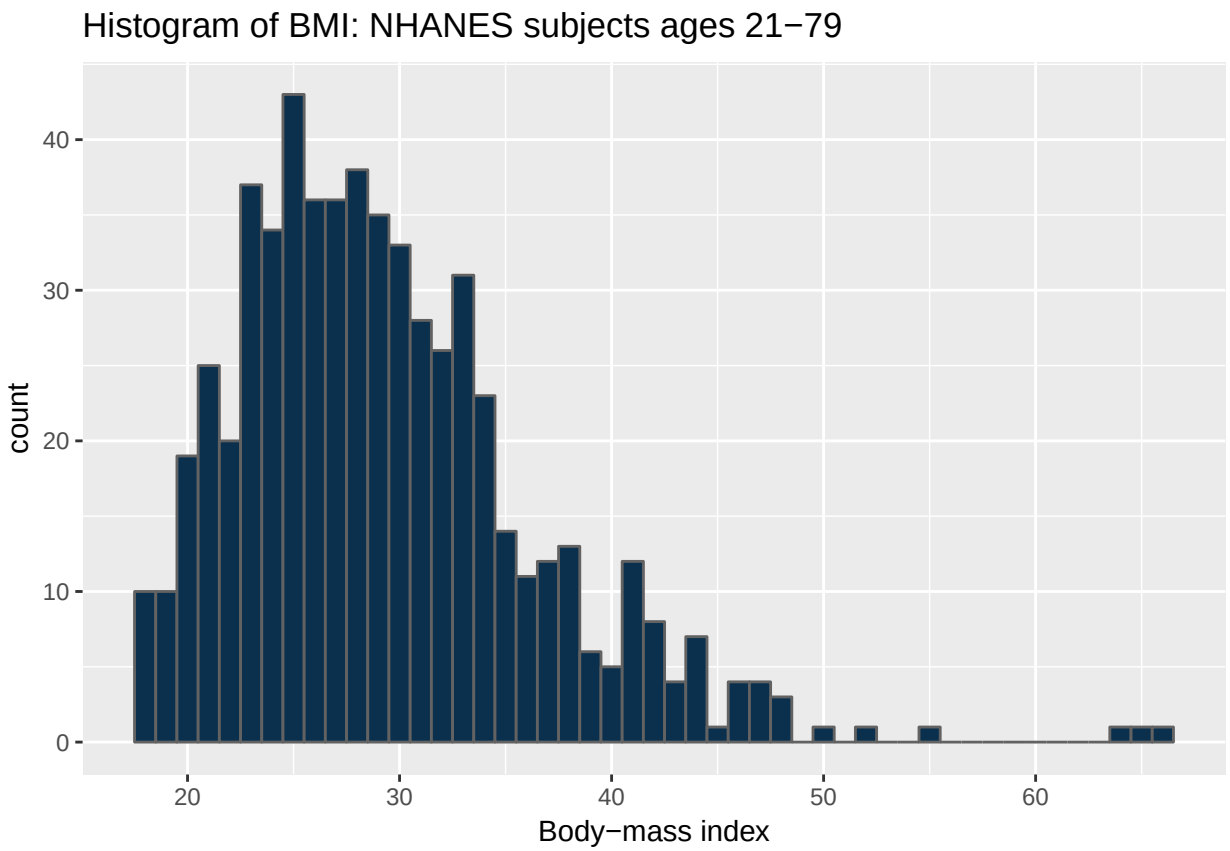
Let's look at a different outcome, the *body-mass index*, or BMI. The definition of BMI for adult subjects (which is expressed in units of kg/m^2) is:

$$\text{BMI} = \frac{\text{weight in kg}}{(\text{height in meters})^2} = 703 \times \frac{\text{weight in pounds}}{(\text{height in inches})^2}$$

> [BMI is essentially] ... a measure of a person's *thinness* or *thickness*... BMI was designed for use as a simple means of classifying average sedentary (physically inactive) populations, with an average body composition. For these individuals, the current value recommendations are as follow: a BMI from 18.5 up to 25 may indicate optimal weight, a BMI lower than 18.5 suggests the person is underweight, a number from 25 up to 30 may indicate the person is overweight, and a number from 30 upwards suggests the person is obese.
>
> Wikipedia, https://en.wikipedia.org/wiki/Body_mass_index

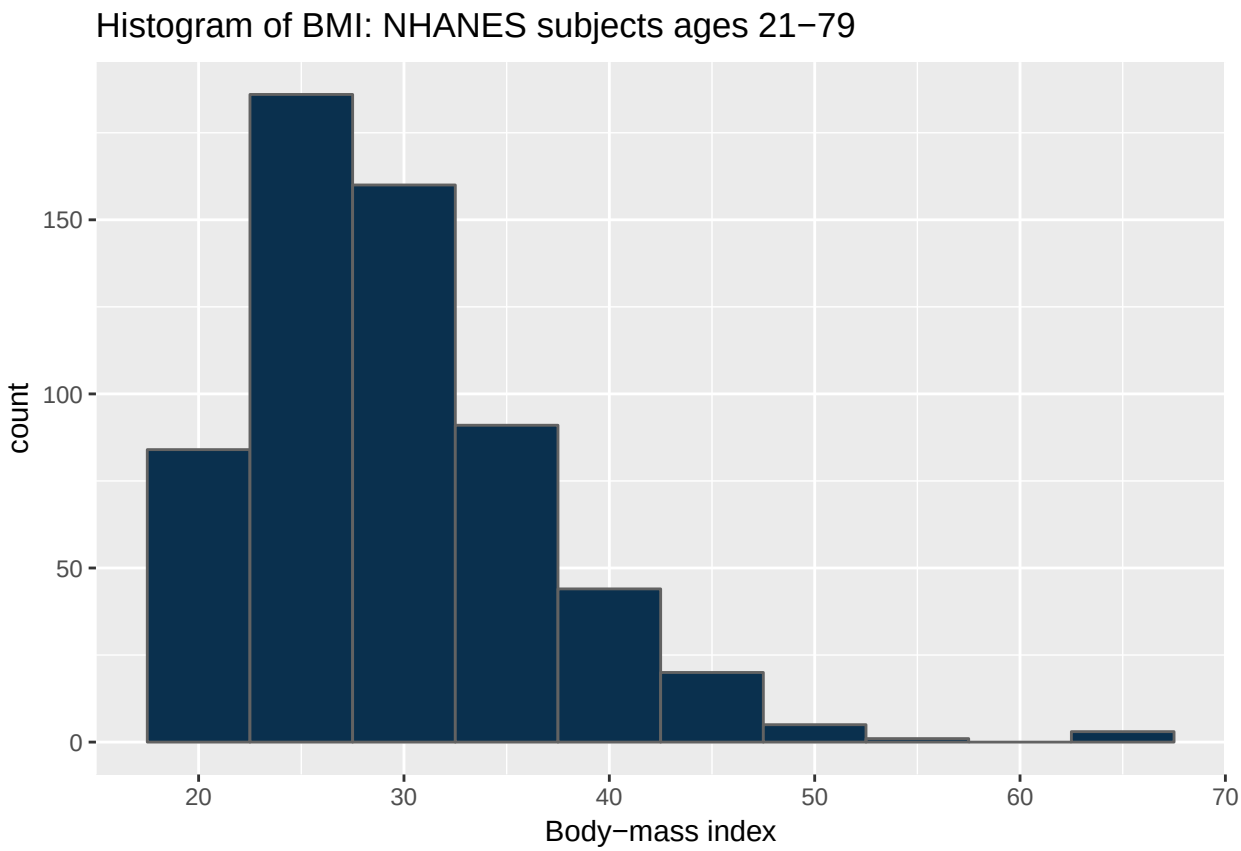
Here's a histogram, again with CWRU colors, for the BMI data.

```
ggplot(data = nh_data_2179, aes(x = BMI)) +
    geom_histogram(binwidth = 1, fill = cwru.blue, col = cwru.gray) +
    labs(title = "Histogram of BMI: NHANES subjects ages 21-79",
         x = "Body-mass index")
```



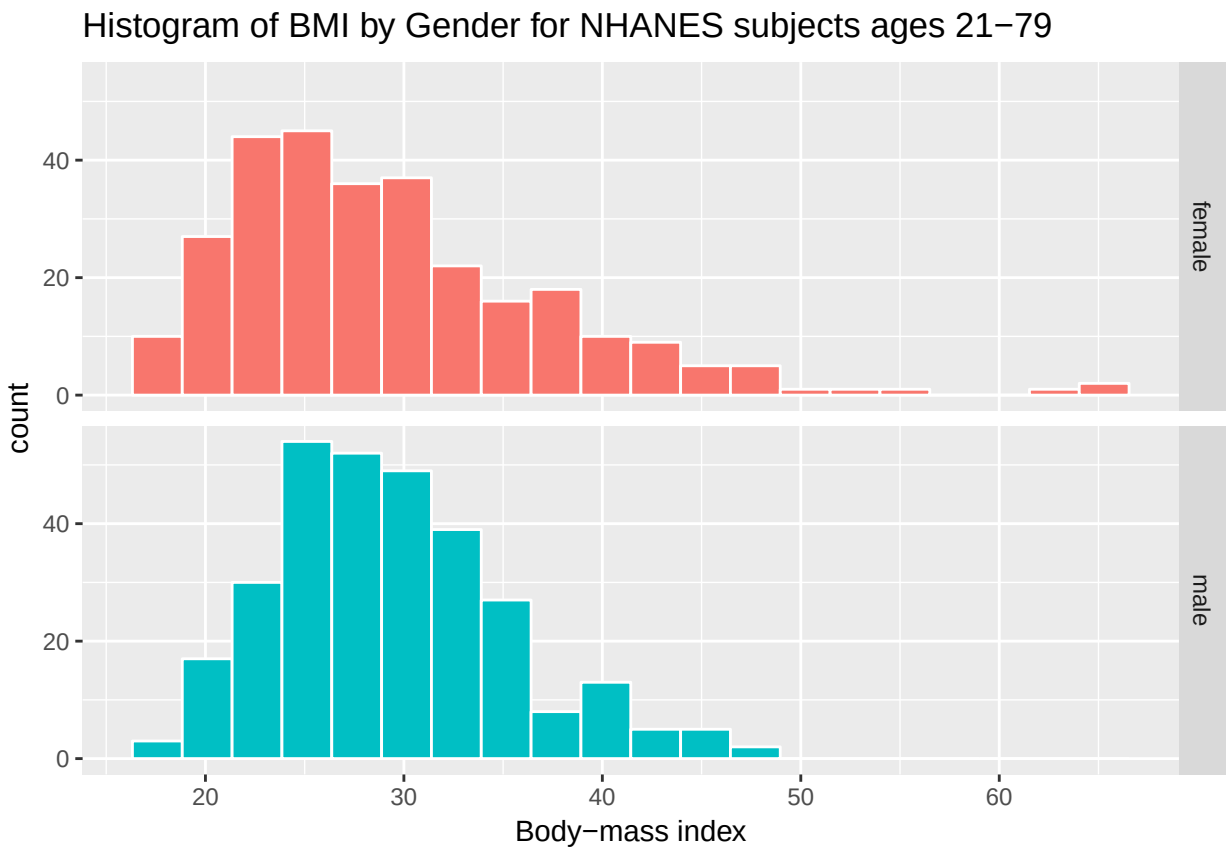
Note how different this picture looks if instead we bin up groups of 5 kg/m^2 at a time. Which is the more useful representation will depend a lot on what questions you're trying to answer.

```
ggplot(data = nh_data_2179, aes(x = BMI)) +
    geom_histogram(binwidth = 5, fill = cwru.blue, col = cwru.gray) +
    labs(title = "Histogram of BMI: NHANES subjects ages 21-79",
         x = "Body-mass index")
```



3.8.1 BMI by Gender

```
ggplot(data = nh_data_2179, aes(x = BMI, fill = Gender)) +
    geom_histogram(color = "white", bins = 20) +
    labs(title = "Histogram of BMI by Gender for NHANES subjects ages 21-79",
         x = "Body-mass index") +
    guides(fill = FALSE) +
    facet_grid(Gender ~ .)
```



As an accompanying numerical summary, we might ask how many people fall into each of these Gender categories, and what is their "average" BMI.

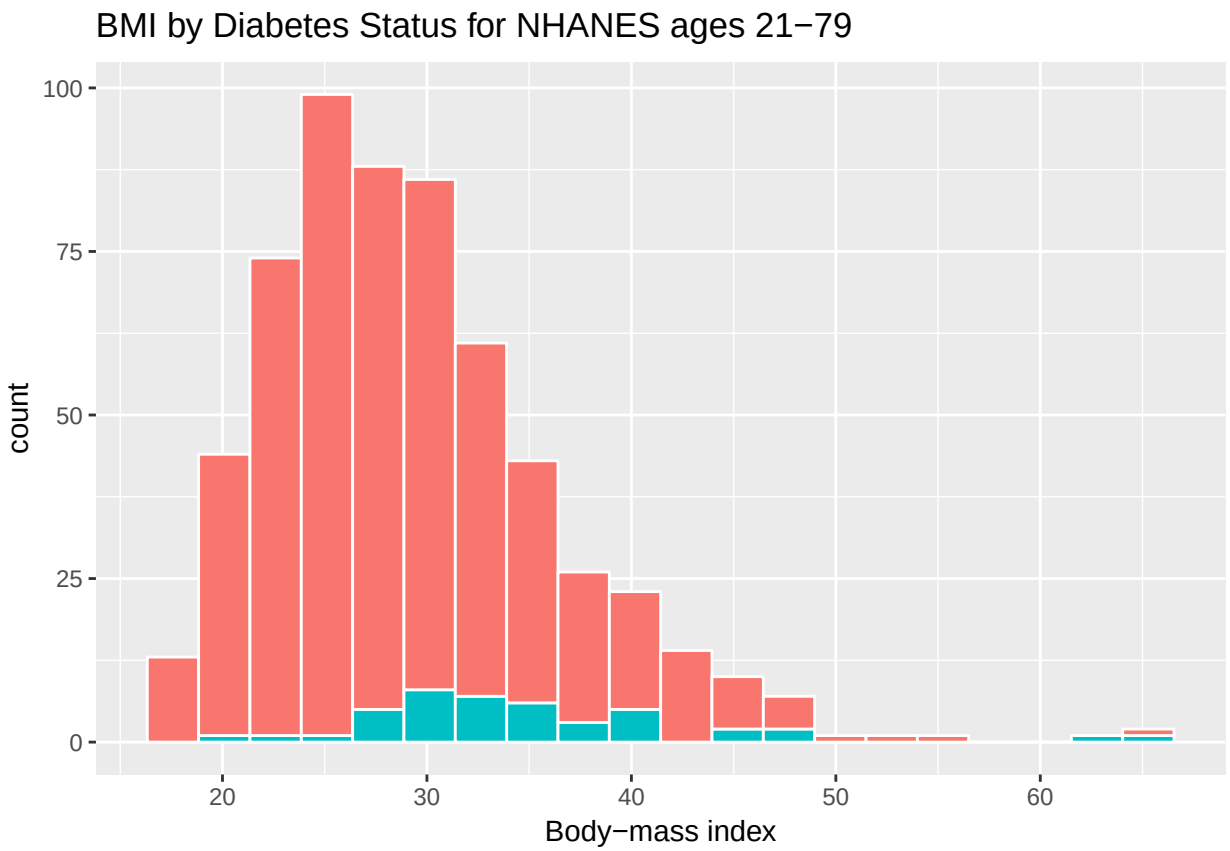
```
nh_data_2179 %>%
    group_by(Gender) %>%
    summarize(count = n(), mean(BMI), median(BMI)) %>%
    knitr::kable()
```

Gender	count	mean(BMI)	median(BMI)
female	290	29.35486	27.43
male	304	29.35773	28.69

3.8.2 BMI and Diabetes

We can split up our histogram into groups based on whether the subjects have been told they have diabetes.

```
ggplot(data = nh_data_2179, aes(x = BMI, fill = Diabetes)) +
    geom_histogram(color = "white", bins = 20) +
    labs(title = "BMI by Diabetes Status for NHANES ages 21-79",
         x = "Body-mass index") +
    guides(fill = FALSE)
```



How many people fall into each of these Diabetes categories, and what is their "average" BMI?

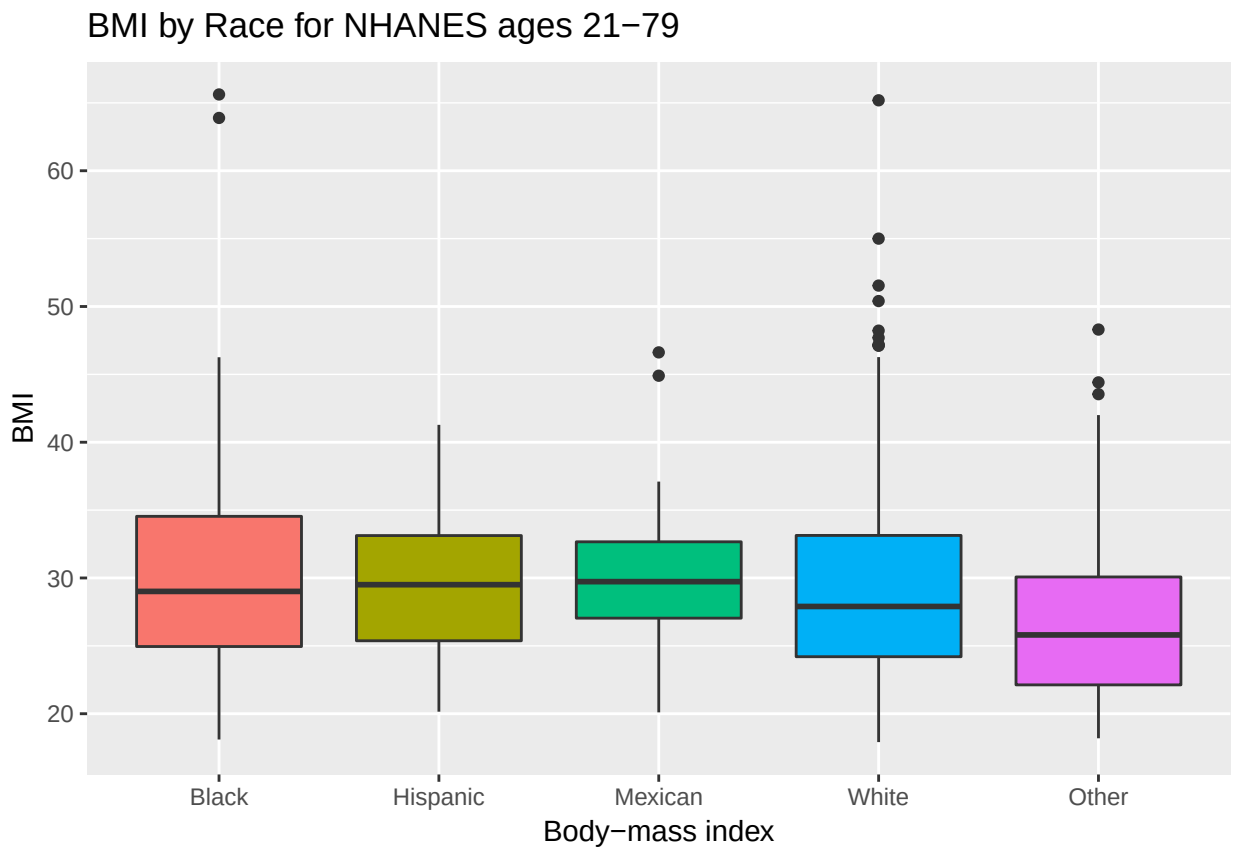
```
nh_data_2179 %>%
    group_by(Diabetes) %>%
    summarize(count = n(), mean(BMI), median(BMI)) %>%
    knitr::kable()
```

Diabetes	count	mean(BMI)	median(BMI)
No	551	28.89544	27.89
Yes	43	35.26209	33.43

3.8.3 BMI and Race

We can compare the distribution of BMI across Race groups, as well.

```
ggplot(data = nh_data_2179, aes(x = Race1, y = BMI, fill = Race1)) +
    geom_boxplot() +
    labs(title = "BMI by Race for NHANES ages 21-79",
         x = "Body-mass index") +
    guides(fill = FALSE)
```



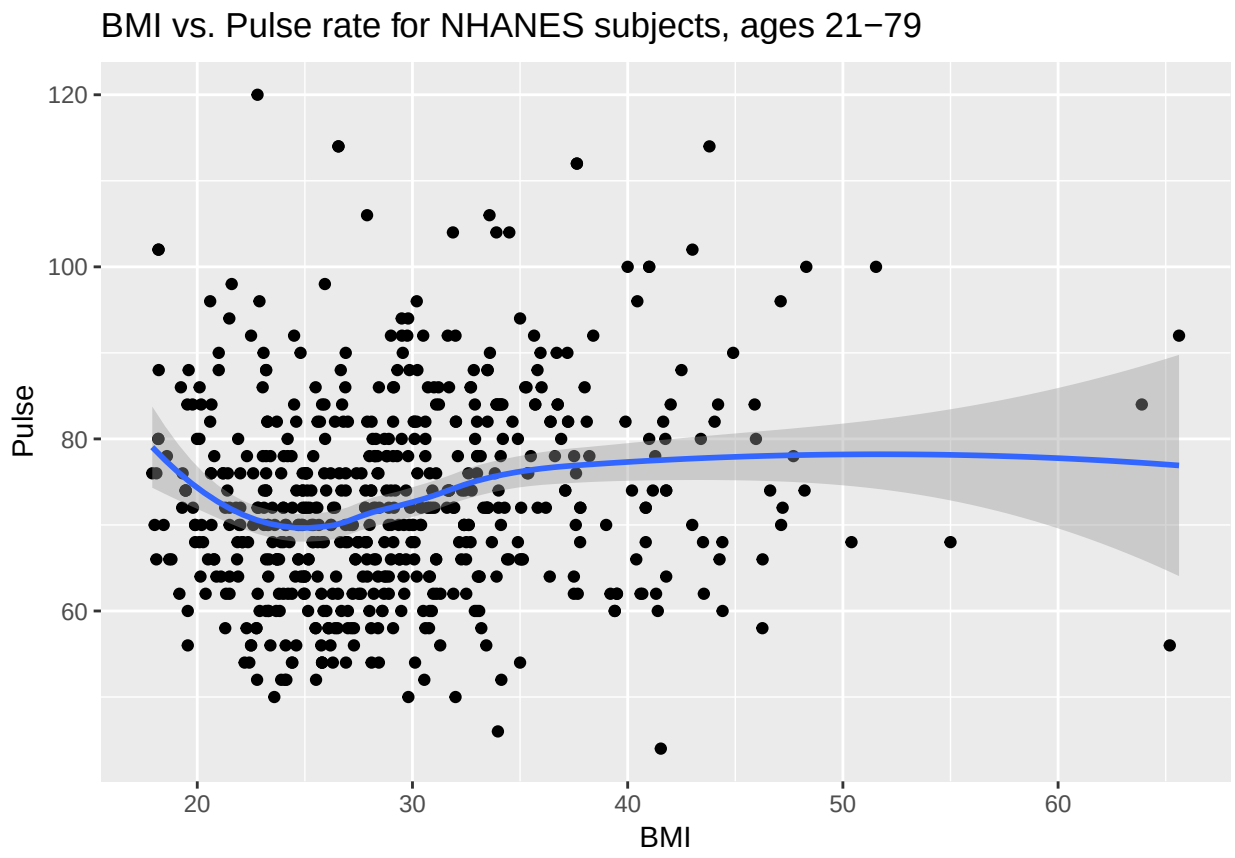
How many people fall into each of these Race1 categories, and what is their "average" BMI?

```
nh_data_2179 %>%
    group_by(Race1) %>%
    summarize(count = n(), mean(BMI), median(BMI)) %>%
    knitr::kable()
```

Race1	count	mean(BMI)	median(BMI)
Black	63	31.04444	29.010
Hispanic	44	29.36227	29.505
Mexican	50	29.97040	29.730
White	387	29.27326	27.900
Other	50	27.25300	25.805

3.8.4 BMI and Pulse Rate

```
ggplot(data = nh_data_2179, aes(x = BMI, y = Pulse)) +
    geom_point() +
    geom_smooth(method = "loess") +
    labs(title = "BMI vs. Pulse rate for NHANES subjects, ages 21-79")
```

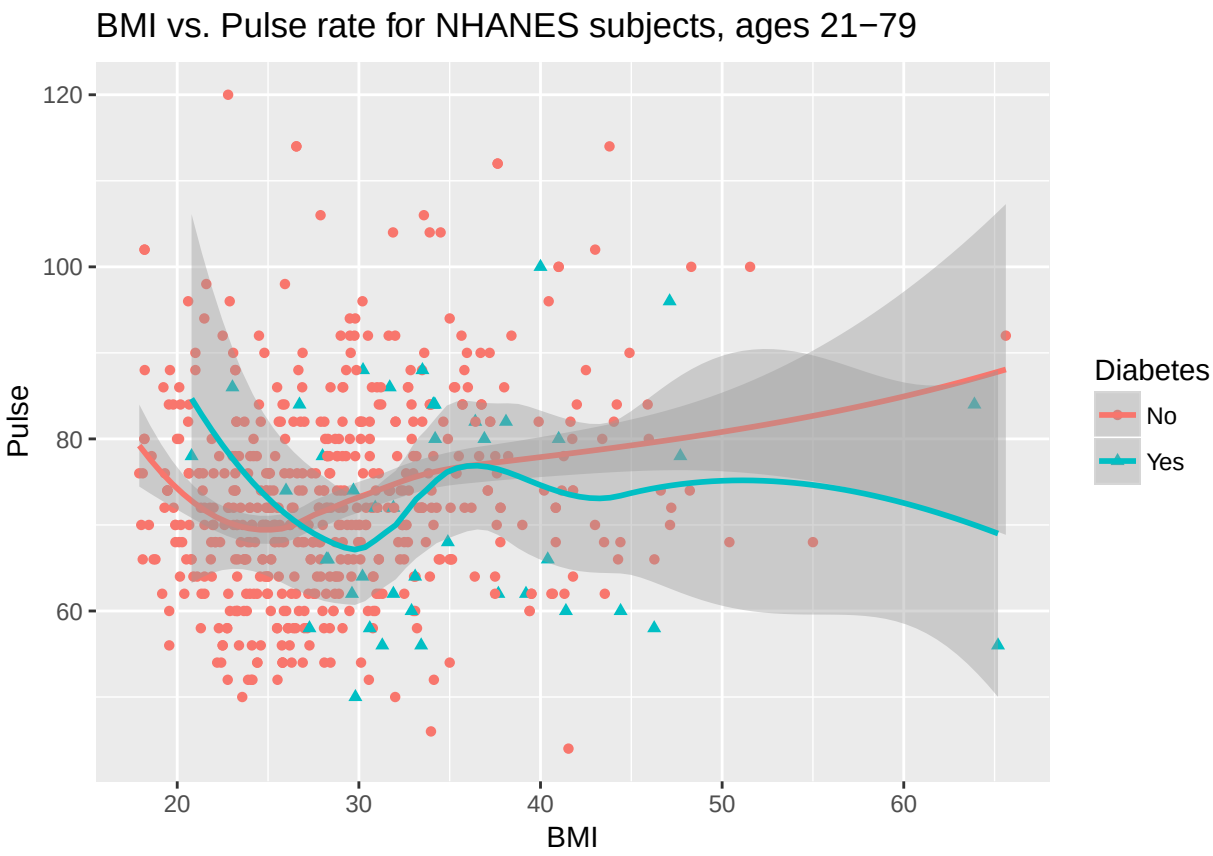


3.8.5 Diabetes vs. No Diabetes

Could we see whether subjects who have been told they have diabetes show different BMI-pulse rate patterns than the subjects who haven't?

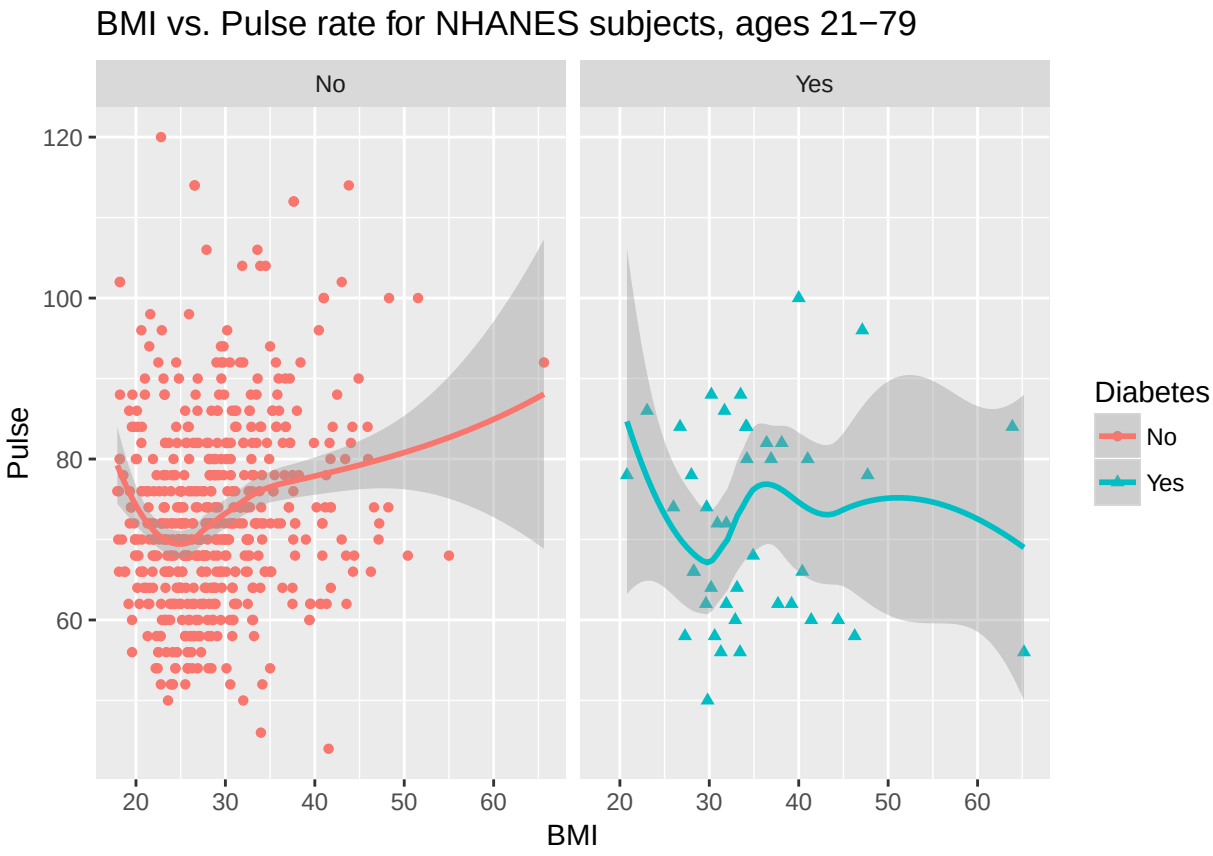
- Let's try doing this by changing the shape *and* the color of the points based on diabetes status.

```
ggplot(data = nh_data_2179,
       aes(x = BMI, y = Pulse,
           color = Diabetes, shape = Diabetes)) +
    geom_point() +
    geom_smooth(method = "loess") +
    labs(title = "BMI vs. Pulse rate for NHANES subjects, ages 21-79")
```



This plot might be easier to interpret if we faceted by Diabetes status, as well.

```
ggplot(data = nh_data_2179,
       aes(x = BMI, y = Pulse,
           color = Diabetes, shape = Diabetes)) +
    geom_point() +
    geom_smooth(method = "loess") +
    labs(title = "BMI vs. Pulse rate for NHANES subjects, ages 21-79") +
    facet_wrap(~ Diabetes)
```



3.9 General Health Status

Here's a Table of the General Health Status results. This is a self-reported rating of each subject's health on a five point scale (Excellent, Very Good, Good, Fair, Poor.)

```
nh_data_2179 %>%
    select(HealthGen) %>%
    table()
```

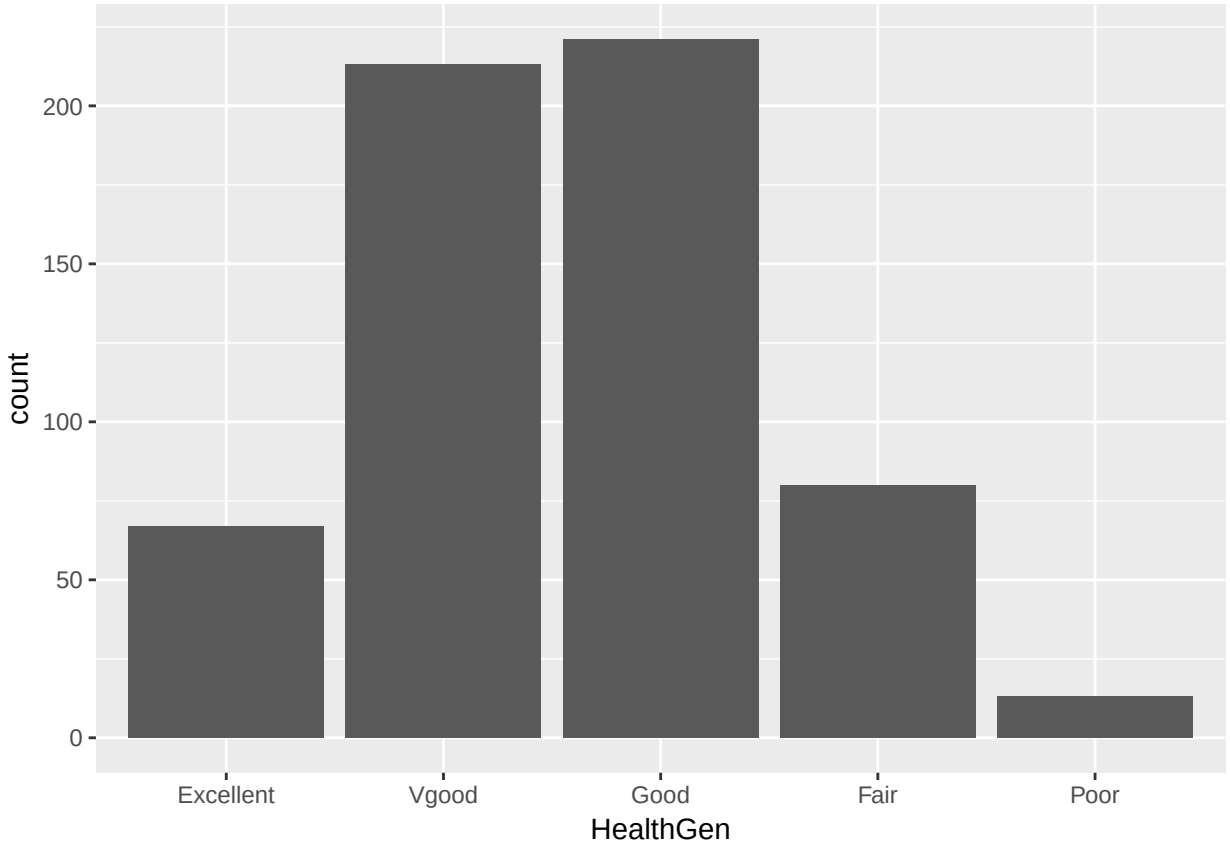
```
.
Excellent     Vgood      Good      Fair      Poor
       67       213       221        80        13
```

The HealthGen data are categorical, which means that summarizing them with averages isn't as appealing as looking at percentages, proportions and rates.

3.9.1 Bar Chart for Categorical Data

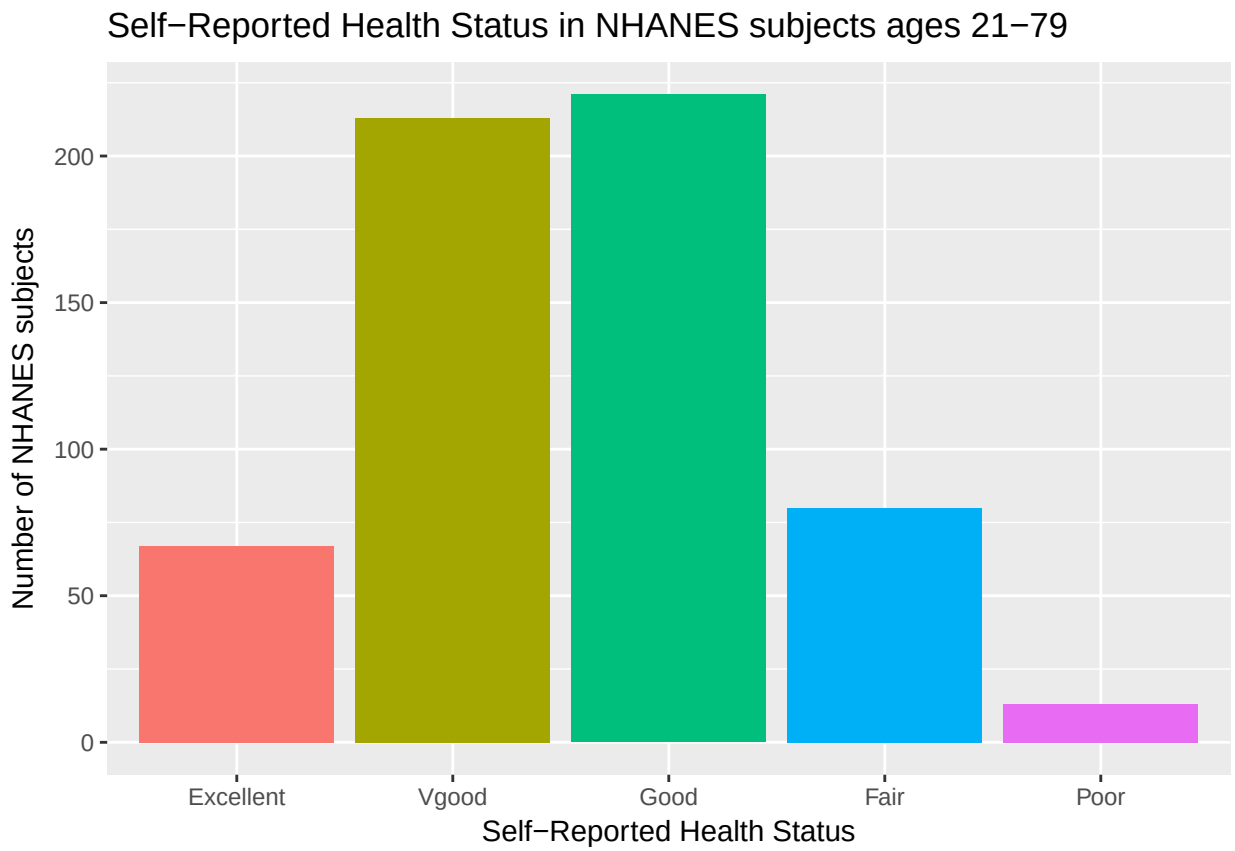
Usually, a **bar chart** is the best choice for a graphing a variable made up of categories.

```
ggplot(data = nh_data_2179, aes(x = HealthGen)) +
    geom_bar()
```



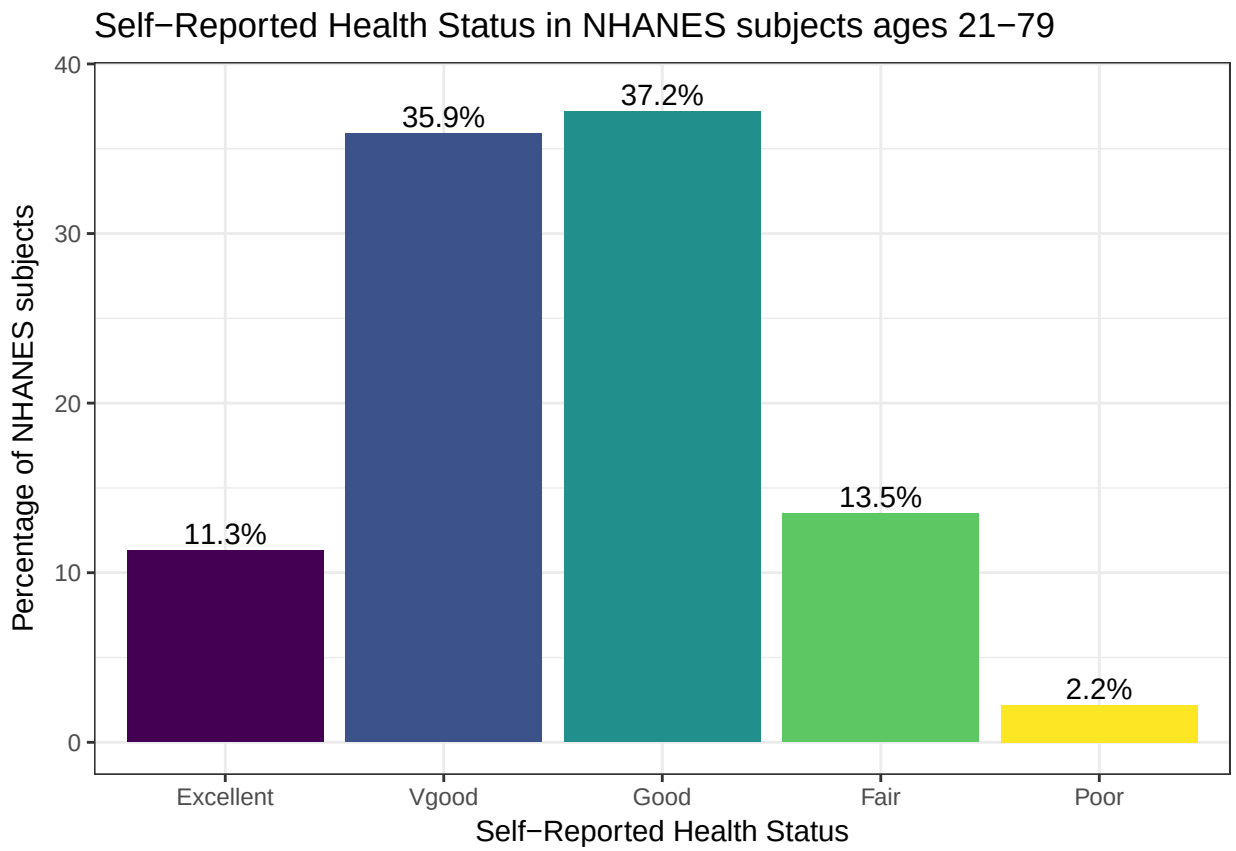
There are lots of things we can do to make this plot fancier.

```
ggplot(data = nh_data_2179, aes(x = HealthGen, fill = HealthGen)) +
    geom_bar() +
    guides(fill = FALSE) +
    labs(x = "Self-Reported Health Status",
         y = "Number of NHANES subjects",
         title = "Self-Reported Health Status in NHANES subjects ages 21-79")
```



Or, we can really go crazy...

```
nh_data_2179 %>%
    count(HealthGen) %>%
    ungroup() %>%
    mutate(pct = round(prop.table(n) * 100, 1)) %>%
    ggplot(aes(x = HealthGen, y = pct, fill = HealthGen)) +
    geom_bar(stat = "identity", position = "dodge") +
    scale_fill_viridis(discrete = TRUE) +
    guides(fill = FALSE) +
    geom_text(aes(y = pct + 1,    # nudge above top of bar
                  label = paste0(pct, '%')),  # prettify
              position = position_dodge(width = .9),
              size = 4) +
    labs(x = "Self-Reported Health Status",
         y = "Percentage of NHANES subjects",
         title = "Self-Reported Health Status in NHANES subjects ages 21-79") +
    theme_bw()
```



3.9.2 Working with Tables

We can add a marginal total, and compare subjects by Gender, as follows...

```
nh_data_2179 %>%
    select(Gender, HealthGen) %>%
    table() %>%
    addmargins()
```

```
        HealthGen
Gender   Excellent Vgood Good Fair Poor Sum
  female        34   107  107   34    8 290
  male          33   106  114   46    5 304
  Sum           67   213  221   80   13 594
```

If we like, we can make this look a little more polished with the `knitr::kable` function...

```
nh_data_2179 %>%
    select(Gender, HealthGen) %>%
    table() %>%
    addmargins() %>%
    knitr::kable()
```

	Excellent	Vgood	Good	Fair	Poor	Sum
female	34	107	107	34	8	290
male	33	106	114	46	5	304
Sum	67	213	221	80	13	594

If we want the proportions of patients within each Gender that fall in each HealthGen category (the row percentages), we can get them, too.

```
nh_data_2179 %>%
    select(Gender, HealthGen) %>%
    table() %>%
    prop.table(.,1) %>%
    knitr::kable()
```

	Excellent	Vgood	Good	Fair	Poor
female	0.1172414	0.3689655	0.3689655	0.1172414	0.0275862
male	0.1085526	0.3486842	0.3750000	0.1513158	0.0164474

To make this a little easier to use, we might consider rounding.

```
nh_data_2179 %>%
    select(Gender, HealthGen) %>%
    table() %>%
    prop.table(.,1) %>%
    round(.,2) %>%
    knitr::kable()
```

	Excellent	Vgood	Good	Fair	Poor
female	0.12	0.37	0.37	0.12	0.03
male	0.11	0.35	0.38	0.15	0.02

Another possibility would be to show the percentages, rather than the proportions (which requires multiplying the proportion by 100.) Note the strange "*" function, which is needed to convince R to multiply each entry by 100 here.

```
nh_data_2179 %>%
    select(Gender, HealthGen) %>%
    table() %>%
    prop.table(.,1) %>%
    "*"(100) %>%
    round(.,2)  %>%
    knitr::kable()
```

	Excellent	Vgood	Good	Fair	Poor
female	11.72	36.90	36.9	11.72	2.76
male	10.86	34.87	37.5	15.13	1.64

And, if we wanted the column percentages, to determine which gender had the higher rate of each HealthGen status level, we can get that by changing the prop.table to calculate 2 (column) proportions, rather than 1 (rows.)

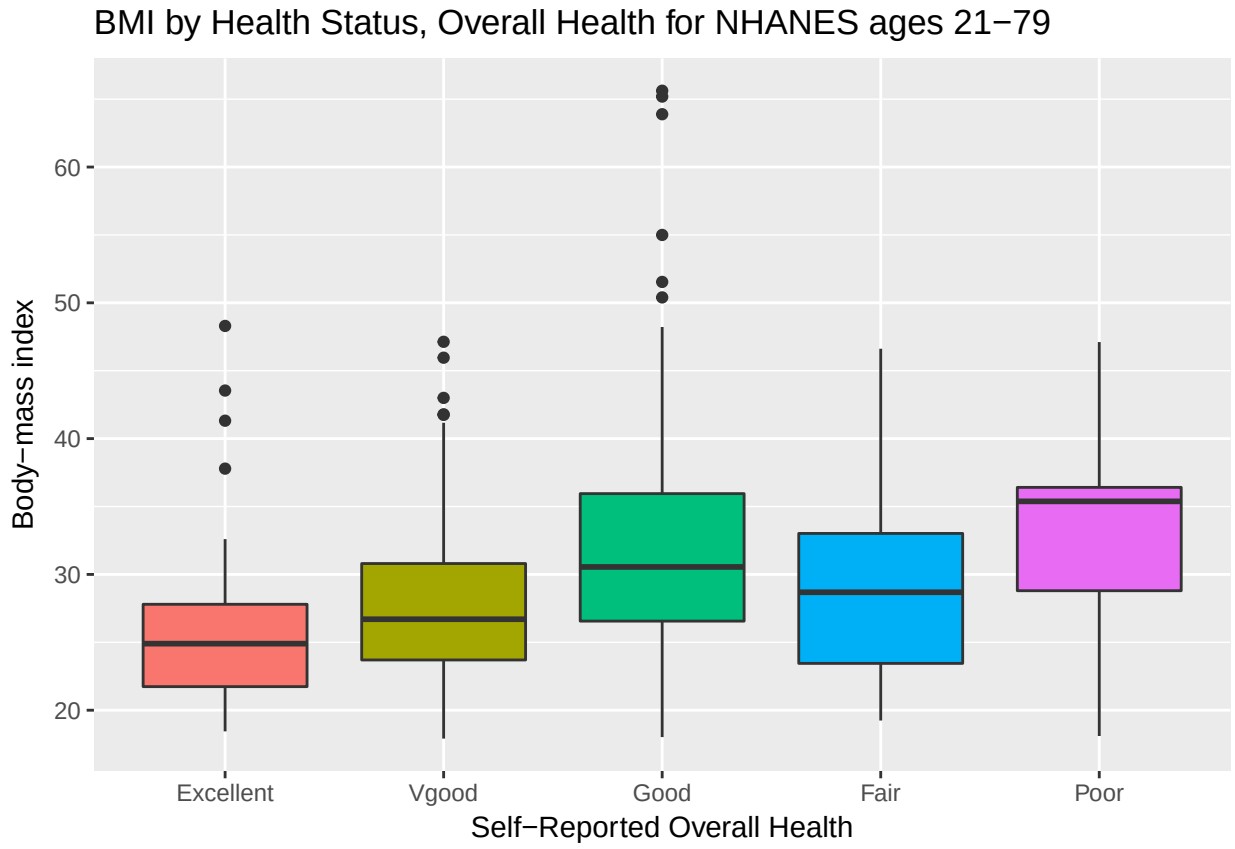
```
nh_data_2179 %>%
    select(Gender, HealthGen) %>%
    table() %>%
    prop.table(.,2) %>%
    "*"(100) %>%
    round(.,2)  %>%
    knitr::kable()
```

	Excellent	Vgood	Good	Fair	Poor
female	50.75	50.23	48.42	42.5	61.54
male	49.25	49.77	51.58	57.5	38.46

3.9.3 BMI by General Health Status

Let's consider now the relationship between self-reported overall health and body-mass index.

```
ggplot(data = nh_data_2179, aes(x = HealthGen, y = BMI, fill = HealthGen)) +
    geom_boxplot() +
    labs(title = "BMI by Health Status, Overall Health for NHANES ages 21-79",
         y = "Body-mass index", x = "Self-Reported Overall Health") +
    guides(fill = FALSE)
```



We can see that not too many people self-identify with the "Poor" health category.

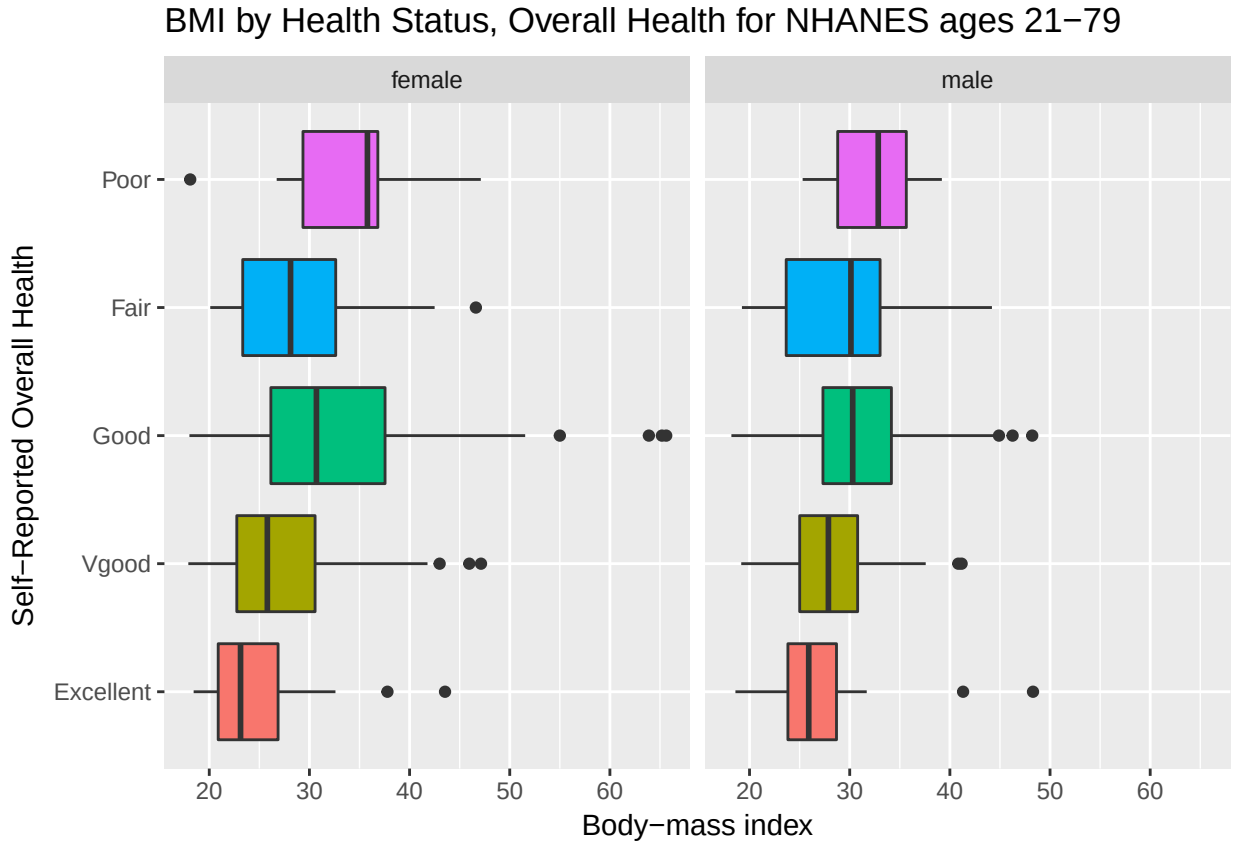
```
nh_data_2179 %>%
    group_by(HealthGen) %>%
    summarize(count = n(), mean(BMI), median(BMI)) %>%
    knitr::kable()
```

HealthGen	count	mean(BMI)	median(BMI)
Excellent	67	25.70060	24.900
Vgood	213	27.55878	26.700
Good	221	32.00321	30.550
Fair	80	29.28663	28.685
Poor	13	33.08154	35.380

3.9.4 BMI by Gender and General Health Status

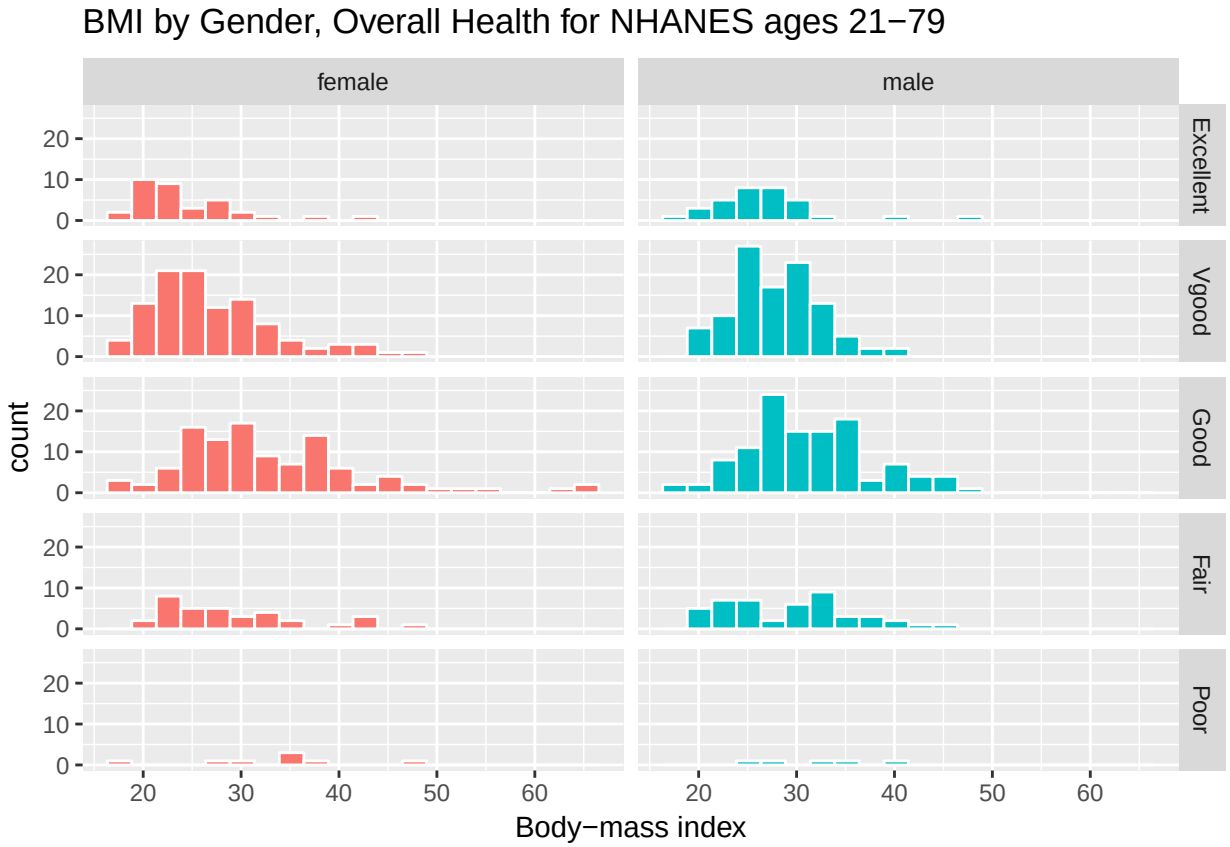
We'll start with two panels of boxplots to try to understand the relationships between BMI, General Health Status and Gender. Note the use of `coord_flip` to rotate the graph 90 degrees.

```
ggplot(data = nh_data_2179, aes(x = HealthGen, y = BMI, fill = HealthGen)) +
    geom_boxplot() +
    labs(title = "BMI by Health Status, Overall Health for NHANES ages 21-79",
         y = "Body-mass index", x = "Self-Reported Overall Health") +
    guides(fill = FALSE) +
    facet_wrap(~ Gender) +
    coord_flip()
```



Here's a plot of faceted histograms, which might be used to address similar questions.

```
ggplot(data = nh_data_2179, aes(x = BMI, fill = Gender)) +
    geom_histogram(color = "white", bins = 20) +
    labs(title = "BMI by Gender, Overall Health for NHANES ages 21-79",
         x = "Body-mass index") +
    guides(fill = FALSE) +
    facet_grid(HealthGen ~ Gender)
```



3.10 Conclusions

This is just a small piece of the toolbox for visualizations that we'll create in this class. Many additional tools are on the way, but the main idea won't change. Using the `ggplot2` package, we can accomplish several critical tasks in creating a visualization, including:

- Identifying (and labeling) the axes and titles
- Identifying a type of `geom` to use, like a point, bar or histogram
- Changing fill, color, shape, size to facilitate comparisons
- Building "small multiples" of plots with faceting

Good data visualizations make it easy to see the data, and `ggplot2`'s tools make it relatively difficult to make a really bad graph.

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