Understanding and Visualizing Data with Python

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2 Lecture notes

A great resource that you can explore is the This is Statistics website, created by the American Statistical Association. This insightful and motivating campaign has countless links, videos, and resources to raise awareness of the wide variety of fascinating careers within statistics.

2.1 Definitions

- The **mean (average)** of a data set is found by adding all numbers in the data set and then dividing by the number of values in the set. Its highly affected by outliers.
- The **median** is the middle value when a data set is ordered from least to greatest.
- The mode is the number that occurs most often in a data set.
- I.i.d. data = Independent and identically distributed data. Here each random variable has the same probability distribution as the others and all are mutually independent
- **Range**: the difference between the highest and lowest values.
- **Interquartile range**: the range of the middle half of a distribution. Q3-Q3
- **Standard deviation**: average distance from the mean.

2.2 Standard Score (Empirical Rule)

In statistics, the **standard score** is the number of standard deviations by which the value of a raw score (i.e., an observed value or data point) is above or below the mean value of what is being observed or measured.

It is calculated by subtracting the population mean from an individual raw score and then dividing the difference by the population standard deviation.

Standard scores are most commonly called **z-scores**.

A bell-shaped or normal distributions is sometimes referred to as the **68-95-99.7 rule**: 68% of the observations are within 1 standard deviation of the mean. 95% of the observations are within 2 standard deviation of the mean. 99.7% of the observations are within 3 standard deviation of the mean.

2.3 Multivariate data

Univariate statistics summarize only one variable at a time. Bivariate statistics compare two variables. Multivariate statistics compare more than two variables.

A **mosaic plot** is a special type of stacked bar chart that shows percentages of data in groups. The plot is a graphical representation of a contingency table. These plots are a way to display qualitative multivariate data.

2.3.1 Scatter plots

Scatter plots are a good way to display multivariate quantitative data

Looking at association in scatter plots:

- Linear: The pattern in a plot is a line
- Quadratic association: The pattern is parabolic, i.e. the pattern goes up at the beginning and goes back down latter
- No association: there is no pattern

Looking at the direction of the association:

- Positive linear association: the pattern has a positive slope, i.e. when x increases, y decreases
- Negative linear association

Looking at the strength of the association:

- Weak linear association: the points are largely scattered along the line
- Moderate linear association: Partial scattering of points
- Strong linear association: Points are minimally scattered

Quantify the strength and direction via **correlation**:

Pearson correlation (R or p): number between -1 and 1 that indicates the strength and direction of association between two variables. The sign of the correlation indicates the

direction, i.e. negative –> negative linear association. The closer the number is to 1 or -1 the stronger the association is.

One caveat with correlations: Correlation does NOT imply causation. I.e. age might not be the reason to why blood pressure is increasing even though we might see a positive correlation.

2.3.2 Outliers

Outliers are extreme data points that deviate from patterns observed in the rest of the data.

2.4 Simpson's Paradox

A **confounding variable** is an outside influence that changes the relationship between the independent and the dependent variable (ie. a third variable in a study examining a potential cause-and-effect relationship). It oftentimes works by affecting the causal relationship between the primary independent variable and the dependent variable. This confounding variable confuses the relationship between two other variables; it may act by hiding, obscuring, or enhancing the existing relationship.

For example, suppose that you are interested in examining how activity level affects weight change. Other factors, like diet, age, and gender may also affect weight change and come into play when looking at the relationship between activity level and weight change. If one doesn't control for these factors, the relationship between activity level and weight change can be distorted.

2.5 Populations and samples

2.5.1 Sampling from populations intro

How to make inferential statements about a population?

1. Conduct a **census**, i.e. measure everyone in a population. So only doable for small populations and can get easily get expensive, so requires careful cost evaluation.

2. Selected a **probability sample from the population** and measure all units in that sample. Here, we construct a list of all units in a population, i.e. a sampling frame and then we determine a probability of selection for every unit on that list. Then select units from that list at random where sampling rates for different subgroups are determined by the probabilities of selection. Finally, measure those randomly selected units.
3. Select a **non-probability sample** from the population. This process doesn't involve random selection of individuals, according to probability of selection, so there is no statistical basis for making inferences about the target population –> high potential for bias. Examples are opt-in web surveys, quota sampling, snowball sampling or convenience sampling.

Why probability sampling?

The known probabilities of selection for all units allow us to make unbiased statements about population features and the uncertainty in survey estimates. The random selection of units protects us against bias from the sample selection mechanisms –> allows us to make population inferences based on sampling distributions.

2.5.2 Simple random sampling (SRS)

- We start with a known list of N population units (N = size of the population) and randomly select n units from the list (n = the size of our sample)
- Every unit has equal probability of selection of n/N
- All possible samples of size n are equally likely
- Estimates of means, proportions and totals based on SRS are unbiased (i.e. equal to the population averages on average)
- Can be with replacement or without replacement
  - **With replacement** means that when we select somebody from a larger list, we've replaced them in that list. And we give them a chance of being selected again in the sample.
  - More common is that simple random sampling is done **without replacement**. So once an individual unit is sampled from a given list, they can't be sampled again.
  - For both: The probability of selection for each unit is still n/N
- Rarely used in practice: Collecting data from n randomly sampled units in a large population can be expensive
- Example: We have 1000 email conversations and want to check 100 manually for some things, then we can design a random nr. generator to pull out a simple, random sample from our population of emails.

2.5.3 Working with complex samples

Key features of complex samples:

- Population is divided into different **strata**, and part of the sample is allocated to each stratum. This ensures the a sample representation from each stratum and reduces variance of survey estimates (this technique is known as **stratification**)
- **Clusters** of population units (e.g. counties) are randomly samples first (with a known probability) within strata, to save costs of data collection (i.e. we collect data from cases close to each other geographically for the county example)
- **Units** are randomly sampled from within clusters, according to some probability of selection, and measured
- The inverse of a person's probability of selection is called their **sampling weight**. I.e. if my probability of selection is 1/100 then my weight is 100 and I represent myself and 99 others of the population.
- These weights are used to compute **unbiased estimates** of population quantities, i.e. the mean BMI, accounting for different probabilities of selection
- Probabilities of selection play a direct and essential role in computation of unbiased population estimates

A unit's probability of selection is determined by:

- The number of clusters sampled from each stratum
- The total number of clusters in the population of each stratum
- The number of units ultimately sampled from within each randomly selected cluster
- The total number of units in the population in each cluster

An example for finding a unit's probability of selection:

- We want to select a out of A clusters at random in a given stratum
- Then we select b out of B units at random from within each selected cluster
- The probability of selection is: $(a/A)(b/B)$

2.5.4 Non-probability sampling

- Features of non-probability samples:
  - Probabilities of selection can't be determined for sampled units a priori (i.e. before you begin the study)
  - Non random selection of individual units
  - Sample can sometimes be divided into groups (strata) or clusters, but clusters are not randomly sampled in earlier stages

  - Data collection often very cheap compared to probability sampling
  - Examples: Studies of volunteers for i.e. clinical studies, opt-in/intercept web surveys, snowball samples, convenience sample or quota samples

- Problem of not having probabilities of selection:
  - We have no statistical basis for making an inference about the larger population from which the sample is selected
  - If we do know the probabilities of selection (in addition to population strata and randomly sampled clusters) then we estimate features of the sampling distribution (if we were to take many random samples using the same design)
  - Another issue we have is that sampled units are not selected at random and we have a strong risk of sampling bias
  - Sampled units are generally not representative of the large population of interest
  - Big data often from non-probability samples, so we need to be careful about what we infer from the data for populations as a whole

- So what can we do, since many data sets arise from non-probability samples, can we say anything about a larger population?
  - There are two possible approaches:
    * Pseudo-randomization
    * Calibration

2.5.4.1 Pseudo-randomization approach

- Combine non-probability sample with a probability sample that collected similar measurements (we "stack" data sets together)
- Then we estimate the probability of being included in the non-probability sample as function of the auxiliary information available from both samples
- We then treat the estimated probabilities of selection as being "known" for the non-probability sample and use probability sampling methods for the further analysis

2.5.4.2 Calibration approach

- We compute the weights for responding units in a non-probability sample that allow weighted sample to mirror a know population,
- i.e. we might have a non probability sample with 70% and 30% male and know we have 50% females and 50% males in the target population. In this example we could then down-weight females and up-weight males
- Limitation: If the weighting factor is not related to the variable(s) of interest then we will not reduce possible sampling biases

2.5.5 Sampling Variance & Sampling Distributions

2.5.5.1 Sampling distribution

- We generally assume that the values of a variable of interest follow a certain distribution if we could measure the entire population, i.e. a normal distribution (bell curve)
- A **sampling distribution** is the distribution of survey estimates (not the distribution of values of a variable of interest) that we would see IF we selected many random samples using the same sampling design and computed an estimate for each
- Key properties of sampling distributions:
  - They are hypothetical and us asking what would happen if we had the luxury of drawing thousands of probability samples and measure each of them.
  - Generally very different appearance from the distribution of values from a single variable of interest
  - With large enough probability sample size, the sampling distribution estimated will look like a normal distribution, regardless of what estimates are computed due to something called the **Central limit theorem (CLT)**

2.5.5.2 Sampling variance

- The variability in the estimates described by the sampling distribution
- Because we select a sample (and are not measuring everyone in the population) a survey estimate based on a single sample WILL NOT be exactly equal to the population quantity of interest. This is called **sampling error**
- Across hypothetical repeated samples the sampling error will randomly vary (sometimes positive, sometimes negative, . . .)
- The variability of these sampling errors describes the variance of the sampling distribution
- If every sample estimate of interest would be equal to the population quantity of interest (i.e. in case of a Census) there would be no sampling error and no sampling variance
- With a larger probability sample size, i.e. sampling more from a given population –> in theory there will be less sampling error and sampling errors will be less variable
- Larger samples –> Less sampling variance, more precise estimated and more confidence in inferential statements BUT more costly
- Spread of sampling distribution becomes smaller as the sampling size becomes larger

We can play with some data using this tool.

2.5.6 Beyond Means: Sampling Distributions of Other Common Statistics

A **correlation coefficient** is a statistical measure of the degree to which changes to the value of one variable predict change to the value of another. In positively correlated variables, the value increases or decreases in tandem.

Linear regression analysis is used to predict the value of a variable based on the value of another variable. The variable you want to predict is called the dependent variable (x). The variable you are using to predict the other variable's value is called the independent variable (y).

2.6 Making Population Inference Based on only one Sample

A key assumption to make an inference on a sample is that we have a normal distribution. So approaches to make such inferences assume that sampling distributions for the thing we want to estimate are (approximately) normal, which is often met if the sample size is large enough.

There are two General approaches to making population inferences based on estimated features of sampling distributions:

1. Estimating a confidence interval
2. Hypothesis testing

2.6.1 Estimate a confidence interval for the parameters of interest

2.6.1.1 Step1

- Compute the **point estimate** , i.e. an unbiased point estimate of the parameter of interest
- Unbiased point estimate: average of all possible values for a point estimate is equal to the true parameter value
- This means that the sampling distribution is centered around the truth value
- If cases had unequal probabilities of selection, those weights need to be used when computing the point estimate

2.6.1.2 Step2

- Estimate the **sampling variance** for the point of estimate, i.e. compute an unbiased estimate of the variance of the sampling distribution for the particular point estimate
- An unbiased variance estimate correctly described the variance of the sampling distribution under the sample design that was used
- The square root of the variance that we try to estimate is also referred to as the Standard Error of the point estimate

To form a confidence interval we take our best estimate and add/subtract the **margin of error** (i.e. we allow for sampling variable). Margin error refers to "a few" estimated standard errors. "A few" generally refers to a multiplier from an appropriate distribution based on the desired confidence level and sample design. I.e. 95% confidence level <–> 0.05 Significance

2.6.2 Hypothesis testing

- Hypothesis: Asking if the value of a parameter could be XYZ (i.e. use a hypothesized or "null" value)?
- Thereby we want to answer the question whether the point estimate for the parameter is close to this null value or far away
- We use the standard error point estimates as a yardstick
- A common test statistic is:

$$Test.statistic = \frac{(estimate - null.value)}{standard.error}$$

- If the null is true, then we can look at the probability of seeing a seeing a test statistic this extreme (or more extreme). If the probability of seeing a test statistic this large under the null hypothesis is small, then we can reject null.

2.7 Resource: Seeing Theory

Seeing Theory is a site developed by Brown University that includes many interactive tools that help to visualize statistical concepts.

The site is broken into six chapters, which includes:

- Basic Probability
- Compound Probability
- Probability distributions

- Frequentist Inference
- Bayesian Inference
- Regression Analysis

2.8 Preventing Bad/Biased Samples

Many so-called "standard" statistical analyses that are presented and discussed in introductory statistics courses make the assumption that the data of interest are independent and identically distributed (or "i.i.d.") observations.

As discussed in the lectures earlier this week, **simple random sampling (SRS)** is the closest probability sampling analog to i.i.d., in that the sampling mechanism used to generate the observations will produce independent and identically distributed observations. While this type of sampling will produce samples with this nice "i.i.d." statistical property, facilitating "standard" statistical analyses, SRS is seldom used when sampling from real populations.

Consider, for example, a national sample of 1,000 cell phone numbers selected using SRS. While in expectation any one given sample will include a representative random sampling of numbers from area codes across the nation, all possible random samples using SRS are equally likely. What this means is that a simple random sample of cell phone numbers that only includes area codes from Florida is just as likely as a simple random sample of numbers that includes a representative selection across the states. Ideally, we would like to use design strategies to reduce the chances of such a "bad sample" occurring, especially if our variable of interest tends to take on very different values in the state of Florida! The major statistical problem with the simple random "Florida" sample is that any estimate that we compute after collecting data from the sample will likely be very different from the true population parameter that we are trying to estimate (especially if the variable of interest tends to take on very different values in Florida relative to the rest of the nation). Because the probability of selecting these extreme samples is equal to the probability of selecting more representative samples, the sampling distribution for simple random samples can tend to be quite variable.

A very common sampling technique used to minimize the sampling variance that can arise from these so-called "bad samples" in SRS is **stratification**. When we conduct stratified sampling, we first allocate portions of our sample to all possible divisions (or "strata") of the population of interest (e.g., states). This ensures that some sample will be selected from all of these possible divisions, and that the overall sample will therefore be representative of the target population. For example, using a technique known as proportionate allocation, suppose that we knew that 55% of students enrolled in a particular college were females, and 45% were males. If we wanted to draw a sample of 1,000 students from this college, we

would randomly selected 550 females from a list of all females enrolled, and 450 males from a list of all males enrolled. This ensures that our entire sample of size 1,000 won't include only females!

Another nice property of stratified sampling is that it shrinks the variance of sampling distributions. In SRS, all of the variance within strata and between strata in terms of the variable of interest contributes to the overall sampling variance. In stratified sampling, when we allocate a certain number of sampled units to be selected from each stratum, we remove the between-stratum variance from the overall sampling variance! This is because every hypothetical repeated sample would use the same stratified design, and the same allocation; assuming reasonable response rates, we will have representation from each of the strata where we allocated a portion of the sample.

When analyzing data, we always have to think carefully about the process used to ultimately produce the data that we are analyzing. We may dedicate substantial resources to a carefully designed stratified sample of some population that will produce unbiased estimates by design; however, there is no guarantee that every unit sampled will agree to provide data. If a sampled unit refuses to provide data after being sampled, this situation is known as **unit nonresponse** . Unit nonresponse can have a particularly negative impact on the quality of a given sample when the units that ultimately agree to provide data differ significantly from the units that do not agree to provide data on the variables of interest.

For example, suppose that people with lower income tend to respond to a survey of a nationally representative sample of individuals at higher rates than people with higher income. Because the resulting sample of respondents to the survey request tends to feature people with lower income, any estimates related to income (which will always be computed using data from the respondents, or the units that agree to provide data!) will be subject to another form of selection bias, namely **nonresponse bias**. In short, nonresponse bias occurs when there is a tendency for the units in a sample that agree to provide data to be systematically different from the units in the sample that do not provide data (in terms of the variable of interest). This type of bias can also occur for estimates based on specific variables, when sampled units may agree to provide data in general, but not on specific variables. For instance, a survey respondent may agree to participate in the survey, but refuse to share their income. This type of nonresponse is known as **item nonresponse**.

Whereas stratified sampling is a design tool that can be used to reduce selection bias from a sampling perspective, the selection bias introduced by unit or item nonresponse can either be addressed during the data collection process or via post-survey adjustments to the estimates based on a respondent sample. For example, sampled units reluctant to provide data may be offered additional incentives for their participation, or offered different methods for providing their data (e.g., over the web, rather than speaking to an interviewer). Such units may also receive additional effort from a data collection organization (e.g., more follow-up contact attempts). After the survey is over, if there is still evidence that the

respondent sample somehow differs systematically from the full sample, respondents who had a lower probability of responding may receive larger weight in the overall analysis. Item nonresponse may be addressed via statistical models used to predict the missing values as a function of other observed data. There are all tools designed to reduce the type of selection bias that can arise from nonresponse.

2.9 Inference for single, non-probability samples

- Non-probability samples do not let us rely on sampling theory for making population inferences based on expected sampling distributions
- There are two approaches to work with these samples:
  - Quasi-randomization (or pseudo-randomization)
  - Population modelling

2.9.1 Quasi-randomization

- In this approach we combine data from a separate, independent non-probability sample with data from a probability sample that collected the same type of measures
- I.e. when collecting BMI or other health data from volunteers we could combine it with data from the NHANES dataset that also collected the same health measures
- To do this we stack the two datasets together (i.e. concatenate them) and the non-probability sample may have other response variables that we are really interested in
- We code the data, i.e. give it an extra variable (NPSAMPLE), so that we know whether or not they came from a non-prob (1) or prob sample (0)
- Then we can fit a logistic regression models: We use this to predict the NPSAMPLE with common variables weighting non-prob cases by 1 and prob cases by their survey weights. I.e. we're trying predict the probability of having a one on the NPSAMPLE variable that we just formed, or in other words, the probability of being in the non-probability sample with those common variables, like bmi, age, and blood pressure, and race ethnicity
- So the idea is that we can predict the probability of an individual of being in a non-prob sample within whatever population is represented by the prob sample
- Then we can invert the predicted probabilities for the non-prob sample, treat them as survey weight in standard weighted survey analysis

$survey.weight = \frac{1}{predicted.probability}$

- The issue in this approach is the issue of estimating sampling variance and some kind of replication method is recommended (i.e. computing weighted estimates in bootstrap samples or jackknife samples of the original units)

2.9.2 Population modelling

- In this approach the idea is to use predictive modeling to predict aggregate sample quantities (usually totals) on key variables of interest for population units that are not included in the non-prob sample
- Given the predictions of the variables of interests for everybody else who was not included in the non-probability sample, we compute our estimates of interests using estimated totals on the variables of interest based on those predictions
- i.e. for computing a weighted mean, we would calculate the overall total of a variable of interest for everyone in the population using the observed values in a non-probability sample, and the predicted values for everybody else who was not included in the non-probability sample. Then, we would divide that predicted total by the estimated population size, and that gives us an estimate of our overall population mean

$$weighted.mean = \frac{predicted.total.estimate}{estimated.population.size}$$

- The key difference to quasi-randomization is that we don't need a probability sample with the same measures
- This approach relies on having good regression models to predict the key variables using other auxiliary information available at aggregate level (i.e. totals for an overall population)
- Standard errors can be based on fitted regression models or using similar replication methods

2.10 Complex samples

A **complex sample** is any probability sample where the design involves anything more than a Simple Random Sampling (SRS).

2.10.1 Features of complex samples: Stratification

- One important feature of this type of sampling design is called **stratification**. So stratification is defined as the allocation of an overall sample to different strata or mutually exclusive divisions of the larger population. So, for example, in a large

national sample from the United States, these could be different regions in the United States.

- There are several different potential allocation schemes in this case for stratification. Either way, or either allocation scheme that we use, our aim is to minimize sampling variance for particular variables given fixed costs.
- Stratification has the very attractive property of eliminating between strata variance in means or totals of interest on the variable of interest from the overall sampling variance
- So it's very important to account for this kind of stratification in our analysis. Otherwise, our sampling variance may be artificially large resulting in too conservative inferences and confidence intervals that are too wide.

2.10.2 Features of complex samples: Cluster sampling (i.e. Clustering)

- In cluster sampling, random sampling of larger clusters of population elements occurs, possibly across multiple stages.
- For example, the national sample, we might first sample US counties. And then within those US counties, we might sample area segments. And within those area segments, we might sample households.
- This idea of cluster sampling is used in practice to reduce the cost of data collection. It's very expensive to visit little n randomly sampled units from a large and widespread population. Instead, we draw random samples of clusters according to a probability sampling design. And then we visit those clusters and collect data from that small clustered area.
- But Clustering tends to increase the sampling variance of estimates because units coming from the same cluster tend to have similar or correlated values on the variables of interest. We're not measuring unique information when we draw the cluster sampling. So we do it to save costs, but we don't pick up on as much unique information as we could if we weren't drawing a cluster sample.
- So much like with stratification, it's important to account for cluster sampling when we analyze the survey data. Otherwise, our inferences might become too narrow, unlike stratification.

2.10.3 Features of complex samples: Weighting

- Remember, complex samples are probability samples but if there are certain subgroups of the population that are sampled at higher rates, this idea of oversampling from particular population subgroups, we end up with unequal probabilities of selection

for different population units. So the probability of being included in the probability sample could be very different for different people

- If there are in fact unequal probabilities of selection for different people in the overall population, we need to account for these unequal probabilities to make unbiased population inferences.
- weights and complex samples are defined by the inverse of a given person's probability of selection. And these are the weights, again, that we would ultimately use when analyzing the data
- I.e. if my probability of selected is 1/100 –> my weight is 100 and I represent myself and 99 others in the population
- Weights can also be adjusted for different possibilities of responding to a given survey request and different subgroups
- I.e. if my prob is 1/100 but if I belong to a subgroup were only 50% of this subgroup responded then I can adjust my weight as follows: (1/0.01) * (1/0.5) = 200
- The drawback of using weights in analysis is that much like cluster sampling, highly variable adjusted survey weights tend to increase the sampling variance of weighted estimates. So there's a lot of variability in our weights, that means there's a lot of uncertainty in terms of who we're actually sampling and who they represent

2.10.4 Summary

- Stratification reduces sampling variance. It gives us more precise estimates, because we're removing that between strata variability from the overall sampling variability
- Cluster sampling and weighting, on the other hand, they tend to increase sampling variants
- The net multiplicative effect of all of these three complex sample design features on the standard error is what we refer to as a **design effect**. This is the net multiplicative change in the variance of an estimate relative to simple random sampling
- A failure to identify those features of complex samples when performing data analysis is what's often referred to as **analytic error**.
- So when you're scouring documentation for survey data, you can think of a couple important keywords that you can look for that would indicate the fact that complex sampling was actually performed. Things like multistage sampling, or weights, or stratification, or cluster sampling, or design effects, these are all words to look for in your documentation to see if this kind of complex sampling was actually performed

3 What is Jupyter Notebooks?

Jupyter is a web-based interactive development environment that supports multiple programming languages, however most commonly used with the Python programming language.

The interactive environment that Jupyter provides enables students, scientists, and researchers to create reproducible analysis and formulate a story within a single document.

Lets take a look at an example of a completed Jupyter Notebook: Example Notebook

3.0.1 Jupyter Notebook Features

- File Browser
- Markdown Cells & Syntax
- Kernels, Variables, & Environment
- Command vs. Edit Mode & Shortcuts

3.0.2 What is Markdown?

Markdown is a markup language that uses plain text formatting syntax. This means that we can modify the formatting our text with the use of various symbols on our keyboard as indicators.

Some examples include:

- Headers
- Text modifications such as italics and bold
- Ordered and Unordered lists
- Links
- Tables
- Images
- Etc.

Now I'll showcase some examples of how this formatting is done:

Headers:

4 H1

4.1 H2

4.1.1 H3

4.1.1.1 H4

4.1.1.1.1 H5

4.1.1.1.1.1 H6

Text modifications:

Emphasis, aka italics, with *asterisks* or *underscores*.

Strong emphasis, aka bold, with **asterisks** or **underscores**.

Combined emphasis with **asterisks and *underscores***.

Strikethrough uses two tildes. ~~Scratch this.~~

Lists:

1. First ordered list item
2. Another item

- Unordered sub-list.

1. Actual numbers don't matter, just that it's a number
2. Ordered sub-list
3. And another item.

- Unordered list can use asterisks
- Or minuses
- Or pluses

Links:

http://www.umich.edu

http://www.umich.edu

The University of Michigan's Homepage

To look into more examples of Markdown syntax and features such as tables, images, etc. head to the following link: Markdown Reference

4.1.2 Kernels, Variables, and Environment

A notebook kernel is a "computational engine" that executes the code contained in a Notebook document. There are kernels for various programming languages, however we are solely using the python kernel which executes python code.

When a notebook is opened, the associated kernel is automatically launched for our convenience.

```
### This is python
print("This is a python code cell")
```

```
This is a python code cell
```

A kernel is the back-end of our notebook which not only executes our python code, but stores our initialized variables.

```
### For example, lets initialize variable x

x = 1738

print("x has been set to " + str(x))
```

```
x has been set to 1738
```

```
### Print x

print(x)
```

1738

Issues arrise when we restart our kernel and attempt to run code with variables that have not been reinitialized.

If the kernel is reset, make sure to rerun code where variables are intialized.

```
## We can also run code that accepts input

name = input("What is your name? ")

print("The name you entered is " + name)
```

It is important to note that Jupyter Notebooks have in-line cell execution. This means that a prior executing cell must complete its operations prior to another cell being executed. A cell still being executing is indicated by the [*] on the left-hand side of the cell.

```
print("This won't print until all prior cells have finished
↪  executing.")
```

4.1.3 Command vs. Edit Mode & Shortcuts

There is an edit and a command mode for jupyter notebooks. The mode is easily identifiable by the color of the left border of the cell.

Blue = Command Mode.

Green = Edit Mode.

Command Mode can be toggled by pressing **esc** on your keyboard.

Commands can be used to execute notebook functions. For example, changing the format of a markdown cell or adding line numbers.

Lets toggle line numbers while in command mode by pressing **L**.

4.1.3.1 Additional Shortcuts

There are a lot of shortcuts that can be used to improve productivity while using Jupyter Notebooks.

Here is a list:

Command Mode (press Esc to enable)	
Enter	enter edit mode
Shift-Enter	run cell, select below
Ctrl-Enter	run cell
Alt-Enter	run cell, insert below
Y	to code
M	to markdown
R	to raw
1	to heading 1
2,3,4,5,6	to heading 2,3,4,5,6
Up/K	select cell above
Down/J	select cell below
A/B	insert cell above/below
X	cut selected cell
C	copy selected cell
Shift-V	paste cell above
V	paste cell below
Z	undo last cell deletion
D,D	delete selected cell
Shift-M	merge cell below
Ctrl-S	Save and Checkpoint
L	toggle line numbers
O	toggle output
Shift-O	toggle output scrolling
Esc	close pager
H	show keyboard shortcut help dialog
I,I	interrupt kernel
0,0	restart kernel
Space	scroll down
Shift-Space	scroll up
Shift	ignore

Edit Mode (press Enter to enable)	
Tab	code completion or indent
Shift-Tab	tooltip
Ctrl-]	indent
Ctrl-[	dedent
Ctrl-A	select all
Ctrl-Z	undo
Ctrl-Shift-Z	redo
Ctrl-Y	redo
Ctrl-Home	go to cell start
Ctrl-Up	go to cell start
Ctrl-End	go to cell end
Ctrl-Down	go to cell end
Ctrl-Left	go one word left
Ctrl-Right	go one word right
Ctrl-Backspace	delete word before
Ctrl-Delete	delete word after
Esc	command mode
Ctrl-M	command mode
Shift-Enter	run cell, select below
Ctrl-Enter	run cell
Alt-Enter	run cell, insert below
Ctrl-Shift-Subtract	split cell
Ctrl-Shift--	split cell
Ctrl-S	Save and Checkpoint
Up	move cursor up or previous cell
Down	move cursor down or next cell
Ctrl-/	toggle comment on current or selected lines

Figure 4.1: Jupyter Notebook Shortcuts

4.1.4 How do you install Jupyter Notebooks?

Note: *Coursera provides embedded jupyter notebooks within the course, thus the download is not a requirement unless you wish to explore jupyter further on your own computer.*

Official Installation Guide: https://jupyter.readthedocs.io/en/latest/install.html

Jupyter recommends utilizing Anaconda, which is a platform compatible with Windows, macOS, and Linux systems.

Anaconda Download: https://www.anaconda.com/download/#macos

5 Data Types in Python

The following data types can be used in base python: * **boolean** * **integer** * **float** * **string** * **list** * **None** * complex * object * set * dictionary

We will only focus on the **bolded** ones

Let's connect these data types to the the variable types we learned from the Variable Types video.

5.0.1 Numerical or Quantitative (taking the mean makes sense)

- Discrete
  - Integer (int) #Stored exactly, i.e. a whole number
- Continuous
  - Float (float) #Stored similarly to scientific notation. Allows for decimal places but loses precision.

```
import math
```

```
#the type function tells us with what data type we are working
type(4)
```

```
int
```

```
type(0)
```

```
int
```

```
type(-3)
```

```
int
```

```
#try taking the mean
numbers = [2, 3, 4, 5]
print(sum(numbers)/len(numbers))
type(sum(numbers)/len(numbers)) #In Python 3 returns float, but in
↪  Python 2 would return int
```

```
3.5

float
```

Floats

```
3/5
```

```
0.6
```

```
6*10**(-1)
```

```
0.6000000000000001
```

```
type(3/5)
```

```
float
```

```
type(math.pi)
```

```
float
```

```
type(4.0)
```

```
float
```

```
# Try taking the mean
numbers = [math.pi, 3/5, 4.1]
type(sum(numbers)/len(numbers))
```

```
float
```

5.0.2 Categorical or Qualitative

- Nominal
  - Boolean (bool)
  - String (str)
  - None (NoneType)
- Ordinal
  - Only defined by how you use the data
  - Often important when creating visuals
  - Lists can hold ordinal information because they have indices

Boolean

Booleans essentially are stored as True or False. I.e. below we see that True is a reservered word in python.

```
# Boolean
type(True)
```

```
bool
```

We also can make our own booleans:

```
type(bool('yes'))
```

```
bool
```

We can also use booleans in if statements, i.e. If the below is true, print something.

```
# Boolean
if 4 < 5:
    print("Yes!")
```

```
Yes!
```

```
myList = [True, 6<5, 1==3, None is None]
for element in myList:
    print(type(element))
```

```
<class 'bool'>
<class 'bool'>
<class 'bool'>
<class 'bool'>
```

For booleans, True equals to the value of 1 and False to the value of 0. This is why we can do math with booleans. Below we get a value of 0.5, since half of the statements above are true.

```
print(sum(myList)/len(myList))
type(sum(myList)/len(myList))
```

```
0.5
```

```
float
```

String

```
type("This sentence makes sense")
```

```
str
```

```
type("Makes sentense this sense")
```

```
str
```

```
type("math.pi")
```

```
str
```

```
strList = ['dog', 'koala', 'goose']

#the code below gives an error because we can not calculate the mean
↪  on a string
#sum(strList)/len(strList)
```

Nonetype

```
# None
type(None)
```

```
NoneType
```

```
# None
x = None
type(x)
```

```
NoneType
```

```
noneList = [None]*5

##the code below gives an error because we can not calculate the mean
↪  on a NoneType
#sum(nonList)/len(nonList)
```

Lists

A list can hold many types and can also be used to store ordinal information.

```
# List
myList = [1, 1.1, "This is a sentence", None]

for element in myList:
    print(type(element))
```

```
<class 'int'>
<class 'float'>
<class 'str'>
<class 'NoneType'>
```

```
#this would give an error because the list contains categorical data
#sum(myList)/len(myList)
```

```
# List
myList = [1, 2, 3]

for element in myList:
    print(type(element))

sum(myList)/len(myList) # note that this outputs a float
```

```
<class 'int'>
<class 'int'>
<class 'int'>
```

```
2.0
```

While we would see the order in the list below, by default Python does not see this as an ordinal category:

```
myList = ['third', 'first', 'medium', 'small', 'large']

#use an index to access data
myList[0]
```

```
'third'
```

```
myList.sort()
myList
```

```
['first', 'large', 'medium', 'small', 'third']
```

There are more datatypes available when using different libraries such as Pandas and Numpy, which we will introduce to you as we use them.

6 Python Libraries

Python, like other programming languages, has an abundance of additional modules or libraries that augument the base framework and functionality of the language.

Think of a library as a collection of functions that can be accessed to complete certain programming tasks without having to write your own algorithm.

For this course, we will focus primarily on the following libraries:

- **Numpy** is a library for working with arrays of data.
- **Pandas** provides high-performance, easy-to-use data structures and data analysis tools.
- **Scipy** is a library of techniques for numerical and scientific computing.
- **Matplotlib** is a library for making graphs.
- **Seaborn** is a higher-level interface to Matplotlib that can be used to simplify many graphing tasks.
- **Statsmodels** is a library that implements many statistical techniques.

7 Documentation

Reliable and accesible documentation is an absolute necessity when it comes to knowledge transfer of programming languages. Luckily, python provides a significant amount of detailed documentation that explains the ins and outs of the language syntax, libraries, and more.

Understanding how to read documentation is crucial for any programmer as it will serve as a fantastic resource when learning the intricacies of python.

Here is the link to the documentation of the python standard library: Python Standard Library

7.0.1 Importing Libraries

When using Python, you must always begin your scripts by importing the libraries that you will be using.

The following statement imports the numpy and pandas library, and gives them abbreviated names:

```
import numpy as np
import pandas as pd
```

7.0.2 Utilizing Library Functions

After importing a library, its functions can then be called from your code by prepending the library name to the function name. For example, to use the '`dot`' function from the '`numpy`' library, you would enter '`numpy.dot`'. To avoid repeatedly having to type the libary name in your scripts, it is conventional to define a two or three letter abbreviation for each library, e.g. '`numpy`' is usually abbreviated as '`np`'. This allows us to use '`np.dot`' instead of '`numpy.dot`'. Similarly, the Pandas library is typically abbreviated as '`pd`'.

The next cell shows how to call functions within an imported library:

```
a = np.array([0,1,2,3,4,5,6,7,8,9,10])
np.mean(a)
```

```
5.0
```

As you can see, we used the mean() function within the numpy library to calculate the mean of the numpy 1-dimensional array.

8 Data Management

Data management is a crucial component to statistical analysis and data science work. The following code will show how to import data via the pandas library, view your data, and transform your data.

The main data structure that Pandas works with is called a **Data Frame**. This is a two-dimensional table of data in which the rows typically represent cases (e.g. Cartwheel Contest Participants), and the columns represent variables. Pandas also has a one-dimensional data structure called a **Series** that we will encounter when accessing a single column of a Data Frame.

Pandas has a variety of functions named '`read_xxx`' for reading data in different formats. Right now we will focus on reading '`csv`' files, which stands for comma-separated values. However the other file formats include excel, json, and sql just to name a few.

This is a link to the .csv that we will be exploring in this tutorial: Cartwheel Data (Link goes to the dataset section of the Resources for this course)

There are many other options to '`read_csv`' that are very useful. For example, you would use the option `sep='\t'` instead of the default `sep=','` if the fields of your data file are delimited by tabs instead of commas. See here for the full documentation for '`read_csv`'.

8.0.1 Importing Data

```
# Store the url string that hosts our .csv file (note that this is a
↪  different url than in the video)
url = "../data/Cartwheeldata.csv"

# Read the .csv file and store it as a pandas Data Frame
df = pd.read_csv(url)

# Output object type
type(df)
```

```
pandas.core.frame.DataFrame
```

8.0.2 Viewing Data

```
# We can view our Data Frame by calling the head() function
df.head()
```

	ID	Age	Gender	GenderGroup	Glasses	GlassesGroup	Height	Wingspan	CWDistance	Comp
0	1	56	F	1	Y	1	62.0	61.0	79	Y
1	2	26	F	1	Y	1	62.0	60.0	70	Y
2	3	33	F	1	Y	1	66.0	64.0	85	Y
3	4	39	F	1	N	0	64.0	63.0	87	Y
4	5	27	M	2	N	0	73.0	75.0	72	N

The head() function simply shows the first 5 rows of our Data Frame. If we wanted to show the entire Data Frame we would simply write the following:

```
# Output entire Data Frame
df
```

	ID	Age	Gender	GenderGroup	Glasses	GlassesGroup	Height	Wingspan	CWDistance	Com
0	1	56	F	1	Y	1	62.00	61.0	79	Y
1	2	26	F	1	Y	1	62.00	60.0	70	Y
2	3	33	F	1	Y	1	66.00	64.0	85	Y
3	4	39	F	1	N	0	64.00	63.0	87	Y
4	5	27	M	2	N	0	73.00	75.0	72	N
5	6	24	M	2	N	0	75.00	71.0	81	N
6	7	28	M	2	N	0	75.00	76.0	107	Y
7	8	22	F	1	N	0	65.00	62.0	98	Y
8	9	29	M	2	Y	1	74.00	73.0	106	N
9	10	33	F	1	Y	1	63.00	60.0	65	Y
10	11	30	M	2	Y	1	69.50	66.0	96	Y
11	12	28	F	1	Y	1	62.75	58.0	79	Y
12	13	25	F	1	Y	1	65.00	64.5	92	Y
13	14	23	F	1	N	0	61.50	57.5	66	Y
14	15	31	M	2	Y	1	73.00	74.0	72	Y

	ID	Age	Gender	GenderGroup	Glasses	GlassesGroup	Height	Wingspan	CWDistance	Com
15	16	26	M	2	Y	1	71.00	72.0	115	Y
16	17	26	F	1	N	0	61.50	59.5	90	N
17	18	27	M	2	N	0	66.00	66.0	74	Y
18	19	23	M	2	Y	1	70.00	69.0	64	Y
19	20	24	F	1	Y	1	68.00	66.0	85	Y
20	21	23	M	2	Y	1	69.00	67.0	66	N
21	22	29	M	2	N	0	71.00	70.0	101	Y
22	23	25	M	2	N	0	70.00	68.0	82	Y
23	24	26	M	2	N	0	69.00	71.0	63	Y
24	25	23	F	1	Y	1	65.00	63.0	67	N

As you can see, we have a 2-Dimensional object where each row is an independent observation of our cartwheel data.

To gather more information regarding the data, we can view the column names and data types of each column with the following functions:

```
df.columns
```

```
Index([u'ID', u'Age', u'Gender', u'GenderGroup', u'Glasses', u'GlassesGroup',
       u'Height', u'Wingspan', u'CWDistance', u'Complete', u'CompleteGroup',
       u'Score'],
      dtype='object')
```

Lets say we would like to splice our data frame and select only specific portions of our data. There are three different ways of doing so.

1. .loc()
2. .iloc()
3. .ix()

We will cover the .loc() and .iloc() splicing functions.

8.0.3 .loc()

.loc() takes two single/list/range operator separated by ‘,’. The first one indicates the row and the second one indicates columns.

```
# Return all observations of CWDistance
df.loc[:,"CWDistance"]
```

```
0      79
1      70
2      85
3      87
4      72
5      81
6     107
7      98
8     106
9      65
10     96
11     79
12     92
13     66
14     72
15    115
16     90
17     74
18     64
19     85
20     66
21    101
22     82
23     63
24     67
Name: CWDistance, dtype: int64
```

```
# Select all rows for multiple columns, ["CWDistance", "Height",
↪  "Wingspan"]
df.loc[:,["CWDistance", "Height", "Wingspan"]]
```

	CWDistance	Height	Wingspan
0	79	62.00	61.0
1	70	62.00	60.0

	CWDistance	Height	Wingspan
2	85	66.00	64.0
3	87	64.00	63.0
4	72	73.00	75.0
5	81	75.00	71.0
6	107	75.00	76.0
7	98	65.00	62.0
8	106	74.00	73.0
9	65	63.00	60.0
10	96	69.50	66.0
11	79	62.75	58.0
12	92	65.00	64.5
13	66	61.50	57.5
14	72	73.00	74.0
15	115	71.00	72.0
16	90	61.50	59.5
17	74	66.00	66.0
18	64	70.00	69.0
19	85	68.00	66.0
20	66	69.00	67.0
21	101	71.00	70.0
22	82	70.00	68.0
23	63	69.00	71.0
24	67	65.00	63.0

```
# Select few rows for multiple columns, ["CWDistance", "Height",
↪  "Wingspan"]
df.loc[:9, ["CWDistance", "Height", "Wingspan"]]
```

	CWDistance	Height	Wingspan
0	79	62.0	61.0
1	70	62.0	60.0
2	85	66.0	64.0
3	87	64.0	63.0
4	72	73.0	75.0
5	81	75.0	71.0
6	107	75.0	76.0

	CWDistance	Height	Wingspan
7	98	65.0	62.0
8	106	74.0	73.0
9	65	63.0	60.0

```
# Select range of rows for all columns
df.loc[10:15]
```

	ID	Age	Gender	GenderGroup	Glasses	GlassesGroup	Height	Wingspan	CWDistance	Com
10	11	30	M	2	Y	1	69.50	66.0	96	Y
11	12	28	F	1	Y	1	62.75	58.0	79	Y
12	13	25	F	1	Y	1	65.00	64.5	92	Y
13	14	23	F	1	N	0	61.50	57.5	66	Y
14	15	31	M	2	Y	1	73.00	74.0	72	Y
15	16	26	M	2	Y	1	71.00	72.0	115	Y

The .loc() function requires to arguments, the indices of the rows and the column names you wish to observe.

In the above case **:** specifies all rows, and our column is **CWDistance**. df.loc[**:,"CWDistance"**]

Now, let's say we only want to return the first 10 observations:

```
df.loc[:9, "CWDistance"]
```

```
0     79
1     70
2     85
3     87
4     72
5     81
6    107
7     98
8    106
9     65
Name: CWDistance, dtype: int64
```

8.0.4 .iloc()

.iloc() is integer based slicing, whereas .loc() used labels/column names. Here are some examples:

```
#returnrn the first 4 rows up to but not including index 4:
df.iloc[:4]
```

	ID	Age	Gender	GenderGroup	Glasses	GlassesGroup	Height	Wingspan	CWDistance	Comp
0	1	56	F	1	Y	1	62.0	61.0	79	Y
1	2	26	F	1	Y	1	62.0	60.0	70	Y
2	3	33	F	1	Y	1	66.0	64.0	85	Y
3	4	39	F	1	N	0	64.0	63.0	87	Y

```
df.iloc[1:5, 2:4]
```

	Gender	GenderGroup
1	F	1
2	F	1
3	F	1
4	M	2

```
#loc does not allow for labels, so below gives an error:
#df.iloc[1:5, ["Gender", "GenderGroup"]]
```

8.1 Explore what datatypes we work with using dtypes

We can view the data types of our data frame columns with by calling .dtypes on our data frame:

```
df.dtypes
```

```
ID                int64
Age               int64
Gender           object
GenderGroup       int64
Glasses          object
GlassesGroup      int64
Height          float64
Wingspan        float64
CWDistance        int64
Complete         object
CompleteGroup     int64
Score             int64
dtype: object
```

The output indicates we have integers, floats, and objects with our Data Frame.

8.2 Print unique values

We may also want to observe the different unique values within a specific column, lets do this for Gender:

```
# List unique values in the df['Gender'] column
df.Gender.unique()
```

```
array(['F', 'M'], dtype=object)
```

```
# Lets explore df["GenderGroup] as well
df.GenderGroup.unique()
```

```
array([1, 2])
```

It seems that these fields may serve the same purpose, which is to specify male vs. female. Lets check this quickly by observing only these two columns:

```
# Use .loc() to specify a list of mulitple column names
df.loc[:,["Gender", "GenderGroup"]]
```

	Gender	GenderGroup
0	F	1
1	F	1
2	F	1
3	F	1
4	M	2
5	M	2
6	M	2
7	F	1
8	M	2
9	F	1
10	M	2
11	F	1
12	F	1
13	F	1
14	M	2
15	M	2
16	F	1
17	M	2
18	M	2
19	F	1
20	M	2
21	M	2
22	M	2
23	M	2
24	F	1

8.3 Summarizing multiple columns using groupby

From eyeballing the output, it seems to check out. We can streamline this by utilizing the groupby() and size() functions.

```
df.groupby(['Gender','GenderGroup']).size()
```

```
Gender  GenderGroup
F       1              12
M       2              13
dtype: int64
```

This output indicates that we have two types of combinations.

- Case 1: Gender = F & Gender Group = 1
- Case 2: Gender = M & GenderGroup = 2.

This validates our initial assumption that these two fields essentially portray the same information.

9 Using Python to read data files and explore their contents

This notebook demonstrates using the Pandas data processing library to read a dataset into Python, and obtain a basic understanding of its contents.

Note that Python by itself is a general-purpose programming language and does not provide high-level data processing capabilities. The Pandas library was developed to meet this need. Pandas is the most popular Python library for data manipulation, and we will use it extensively in this course.

In addition to Pandas, we will also make use of the following Python libraries

- Numpy is a library for working with arrays of data
- Matplotlib is a library for making graphs
- Seaborn is a higher-level interface to Matplotlib that can be used to simplify many graphing tasks
- Statsmodels is a library that implements many statistical techniques
- Scipy is a library of techniques for numerical and scientific computing

9.0.1 Importing libraries

When using Python, you must always begin your scripts by importing the libraries that you will be using. After importing a library, its functions can then be called from your code by prepending the library name to the function name. For example, to use the '`dot`' function from the '`numpy`' library, you would enter '`numpy.dot`'. To avoid repeatedly having to type the libary name in your scripts, it is conventional to define a two or three letter abbreviation for each library, e.g. '`numpy`' is usually abbreviated as '`np`'. This allows us to use '`np.dot`' instead of '`numpy.dot`'. Similarly, the Pandas library is typically abbreviated as '`pd`'.

The following statement imports the Pandas library, and gives it the abbreviated name 'pd'.

```
import pandas as pd
```

9.0.2 Reading a data file

We will be working with the NHANES (National Health and Nutrition Examination Survey) data from the 2015-2016 wave, which has been discussed earlier in this course. The raw data for this study are available here:

https://wwwn.cdc.gov/nchs/nhanes/Default.aspx

As in many large studies, the NHANES data are spread across multiple files. The NHANES files are stored in SAS transport (Xport) format. This is a somewhat obscure format, and while Pandas is perfectly capable of reading the NHANES data directly from the xport files, accomplishing this task is a more advanced topic than we want to get into here. Therefore, for this course we have prepared some merged datasets in text/csv format.

Pandas is a large and powerful library. Here we will only use a few of its basic features. The main data structure that Pandas works with is called a "data frame". This is a two-dimensional table of data in which the rows typically represent cases (e.g. NHANES subjects), and the columns represent variables. Pandas also has a one-dimensional data structure called a `Series` that we will encounter occasionally.

Pandas has a variety of functions named with the pattern '`read_xxx`' for reading data in different formats into Python. Right now we will focus on reading '`csv`' files, so we are using the '`read_csv`' function, which can read csv (and "tsv") format files that are exported from spreadsheet software like Excel. The '`read_csv`' function by default expects the first row of the data file to contain column names.

Using '`read_csv`' in its default mode is fairly straightforward. There are many options to '`read_csv`' that are useful for handling less-common situations. For example, you would use the option `sep='\t'` instead of the default `sep=','` if the fields of your data file are delimited by tabs instead of commas. See here for the full documentation for '`read_csv`'.

Pandas can read a data file over the internet when provided with a URL, which is what we will do below. In the Python script we will name the data set '`da`', i.e. this is the name of the Python variable that will hold the data frame after we have loaded it.

The variable '`url`' holds a string (text) value, which is the internet URL where the data are located. If you have the data file in your local filesystem, you can also use '`read_csv`' to read the data from this file. In this case you would pass a file path instead of a URL, e.g. `pd.read_csv("my_file.csv")` would read a file named `my_file.csv` that is located in your current working directory.

```
url = "../data/nhanes_2015_2016.csv"
da = pd.read_csv(url)
```

To confirm that we have actually obtained the data the we are expecting, we can display the shape (number of rows and columns) of the data frame in the notebook. Note that the final expression in any Jupyter notebook cell is automatically printed, but you can force other expressions to be printed by using the '`print`' function, e.g. '`print(da.shape)`'.

Based on what we see below, the data set being read here has 5735 rows, corresponding to 5735 people in this wave of the NHANES study, and 28 columns, corresponding to 28 variables in this particular data file. Note that NHANES collects thousands of variables on each study subject, but here we are working with a reduced file that contains a limited number of variables.

```
da.shape
```

```
(5735, 28)
```

9.0.3 Exploring the contents of a data set

Pandas has a number of basic ways to understand what is in a data set. For example, above we used the '`shape`' method to determine the numbers of rows and columns in a data set. The columns in a Pandas data frame have names, to see the names, use the '`columns`' method:

```
da.columns
```

```
Index(['SEQN', 'ALQ101', 'ALQ110', 'ALQ130', 'SMQ020', 'RIAGENDR', 'RIDAGEYR',
       'RIDRETH1', 'DMDCITZN', 'DMDEDUC2', 'DMDMARTL', 'DMDHHSIZ', 'WTINT2YR',
       'SDMVPSU', 'SDMVSTRA', 'INDFMPIR', 'BPXSY1', 'BPXDI1', 'BPXSY2',
       'BPXDI2', 'BMXWT', 'BMXHT', 'BMXBMI', 'BMXLEG', 'BMXARML', 'BMXARMC',
       'BMXWAIST', 'HIQ210'],
      dtype='object')
```

These names correspond to variables in the NHANES study. For example, `SEQN` is a unique identifier for one person, and `BMXWT` is the subject's weight in kilograms ("BMX" is the NHANES prefix for body measurements). The variables in the NHANES data set are

documented in a set of "codebooks" that are available on-line. The codebooks for the 2015-2016 wave of NHANES can be found by following the links at the following page:

https://wwwn.cdc.gov/nchs/nhanes/continuousnhanes/default.aspx?BeginYear=2015

For convenience, direct links to some of the code books are included below:

- Demographics code book
- Body measures code book
- Blood pressure code book
- Alcohol questionaire code book
- Smoking questionaire code book

Every variable in a Pandas data frame has a data type. There are many different data types, but most commonly you will encounter floating point values (real numbers), integers, strings (text), and date/time values. When Pandas reads a text/csv file, it guesses the data types based on what it sees in the first few rows of the data file. Usually it selects an appropriate type, but occasionally it does not. To confirm that the data types are consistent with what the variables represent, inspect the '`dtypes`' attribute of the data frame.

```
da.dtypes
```

```
SEQN          int64
ALQ101      float64
ALQ110      float64
ALQ130      float64
SMQ020        int64
RIAGENDR      int64
RIDAGEYR      int64
RIDRETH1      int64
DMDCITZN    float64
DMDEDUC2    float64
DMDMARTL    float64
DMDHHSIZ      int64
WTINT2YR    float64
SDMVPSU       int64
SDMVSTRA      int64
INDFMPIR    float64
BPXSY1      float64
```

```
BPXDI1      float64
BPXSY2      float64
BPXDI2      float64
BMXWT       float64
BMXHT       float64
BMXBMI      float64
BMXLEG      float64
BMXARML     float64
BMXARMC     float64
BMXWAIST    float64
HIQ210      float64
dtype: object
```

As we see here, most of the variables have floating point or integer data type. Unlike many data sets, NHANES does not use any text values in its data. For example, while many datasets would use text labels like "F" or "M" to denote a subject's gender, this information is represented in NHANES with integer codes. The actual meanings of these codes can be determined from the codebooks. For example, the variable `RIAGENDR` contains each subject's gender, with male gender coded as `1` and female gender coded as `2`. The `RIAGENDR` variable is part of the demographics component of NHANES, so this coding can be found in the demographics codebook.

Variables like `BMXWT` which represent a quantitative measurement will typically be stored as floating point data values.

9.0.4 Slicing a data set

As discussed above, a Pandas data frame is a rectangular data table, in which the rows represent cases and the columns represent variables. One common manipulation of a data frame is to extract the data for one case or for one variable. There are several ways to do this, as shown below.

To extract all the values for one variable, the following three approaches are equivalent ("DMDEDUC2" here is an NHANES variable containing a person's educational attainment). In these four lines of code, we are assigning the data from one column of the data frame `da` into new variables `w`, `x`, `y`, and `z`. The first three approaches access the variable by name. The fourth approach accesses the variable by position (note that `DMDEDUC2` is in position 9 of the `da.columns` array shown above – remember that Python counts starting at position zero).

```
w = da["DMDEDUC2"]
x = da.loc[:, "DMDEDUC2"]
y = da.DMDEDUC2
z = da.iloc[:, 9]  # DMDEDUC2 is in column 9
```

Another reason to slice a variable out of a data frame is so that we can then pass it into a function. For example, we can find the maximum value over all `DMDEDUC2` values using any one of the following four lines of code:

```
print(da["DMDEDUC2"].max())
print(da.loc[:, "DMDEDUC2"].max())
print(da.DMDEDUC2.max())
print(da.iloc[:, 9].max())
```

```
9.0
9.0
9.0
9.0
```

Every value in a Python program has a type, and the type information can be obtained using Python's '`type`' function. This can be useful, for example, if you are looking for the documentation associated with some value, but you do not know what the value's type is.

Here we see that the variable `da` has type 'DataFrame', while one column of `da` has type 'Series'. As noted above, a Series is a Pandas data structure for holding a single column (or row) of data.

```
print(type(da)) # The type of the variable
print(type(da.DMDEDUC2)) # The type of one column of the data frame
print(type(da.iloc[2,:])) # The type of one row of the data frame
```

```
<class 'pandas.core.frame.DataFrame'>
<class 'pandas.core.series.Series'>
<class 'pandas.core.series.Series'>
```

It may also be useful to slice a row (case) out of a data frame. Just as a data frame's columns have names, the rows also have names, which are called the "index". However many data sets do not have meaningful row names, so it is more common to extract a row

of a data frame using its position. The `iloc` method slices rows or columns from a data frame by position (counting from 0). The following line of code extracts row 3 from the data set (which is the fourth row, counting from zero).

```
x = da.iloc[3, :]
```

Another important data frame manipulation is to extract a contiguous block of rows or columns from the data set. Below we slice by position, in the first case taking row positions 3 and 4 (counting from 0, which are rows 4 and 5 counting from 1), and in the second case taking columns 2, 3, and 4 (columns 3, 4, 5 if counting from 1).

```
x = da.iloc[3:5, :]
y = da.iloc[:, 2:5]
```

9.0.5 Missing values

When reading a dataset using Pandas, there is a set of values including 'NA', 'NULL', and 'NaN' that are taken by default to represent a missing value. The full list of default missing value codes is in the '`read_csv`' documentation here. This document also explains how to change the way that '`read_csv`' decides whether a variable's value is missing.

Pandas has functions called `isnull` and `notnull` that can be used to identify where the missing and non-missing values are located in a data frame. Below we use these functions to count the number of missing and non-missing `DMDEDUC2` values.

```
print(pd.isnull(da.DMDEDUC2).sum())
print(pd.notnull(da.DMDEDUC2).sum())
```

```
261
5474
```

As an aside, note that there may be a variety of distinct forms of missingness in a variable, and in some cases it is important to keep these values distinct. For example, in case of the DMDEDUC2 variable, in addition to the blank or NA values that Pandas considers to be missing, three people responded "don't know" (code value 9). In many analyses, the "don't know" values will also be treated as missing, but at this point we are considering "don't know" to be a distinct category of observed response.

10 Python Resources

The purpose of this document is to direct you to resources that you may find useful if you decide to do a deeper dive into Python. This course is not meant to be an introduction to programming, nor an introduction to Python, but if you find yourself interested in exploring Python further, or feel as if this is a useful skill, this document aims to direct you to resources that you may find useful. If you have a background in Python or programming, a style guides are included below to show how Python may differ from other programming languages or give you a launching point for diving deeper into more advanced packages. This course does not endorse the use or non-use of any particular resource, but the author has found these resources useful in their exploration of programming and Python in particular

10.0.1 The Python Documentation

Any reference that does not begin with the Python documentation would not be complete. The authors of the language, as well as the community that supports it, have developed a great set of tutorials, documentation, and references around Python. When in doubt, this is often the first place that you should look if you run into a scary error or would like to learn more about a specific function. The documentation can be found here: Python Documentation

10.0.2 Python Programming Introductions

Below are resources to help you along your way in learning Python. While it is great to consume material, in programming there is no substitute for actually writing code. For every hour that you spend learning, you should spend about twice that amount of time writing code for cool problems or working out examples. Coding is best learned through actually coding!

- Coursera has several offerings for Python that you can take in addition to this course. These courses will go into depth into Python programming and how to use it in an applied setting

- Code Academy is another resources that is great for learning Python (and other programming languages). While not as focused as Cousera, this is a quick way to get up-and-running with Python
- YouTube is another great resource for online learning and there are several "courses" for learning Python. We recommend trying several sets of videos to see which you like best and using multiple video series to learn since each will present the material in a slightly different way
- There are tens of books on programming in Python that are great if you prefer to read. More so than the other resources, be sure to code what you learn. It is easy to read about coding, but you really learn to code by coding!
- If you have a background in coding, the authors have found the tutorial at Tutorials Point to be useful in getting started with Python. This tutorial assumes that you have some background in coding in another language

10.0.3 Cheatsheets and References

There are a variety of one-pagers and cheat-sheets available for Python that summarize the language in a few simple pages. These resources tend to be more aimed at someone who knows the language, or has experience in the language, but would like a refresher course in how the language works.

- Cheatsheet for Numpy
- Cheatsheet for Datawrangling
- Cheatsheet for Pandas
- Cheatsheet for SciPy
- Cheatsheet for Matplotlib

10.0.4 Python Style Guides

As you learn to code, you will find that you will begin to develop your own style. Sometimes this is good. Most times, this can be detrimental to your code readability and, worse, can hinder you from finding bugs in your own code in extreme cases.

It is best to learn good coding habits from the beginning and the Google Style Guide is a great place to start. We will mention some of these best practices here.

10.0.4.1 Consistent Indenting

Python will generally 'yell' at you if your indenting is incorrect. It is good to use an editor that takes care of this for you. In general, four spaces are preferred for indenting and you should not mix tabs and spaces.

```
# Good Indenting - four spaces are standard but consistiency is key
result = []
for x in range(10):
    for y in range(5):
        if x * y > 10:
            result.append((x, y))
print (result)

# Bad indenting
result = []
for x in range(10):
  for y in range(5):
     if x * y > 10:
                result.append((x, y))
print (result)
```

10.0.4.2 Commenting

Comments seem weird when you first begin programming - why would I include 'code' that doesn't run? Comments are probably some of the most important aspects of code. They help other read code that is difficult for them to understand, and they, more importantly, are helpful for yourself if you look at the code in a few weeks and need clarity on why you did something. Always comment and comment well.

```
################################################################################
#
↪  #
#                                Good Commenting
↪  #
#
↪  #
################################################################################
```

```
################################ Bad Commenting
↪  ################################

# My loop
for x in range(10):
    print (x)

############################## Better Commenting
↪  ##############################

# Looping from zero to ten
for x in range(10):
    print (x)

############################## Preferred Commenting
↪  ##############################

# Print out the numbers from zero to ten
for x in range(10):
    print (x)
```

```
###############################################################################
#
↪  #
#                          Mixing Commenting Strategies
↪  #
#
↪  #
###############################################################################

# Try not to mix commenting styles in the same blocks - just be
↪  consistient

########### Bad - mixing doc-strings commenting and line commenting
↪  ############

''' Printing one to five, a six, and then six to nine'''
```

```
for x in range(10):
    # If x > 5, then print the value
    if x > 5:
        print (x)
    else:
        print (x + 1)

###################### Good - no mixing of comment types
↪  ########################

# Printing one to five, a six, and then six to nine
for x in range(10):
    # If x > 5, then print the value
    if x > 5:
        print (x)
    else:
        print (x + 1)
```

10.0.4.3 Line Length

Try to avoid excessively long lines. Standard practice is to keep lines to no longer than 80 characters. While this is not a hard rule, it is a good practice to follow for readability

```
########################## Bad - This code is too long
↪  ############################

my_random_array = [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 1, 2, 3, 4, 5, 6,
↪  7, 8, 9, 10, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 1, 2, 3, 4, 5, 6, 7,
↪  8, 9, 10]

############ Good - this code is wrapped to avoid excessive length
↪  #############

my_random_array = [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 1, 2, 3, 4, 5, 6,
↪  7, 8, 9,
                   10, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 1, 2, 3, 4, 5,
                   ↪  6, 7, 8,
                   9, 10]
```

10.0.4.4 White Space

Utilizing Whitespace is a great way to improve the way that your code looks. In general the following can be helpful to improve the look of your code

- Try to space out your code and introduce whitespace to improve readability
- Use spacing to separate function arguments
- Do not over-do spacing. Too many spaces between code blocks makes it difficult to organize code well

```
################ Bad - this code has bad whitespace management
↪  #################

my_player = player()
player_attributes = get_player_attributes(my_player,height,weight,
↪  birthday)


player_attributes[0]*=12 # convert from feet to inches




player.shoot_ball()


########################## Good whitespace management
↪  ##########################

my_player = player()
player_attributes = get_player_attributes(my_player, height, weight,
↪  birthday)

# convert from feet to inches
player_attributes[0] *= 12

player.shoot_ball()
```

10.0.4.5 The tip of the iceberg

Take a look at code out in the wild if you are really curious. How are they coding specific things? How do they manage spacing in loops? How do they manage the whitespace in argument list?

You will learn to code by coding, and you will develop your own style but starting out with good habits ensures that your code is easy to read by others and, most importantly, yourself. Good luck!

11 Python Libraries

For this tutorial, we are going to outline the most common uses for each of the following libraries:

- **Numpy** is a library for working with arrays of data.
- **Scipy** is a library of techniques for numerical and scientific computing.
- **Matplotlib** is a library for making visualizations.
- **Seaborn** is a higher-level interface to Matplotlib that can be used to simplify many visualization tasks.

***Important**: While this tutorial provides insight into the basics of these libraries, I recommend digging into the documentation that is available online.*

11.1 NumPy

NumPy is the fundamental package for scientific computing with Python. It contains among other things:

- a powerful N-dimensional array object
- sophisticated (broadcasting) functions
- tools for integrating C/C++ and Fortran code
- useful linear algebra, Fourier transform, and random number capabilities

We will focus on the numpy array object.

11.1.1 Numpy Array

A numpy array is a grid of values, all of the same type, and is indexed by a tuple of nonnegative integers. The number of dimensions is the rank of the array; the shape of an array is a tuple of integers giving the size of the array along each dimension.

```
import numpy as np
```

```
### Create a 3x1 numpy array
a = np.array([1,2,3])
print(a)

### Print object type
print(type(a))
```

```
[1 2 3]
<class 'numpy.ndarray'>
```

```
### Print shape
#we have a one dimensional object with 3 values
print(a.shape)
```

```
(3,)
```

```
### Print some values in a
print(a[0], a[1], a[2])
```

```
1 2 3
```

```
### Create a 2x2 numpy array using a nested list
b = np.array([[1,2],[3,4]])
print(b)
```

```
[[1 2]
 [3 4]]
```

```
### Print shape
# we now have a two dimensional array (with 2 rows and 2 columns)
```

```
print(b.shape)
```

```
(2, 2)
```

```
#in row two, access the the first value
#here we index, specifying the row first and then the column position
#don't forget: in py we start counting at 0
print(b[1,0])
```

```
3
```

```
## Print several values in b
print(b[0,0], b[0,1], b[1,1])
```

```
1 2 4
```

```
### Create a 3x2 numpy array
c = np.array([[1,2],[3,4],[5,6]])
c
```

```
array([[1, 2],
       [3, 4],
       [5, 6]])
```

```
### Print shape
print(c.shape)
```

```
(3, 2)
2 3 5 6
```

```
### Print some values in c
print(c[0,1], c[1,0], c[2,0], c[2,1])
```

```
2 3 5 6
```

11.1.1.1 Create numpy arrays with different automatic numberings

```
### create a 2x3 zero array with only 0s
d = np.zeros((2,3))

print(d)
```

```
[[0. 0. 0.]
 [0. 0. 0.]]
```

```
### 4x2 array of ones
e = np.ones((4,2))

print(e)
```

```
[[1. 1.]
 [1. 1.]
 [1. 1.]
 [1. 1.]]
```

```
### create 2x2 constant array with a specified value
#we first give the nr of rows and columns we want, followed by the
 ↪  constant value
f = np.full((2,2), 9)

print(f)
```

```
[[9 9]
 [9 9]]
```

```
### create a 3x3 random array with random nrs
g = np.random.random((3,3))

print(g)
```

```
[[0.75578673 0.52378499 0.68715926]
 [0.09153656 0.89729222 0.85334664]
 [0.34651959 0.06094491 0.15857276]]
```

11.1.2 Array Indexing

```
### Create 3x4 array
h = np.array([[1,2,3,4,], [5,6,7,8], [9,10,11,12]])

print(h)
```

```
[[ 1  2  3  4]
 [ 5  6  7  8]
 [ 9 10 11 12]]
```

```
print(h[0,1])
```

```
2
```

```
### Slice array to make a 2x2 sub-array
#first we select rows with index 0 and 1 (so up to but not including
↪  2)
#then we further select columns with index 1 and 2
i = h[:2, 1:3]

print(i)
```

```
[[2 3]
 [6 7]]
```

```
### Modify something in the slice
i[0,0] = 1738
print(i)
```

```
[[1738    3]
 [   6    7]]
```

```
#notice how this value is also changed in our original array h!
print(h)
```

```
[[   1 1738    3    4]
 [   5    6    7    8]
 [   9   10   11   12]]
```

11.1.3 Datatypes in Arrays

```
### Integer
j = np.array([1, 2])
print(j)
print(j.dtype)
```

```
[1 2]
int64
```

```
### Float
k = np.array([1.2, 2.0])
print(k)
print(k.dtype)
```

```
[1.2 2. ]
float64
```

```
### Force Data Type
l = np.array([1.0, 2.0], dtype = np.int64)
print(l)
print(l.dtype)
```

```
[1 2]
int64
```

11.1.4 Array Math

Basic mathematical functions operate elementwise on arrays, and are available both as operator overloads and as functions in the numpy module:

```
x = np.array([[1,2],[3,4]], dtype = np.float64)
y = np.array([[5,6],[7,8]], dtype = np.float64)
print(x)
```

```
[[1. 2.]
 [3. 4.]]
```

```
print(y)
```

```
[[5. 6.]
 [7. 8.]]
```

```
# Elementwise sum; both produce the array
# [[ 6.0  8.0]
#  [10.0 12.0]]
print(x + y)
```

```
[[ 6.  8.]
 [10. 12.]]
```

```
print(np.add(x, y))
```

```
[[ 6.  8.]
 [10. 12.]]
```

```
# Elementwise difference; both produce the array
# [[-4.0 -4.0]
#  [-4.0 -4.0]]
print(x - y)
```

```
[[-4. -4.]
 [-4. -4.]]
```

```
print(np.subtract(x, y))
```

```
[[-4. -4.]
 [-4. -4.]]
```

```
# Elementwise product; both produce the array
# [[ 5.0 12.0]
#  [21.0 32.0]]
print(x * y)
```

```
[[ 5. 12.]
 [21. 32.]]
```

```
print(np.multiply(x, y))
```

```
[[ 5. 12.]
 [21. 32.]]
```

```
# Elementwise division; both produce the array
# [[ 0.2         0.33333333]
#  [ 0.42857143  0.5       ]]
print(x / y)
```

```
[[0.2        0.33333333]
 [0.42857143 0.5       ]]
```

```
print(np.divide(x, y))
```

```
[[0.2        0.33333333]
 [0.42857143 0.5       ]]
```

```
# Elementwise square root; produces the array
# [[ 1.          1.41421356]
#  [ 1.73205081  2.        ]]
print(np.sqrt(x))
```

```
[[1.         1.41421356]
 [1.73205081 2.        ]]
```

11.1.5 Descriptive statistics with numpy

```
x = np.array([[1,2],[3,4]])
x
```

```
array([[1, 2],
       [3, 4]])
```

```
### Compute sum of all elements; prints "10"
print(np.sum(x))
```

```
10
```

```
### Compute sum of each column; prints "[4 6]"
print(np.sum(x, axis=0))
```

```
[4 6]
```

```
### Compute sum of each row; prints "[3 7]"
print(np.sum(x, axis=1))
```

```
[3 7]
```

```
### Compute mean of all elements; prints "2.5"
print(np.mean(x))
```

```
2.5
```

```
### Compute mean of each column; prints "[2 3]"
print(np.mean(x, axis=0))
```

```
[2. 3.]
```

```
### Compute mean of each row; prints "[1.5 3.5]"
print(np.mean(x, axis=1))
```

```
[1.5 3.5]
```

11.2 SciPy

Numpy provides a high-performance multidimensional array and basic tools to compute with and manipulate these arrays. SciPy builds on this, and provides a large number of functions that operate on numpy arrays and are useful for different types of scientific and engineering applications.

For this course, we will primariyl be using the **SciPy.Stats** sub-library.

11.2.1 SciPy.Stats

The SciPy.Stats module contains a large number of probability distributions as well as a growing library of statistical functions such as:

- Continuous and Discrete Distributions (i.e Normal, Uniform, Binomial, etc.)
- Descriptive Statistcs
- Statistical Tests (i.e T-Test)

```
from scipy import stats
import numpy as np
```

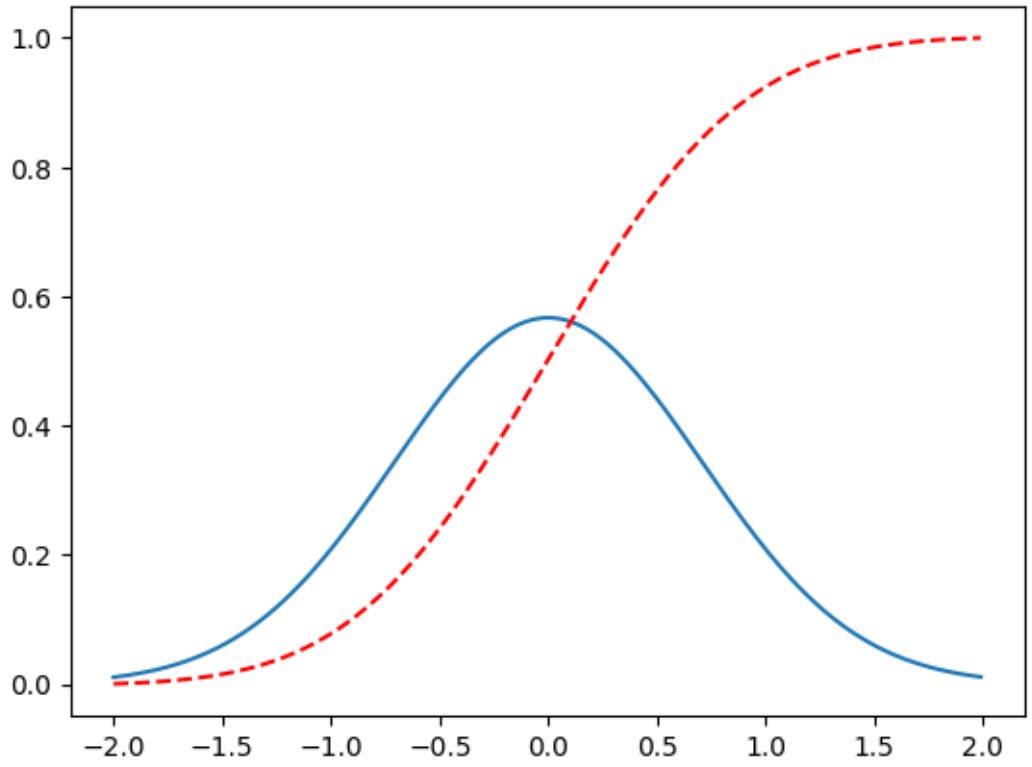
```
### Print 10 Normal Random Variables
print(stats.norm.rvs(size = 10))
```

```
[ 1.2273344  -1.18292396  0.06328786 -1.08124849 -0.6143745   0.703326
  1.11746254  1.06465073  0.64391558 -1.8944723 ]
```

```
from pylab import *

# Create some test data
dx = .01
X  = np.arange(-2,2,dx)
Y  = exp(-X**2)

#print(X)
#print(Y)
```

```
# Normalize the data to a proper PDF
Y /= (dx*Y).sum()

# Compute the CDF
CY = np.cumsum(Y*dx)

# Plot both
plot(X,Y)
```

```
plot(X,CY,'r--')

show()
```




```
### Compute the Normal CDF of certain values.
#this returns some probabilites based on the plot above
print(stats.norm.cdf(np.array([1,-1., 0, 1, 3, 4, -2, 6])))
```

```
[0.84134475 0.15865525 0.5        0.84134475 0.9986501  0.99996833
 0.02275013 1.        ]
```

11.2.1.1 Descriptive Statistics

```
np.random.seed(282629734)

# Generate 1000 Student's T continuous random variables.
x = stats.t.rvs(10, size=1000)
```

```
# Do some descriptive statistics
print(x.min())   # equivalent to np.min(x)
```

```
-3.7897557242248197
```

```
print(x.max())   # equivalent to np.max(x)
```

```
5.263277329807165
```

```
print(x.mean())  # equivalent to np.mean(x)
```

```
0.014061066398468422
```

```
print(x.var())   # equivalent to np.var(x))
```

```
1.288993862079285
```

```
stats.describe(x)
```

```
DescribeResult(nobs=1000, minmax=(-3.7897557242248197, 5.263277329807165), mean=0.014061066
```

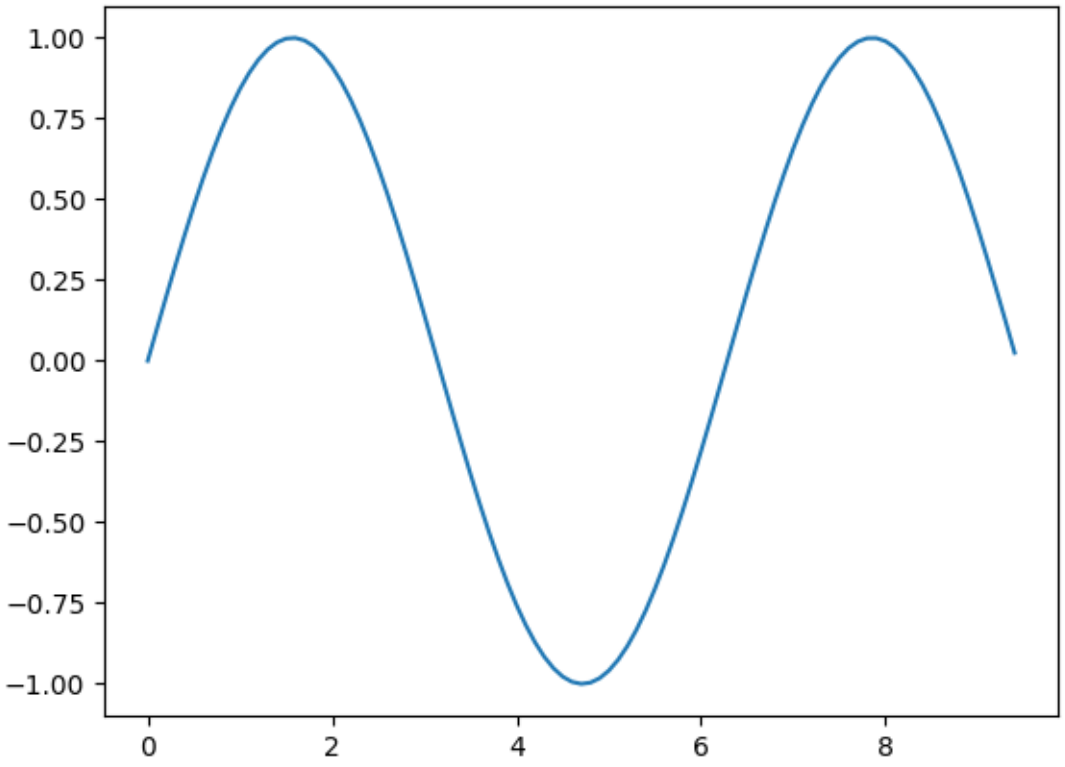
Later in the course, we will discuss distributions and statistical tests such as a T-Test. SciPy has built in functions for these operations.

11.3 MatPlotLib

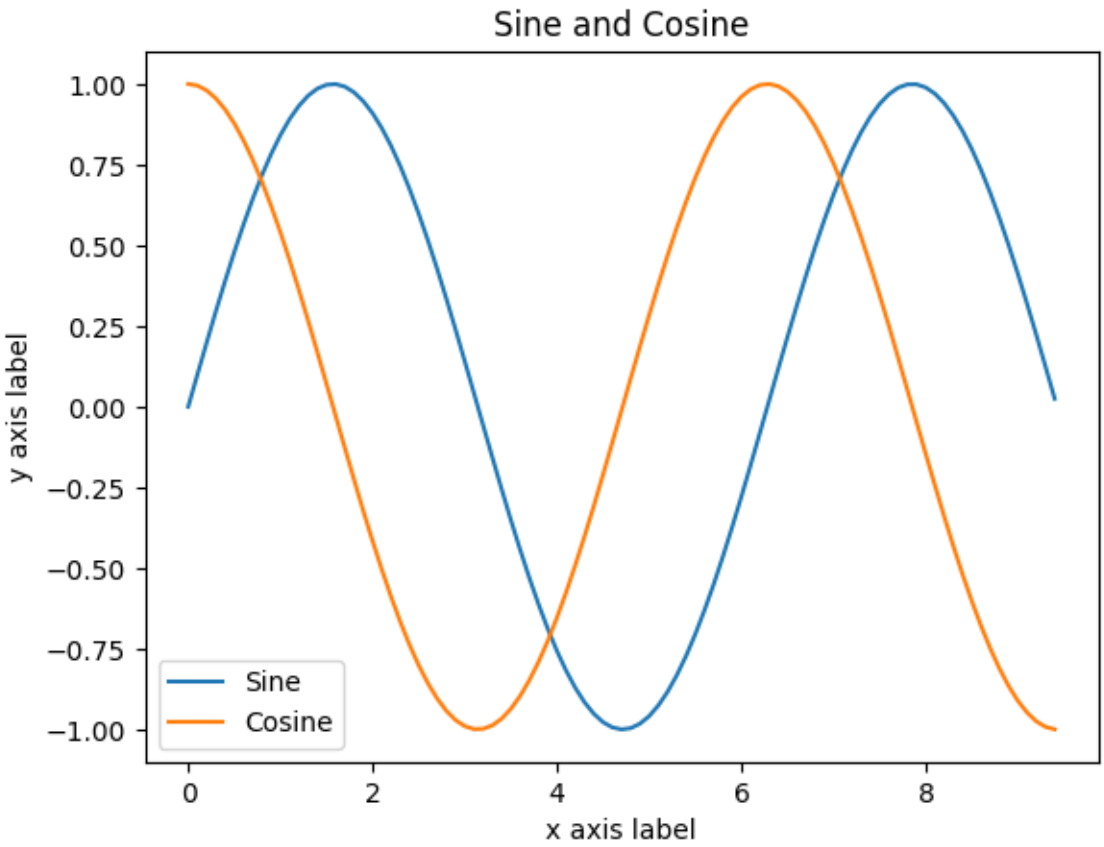
Matplotlib is a plotting library. In this section give a brief introduction to the matplotlib.pyplot module.

```
import numpy as np
import matplotlib.pyplot as plt
```

```
# Compute the x and y coordinates for points on a sine curve
x = np.arange(0, 3 * np.pi, 0.1)
y = np.sin(x)

# Plot the points using matplotlib
plt.plot(x, y)
plt.show()  # You must call plt.show() to make graphics appear.
```

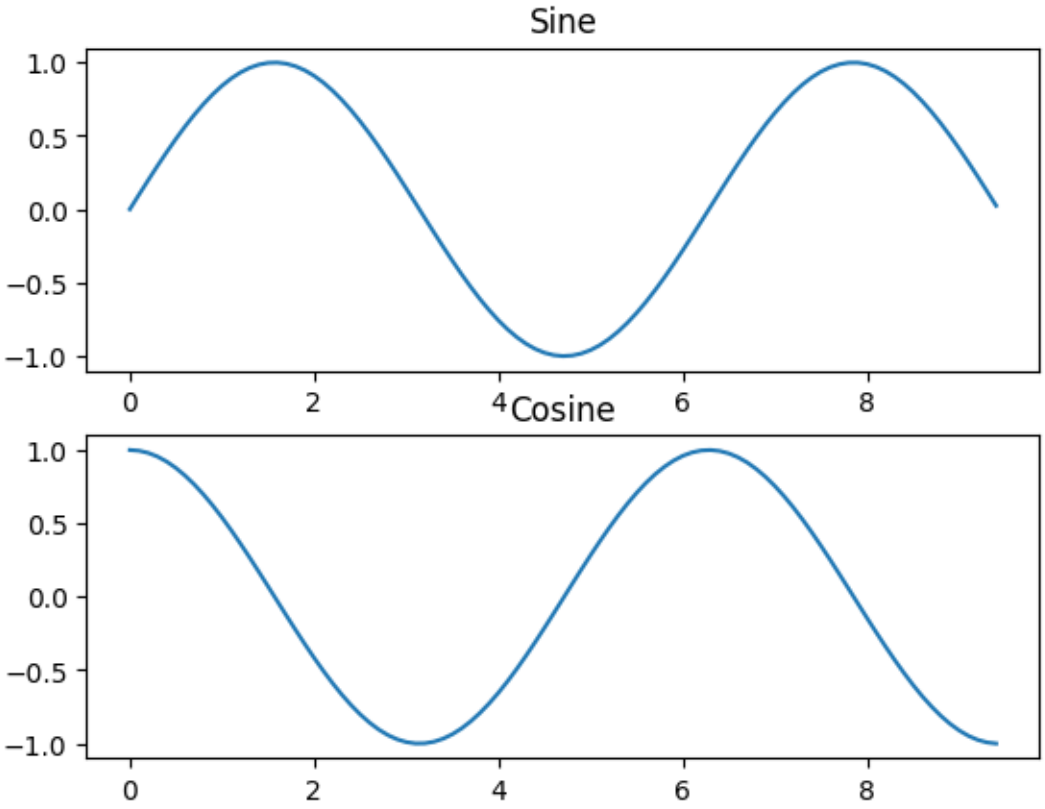


```
# Compute the x and y coordinates for points on sine and cosine
↪  curves
x = np.arange(0, 3 * np.pi, 0.1)
y_sin = np.sin(x)
y_cos = np.cos(x)

# Plot the points using matplotlib
plt.plot(x, y_sin)
plt.plot(x, y_cos)
plt.xlabel('x axis label')
plt.ylabel('y axis label')
plt.title('Sine and Cosine')
plt.legend(['Sine', 'Cosine'])
plt.show()
```



11.3.0.1 Subplots

```
import numpy as np
import matplotlib.pyplot as plt

# Compute the x and y coordinates for points on sine and cosine
↪  curves
x = np.arange(0, 3 * np.pi, 0.1)
y_sin = np.sin(x)
y_cos = np.cos(x)

# Set up a subplot grid that has height 2 and width 1,
# and set the first such subplot as active.
plt.subplot(2, 1, 1)

# Make the first plot
plt.plot(x, y_sin)
plt.title('Sine')

# Set the second subplot as active, and make the second plot.
plt.subplot(2, 1, 2)
plt.plot(x, y_cos)
plt.title('Cosine')

# Show the figure.
plt.show()
```



11.4 Seaborn

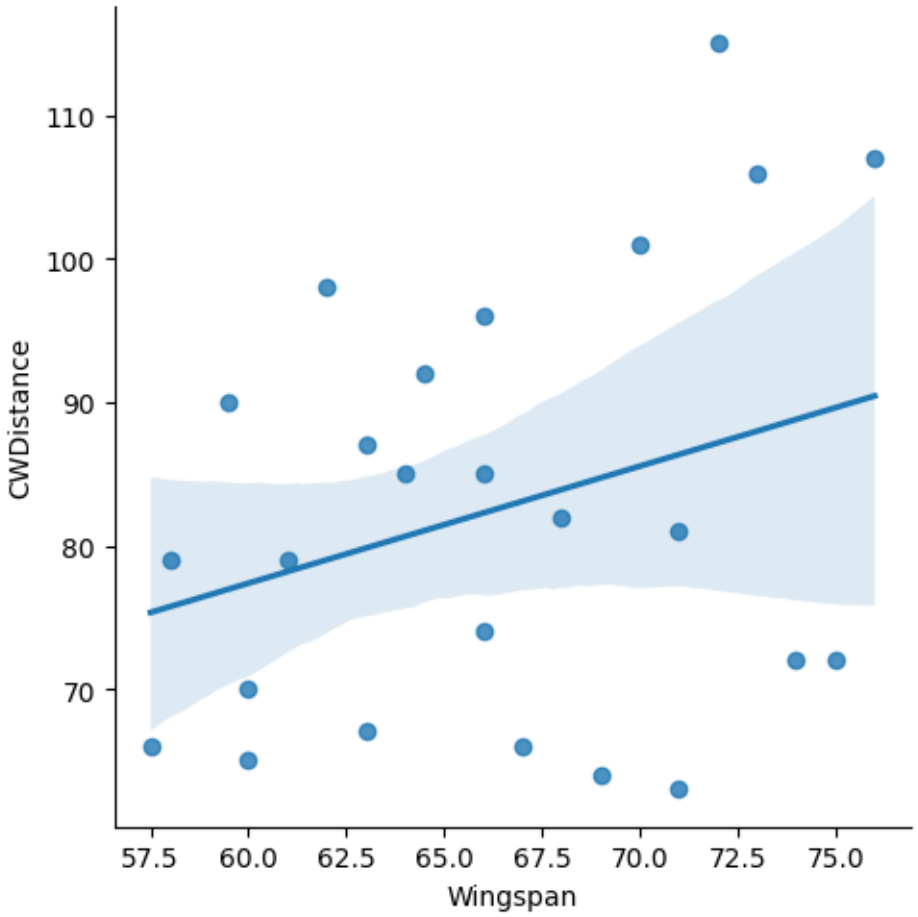
Seaborn is complimentary to Matplotlib and it specifically targets statistical data visualization. But it goes even further than that: Seaborn extends Matplotlib and makes generating visualizations convenient.

While Matplotlib is a robust solution for various problems, Seaborn utilizes more concise parameters for ease-of-use.

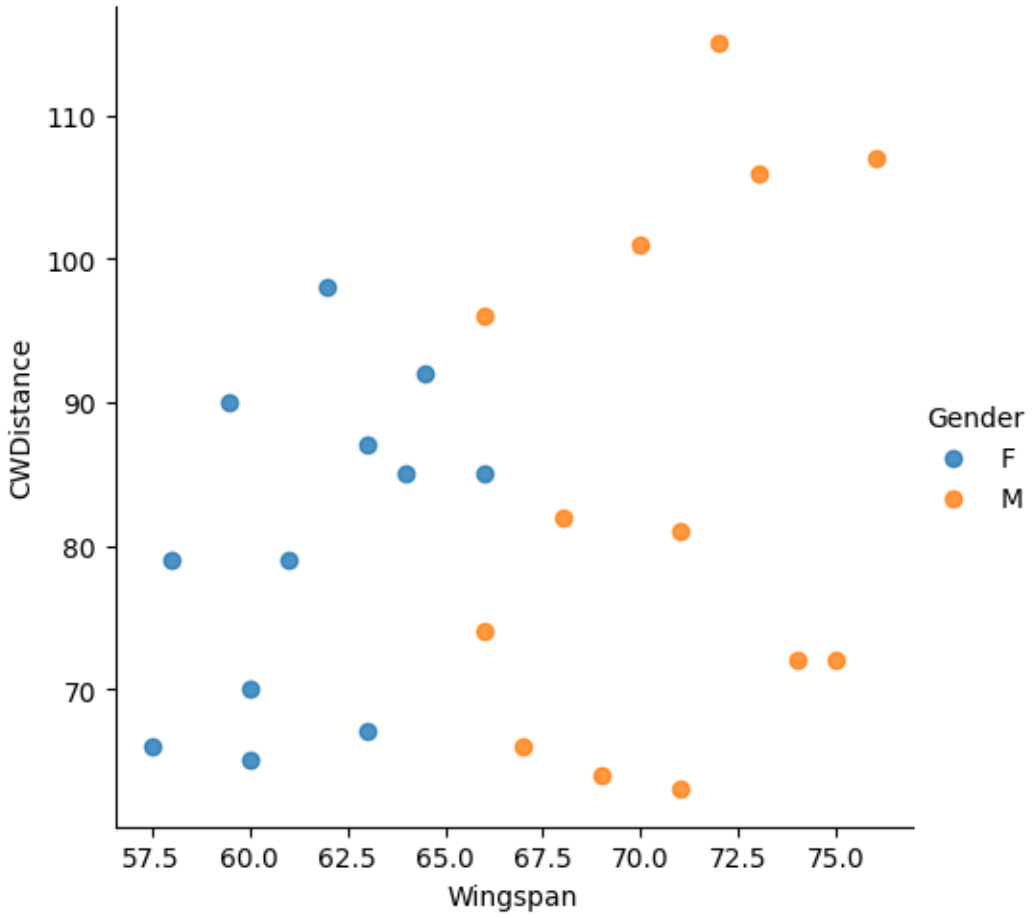
11.4.0.1 Scatterplots

```
# Import necessary libraries
import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd
```

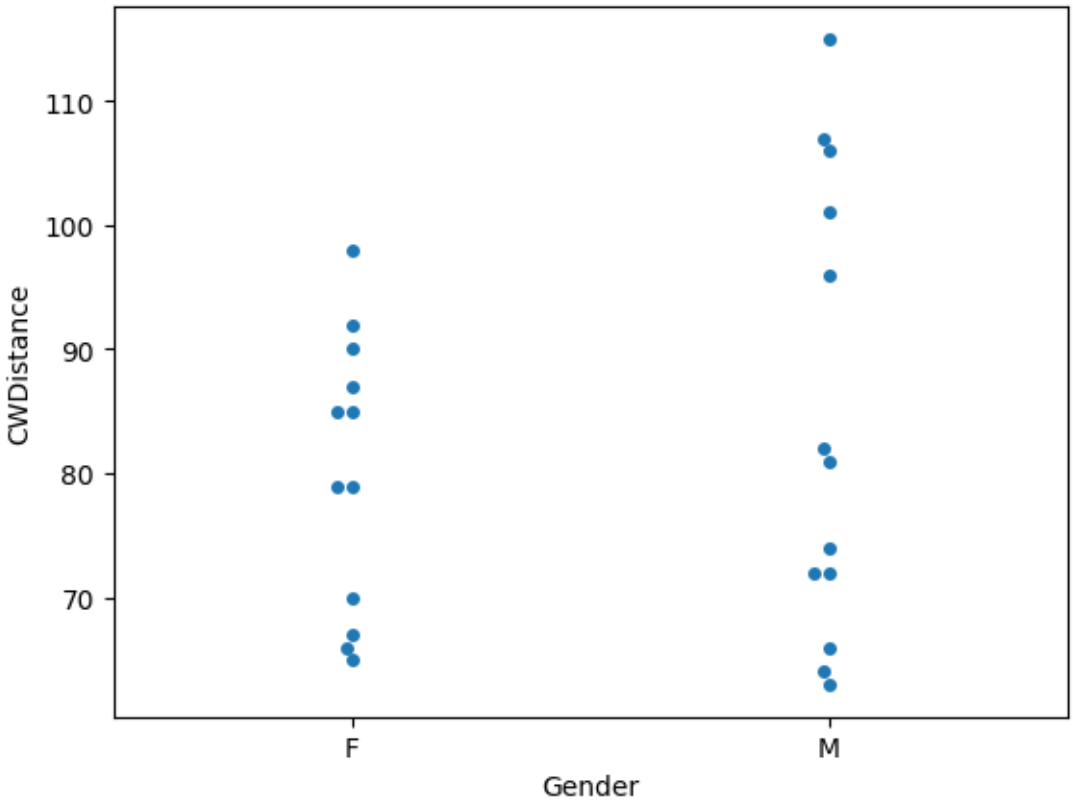
```
# Store the url string that hosts our .csv file
url = "../data/Cartwheeldata.csv"

# Read the .csv file and store it as a pandas Data Frame
df = pd.read_csv(url)

# Create Scatterplot
sns.lmplot(x='Wingspan', y='CWDistance', data=df)

plt.show()
```




```
# Scatterplot arguments
sns.lmplot(x='Wingspan', y='CWDistance', data=df,
           fit_reg=False, # No regression line
           hue='Gender')   # Color by evolution stage

plt.show()
```

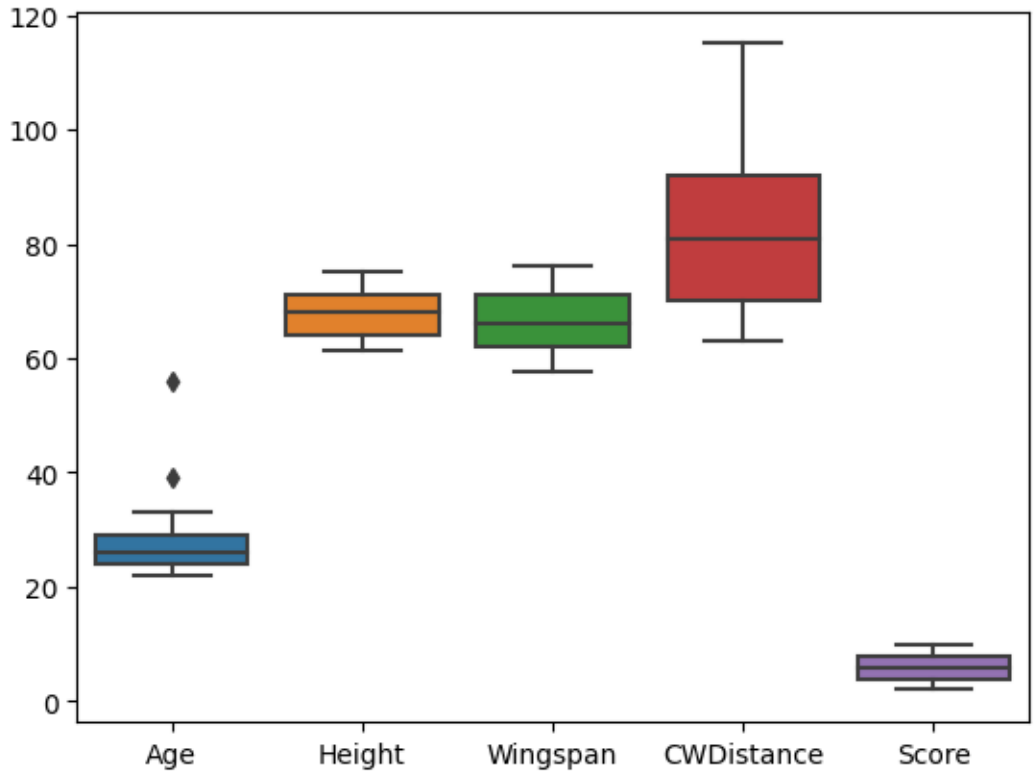



```
# Construct Cartwheel distance plot
sns.swarmplot(x="Gender", y="CWDistance", data=df)

plt.show()
```

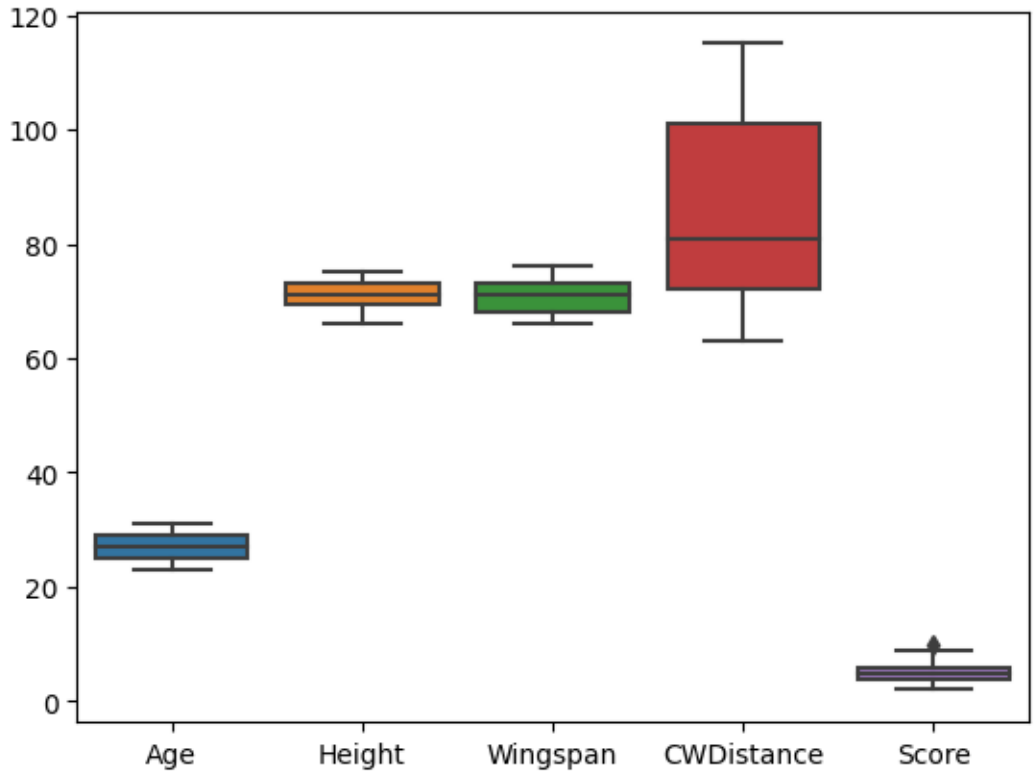


11.4.0.2 Boxplots

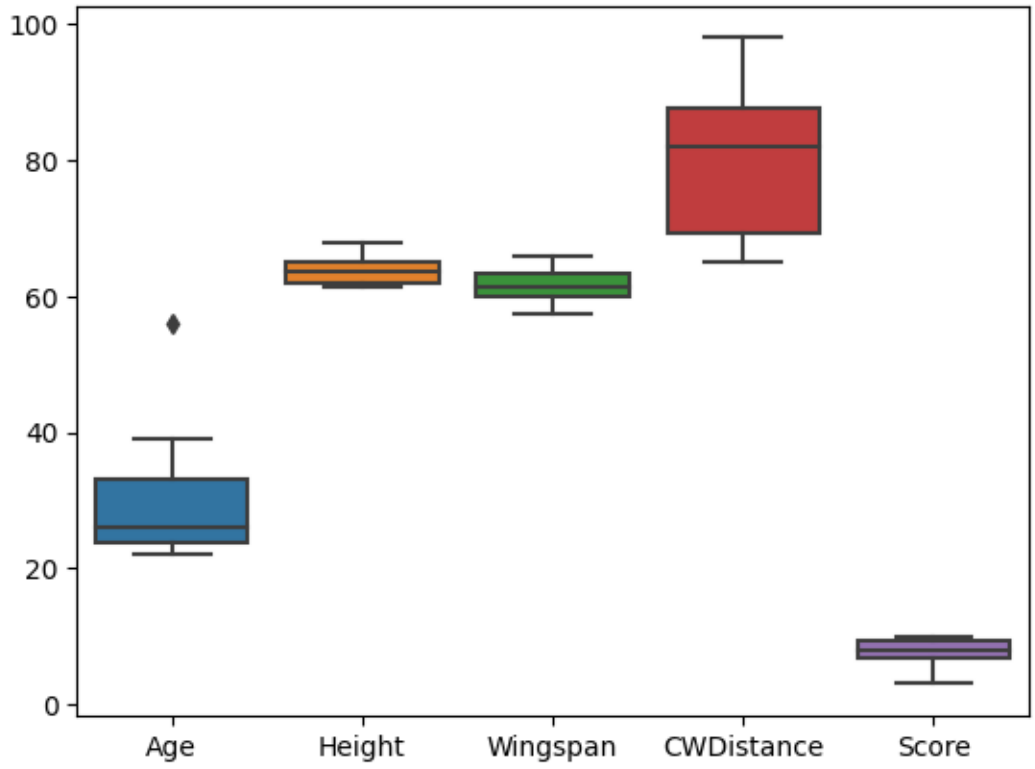
```
sns.boxplot(data=df.loc[:, ["Age", "Height", "Wingspan",
↪  "CWDistance", "Score"]])

plt.show()
```



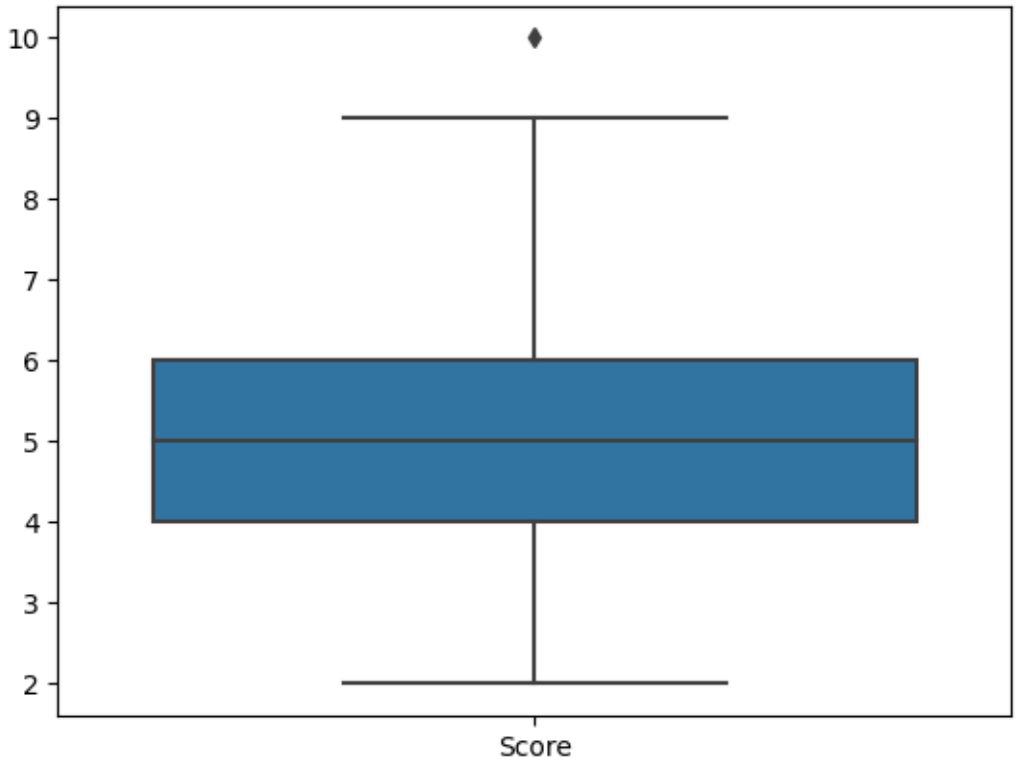

```
# Male Boxplot
sns.boxplot(data=df.loc[df['Gender'] == 'M', ["Age", "Height",
↪  "Wingspan", "CWDistance", "Score"]])

plt.show()
```




```
# Female Boxplot
sns.boxplot(data=df.loc[df['Gender'] == 'F', ["Age", "Height",
↪  "Wingspan", "CWDistance", "Score"]])

plt.show()
```



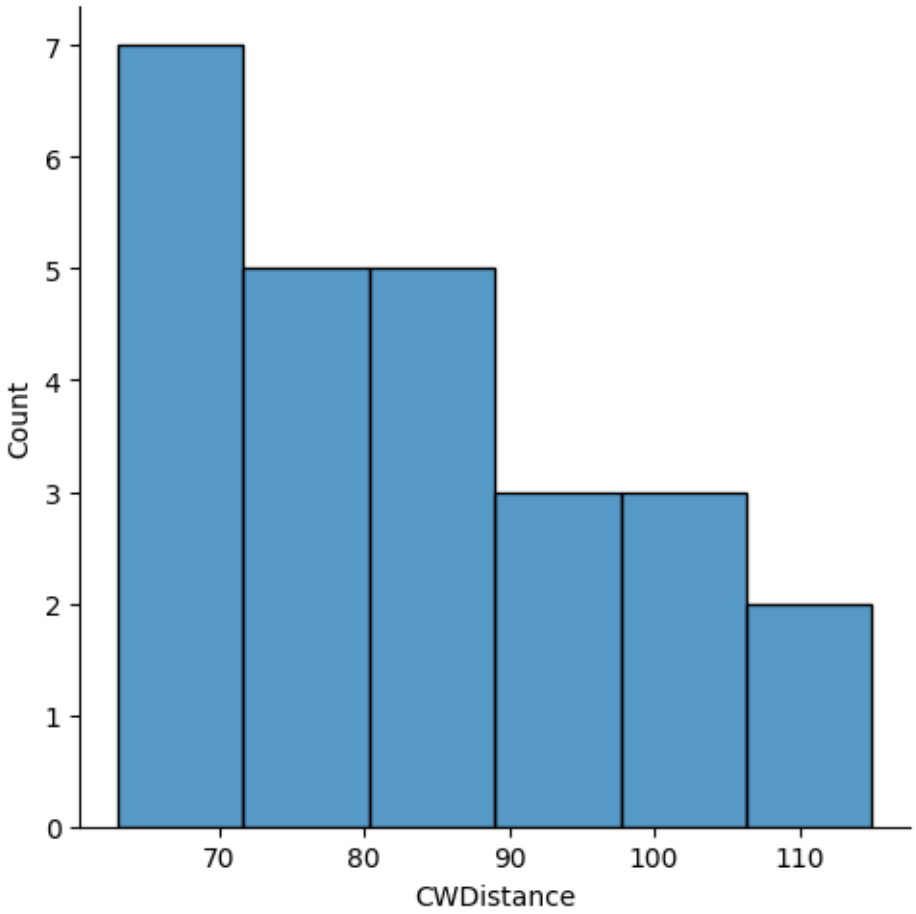

```
# Male Boxplot
sns.boxplot(data=df.loc[df['Gender'] == 'M', ["Score"]])

plt.show()
```




```
# Female Boxplot
sns.boxplot(data=df.loc[df['Gender'] == 'F', ["Score"]])

plt.show()
```

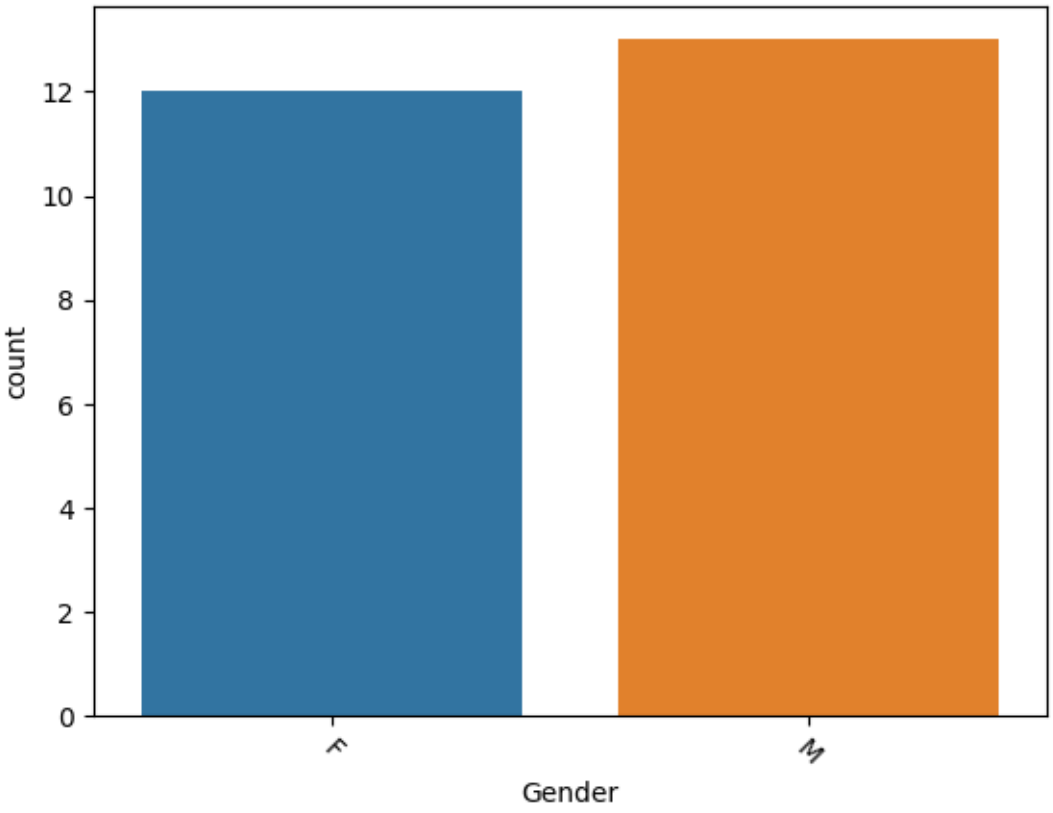
11.4.0.3 Histogram

```
# Distribution Plot (a.k.a. Histogram)
sns.displot(df.CWDistance)

plt.show()
```



11.4.0.4 Count Plot

```
# Count Plot (a.k.a. Bar Plot)
sns.countplot(x='Gender', data=df)

plt.xticks(rotation=-45)

plt.show()
```


12
10
8
6
4
2
0
count
F
M
Gender

12 Visualizing Data in Python

12.0.0.1 Tables, Histograms, Boxplots, and Slicing for Statistics

When working with a new dataset, one of the most useful things to do is to begin to visualize the data. By using tables, histograms, box plots, and other visual tools, we can get a better idea of what the data may be trying to tell us, and we can gain insights into the data that we may have not discovered otherwise.

Today, we will be going over how to perform some basic visualisations in Python, and, most importantly, we will learn how to begin exploring data from a graphical perspective.

```
# We first need to import the packages that we will be using
import seaborn as sns # For plotting
import matplotlib.pyplot as plt # For showing plots

# Load in the data set
tips_data = sns.load_dataset("tips")
```

12.0.0.2 Visualizing the Data - Tables

When you begin working with a new data set, it is often best to print out the first few rows before you begin other analysis. This will show you what kind of data is in the dataset, what data types you are working with, and will serve as a reference for the other plots that we are about to make.

```
# Print out the first few rows of the data
tips_data.head()
```

	total_bill	tip	sex	smoker	day	time	size
0	16.99	1.01	Female	No	Sun	Dinner	2
1	10.34	1.66	Male	No	Sun	Dinner	3

	total_bill	tip	sex	smoker	day	time	size
2	21.01	3.50	Male	No	Sun	Dinner	3
3	23.68	3.31	Male	No	Sun	Dinner	2
4	24.59	3.61	Female	No	Sun	Dinner	4

12.0.0.3 Describing Data

Summary statistics, which include things like the mean, min, and max of the data, can be useful to get a feel for how large some of the variables are and what variables may be the most important.

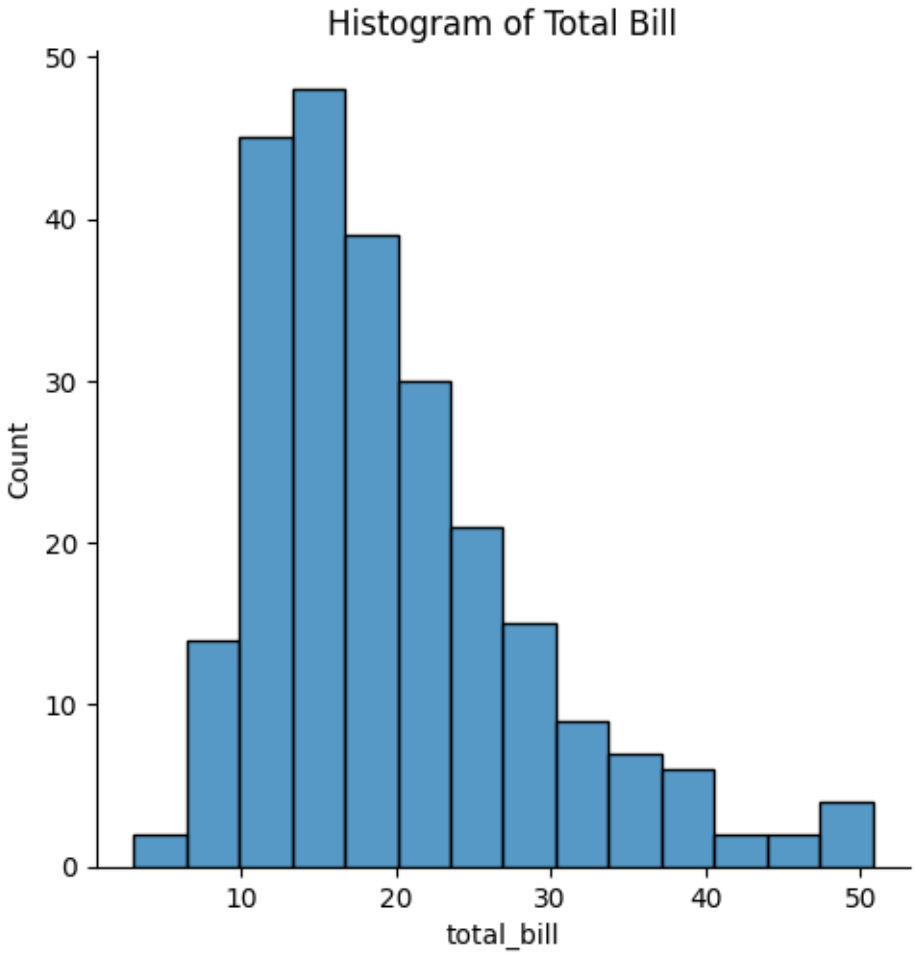
```
# Print out the summary statistics for the quantitative variables
tips_data.describe()
```

	total_bill	tip	size
count	244.000000	244.000000	244.000000
mean	19.785943	2.998279	2.569672
std	8.902412	1.383638	0.951100
min	3.070000	1.000000	1.000000
25%	13.347500	2.000000	2.000000
50%	17.795000	2.900000	2.000000
75%	24.127500	3.562500	3.000000
max	50.810000	10.000000	6.000000

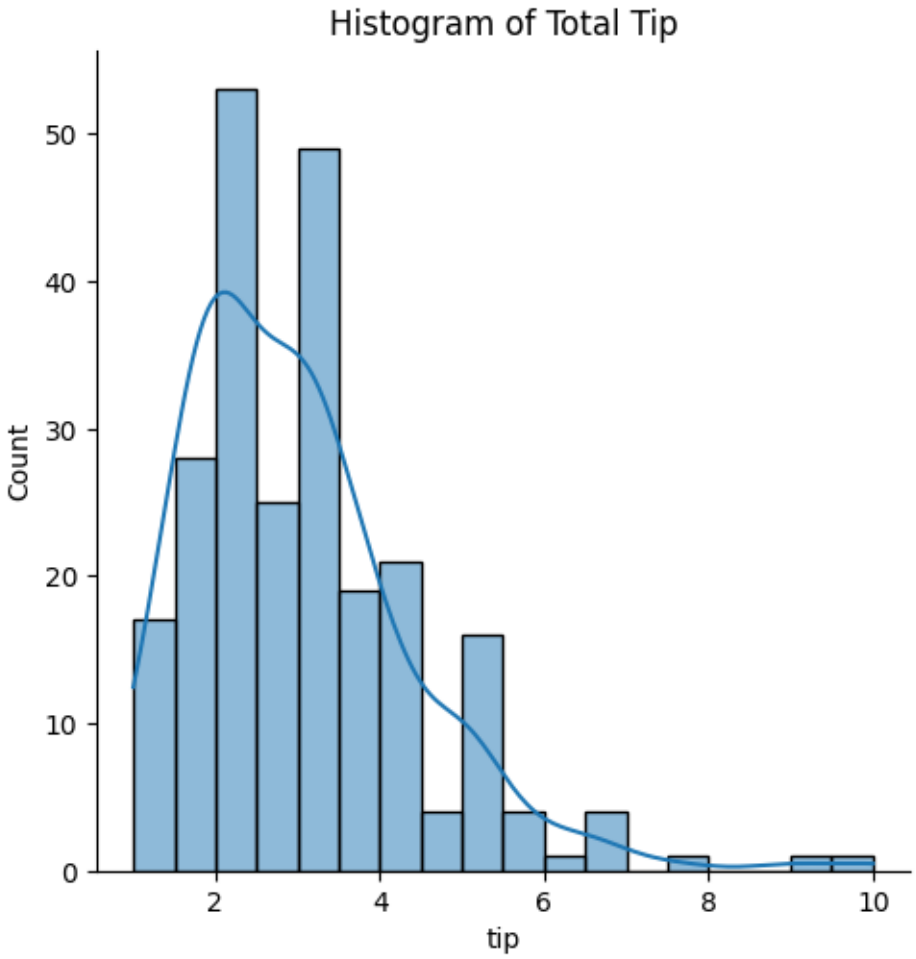
12.0.0.4 Creating a Histogram

After we have a general 'feel' for the data, it is often good to get a feel for the shape of the distribution of the data.

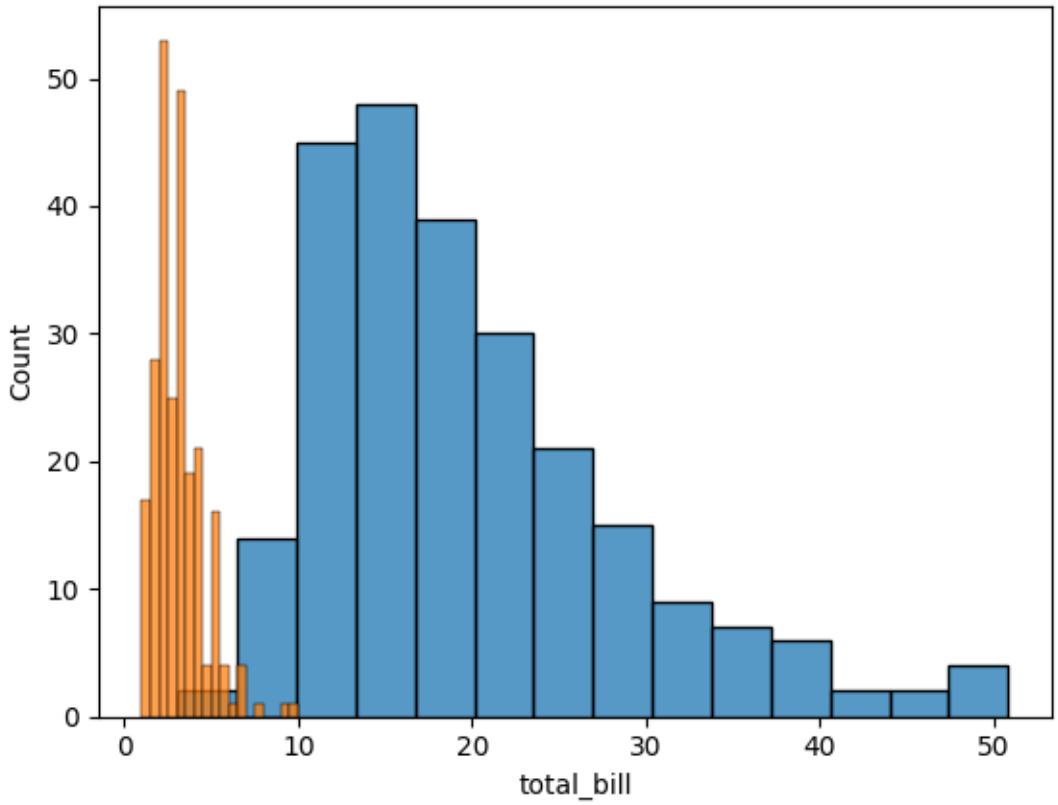
```
# Plot a histogram of the total bill
#kde --> whether or not to display a density plot
plot = sns.displot(tips_data["total_bill"], kde = False)
plt.title("Histogram of Total Bill")
plt.show()
```



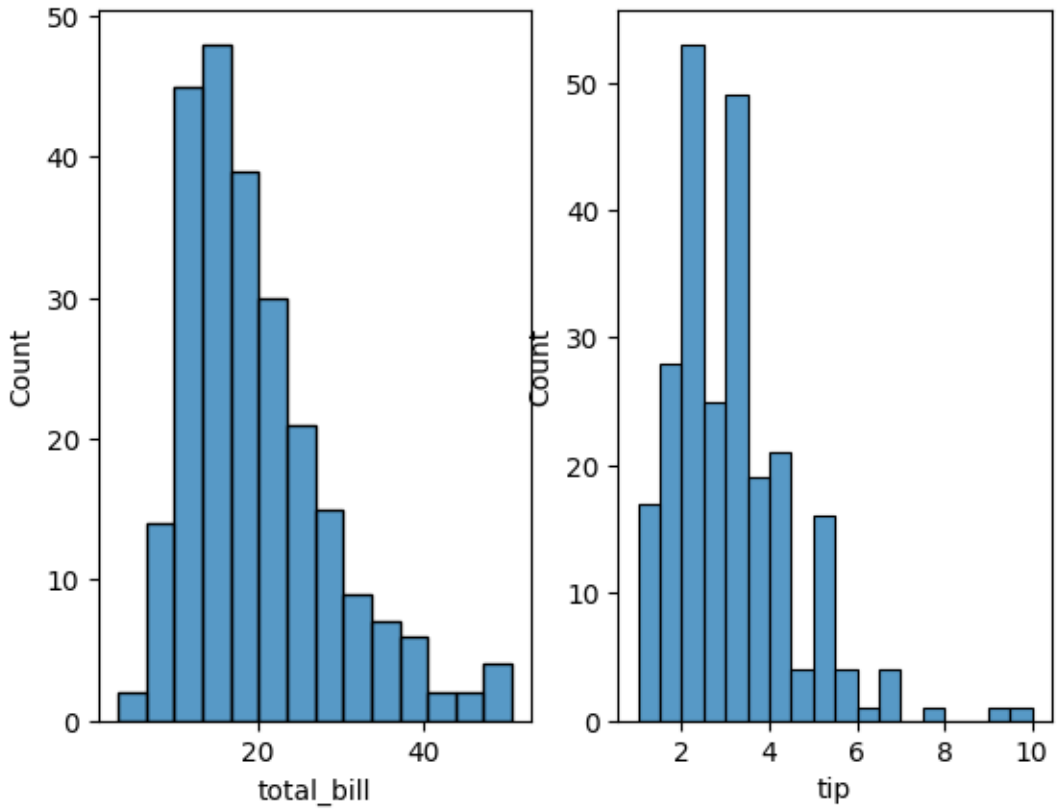

```
# Plot a histogram of the Tips only
sns.displot(tips_data["tip"], kde = True)
plt.title("Histogram of Total Tip")
plt.show()
```




```
# Plot a histogram of both the total bill and the tips'
sns.histplot(tips_data["total_bill"], kde = False)
sns.histplot(tips_data["tip"], kde = False)
plt.show()
```



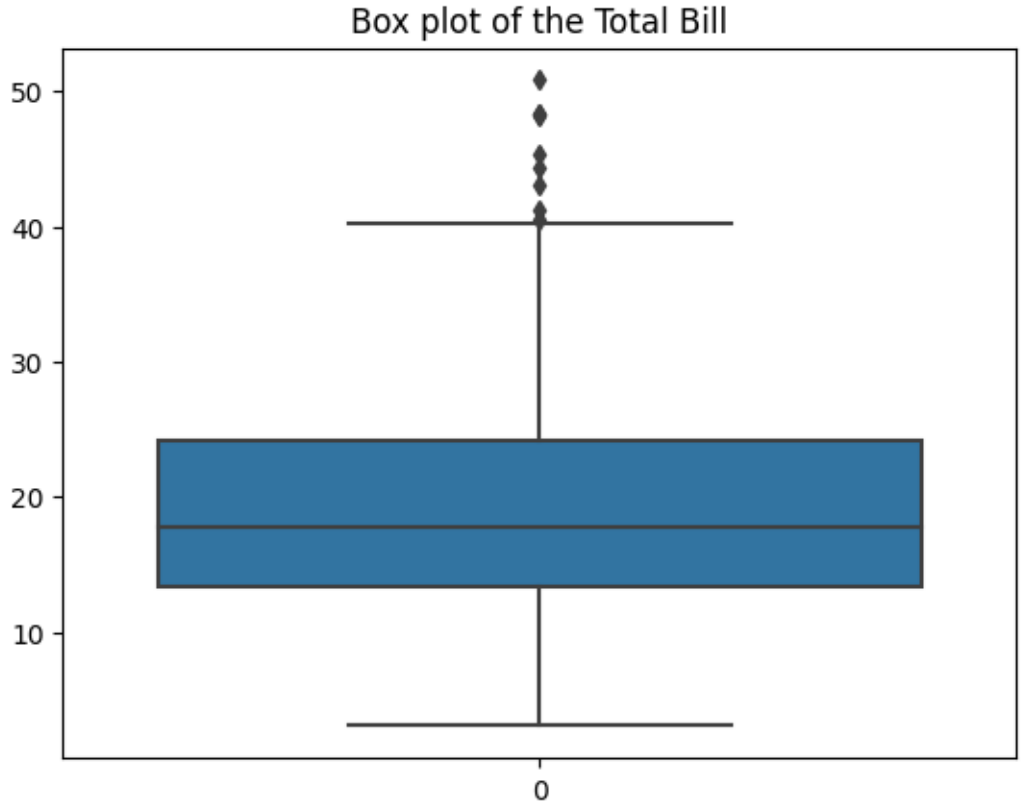

```
#alternative
fig, ax =plt.subplots(1,2)
sns.histplot(tips_data["total_bill"], kde = False, ax = ax[0])
sns.histplot(tips_data["tip"], kde = False, ax = ax[1])
plt.show()
```



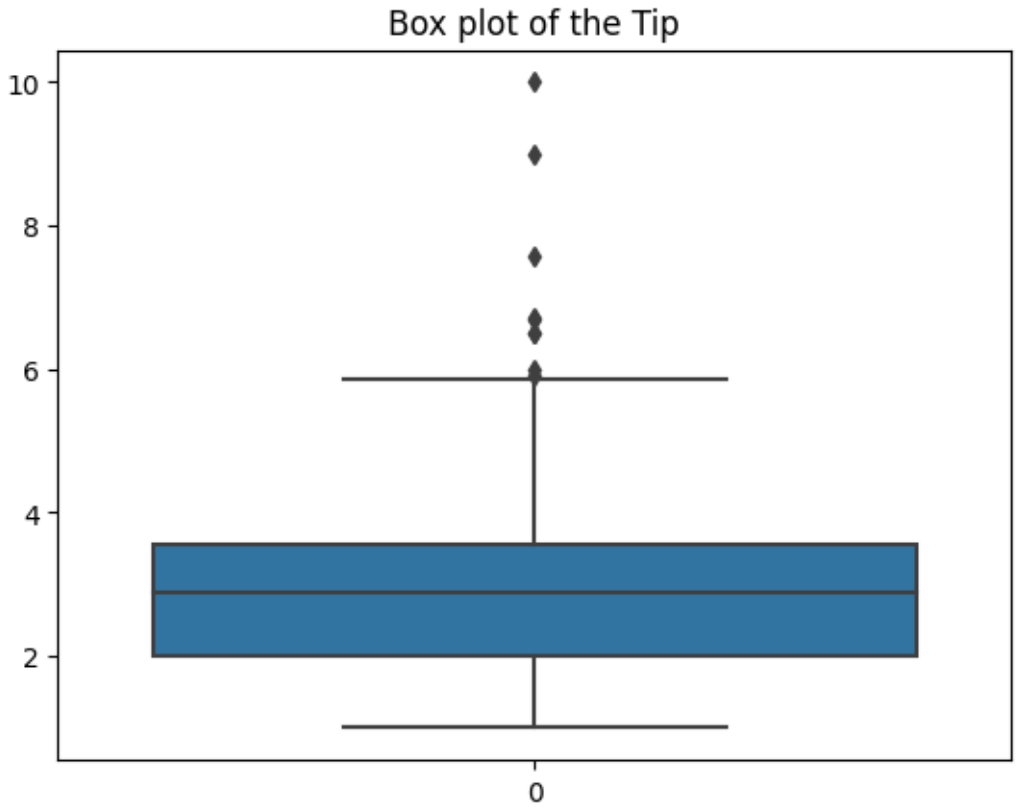
12.0.0.5 Creating a Boxplot

Boxplots do not show the shape of the distribution, but they can give us a better idea about the center and spread of the distribution as well as any potential outliers that may exist. Boxplots and Histograms often complement each other and help an analyst get more information about the data

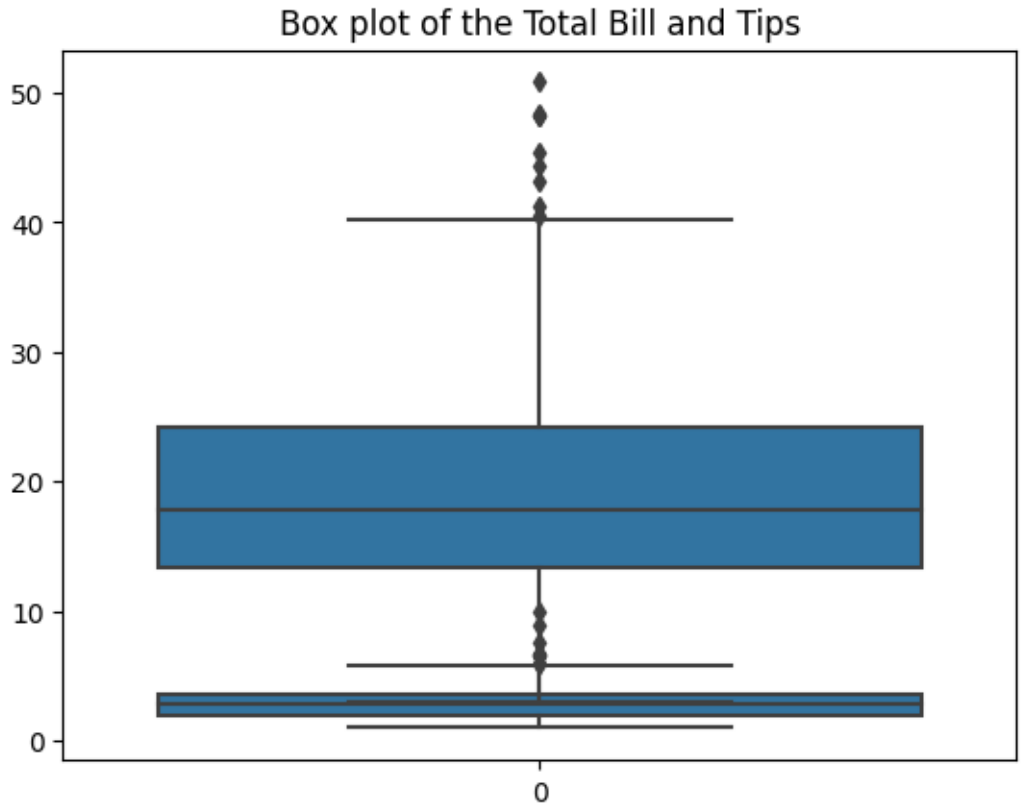
```
# Create a boxplot of the total bill amounts
sns.boxplot(tips_data["total_bill"])
plt.title("Box plot of the Total Bill")

plt.show()
```




```
# Create a boxplot of the tips amounts
sns.boxplot(tips_data["tip"])
plt.title("Box plot of the Tip")

plt.show()
```



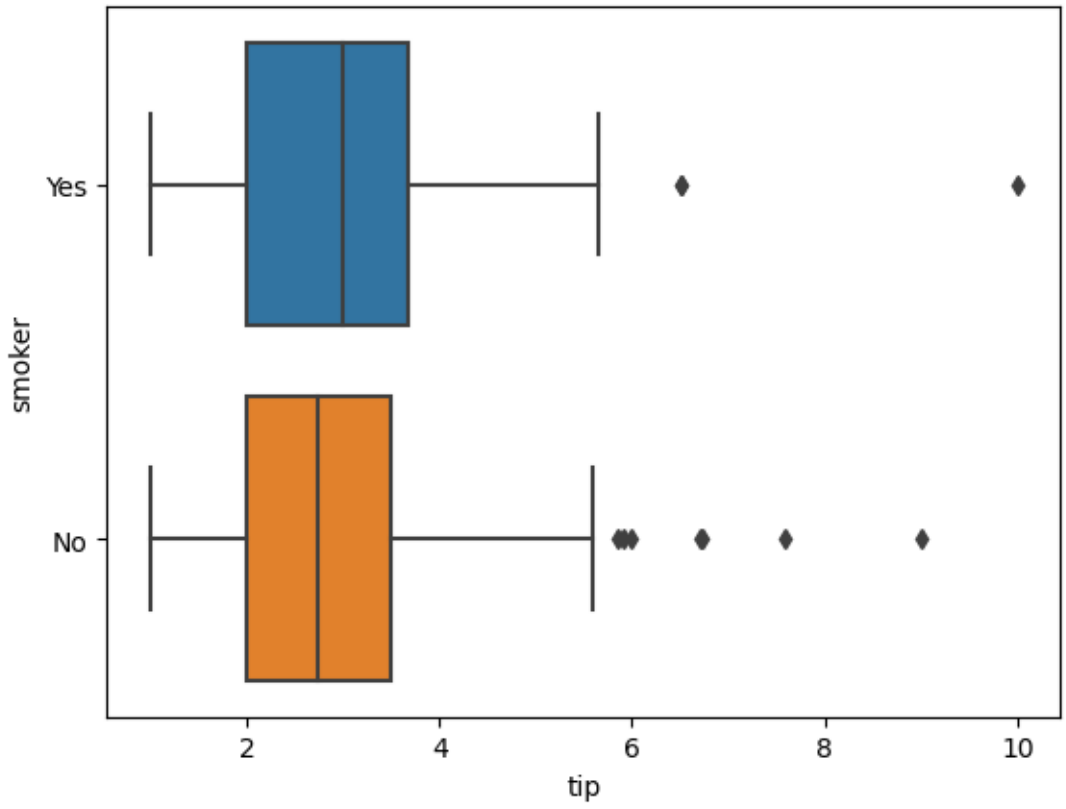

```
# Create a boxplot of the tips and total bill amounts - do not do it
↪  like this
sns.boxplot(tips_data["total_bill"])
plt.title("Box plot of the Total Bill and Tips")
sns.boxplot(tips_data["tip"])

plt.show()
```



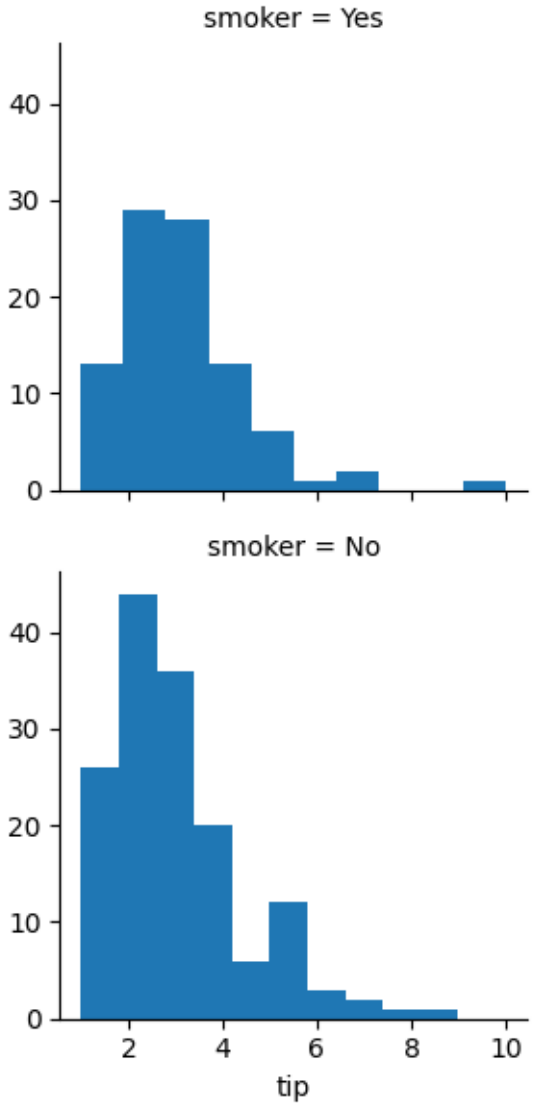
12.0.0.6 Creating Histograms and Boxplots Plotted by Groups

While looking at a single variable is interesting, it is often useful to see how a variable changes in response to another. Using graphs, we can see if there is a difference between the tipping amounts of smokers vs. non-smokers, if tipping varies according to the time of the day, or we can explore other trends in the data as well.

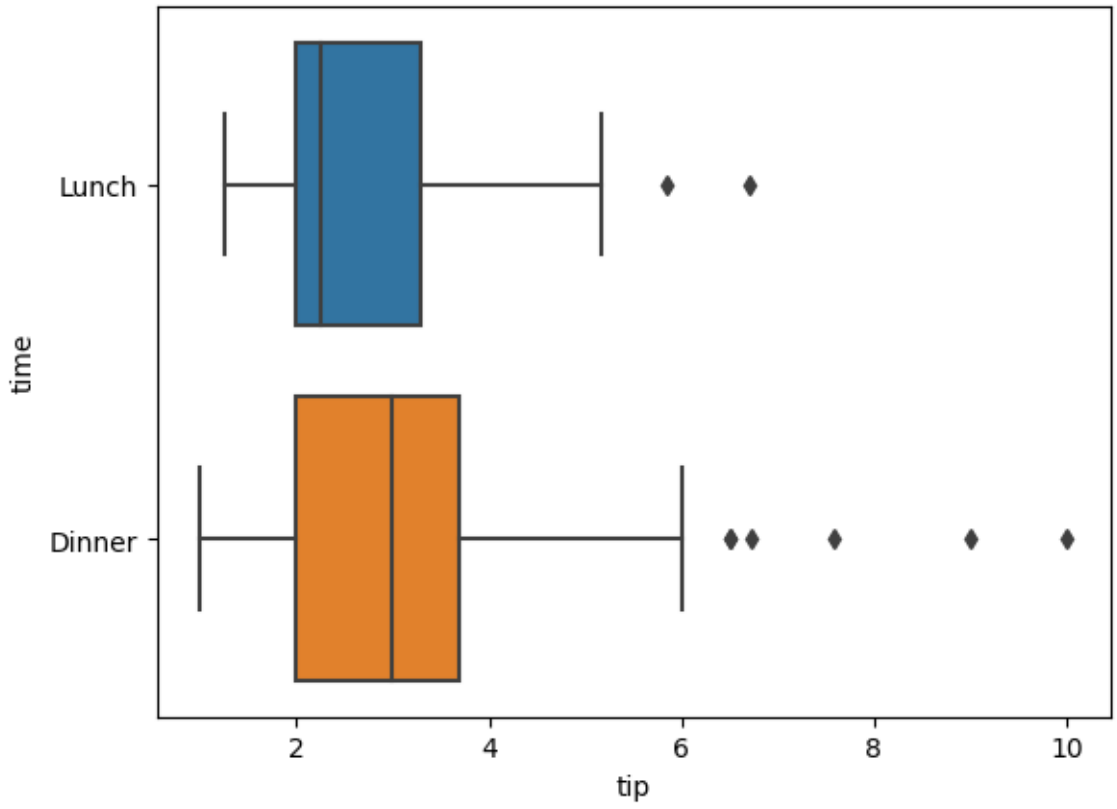
```
# Create a boxplot and histogram of the tips grouped by smoking
↪  status
# x = what I am trying to plot
# y = what I am going to be grouping by
sns.boxplot(x = tips_data["tip"], y = tips_data["smoker"])
plt.show()
```

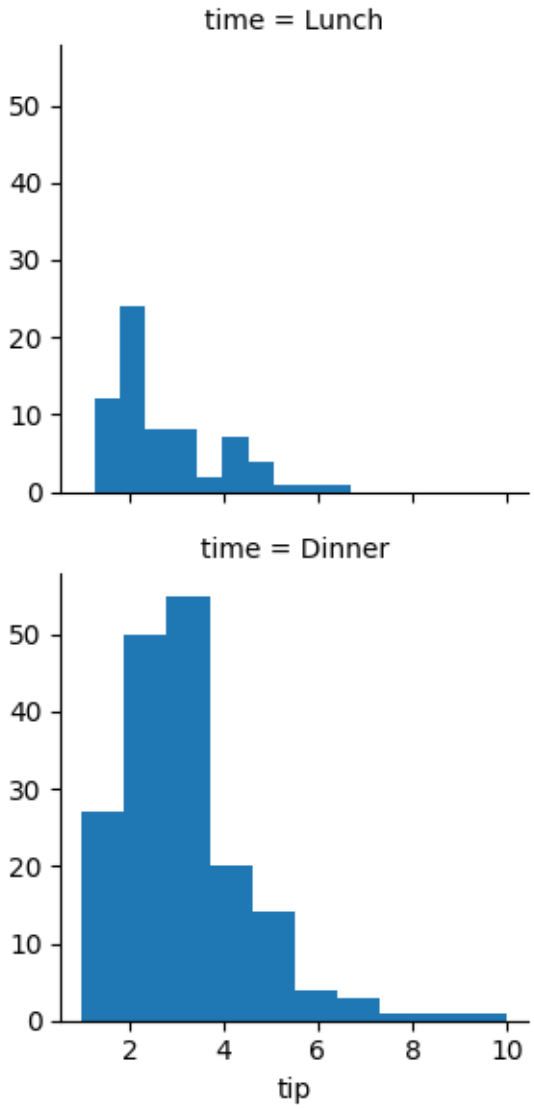



```
# Create histograms of the tips grouped by smoking status

#set up a facet grid by saying we want to have two similar boxes for
↪  our two smoking categories
g = sns.FacetGrid(tips_data, row = "smoker")

#the map fct allows us to take the histrogram feature of plt and map
↪  it across both smoking groups at the same time
g = g.map(plt.hist, "tip")

plt.show()
```

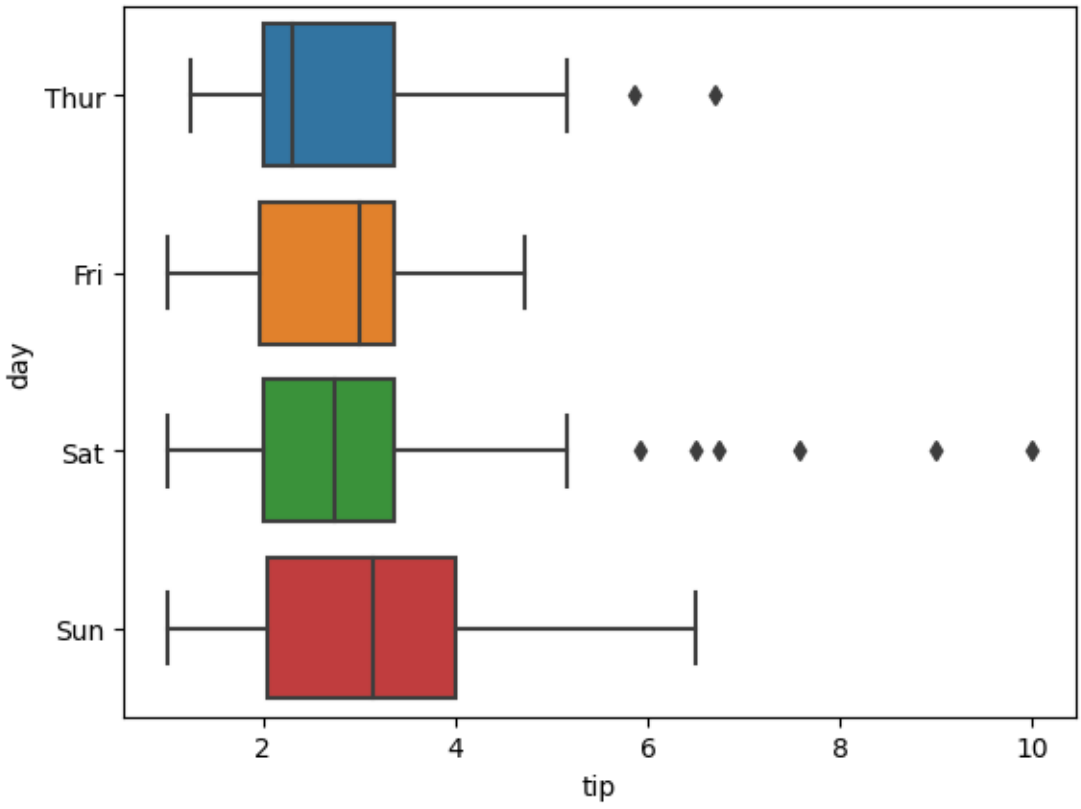


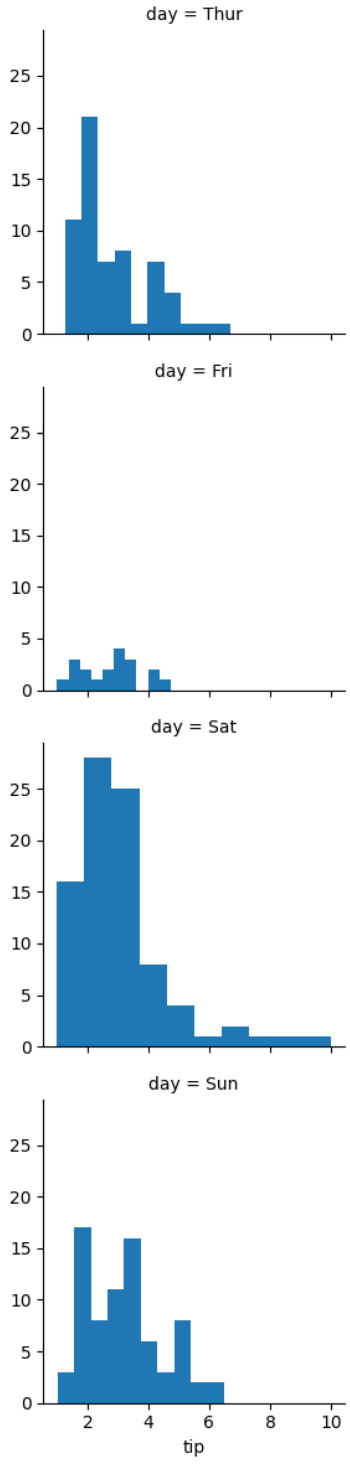

```
# Create a boxplot and histogram of the tips grouped by time of day
sns.boxplot(x = tips_data["tip"], y = tips_data["time"])

g = sns.FacetGrid(tips_data, row = "time")
g = g.map(plt.hist, "tip")
plt.show()
```


Lunch
Dinner
time
2
4
6
8
10
tip




```
# Create a boxplot and histogram of the tips grouped by the day
sns.boxplot(x = tips_data["tip"], y = tips_data["day"])

g = sns.FacetGrid(tips_data, row = "day")
g = g.map(plt.hist, "tip")
plt.show()
```


Thur
Fri
Sat
Sun
day
2
4
6
8
10
tip


day = Thur
day = Fri
day = Sat
day = Sun
0
5
10
15
20
25
2
4
6
8
10
tip

13 Univariate data analyses - NHANES case study

Here we will demonstrate how to use Python and Pandas to perform some basic analyses with univariate data, using the 2015-2016 wave of the NHANES study to illustrate the techniques.

The following import statements make the libraries that we will need available. Note that in a Jupyter notebook, you should generally use the `%matplotlib inline` directive, which would not be used when running a script outside of the Jupyter environment.

```
%matplotlib inline
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
import numpy as np
```

Next we will load the NHANES data from a file.

```
da = pd.read_csv("../data/nhanes_2015_2016.csv")
da.head()
```

	SEQN	ALQ101	ALQ110	ALQ130	SMQ020	RIAGENDR	RIDAGEYR	RIDRETH1	DMDCI
0	83732	1.0	NaN	1.0	1	1	62	3	1.0
1	83733	1.0	NaN	6.0	1	1	53	3	2.0
2	83734	1.0	NaN	NaN	1	1	78	3	1.0
3	83735	2.0	1.0	1.0	2	2	56	3	1.0
4	83736	2.0	1.0	1.0	2	2	42	4	1.0

13.0.1 Frequency tables

The value_counts method can be used to determine the number of times that each distinct value of a variable occurs in a data set. In statistical terms, this is the "frequency distribution" of the variable. Below we show the frequency distribution of the DMDEDUC2 variable, which is a variable that reflects a person's level of educational attainment. The `value_counts` method produces a table with two columns. The first column contains all distinct observed values for the variable. The second column contains the number of times each of these values occurs. Note that the table returned by `value_counts` is actually a Pandas data frame, so can be further processed using any Pandas methods for working with data frames.

The numbers 1, 2, 3, 4, 5, 9 seen below are integer codes for the 6 possible non-missing values of the DMDEDUC2 variable. The meaning of these codes is given in the NHANES codebook located here, and will be discussed further below. This table shows, for example, that 1621 people in the data file have DMDEDUC=4, which indicates that the person has completed some college, but has not graduated with a four-year degree.

```
da.DMDEDUC2.value_counts()
```

```
4.0    1621
5.0    1366
3.0    1186
1.0     655
2.0     643
9.0       3
Name: DMDEDUC2, dtype: int64
```

Note that **the `value_counts` method excludes missing values**. We confirm this below by adding up the number of observations with a DMDEDUC2 value equal to 1, 2, 3, 4, 5, or 9 (there are 5474 such rows), and comparing this to the total number of rows in the data set, which is 5735. This tells us that there are 5735 - 5474 = 261 missing values for this variable (other variables may have different numbers of missing values).

```
print(da.DMDEDUC2.value_counts().sum())
print(1621 + 1366 + 1186 + 655 + 643 + 3) # Manually sum the
↪  frequencies
print(da.shape)
```

```
5474
5474
(5735, 28)
```

Another way to obtain this result is to locate all the null (missing) values in the data set using the isnull Pandas function, and count the number of such locations.

```
pd.isnull(da.DMDEDUC2).sum()
```

```
261
```

13.0.1.1 Replace naming in a column

In some cases it is useful to replace integer codes with a text label that reflects the code's meaning. Below we create a new variable called 'DMDEDUC2x' that is recoded with text labels, then we generate its frequency distribution.

```
da["DMDEDUC2x"] = da.DMDEDUC2.replace({1: "<9", 2: "9-11", 3:
↪  "HS/GED", 4: "Some college/AA", 5: "College",
                                       7: "Refused", 9: "Don't
                                       ↪  know"})

da.DMDEDUC2x.value_counts()
```

```
Some college/AA    1621
College            1366
HS/GED             1186
<9                  655
9-11                643
Don't know            3
Name: DMDEDUC2x, dtype: int64
```

We will also want to have a relabeled version of the gender variable, so we will construct that now as well. We will follow a convention here of appending an 'x' to the end of a categorical variable's name when it has been recoded from numeric to string (text) values.

```
da["RIAGENDRx"] = da.RIAGENDR.replace({1: "Male", 2: "Female"})

da["RIAGENDRx"].value_counts()
```

```
Female    2976
Male      2759
Name: RIAGENDRx, dtype: int64
```

For many purposes it is more relevant to consider the proportion of the sample with each of the possible category values, rather than the number of people in each category. We can do this as follows:

```
x = da.DMDEDUC2x.value_counts()  # x is just a name to hold this
↪  value temporarily
x / x.sum() * 100
```

```
Some college/AA    29.612715
College            24.954330
HS/GED             21.666058
<9                 11.965656
9-11               11.746438
Don't know          0.054805
Name: DMDEDUC2x, dtype: float64
```

13.0.1.2 Replace NAs with another category

In some cases we will want to treat the missing response category as another category of observed response, rather than ignoring it when creating summaries. Below we create a new category called "Missing", and assign all missing values to it usig fillna. Then we recalculate the frequency distribution. We see that 4.6% of the responses are missing.

```
da["DMDEDUC2x"] = da.DMDEDUC2x.fillna("Missing")
x = da.DMDEDUC2x.value_counts()
x / x.sum() * 100
```

```
Some college/AA    28.265039
College            23.818657
HS/GED             20.680035
<9                 11.421099
9-11               11.211857
Missing             4.551003
Don't know          0.052310
Name: DMDEDUC2x, dtype: float64
```

13.0.2 Numerical summaries

A quick way to get a set of numerical summaries for a quantitative variable is with the describe data frame method. Below we demonstrate how to do this using the body weight variable (BMXWT). As with many surveys, some data values are missing, so we explicitly drop the missing cases using the dropna method before generating the summaries.

```
da.BMXWT.dropna().describe()
```

```
count    5666.000000
mean       81.342676
std        21.764409
min        32.400000
25%        65.900000
50%        78.200000
75%        92.700000
max       198.900000
Name: BMXWT, dtype: float64
```

It's also possible to calculate individual summary statistics from one column of a data set. This can be done using Pandas methods, or with numpy functions:

```
x = da.BMXWT.dropna()  # Extract all non-missing values of BMXWT into
↪  a variable called 'x'
print(x.mean()) # Pandas method
print(np.mean(x)) # Numpy function

print(x.median())
print(np.percentile(x, 50))  # 50th percentile, same as the median
```

```
print(np.percentile(x, 75))  # 75th percentile
print(x.quantile(0.75)) # Pandas method for quantiles, equivalent to
↪  75th percentile
```

```
81.34267560889516
81.34267560889516
78.2
78.2
92.7
92.7
```

Next we look at frequencies for a systolic blood pressure measurement (BPXSY1). "BPX" here is the NHANES prefix for blood pressure measurements, "SY" stands for "systolic" blood pressure (blood pressure at the peak of a heartbeat cycle), and "1" indicates that this is the first of three systolic blood presure measurements taken on a subject.

A person is generally considered to have pre-hypertension when their systolic blood pressure is between 120 and 139, or their diastolic blood pressure is between 80 and 89. Considering only the systolic condition, we can calculate the proprotion of the NHANES sample who would be considered to have pre-hypertension.

```
np.mean((da.BPXSY1 >= 120) & (da.BPXSY2 <= 139))  # "&" means "and"
```

```
0.3741935483870968
```

Next we calculate the propotion of NHANES subjects who are pre-hypertensive based on diastolic blood pressure.

```
np.mean((da.BPXDI1 >= 80) & (da.BPXDI2 <= 89))
```

```
0.14803836094158676
```

Finally we calculate the proportion of NHANES subjects who are pre-hypertensive based on either systolic or diastolic blood pressure. Since some people are pre-hypertensive under both criteria, the proportion below is less than the sum of the two proportions calculated above.

Since the combined systolic and diastolic condition for pre-hypertension is somewhat complex, below we construct temporary variables 'a' and 'b' that hold the systolic and diastolic pre-hypertensive status separately, then combine them with a "logical or" to obtain the final status for each subject.

```
a = (da.BPXSY1 >= 120) & (da.BPXSY2 <= 139)
b = (da.BPXDI1 >= 80) & (da.BPXDI2 <= 89)
print(np.mean(a | b))  # "|" means "or"
```

```
0.43975588491717527
```

Blood pressure measurements are affected by a phenomenon called "white coat anxiety", in which a subject's bood pressure may be slightly elevated if they are nervous when interacting with health care providers. Typically this effect subsides if the blood pressure is measured several times in sequence. In NHANES, both systolic and diastolic blood pressure are meausred three times for each subject (e.g. BPXSY2 is the second measurement of systolic blood pressure). We can calculate the extent to which white coat anxiety is present in the NHANES data by looking a the mean difference between the first two systolic or diastolic blood pressure measurements.

```
print(np.mean(da.BPXSY1 - da.BPXSY2))
print(np.mean(da.BPXDI1 - da.BPXDI2))
```

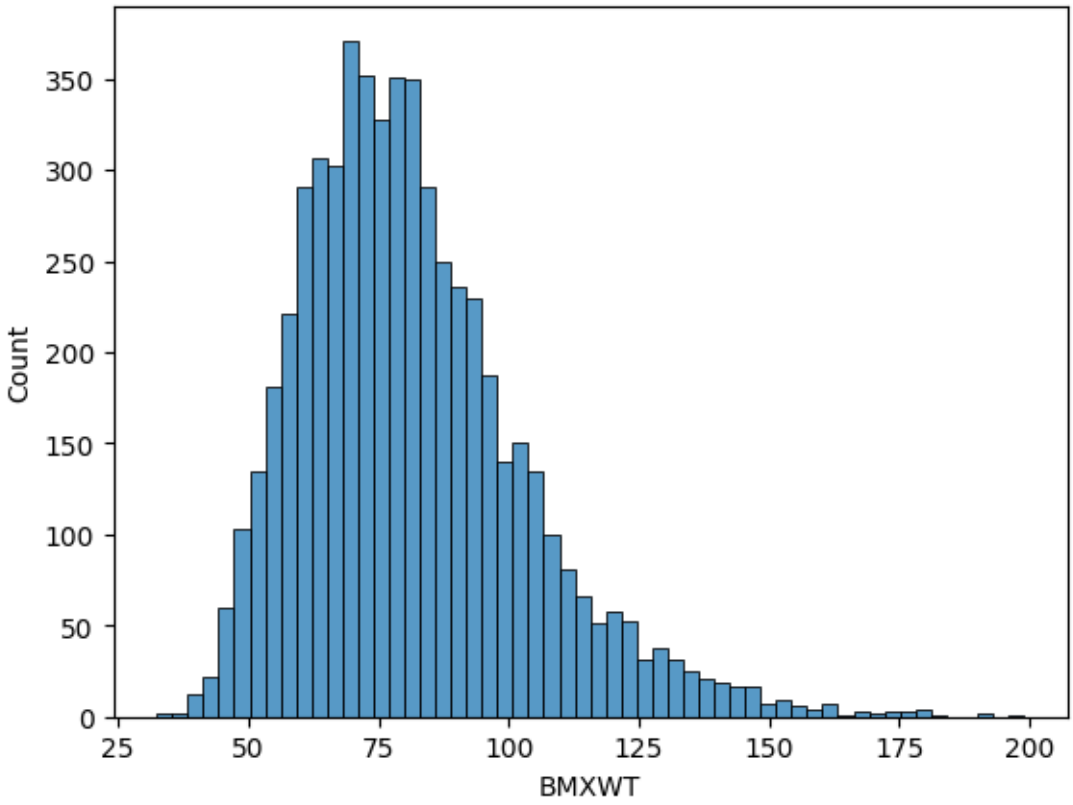
```
0.6749860309182343
0.3490407897187558
```

13.0.3 Graphical summaries

Quantitative variables can be effectively summarized graphically. Below we see the distribution of body weight (in Kg), shown as a histogram. It is evidently right-skewed.

```
sns.histplot(da.BMXWT.dropna())
```

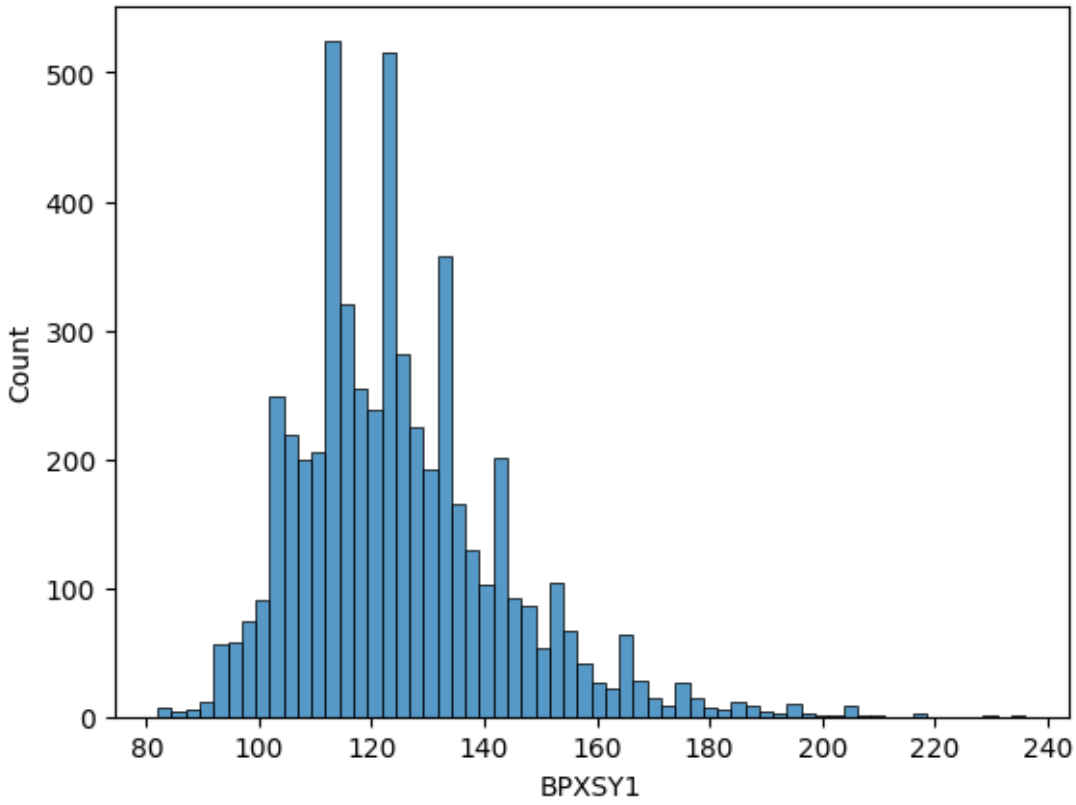
```
<AxesSubplot:xlabel='BMXWT', ylabel='Count'>
```



Next we look at the histogram of systolic blood pressure measurements. You can see that there is a tendency for the measurements to be rounded to the nearest 5 or 10 units.

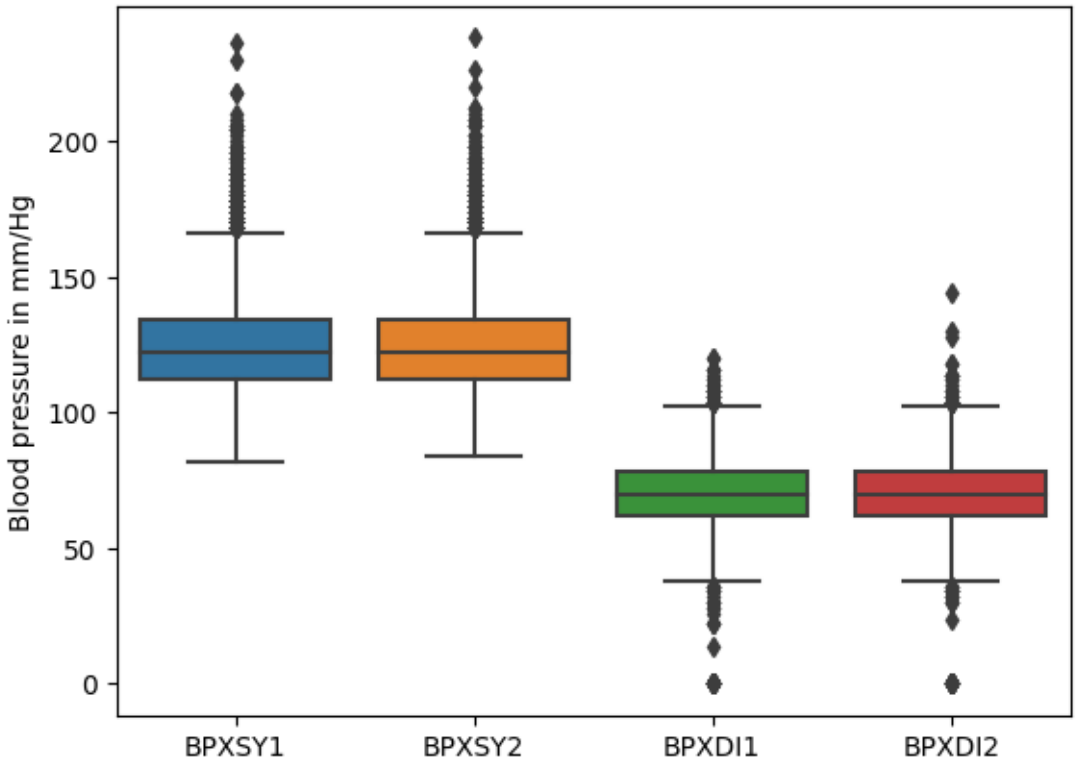
```
sns.histplot(da.BPXSY1.dropna())
```

```
<AxesSubplot:xlabel='BPXSY1', ylabel='Count'>
```



To compare several distributions, we can use side-by-side boxplots. Below we compare the distributions of the first and second systolic blood pressure measurements (BPXSY1, BPXSY2), and the first and second diastolic blood pressure measurements (BPXDI1, BPXDI2). As expected, diastolic measurements are substantially lower than systolic measurements. Above we saw that the second blood pressure reading on a subject tended on average to be slightly lower than the first measurement. This difference was less than 1 mm/Hg, so is not visible in the "marginal" distributions shown below.

```
bp = sns.boxplot(data=da[["BPXSY1", "BPXSY2", "BPXDI1", "BPXDI2"]])
_ = bp.set_ylabel("Blood pressure in mm/Hg")
```



13.0.4 Stratification

One of the most effective ways to get more information out of a dataset is to divide it into smaller, more uniform subsets, and analyze each of these "strata" on its own. We can then formally or informally compare the findings in the different strata. When working with human subjects, it is very common to stratify on demographic factors such as age, sex, and race.

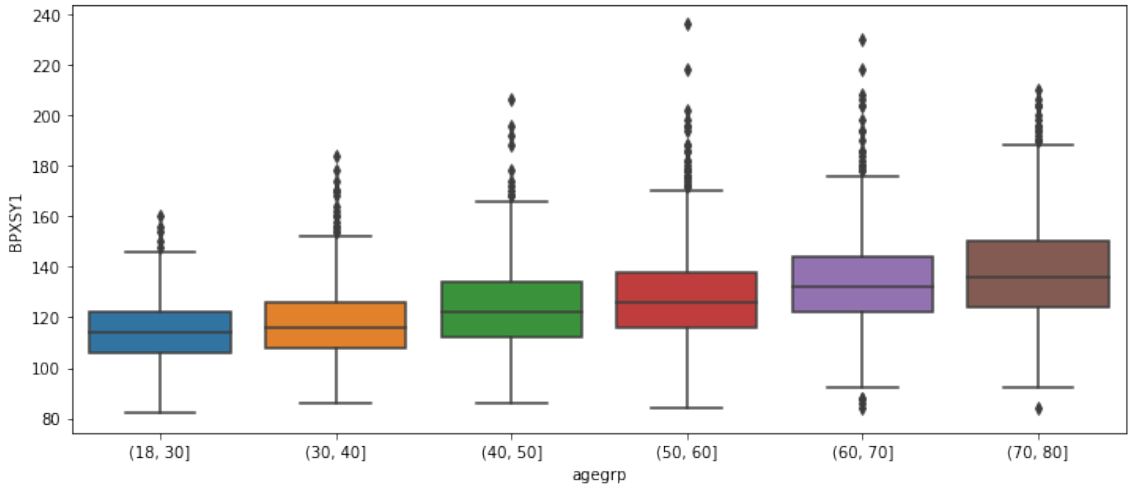
To illustrate this technique, consider blood pressure, which is a value that tends to increase with age. To see this trend in the NHANES data, we can partition the data into age strata, and construct side-by-side boxplots of the systolic blood pressure (SBP) distribution within each stratum. Since age is a quantitative variable, we need to create a series of "bins" of similar SBP values in order to stratify the data. Each box in the figure below is a summary of univariate data within a specific population stratum (here defined by age).

```
da.RIDAGEYR.value_counts()
```

```
80     343
18     133
19     128
60     119
61     112
      ...
74      52
78      47
76      44
77      43
79      35
Name: RIDAGEYR, Length: 63, dtype: int64
```

```
da["agegrp"] = pd.cut(da.RIDAGEYR, [18, 30, 40, 50, 60, 70, 80]) #
↪  Create age strata based on these cut points

plt.figure(figsize=(12, 5))  # Make the figure wider than default
↪  (12cm wide by 5cm tall)
sns.boxplot(x="agegrp", y="BPXSY1", data=da)  # Make boxplot of
↪  BPXSY1 stratified by age group
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f8388799ef0>
```

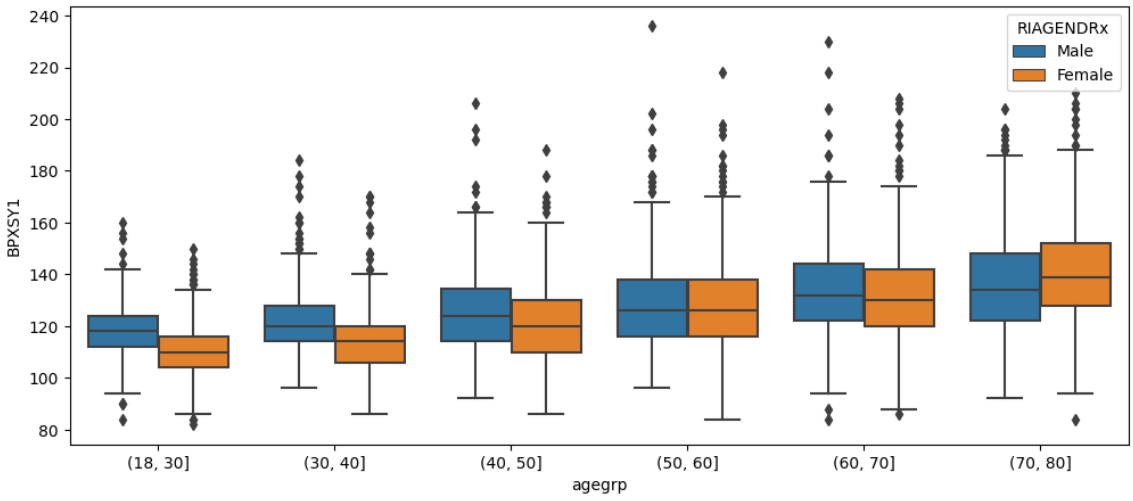


Taking this a step further, it is also the case that blood pressure tends to differ between women and men. While we could simply make two side-by-side boxplots to illustrate this contrast, it would be a bit odd to ignore age after already having established that it is strongly associated with blood pressure. Therefore, we will doubly stratify the data by gender and age.

We see from the figure below that within each gender, older people tend to have higher blood pressure than younger people. However within an age band, the relationship between gender and systolic blood pressure is somewhat complex – in younger people, men have substantially higher blood pressures than women of the same age. However for people older than 50, this relationship becomes much weaker, and among people older than 70 it appears to reverse. It is also notable that the variation of these distributions, reflected in the height of each box in the boxplot, increases with age.

```
da["agegrp"] = pd.cut(da.RIDAGEYR, [18, 30, 40, 50, 60, 70, 80])

plt.figure(figsize=(12, 5))
sns.boxplot(x="agegrp", y="BPXSY1", hue="RIAGENDRx", data = da)
```

```
<AxesSubplot:xlabel='agegrp', ylabel='BPXSY1'>
```

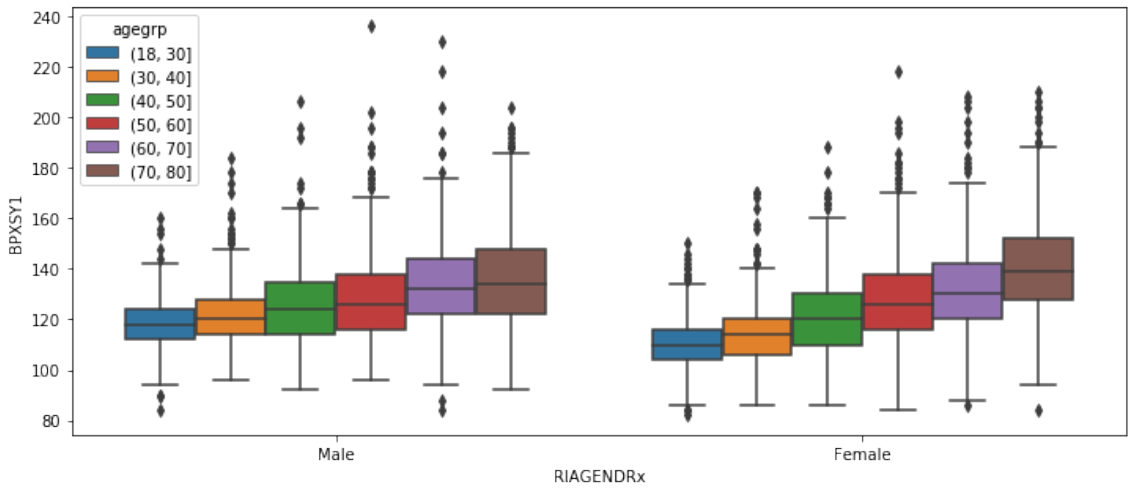


When stratifying on two factors (here age and gender), we can group the boxes first by age, and within age bands by gender, as above, or we can do the opposite – group first by

gender, and then within gender group by age bands. Each approach highlights a different aspect of the data.

```
da["agegrp"] = pd.cut(da.RIDAGEYR, [18, 30, 40, 50, 60, 70, 80])

plt.figure(figsize=(12, 5))
sns.boxplot(x="RIAGENDRx", y="BPXSY1", hue="agegrp", data=da)
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f838880ed68>
```



Stratification can also be useful when working with categorical variables. Below we look at the frequency distribution of educational attainment ("DMDEDUC2") within 10-year age bands. While "some college" is the most common response in all age bands, up to around age 60 the second most common response is "college" (i.e. the person graduated from college with a four-year degree). However for people over 50, there are as many or more people with only high school or general equivalency diplomas (HS/GED) than there are college graduates.

Note on causality and confounding: An important role of statistics is to aid researchers in identifying causes underlying observed differences. Here we have seen differences in both blood pressure and educational attainment based on age. It is plausible that aging directly causes blood pressure to increase. But in the case of educational attainment, this is actually a "birth cohort effect". NHANES is a cross sectional survey (all data for one wave were collected at a single point in time). People who were, say, 65 in 2015 (when these

data were collected), were college-aged around 1970, while people who were in their 20's in 2015 were college-aged in around 2010 or later. Over the last few decades, it has become much more common for people to at least begin a college degree than it was in the past. Therefore, younger people as a group have higher educational attainment than older people as a group. As these young people grow older, the cross sectional relationship between age and educational attainment will change.

```
da.groupby("agegrp")["DMDEDUC2x"].value_counts()
```

```
agegrp    DMDEDUC2x
(18, 30]  Some college/AA    364
          College            278
          HS/GED             237
          Missing            128
          9-11                99
          <9                  47
(30, 40]  Some college/AA    282
          College            264
          HS/GED             182
          9-11               111
          <9                  93
(40, 50]  Some college/AA    262
          College            260
          HS/GED             171
          9-11               112
          <9                  98
(50, 60]  Some college/AA    258
          College            220
          HS/GED             220
          9-11               122
          <9                 104
(60, 70]  Some college/AA    238
          HS/GED             192
          College            188
          <9                 149
          9-11               111
(70, 80]  Some college/AA    217
          HS/GED             184
          <9                 164
          College            156
```

```
          9-11                88
          Don't know           3
Name: DMDEDUC2x, dtype: int64
```

We can also stratify jointly by age and gender to explore how educational attainment varies by both of these factors simultaneously. In doing this, it is easier to interpret the results if we pivot the education levels into the columns, and normalize the counts so that they sum to 1. After doing this, the results can be interpreted as proportions or probabilities. One notable observation from this table is that for people up to age around 60, women are more likely to have graduated from college than men, but for people over aged 60, this relationship reverses.

```
# Eliminate rare/missing values
dx = da.loc[~da.DMDEDUC2x.isin(["Don't know", "Missing"]), :]

#group data
dx = dx.groupby(["agegrp", "RIAGENDRx"])["DMDEDUC2x"]
dx = dx.value_counts()
dx.head()
```

```
agegrp    RIAGENDRx  DMDEDUC2x
(18, 30]  Female     Some college/AA    207
                     College            156
                     HS/GED             119
                     9-11                44
                     <9                  27
Name: DMDEDUC2x, dtype: int64
```

```
dx = dx.unstack() # Restructure the results from 'long' to 'wide'
dx.head()
```

agegrp	DMDEDUC2x RIAGENDRx	9-11	<9	College	HS/GED	Some college/AA
(18, 30]	Female	44	27	156	119	207
	Male	55	20	122	118	157
(30, 40]	Female	42	46	149	78	159
	Male	69	47	115	104	123

agegrp	DMDEDUC2x RIAGENDRx	9-11	<9	College	HS/GED	Some college/AA
(40, 50]	Female	55	53	150	87	157

```
# Normalize within each stratum to get proportions
dx = dx.apply(lambda x: x/x.sum(), axis=1)
dx.head()
```

agegrp	DMDEDUC2x RIAGENDRx	9-11	<9	College	HS/GED	Some college/AA
(18, 30]	Female	0.079566	0.048825	0.282098	0.215190	0.374322
	Male	0.116525	0.042373	0.258475	0.250000	0.332627
(30, 40]	Female	0.088608	0.097046	0.314346	0.164557	0.335443
	Male	0.150655	0.102620	0.251092	0.227074	0.268559
(40, 50]	Female	0.109562	0.105578	0.298805	0.173307	0.312749

```
print(dx.to_string(float_format="%.3f"))  # Limit display to 3
↪  decimal places
```

```
DMDEDUC2x                 9-11    <9  College  HS/GED  Some college/AA
agegrp   RIAGENDRx
(18, 30] Female          0.080 0.049    0.282   0.215            0.374
         Male            0.117 0.042    0.258   0.250            0.333
(30, 40] Female          0.089 0.097    0.314   0.165            0.335
         Male            0.151 0.103    0.251   0.227            0.269
(40, 50] Female          0.110 0.106    0.299   0.173            0.313
         Male            0.142 0.112    0.274   0.209            0.262
(50, 60] Female          0.117 0.102    0.245   0.234            0.302
         Male            0.148 0.123    0.231   0.242            0.256
(60, 70] Female          0.118 0.188    0.195   0.206            0.293
         Male            0.135 0.151    0.233   0.231            0.249
(70, 80] Female          0.105 0.225    0.149   0.240            0.281
         Male            0.113 0.180    0.237   0.215            0.255
```

14 Practice notebook for univariate analysis using NHANES data

This notebook will give you the opportunity to perform some univariate analyses on your own using the NHANES. These analyses are similar to what was done in the week 2 NHANES case study notebook.

You can enter your code into the cells that say "enter your code here", and you can type responses to the questions into the cells that say "Type Markdown and Latex".

Note that most of the code that you will need to write below is very similar to code that appears in the case study notebook. You will need to edit code from that notebook in small ways to adapt it to the prompts below.

To get started, we will use the same module imports and read the data in the same way as we did in the case study:

```
%matplotlib inline
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
import statsmodels.api as sm
import numpy as np

da = pd.read_csv("../data/nhanes_2015_2016.csv")
da.head()
```

	SEQN	ALQ101	ALQ110	ALQ130	SMQ020	RIAGENDR	RIDAGEYR	RIDRETH1	DMDCI
0	83732	1.0	NaN	1.0	1	1	62	3	1.0
1	83733	1.0	NaN	6.0	1	1	53	3	2.0
2	83734	1.0	NaN	NaN	1	1	78	3	1.0
3	83735	2.0	1.0	1.0	2	2	56	3	1.0
4	83736	2.0	1.0	1.0	2	2	42	4	1.0

14.1 Question 1

Relabel the marital status variable DMDMARTL to have brief but informative character labels. Then construct a frequency table of these values for all people, then for women only, and for men only. Then construct these three frequency tables using only people whose age is between 30 and 40.

```
# relabel colum
da['DMDMARTLx'] = da['DMDMARTL'].replace({1:'Married', 2:'Widowed',
↪  3:'Divorced', 4:'Separated', 5:'Never married', 6:'Living with
↪  partner', 77:'Refused', 99:'Unknown' }).fillna('Missing')
da['RIAGENDRx'] = da['RIAGENDR'].replace({1:'Male', 2:'Female'})

#create freq table
x = da['DMDMARTLx'].value_counts()
x / x.sum()*100
```

```
Married                48.474281
Never married          17.506539
Divorced               10.095902
Living with partner     9.189189
Widowed                 6.904969
Missing                 4.551003
Separated               3.243243
Refused                 0.034874
Name: DMDMARTLx, dtype: float64
```

```
#freq table for women only
x = da[da['RIAGENDR']==2]['DMDMARTLx'].value_counts()
x / x.sum()*100
```

```
Married                43.783602
Never married          17.473118
Divorced               11.760753
Widowed                 9.946237
Living with partner     8.803763
Missing                 4.233871
Separated               3.965054
```

```
Refused                  0.033602
Name: DMDMARTLx, dtype: float64
```

```
#freq table for male only
x = da[da['RIAGENDR']==1]['DMDMARTLx'].value_counts()
x / x.sum()*100
```

```
Married                 53.533889
Never married           17.542588
Living with partner      9.604929
Divorced                 8.300109
Missing                  4.893077
Widowed                  3.624502
Separated                2.464661
Refused                  0.036245
Name: DMDMARTLx, dtype: float64
```

```
#freq table for all people, age 30-40
age30_40 = da[(da['RIDAGEYR'] >= 30) & (da['RIDAGEYR'] <= 40)]
x = age30_40['DMDMARTLx'].value_counts()
x / x.sum()*100
```

```
Married                 54.580897
Never married           21.150097
Living with partner     13.937622
Divorced                 6.822612
Separated                2.923977
Widowed                  0.487329
Refused                  0.097466
Name: DMDMARTLx, dtype: float64
```

```
#freq table for females, age 30-40
x = age30_40[age30_40['RIAGENDR']==2]['DMDMARTLx'].value_counts()
x / x.sum()*100
```

```
Married                 53.571429
Never married           21.804511
Living with partner     12.218045
Divorced                 8.646617
Separated                3.383459
Widowed                  0.375940
Name: DMDMARTLx, dtype: float64
```

```
#freq table for males, age 30-40
x = age30_40[age30_40['RIAGENDR']==1]['DMDMARTLx'].value_counts()
x / x.sum()*100
```

```
Married                 55.668016
Never married           20.445344
Living with partner     15.789474
Divorced                 4.858300
Separated                2.429150
Widowed                  0.607287
Refused                  0.202429
Name: DMDMARTLx, dtype: float64
```

Q1a. Briefly comment on some of the differences that you observe between the distribution of marital status between women and men, for people of all ages.

There are less married women and that seems to be due to more women being divorced

Q1b. Briefly comment on the differences that you observe between the distribution of marital status states for women between the overall population, and for women between the ages of 30 and 40.

More women between 30-40 are married compared to the whole population and this group as less rates of widowed women

Q1c. Repeat part b for the men.

More man in their 30-4o live with a partner

14.2 Question 2

Restricting to the female population, stratify the subjects into age bands no wider than ten years, and construct the distribution of marital status within each age band. Within each age band, present the distribution in terms of proportions that must sum to 1.

```
#subset df
females = da[da['RIAGENDR'] == 2].copy()

#stratify
females['agegr'] = pd.cut(females['RIDAGEYR'], [18, 30, 40, 50, 60,
↪  70, 80])

#group data
df
↪  =females.groupby("agegr")["DMDMARTLx"].value_counts().unstack().fillna(0)

#normalize
df = df.apply(lambda x : x/x.sum() * 100, axis = 1)

df
```

DMDMARTLx agegr	Divorced	Living with partner	Married	Missing	Never married	Refused	Separ
(18, 30]	1.806240	18.719212	25.944171	9.195402	42.528736	0.000000	1.806
(30, 40]	9.071730	12.025316	54.430380	0.000000	20.464135	0.000000	3.586
(40, 50]	13.745020	7.370518	57.370518	0.000000	12.549801	0.000000	6.573
(50, 60]	17.659574	6.808511	54.680851	0.000000	8.936170	0.212766	5.744
(60, 70]	19.274376	4.308390	48.072562	0.000000	8.616780	0.000000	4.988
(70, 80]	14.390244	0.731707	31.707317	0.000000	5.121951	0.000000	1.951

Q2a. Comment on the trends that you see in this series of marginal distributions.

We see an increase in: divorce over age groups We see a decrease in the proportion of females living with a partner + women never married There is a big spike in marriages (up to 50%) from age group 18-30 to 30-40 and then a slow decline The largest group of widowed women is in the oldest age group

Q2b. Repeat the construction for males.

```
#subset df
males = da[da['RIAGENDR'] == 1].copy()

#stratify
males['agegr'] = pd.cut(males['RIDAGEYR'], [18, 30, 40, 50, 60, 70,
↪  80])

#group data
df
↪  =males.groupby("agegr")["DMDMARTLx"].value_counts().unstack().fillna(0)

#normalize
df = df.apply(lambda x : x/x.sum() * 100, axis = 1)

df
```

DMDMARTLx agegr	Divorced	Living with partner	Married	Missing	Never married	Refused	Sepa
(18, 30]	0.367647	17.463235	19.117647	13.235294	48.161765	0.000000	1.28
(30, 40]	5.240175	15.720524	56.331878	0.000000	19.432314	0.218341	2.62
(40, 50]	8.478803	8.229426	70.324190	0.000000	9.725686	0.000000	2.74
(50, 60]	12.555066	7.488987	65.198238	0.000000	10.352423	0.000000	2.20
(60, 70]	12.585812	5.034325	66.590389	0.000000	8.695652	0.000000	3.20
(70, 80]	14.179104	2.238806	61.194030	0.000000	2.238806	0.000000	3.48

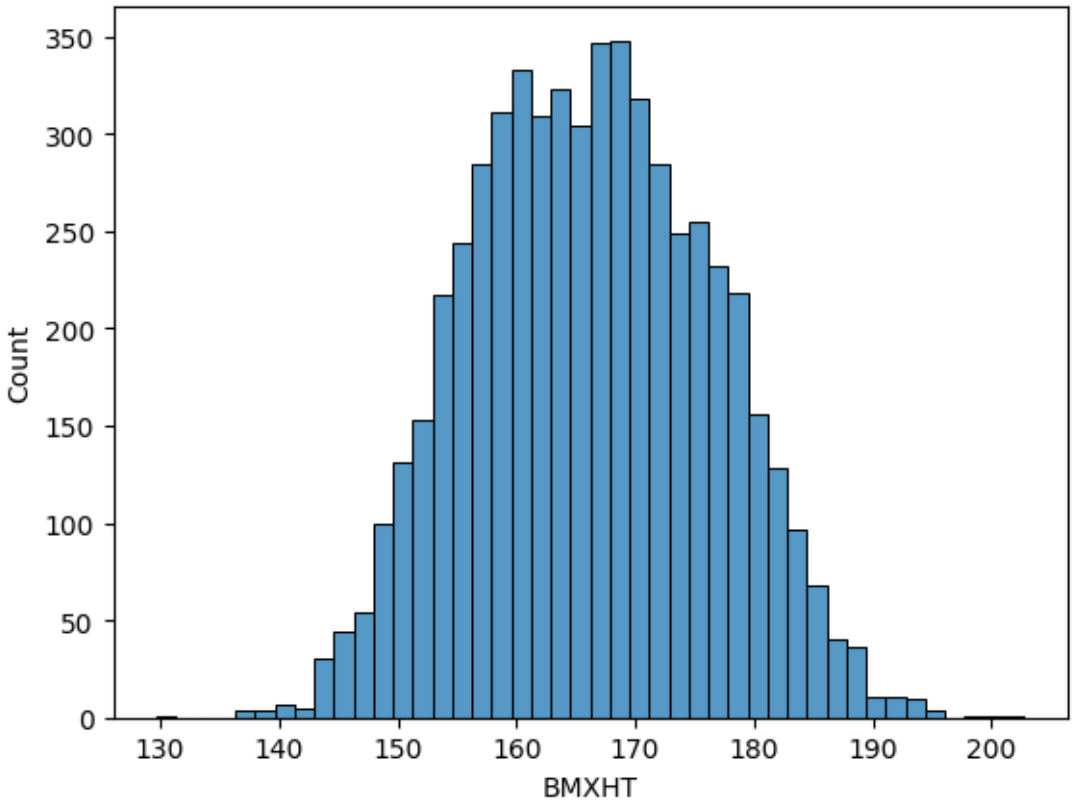
Q2c. Comment on any notable differences that you see when comparing these results for females and for males.

Increase in divorce over time Decrease of males living with a partner and males that never married Largest increase in married males in group 30-40 and then slow decrease (but not to levels as for females) Separated relatively constant Largest increase in widowed men in the last group (but small compared to females)

14.3 Question 3

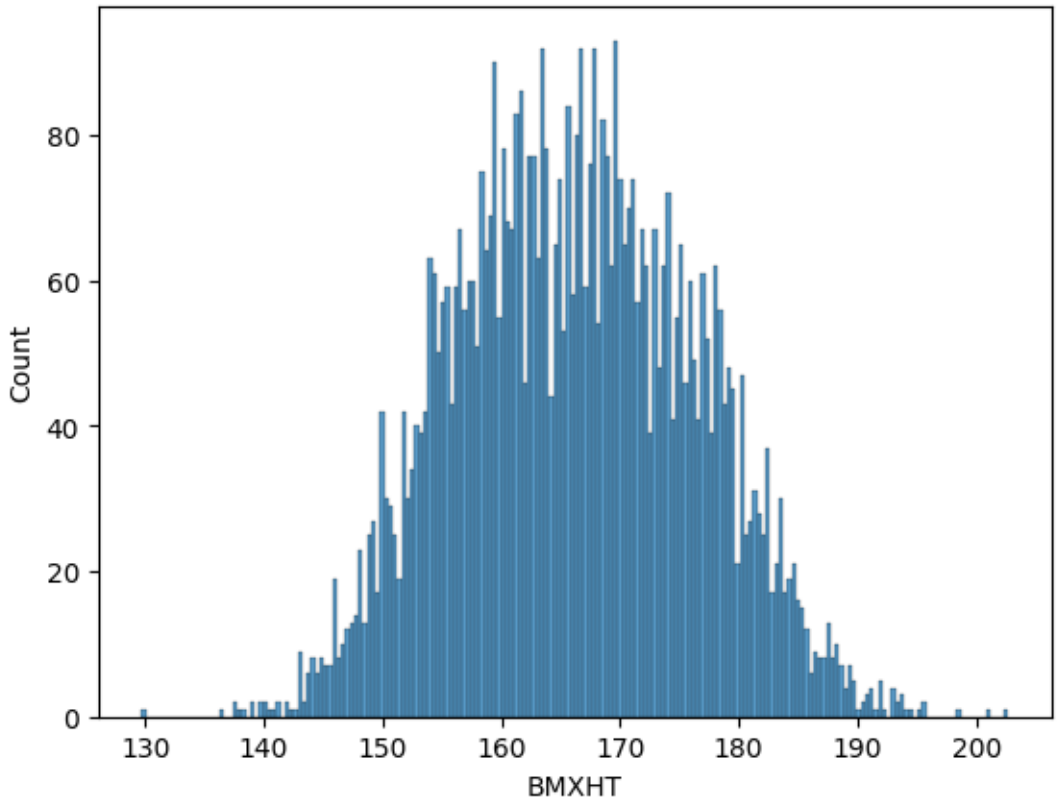
Construct a histogram of the distribution of heights using the BMXHT variable in the NHANES sample.

```
sns.histplot(da.BMXHT)
plt.show()
```



Q3a. Use the `bins` argument to distplot to produce histograms with different numbers of bins. Assess whether the default value for this argument gives a meaningful result, and comment on what happens as the number of bins grows excessively large or excessively small.

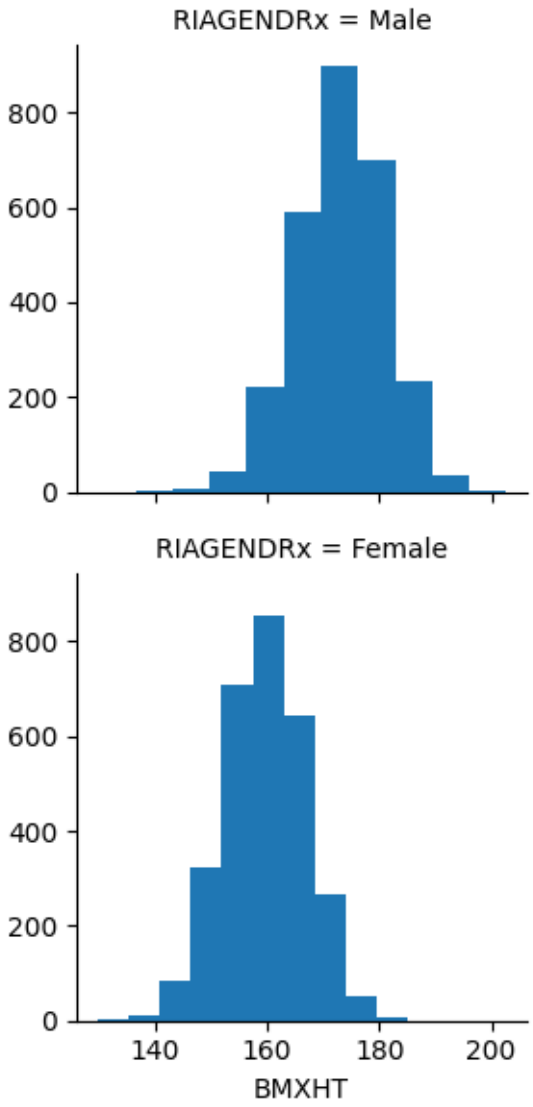
```
sns.histplot(da.BMXHT, bins = 200)
plt.show()
```



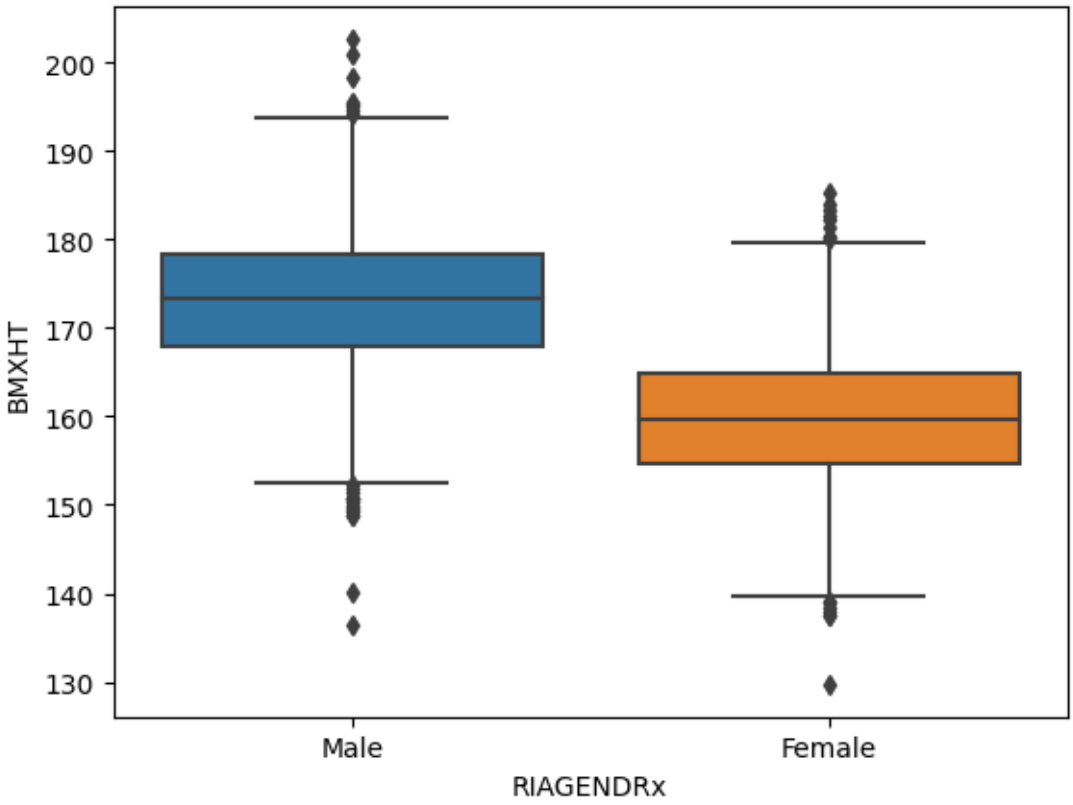
The value looks good

Q3b. Make separate histograms for the heights of women and men, then make a side-by-side boxplot showing the heights of women and men.

```
g = sns.FacetGrid(da, row = 'RIAGENDRx')
g = g.map(plt.hist, "BMXHT")
plt.show()
```




```
sns.boxplot(y = da['BMXHT'], x = da['RIAGENDRx'])
plt.show()
```



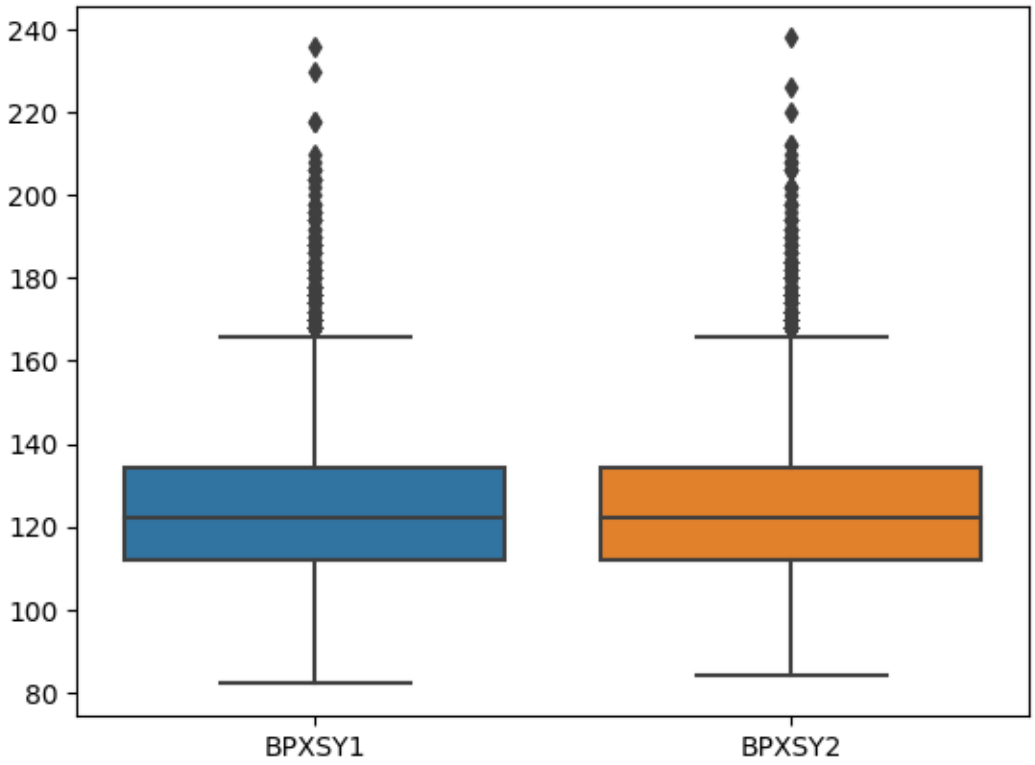
Q3c. Comment on what features, if any are not represented clearly in the boxplots, and what features, if any, are easier to see in the boxplots than in the histograms.

Males are larger than females (we can see this in both plots, however the median is easier to see in the boxplot). There are outliers on both ends (clearer in the boxplot)

14.4 Question 4

Make a boxplot showing the distribution of within-subject differences between the first and second systolic blood pressure measurents (BPXSY1 and BPXSY2).

```
sns.boxplot(da[['BPXSY1', 'BPXSY2']])
plt.show()
```

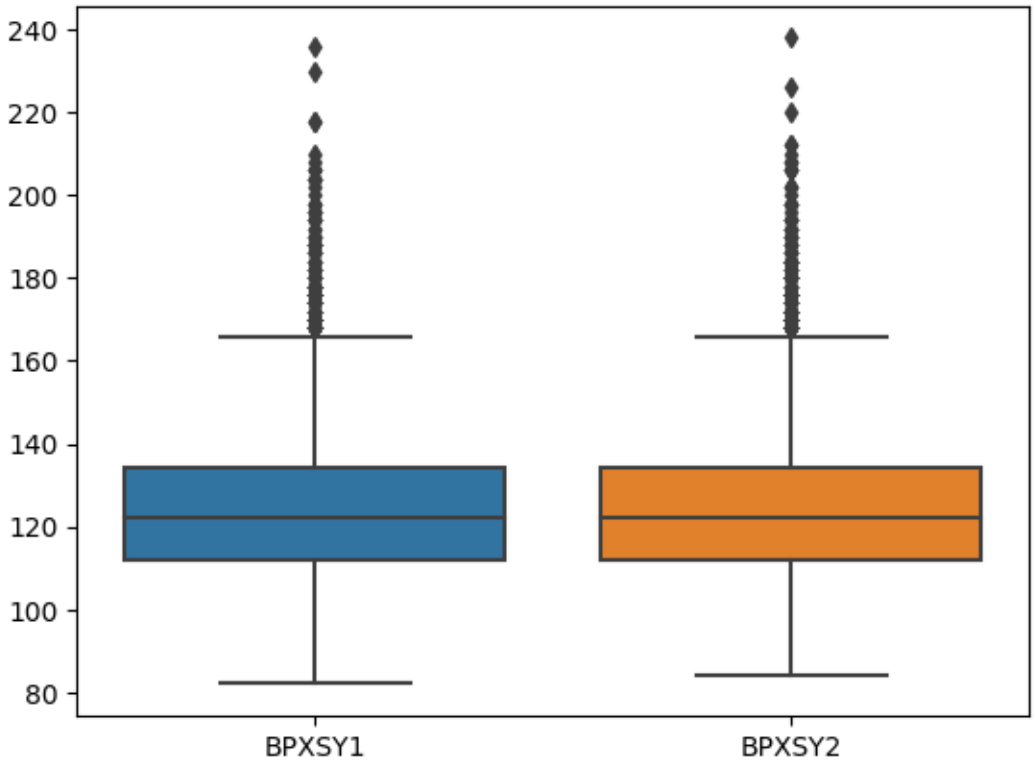


Q4a. What proportion of the subjects have a lower SBP on the second reading compared to the first?

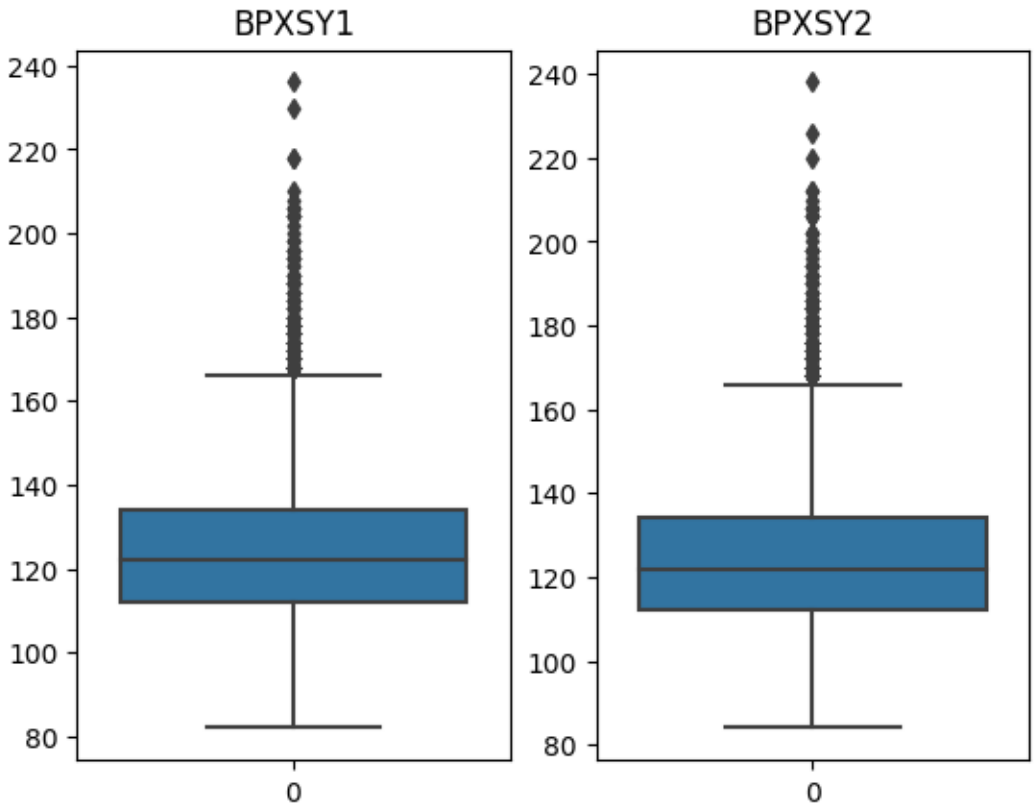
```
# insert your code here
```

Q4b. Make side-by-side boxplots of the two systolic blood pressure variables.

```
sns.boxplot(da[['BPXSY1', 'BPXSY2']])
plt.show()
```




```
fig, ax =plt.subplots(1,2)
sns.boxplot(da['BPXSY1'], ax = ax[0]).set_title("BPXSY1")
sns.boxplot(da['BPXSY2'], ax = ax[1]).set_title("BPXSY2")
plt.show()
```



Q4c. Comment on the variation within either the first or second systolic blood pressure measurements, and the variation in the within-subject differences between the first and second systolic blood pressure measurements.

14.5 Question 5

Construct a frequency table of household sizes for people within each educational attainment category (the relevant variable is DMDEDUC2). Convert the frequencies to proportions.

```
dx = da.groupby(["DMDEDUC2"])["DMDHHSIZ"].value_counts().unstack()
dx = dx.apply(lambda x: x/x.sum(), axis=1)
dx
#print(dx.to_string(float_format="%.2f"))
```

DMDHHSIZ DMDEDUC2	1	2	3	4	5	6	7
1.0	0.109924	0.224427	0.146565	0.132824	0.148092	0.108397	0.129771
2.0	0.116641	0.222395	0.163297	0.152411	0.146190	0.113530	0.085537
3.0	0.152614	0.270658	0.171164	0.161889	0.109612	0.065767	0.068297
4.0	0.151141	0.268970	0.193091	0.169031	0.122147	0.050586	0.045034
5.0	0.142753	0.347731	0.193997	0.165447	0.095168	0.029283	0.025622
9.0	NaN	0.666667	NaN	NaN	0.333333	NaN	NaN

Q5a. Comment on any major differences among the distributions.

Q5b. Restrict the sample to people between 30 and 40 years of age. Then calculate the median household size for women and men within each level of educational attainment.

```
da[(da.RIDAGEYR >= 30) & (da.RIDAGEYR <= 40)].groupby(["DMDEDUC2",
↪  "RIAGENDR"])["DMDHHSIZ"].median()
```

```
DMDEDUC2  RIAGENDR
1.0       1           5.0
          2           5.0
2.0       1           4.5
          2           5.0
3.0       1           4.0
          2           5.0
4.0       1           4.0
          2           4.0
5.0       1           3.0
          2           3.0
Name: DMDHHSIZ, dtype: float64
```

14.6 Question 6

The participants can be clustered into "maked variance units" (MVU) based on every combination of the variables SDMVSTRA and SDMVPSU. Calculate the mean age (RIDAGEYR), height (BMXHT), and BMI (BMXBMI) for each gender (RIAGENDR), within each MVU, and report the ratio between the largest and smallest mean (e.g. for height) across the MVUs.

```
da.groupby(['SDMVSTRA', 'SDMVPSU', 'RIAGENDR']) \
    [['RIDAGEYR', 'BMXHT', 'BMXBMI']] \
    .mean().unstack()
```

		RIDAGEYR		BMXHT		BMXBMI	
	RIAGENDR	1	2	1	2	1	2
SDMVSTRA	SDMVPSU						
119	1	47.861111	47.663265	172.741667	159.570408	26.958333	30.052041
	2	54.363636	52.987952	172.906818	159.244578	27.160465	27.849398
120	1	43.130000	43.636364	169.537755	155.402041	30.939175	32.419388
	2	45.219178	43.736111	173.075342	159.218056	27.727397	27.400000
121	1	46.750000	44.397959	172.177885	158.871579	29.416505	30.856842
	2	42.063158	44.376344	174.764516	160.229032	26.273118	26.470968
122	1	44.653061	42.897436	173.998969	161.315385	28.528866	29.447436
	2	44.320000	47.333333	170.332323	157.231111	25.744444	26.611111
123	1	47.829787	44.841121	174.315217	162.059615	29.231522	29.905769
	2	52.126582	46.457447	174.454430	160.476596	28.811392	30.641489
124	1	50.750000	51.664000	172.109009	158.788710	28.614414	29.533065
	2	48.245614	42.541667	174.291228	162.853521	27.714035	28.640845
125	1	55.165289	50.900901	173.631092	160.762385	29.727731	30.385321
	2	49.705882	51.660000	174.456863	160.021429	29.143564	28.564286
126	1	48.416667	46.229167	175.149398	160.387500	29.033333	31.262500
	2	48.666667	47.205882	174.713043	160.892000	29.039130	29.612121
127	1	53.137931	49.694444	171.545349	157.422430	31.062353	32.189720
	2	54.070588	51.486239	173.366667	159.022936	30.557831	30.770642
128	1	53.673267	55.638462	169.325000	156.339063	31.749000	32.303125
	2	45.822785	45.589744	172.400000	160.437179	26.835443	27.491026
129	1	43.922222	45.329787	171.094318	156.900000	26.493182	29.019149
	2	45.775510	43.500000	173.138298	161.034259	28.961702	29.429630
130	1	50.516854	47.810526	176.974157	161.977895	30.337079	30.700000
	2	50.535354	50.833333	175.061224	160.060577	29.237755	31.490385
131	1	53.140187	54.893617	175.610476	161.989362	28.259615	30.061702
	2	46.778846	45.000000	175.091346	161.673810	30.077885	32.984127
132	1	42.380435	43.210526	172.534066	161.508421	28.546154	29.848421
	2	49.038760	51.700000	172.809524	159.138281	28.966667	30.540625
133	1	44.054795	45.105882	171.509722	158.295122	27.495833	27.959259
	2	47.489796	47.063158	171.179167	158.627368	27.966667	29.000000

Q6a. Comment on the extent to which mean age, height, and BMI vary among the MVUs.

Q6b. Calculate the inter-quartile range (IQR) for age, height, and BMI for each gender and each MVU. Report the ratio between the largest and smalles IQR across the MVUs.

```
# insert your code here
```

Q6c. Comment on the extent to which the IQR for age, height, and BMI vary among the MVUs.

15 How to select dataframe subsets from multivariate data

```
import numpy as np
import pandas as pd

# Show all columns when looking at dataframe
pd.set_option('display.max_columns', 100)
```

```
# Download NHANES 2015-2016 data
df = pd.read_csv("../data/nhanes_2015_2016.csv")
```

```
df.head()
```

	SEQN	ALQ101	ALQ110	ALQ130	SMQ020	RIAGENDR	RIDAGEYR	RIDRETH1	DMDCI
0	83732	1.0	NaN	1.0	1	1	62	3	1.0
1	83733	1.0	NaN	6.0	1	1	53	3	2.0
2	83734	1.0	NaN	NaN	1	1	78	3	1.0
3	83735	2.0	1.0	1.0	2	2	56	3	1.0
4	83736	2.0	1.0	1.0	2	2	42	4	1.0

15.0.1 Selecting columns

15.0.1.1 Selecting columns using list comprehensions

Keep only body measures columns, so only columns with "BMX" in the name

```
# get columns names
col_names = df.columns
```

```
col_names
```

```
Index(['SEQN', 'ALQ101', 'ALQ110', 'ALQ130', 'SMQ020', 'RIAGENDR', 'RIDAGEYR',
       'RIDRETH1', 'DMDCITZN', 'DMDEDUC2', 'DMDMARTL', 'DMDHHSIZ', 'WTINT2YR',
       'SDMVPSU', 'SDMVSTRA', 'INDFMPIR', 'BPXSY1', 'BPXDI1', 'BPXSY2',
       'BPXDI2', 'BMXWT', 'BMXHT', 'BMXBMI', 'BMXLEG', 'BMXARML', 'BMXARMC',
       'BMXWAIST', 'HIQ210'],
      dtype='object')
```

```
# One way to get the column names we want to keep is simply by
↪  copying from the above output and storing in a list
keep = ['BMXWT', 'BMXHT', 'BMXBMI', 'BMXLEG', 'BMXARML', 'BMXARMC',
        'BMXWAIST']
```

```
# Another way to get only column names that include 'BMX' is with
↪  list comprehension
# [keep x for x in list if condition met]
[column for column in col_names if 'BMX' in column]
```

```
['BMXWT', 'BMXHT', 'BMXBMI', 'BMXLEG', 'BMXARML', 'BMXARMC', 'BMXWAIST']
```

```
keep = [column for column in col_names if 'BMX' in column]
```

```
# use [] notation to keep columns
df_BMX = df[keep]
```

```
df_BMX.head()
```

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
0	94.8	184.5	27.8	43.3	43.6	35.9	101.1
1	90.4	171.4	30.8	38.0	40.0	33.2	107.9
2	83.4	170.1	28.8	35.6	37.0	31.0	116.5
3	109.8	160.9	42.4	38.5	37.7	38.3	110.1

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
4	55.2	164.9	20.3	37.4	36.0	27.2	80.4

There are two methods for selecting by row and column.

15.0.1.2 Selecting columns using loc

link for pandas cheat sheets

- df.loc[row labels or bool, col labels or bool]
- df.iloc[row int or bool, col int or bool]

From pandas docs:

☐ column indexing
- .loc is primarily label based, but may also be used with a boolean array.

- .iloc is primarily integer position based (from 0 to length-1 of the axis), but may also be used with a boolean array.

```
df.loc[:, keep].head()
```

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
0	94.8	184.5	27.8	43.3	43.6	35.9	101.1
1	90.4	171.4	30.8	38.0	40.0	33.2	107.9
2	83.4	170.1	28.8	35.6	37.0	31.0	116.5
3	109.8	160.9	42.4	38.5	37.7	38.3	110.1
4	55.2	164.9	20.3	37.4	36.0	27.2	80.4

15.0.1.3 Selecting columns using numpy

```
index_bool = np.isin(df.columns, keep)
```

```
index_bool
```

```
array([False, False, False, False, False, False, False, False, False,
       False, False, False, False, False, False, False, False, False,
       False, False,  True,  True,  True,  True,  True,  True,  True,
       False])
```

```
df.iloc[:,index_bool].head() # Indexing with boolean list
```

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
0	94.8	184.5	27.8	43.3	43.6	35.9	101.1
1	90.4	171.4	30.8	38.0	40.0	33.2	107.9
2	83.4	170.1	28.8	35.6	37.0	31.0	116.5
3	109.8	160.9	42.4	38.5	37.7	38.3	110.1
4	55.2	164.9	20.3	37.4	36.0	27.2	80.4

15.0.2 Selection by conditions

```
# Lets only look at rows who 'BMXWAIST' is larger than the median
# get the median of 'BMXWAIST'
waist_median = pd.Series.median(df_BMX['BMXWAIST'])
```

```
#alternative code
df_BMX['BMXWAIST'].median()
```

```
98.3
```

```
waist_median
```

```
98.3
```

```
#subset the dataframe
df_BMX[df_BMX['BMXWAIST'] > waist_median].head()
```

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
0	94.8	184.5	27.8	43.3	43.6	35.9	101.1
1	90.4	171.4	30.8	38.0	40.0	33.2	107.9
2	83.4	170.1	28.8	35.6	37.0	31.0	116.5
3	109.8	160.9	42.4	38.5	37.7	38.3	110.1
9	108.3	179.4	33.6	46.0	44.1	38.5	116.0

```
# Lets add another condition, that 'BMXLEG' must be less than 32
condition1 = df_BMX['BMXWAIST'] > waist_median
condition2 = df_BMX['BMXLEG'] < 32

# Subset the data using [] method
# Note: can't use 'and' instead of '&'
df_BMX[condition1 & condition2].head()
```

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
15	80.5	150.8	35.4	31.6	32.7	33.7	113.5
27	75.6	145.2	35.9	31.0	33.1	36.0	108.0
39	63.7	147.9	29.1	26.0	34.0	31.5	110.0
52	105.9	157.7	42.6	29.2	35.0	40.7	129.1
55	77.5	148.3	35.2	30.5	34.0	34.4	107.6

```
# Alternative using df.loc[] method
# note that the conditiona are describing the rows to keep
df_BMX.loc[condition1 & condition2, :].head()
```

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
15	80.5	150.8	35.4	31.6	32.7	33.7	113.5
27	75.6	145.2	35.9	31.0	33.1	36.0	108.0
39	63.7	147.9	29.1	26.0	34.0	31.5	110.0
52	105.9	157.7	42.6	29.2	35.0	40.7	129.1
55	77.5	148.3	35.2	30.5	34.0	34.4	107.6

```
# Lets make a small dataframe and give it a new index so can more
↪  clearly see the differences between .loc and .iloc
# If you use different years than 2015-2016, this my give an error.
↪  Why?
tmp = df_BMX.loc[condition1 & condition2, :].head()
tmp.index = ['a', 'b', 'c', 'd', 'e']
tmp
```

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
a	80.5	150.8	35.4	31.6	32.7	33.7	113.5
b	75.6	145.2	35.9	31.0	33.1	36.0	108.0
c	63.7	147.9	29.1	26.0	34.0	31.5	110.0
d	105.9	157.7	42.6	29.2	35.0	40.7	129.1
e	77.5	148.3	35.2	30.5	34.0	34.4	107.6

```
#use loc
tmp.loc[['a', 'b'],'BMXLEG']
```

```
a    31.6
b    31.0
Name: BMXLEG, dtype: float64
```

```
#use iloc (use only the index values not the label)
tmp.iloc[[0, 1],3]
```

```
a    31.6
b    31.0
Name: BMXLEG, dtype: float64
```

15.0.3 Common errors and how to read them

```
#Gives an an invalid key error, we need to use iloc or the regular
↪  loc
#tmp[:, 'BMXBMI']
```

15.0.4 Problem

The above gives: TypeError: unhashable type: 'slice'

The [ ] method uses hashes to identify the columns to keep, and each column has an associated hash. A 'slice' (a subset of rows and columns) does not have an associated hash, thus causing this TypeError.

```
tmp.loc[:, 'BMXBMI']
```

```
a    35.4
b    35.9
c    29.1
d    42.6
e    35.2
Name: BMXBMI, dtype: float64
```

```
tmp.loc[:, 'BMXBMI'].values
```

```
array([35.4, 35.9, 29.1, 42.6, 35.2])
```

```
#this will also give an error because iloc just takes indices
#tmp.iloc[:, 'BMXBMI']
```

15.0.5 Problem

The above gives: ValueError: Location based indexing can only have [integer, integer slice (START point is INCLUDED, END point is EXCLUDED), listlike of integers, boolean array] types

'BMXBMI' is not an integer that is less than or equal number of columns -1, or a list of boolean values, so it is the wrong value type.

```
tmp.iloc[:, 2]
```

```
a    35.4
b    35.9
c    29.1
d    42.6
e    35.2
Name: BMXBMI, dtype: float64
```

```
#this gives a key error , because no column is named 2
#tmp.loc[:, 2]
```

15.0.6 Problem

The above code gives: `TypeError: cannot do label indexing on <class 'pandas.core.indexes.base.I with these indexers [2] of <class 'int'>`

2 is not one of the labels (i.e. column names) in the dataframe

```
# Here is another example of using a boolean list for indexing
↪  columns
tmp.loc[:, [False, False, True] +[False]*4]
```

	BMXBMI
a	35.4
b	35.9
c	29.1
d	42.6

	BMXBMI
e	35.2

```
tmp.iloc[:, 2]
```

```
a    35.4
b    35.9
c    29.1
d    42.6
e    35.2
Name: BMXBMI, dtype: float64
```

15.0.7 Change values inside a df

```
# We can use the .loc and .iloc methods to change values within the
↪  dataframe
tmp.iloc[0:3,2] = [0]*3
tmp.iloc[:,2]
```

```
a     0.0
b     0.0
c     0.0
d    42.6
e    35.2
Name: BMXBMI, dtype: float64
```

```
tmp.loc['a':'c','BMXBMI'] = [1]*3
tmp.loc[:,'BMXBMI']
```

```
a     1.0
b     1.0
c     1.0
d    42.6
e    35.2
Name: BMXBMI, dtype: float64
```

```
# We can use the [] method when changing all the values of a column
tmp['BMXBMI'] = range(0, 5)
tmp
```

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
a	80.5	150.8	0	31.6	32.7	33.7	113.5
b	75.6	145.2	1	31.0	33.1	36.0	108.0
c	63.7	147.9	2	26.0	34.0	31.5	110.0
d	105.9	157.7	3	29.2	35.0	40.7	129.1
e	77.5	148.3	4	30.5	34.0	34.4	107.6

```
# We will get a warning when using the [] method with conditions to
↪  set new values in our dataframe
tmp[tmp.BMXBMI > 2]['BMXBMI'] = [10]*2

# Setting new values to a copy of tmp, but not tmp itself
# You can see that the above code did not change our dataframe 'tmp'.
tmp
```

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
a	80.5	150.8	0	31.6	32.7	33.7	113.5
b	75.6	145.2	1	31.0	33.1	36.0	108.0
c	63.7	147.9	2	26.0	34.0	31.5	110.0
d	105.9	157.7	3	29.2	35.0	40.7	129.1
e	77.5	148.3	4	30.5	34.0	34.4	107.6

```
# The correct way to do the above is with .loc or .iloc
tmp.loc[tmp.BMXBMI > 2, 'BMXBMI']  = [10]*2
tmp
```

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
a	80.5	150.8	0	31.6	32.7	33.7	113.5
b	75.6	145.2	1	31.0	33.1	36.0	108.0
c	63.7	147.9	2	26.0	34.0	31.5	110.0

	BMXWT	BMXHT	BMXBMI	BMXLEG	BMXARML	BMXARMC	BMXWAIST
d	105.9	157.7	10	29.2	35.0	40.7	129.1
e	77.5	148.3	10	30.5	34.0	34.4	107.6

16 Plot Multivariate Distributions in Python

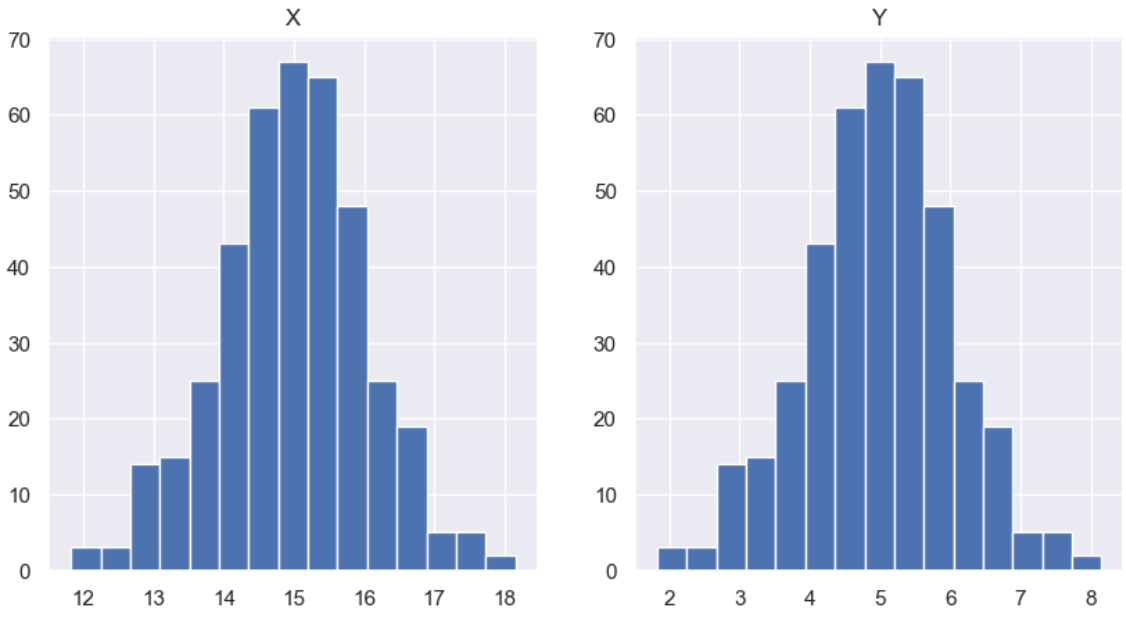
Sometimes we can get a lot of information about how two variables (or more) relate if we plot them together. This tutorial aims to show how plotting two variables together can give us information that plotting each one separately may miss.

```
# import the packages we are going to be using
import numpy as np # for getting our distribution
import matplotlib.pyplot as plt # for plotting
import seaborn as sns; sns.set() # For a different plotting theme
```

```
# Don't worry so much about what rho is doing here
# Just know if we have a rho of 1 then we will get a perfectly
# upward sloping line, and if we have a rho of -1, we will get
# a perfectly downward slopping line. A rho of 0 will
# get us a 'cloud' of points
r = 1

# Don't worry so much about the following three lines of code for now
# this is just getting the data for us to plot
mean = [15, 5]
cov = [[1, r], [r, 1]]

#create two vectors,x and y, both having a normal distribution
x, y = x, y = np.random.multivariate_normal(mean, cov, 400).T
```

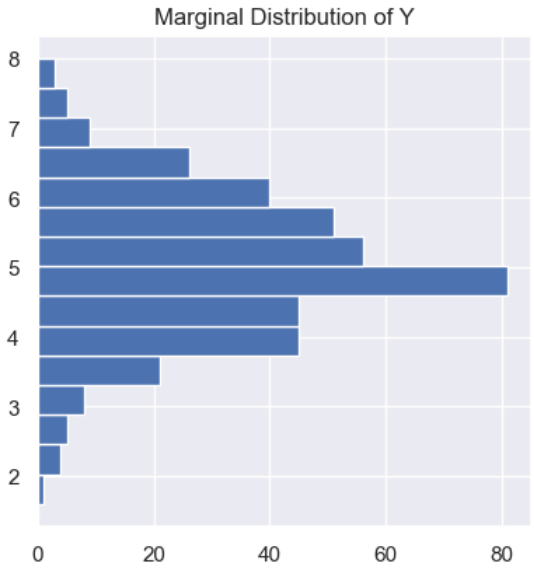
```
# Adjust the figure size
plt.figure(figsize=(10,5))

# Plot the histograms of X and Y next to each other
#create first plot
plt.subplot(1,2,1)
```

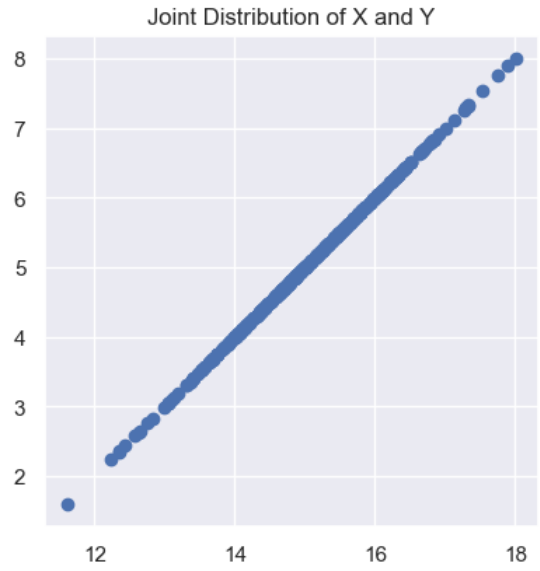
```
plt.hist(x = x, bins = 15)
plt.title("X")

#Plot second plot
plt.subplot(1,2,2)
plt.hist(x = y, bins = 15)
plt.title("Y")

plt.show()
```

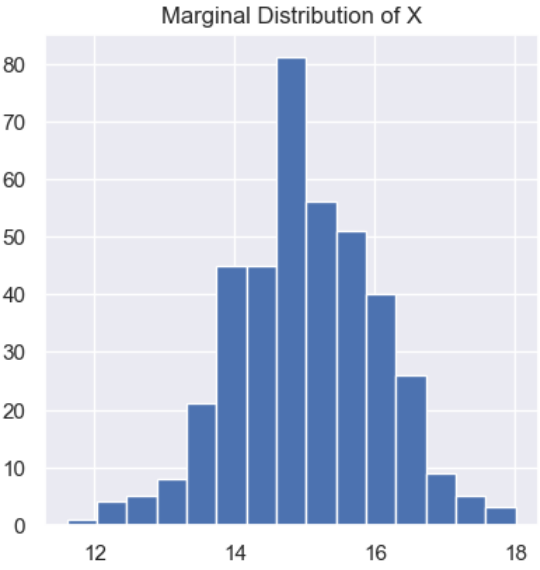



```
# Plot the data by including a scatterplot
plt.figure(figsize=(10,10))

#create the scatterplot
#we create a two by two plot and plot the scatter in the upper right
↪  corner
plt.subplot(2,2,2)
plt.scatter(x = x, y = y)
plt.title("Joint Distribution of X and Y")
```

```
# Plot the Marginal X Distribution at the bottom right (position 4)
plt.subplot(2,2,4)
plt.hist(x = x, bins = 15)
plt.title("Marginal Distribution of X")

# Plot the Marginal Y Distribution
plt.subplot(2,2,1)
plt.hist(x = y, orientation = "horizontal", bins = 15)
plt.title("Marginal Distribution of Y")

# Show the plots
plt.show()
```


Marginal Distribution of Y
8
7
6
5
4
3
2
0
20
40
60
80


Joint Distribution of X and Y
8
7
6
5
4
3
2
12
14
16
18


Marginal Distribution of X
80
70
60
50
40
30
20
10
0
12
14
16
18

17 Unit Testing

While we will not cover the unit testing library that python has, we wanted to introduce you to a simple way that you can test your code.

Unit testing is important because it the only way you can be sure that your code is do what you think it is doing.

Remember, just because ther are no errors does not mean your code is correct.

```
import numpy as np
import pandas as pd
import matplotlib as plt
pd.set_option('display.max_columns', 100) # Show all columns when
↪  looking at dataframe
```

```
# Download NHANES 2015-2016 data
df = pd.read_csv("../data/nhanes_2015_2016.csv")
df.index = range(1,df.shape[0]+1)
```

```
df.head()
```

	SEQN	ALQ101	ALQ110	ALQ130	SMQ020	RIAGENDR	RIDAGEYR	RIDRETH1	DMDCI
1	83732	1.0	NaN	1.0	1	1	62	3	1.0
2	83733	1.0	NaN	6.0	1	1	53	3	2.0
3	83734	1.0	NaN	NaN	1	1	78	3	1.0
4	83735	2.0	1.0	1.0	2	2	56	3	1.0
5	83736	2.0	1.0	1.0	2	2	42	4	1.0

17.0.1 Goal

We want to find the mean of first 100 rows of 'BPXSY1' when 'RIDAGEYR' > 60

```
# One possible way of doing this is:
# Current version of python will include this warning, older versions
↪  will not
#this gives an index error
#pd.Series.mean(df[df.RIDAGEYR > 60].loc[range(0,100), 'BPXSY1'])
```

```
df[df.RIDAGEYR > 60]['BPXSY1'].head(100).mean()
```

```
136.29166666666666
```

```
# test our code on only ten rows so we can easily check
test = pd.DataFrame({'col1': np.repeat([3,1],5), 'col2':
↪  range(3,13)}, index=range(1,11))
test
```

	col1	col2
1	3	3
2	3	4
3	3	5
4	3	6
5	3	7
6	1	8
7	1	9
8	1	10
9	1	11
10	1	12

```
# pd.Series.mean(df[df.RIDAGEYR > 60].loc[range(0,5), 'BPXSY1'])
# should return 5

#the code below would give the wrong number but returns an error
#pd.Series.mean(test[test.col1 > 2].loc[range(0,5), 'col2'])
test[test.col1 > 2]['col2'].head(5).mean()
```

```
5.0
```

What went wrong?

```
#test[test.col1 > 2].loc[range(0,5), 'col2']
# 0 is not in the row index labels because the second row's value is
↪  < 2. For now, pandas defaults to filling this
# with NaN
```

```
# Using the .iloc method instead, we are correctly choosing the first
↪  5 rows, regardless of their row labels
test[test.col1 >2].iloc[range(0,5), 1]
```

```
1    3
2    4
3    5
4    6
5    7
Name: col2, dtype: int64
```

```
pd.Series.mean(test[test.col1 >2].iloc[range(0,5), 1])
```

```
5.0
```

```
# We can compare what our real dataframe looks like with the
↪  incorrect and correct methods
#Filled with NaN whenever a row label does not meet the condition
#df[df.RIDAGEYR > 60].loc[range(0,5), :] #
```

```
#This Correctly picks the first fice rows such that 'RIDAGEYR" > 60
df[df.RIDAGEYR > 60].iloc[range(0,5), :]
```

	SEQN	ALQ101	ALQ110	ALQ130	SMQ020	RIAGENDR	RIDAGEYR	RIDRETH1	DMDC
1	83732	1.0	NaN	1.0	1	1	62	3	1.0
3	83734	1.0	NaN	NaN	1	1	78	3	1.0
6	83737	2.0	2.0	NaN	2	2	72	1	2.0

	SEQN	ALQ101	ALQ110	ALQ130	SMQ020	RIAGENDR	RIDAGEYR	RIDRETH1	DMDC
14	83754	2.0	1.0	1.0	2	2	67	2	1.0
15	83755	1.0	NaN	3.0	2	1	67	4	1.0

```
# Applying the correct method to the original question about BPXSY1
print(pd.Series.mean(df[df.RIDAGEYR > 60].iloc[range(0,100), 16]))
```

```
136.29166666666666
```

```
# Another way to reference the BPXSY1 variable
print(pd.Series.mean(df[df.RIDAGEYR > 60].iloc[range(0,100),
↪  df.columns.get_loc('BPXSY1')]))
```

```
136.29166666666666
```

18 Analysis of multivariate data - NHANES case study

In this notebook, we illustrate several basic techniques for exploring data using methods for understanding multivariate relationships. The statistical methods discussed here will parallel the methods discussed in the multivariate methods section of the course, and build on the univariate analysis discussed earlier. As with the univariate notebook, we use here the 2015-2016 wave of the NHANES study for illustration.

Many of the analyses presented in this notebook use the Matplotlib and Seaborn libraries for data visualization. These are very powerful tools that give you a vast number of options when constructing plots. We will not explain every option to every function in the examples below. You can use the Matplotlib and Seaborn documentation to fully understand the options, and you can experiment with these and other plots on your own to get a better sense of what can be done.

We start with the usual library import statements:

```
%matplotlib inline
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
import numpy as np
from scipy import stats
```

Next we load the NHANES data, just as we did for the univariate analyes.

```
da = pd.read_csv("../data/nhanes_2015_2016.csv")
da.head()
```

	SEQN	ALQ101	ALQ110	ALQ130	SMQ020	RIAGENDR	RIDAGEYR	RIDRETH1	DMDCI
0	83732	1.0	NaN	1.0	1	1	62	3	1.0
1	83733	1.0	NaN	6.0	1	1	53	3	2.0

	SEQN	ALQ101	ALQ110	ALQ130	SMQ020	RIAGENDR	RIDAGEYR	RIDRETH1	DMDCI
2	83734	1.0	NaN	NaN	1	1	78	3	1.0
3	83735	2.0	1.0	1.0	2	2	56	3	1.0
4	83736	2.0	1.0	1.0	2	2	42	4	1.0

18.0.1 Quantitative bivariate data

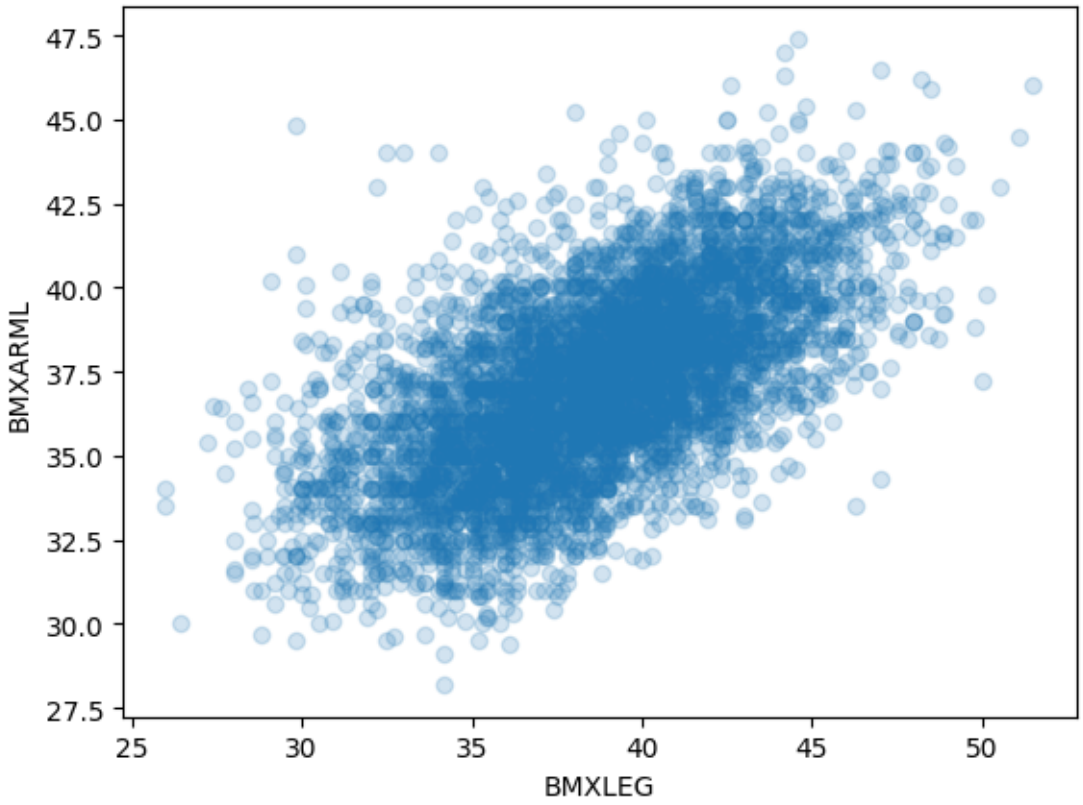
Bivariate data arise when every "unit of analysis" (e.g. a person in the NHANES dataset) is assessed with respect to two traits (the NHANES subjects were assessed for many more than two traits, but we can consider two traits at a time here).

A scatterplot is a very common and easily-understood visualization of quantitative bivariate data. Below we make a scatterplot of arm length against leg length. This means that arm length (BMXARML) is plotted on the vertical axis and leg length (BMXLEG) is plotted on the horizontal axis). We see a positive dependence between the two measures – people with longer arms tend to have longer legs, and vice-versa. However it is far from a perfect relationship.

In a scatterplot with more than around 100 points, "overplotting" becomes an issue. This means that many points fall on top of each other in the plot, which obscures relationships in the middle of the distribution and over-emphasizes the extremes. One way to mitigate overplotting is to use an "alpha" channel to make the points semi-transparent, as we have done below.

```
sns.regplot(x="BMXLEG", y="BMXARML", data=da, fit_reg=False,
↪  scatter_kws={"alpha": 0.2})
```

```
<AxesSubplot:xlabel='BMXLEG', ylabel='BMXARML'>
```

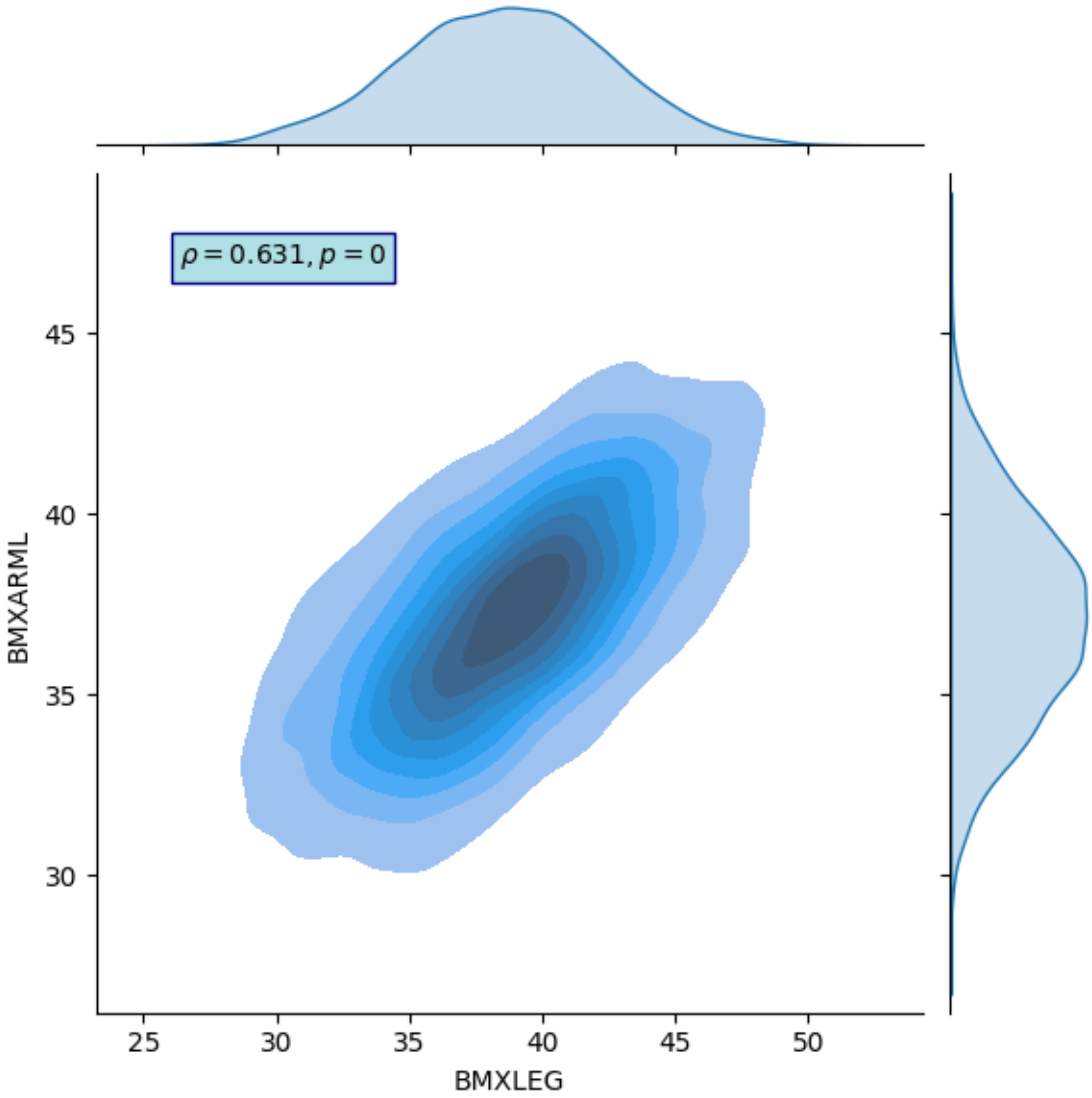


Another way to avoid overplotting is to make a plot of the "density" of points. In the plots below, darker colors indicate where a greater number of points fall. The two plot margins show the densities for the arm lengths and leg lengths separately, while the plot in the center shows their density jointly.

This plot also shows the Pearson correlation coefficient between the arm length and leg length, which is 0.62. As discussed in the course, the Pearson correlation coefficient ranges from -1 to 1, with values approaching 1 indicating a more perfect positive dependence. In many settings, a correlation of 0.62 would be considered a moderately strong positive dependence.

```
g = sns.jointplot(x="BMXLEG", y="BMXARML", kind='kde', fill=True,
↪  data=da)
r, p = stats.spearmanr(da['BMXLEG'], da['BMXARML'],
↪  nan_policy='omit')
g.ax_joint.annotate(f'$\\rho = {r:.3f}, p = {p:3g}$',
```

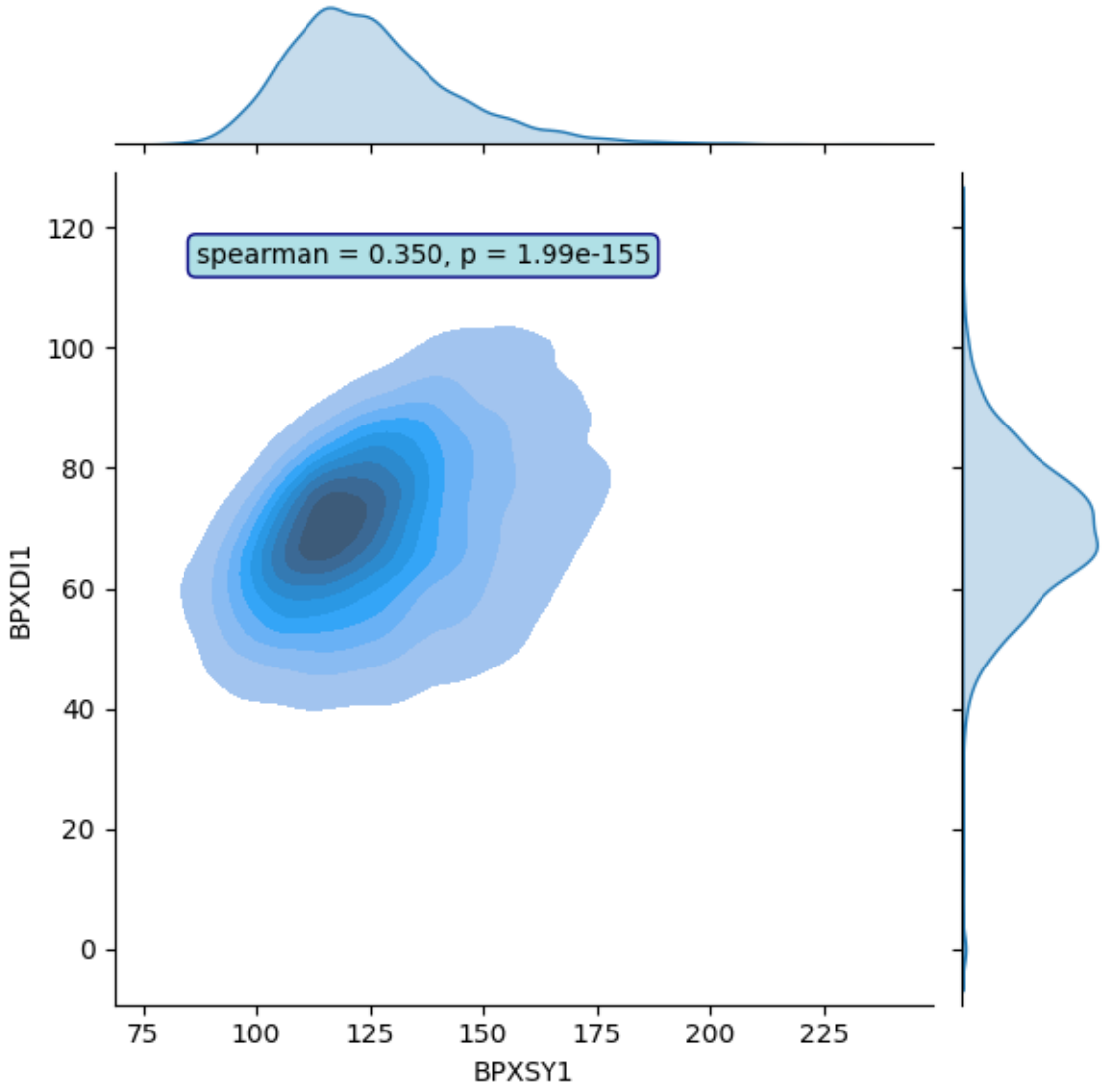
```
                    xy=(0.1, 0.9), xycoords='axes fraction',
                    ha='left', va='center',
                    bbox={'boxstyle': 'square', 'fc': 'powderblue',
↪  'ec': 'navy'})
plt.show()
```



As another example with slightly different behavior, we see that systolic and diastolic blood

pressure (essentially the maximum and minimum blood pressure between two consecutive heart beats) are more weakly correlated than arm and leg length, with a correlation coefficient of 0.32. This weaker correlation indicates that some people have unusually high systolic blood pressure but have average diastolic blood pressure, and vice versa.

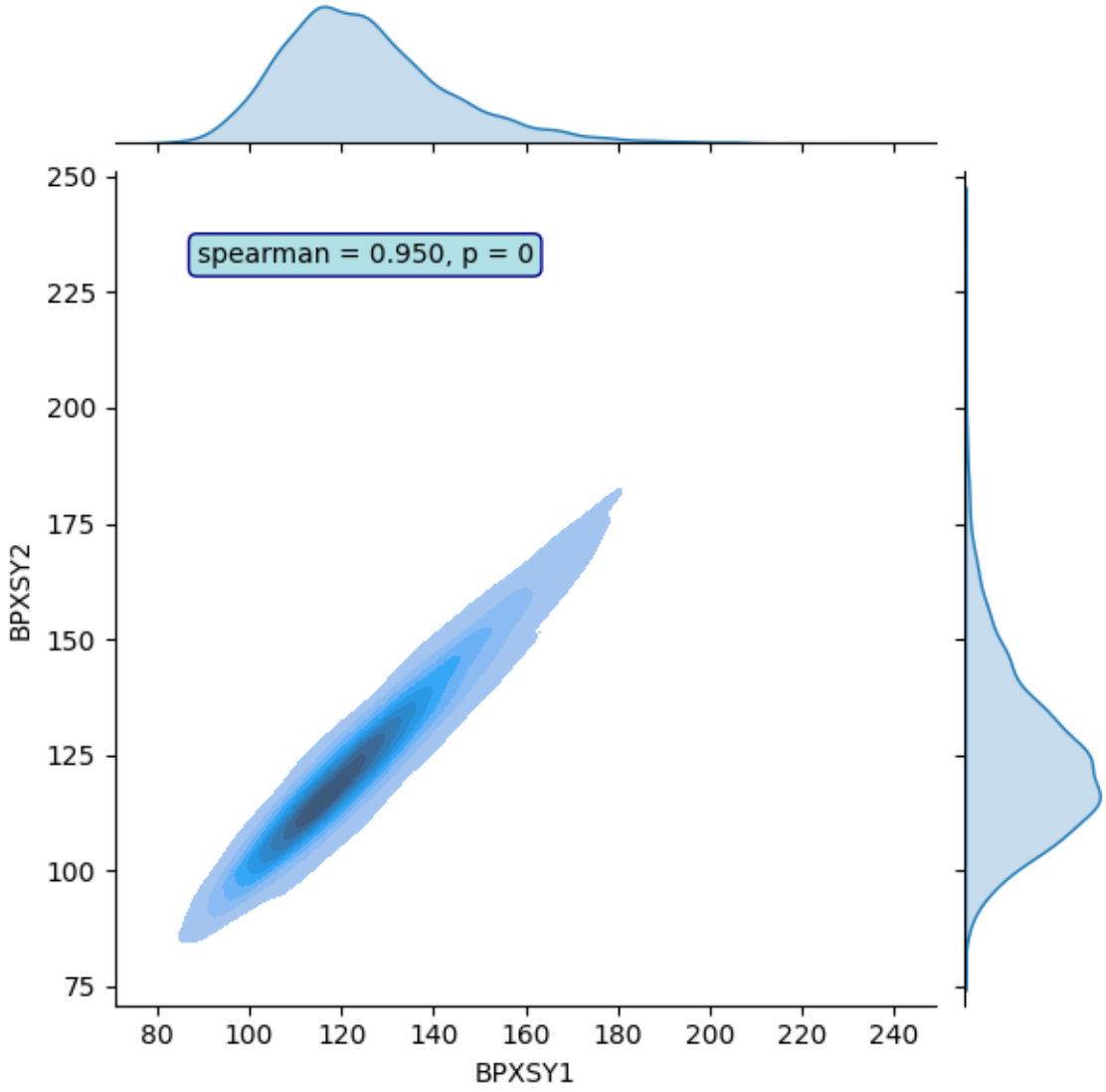
```
g = sns.jointplot(x="BPXSY1", y="BPXDI1", kind='kde', fill = True,
↪  data=da)
r, p = stats.spearmanr(da['BPXSY1'], da['BPXDI1'], nan_policy='omit')
g.ax_joint.annotate(f'spearman = {r:.3f}, p = {p:.3g}',
                    xy=(0.1, 0.9), xycoords='axes fraction',
                    ha='left', va='center',
                    bbox={'boxstyle': 'round', 'fc': 'powderblue',
↪  'ec': 'navy'})
plt.show()
```



Next we look at two repeated measures of systolic blood pressure, taken a few minutes apart on the same person. These values are very highly correlated, with a correlation coefficient of around 0.96.

```
g = sns.jointplot(x="BPXSY1", y="BPXSY2", kind='kde', fill = True,
↪  data=da)
r, p = stats.spearmanr(da['BPXSY1'], da['BPXSY2'], nan_policy='omit')
```

```
g.ax_joint.annotate(f'spearman = {r:.3f}, p = {p:.3g}',
                    xy=(0.1, 0.9), xycoords='axes fraction',
                    ha='left', va='center',
                    bbox={'boxstyle': 'round', 'fc': 'powderblue',
↪  'ec': 'navy'})
plt.show()
```



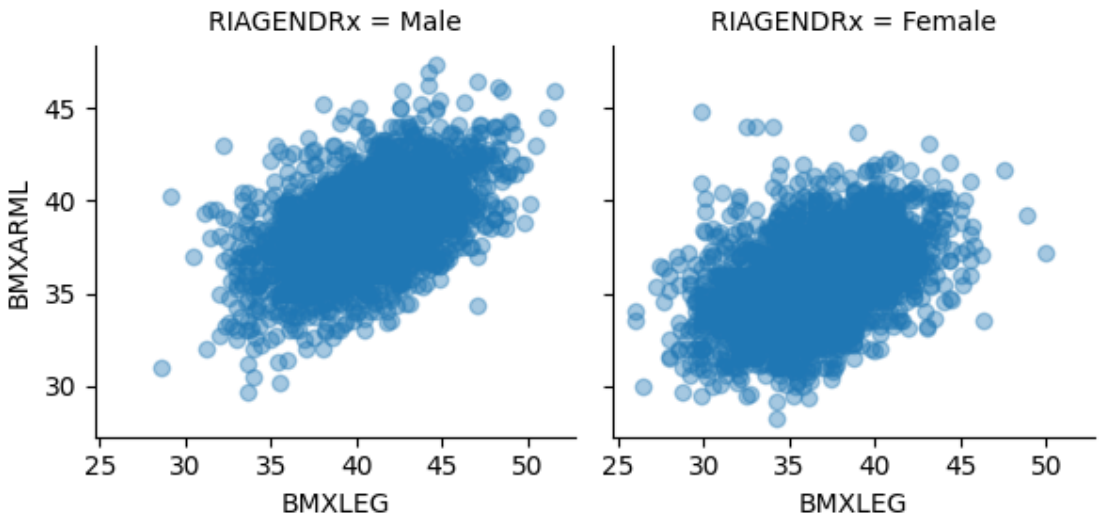
18.0.2 Heterogeneity and stratification

Most human characteristics are complex – they vary by gender, age, ethnicity, and other factors. This type of variation is often referred to as "heterogeneity". When such heterogeneity is present, it is usually productive to explore the data more deeply by stratifying on relevant factors, as we did in the univariate analyses.

Below, we continue to probe the relationship between leg length and arm length, stratifying first by gender, then by gender and ethnicity. The gender-stratified plot indicates that men tend to have somewhat longer arms and legs than women – this is reflected in the fact that the cloud of points on the left is shifted slightly up and to the right relative to the cloud of points on the right. In addition, the correlation between arm length and leg length appears to be somewhat weaker in women than in men.

```
da["RIAGENDRx"] = da.RIAGENDR.replace({1: "Male", 2: "Female"})
sns.FacetGrid(da, col="RIAGENDRx").map(plt.scatter, "BMXLEG",
↪  "BMXARML", alpha=0.4).add_legend()
```

```
<seaborn.axisgrid.FacetGrid at 0x7fd4f55a0710>
```



Consistent with the scatterplot, a slightly weaker correlation between arm length and leg length in women (compared to men) can be seen by calculating the correlation coefficient separately within each gender.

The '`corr`' method of a dataframe calculates the correlation coefficients for every pair of variables in the dataframe. This method returns a "correlation matrix", which is a table containing the correlations between every pair of variables in the data set. Note that the diagonal of a correlation matrix always contains 1's, since a variable always has correlation 1 with itself. The correlation matrix is also symmetric around this diagonal, since the correlation between two variables '`X`' and '`Y`' does not depend on the order in which we consider the two variables.

In the results below, we see that the correlation between leg length and arm length in men is 0.50, while in women the correlation is 0.43.

```
print(da.loc[da.RIAGENDRx=="Female", ["BMXLEG",
↪  "BMXARML"]].dropna().corr())
```

```
           BMXLEG   BMXARML
BMXLEG   1.000000  0.434703
BMXARML  0.434703  1.000000
```

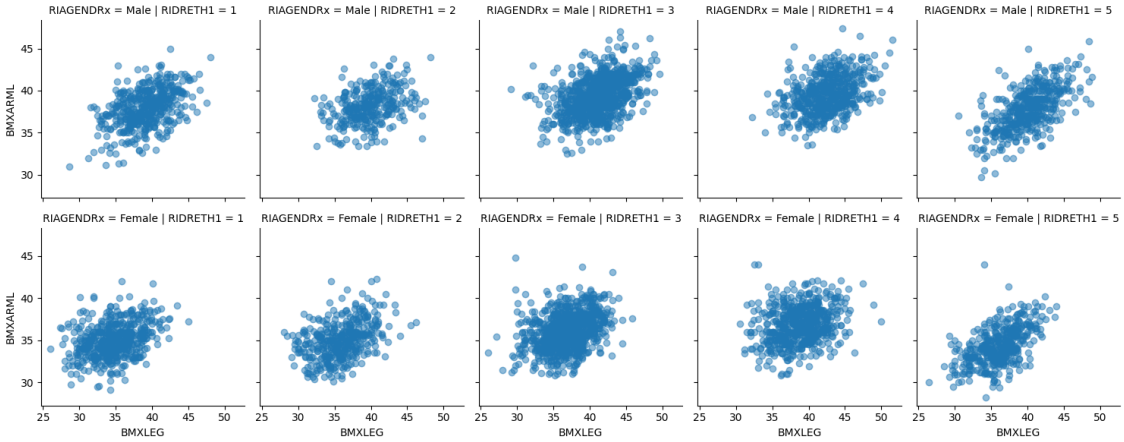
```
print(da.loc[da.RIAGENDRx=="Male", ["BMXLEG",
↪  "BMXARML"]].dropna().corr())
```

```
           BMXLEG   BMXARML
BMXLEG   1.000000  0.505426
BMXARML  0.505426  1.000000
```

Next we look to stratifying the data by both gender and ethnicity. This results in 2 x 5 = 10 total strata, since there are 2 gender strata and 5 ethnicity strata. These scatterplots reveal differences in the means as well a diffrences in the degree of association (correlation) between different pairs of variables. We see that although some ethnic groups tend to have longer/shorter arms and legs than others, the relationship between arm length and leg length within genders is roughly similar across the ethnic groups.

One notable observation is that ethnic group 5, which consists of people who report being multi-racial or are of any race not treated as a separate group (due to small sample size), the correlation between arm length and leg length is stronger, especially for men. This is not surprising, as greater heterogeneity can allow correlations to emerge that are indiscernible in more homogeneous data.

```
_ = sns.FacetGrid(da, col="RIDRETH1",
↪  row="RIAGENDRx").map(plt.scatter, "BMXLEG", "BMXARML",
↪  alpha=0.5).add_legend()
```



18.0.3 Categorical bivariate data

In this section we discuss some methods for working with bivariate data that are categorical. We can start with a contingency table, which counts the number of people having each combination of two factors. To illustrate, we will consider the NHANES variables for marital status and education level.

First, we create new versions of these two variables using text labels instead of numbers to represent the categories. We also create a new data set that omits people who responded "Don't know" or who refused to answer these questions.

```
#CLEAN up df
da["DMDEDUC2x"] = da.DMDEDUC2.replace({1: "<9", 2: "9-11", 3:
↪  "HS/GED", 4: "Some college/AA", 5: "College",
                                        7: "Refused", 9: "Don't
                                        ↪  know"})
da["DMDMARTLx"] = da.DMDMARTL.replace({1: "Married", 2: "Widowed", 3:
↪  "Divorced", 4: "Separated", 5: "Never married",
                                      6: "Living w/partner", 77:
                                      ↪  "Refused"})
```

```
db = da.loc[(da.DMDEDUC2x != "Don't know") & (da.DMDMARTLx !=
↪  "Refused"), :]
```

18.0.4 Create count table with pd.crosstab

Now we can create a contingency table, counting the number of people in each cell defined by a combination of education and marital status.

```
x = pd.crosstab(db.DMDEDUC2x, da.DMDMARTLx)
x
```

DMDMARTLx DMDEDUC2x	Divorced	Living w/partner	Married	Never married	Separated	Widowed
9-11	62	80	305	117	39	40
<9	52	66	341	65	43	88
College	120	85	827	253	22	59
HS/GED	127	133	550	237	40	99
Some college/AA	217	163	757	332	42	108

The results will be easier to interpret if we normalize the data. A contingency table can be normalized in three ways – we can make the rows sum to 1, the columns sum to 1, or the whole table sum to 1. Below we normalize within rows. This gives us the proportion of people in each educational attainment category who fall into each group of the marital status variable.

The modal (most common) marital status for people within each educational attainment group is "married". However quantitatively, the proportion of people who are married varies substantially, and is notably higher for college graduates (around 61%) compared to groups with lower educational attainment.

```
x.apply(lambda z: z/z.sum() * 100, axis=1)
```

DMDMARTLx DMDEDUC2x	Divorced	Living w/partner	Married	Never married	Separated	Widowed
9-11	9.642302	12.441680	47.433904	18.195956	6.065319	6.220840
<9	7.938931	10.076336	52.061069	9.923664	6.564885	13.435115

DMDMARTLx DMDEDUC2x	Divorced	Living w/partner	Married	Never married	Separated	Widowed
College	8.784773	6.222548	60.541728	18.521230	1.610542	4.319180
HS/GED	10.708263	11.214165	46.374368	19.983137	3.372681	8.347386
Some college/AA	13.403335	10.067943	46.757258	20.506485	2.594194	6.670784

We can also normalize within the columns instead of normalizing within the rows. This gives us the proportion of people with each marital status group who have each level of educational attainment.

```
x.apply(lambda z: z/z.sum() * 100, axis=0)
```

DMDMARTLx DMDEDUC2x	Divorced	Living w/partner	Married	Never married	Separated	Widowed
9-11	10.726644	15.180266	10.971223	11.653386	20.967742	10.152284
<9	8.996540	12.523719	12.266187	6.474104	23.118280	22.335025
College	20.761246	16.129032	29.748201	25.199203	11.827957	14.974619
HS/GED	21.972318	25.237192	19.784173	23.605578	21.505376	25.126904
Some college/AA	37.543253	30.929791	27.230216	33.067729	22.580645	27.411168

We see here that the plurality of divorced people have some college but have not graduated from college, while the plurality of married people are college graduates.

It is quite plausible that there are gender differences in the relationship between educational attainment and marital status. Therefore we can look at the proportion of people in each marital status category, for each combination of the gender and education variables. This analyses yields some interesting trends, notably that women are much more likely to be widowed or divorced than men (e.g. women in the HS/GED group are around 3 times more likely to be widowed than men in the HS/GED group).

```
# The following line does these steps, reading the code from left to
↪ right:
# 1 Group the data by every combination of gender, education, and
↪ marital status
# 2 Count the number of people in each cell using the 'size' method
# 3 Pivot the marital status results into the columns (using unstack)
# 4 Fill any empty cells with 0
```

```
# 5 Normalize the data by row
db.groupby(["RIAGENDRx", "DMDEDUC2x",
↪  "DMDMARTLx"]).size().unstack().fillna(0).apply(lambda x:
↪  x/x.sum() * 100, axis=1)
```

RIAGENDRx	DMDMARTLx DMDEDUC2x	Divorced	Living w/partner	Married	Never married	Separated
	9-11	11.340206	12.371134	41.237113	17.182131	7.560137
	<9	9.169054	9.169054	42.406877	10.888252	8.882521
Female	College	11.018131	5.578801	57.740586	18.270572	1.673640
	HS/GED	12.178388	10.977702	41.337907	18.867925	4.116638
	Some college/AA	14.867841	9.911894	41.850220	21.035242	3.193833
	9-11	8.238636	12.500000	52.556818	19.034091	4.829545
	<9	6.535948	11.111111	63.071895	8.823529	3.921569
Male	College	6.317411	6.933744	63.636364	18.798151	1.540832
	HS/GED	9.286899	11.442786	51.243781	21.061360	2.653400
	Some college/AA	11.533052	10.267229	53.023910	19.831224	1.828411

One factor behind the greater number of women who are divorced and widowed could be that women live longer than men. To minimize the impact of this factor, we can recalculate the above table using a few narrow bands of ages. To simplify here, we collapse the marital status data to characterize people as being either "married" or "unmarried" This allows us to focus on the marriage rate, which is a widely-studied variable in social science research.

There are a number of intriguing results here. For example, the marriage rate seems to drop as college-educated people get older (e.g. 71% of college educated women between 49 and 50 are married, but only 65% of college educated women between 50 and 59 are married, an even larger drop occurs for men). However in people with a HS/GED level of education, the marriage rate is higher for older people (although it is lower compared to the college educated sample). There are a number of possible explanations for this, for example, that remarriage after divorce is less common among college graduates.

```
#look at narrower age group
dx = db.loc[(db.RIDAGEYR >= 40) & (db.RIDAGEYR < 50)]
a = dx.groupby(["RIAGENDRx", "DMDEDUC2x",
↪  "DMDMARTLx"]).size().unstack().fillna(0).apply(lambda x:
↪  x/x.sum(), axis=1)
a
```

RIAGENDRx	DMDMARTLx DMDEDUC2x	Divorced	Living w/partner	Married	Never married	Separated	W
	9-11	0.090909	0.072727	0.581818	0.163636	0.090909	0.
	<9	0.089286	0.142857	0.464286	0.142857	0.125000	0.
Female	College	0.121019	0.019108	0.713376	0.108280	0.012739	0.
	HS/GED	0.151163	0.127907	0.476744	0.116279	0.104651	0.
	Some college/AA	0.184713	0.082803	0.509554	0.152866	0.057325	0.
	9-11	0.092593	0.129630	0.574074	0.166667	0.037037	0.
	<9	0.023810	0.142857	0.714286	0.095238	0.000000	0.
Male	College	0.051724	0.034483	0.879310	0.034483	0.000000	0.
	HS/GED	0.093023	0.081395	0.616279	0.162791	0.046512	0.
	Some college/AA	0.125000	0.125000	0.625000	0.096154	0.019231	0.

```
#look at another age group
dx = db.loc[(db.RIDAGEYR >= 50) & (db.RIDAGEYR < 60)]
b = dx.groupby(["RIAGENDRx", "DMDEDUC2x",
↪  "DMDMARTLx"]).size().unstack().fillna(0).apply(lambda x:
↪  x/x.sum(), axis=1)
```

```
#view the two dfs for the married group
print(a.loc[:, ["Married"]].unstack())
```

```
DMDMARTLx   Married
DMDEDUC2x      9-11        <9   College    HS/GED Some college/AA
RIAGENDRx
Female     0.581818  0.464286  0.713376  0.476744        0.509554
Male       0.574074  0.714286  0.879310  0.616279        0.625000
```

```
print(b.loc[:, ["Married"]].unstack())
```

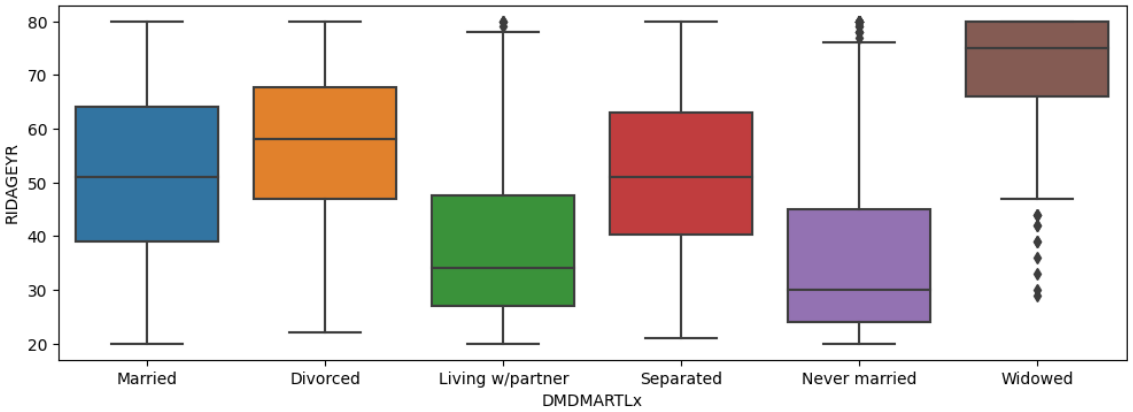
```
DMDMARTLx   Married
DMDEDUC2x      9-11        <9   College    HS/GED Some college/AA
RIAGENDRx
Female     0.490566  0.511111  0.648649  0.563107        0.496403
Male       0.666667  0.622642  0.737374  0.637255        0.555556
```

We conclude this section by noting that marital status is associated with many factors, including gender and eduational status, but also varies strongly by age and birth cohort. For example, it is unlikely for young people to be widowed, and it is less likely for older people to be "never married", since a person can transition from "never married" into one of the other categories, but can never move back. Below we will consider the role of age in more detail, and later in the course we will revisit these questions using more sophisticated analytic methods that can account for all of these factors simultaneously. However, since NHANES is a cross-sectional study, there are certain important questions that it cannot be used to answer. For example, while we know each person's current marital status, we do not know their full marital history (e.g. how many times and at what ages they were married or divorced).

18.0.5 Mixed categorical and quantitative data

Another situation that commonly arises in data analysis is when we wish to analyze bivariate data consisting of one quantitative and one categorical variable. To illustrate methods that can be used in this setting, we consider the relationship between marital status and age in the NHANES data. Specifically, we consider the distribution of ages for people who are currently in each marital status category. A natural tool in this setting is side-by-side boxplots. Here we see some unsurprising things – widowed people tend to be older, and never-married people tend to be younger.

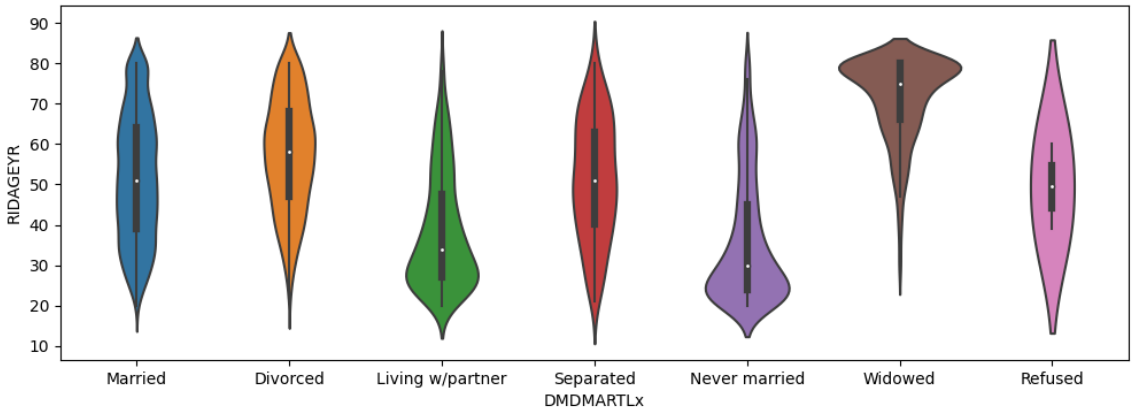
```
plt.figure(figsize=(12, 4))
a = sns.boxplot(x = db.DMDMARTLx, y = db.RIDAGEYR)
```



When we have enough data, a "violinplot" gives a bit more insight into the shapes of the

distributions compared to a traditional boxplot. The violinplot below is based on the same data as the boxplot above. We can see quite clearly that the distributions with low mean (living with partner, never married) are strongly right-skewed, while the distribution with high mean (widowed) is strongly left-skewed. The other distributions have intermediate mean values, and are approximately symmetrically distributed. Note also that the never-married distribution has a long shoulder, suggesting that this distributions includes many people who are never-married because they are young, and have not yet reached the ages when people typically marry, but also a substantial number of people will marry for the first time anywhere from their late 30's to their mid-60's.

```
plt.figure(figsize=(12, 4))
a = sns.violinplot(x = da.DMDMARTLx, y = da.RIDAGEYR)
```



19 Practice notebook for multivariate analysis using NHANES data

This notebook will give you the opportunity to perform some multivariate analyses on your own using the NHANES study data. These analyses are similar to what was done in the week 3 NHANES case study notebook.

You can enter your code into the cells that say "enter your code here", and you can type responses to the questions into the cells that say "Type Markdown and Latex".

Note that most of the code that you will need to write below is very similar to code that appears in the case study notebook. You will need to edit code from that notebook in small ways to adapt it to the prompts below.

To get started, we will use the same module imports and read the data in the same way as we did in the case study:

```
%matplotlib inline
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
import statsmodels.api as sm
import numpy as np

da = pd.read_csv("../data/nhanes_2015_2016.csv")

#have a more descriptive name for some columns
da["RIAGENDRx"] = da.RIAGENDR.replace({1: "Male", 2: "Female"})
da["DMDEDUC2x"] = da.DMDEDUC2.replace({1: "<9", 2: "9-11", 3:
↪  "HS/GED", 4: "Some college/AA", 5: "College",
                                       7: "Refused", 9: "Don't
                                       ↪  know"})
da["DMDMARTLx"] = da.DMDMARTL.replace({1: "Married", 2: "Widowed", 3:
↪  "Divorced", 4: "Separated", 5: "Never married",
```

```
                                        6: "Living w/partner", 77:
                                        ↪  "Refused"})

da.columns
```

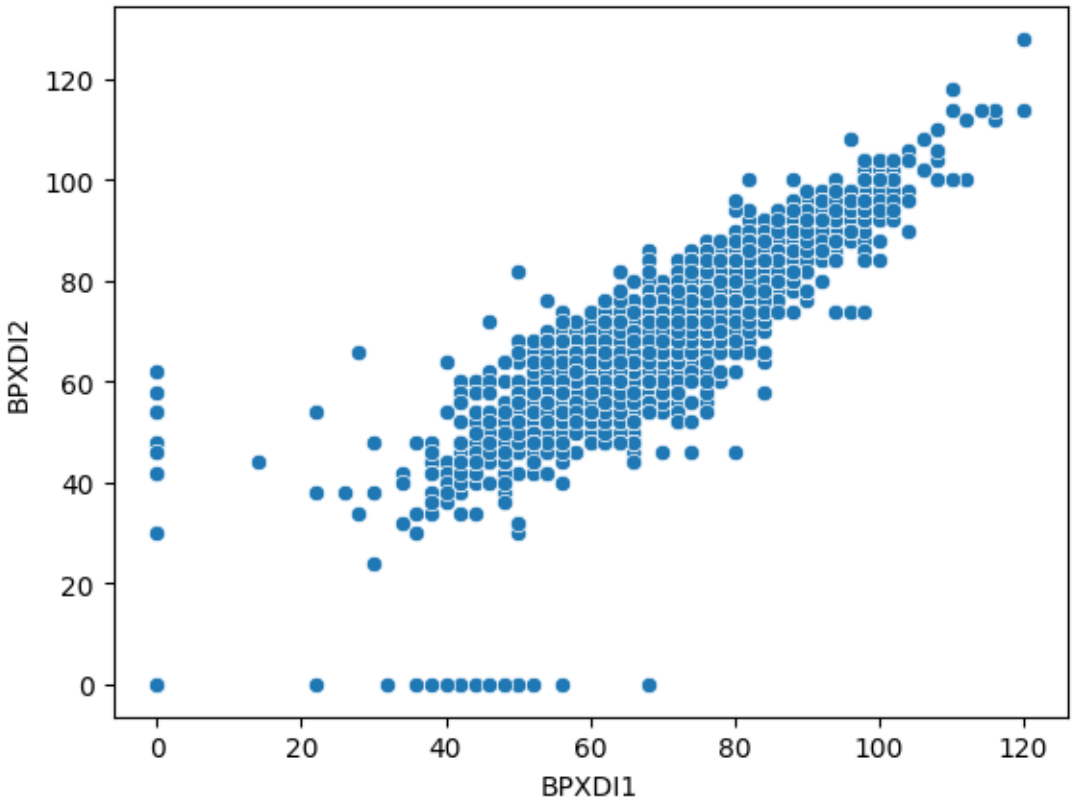
```
Index(['SEQN', 'ALQ101', 'ALQ110', 'ALQ130', 'SMQ020', 'RIAGENDR', 'RIDAGEYR',
       'RIDRETH1', 'DMDCITZN', 'DMDEDUC2', 'DMDMARTL', 'DMDHHSIZ', 'WTINT2YR',
       'SDMVPSU', 'SDMVSTRA', 'INDFMPIR', 'BPXSY1', 'BPXDI1', 'BPXSY2',
       'BPXDI2', 'BMXWT', 'BMXHT', 'BMXBMI', 'BMXLEG', 'BMXARML', 'BMXARMC',
       'BMXWAIST', 'HIQ210', 'RIAGENDRx', 'DMDEDUC2x', 'DMDMARTLx'],
      dtype='object')
```

19.1 Question 1

Make a scatterplot showing the relationship between the first and second measurements of diastolic blood pressure (BPXDI1 and BPXDI2). Also obtain the 4x4 matrix of correlation coefficients among the first two systolic and the first two diastolic blood pressure measures.

```
# show scatterplot
sns.scatterplot(x='BPXDI1', y='BPXDI2', data = da)
```

```
<AxesSubplot:xlabel='BPXDI1', ylabel='BPXDI2'>
```




```
#generate correlation matrix
print(da.loc[:,["BPXDI1", "BPXDI2","BPXSY1",
↪  "BPXSY2"]].dropna().corr())
```

```
          BPXDI1    BPXDI2    BPXSY1    BPXSY2
BPXDI1  1.000000  0.884722  0.317497  0.329843
BPXDI2  0.884722  1.000000  0.277681  0.298392
BPXSY1  0.317497  0.277681  1.000000  0.962287
BPXSY2  0.329843  0.298392  0.962287  1.000000
```

Q1a. How does the correlation between repeated measurements of diastolic blood pressure relate to the correlation between repeated measurements of systolic blood pressure?

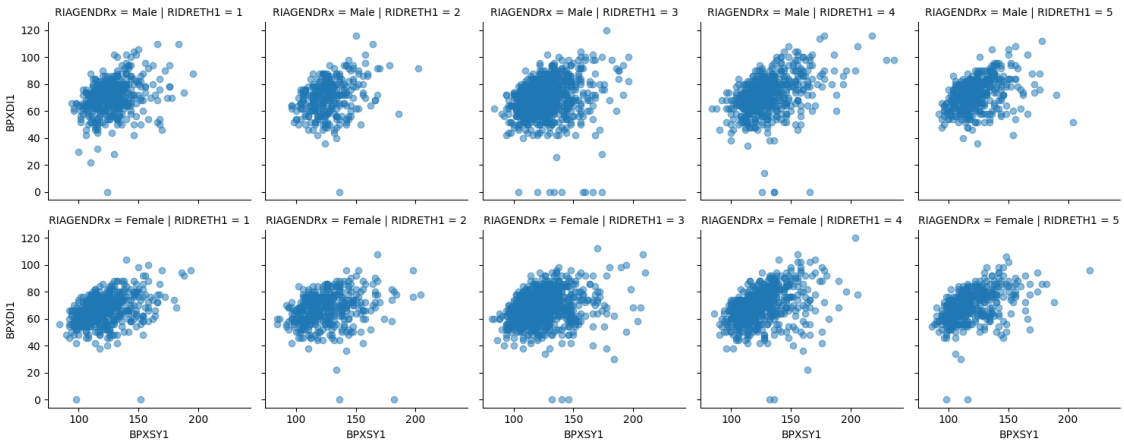
There is a better correlation between repeated systolic compared to diastolic measurements.

Q2a. Are the second systolic and second diastolic blood pressure measure more correlated or less correlated than the first systolic and first diastolic blood pressure measure?

19.2 Question 2

Construct a grid of scatterplots between the first systolic and the first diastolic blood pressure measurement. Stratify the plots by gender (rows) and by race/ethnicity groups (columns).

```
_ = sns.FacetGrid(da, col="RIDRETH1",
↪  row="RIAGENDRx").map(plt.scatter, "BPXSY1", "BPXDI1",
↪  alpha=0.5).add_legend()
```



Q3a. Comment on the extent to which these two blood pressure variables are correlated to different degrees in different demographic subgroups.

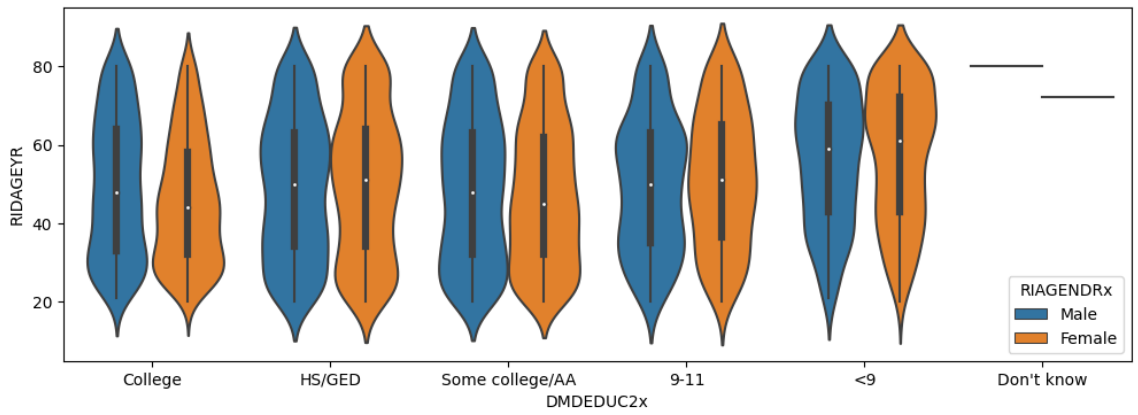
For all groups we see a positive correlation, but the slop esp. in ETH group 1 and 2 seems steeper for males compared to females.

19.3 Question 3

Use "violin plots" to compare the distributions of ages within groups defined by gender and educational attainment.

```
plt.figure(figsize = (12,4))
sns.violinplot(data=da, x="DMDEDUC2x", y="RIDAGEYR", hue="RIAGENDRx")
```

```
<AxesSubplot:xlabel='DMDEDUC2x', ylabel='RIDAGEYR'>
```



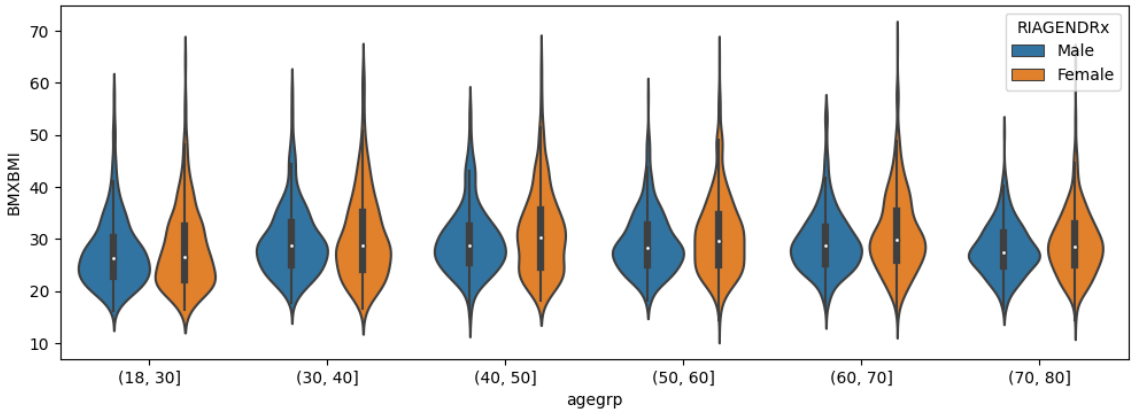
Q4a. Comment on any evident differences among the age distributions in the different demographic groups.

19.4 Question 4

Use violin plots to compare the distributions of BMI within a series of 10-year age bands. Also stratify these plots by gender.

```
#create age bands
da["agegrp"] = pd.cut(da.RIDAGEYR, [18, 30, 40, 50, 60, 70, 80])

#plot
plt.figure(figsize = (12,4))
sns.violinplot(data=da, y="BMXBMI", x="agegrp", hue="RIAGENDRx")
```

```
<AxesSubplot:xlabel='agegrp', ylabel='BMXBMI'>
```



Q5a. Comment on the trends in BMI across the demographic groups.

19.5 Question 5

Construct a frequency table for the joint distribution of ethnicity groups (RIDRETH1) and health-insurance status (HIQ210). Normalize the results so that the values within each ethnic group are proportions that sum to 1.

```
da.groupby(["RIDRETH1",
↪  "HIQ210"]).size().unstack().fillna(0).apply(lambda x: x/x.sum() *
↪  100, axis=1)
```

HIQ210 RIDRETH1	1.0	2.0	9.0
1	13.798220	85.756677	0.445104
2	12.869565	87.130435	0.000000
3	6.735437	93.143204	0.121359
4	10.865385	89.038462	0.096154
5	8.176101	91.572327	0.251572

Q6a. Which ethnic group has the highest rate of being uninsured in the past year?

Group 1 has the highest rate of not being ensured (category 1)

20 Sampling from a Biased Population

In this tutorial we will go over some code that recreates the visualizations in the Interactive Sampling Distribution Demo. This demo looks at a hypothetical problem that illustrates what happens when we sample from a biased population and not the entire population we are interested in. This tutorial assumes that you have seen that demo, for context, and understand the statistics behind the graphs.

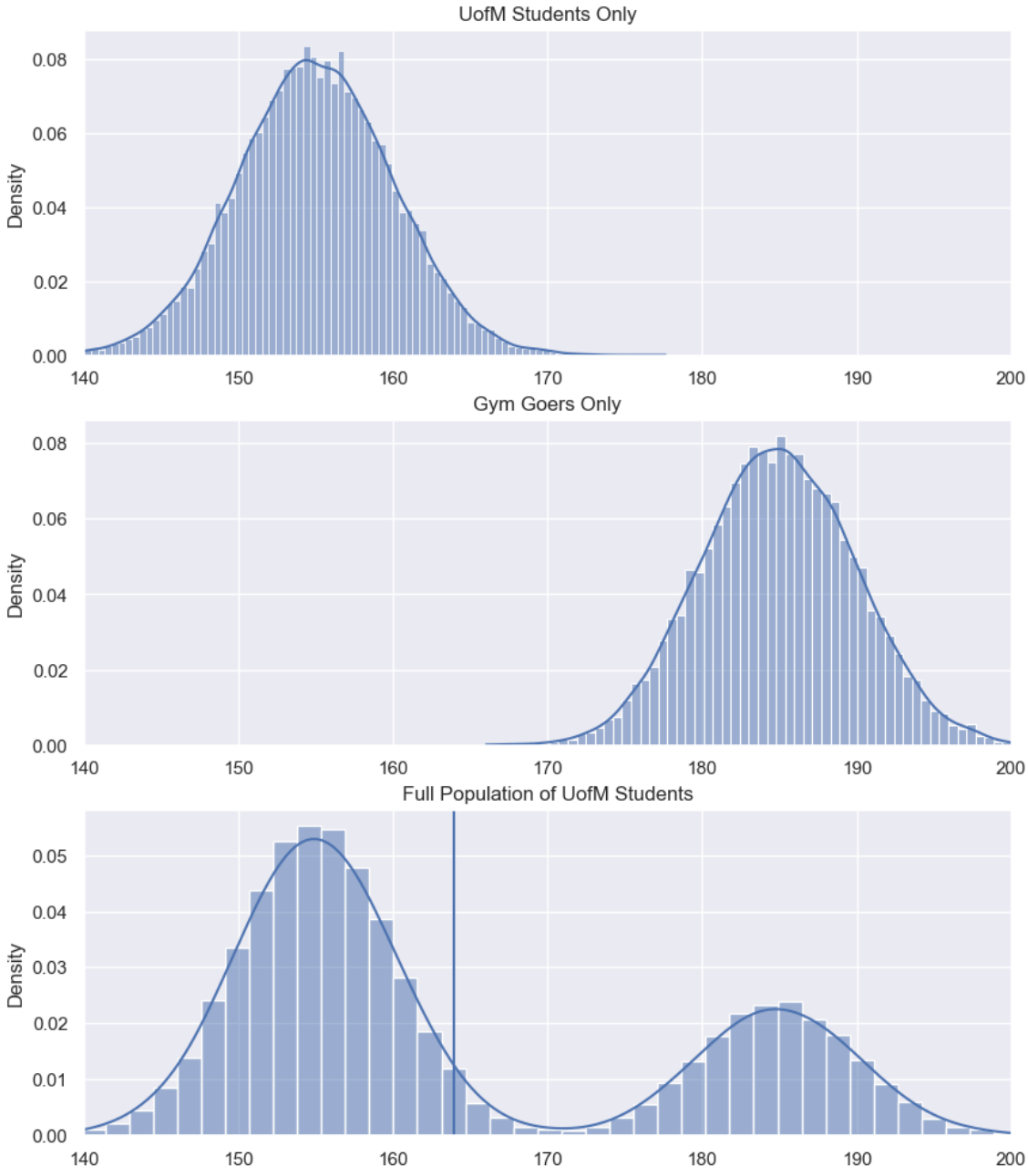
```
# Import the packages that we will be using for the tutorial
import numpy as np # for sampling for the distributions
import matplotlib.pyplot as plt # for basic plotting
import seaborn as sns; sns.set() # for plotting of the histograms

# Recreate the simulations from the video
mean_uofm = 155
sd_uofm = 5
mean_gym = 185
sd_gym = 5
gymperc = .3
totalPopSize = 40000

# Create the two subgroups
uofm_students = np.random.normal(mean_uofm, sd_uofm, int(totalPopSize
↪  * (1 - gymperc)))
students_at_gym = np.random.normal(mean_gym, sd_gym, int(totalPopSize
↪  * (gymperc)))
print(len(uofm_students))
print(len(students_at_gym))
```

```
28000
12000
```

```
# Create the population from the subgroups
population = np.append(uofm_students, students_at_gym)
population.shape
```

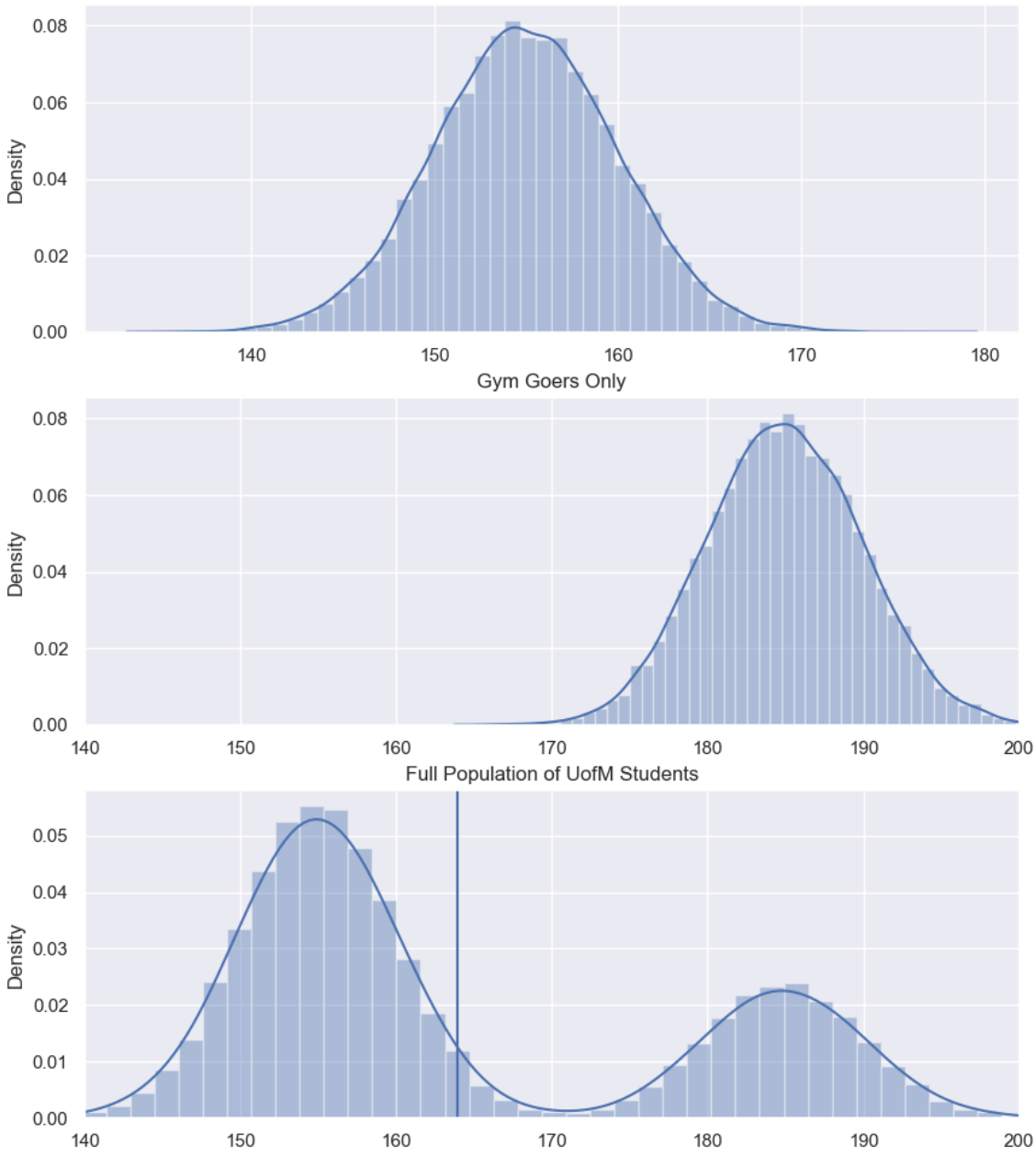
```
(40000,)
```

```
# Plot the UofM students only (edited)
fig, axes = plt.subplots(3, 1, figsize=(10, 12))
sns.histplot(ax=axes[0], data = uofm_students, stat="density",
↪  kde=True)
axes[0].set_title("UofM Students Only")
axes[0].set_xlim([140,200])

sns.histplot(ax=axes[1], data = students_at_gym, stat="density",
↪  kde=True)
axes[1].set_title("Gym Goers Only")
axes[1].set_xlim([140,200])

sns.histplot(ax=axes[2], data = population, stat="density", kde=True)
axes[2].set_title("Full Population of UofM Students")
axes[2].axvline(x = np.mean(population))
axes[2].set_xlim([140,200])

plt.show()
plt.close()
```




```
# Set up the figure for plotting (original)
plt.figure(figsize=(10,12))
```

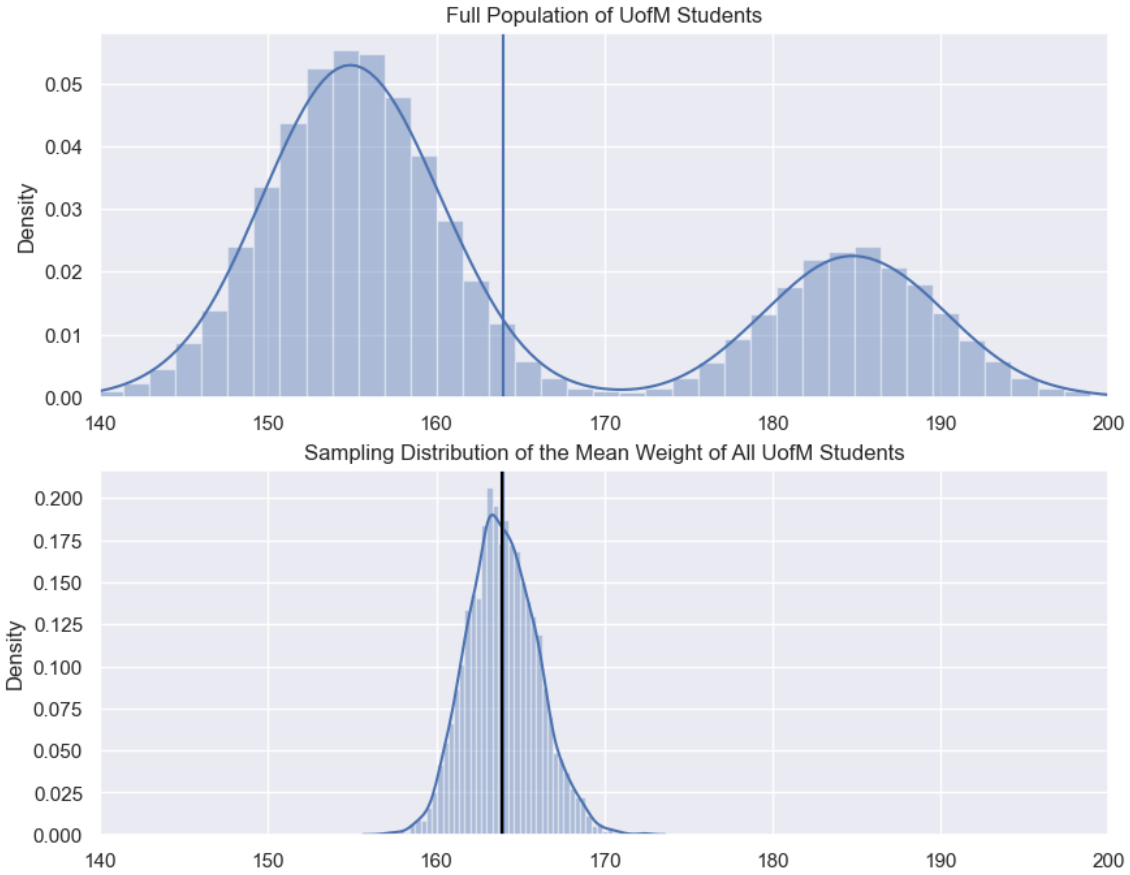
```
# Plot the UofM students only
plt.subplot(3,1,1)
sns.distplot( uofm_students)
axes[0].set_title("UofM Students Only")
axes[0].set_xlim([140,200])

# Plot the Gym Goers only
plt.subplot(3,1,2)
sns.distplot(students_at_gym)
plt.title("Gym Goers Only")
plt.xlim([140,200])

# Plot both groups together
plt.subplot(3,1,3)
sns.distplot(population)
plt.title("Full Population of UofM Students")
plt.axvline(x = np.mean(population))
plt.xlim([140,200])

plt.show()
plt.close()
```



20.1 What Happens if We Sample from the Entire Population?

We will sample randomly from all students at the University of Michigan.

```
# Simulation parameters
numberSamps = 5000
sampSize = 50

# Get the sampling distribution of the mean from only the gym
mean_distribution = np.empty(numberSamps)
for i in range(numberSamps):
    random_students = np.random.choice(population, sampSize)
    mean_distribution[i] = np.mean(random_students)

# Plot the population and the biased sampling distribution
plt.figure(figsize = (10,8))

# Plotting the population again
plt.subplot(2,1,1)
sns.distplot(population)
plt.title("Full Population of UofM Students")
plt.axvline(x = np.mean(population))
plt.xlim([140,200])

# Plotting the sampling distribution
plt.subplot(2,1,2)
sns.distplot(mean_distribution)
plt.title("Sampling Distribution of the Mean Weight of All UofM
↪  Students")
plt.axvline(x = np.mean(population))
plt.axvline(x = np.mean(mean_distribution), color = "black")
plt.xlim([140,200])

plt.show()
```

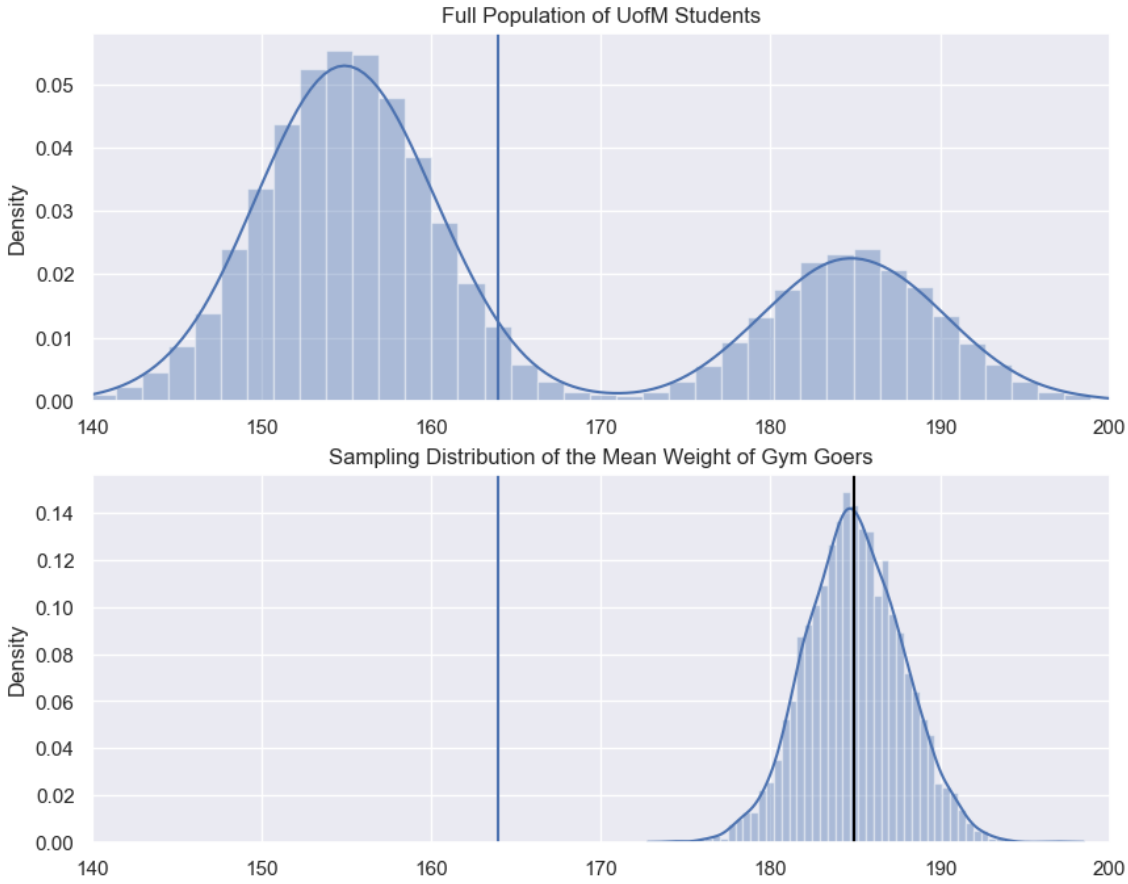


20.2 What Happens if We take a Non-Representative Sample?

What happens if I only go to the gym to get the weight of individuals, and I don't sample randomly from all students at the University of Michigan?

```
# Simulation parameters
numberSamps = 5000
sampSize = 3

# Get the sampling distribution of the mean from only the gym
mean_distribution = np.empty(numberSamps)
for i in range(numberSamps):
```

```
    random_students = np.random.choice(students_at_gym, sampSize)
    mean_distribution[i] = np.mean(random_students)


# Plot the population and the biased sampling distribution
plt.figure(figsize = (10,8))

# Plotting the population again
plt.subplot(2,1,1)
sns.distplot(population)
plt.title("Full Population of UofM Students")
plt.axvline(x = np.mean(population))
plt.xlim([140,200])

# Plotting the sampling distribution
plt.subplot(2,1,2)
sns.distplot(mean_distribution)
plt.title("Sampling Distribution of the Mean Weight of Gym Goers")
plt.axvline(x = np.mean(population))
plt.axvline(x = np.mean(students_at_gym), color = "black")
plt.xlim([140,200])

plt.show()
```


Full Population of UofM Students
Density
0.05
0.04
0.03
0.02
0.01
0.00
140
150
160
170
180
190
200
Sampling Distribution of the Mean Weight of Gym Goers
Density
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
140
150
160
170
180
190
200