

Hands-On

Data Analysis

with Pandas

Second Edition

A Python data science handbook for data collection,
wrangling, analysis, and visualization

Stefanie Molin
Foreword by Ken Jee



Hands-On Data Analysis with Pandas – Second Edition

A Python data science handbook for data collection,
wrangling, analysis, and visualization

Stefanie Molin



BIRMINGHAM—MUMBAI

Hands-On Data Analysis with Pandas

Second Edition

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To everyone that made the first edition such a success.

Foreword to the Second Edition

As educators, we are inclined to teach across the medium that we best learn from. I personally gravitated towards video content early in my career. As I produce more online content, surprisingly, one of the most frequently asked questions I get is: *What book would you recommend for someone getting started in data science?*

Initially, I was baffled at why people would turn to books when there are so many great online resources out there. However, after reading *Hands-On Data Analysis with Pandas*, my perception of books for learning data science began to change.

The first thing I loved about *Hands-On Data Analysis with Pandas* was the structure. The book gives you just the right amount of information at the right time to keep you progressing at a natural pace. Starting with light foundations in statistics and concepts gives the perfect amount of cognitive glue to keep theory and practice comfortably bound together.

After the foundations, you are introduced to the star of the show: pandas. Stefanie uses practical examples (not the same old datasets you have used before) to bring the module to life. I use pandas almost every day, and I still learned quite a few tricks across these sections.

As a software engineer, Stefanie knows the importance of quality documentation. She has all of the data, examples, and more in a tidy GitHub repo. Through these examples, the book truly earns the "Hands-On" moniker in its title.

The latter portion of the book gives the reader a taste of what is possible with a strong foundation in pandas. Stefanie leads you just a little bit deeper into the more advanced machine learning concepts. Once again, she provides just enough information to get you excited about taking the next step in your learning journey without inundating you with overly technical jargon.

I could sense the pride Stefanie took in this work through our conversations. While the book is a great resource for people looking to learn data science tools, it was also a way for her to solidify her own knowledge and push her boundaries. In my opinion, you want to learn from people that are creating not only for the community but also for their own learning. People with intrinsic motivation like this are willing to go the extra mile to make that extra revision or get the wording perfect.

I hope you enjoy learning from this book as much as I did. To those who asked me the question above, I have a simple answer: This one.

*Ken Jee
YouTuber & Head of Data Science @ Scouts Consulting Group
Honolulu, HI (03/09/2021)*

Foreword to the First Edition

Recent advancements in computing and artificial intelligence have completely changed the way we understand the world. Our current ability to record and analyze data has already transformed industries and inspired big changes in society.

Stefanie Molin's *Hands-On Data Analysis with Pandas* is much more than an introduction to the subject of data analysis or the pandas Python library; it's a guide to help you become part of this transformation.

Not only will this book teach you the fundamentals of using Python to collect, analyze, and understand data, but it will also expose you to important software engineering, statistical, and machine learning concepts that you will need to be successful.

Using examples based on real data, you will be able to see firsthand how to apply these techniques to extract value from data. In the process, you will learn important software development skills, including writing simulations, creating your own Python packages, and collecting data from APIs.

Stefanie possesses a rare combination of skills that makes her uniquely qualified to guide you through this process. Being both an expert data scientist and a strong software engineer, she can not only talk authoritatively about the intricacies of the data analysis workflow but also about how to implement it correctly and efficiently in Python.

Whether you are a Python programmer interested in learning more about data analysis, or a data scientist learning how to work in Python, this book will get you up to speed fast, so you can begin to tackle your own data analysis projects right away.

Felipe Moreno

New York, June 10, 2019.

Felipe Moreno has been working in information security for the last two decades. He currently works for Bloomberg LP, where he leads the Security Data Science team within the Chief Information Security Office and focuses on applying statistics and machine learning to security problems.

Contributors

About the author

Stefanie Molin is a data scientist and software engineer at Bloomberg LP in NYC, tackling tough problems in information security, particularly revolving around anomaly detection, building tools for gathering data, and knowledge sharing. She has extensive experience in data science, designing anomaly detection solutions, and utilizing machine learning in both R and Python in the AdTech and FinTech industries. She holds a B.S. in operations research from Columbia University's Fu Foundation School of Engineering and Applied Science, with minors in economics, and entrepreneurship and innovation. In her free time, she enjoys traveling the world, inventing new recipes, and learning new languages spoken among both people and computers.

Writing this book was a tremendous amount of work, but I have grown a lot through the experience: as a writer, as a technologist, and as a person. This wouldn't have been possible without the help of my friends, family, and colleagues. I'm very grateful to you all. In particular, I want to thank Aliki Mavromoustaki, Felipe Moreno, Suphannee Sivakorn, Lucy Hao, Javon Thompson, and Ken Jee. (The full version of my acknowledgments can be found in the code repository; see the preface for the link.)

About the reviewer

Aliki Mavromoustaki is the lead data scientist at Tasman Analytics. She works with direct-to-consumer companies to deliver scalable infrastructure and implement event-driven analytics. Previously, she worked at Criteo, an AdTech company that employs machine learning to help digital commerce companies target valuable customers. Aliki has worked on optimizing marketing campaigns and designed statistical experiments comparing Criteo products. Aliki holds a PhD in fluid dynamics from Imperial College London and was an assistant adjunct professor in applied mathematics at UCLA.

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Preface

Data science is often described as an interdisciplinary field where programming skills, statistical know-how, and domain knowledge intersect. It has quickly become one of the hottest fields of our society, and knowing how to work with data has become essential in today's careers. Regardless of the industry, role, or project, data skills are in high demand, and learning data analysis is key to making an impact.

Fields in data science cover many different aspects of the spectrum: data analysts focus more on extracting business insights, while data scientists focus more on applying machine learning techniques to the business's problems. Data engineers focus on designing, building, and maintaining data pipelines used by data analysts and scientists. Machine learning engineers share much of the skill set of data scientists and, like data engineers, are adept software engineers. The data science landscape encompasses many fields, but for all of them, data analysis is a fundamental building block. This book will give you the skills to get started, wherever your journey may take you.

The traditional skill set in data science involves knowing how to collect data from various sources, such as databases and APIs, and process it. Python is a popular language for data science that provides the means to collect and process data, as well as to build production-quality data products. Since it is open source, it is easy to get started with data science by taking advantage of the libraries written by others to solve common data tasks and issues.

Pandas is the powerful and popular library synonymous with data science in Python. This book will give you a hands-on introduction to data analysis using pandas on real-world datasets, such as those dealing with the stock market, simulated hacking attempts, weather trends, earthquakes, wine, and astronomical data. Pandas makes data wrangling and visualization easy by giving us the ability to work efficiently with tabular data.

Once we have learned how to conduct data analysis, we will explore a number of applications. We will build Python packages and try our hand at stock analysis, anomaly detection, regression, clustering, and classification with the help of additional libraries commonly used for data visualization, data wrangling, and machine learning, such as Matplotlib, Seaborn, NumPy, and Scikit-learn. By the time you finish this book, you will be well equipped to take on your own data science projects in Python.

Who this book is for

This book is written for people with varying levels of experience who want to learn about data science in Python, perhaps to apply it to a project, collaborate with data scientists, and/or progress to working on machine learning production code with software engineers. You will get the most out of this book if your background is similar to one (or both) of the following:

- You have prior data science experience in another language, such as R, SAS, or MATLAB, and want to learn pandas in order to move your workflow to Python.
- You have some Python experience and are looking to learn about data science using Python.

What this book covers

Chapter 1, Introduction to Data Analysis, teaches you the fundamentals of data analysis, gives you a foundation in statistics, and guides you through getting your environment set up for working with data in Python and using Jupyter Notebooks.

Chapter 2, Working with Pandas DataFrames, introduces you to the pandas library and shows you the basics of working with DataFrames.

Chapter 3, Data Wrangling with Pandas, discusses the process of data manipulation, shows you how to explore an API to gather data, and guides you through data cleaning and reshaping with pandas.

Chapter 4, Aggregating Pandas DataFrames, teaches you how to query and merge DataFrames, how to perform complex operations on them, including rolling calculations and aggregations, and how to work effectively with time series data.

Chapter 5, Visualizing Data with Pandas and Matplotlib, shows you how to create your own data visualizations in Python, first using the matplotlib library, and then from pandas objects directly.

Chapter 6, Plotting with Seaborn and Customization Techniques, continues the discussion on data visualization by teaching you how to use the `seaborn` library to visualize your long-form data and giving you the tools you need to customize your visualizations, making them presentation-ready.

Chapter 7, Financial Analysis – Bitcoin and the Stock Market, walks you through the creation of a Python package for analyzing stocks, building upon everything learned from *Chapter 1, Introduction to Data Analysis*, through *Chapter 6, Plotting with Seaborn and Customization Techniques*, and applying it to a financial application.

Chapter 8, Rule-Based Anomaly Detection, covers simulating data and applying everything learned from *Chapter 1, Introduction to Data Analysis*, through *Chapter 6, Plotting with Seaborn and Customization Techniques*, to catch hackers attempting to authenticate to a website, using rule-based strategies for anomaly detection.

Chapter 9, Getting Started with Machine Learning in Python, introduces you to machine learning and building models using the `scikit-learn` library.

Chapter 10, Making Better Predictions – Optimizing Models, shows you strategies for tuning and improving the performance of your machine learning models.

Chapter 11, Machine Learning Anomaly Detection, revisits anomaly detection on login attempt data, using machine learning techniques, all while giving you a taste of how the workflow looks in practice.

Chapter 12, The Road Ahead, covers resources for taking your skills to the next level and further avenues for exploration.

To get the most out of this book

You should be familiar with Python, particularly Python 3 and up. You should also know how to write functions and basic scripts in Python, understand standard programming concepts such as variables, data types, and control flow (`if/else`, `for/while` loops), and be able to use Python as a functional programming language. Some basic knowledge of object-oriented programming may be helpful but is not necessary. If your Python prowess isn't yet at this level, the Python documentation includes a helpful tutorial for quickly getting up to speed: <https://docs.python.org/3/tutorial/index.html>.

The accompanying code for this book can be found on GitHub at <https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition>. To get the most out of this book, you should follow along in the Jupyter Notebooks as you read through each chapter. We will cover setting up your environment and obtaining these files in *Chapter 1, Introduction to Data Analysis*. Note that there is also a Python 101 notebook that provides a crash course/refresher, if needed: https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/blob/master/ch_01/python_101.ipynb.

Lastly, be sure to do the exercises at the end of each chapter. Some of them may be quite challenging, but they will make you much stronger with the material. Solutions for each chapter's exercises can be found at <https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/solutions> in their respective folders.

Download the color images

We also provide a PDF file that has color images of the screenshots/diagrams used in this book. You can download it here: https://static.packt-cdn.com/downloads/9781800563452_ColorImages.pdf.

Conventions used

There are a number of text conventions used throughout this book.

Code in text: Indicates code words in text, database table names, folder names, filenames, file extensions, pathnames, dummy URLs, and user input. Here is an example: "Use pip to install the packages in the `requirements.txt` file."

A block of code is set as follows. The start of the line will be preceded by `>>>` and continuations of that line will be preceded by `...`:

```
>>> df = pd.read_csv(  
...     'data/fb_2018.csv', index_col='date', parse_dates=True  
... )  
>>> df.head()
```

Any code without the preceding `>>>` or `...` is not something we will run—it is for reference:

```
try:  
    del df['ones']  
except KeyError:  
    pass # handle the error here
```

When we wish to draw your attention to a particular part of a code block, the relevant lines or items are set in bold:

```
>>> df.price.plot(  
...     title='Price over Time', ylim=(0, None)  
... )
```

Results will be shown without anything preceding the lines:

```
>>> pd.Series(np.random.rand(2), name='random')  
0 0.235793  
1 0.257935  
Name: random, dtype: float64
```

Any command-line input or output is written as follows:

```
# Windows:  
C:\path\of\your\choosing> mkdir pandas_exercises  
  
# Linux, Mac, and shorthand:  
$ mkdir pandas_exercises
```

Bold: Indicates a new term, an important word, or words that you see onscreen. For example, words in menus or dialog boxes appear in the text like this. Here is an example: "Using the **File Browser** pane, double-click on the **ch_01** folder, which contains the Jupyter Notebook that we will use to validate our setup."

Tips or important notes

Appear like this.

Get in touch

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Section 1: Getting Started with Pandas

Our journey begins with an introduction to data analysis and statistics, which will lay a strong foundation for the concepts we will cover throughout the book. Then, we will set up our Python data science environment, which contains everything we will need to work through the examples, and get started with learning the basics of pandas.

This section comprises the following chapters:

- *Chapter 1, Introduction to Data Analysis*
- *Chapter 2, Working with Pandas DataFrames*

1

Introduction to Data Analysis

Before we can begin our hands-on introduction to data analysis with pandas, we need to learn about the fundamentals of data analysis. Those who have ever looked at the documentation for a software library know how overwhelming it can be if you have no clue what you are looking for. Therefore, it is essential that we master not only the coding aspect but also the thought process and workflow required to analyze data, which will prove the most useful in augmenting our skill set in the future.

Much like the scientific method, data science has some common workflows that we can follow when we want to conduct an analysis and present the results. The backbone of this process is **statistics**, which gives us ways to describe our data, make predictions, and also draw conclusions about it. Since prior knowledge of statistics is not a prerequisite, this chapter will give us exposure to the statistical concepts we will use throughout this book, as well as areas for further exploration.

After covering the fundamentals, we will get our Python environment set up for the remainder of this book. Python is a powerful language, and its uses go way beyond data science: building web applications, software, and web scraping, to name a few. In order to work effectively across projects, we need to learn how to make **virtual environments**, which will isolate each project's dependencies. Finally, we will learn how to work with Jupyter Notebooks in order to follow along with the text.

The following topics will be covered in this chapter:

- The fundamentals of data analysis
- Statistical foundations
- Setting up a virtual environment

Chapter materials

All the files for this book are on GitHub at <https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition>. While having a GitHub account isn't necessary to work through this book, it is a good idea to create one, as it will serve as a portfolio for any data/coding projects. In addition, working with Git will provide a version control system and make collaboration easy.

Tip

Check out this article to learn some Git basics: <https://www.freecodecamp.org/news/learn-the-basics-of-git-in-under-10-minutes-da548267cc91/>.

In order to get a local copy of the files, we have a few options (ordered from least useful to most useful):

- Download the ZIP file and extract the files locally.
- Clone the repository without forking it.
- Fork the repository and then clone it.

This book includes exercises for every chapter; therefore, for those who want to keep a copy of their solutions along with the original content on GitHub, it is highly recommended to **fork** the repository and **clone** the forked version. When we fork a repository, GitHub will make a repository under our own profile with the latest version of the original. Then, whenever we make changes to our version, we can push the changes back up. Note that if we simply clone, we don't get this benefit.

The relevant buttons for initiating this process are circled in the following screenshot:

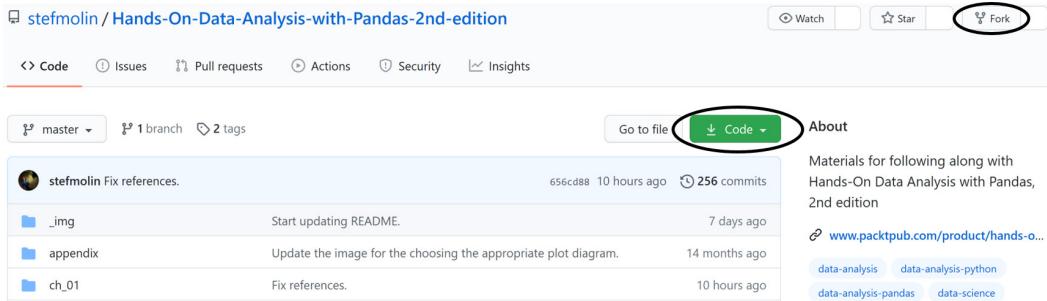


Figure 1.1 – Getting a local copy of the code for following along

Important note

The cloning process will copy the files to the current working directory in a folder called `Hands-On-Data-Analysis-with-Pandas-2nd-edition`. To make a folder to put this repository in, we can use `mkdir my_folder && cd my_folder`. This will create a new folder (directory) called `my_folder` and then change the current directory to that folder, after which we can clone the repository. We can chain these two commands (and any number of commands) together by adding `&&` in between them. This can be thought of as *and then* (provided the first command succeeds).

This repository has folders for each chapter. This chapter's materials can be found at https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_01. While the bulk of this chapter doesn't involve any coding, feel free to follow along in the `introduction_to_data_analysis.ipynb` notebook on the GitHub website until we set up our environment toward the end of the chapter. After we do so, we will use the `check_your_environment.ipynb` notebook to get familiar with Jupyter Notebooks and to run some checks to make sure that everything is set up properly for the rest of this book.

Since the code that's used to generate the content in these notebooks is not the main focus of this chapter, the majority of it has been separated into the `visual_aids` package, which is used to create visuals for explaining concepts throughout the book, and the `check_environment.py` file. If you choose to inspect these files, don't be overwhelmed; everything that's relevant to data science will be covered in this book.

Every chapter includes exercises; however, for this chapter only, there is an `exercises.ipynb` notebook, with code to generate some initial data. Knowledge of basic Python will be necessary to complete these exercises. For those who would like to review the basics, make sure to run through the `python_101.ipynb` notebook, included in the materials for this chapter, for a crash course. The official Python tutorial is a good place to start for a more formal introduction: <https://docs.python.org/3/tutorial/index.html>.

The fundamentals of data analysis

Data analysis is a highly iterative process involving collection, preparation (wrangling), **exploratory data analysis (EDA)**, and drawing conclusions. During an analysis, we will frequently revisit each of these steps. The following diagram depicts a generalized workflow:

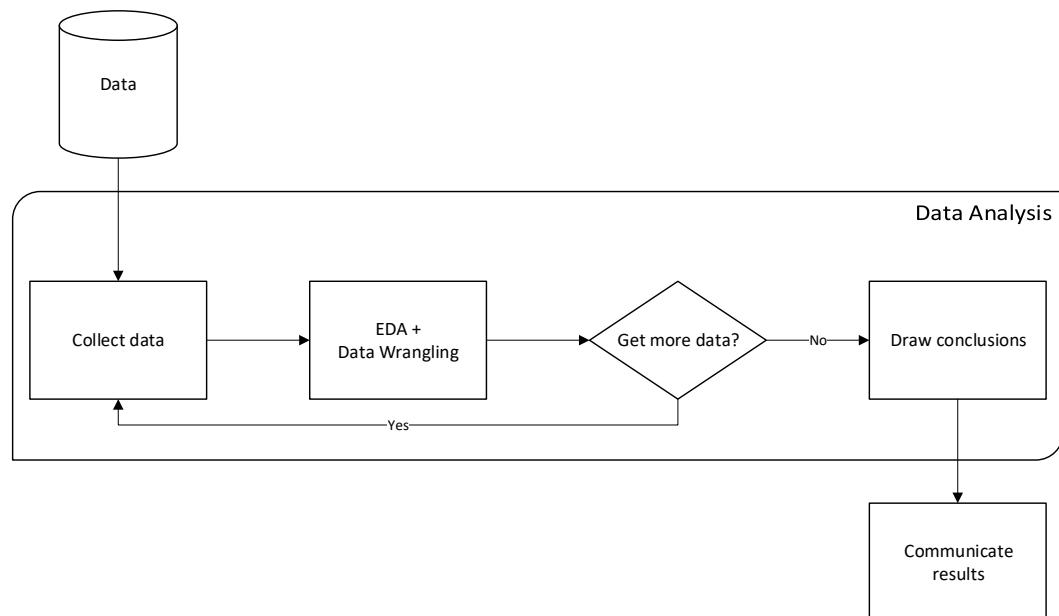


Figure 1.2 – The data analysis workflow

Over the next few sections, we will get an overview of each of these steps, starting with data collection. In practice, this process is heavily skewed toward the data preparation side. Surveys have found that although data scientists enjoy the data preparation side of their job the least, it makes up 80% of their work (<https://www.forbes.com/sites/gilpress/2016/03/23/data-preparation-most-time-consuming-least-enjoyable-data-science-task-survey-says/>). This data preparation step is where pandas really shines.

Data collection

Data collection is the natural first step for any data analysis—we can't analyze data we don't have. In reality, our analysis can begin even before we have the data. When we decide what we want to investigate or analyze, we have to think about what kind of data we can collect that will be useful for our analysis. While data can come from anywhere, we will explore the following sources throughout this book:

- Web scraping to extract data from a website's HTML (often with Python packages such as `selenium`, `requests`, `scrapy`, and `beautifulsoup`)
- **Application programming interfaces (APIs)** for web services from which we can collect data with HTTP requests (perhaps using `cURL` or the `requests` Python package)
- Databases (data can be extracted with SQL or another database-querying language)
- Internet resources that provide data for download, such as government websites or Yahoo! Finance
- Log files

Important note

Chapter 2, Working with Pandas DataFrames, will give us the skills we need to work with the aforementioned data sources. *Chapter 12, The Road Ahead*, provides numerous resources for finding data sources.

We are surrounded by data, so the possibilities are limitless. It is important, however, to make sure that we are collecting data that will help us draw conclusions. For example, if we are trying to determine whether hot chocolate sales are higher when the temperature is lower, we should collect data on the amount of hot chocolate sold and the temperatures each day. While it might be interesting to see how far people traveled to get the hot chocolate, it's not relevant to our analysis.

Don't worry too much about finding the perfect data before beginning an analysis. Odds are, there will always be something we want to add/remove from the initial dataset, reformat, merge with other data, or change in some way. This is where data wrangling comes into play.

Data wrangling

Data wrangling is the process of preparing the data and getting it into a format that can be used for analysis. The unfortunate reality of data is that it is often dirty, meaning that it requires cleaning (preparation) before it can be used. The following are some issues we may encounter with our data:

- **Human errors:** Data is recorded (or even collected) incorrectly, such as putting 100 instead of 1000, or typos. In addition, there may be multiple versions of the same entry recorded, such as New York City, NYC, and nyc.
- **Computer error:** Perhaps we weren't recording entries for a while (missing data).
- **Unexpected values:** Maybe whoever was recording the data decided to use a question mark for a missing value in a numeric column, so now all the entries in the column will be treated as text instead of numeric values.
- **Incomplete information:** Think of a survey with optional questions; not everyone will answer them, so we will have missing data, but not due to computer or human error.
- **Resolution:** The data may have been collected per second, while we need hourly data for our analysis.
- **Relevance of the fields:** Often, data is collected or generated as a product of some process rather than explicitly for our analysis. In order to get it to a usable state, we will have to clean it up.
- **Format of the data:** Data may be recorded in a format that isn't conducive to analysis, which will require us to reshape it.
- **Misconfigurations in the data-recording process:** Data coming from sources such as misconfigured trackers and/or webhooks may be missing fields or passed in the wrong order.

Most of these data quality issues can be remedied, but some cannot, such as when the data is collected daily and we need it on an hourly resolution. It is our responsibility to carefully examine our data and handle any issues so that our analysis doesn't get distorted. We will cover this process in depth in *Chapter 3, Data Wrangling with Pandas*, and *Chapter 4, Aggregating Pandas DataFrames*.

Once we have performed an initial cleaning of the data, we are ready for EDA. Note that during EDA, we may need some additional data wrangling; these two steps are highly intertwined.

Exploratory data analysis

During EDA, we use visualizations and summary statistics to get a better understanding of the data. Since the human brain excels at picking out visual patterns, data visualization is essential to any analysis. In fact, some characteristics of the data can only be observed in a plot. Depending on our data, we may create plots to see how a variable of interest has evolved over time, compare how many observations belong to each category, find outliers, look at distributions of continuous and discrete variables, and much more. In *Chapter 5, Visualizing Data with Pandas and Matplotlib*, and *Chapter 6, Plotting with Seaborn and Customization Techniques*, we will learn how to create these plots for both EDA and presentation.

Important note

Data visualizations are very powerful; unfortunately, they can often be misleading. One common issue stems from the scale of the *y*-axis because most plotting tools will zoom in by default to show the pattern up close. It would be difficult for software to know what the appropriate axis limits are for every possible plot; therefore, it is our job to properly adjust the axes before presenting our results. You can read about some more ways that plots can be misleading at <https://venngage.com/blog/misleading-graphs/>.

In the workflow diagram we saw earlier (*Figure 1.2*), EDA and data wrangling shared a box. This is because they are closely tied:

- Data needs to be prepped before EDA.
- Visualizations that are created during EDA may indicate the need for additional data cleaning.
- Data wrangling uses summary statistics to look for potential data issues, while EDA uses them to understand the data. Improper cleaning will distort the findings when we're conducting EDA. In addition, data wrangling skills will be required to get summary statistics across subsets of the data.

When calculating summary statistics, we must keep the type of data we collected in mind. Data can be **quantitative** (measurable quantities) or **categorical** (descriptions, groupings, or categories). Within these classes of data, we have further subdivisions that let us know what types of operations we can perform on them.

For example, categorical data can be **nominal**, where we assign a numeric value to each level of the category, such as `on = 1/off = 0`. Note that the fact that `on` is greater than `off` is meaningless because we arbitrarily chose those numbers to represent the states `on` and `off`. When there is a ranking among the categories, they are **ordinal**, meaning that we can order the levels (for instance, we can have `low < medium < high`).

Quantitative data can use an **interval scale** or a **ratio scale**. The interval scale includes things such as temperature. We can measure temperatures in Celsius and compare the temperatures of two cities, but it doesn't mean anything to say one city is twice as hot as the other. Therefore, interval scale values can be meaningfully compared using addition/subtraction, but not multiplication/division. The ratio scale, then, are those values that can be meaningfully compared with ratios (using multiplication and division). Examples of the ratio scale include prices, sizes, and counts.

When we complete our EDA, we can decide on the next steps by drawing conclusions.

Drawing conclusions

After we have collected the data for our analysis, cleaned it up, and performed some thorough EDA, it is time to draw conclusions. This is where we summarize our findings from EDA and decide the next steps:

- Did we notice any patterns or relationships when visualizing the data?
- Does it look like we can make accurate predictions from our data? Does it make sense to move to modeling the data?
- Should we handle missing data points? How?
- How is the data distributed?
- Does the data help us answer the questions we have or give insight into the problem we are investigating?
- Do we need to collect new or additional data?

If we decide to model the data, this falls under machine learning and statistics. While not technically data analysis, it is usually the next step, and we will cover it in *Chapter 9, Getting Started with Machine Learning in Python*, and *Chapter 10, Making Better Predictions – Optimizing Models*. In addition, we will see how this entire process will work in practice in *Chapter 11, Machine Learning Anomaly Detection*. As a reference, in the *Machine learning workflow* section in the *Appendix*, there is a workflow diagram depicting the full process from data analysis to machine learning. *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*, and *Chapter 8, Rule-Based Anomaly Detection*, will focus on drawing conclusions from data analysis, rather than building models.

The next section will be a review of statistics; those with knowledge of statistics can skip ahead to the *Setting up a virtual environment* section.

Statistical foundations

When we want to make observations about the data we are analyzing, we often, if not always, turn to statistics in some fashion. The data we have is referred to as the **sample**, which was observed from (and is a subset of) the **population**. Two broad categories of statistics are descriptive and inferential statistics. With **descriptive statistics**, as the name implies, we are looking to *describe* the sample. **Inferential statistics** involves using the sample statistics to *infer*, or deduce, something about the population, such as the underlying distribution.

Important note

Sample statistics are used as **estimators** of the population parameters, meaning that we have to quantify their bias and variance. There is a multitude of methods for this; some will make assumptions on the shape of the distribution (parametric) and others won't (non-parametric). This is all well beyond the scope of this book, but it is good to be aware of.

Often, the goal of an analysis is to create a story for the data; unfortunately, it is very easy to misuse statistics. It's the subject of a famous quote:

"There are three kinds of lies: lies, damned lies, and statistics."

— Benjamin Disraeli

This is especially true of inferential statistics, which is used in many scientific studies and papers to show the significance of the researchers' findings. This is a more advanced topic and, since this isn't a statistics book, we will only briefly touch upon some of the tools and principles behind inferential statistics, which can be pursued further. We will focus on descriptive statistics to help explain the data we are analyzing.

Sampling

There's an important thing to remember before we attempt any analysis: our sample must be a **random sample** that is representative of the population. This means that the data must be sampled without bias (for example, if we are asking people whether they like a certain sports team, we can't only ask fans of the team) and that we should have (ideally) members of all distinct groups from the population in our sample (in the sports team example, we can't just ask men).

When we discuss machine learning in *Chapter 9, Getting Started with Machine Learning in Python*, we will need to sample our data, which will be a sample to begin with. This is called **resampling**. Depending on the data, we will have to pick a different method of sampling. Often, our best bet is a **simple random sample**: we use a random number generator to pick rows at random. When we have distinct groups in the data, we want our sample to be a **stratified random sample**, which will preserve the proportion of the groups in the data. In some cases, we don't have enough data for the aforementioned sampling strategies, so we may turn to random sampling with replacement (**bootstrapping**); this is called a **bootstrap sample**. Note that our underlying sample needs to have been a random sample or we risk increasing the bias of the estimator (we could pick certain rows more often because they are in the data more often if it was a convenience sample, while in the true population these rows aren't as prevalent). We will see an example of bootstrapping in *Chapter 8, Rule-Based Anomaly Detection*.

Important note

A thorough discussion of the theory behind bootstrapping and its consequences is well beyond the scope of this book, but watch this video for a primer: <https://www.youtube.com/watch?v=gcPIyeqymOU>.

You can read more about sampling methods, along with their strengths and weaknesses, at <https://www.khanacademy.org/math/statistics-probability/designing-studies/sampling-methods-stats/a/sampling-methods-review>.

Descriptive statistics

We will begin our discussion of descriptive statistics with **univariate statistics**; univariate simply means that these statistics are calculated from one (**uni**) variable. Everything in this section can be extended to the whole dataset, but the statistics will be calculated per variable we are recording (meaning that if we had 100 observations of speed and distance pairs, we could calculate the averages across the dataset, which would give us the average speed and average distance statistics).

Descriptive statistics are used to describe and/or summarize the data we are working with. We can start our summarization of the data with a measure of **central tendency**, which describes where most of the data is centered around, and a measure of **spread** or **dispersion**, which indicates how far apart values are.

Measures of central tendency

Measures of central tendency describe the center of our distribution of data. There are three common statistics that are used as measures of center: mean, median, and mode. Each has its own strengths, depending on the data we are working with.

Mean

Perhaps the most common statistic for summarizing data is the average, or **mean**. The population mean is denoted by μ (the Greek letter *mu*), and the sample mean is written as \bar{x} (pronounced *X-bar*). The sample mean is calculated by summing all the values and dividing by the count of values; for example, the mean of the numbers 0, 1, 1, 2, and 9 is $2.6 ((0 + 1 + 1 + 2 + 9) / 5)$:

$$\bar{x} = \frac{\sum_1^n x_i}{n}$$

We use x_i to represent the i^{th} observation of the variable X . Note how the variable as a whole is represented with a capital letter, while the specific observation is lowercase. Σ (the Greek capital letter *sigma*) is used to represent a summation, which, in the equation for the mean, goes from 1 to n , which is the number of observations.

One important thing to note about the mean is that it is very sensitive to **outliers** (values created by a different generative process than our distribution). In the previous example, we were dealing with only five values; nevertheless, the 9 is much larger than the other numbers and pulled the mean higher than all but the 9. In cases where we suspect outliers to be present in our data, we may want to instead use the median as our measure of central tendency.

Median

Unlike the mean, the **median** is robust to outliers. Consider income in the US; the top 1% is much higher than the rest of the population, so this will skew the mean to be higher and distort the perception of the average person's income. However, the median will be more representative of the average income because it is the 50th percentile of our data; this means that 50% of the values are greater than the median and 50% are less than the median.

Tip

The i^{th} percentile is the value at which $i\%$ of the observations are less than that value, so the 99th percentile is the value in X where 99% of the x 's are less than it.

The median is calculated by taking the middle value from an ordered list of values; in cases where we have an even number of values, we take the mean of the middle two values. If we take the numbers 0, 1, 1, 2, and 9 again, our median is 1. Notice that the mean and median for this dataset are different; however, depending on the distribution of the data, they may be the same.

Mode

The **mode** is the most common value in the data (if we, once again, have the numbers 0, 1, 1, 2, and 9, then 1 is the mode). In practice, we will often hear things such as *the distribution is bimodal or multimodal* (as opposed to unimodal) in cases where the distribution has two or more most popular values. This doesn't necessarily mean that each of them occurred the same amount of times, but rather, they are more common than the other values by a significant amount. As shown in the following plots, a unimodal distribution has only one mode (at **0**), a bimodal distribution has two (at **-2** and **3**), and a multimodal distribution has many (at **-2**, **0.4**, and **3**):

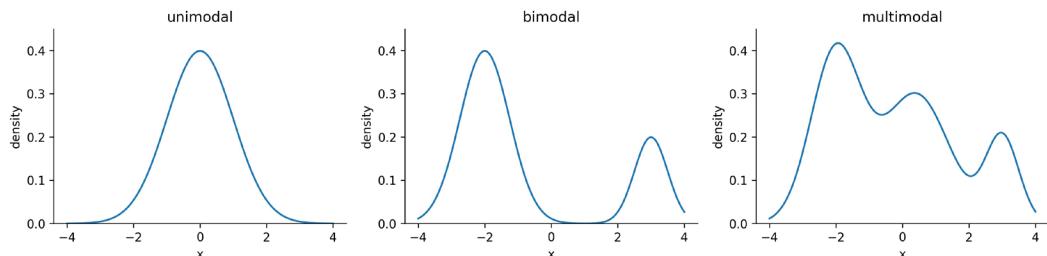


Figure 1.3 – Visualizing the mode with continuous data

Understanding the concept of the mode comes in handy when describing continuous distributions; however, most of the time when we're describing our continuous data, we will use either the mean or the median as our measure of central tendency. When working with categorical data, on the other hand, we will typically use the mode.

Measures of spread

Knowing where the center of the distribution is only gets us partially to being able to summarize the distribution of our data—we need to know how values fall around the center and how far apart they are. Measures of spread tell us how the data is dispersed; this will indicate how thin (low dispersion) or wide (very spread out) our distribution is. As with measures of central tendency, we have several ways to describe the spread of a distribution, and which one we choose will depend on the situation and the data.

Range

The **range** is the distance between the smallest value (**minimum**) and the largest value (**maximum**). The units of the range will be the same units as our data. Therefore, unless two distributions of data are in the same units and measuring the same thing, we can't compare their ranges and say one is more dispersed than the other:

$$\text{range} = \max(X) - \min(X)$$

Just from the definition of the range, we can see why it wouldn't always be the best way to measure the spread of our data. It gives us upper and lower bounds on what we have in the data; however, if we have any outliers in our data, the range will be rendered useless.

Another problem with the range is that it doesn't tell us how the data is dispersed around its center; it really only tells us how dispersed the entire dataset is. This brings us to the variance.

Variance

The **variance** describes how far apart observations are spread out from their average value (the mean). The population variance is denoted as σ^2 (pronounced *sigma-squared*), and the sample variance is written as s^2 . It is calculated as the average squared distance from the mean. Note that the distances must be squared so that distances below the mean don't cancel out those above the mean.

If we want the sample variance to be an unbiased estimator of the population variance, we divide by $n - 1$ instead of n to account for using the sample mean instead of the population mean; this is called Bessel's correction (https://en.wikipedia.org/wiki/Bessel%27s_correction). Most statistical tools will give us the sample variance by default, since it is *very* rare that we would have data for the entire population:

$$s^2 = \frac{\sum_1^n (x_i - \bar{x})^2}{n - 1}$$

The variance gives us a statistic with *squared* units. This means that if we started with data on income in dollars (\$), then our variance would be in dollars squared ($\2). This isn't really useful when we're trying to see how this describes the data; we can use the **magnitude** (size) itself to see how spread out something is (large values = large spread), but beyond that, we need a measure of spread with units that are the same as our data. For this purpose, we use the standard deviation.

Standard deviation

We can use the **standard deviation** to see how far from the mean data points are *on average*. A small standard deviation means that values are close to the mean, while a large standard deviation means that values are dispersed more widely. This is tied to how we would imagine the distribution curve: the smaller the standard deviation, the thinner the peak of the curve (0.5); the larger the standard deviation, the wider the peak of the curve (2):

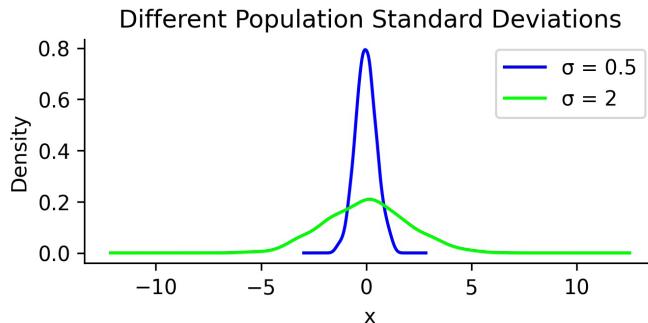


Figure 1.4 – Using standard deviation to quantify the spread of a distribution

The standard deviation is simply the square root of the variance. By performing this operation, we get a statistic in units that we can make sense of again (\$) for our income example):

$$s = \sqrt{\frac{\sum_1^n (x_i - \bar{x})^2}{n - 1}} = \sqrt{s^2}$$

Note that the population standard deviation is represented as σ , and the sample standard deviation is denoted as s .

Coefficient of variation

When we moved from variance to standard deviation, we were looking to get to units that made sense; however, if we then want to compare the level of dispersion of one dataset to another, we would need to have the same units once again. One way around this is to calculate the **coefficient of variation (CV)**, which is unitless. The CV is the ratio of the standard deviation to the mean:

$$CV = \frac{s}{\bar{x}}$$

We will use this metric in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*; since the CV is unitless, we can use it to compare the volatility of different assets.

Interquartile range

So far, other than the range, we have discussed mean-based measures of dispersion; now, we will look at how we can describe the spread with the median as our measure of central tendency. As mentioned earlier, the median is the 50th percentile or the 2nd **quartile (Q₂)**. Percentiles and quartiles are both **quantiles**—values that divide data into equal groups each containing the same percentage of the total data. Percentiles divide the data into 100 parts, while quartiles do so into four (25%, 50%, 75%, and 100%).

Since quantiles neatly divide up our data, and we know how much of the data goes in each section, they are a perfect candidate for helping us quantify the spread of our data. One common measure for this is the **interquartile range (IQR)**, which is the distance between the 3rd and 1st quartiles:

$$IQR = Q_3 - Q_1$$

The IQR gives us the spread of data around the median *and* quantifies how much dispersion we have in the middle 50% of our distribution. It can also be useful when checking the data for outliers, which we will cover in *Chapter 8, Rule-Based Anomaly Detection*. In addition, the IQR can be used to calculate a unitless measure of dispersion, which we will discuss next.

Quartile coefficient of dispersion

Just like we had the coefficient of variation when using the mean as our measure of central tendency, we have the **quartile coefficient of dispersion** when using the median as our measure of center. This statistic is also unitless, so it can be used to compare datasets. It is calculated by dividing the **semi-quartile range** (half the IQR) by the **midhinge** (midpoint between the first and third quartiles):

$$QCD = \frac{\frac{Q_3 - Q_1}{2}}{\frac{Q_1 + Q_3}{2}} = \frac{Q_3 - Q_1}{Q_3 + Q_1}$$

We will see this metric again in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*, when we assess stock volatility. For now, let's take a look at how we can use measures of central tendency and dispersion to summarize our data.

Summarizing data

We have seen many examples of descriptive statistics that we can use to summarize our data by its center and dispersion; in practice, looking at the **5-number summary** and visualizing the distribution prove to be helpful first steps before diving into some of the other aforementioned metrics. The 5-number summary, as its name indicates, provides five descriptive statistics that summarize our data:

	Quartile	Statistic	Percentile
1.	Q_0	minimum	0^{th}
2.	Q_1	N/A	25^{th}
3.	Q_2	median	50^{th}
4.	Q_3	N/A	75^{th}
5.	Q_4	maximum	100^{th}

Figure 1.5 – The 5-number summary

A **box plot** (or box and whisker plot) is a visual representation of the 5-number summary. The median is denoted by a thick line in the box. The top of the box is Q_3 and the bottom of the box is Q_1 . Lines (whiskers) extend from both sides of the box boundaries toward the minimum and maximum. Based on the convention our plotting tool uses, though, they may only extend to a certain statistic; any values beyond these statistics are marked as outliers (using points). For this book in general, the lower bound of the whiskers will be $Q_1 - 1.5 * IQR$ and the upper bound will be $Q_3 + 1.5 * IQR$, which is called the **Tukey box plot**:

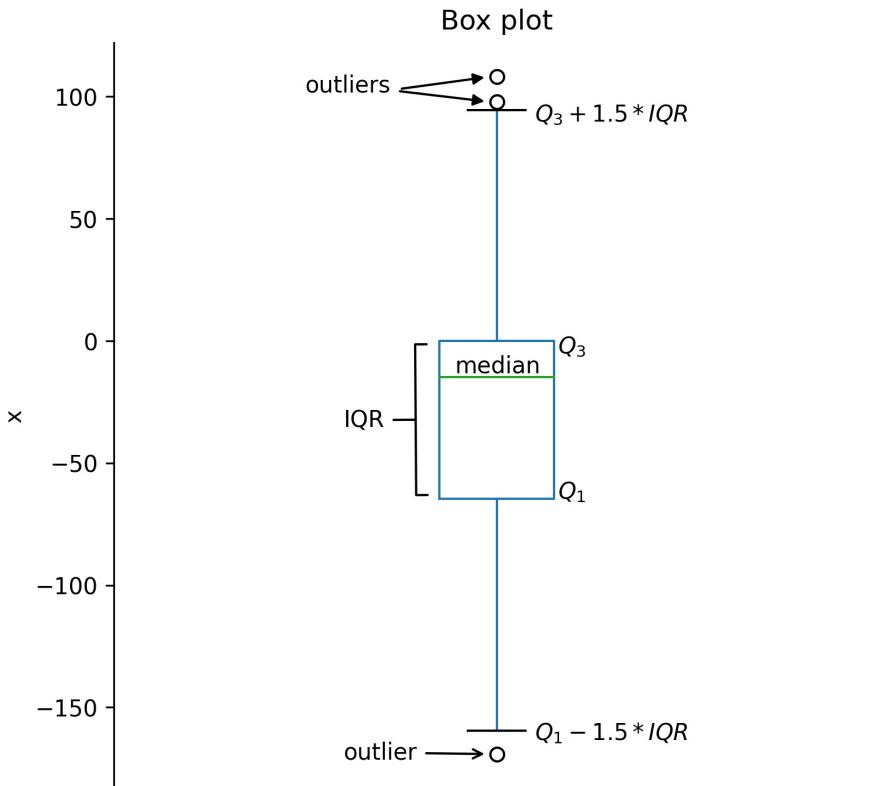


Figure 1.6 – The Tukey box plot

While the box plot is a great tool for getting an initial understanding of the distribution, we don't get to see how things are distributed inside each of the quartiles. For this purpose, we turn to **histograms** for **discrete** variables (for instance, the number of people or books) and **kernel density estimates (KDEs)** for **continuous** variables (for instance, heights or time). There is nothing stopping us from using KDEs on discrete variables, but it is easy to confuse people that way. Histograms work for both discrete and continuous variables; however, in both cases, we must keep in mind that the number of bins we choose to divide the data into can easily change the shape of the distribution we see.

To make a histogram, a certain number of equal-width bins are created, and then bars with heights for the number of values we have in each bin are added. The following plot is a histogram with 10 bins, showing the three measures of central tendency for the same data that was used to generate the box plot in *Figure 1.6*:

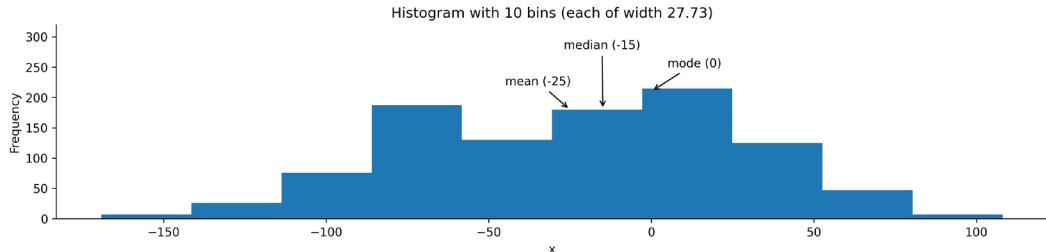


Figure 1.7 – Example histogram

Important note

In practice, we need to play around with the number of bins to find the best value. However, we have to be careful as this can misrepresent the shape of the distribution.

KDEs are similar to histograms, except rather than creating bins for the data, they draw a smoothed curve, which is an estimate of the distribution's **probability density function (PDF)**. The PDF is for continuous variables and tells us how probability is distributed over the values. Higher values for the PDF indicate higher likelihoods:

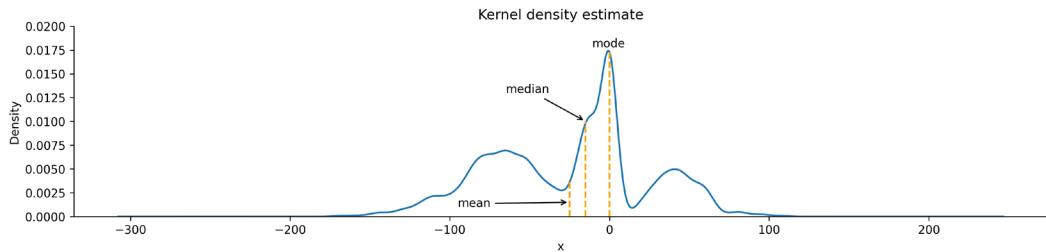


Figure 1.8 – KDE with marked measures of center

When the distribution starts to get a little lopsided with long tails on one side, the mean measure of center can easily get pulled to that side. Distributions that aren't symmetric have some **skew** to them. A **left (negative) skewed distribution** has a long tail on the left-hand side; a **right (positive) skewed distribution** has a long tail on the right-hand side. In the presence of negative skew, the mean will be less than the median, while the reverse happens with a positive skew. When there is no skew, both will be equal:

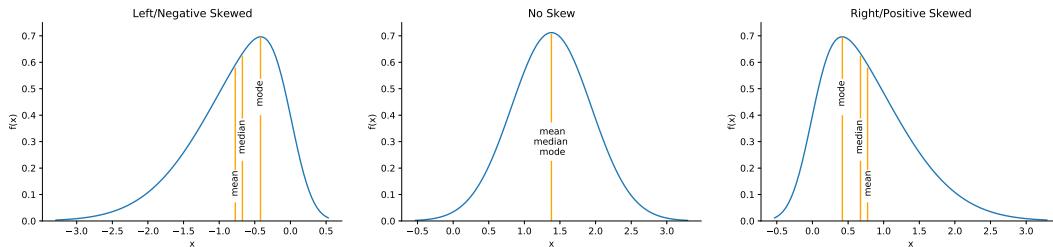


Figure 1.9 – Visualizing skew

Important note

There is also another statistic called **kurtosis**, which compares the density of the center of the distribution with the density at the tails. Both skewness and kurtosis can be calculated with the SciPy package.

Each column in our data is a **random variable**, because every time we observe it, we get a value according to the underlying distribution—it's not static. When we are interested in the probability of getting a value of x or less, we use the **cumulative distribution function (CDF)**, which is the integral (area under the curve) of the PDF:

$$CDF = F(x) = \int_{-\infty}^x f(t)dt$$

where $f(t)$ is the PDF and $\int_{-\infty}^{\infty} f(t)dt = 1$

The probability of the random variable X being less than or equal to the specific value of x is denoted as $P(X \leq x)$. With a continuous variable, the probability of getting exactly x is 0. This is because the probability will be the integral of the PDF from x to x (area under a curve with zero width), which is 0:

$$P(X = x) = \int_x^x f(t)dt = 0$$

In order to visualize this, we can find an estimate of the CDF from the sample, called the **empirical cumulative distribution function** (ECDF). Since this is cumulative, at the point where the value on the x -axis is equal to x , the y value is the cumulative probability of $P(X \leq x)$. Let's visualize $P(X \leq 50)$, $P(X = 50)$, and $P(X > 50)$ as an example:

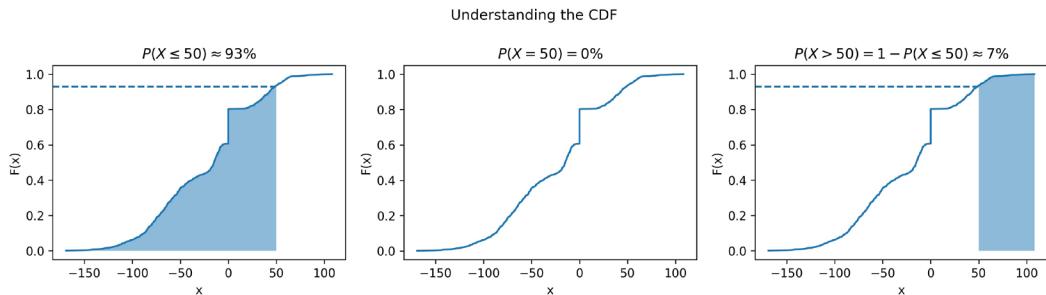


Figure 1.10 – Visualizing the CDF

In addition to examining the distribution of our data, we may find the need to utilize probability distributions for uses such as simulation (discussed in *Chapter 8, Rule-Based Anomaly Detection*) or hypothesis testing (see the *Inferential statistics* section); let's take a look at a few distributions that we are likely to come across.

Common distributions

While there are many probability distributions, each with specific use cases, there are some that we will come across often. The **Gaussian**, or **normal**, looks like a bell curve and is parameterized by its mean (μ) and standard deviation (σ). The **standard normal** (Z) has a mean of 0 and a standard deviation of 1. Many things in nature happen to follow the normal distribution, such as heights. Note that testing whether a distribution is normal is not trivial—check the *Further reading* section for more information.

The **Poisson distribution** is a discrete distribution that is often used to model arrivals. The time between arrivals can be modeled with the **exponential distribution**. Both are defined by their mean, lambda (λ). The **uniform distribution** places equal likelihood on each value within its bounds. We often use this for random number generation. When we generate a random number to simulate a single success/failure outcome, it is called a **Bernoulli trial**. This is parameterized by the probability of success (p). When we run the same experiment multiple times (n), the total number of successes is then a **binomial** random variable. Both the Bernoulli and binomial distributions are discrete.

We can visualize both discrete and continuous distributions; however, discrete distributions give us a **probability mass function** (PMF) instead of a PDF:

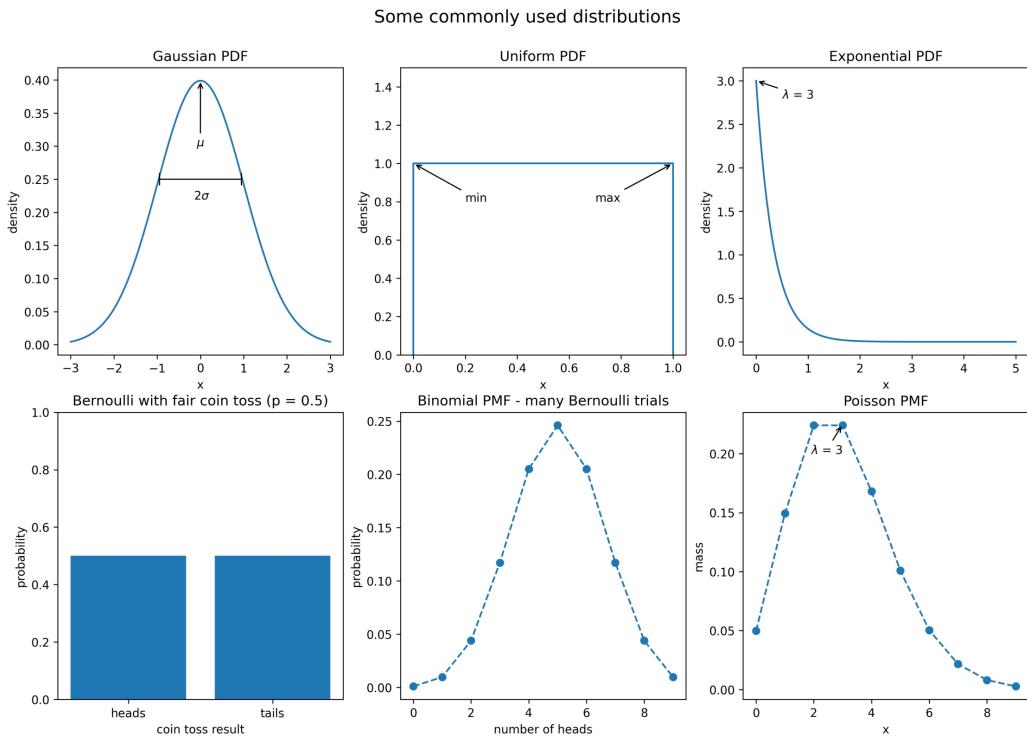


Figure 1.11 – Visualizing some commonly used distributions

We will use some of these distributions in *Chapter 8, Rule-Based Anomaly Detection*, when we simulate some login attempt data for anomaly detection.

Scaling data

In order to compare variables from different distributions, we would have to **scale** the data, which we could do with the range by using **min-max scaling**. We take *each* data point, subtract the minimum of the dataset, then divide by the range. This **normalizes** our data (scales it to the range $[0, 1]$):

$$x_{scaled} = \frac{x - \min(X)}{\text{range}(X)}$$

This isn't the only way to scale data; we can also use the mean and standard deviation. In this case, we would subtract the mean from each observation and then divide by the standard deviation to **standardize** the data. This gives us what is known as a **Z-score**:

$$z_i = \frac{x_i - \bar{x}}{s}$$

We are left with a normalized distribution with a mean of 0 and a standard deviation (and variance) of 1. The Z-score tells us how many standard deviations from the mean each observation is; the mean has a Z-score of 0, while an observation of 0.5 standard deviations below the mean will have a Z-score of -0.5.

There are, of course, additional ways to scale our data, and the one we end up choosing will be dependent on our data and what we are trying to do with it. By keeping the measures of central tendency and measures of dispersion in mind, you will be able to identify how the scaling of data is being done in any other methods you come across.

Quantifying relationships between variables

In the previous sections, we were dealing with univariate statistics and were only able to say something about the variable we were looking at. With multivariate statistics, we seek to quantify relationships between variables and attempt to make predictions for future behavior.

The **covariance** is a statistic for quantifying the relationship between variables by showing how one variable changes with respect to another (also referred to as their joint variance):

$$\text{cov}(X, Y) = E[(X - E[X])(Y - E[Y])]$$

Important note

$E[X]$ is a new notation for us. It is read as *the expected value of X* or *the expectation of X*, and it is calculated by summing all the possible values of X multiplied by their probability—it's the long-run average of X.

The magnitude of the covariance isn't easy to interpret, but its sign tells us whether the variables are positively or negatively correlated. However, we would also like to quantify how *strong* the relationship is between the variables, which brings us to correlation.

Correlation tells us how variables change together both in direction (same or opposite) and magnitude (strength of the relationship). To find the correlation, we calculate the **Pearson correlation coefficient**, symbolized by ρ (the Greek letter *rho*), by dividing the covariance by the product of the standard deviations of the variables:

$$\rho_{X,Y} = \frac{\text{cov}(X, Y)}{s_X s_Y}$$

This normalizes the covariance and results in a statistic bounded between -1 and 1, making it easy to describe both the direction of the correlation (sign) and the strength of it (magnitude). Correlations of 1 are said to be perfect positive (linear) correlations, while those of -1 are perfect negative correlations. Values near 0 aren't correlated. If correlation coefficients are near 1 in absolute value, then the variables are said to be strongly correlated; those closer to 0.5 are said to be weakly correlated.

Let's look at some examples using scatter plots. In the leftmost subplot of *Figure 1.12* ($\rho = 0.11$), we see that there is no correlation between the variables: they appear to be random noise with no pattern. The next plot with $\rho = -0.52$ has a weak negative correlation: we can see that the variables appear to move together with the x variable increasing, while the y variable decreases, but there is still a bit of randomness. In the third plot from the left ($\rho = 0.87$), there is a strong positive correlation: x and y are increasing together. The rightmost plot with $\rho = -0.99$ has a near-perfect negative correlation: as x increases, y decreases. We can also see how the points form a line:

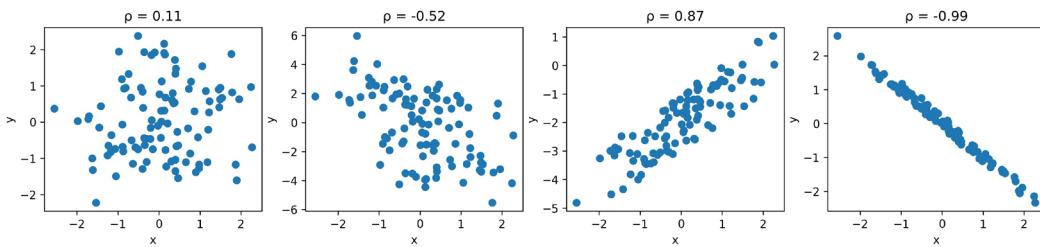


Figure 1.12 – Comparing correlation coefficients

To quickly eyeball the strength and direction of the relationship between two variables (and see whether there even seems to be one), we will often use scatter plots rather than calculating the exact correlation coefficient. This is for a couple of reasons:

- It's easier to find patterns in visualizations, but it's more work to arrive at the same conclusion by looking at numbers and tables.
- We might see that the variables seem related, but they may not be *linearly* related. Looking at a visual representation will make it easy to see if our data is actually quadratic, exponential, logarithmic, or some other non-linear function.

Both of the following plots depict data with strong positive correlations, but it's pretty obvious when looking at the scatter plots that these are not linear. The one on the left is logarithmic, while the one on the right is exponential:

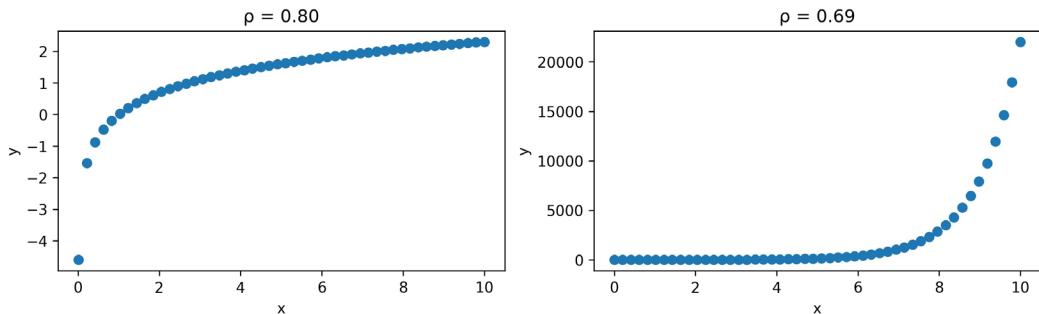


Figure 1.13 – The correlation coefficient can be misleading

It's very important to remember that while we may find a correlation between X and Y , it doesn't mean that X causes Y or that Y causes X . There could be some Z that actually causes both; perhaps X causes some intermediary event that causes Y , or it is actually just a coincidence. Keep in mind that we often don't have enough information to report causation—*correlation does not imply causation*.

Tip

Be sure to check out Tyler Vigen's *Spurious Correlations* blog (<https://www.tylervigen.com/spurious-correlations>) for some interesting correlations.

Pitfalls of summary statistics

There is a very interesting dataset illustrating how careful we must be when only using summary statistics and correlation coefficients to describe our data. It also shows us that plotting is not optional. **Anscombe's quartet** is a collection of four different datasets that have identical summary statistics and correlation coefficients, but when plotted, it is obvious they are not similar:

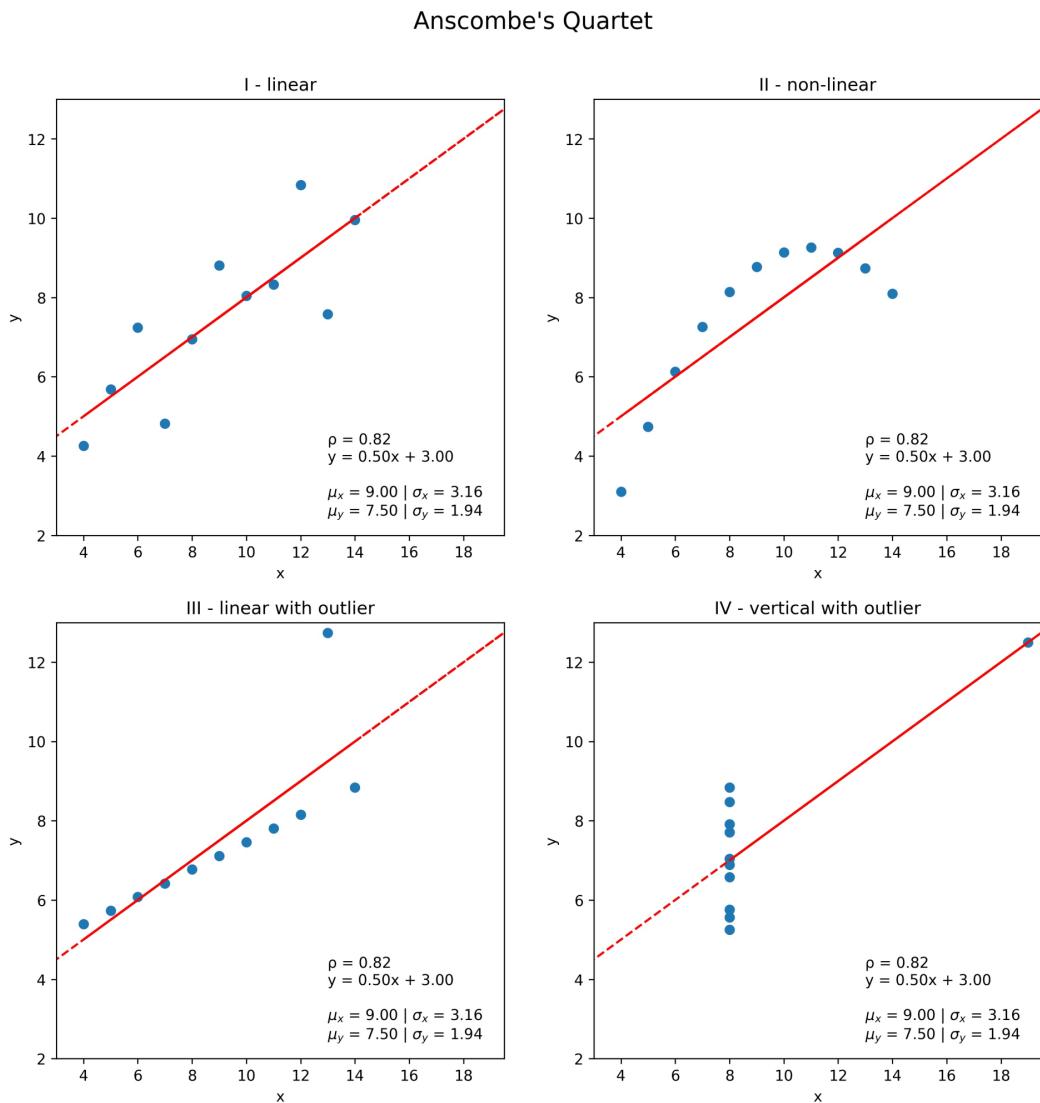


Figure 1.14 – Summary statistics can be misleading

Notice that each of the plots in *Figure 1.14* has an identical best-fit line defined by the equation $y = 0.50x + 3.00$. In the next section, we will discuss, at a high level, how this line is created and what it means.

Important note

Summary statistics are very helpful when we're getting to know the data, but be wary of relying exclusively on them. Remember, statistics can be misleading; be sure to also plot the data before drawing any conclusions or proceeding with the analysis. You can read more about Anscombe's quartet at https://en.wikipedia.org/wiki/Anscombe%27s_quartet. Also, be sure to check out the **Datasaurus Dozen**, which are 13 datasets that also have the same summary statistics, at <https://www.autodeskresearch.com/publications/samestats>.

Prediction and forecasting

Say our favorite ice cream shop has asked us to help predict how many ice creams they can expect to sell on a given day. They are convinced that the temperature outside has a strong influence on their sales, so they have collected data on the number of ice creams sold at a given temperature. We agree to help them, and the first thing we do is make a scatter plot of the data they collected:

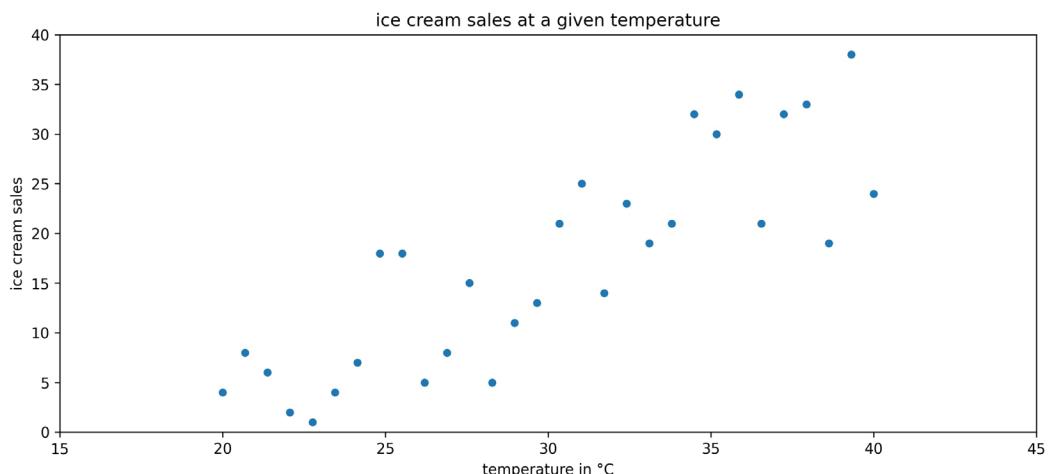


Figure 1.15 – Observations of ice cream sales at various temperatures

We can observe an upward trend in the scatter plot: more ice creams are sold at higher temperatures. In order to help out the ice cream shop, though, we need to find a way to make predictions from this data. We can use a technique called **regression** to model the relationship between temperature and ice cream sales with an equation. Using this equation, we will be able to **predict** ice cream sales at a given temperature.

Important note

Remember that correlation does not imply causation. People may buy ice cream when it is warmer, but warmer temperatures don't necessarily cause people to buy ice cream.

In *Chapter 9, Getting Started with Machine Learning in Python*, we will go over regression in depth, so this discussion will be a high-level overview. There are many types of regression that will yield a different type of equation, such as linear (which we will use for this example) and logistic. Our first step will be to identify the **dependent variable**, which is the quantity we want to predict (ice cream sales), and the variables we will use to predict it, which are called **independent variables**. While we can have many independent variables, our ice cream sales example only has one: temperature. Therefore, we will use simple linear regression to model the relationship as a line:

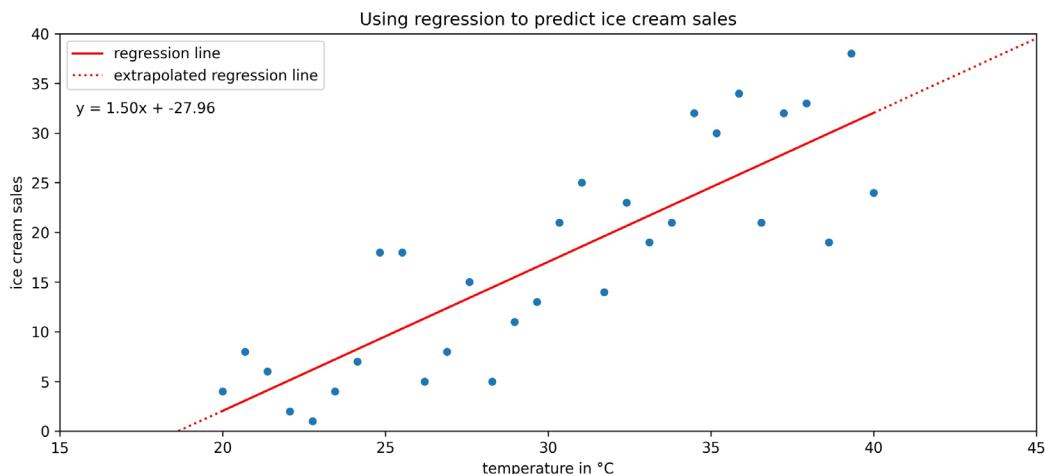


Figure 1.16 – Fitting a line to the ice cream sales data

The regression line in the previous scatter plot yields the following equation for the relationship:

$$\text{ice cream sales} = 1.50 \times \text{temperature} - 27.96$$

Suppose that today the temperature is 35°C—we would plug that in for *temperature* in the equation. The result predicts that the ice cream shop will sell 24.54 ice creams. This prediction is along the red line in the previous plot. Note that the ice cream shop can't actually sell fractions of ice cream.

Before leaving the model in the hands of the ice cream shop, it's important to discuss the difference between the dotted and solid portions of the regression line that we obtained. When we make predictions using the solid portion of the line, we are using **interpolation**, meaning that we will be predicting ice cream sales for temperatures the regression was created on. On the other hand, if we try to predict how many ice creams will be sold at 45°C, it is called **extrapolation** (the dotted portion of the line), since we didn't have any temperatures this high when we ran the regression. Extrapolation can be very dangerous as many trends don't continue indefinitely. People may decide not to leave their houses because it is so hot. This means that instead of selling the predicted 39.54 ice creams, they would sell zero.

When working with time series, our terminology is a little different: we often look to **forecast** future values based on past values. Forecasting is a type of prediction for time series. Before we try to model the time series, however, we will often use a process called **time series decomposition** to split the time series into components, which can be combined in an additive or multiplicative fashion and may be used as parts of a model.

The **trend** component describes the behavior of the time series in the **long term** without accounting for seasonal or cyclical effects. Using the trend, we can make broad statements about the time series in the long run, such as *the population of Earth is increasing* or *the value of a stock is stagnating*. The **seasonality** component explains the systematic and calendar-related movements of a time series. For example, the number of ice cream trucks on the streets of New York City is high in the summer and drops to nothing in the winter; this pattern repeats every year, regardless of whether the actual amount each summer is the same. Lastly, the **cyclical** component accounts for anything else unexplained or irregular with the time series; this could be something such as a hurricane driving the number of ice cream trucks down in the **short term** because it isn't safe to be outside. This component is difficult to anticipate with a forecast due to its unexpected nature.

We can use Python to **decompose** the time series into trend, seasonality, and **noise** or **residuals**. The cyclical component is captured in the noise (random, unpredictable data); after we remove the trend and seasonality from the time series, what we are left with is the residual:

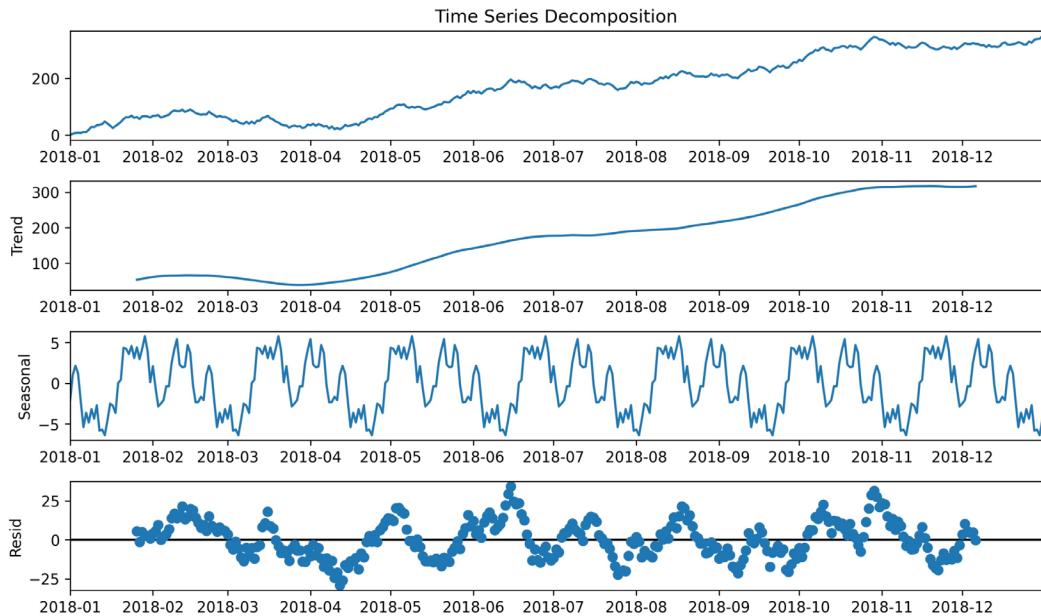


Figure 1.17 – An example of time series decomposition

When building models to forecast time series, some common methods include exponential smoothing and ARIMA-family models. **ARIMA** stands for **autoregressive (AR)**, **integrated (I)**, **moving average (MA)**. **Autoregressive** models take advantage of the fact that an observation at time t is *correlated* to a previous observation, for example, at time $t - 1$. In *Chapter 5, Visualizing Data with Pandas and Matplotlib*, we will look at some techniques for determining whether a time series is autoregressive; note that not all time series are. The **integrated** component concerns the **differenced** data, or the *change* in the data from one time to another. For example, if we were concerned with a **lag** (distance between times) of 1, the differenced data would be the value at time t subtracted by the value at time $t - 1$. Lastly, the **moving average** component uses a sliding window to average the last x observations, where x is the length of the sliding window. If, for example, we have a 3-period moving average, by the time we have all of the data up to time 5, our moving average calculation only uses time periods 3, 4, and 5 to forecast time 6. We will build an ARIMA model in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*.

The moving average puts equal weight on each time period in the past involved in the calculation. In practice, this isn't always a realistic expectation of our data. Sometimes, *all* past values are important, but they *vary* in their influence on future data points. For these cases, we can use **exponential smoothing**, which allows us to put more weight on more recent values and less weight on values further away from what we are predicting.

Note that we aren't limited to predicting numbers; in fact, depending on the data, our predictions could be categorical in nature—things such as determining which flavor of ice cream will sell the most on a given day or whether an email is spam or not. This type of prediction will be introduced in *Chapter 9, Getting Started with Machine Learning in Python*.

Inferential statistics

As mentioned earlier, inferential statistics deals with inferring or deducing things from the sample data we have in order to make statements about the population as a whole. When we're looking to state our conclusions, we have to be mindful of whether we conducted an observational study or an experiment. With an **observational study**, the independent variable is not under the control of the researchers, and so we are *observing* those taking part in our study (think about studies on smoking—we can't force people to smoke). The fact that we can't control the independent variable means that we *cannot* conclude causation.

With an **experiment**, we are able to directly influence the independent variable and randomly assign subjects to the control and test groups, such as A/B tests (for anything from website redesigns to ad copy). Note that the control group doesn't receive treatment; they can be given a placebo (depending on what the study is). The ideal setup for this is **double-blind**, where the researchers administering the treatment don't know which treatment is the placebo and also don't know which subject belongs to which group.

Important note

We can often find reference to Bayesian inference and frequentist inference. These are based on two different ways of approaching probability. Frequentist statistics focuses on the frequency of the event, while Bayesian statistics uses a degree of belief when determining the probability of an event. We will see an example of Bayesian statistics in *Chapter 11, Machine Learning Anomaly Detection*. You can read more about how these methods differ at <https://www.probabilisticworld.com/frequentist-bayesian-approaches-inferential-statistics/>.

Inferential statistics gives us tools to translate our understanding of the sample data to a statement about the population. Remember that the sample statistics we discussed earlier are estimators for the population parameters. Our estimators need **confidence intervals**, which provide a point estimate and a margin of error around it. This is the range that the true population parameter will be in at a certain **confidence level**. At the 95% confidence level, 95% of the confidence intervals that are calculated from random samples of the population contain the true population parameter. Frequently, 95% is chosen for the confidence level and other purposes in statistics, although 90% and 99% are also common; the higher the confidence level, the wider the interval.

Hypothesis tests allow us to test whether the true population parameter is less than, greater than, or not equal to some value at a certain **significance level** (called **alpha**). The process of performing a hypothesis test starts with stating our initial assumption or **null hypothesis**: for example, *the true population mean is 0*. We pick a level of statistical significance, usually 5%, which is the probability of rejecting the null hypothesis when it is true. Then, we calculate the critical value for the test statistic, which will depend on the amount of data we have and the type of statistic (such as the mean of one population or the proportion of votes for a candidate) we are testing. The critical value is compared to the test statistic from our data and, based on the result, we either reject or fail to reject the null hypothesis. Hypothesis tests are closely related to confidence intervals. The significance level is equivalent to 1 minus the confidence level. This means that a result is statistically significant if the null hypothesis value is not in the confidence interval.

Important note

There are many things we have to be aware of when picking the method to calculate a confidence interval or the proper test statistic for a hypothesis test. This is beyond the scope of this book, but check out the link in the *Further reading* section at the end of this chapter for more information. Also, be sure to look at some of the mishaps with the p-values used in hypothesis testing, such as p-hacking, at https://en.wikipedia.org/wiki/Misuse_of_p-values.

Now that we have an overview of statistics and data analysis, we are ready to get started with the Python portion of this book. Let's start by setting up a virtual environment.

Setting up a virtual environment

This book was written using Python 3.7.3, but the code should work for Python 3.7.1+, which is available on all major operating systems. In this section, we will go over how to set up the virtual environment in order to follow along with this book. If Python isn't already installed on your computer, read through the following sections on virtual environments first, and then decide whether to install Anaconda, since it will also install Python. To install Python without Anaconda, download it from <https://www.python.org/downloads/>, and then follow the *venv* section instead of the *conda* section.

Important note

To check whether Python is already installed, run `where python3` from the command line on Windows or `which python3` from the command line on Linux/macOS. If this returns nothing, try running it with just `python` (instead of `python3`). If Python is installed, check the version by running `python3 --version`. Note that if `python3` works, then you should use that throughout the book (and conversely, use `python` if `python3` doesn't work).

Virtual environments

Most of the time, when we want to install software on our computer, we simply download it, but the nature of programming languages where packages are constantly being updated and rely on specific versions of others means this can cause issues. We could be working on a project one day where we need a certain version of a Python package (say 0.9.1), but the next day be working on an analysis where we need the most recent version of that same package to access some newer functionality (1.1.0). Sounds like there wouldn't be an issue, right? Well, what happens if this update causes a breaking change to the first project or another package in our project that relies on this one? This is a common enough problem that a solution already exists to prevent this from being an issue: virtual environments.

A **virtual environment** allows us to create separate environments for each of our projects. Each of our environments will only have the packages that it needs installed. This makes it easy to share our environment with others, have multiple versions of the same package installed on our machine for different projects without interfering with each other, and avoid unexpected side effects from installing packages that update or have dependencies on others. It's good practice to make a dedicated virtual environment for any projects we work on.

We will discuss two common ways to achieve this setup, and you can decide which fits best. Note that all the code in this section will be executed on the command line.

venv

Python 3 comes with the `venv` module, which will create a virtual environment in the location of our choice. The process of setting up and using a development environment is as follows (after Python is installed):

1. Create a folder for the project.
2. Use `venv` to create an environment in this folder.
3. Activate the environment.
4. Install Python packages in the environment with `pip`.
5. Deactivate the environment when finished.

In practice, we will create environments for each project we work on, so our first step will be to create a directory for all of our project files. For this, we can use the `mkdir` command. Once this has been created, we will change our current directory to the newly created one using the `cd` command. Since we already obtained the project files (from the instructions in the *Chapter materials* section), the following is for reference only. To make a new directory and move to that directory, we can use the following command:

```
$ mkdir my_project && cd my_project
```

Tip

`cd <path>` changes the current directory to the path specified in `<path>`, which can be an **absolute** (full) path or **relative** (how to get there from the current directory) path.

Before moving on, use `cd` to navigate to the directory containing this book's repository. Note that the path will depend on where it was cloned/downloaded:

```
$ cd path/to/Hands-On-Data-Analysis-with-Pandas-2nd-edition
```

Since there are slight differences in operating systems for the remaining steps, we will go over Windows and Linux/macOS separately. Note that if you have both Python 2 and Python 3, make sure you use `python3` and not `python` in the following commands.

Windows

To create our environment for this book, we will use the `venv` module from the standard library. Note that we must provide a name for our environment (`book_env`). Remember, if your Windows setup has `python` associated with Python 3, then use `python` instead of `python3` in the following command:

```
C:\...> python3 -m venv book_env
```

Now, we have a folder for our virtual environment named `book_env` inside the repository folder that we cloned/downloaded earlier. In order to use the environment, we need to activate it:

```
C:\...> %cd%\book_env\Scripts\activate.bat
```

Tip

Windows replaces `%cd%` with the path to the current directory. This saves us from having to type the full path up to the `book_env` part.

Note that after we activate the virtual environment, we can see `(book_env)` in front of our prompt on the command line; this lets us know we are in the environment:

```
(book_env) C:\...>
```

When we are finished using the environment, we simply deactivate it:

```
(book_env) C:\...> deactivate
```

Any packages that are installed in the environment don't exist outside the environment. Note that we no longer have `(book_env)` in front of our prompt on the command line. You can read more about `venv` in the Python documentation at <https://docs.python.org/3/library/venv.html>.

Now that the virtual environment is created, activate it and then head to the *Installing the required Python packages* section for the next step.

Linux/macOS

To create our environment for this book, we will use the `venv` module from the standard library. Note that we must provide a name for our environment (`book_env`):

```
$ python3 -m venv book_env
```

Now, we have a folder for our virtual environment named `book_env` inside of the repository folder we cloned/downloaded earlier. In order to use the environment, we need to activate it:

```
$ source book_env/bin/activate
```

Note that after we activate the virtual environment, we can see `(book_env)` in front of our prompt on the command line; this lets us know we are in the environment:

```
(book_env) $
```

When we are finished using the environment, we simply deactivate it:

```
(book_env) $ deactivate
```

Any packages that are installed in the environment don't exist outside the environment. Note that we no longer have `(book_env)` in front of our prompt on the command line. You can read more about `venv` in the Python documentation at <https://docs.python.org/3/library/venv.html>.

Now that the virtual environment is created, activate it and then head to the *Installing the required Python packages* section for the next step.

conda

Anaconda provides a way to set up a Python environment specifically for data science. It includes some of the packages we will use in this book, along with several others that may be necessary for tasks that aren't covered in this book (and also deals with dependencies outside of Python that might be tricky to install otherwise). Anaconda uses `conda` as the environment and package manager instead of `pip`, although packages can still be installed with `pip` (as long as the `pip` installed by Anaconda is called). Note that some packages may not be available with `conda`, in which case we will have to use `pip`. Consult this page in the `conda` documentation for a comparison of commands used with `conda`, `pip`, and `venv`: <https://conda.io/projects/conda/en/latest/commands.html#conda-vs-pip-vs-virtualenv-commands>.

Important note

Be warned that Anaconda is a very large install (although the Miniconda version is much lighter). Those who use Python for purposes aside from data science may prefer the `venv` method we discussed earlier in order to have more control over what gets installed.

Anaconda can also be packaged with the Spyder **integrated development environment (IDE)** and Jupyter Notebooks, which we will discuss later. Note that we can use Jupyter with the venv option as well.

You can read more about Anaconda and how to install it at the following pages in their official documentation:

- **Windows**: <https://docs.anaconda.com/anaconda/install/windows/>
- **macOS**: <https://docs.anaconda.com/anaconda/install/mac-os/>
- **Linux**: <https://docs.anaconda.com/anaconda/install/linux/>
- **User guide**: <https://docs.anaconda.com/anaconda/user-guide/>

Once you have installed either Anaconda or Miniconda, confirm that it is properly installed by running `conda -V` on the command line to display the version. Note that on Windows, all `conda` commands need to be run in **Anaconda Prompt** (as opposed to **Command Prompt**).

To create a new `conda` environment for this book, called `book_env`, run the following:

```
(base) $ conda create --name book_env
```

Running `conda env list` will show all the `conda` environments on the system, which will now include `book_env`. The current active environment will have an asterisk (*) next to it—by default, `base` will be active until we activate another environment:

```
(base) $ conda env list
# conda environments:
#
base                  * /miniconda3
book_env               /miniconda3/envs/book_env
```

To activate the `book_env` environment, we run the following command:

```
(base) $ conda activate book_env
```

Note that after we activate the virtual environment, we can see `(book_env)` in front of our prompt on the command line; this lets us know we are in the environment:

```
(book_env) $
```

When we are finished using the environment, we deactivate it:

```
(book_env) $ conda deactivate
```

Any packages that are installed in the environment don't exist outside the environment. Note that we no longer have (book_env) in front of our prompt on the command line. You can read more about how to use conda to manage virtual environments at <https://www.freecodecamp.org/news/why-you-need-python-environments-and-how-to-manage-them-with-conda-85f155f4353c/>.

In the next section, we will install the Python packages required for following along with this book, so be sure to activate the virtual environment now.

Installing the required Python packages

We can do a lot with the Python standard library; however, we will often find the need to install and use an outside package to extend functionality. The `requirements.txt` file in the repository contains all the packages we need to install to work through this book. It will be in our current directory, but it can also be found at <https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/blob/master/requirements.txt>. This file can be used to install a bunch of packages at once with the `-r` flag in the call to `pip3 install` and has the advantage of being easy to share.

Before installing anything, be sure to activate the virtual environment that you created with either `venv` or `conda`. Be advised that if the environment is not activated before running the following command, the packages will be installed outside the environment:

```
(book_env) $ pip3 install -r requirements.txt
```

Tip

If you encounter any issues, report them at <https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/issues>.

Why pandas?

When it comes to data science in Python, the `pandas` library is pretty much ubiquitous. It is built on top of the NumPy library, which allows us to perform mathematical operations on arrays of single-type data efficiently. Pandas expands this to **dataframes**, which can be thought of as tables of data. We will get a more formal introduction to dataframes in *Chapter 2, Working with Pandas DataFrames*.

Aside from efficient operations, pandas also provides **wrappers** around the `matplotlib` plotting library, making it very easy to create a variety of plots without needing to write many lines of `matplotlib` code. We can always tweak our plots using `matplotlib`, but for quickly visualizing our data, we only need one line of code in pandas. We will explore this functionality in *Chapter 5, Visualizing Data with Pandas and Matplotlib*, and *Chapter 6, Plotting with Seaborn and Customization Techniques*.

Important note

Wrapper functions wrap around code from another library, obscuring some of its complexity and leaving us with a simpler interface for repeating that functionality. This is a core principle of **object-oriented programming (OOP)** called **abstraction**, which reduces complexity and the duplication of code. We will create our own wrapper functions throughout this book.

In addition to pandas, this book makes use of Jupyter Notebooks. While you are free to choose not to use them, it's important to be familiar with Jupyter Notebooks as they are very common in the data world. As an introduction, we will use a Jupyter Notebook to validate our setup in the next section.

Jupyter Notebooks

Each chapter of this book includes Jupyter Notebooks for following along. Jupyter Notebooks are omnipresent in Python data science because they make it very easy to write and test code in more of a discovery environment compared to writing a program. We can execute one block of code at a time and have the results printed to the notebook, directly beneath the code that generated it. In addition, we can use **Markdown** to add text explanations to our work. Jupyter Notebooks can be easily packaged up and shared; they can be pushed to GitHub (where they will be rendered), converted into HTML or PDF, sent to someone else, or presented.

Launching JupyterLab

JupyterLab is an IDE that allows us to create Jupyter Notebooks and Python scripts, interact with the terminal, create text documents, reference documentation, and much more from a clean web interface on our local machine. There are lots of keyboard shortcuts to master before really becoming a power user, but the interface is pretty intuitive. When we created our environment, we installed everything we needed to run JupyterLab, so let's take a quick tour of the IDE and make sure that our environment is set up properly. First, we activate our environment, and then we launch JupyterLab:

```
(book_env) $ jupyter lab
```

This will then launch a window in the default browser with JupyterLab. We will be greeted with the **Launcher** tab and the **File Browser** pane to the left:

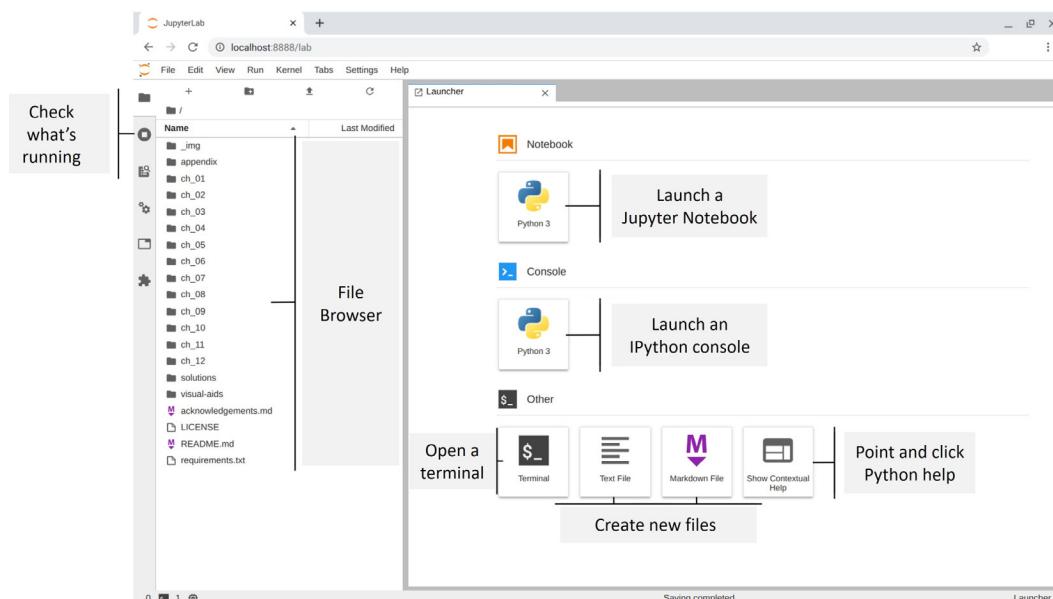


Figure 1.18 – Launching JupyterLab

Using the **File Browser** pane, double-click on the **ch_01** folder, which contains the Jupyter Notebook that we will use to validate our setup.

Validating the virtual environment

Open the `checking_your_setup.ipynb` notebook in the `ch_01` folder, as shown in the following screenshot:

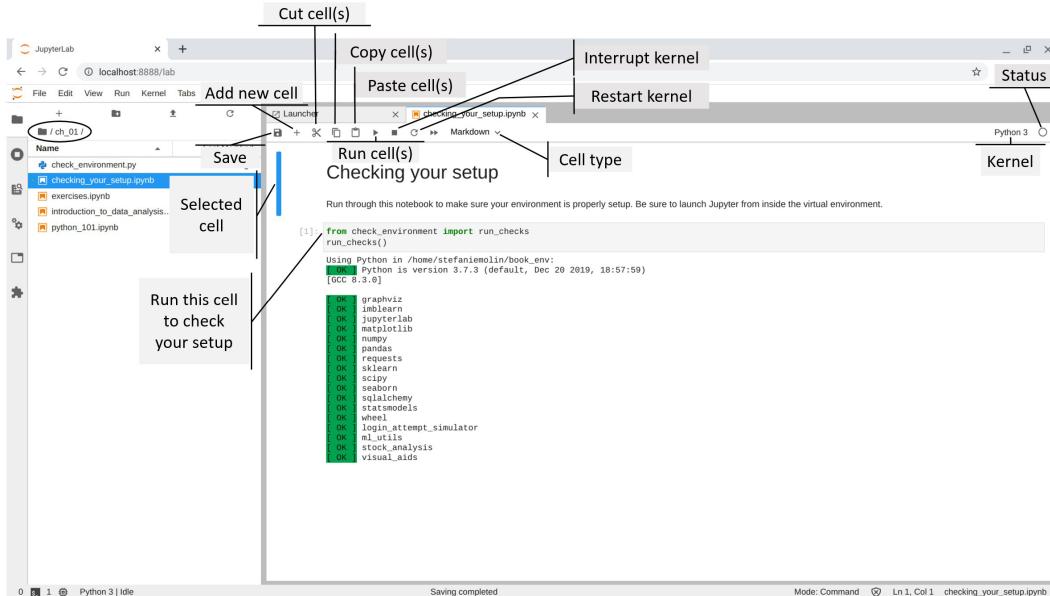


Figure 1.19 – Validating the virtual environment setup

Important note

The **kernel** is the process that runs and introspects our code in a Jupyter Notebook. Note that we aren't limited to running Python—we can run kernels for R, Julia, Scala, and other languages as well. By default, we will be running Python using the IPython kernel. We will learn a little more about IPython throughout the book.

Click on the code cell indicated in the previous screenshot and run it by clicking the play (►) button. If everything shows up in green, the environment is all set up. However, if this isn't the case, run the following command from the virtual environment to create a special kernel with the `book_env` virtual environment for use with Jupyter:

```
(book_env) $ ipython kernel install --user --name=book_env
```

This adds an additional option in the **Launcher** tab, and we can now switch to the `book_env` kernel from a Jupyter Notebook as well:

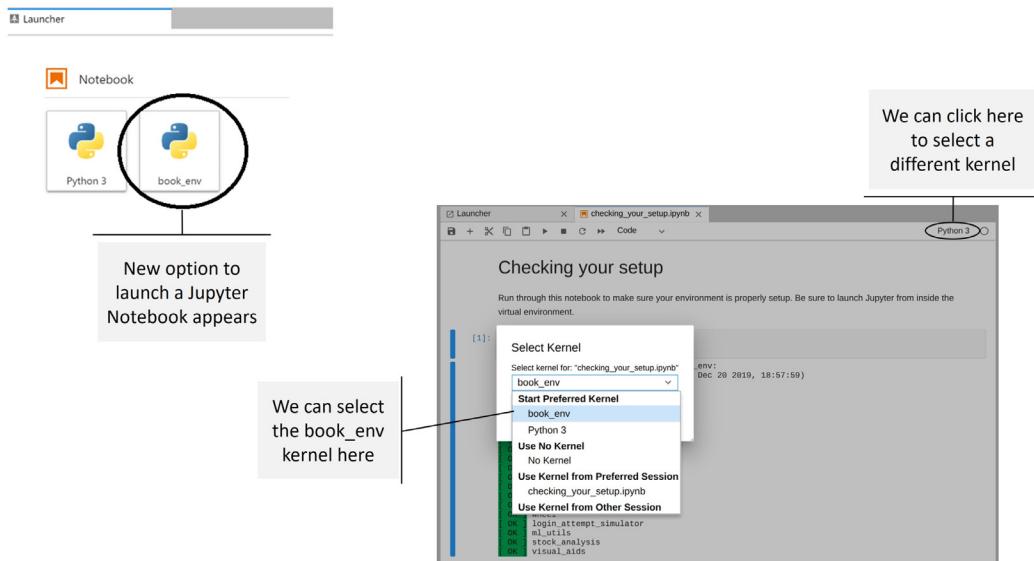


Figure 1.20 – Selecting a different kernel

It's important to note that Jupyter Notebooks will retain the values we assign to variables while the kernel is running, and the results in the `Out[#]` cells will be saved when we save the file. Closing the file doesn't stop the kernel and neither does closing the JupyterLab tab in the browser.

Closing JupyterLab

Closing the browser with JupyterLab in it doesn't stop JupyterLab or the kernels it is running (we also won't get the command-line interface back). To shut down JupyterLab entirely, we need to hit `Ctrl + C` (which is a keyboard interrupt signal that lets JupyterLab know we want to shut it down) a couple of times in the terminal until we get the prompt back:

```
...
[I 17:36:53.166 LabApp] Interrupted...
[I 17:36:53.168 LabApp] Shutting down 1 kernel
[I 17:36:53.770 LabApp] Kernel shutdown: a38e1[...]b44f
(book_env) $
```

For more information about Jupyter, including a tutorial, check out <http://jupyter.org/>. Learn more about JupyterLab at <https://jupyterlab.readthedocs.io/en/stable/>.

Summary

In this chapter, we learned about the main processes in conducting data analysis: data collection, data wrangling, EDA, and drawing conclusions. We followed that up with an overview of descriptive statistics and learned how to describe the central tendency and spread of our data; how to summarize it both numerically and visually using the 5-number summary, box plots, histograms, and kernel density estimates; how to scale our data; and how to quantify relationships between variables in our dataset.

We got an introduction to prediction and time series analysis. Then, we had a very brief overview of some core topics in inferential statistics that can be explored after mastering the contents of this book. Note that while all the examples in this chapter were of one or two variables, real-life data is often high-dimensional. *Chapter 10, Making Better Predictions – Optimizing Models*, will touch on some ways to address this. Lastly, we set up our virtual environment for this book and learned how to work with Jupyter Notebooks.

Now that we have built a strong foundation, we will start working with data in Python in the next chapter.

Exercises

Run through the `introduction_to_data_analysis.ipynb` notebook for a review of this chapter's content, review the `python_101.ipynb` notebook (if needed), and then complete the following exercises to practice working with JupyterLab and calculating summary statistics in Python:

1. Explore the JupyterLab interface and look at some of the shortcuts that are available. Don't worry about memorizing them for now (eventually, they will become second nature and save you a lot of time)—just get comfortable using Jupyter Notebooks.
2. Is all data normally distributed? Explain why or why not.
3. When would it make more sense to use the median instead of the mean for the measure of center?
4. Run the code in the first cell of the `exercises.ipynb` notebook. It will give you a list of 100 values to work with for the rest of the exercises in this chapter. Be sure to treat these values as a sample of the population.

5. Using the data from *exercise 4*, calculate the following statistics without importing anything from the `statistics` module in the standard library (<https://docs.python.org/3/library/statistics.html>), and then confirm your results match up to those that are obtained when using the `statistics` module (where possible):
 - a) Mean
 - b) Median
 - c) Mode (hint: check out the `Counter` class in the `collections` module of the standard library at <https://docs.python.org/3/library/collections.html#collections.Counter>)
 - d) Sample variance
 - e) Sample standard deviation
6. Using the data from *exercise 4*, calculate the following statistics using the functions in the `statistics` module where appropriate:
 - a) Range
 - b) Coefficient of variation
 - c) Interquartile range
 - d) Quartile coefficient of dispersion
7. Scale the data created in *exercise 4* using the following strategies:
 - a) Min-max scaling (normalizing)
 - b) Standardizing
8. Using the scaled data from *exercise 7*, calculate the following:
 - a) The covariance between the standardized and normalized data
 - b) The Pearson correlation coefficient between the standardized and normalized data (this is actually 1, but due to rounding along the way, the result will be slightly less)

Further reading

The following are some resources that you can use to become more familiar with Jupyter:

- *Jupyter Notebook Basics*: <https://nbviewer.jupyter.org/github/jupyter/notebook/blob/master/docs/source/examples/Notebook/Notebook%20Basics.ipynb>
- *JupyterLab introduction*: <https://blog.jupyter.org/jupyterlab-is-ready-for-users-5a6f039b8906>
- *Learning Markdown to make your Jupyter Notebooks presentation-ready*: <https://medium.com/ibm-data-science-experience/markdown-for-jupyter-notebooks-cheatsheet-386c05aeebed>
- *28 Jupyter Notebook Tips, Tricks, and Shortcuts*: <https://www.dataquest.io/blog/jupyter-notebook-tips-tricks-shortcuts/>

Some resources for learning more advanced concepts of statistics (that we won't cover here) and carefully applying them are as follows:

- *A Gentle Introduction to Normality Tests in Python*: <https://machinelearningmastery.com/a-gentle-introduction-to-normality-tests-in-python/>
- *How Hypothesis Tests Work: Confidence Intervals and Confidence Levels*: <https://statisticsbyjim.com/hypothesis-testing/hypothesis-tests-confidence-intervals-levels/>
- *Intro to Inferential Statistics (Making Predictions with Data) on Udacity*: <https://www.udacity.com/course/intro-to-inferential-statistics--ud201>
- *Lesson 4: Confidence Intervals (Penn State Elementary Statistics)*: <https://online.stat.psu.edu/stat200/lesson/4>
- *Seeing Theory: A visual introduction to probability and statistics*: <https://seeing-theory.brown.edu/index.html>
- *Statistics Done Wrong: The Woefully Complete Guide by Alex Reinhart*: <https://www.statisticsdonewrong.com/>
- *Survey Sampling Methods*: <https://stattrek.com/survey-research/sampling-methods.aspx>

2

Working with Pandas DataFrames

The time has come for us to begin our journey into the pandas universe. This chapter will get us comfortable working with some of the basic, yet powerful, operations we will be performing when conducting our data analyses with pandas.

We will begin with an introduction to the main **data structures** we will encounter when working with pandas. Data structures provide us with a format for organizing, managing, and storing data. Knowledge of pandas data structures will prove infinitely helpful when it comes to troubleshooting or looking up how to perform an operation on the data. Keep in mind that these data structures are different from the standard Python data structures for a reason: they were created for specific analysis tasks. We must remember that a given method may only work on a certain data structure, so we need to be able to identify the best structure for the problem we are looking to solve.

Next, we will bring our first dataset into Python. We will learn how to collect data from an API, create DataFrame objects from other data structures in Python, read in files, and interact with databases. Initially, you may wonder why we would ever need to create a DataFrame object from other Python data structures; however, if we ever want to test something quickly, create our own data, pull data from an API, or repurpose Python code from another project, then we will find this knowledge indispensable. Finally, we will master ways to inspect, describe, filter, and summarize our data.

The following topics will be covered in this chapter:

- Pandas data structures
- Creating DataFrame objects from files, API requests, SQL queries, and other Python objects
- Inspecting DataFrame objects and calculating summary statistics
- Grabbing subsets of the data via selection, slicing, indexing, and filtering
- Adding and removing data

Chapter materials

The files we will be working with in this chapter can be found in the GitHub repository at https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_02. We will be working with earthquake data from the **US Geological Survey (USGS)** by using the USGS API and CSV files, which can be found in the `data/` directory.

There are four CSV files and a SQLite database file, all of which will be used at different points throughout this chapter. The `earthquakes.csv` file contains data that's been pulled from the USGS API for September 18, 2018 through October 13, 2018. For our discussion of data structures, we will work with the `example_data.csv` file, which contains five rows and a subset of the columns from the `earthquakes.csv` file.

The `tsunamis.csv` file is a subset of the data in the `earthquakes.csv` file for all earthquakes that were accompanied by tsunamis during the aforementioned date range. The `quakes.db` file contains a SQLite database with a single table for the tsunamis data. We will use this to learn how to read from and write to a database with `pandas`. Lastly, the `parsed.csv` file will be used for the end-of-chapter exercises, and we will also walk through the creation of it during this chapter.

The accompanying code for this chapter has been divided into six Jupyter Notebooks, which are numbered in the order they are to be used. They contain the code snippets we will be running throughout this chapter, along with the full output of any command that has to be trimmed for this text. Each time we are to switch notebooks, the text will indicate to do so.

In the `1-pandas_data_structures.ipynb` notebook, we will start learning about the main pandas data structures. Afterward, we will discuss the various ways to create `DataFrame` objects in the `2-creating_dataframes.ipynb` notebook. Our discussion on this topic will continue in the `3-making_dataframes_from_api_requests.ipynb` notebook, where we will explore the USGS API to gather data for use with pandas. After learning about how we can collect our data, we will begin to learn how to conduct **exploratory data analysis (EDA)** in the `4-inspecting_dataframes.ipynb` notebook. Then, in the `5-subsetting_data.ipynb` notebook, we will discuss various ways to select and filter data. Finally, we will learn how to add and remove data in the `6-adding_and_removing_data.ipynb` notebook. Let's get started.

Pandas data structures

Python has several data structures already, such as tuples, lists, and dictionaries. Pandas provides two main structures to facilitate working with data: `Series` and `DataFrame`. The `Series` and `DataFrame` data structures each contain another pandas data structure, `Index`, that we must also be aware of. However, in order to understand these data structures, we need to first take a look at NumPy (<https://numpy.org/doc/stable/>), which provides the n-dimensional arrays that pandas builds upon.

The aforementioned data structures are implemented as Python **classes**; when we actually create one, they are referred to as **objects** or **instances**. This is an important distinction, since, as we will see, some actions can be performed using the object itself (a **method**), whereas others will require that we pass our object in as an argument to some **function**. Note that, in Python, class names are traditionally written in CapWords, while objects are written in `snake_case`. (More Python style guidelines can be found at <https://www.python.org/dev/peps/pep-0008/>.)

We use a `pandas` function to read a CSV file into an object of the `DataFrame` class, but we use methods on our `DataFrame` objects to perform actions on them, such as dropping columns or calculating summary statistics. With `pandas`, we will often want to access the **attributes** of the object we are working with. This won't generate an action as a method or function would; rather, we will be given information about our `pandas` object, such as dimensions, column names, data types, and whether it is empty.

Important note

For the remainder of this book, we will refer to `DataFrame` objects as `dataframes`, `Series` objects as `series`, and `Index` objects as `index/indices`, unless we are referring to the class itself.

For this section, we will work in the `1-pandas_data_structures.ipynb` notebook. To begin, we will import `numpy` and use it to read the contents of the `example_data.csv` file into a `numpy.array` object. The data comes from the USGS API for earthquakes (source: <https://earthquake.usgs.gov/fdsnws/event/1/>). Note that this is the only time we will use NumPy to read in a file and that this is being done for illustrative purposes only; the important part is to look at the way the data is represented with NumPy:

```
>>> import numpy as np

>>> data = np.genfromtxt(
...     'data/example_data.csv', delimiter=';',
...     names=True, dtype=None, encoding='UTF'
... )
>>> data
array([(u'2018-10-13 11:10:23.560',
        u'262km NW of Ozernovskiy, Russia',
        u'mww', 6.7, u'green', 1),
       (u'2018-10-13 04:34:15.580',
        u'25km E of Bitung, Indonesia', 'mww', 5.2, 'green', 0),
       (u'2018-10-13 00:13:46.220',
        u'42km WNW of Sola, Vanuatu',
        u'mww', 5.7, u'green', 0),
       (u'2018-10-12 21:09:49.240',
        u'13km E of Nueva Concepcion, Guatemala',
        u'mww', 5.7, u'green', 0),
       (u'2018-10-12 02:52:03.620',
        u'128km SE of Kimbe, Papua New Guinea',
        u'mww', 5.6, u'green', 1)],
      dtype=[('time', '<U23'), ('place', '<U37'),
             ('magType', '<U3'), ('mag', '<f8'),
             ('alert', '<U5'), ('tsunami', '<i8')])
```

We now have our data in a NumPy array. Using the `shape` and `dtype` attributes, we can gather information about the dimensions of the array and the data types it contains, respectively:

```
>>> data.shape
(5,)
>>> data.dtype
dtype([('time', '<U23'), ('place', '<U37'), ('magType', '<U3'),
       ('mag', '<f8'), ('alert', '<U5'), ('tsunami', '<i8')])
```

Each of the entries in the array is a row from the CSV file. NumPy arrays contain a single data type (unlike lists, which allow mixed types); this allows for fast, vectorized operations. When we read in the data, we got an array of `numpy.void` objects, which are used to store flexible types. This is because NumPy had to store several different data types per row: four strings, a float, and an integer. Unfortunately, this means that we can't take advantage of the performance improvements NumPy provides for single data type objects.

Say we want to find the maximum magnitude—we can use a **list comprehension** (<https://www.python.org/dev/peps/pep-0202/>) to select the third index of each row, which is represented as a `numpy.void` object. This makes a list, meaning that we can take the maximum using the `max()` function. We can use the `%%timeit` **magic command** from IPython (a special command preceded by %) to see how long this implementation takes (times will vary):

```
>>> %%timeit
>>> max([row[3] for row in data])
9.74 µs ± 177 ns per loop
(mean ± std. dev. of 7 runs, 100000 loops each)
```

Note that we should use a list comprehension whenever we would write a `for` loop with just a single line under it or want to run an operation against the members of some initial list. This is a rather simple list comprehension, but we can make them more complex with the addition of `if...else` statements. List comprehensions are an extremely powerful tool to have in our arsenal. More information can be found in the Python documentation at <https://docs.python.org/3/tutorial/datastructures.html#list-comprehensions>.

Tip

IPython (<https://ipython.readthedocs.io/en/stable/index.html>) provides an interactive shell for Python. Jupyter Notebooks are built on top of IPython. While knowledge of IPython is not required for this book, it can be helpful to be familiar with some of its functionality. IPython includes a tutorial in their documentation at <https://ipython.readthedocs.io/en/stable/interactive/>.

If we create a NumPy array for each column instead, this operation is much easier (and more efficient) to perform. To do so, we will use a **dictionary comprehension** (<https://www.python.org/dev/peps/pep-0274/>) to make a dictionary where the keys are the column names and the values are NumPy arrays of the data. Again, the important part here is how the data is now represented using NumPy:

```
>>> array_dict = {
...     col: np.array([row[i] for row in data])
...     for i, col in enumerate(data.dtype.names)
... }
>>> array_dict
{'time': array(['2018-10-13 11:10:23.560',
   '2018-10-13 04:34:15.580', '2018-10-13 00:13:46.220',
   '2018-10-12 21:09:49.240', '2018-10-12 02:52:03.620'],
  dtype='|<U23'),
 'place': array(['262km NW of Ozernovskiy, Russia',
    '25km E of Bitung, Indonesia',
    '42km WNW of Sola, Vanuatu',
    '13km E of Nueva Concepcion, Guatemala',
    '128km SE of Kimbe, Papua New Guinea'], dtype='|<U37'),
 'magType': array(['mww', 'mww', 'mww', 'mww', 'mww'],
  dtype='|<U3'),
 'mag': array([6.7, 5.2, 5.7, 5.7, 5.6]),
 'alert': array(['green', 'green', 'green', 'green', 'green'],
  dtype='|<U5'),
 'tsunami': array([1, 0, 0, 0, 1])}
```

Grabbing the maximum magnitude is now simply a matter of selecting the `mag` key and calling the `max()` method on the NumPy array. This is nearly twice as fast as the list comprehension implementation, when dealing with just five entries—imagine how much worse the first attempt will perform on large datasets:

```
>>> %%timeit
>>> array_dict['mag'].max()
5.22 µs ± 100 ns per loop
(mean ± std. dev. of 7 runs, 100000 loops each)
```

However, this representation has other issues. Say we wanted to grab all the information for the earthquake with the maximum magnitude; how would we go about that? We need to find the index of the maximum, and then for each of the keys in the dictionary, grab that index. The result is now a NumPy array of strings (our numeric values were converted), and we are now in the format that we saw earlier:

```
>>> np.array([
...     value[array_dict['mag']].argmax()
...     for key, value in array_dict.items()
... ])
array(['2018-10-13 11:10:23.560',
       '262km NW of Ozernovskiy, Russia',
       'mww', '6.7', 'green', '1'], dtype='|<U31')
```

Consider how we would go about sorting the data by magnitude from smallest to largest. In the first representation, we would have to sort the rows by examining the third index. With the second representation, we would have to determine the order of the indices from the mag column, and then sort all the other arrays with those same indices. Clearly, working with several NumPy arrays containing different data types at once is a bit cumbersome; however, pandas builds on top of NumPy arrays to make this easier. Let's start our exploration of pandas with an overview of the `Series` data structure.

Series

The `Series` class provides a data structure for arrays of a single type, just like the NumPy array. However, it comes with some additional functionality. This one-dimensional representation can be thought of as a column in a spreadsheet. We have a name for our column, and the data we hold in it is of the same type (since we are measuring the same variable):

```
>>> import pandas as pd

>>> place = pd.Series(array_dict['place'], name='place')
>>> place
0           262km NW of Ozernovskiy, Russia
1           25km E of Bitung, Indonesia
2           42km WNW of Sola, Vanuatu
3           13km E of Nueva Concepcion, Guatemala
4           128km SE of Kimbe, Papua New Guinea
Name: place, dtype: object
```

Note the numbers on the left of the result; these correspond to the row number in the original dataset (offset by 1 since, in Python, we start counting at 0). These row numbers form the index, which we will discuss in the following section. Next to the row numbers, we have the actual value of the row, which, in this example, is a string indicating where the earthquake occurred. Notice that we have `dtype: object` next to the name of the `Series` object; this is telling us that the data type of `place` is `object`. A string will be classified as `object` in pandas.

To access attributes of the `Series` object, we use attribute notation of the form `<object>.attribute_name`. The following are some common attributes we will access. Notice that `dtype` and `shape` are available, just as we saw with the NumPy array:

Attribute	Returns
<code>name</code>	The name of the <code>Series</code> object
<code>dtype</code>	The data type of the <code>Series</code> object
<code>shape</code>	Dimensions of the <code>Series</code> object in a tuple of the form <code>(number of rows,)</code>
<code>index</code>	The <code>Index</code> object that is part of the <code>Series</code> object
<code>values</code>	The data in the <code>Series</code> object

Figure 2.1 – Commonly used series attributes

Important note

For the most part, pandas objects use NumPy arrays for their internal data representations. However, for some data types, pandas builds upon NumPy to create its own arrays (<https://pandas.pydata.org/pandas-docs/stable/reference/arrays.html>). For this reason, depending on the data type, `values` can return either a `pandas.array` or a `numpy.array` object. Therefore, if we need to ensure we get a specific type back, it is recommended to use the `array` attribute or `to_numpy()` method, respectively, instead of `values`.

Be sure to bookmark the `pandas.Series` documentation (<https://pandas.pydata.org/pandas-docs/stable/reference/api/pandas.Series.html>) for reference later. It contains more information on how to create a `Series` object, the full list of attributes and methods that are available, as well as a link to the source code. With this high-level introduction to the `Series` class, we are ready to move on to the `Index` class.

Index

The addition of the `Index` class makes the `Series` class significantly more powerful than a NumPy array. The `Index` class gives us row labels, which enable selection by row. Depending on the type, we can provide a row number, a date, or even a string to select our row. It plays a key role in identifying entries in the data and is used for a multitude of operations in pandas, as we will see throughout this book. We can access the index through the `index` attribute:

```
>>> place_index = place.index
>>> place_index
RangeIndex(start=0, stop=5, step=1)
```

Note that this is a `RangeIndex` object. Its values start at 0 and end at 4. The step of 1 indicates that the indices are all 1 apart, meaning that we have all the integers in that range. The default index class is `RangeIndex`; however, we can change the index, as we will discuss in *Chapter 3, Data Wrangling with Pandas*. Often, we will either work with an `Index` object of row numbers or date(time)s.

As with `Series` objects, we can access the underlying data via the `values` attribute. Note that this `Index` object is built on top of a NumPy array:

```
>>> place_index.values
array([0, 1, 2, 3, 4], dtype=int64)
```

Some of the useful attributes of `Index` objects include the following:

Attribute	Returns
<code>name</code>	The name of the <code>Index</code> object
<code>dtype</code>	The data type of the <code>Index</code> object
<code>shape</code>	Dimensions of the <code>Index</code> object
<code>values</code>	The data in the <code>Index</code> object
<code>is_unique</code>	Check if the <code>Index</code> object has all unique values

Figure 2.2 – Commonly used index attributes

Both NumPy and pandas support arithmetic operations, which will be performed element-wise. NumPy will use the position in the array for this:

```
>>> np.array([1, 1, 1]) + np.array([-1, 0, 1])
array([0, 1, 2])
```

With pandas, this element-wise arithmetic is performed on matching index values. If we add a `Series` object with an index from 0 to 4 (stored in `x`) and another, `y`, from 1 to 5, we will only get results were the indices align (1 through 4). In *Chapter 3, Data Wrangling with Pandas*, we will discuss some ways to change and align the index so that we can perform these types of operations without losing data:

```
>>> numbers = np.linspace(0, 10, num=5) # [0, 2.5, 5, 7.5, 10]
>>> x = pd.Series(numbers) # index is [0, 1, 2, 3, 4]
>>> y = pd.Series(numbers, index=pd.Index([1, 2, 3, 4, 5]))
>>> x + y
0      NaN
1    2.5
2    7.5
3   12.5
4   17.5
5      NaN
dtype: float64
```

Now that we have had a primer on both the `Series` and `Index` classes, we are ready to learn about the `DataFrame` class. Note that more information on the `Index` class can be found in the respective documentation at <https://pandas.pydata.org/pandas-docs/stable/reference/api/pandas.Index.html>.

DataFrame

With the `Series` class, we essentially had columns of a spreadsheet, with the data all being of the same type. The `DataFrame` class builds upon the `Series` class and can have many columns, each with its own data type; we can think of it as representing the spreadsheet as a whole. We can turn either of the NumPy representations we built from the example data into a `DataFrame` object:

```
>>> df = pd.DataFrame(array_dict)
>>> df
```

This gives us a dataframe of six series. Note the column before the `time` column; this is the `Index` object for the rows. When creating a `DataFrame` object, pandas aligns all the series to the same index. In this case, it is just the row number, but we could easily use the `time` column for this, which would enable some additional pandas features, as we will see in *Chapter 4, Aggregating Pandas DataFrames*:

	time	place	magType	mag	alert	tsunami
0	2018-10-13 11:10:23.560	262km NW of Ozernovskiy, Russia	mww	6.7	green	1
1	2018-10-13 04:34:15.580	25km E of Bitung, Indonesia	mww	5.2	green	0
2	2018-10-13 00:13:46.220	42km WNW of Sola, Vanuatu	mww	5.7	green	0
3	2018-10-12 21:09:49.240	13km E of Nueva Concepcion, Guatemala	mww	5.7	green	0
4	2018-10-12 02:52:03.620	128km SE of Kimbe, Papua New Guinea	mww	5.6	green	1

Figure 2.3 – Our first dataframe

Our columns each have a single data type, but they don't all share the same data type:

```
>>> df.dtypes
time      object
place     object
magType   object
mag      float64
alert     object
tsunami   int64
dtype: object
```

The values of the dataframe look very similar to the initial NumPy representation we had:

```
>>> df.values
array([['2018-10-13 11:10:23.560',
       '262km NW of Ozernovskiy, Russia',
       'mww', 6.7, 'green', 1],
      ['2018-10-13 04:34:15.580',
       '25km E of Bitung, Indonesia', 'mww', 5.2, 'green', 0],
      ['2018-10-13 00:13:46.220',
       '42km WNW of Sola, Vanuatu', 'mww', 5.7, 'green', 0],
      ['2018-10-12 21:09:49.240',
       '13km E of Nueva Concepcion, Guatemala',
       'mww', 5.7, 'green', 0],
      ['2018-10-12 02:52:03.620',
       '128 km SE of Kimbe, Papua New Guinea', 'mww', 5.6, 'green', 1]],
      dtype=object)
```

We can access the column names via the `columns` attribute. Note that they are actually stored in an `Index` object as well:

```
>>> df.columns  
Index(['time', 'place', 'magType', 'mag', 'alert', 'tsunami'],  
      dtype='object')
```

The following are some commonly used dataframe attributes:

Attribute	Returns
<code>dtypes</code>	The data types of each column
<code>shape</code>	Dimensions of the <code>DataFrame</code> object in a tuple of the form (number of rows, number of columns)
<code>index</code>	The <code>Index</code> object along the rows of the <code>DataFrame</code> object
<code>columns</code>	The name of the columns (as an <code>Index</code> object)
<code>values</code>	The data in the <code>DataFrame</code> object
<code>empty</code>	Check if the <code>DataFrame</code> object is empty

Figure 2.4 – Commonly used dataframe attributes

Note that we can also perform arithmetic on dataframes. For example, we can add `df` to itself, which will sum the numeric columns and concatenate the string columns:

```
>>> df + df
```

Pandas will only perform the operation when both the index and column match. Here, pandas concatenated the string columns (`time`, `place`, `magType`, and `alert`) across dataframes. The numeric columns (`mag` and `tsunami`) were summed:

	time	place	magType	mag	alert	tsunami
0	2018-10-13 11:10:23.5602018-10-13 11:10:23.560	262km NW of Ozernovskiy, Russia262km NW of Oze...	mwwmww	13.4	greengreen	2
1	2018-10-13 04:34:15.5802018-10-13 04:34:15.580	25km E of Bitung, Indonesia25km E of Bitung, I...	mwwmww	10.4	greengreen	0
2	2018-10-13 00:13:46.2202018-10-13 00:13:46.220	42km WNW of Sola, Vanuatu42km WNW of Sola, Van...	mwwmww	11.4	greengreen	0
3	2018-10-12 21:09:49.2402018-10-12 21:09:49.240	13km E of Nueva Concepcion, Guatemala13km E of...	mwwmww	11.4	greengreen	0
4	2018-10-12 02:52:03.6202018-10-12 02:52:03.620	128km SE of Kimbe, Papua New Guinea128km SE of...	mwwmww	11.2	greengreen	2

Figure 2.5 – Adding dataframes

More information on `DataFrame` objects and all the operations that can be performed directly on them is available in the official documentation at <https://pandas.pydata.org/pandas-docs/stable/reference/api/pandas.DataFrame.html>; be sure to bookmark it for future reference. Now, we are ready to begin learning how to create `DataFrame` objects from a variety of sources.

Creating a pandas DataFrame

Now that we understand the data structures we will be working with, we can discuss the different ways we can create them. Before we dive into the code however, it's important to know how to get help right from Python. Should we ever find ourselves unsure of how to use something in Python, we can utilize the built-in `help()` function. We simply run `help()`, passing in the package, module, class, object, method, or function that we want to read the documentation on. We can, of course, look up the documentation online; however, in most cases, the **docstrings** (the documentation text written in the code) that are returned with `help()` will be equivalent to this since they are used to generate the documentation.

Assuming we first ran `import pandas as pd`, we can run `help(pd)` to display information about the `pandas` package; `help(pd.DataFrame)` for all the methods and attributes of `DataFrame` objects (note we can also pass in a `DataFrame` object instead); and `help(pd.read_csv)` to learn more about the `pandas` function for reading CSV files into Python and how to use it. We can also try using the `dir()` function and the `__dict__` attribute, which will give us a list or dictionary of what's available, respectively; these might not be as useful as the `help()` function, though.

Additionally, we can use `?` and `??` to get help, thanks to IPython, which is part of what makes Jupyter Notebooks so powerful. Unlike the `help()` function, we can use question marks by putting them after whatever we want to know more about, as if we were asking Python a question; for example, `pd.read_csv?` and `pd.read_csv??`. These three will yield slightly different outputs: `help()` will give us the docstring; `?` will give the docstring, plus some additional information, depending on what we are inquiring about; and `??` will give us even more information and, if possible, the source code behind it.

Let's now turn to the next notebook, `2-creating_dataframes.ipynb`, and import the packages we will need for the upcoming examples. We will be using `datetime` from the Python standard library, along with the third-party packages `numpy` and `pandas`:

```
>>> import datetime as dt  
>>> import numpy as np  
>>> import pandas as pd
```

Important note

We have **aliased** each of our imports. This allows us to use the `pandas` package by referring to it with the alias we assign to be `pd`, which is the most common way of importing it. In fact, we can only refer to it as `pd`, since that is what we imported into the namespace. Packages need to be imported before we can use them; installation puts the files we need on our computer, but, in the interest of memory, Python won't load every installed package when we start it up—just the ones we tell it to.

We are now ready to begin using `pandas`. First, we will learn how to create `pandas` objects from other Python objects. Then, we will learn how to do so with flat files, tables in a database, and responses from API requests.

From a Python object

Before we cover all the ways we can create a `DataFrame` object from a Python object, we should learn how to make a `Series` object. Remember that a `Series` object is essentially a column in a `DataFrame` object, so, once we know this, it should be easy to understand how to create a `DataFrame` object. Say that we wanted to create a series of five random numbers between 0 and 1. We could use NumPy to generate the random numbers as an array and create the series from that.

Tip

NumPy makes it very easy to generate numerical data. Aside from generating random numbers, we can use it to get evenly-spaced numbers in a certain range with the `np.linspace()` function; obtain a range of integers with the `np.arange()` function; sample from the standard normal with the `np.random.normal()` function; and easily create arrays of all zeros with the `np.zeros()` function and all ones with the `np.ones()` function.

We will be using NumPy throughout this book.

To ensure that the result is reproducible, we will set the seed here. The `seed` gives a starting point for the generation of pseudorandom numbers. No algorithms for random number generation are truly random—they are deterministic, so by setting this starting point, the numbers that are generated will be the same each time the code is run. This is good for testing things, but not for simulation (where we want randomness), which we will look at in *Chapter 8, Rule-Based Anomaly Detection*. In this fashion, we can make a `Series` object with any list-like structure (such as NumPy arrays):

```
>>> np.random.seed(0) # set a seed for reproducibility
>>> pd.Series(np.random.rand(5), name='random')
0    0.548814
1    0.715189
2    0.602763
3    0.544883
4    0.423655
Name: random, dtype: float64
```

Making a `DataFrame` object is an extension of making a `Series` object; it will be composed of one or more series, and each will be distinctly named. This should remind us of dictionary-like structures in Python: the keys are the column names, and the values are the contents of the columns. Note that if we want to turn a single `Series` object into a `DataFrame` object, we can use its `to_frame()` method.

Tip

In computer science, a **constructor** is a piece of code that initializes new instances of a class, preparing them for use. Python classes implement this with the `__init__()` method. When we run `pd.Series()`, Python calls `pd.Series.__init__()`, which contains instructions for instantiating a new `Series` object. We will learn more about the `__init__()` method in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*.

Since columns can all be different data types, let's get a little fancy with this example. We are going to create a `DataFrame` object containing three columns, with five observations each:

- `random`: Five random numbers between 0 and 1 as a NumPy array
- `text`: A list of five strings or `None`
- `truth`: A list of five random Booleans

We will also create a `DatetimeIndex` object with the `pd.date_range()` function. The index will contain five dates (`periods=5`), all one day apart (`freq='1D'`), ending with April 21, 2019 (`end`), and will be called `date`. Note that more information on the values the `pd.date_range()` function accepts for frequencies can be found at https://pandas.pydata.org/pandas-docs/stable/user_guide/timeseries.html#offset-aliases.

All we have to do is package the columns in a dictionary using the desired column names as the keys and pass this in when we call the `pd.DataFrame()` constructor. The index gets passed as the `index` argument:

```
>>> np.random.seed(0) # set seed so result is reproducible
>>> pd.DataFrame(
...     {
...         'random': np.random.rand(5),
...         'text': ['hot', 'warm', 'cool', 'cold', None],
...         'truth': [np.random.choice([True, False])
...                   for _ in range(5)]
...     },
...     index=pd.date_range(
...         end=dt.date(2019, 4, 21),
...         freq='1D', periods=5, name='date'
...     )
... )
```

Important note

By convention, we use `_` to hold variables in a loop that we don't care about. Here, we use `range()` as a counter, and its values are unimportant. More information on the roles `_` plays in Python can be found at <https://hackernoon.com/understanding-the-underscore-of-python-309d1a029edc>.

Having dates in the index makes it easy to select entries by date (or even in a date range), as we will see in *Chapter 3, Data Wrangling with Pandas*:

	random	text	truth
date			
2019-04-17	0.548814	hot	False
2019-04-18	0.715189	warm	True
2019-04-19	0.602763	cool	True
2019-04-20	0.544883	cold	False
2019-04-21	0.423655	None	True

Figure 2.6 – Creating a dataframe from a dictionary

In cases where the data isn't a dictionary, but rather a list of dictionaries, we can still use `pd.DataFrame()`. Data in this format is what we would expect when consuming from an API. Each entry in the list will be a dictionary, where the keys of the dictionary are the column names and the values of the dictionary are the values for that column at that index:

```
>>> pd.DataFrame([
...     {'mag': 5.2, 'place': 'California'},
...     {'mag': 1.2, 'place': 'Alaska'},
...     {'mag': 0.2, 'place': 'California'},
... ])
```

This gives us a dataframe of three rows (one for each entry in the list) with two columns (one for each key in the dictionaries):

	mag	place
0	5.2	California
1	1.2	Alaska
2	0.2	California

Figure 2.7 – Creating a dataframe from a list of dictionaries

In fact, `pd.DataFrame()` also works for lists of tuples. Note that we can also pass in the column names as a list through the `columns` argument:

```
>>> list_of_tuples = [(n, n**2, n**3) for n in range(5)]
>>> list_of_tuples
[(0, 0, 0), (1, 1, 1), (2, 4, 8), (3, 9, 27), (4, 16, 64)]

>>> pd.DataFrame(
...     list_of_tuples,
...     columns=['n', 'n_squared', 'n_cubed']
... )
```

Each tuple is treated like a record and becomes a row in the dataframe:

	n	n_squared	n_cubed
0	0	0	0
1	1	1	1
2	2	4	8
3	3	9	27
4	4	16	64

Figure 2.8 – Creating a dataframe from a list of tuples

We also have the option of using `pd.DataFrame()` with NumPy arrays:

```
>>> pd.DataFrame(  
...     np.array([  
...         [0, 0, 0],  
...         [1, 1, 1],  
...         [2, 4, 8],  
...         [3, 9, 27],  
...         [4, 16, 64]  
...     ]), columns=['n', 'n_squared', 'n_cubed'])  
... )
```

This will have the effect of stacking each entry in the array as rows in a dataframe, giving us a result that's identical to *Figure 2.8*.

From a file

The data we want to analyze will most often come from outside Python. In many cases, we may obtain a **data dump** from a database or website and bring it into Python to sift through it. A data dump gets its name from containing a large amount of data (possibly at a very granular level) and often not discriminating against any of it initially; for this reason, they can be unwieldy.

Often, these data dumps will come in the form of a text file (`.txt`) or a CSV file (`.csv`). Pandas provides many methods for reading in different types of files, so it is simply a matter of looking up the one that matches our file format. Our earthquake data is a CSV file; therefore, we use the `pd.read_csv()` function to read it in. However, we should always do an initial inspection of the file before attempting to read it in; this will inform us of whether we need to pass additional arguments, such as `sep` to specify the delimiter or `names` to provide the column names ourselves in the absence of a header row in the file.

Important note

Windows users: Depending on your setup, the commands in the next few code blocks may not work. The notebook contains alternatives if you encounter issues.

We can perform our due diligence directly in our Jupyter Notebook thanks to IPython, provided we prefix our commands with ! to indicate they are to be run as shell commands. First, we should check how big the file is, both in terms of lines and in terms of bytes. To check the number of lines, we use the wc utility (word count) with the -l flag to count the number of lines. We have 9,333 rows in the file:

```
>>> !wc -l data/earthquakes.csv
9333 data/earthquakes.csv
```

Now, let's check the file's size. For this task, we will use ls on the data directory. This will show us the list of files in that directory. We can add the -lh flag to get information about the files in a human-readable format. Finally, we send this output to the grep utility, which will help us isolate the files we want. This tells us that the earthquakes.csv file is 3.4 MB:

```
>>> !ls -lh data | grep earthquakes.csv
-rw-r--r-- 1 stefanie stefanie 3.4M ... earthquakes.csv
```

Note that IPython also lets us capture the result of the command in a Python variable, so if we aren't comfortable with pipes (|) or grep, we can do the following:

```
>>> files = !ls -lh data
>>> [file for file in files if 'earthquake' in file]
['-rw-r--r-- 1 stefanie stefanie 3.4M ... earthquakes.csv']
```

Now, let's take a look at the top few rows to see if the file comes with headers. We will use the head utility and specify the number of rows with the -n flag. This tells us that the first row contains the headers for the data and that the data is delimited with commas (just because the file has the .csv extension does not mean it is comma-delimited):

```
>>> !head -n 2 data/earthquakes.csv
alert,cdi,code,detail,dmin,felt,gap,ids,mag,magType,mmi,
net,nst,place,rms,sig,sources,status,time,title,tsunami,
type,types,tz,updated,url
,,37389218,https://earthquake.usgs.gov/ [...],0.008693,,85.0,",
ci37389218,",1.35,ml,,ci,26.0,"9km NE of Aguanga,
CA",0.19,28,",ci,",automatic,1539475168010,"M 1.4 -
9km NE of Aguanga, CA",0,earthquake,",geoserve,nearby-
cities,origin,phase-data,",,-480.0,1539475395144,
https://earthquake.usgs.gov/earthquakes/eventpage/ci37389218
```

Note that we should also check the bottom rows to make sure there is no extraneous data that we will need to ignore by using the `tail` utility. This file is fine, so the result won't be reproduced here; however, the notebook contains the result.

Lastly, we may be interested in seeing the column count in our data. While we could just count the fields in the first row of the result of `head`, we have the option of using the `awk` utility (for pattern scanning and processing) to count our columns. The `-F` flag allows us to specify the delimiter (a comma, in this case). Then, we specify what to do for each record in the file. We choose to print `NF`, which is a predefined variable whose value is the number of fields in the current record. Here, we say `exit` immediately after the print so that we print the number of fields in the first row of the file; then, we stop. This will look a little complicated, but this is by no means something we need to memorize:

```
>>> !awk -F',' '{print NF; exit}' data/earthquakes.csv  
26
```

Since we know that the first line of the file contains headers and that the file is comma-separated, we can also count the columns by using `head` to get the headers and Python to parse them:

```
>>> headers = !head -n 1 data/earthquakes.csv  
>>> len(headers[0].split(','))  
26
```

Important note

The ability to run shell commands directly from our Jupyter Notebook dramatically streamlines our workflow. However, if we don't have past experience with the command line, it may be complicated to learn these commands initially. IPython has some helpful information on running shell commands in their documentation at <https://ipython.readthedocs.io/en/stable/interactive/reference.html#system-shell-access>.

To summarize, we now know that the file is 3.4 MB and is comma-delimited with 26 columns and 9,333 rows, with the first one being the header. This means that we can use the `pd.read_csv()` function with the defaults:

```
>>> df = pd.read_csv('earthquakes.csv')
```

Note that we aren't limited to reading in data from files on our local machines; file paths can be URLs as well. As an example, let's read in the same CSV file from GitHub:

```
>>> df = pd.read_csv(
...     'https://github.com/stefmolin/'
...     'Hands-On-Data-Analysis-with-Pandas-2nd-edition'
...     '/blob/master/ch_02/data/earthquakes.csv?raw=True'
... )
```

Pandas is usually very good at figuring out which options to use based on the input data, so we often won't need to add arguments to this call; however, there are many options available should we need them, some of which include the following:

Parameter	Purpose
<code>sep</code>	Specifies the delimiter
<code>header</code>	Row number where the column names are located; the default option has <code>pandas infer</code> whether they are present
<code>names</code>	List of column names to use as the header
<code>index_col</code>	Column to use as the index
<code>usecols</code>	Specifies which columns to read in
<code>dtype</code>	Specifies data types for the columns
<code>converters</code>	Specifies functions for converting data in certain columns
<code>skiprows</code>	Rows to skip
<code>nrows</code>	Number of rows to read at a time (combine with <code>skiprows</code> to read a file bit by bit)
<code>parse_dates</code>	Automatically parse columns containing dates into datetime objects
<code>chunksize</code>	For reading the file in chunks
<code>compression</code>	For reading in compressed files without extracting beforehand
<code>encoding</code>	Specifies the file encoding

Figure 2.9 – Helpful parameters when reading data from a file

Throughout this book, we will be working with CSV files; however, note that we can use the `read_excel()` function to read in Excel files, the `read_json()` function for **JSON (JavaScript Object Notation)** files, and for other delimited files, such as tab (`\t`), we can use the `read_csv()` function with the `sep` argument equal to the delimiter.

It would be remiss if we didn't also learn how to save our dataframe to a file so that we can share it with others. To write our dataframe to a CSV file, we call its `to_csv()` method. We have to be careful here; if our dataframe's index is just row numbers, we probably don't want to write that to our file (it will have no meaning to the consumers of the data), but it is the default. We can write our data without the index by passing in `index=False`:

```
>>> df.to_csv('output.csv', index=False)
```

As with reading from files, `Series` and `DataFrame` objects have methods to write data to Excel (`to_excel()`) and JSON files (`to_json()`). Note that, while we use functions from `pandas` to read our data in, we must use methods to write our data; the reading functions create the `pandas` objects that we want to work with, but the writing methods are actions that we take using the `pandas` object.

Tip

The preceding file paths to read from and write to were **relative** to our **current directory**. The current directory is where we are running our code from. An **absolute** path will be the full path to the file. For example, if the file we want to work with has an absolute path of `/home/myuser/learning/hands_on_pandas/data.csv` and our current directory is `/home/myuser/learning/hands_on_pandas`, then we can simply use the relative path of `data.csv` as the file path.

Pandas provides us with capabilities to read and write from many other data sources, including databases, which we will discuss next; pickle files (containing serialized Python objects—see the *Further reading* section for more information); and HTML pages. Be sure to check out the following resource in the `pandas` documentation for the full list of capabilities: https://pandas.pydata.org/pandas-docs/stable/user_guide/io.html.

From a database

Pandas can interact with SQLite databases without the need for us to install any additional packages; however, the SQLAlchemy package needs to be installed in order to interact with other database flavors. Interaction with a SQLite database can be achieved by opening a connection to the database using the `sqlite3` module in the Python standard library and then using either the `pd.read_sql()` function to query the database or the `to_sql()` method on a `DataFrame` object to write it to the database.

Before we read from a database, let's write to one. We simply call `to_sql()` on our dataframe, telling it which table to write to, which database connection to use, and how to handle if the table already exists. There is already a SQLite database in the folder for this chapter in this book's GitHub repository: `data/quakes.db`. Note that, to create a new database, we can change '`data/quakes.db`' to the path for the new database file. Let's write the tsunami data from the `data/tsunamis.csv` file to a table in the database called `tsunamis`, replacing the table if it already exists:

```
>>> import sqlite3

>>> with sqlite3.connect('data/quakes.db') as connection:
...     pd.read_csv('data/tsunamis.csv').to_sql(
...         'tsunamis', connection, index=False,
...         if_exists='replace'
...     )
```

Querying the database is just as easy as writing to it. Note this will require knowledge of **Structured Query Language (SQL)**. While it's not required for this book, we will use some simple SQL statements to illustrate certain concepts. See the *Further reading* section for a resource on how `pandas` compares to SQL and *Chapter 4, Aggregating Pandas DataFrames*, for some examples of how `pandas` actions relate to SQL statements.

Let's query our database for the full `tsunamis` table. When we write a SQL query, we first state the columns that we want to select, which in our case is all of them, so we write "`SELECT *`". Next, we state the table to select the data from, which for us is `tsunamis`, so we add "`FROM tsunamis`". This is our full query now (of course, it can get much more complicated than this). To actually query the database, we use `pd.read_sql()`, passing in our query and the database connection:

```
>>> import sqlite3

>>> with sqlite3.connect('data/quakes.db') as connection:
...     tsunamis = \
...         pd.read_sql('SELECT * FROM tsunamis', connection)

>>> tsunamis.head()
```

We now have the tsunamis data in a dataframe:

	alert	type	title	place	magType	mag	time
0	None	earthquake	M 5.0 - 165km NNW of Flying Fish Cove, Christm...	165km NNW of Flying Fish Cove, Christmas Island	mww	5.0	1539459504090
1	green	earthquake	M 6.7 - 262km NW of Ozernovskiy, Russia	262km NW of Ozernovskiy, Russia	mww	6.7	1539429023560
2	green	earthquake	M 5.6 - 128km SE of Kimbe, Papua New Guinea	128km SE of Kimbe, Papua New Guinea	mww	5.6	1539312723620
3	green	earthquake	M 6.5 - 148km S of Severo-Kuril'sk, Russia	148km S of Severo-Kuril'sk, Russia	mww	6.5	1539213362130
4	green	earthquake	M 6.2 - 94km SW of Kokopo, Papua New Guinea	94km SW of Kokopo, Papua New Guinea	mww	6.2	1539208835130

Figure 2.10 – Reading data from a database

Important note

The connection object we created in both code blocks is an example of a **context manager**, which, when used with the `with` statement, automatically handles cleanup after the code in the block executes (closing the connection, in this case). This makes cleanup easy and makes sure we don't leave any loose ends. Be sure to check out `contextlib` from the standard library for utilities using the `with` statement and context managers. The documentation is at <https://docs.python.org/3/library/contextlib.html>.

From an API

We can now easily create `Series` and `DataFrame` objects from data we have in Python or from files we obtain, but how can we get data from online resources, such as APIs? There is no guarantee that each data source will give us data in the same format, so we must remain flexible in our approach and be comfortable examining the data source to find the appropriate import method. In this section, we will request some earthquake data from the USGS API and see how we can make a dataframe out of the result. In *Chapter 3, Data Wrangling with Pandas*, we will work with another API to gather weather data.

For this section, we will be working in the `3-making_dataframes_from_api_requests.ipynb` notebook, so we have to import the packages we need once again. As with the previous notebook, we need `pandas` and `datetime`, but we also need the `requests` package to make API requests:

```
>>> import datetime as dt  
>>> import pandas as pd  
>>> import requests
```

Next, we will make a GET request to the USGS API for a JSON payload (a dictionary-like response containing the data that's sent with a request or response) by specifying the format of `geojson`. We will ask for earthquake data for the last 30 days (we can use `dt.timedelta` to perform arithmetic on `datetime` objects). Note that we are using `yesterday` as the end of our date range, since the API won't have complete information for today yet:

```
>>> yesterday = dt.date.today() - dt.timedelta(days=1)  
>>> api = 'https://earthquake.usgs.gov/fdsnws/event/1/query'  
>>> payload = {  
...     'format': 'geojson',  
...     'starttime': yesterday - dt.timedelta(days=30),  
...     'endtime': yesterday  
... }  
>>> response = requests.get(api, params=payload)
```

Important note

GET is an HTTP method. This action tells the server we want to read some data. Different APIs may require that we use different methods to get the data; some will require a POST request, where we authenticate with the server. You can read more about API requests and HTTP methods at <https://nordicapis.com/ultimate-guide-to-all-9-standard-http-methods/>.

Before we try to create a dataframe out of this, we should make sure that our request was successful. We can do this by checking the `status_code` attribute of the `response` object. A listing of status codes and their meanings can be found at https://en.wikipedia.org/wiki/List_of_HTTP_status_codes. A 200 response will indicate that everything is OK:

```
>>> response.status_code  
200
```

Our request was successful, so let's see what the data we got looks like. We asked the API for a JSON payload, which is essentially a dictionary, so we can use dictionary methods on it to get more information about its structure. This is going to be a lot of data; hence, we don't want to print it to the screen just to inspect it. We need to isolate the JSON payload from the HTTP response (stored in the `response` variable), and then look at the keys to view the main sections of the resulting data:

```
>>> earthquake_json = response.json()
>>> earthquake_json.keys()
dict_keys(['type', 'metadata', 'features', 'bbox'])
```

We can inspect what kind of data we have as values for each of these keys; one of them will be the data we are after. The `metadata` portion tells us some information about our request. While this can certainly be useful, it isn't what we are after right now:

```
>>> earthquake_json['metadata']
{'generated': 1604267813000,
 'url': 'https://earthquake.usgs.gov/fdsnws/event/1/query?
format=json&starttime=2020-10-01&endtime=2020-10-31',
 'title': 'USGS Earthquakes',
 'status': 200,
 'api': '1.10.3',
 'count': 13706}
```

The `features` key looks promising; if this does indeed contain all our data, we should check what type it is so that we don't end up trying to print everything to the screen:

```
>>> type(earthquake_json['features'])
list
```

This key contains a list, so let's take a look at the first entry to see if this is the data we want. Note that the USGS data may be altered or added to for dates in the past as more information on the earthquakes comes to light, meaning that querying for the same date range may yield a different number of results later on. For this reason, the following is an example of what an entry looks like:

```
>>> earthquake_json['features'][0]
{'type': 'Feature',
 'properties': {'mag': 1,
 'place': '50 km ENE of Susitna North, Alaska',
 'time': 1604102395919, 'updated': 1604103325550, 'tz': None,
```

```
'url': 'https://earthquake.usgs.gov/earthquakes/eventpage/ak020dz5f85a',
'detail': 'https://earthquake.usgs.gov/fdsnws/event/1/query?eventid=ak020dz5f85a&format=json',
'felt': None, 'cdi': None, 'mmi': None, 'alert': None,
'status': 'reviewed', 'tsunami': 0, 'sig': 15, 'net': 'ak',
'code': '020dz5f85a', 'ids': ',ak020dz5f85a,', 'sources': ',ak,', 'types': ',origin,phase-data,', 'nst': None, 'dmin': None, 'rms': 1.36, 'gap': None, 'magType': 'ml', 'type': 'earthquake', 'title': 'M 1.0 - 50 km ENE of Susitna North, Alaska'}, 'geometry': {'type': 'Point', 'coordinates': [-148.9807, 62.3533, 5]}, 'id': 'ak020dz5f85a'}
```

This is definitely the data we are after, but do we need all of it? Upon closer inspection, we only really care about what is inside the `properties` dictionary. Now, we have a problem because we have a list of dictionaries where we only want a specific key from inside them. How can we pull this information out so that we can make our dataframe? We can use a list comprehension to isolate the `properties` section from each of the dictionaries in the `features` list:

```
>>> earthquake_properties_data = [
...     quake['properties']
...     for quake in earthquake_json['features']
... ]
```

Finally, we are ready to create our dataframe. Pandas knows how to handle data in this format already (a list of dictionaries), so all we have to do is pass in the data when we call `pd.DataFrame()`:

```
>>> df = pd.DataFrame(earthquake_properties_data)
```

Now that we know how to create dataframes from a variety of sources, we can start learning how to work with them.

Inspecting a DataFrame object

The first thing we should do when we read in our data is inspect it; we want to make sure that our dataframe isn't empty and that the rows look as we would expect. Our main goal is to verify that it was read in properly and that all the data is there; however, this initial inspection will also give us ideas with regard to where we should direct our data wrangling efforts. In this section, we will explore ways in which we can inspect our dataframes in the `4-inspecting_dataframes.ipynb` notebook.

Since this is a new notebook, we must once again handle our setup. This time, we need to import `pandas` and `numpy`, as well as read in the CSV file with the earthquake data:

```
>>> import numpy as np  
>>> import pandas as pd  
  
>>> df = pd.read_csv('data/earthquakes.csv')
```

Examining the data

First, we want to make sure that we actually have data in our dataframe. We can check the `empty` attribute to find out:

```
>>> df.empty  
False
```

So far, so good; we have data. Next, we should check how much data we read in; we want to know the number of observations (rows) and the number of variables (columns) we have. For this task, we use the `shape` attribute. Our data contains 9,332 observations of 26 variables, which matches our initial inspection of the file:

```
>>> df.shape  
(9332, 26)
```

Now, let's use the `columns` attribute to see the names of the columns in our dataset:

```
>>> df.columns  
Index(['alert', 'cdi', 'code', 'detail', 'dmin', 'felt', 'gap',  
       'ids', 'mag', 'magType', 'mmi', 'net', 'nst', 'place',  
       'rms', 'sig', 'sources', 'status', 'time', 'title',  
       'tsunami', 'type', 'types', 'tz', 'updated', 'url'],  
      dtype='object')
```

Important note

Having a list of columns doesn't necessarily mean that we know what all of them mean. Especially in cases where our data comes from the Internet, be sure to read up on what the columns mean before drawing any conclusions. Information on the fields in the `geojson` format, including what each field in the JSON payload means (along with some example values), can be found on the USGS website at <https://earthquake.usgs.gov/earthquakes/feed/v1.0/geojson.php>.

We know the dimensions of our data, but what does it actually look like? For this task, we can use the `head()` and `tail()` methods to look at the top and bottom rows, respectively. This will default to five rows, but we can change this by passing a different number to the method. Let's take a look at the first few rows:

```
>>> df.head()
```

The following are the first five rows we get using `head()`:

	alert	...	dmin	felt	...	mag	magType	...	place	...	time	title	tsunami	...	updated	url
0	NaN	...	0.008693	NaN	...	1.35	ml	...	9km NE of Aguanga, CA	...	1539475168010	M 1.4 - 9km NE of Aguanga, CA	0	...	1539475395144	https...
1	NaN	...	0.020030	NaN	...	1.29	ml	...	9km NE of Aguanga, CA	...	1539475129610	M 1.3 - 9km NE of Aguanga, CA	0	...	1539475253925	https...
2	NaN	...	0.021370	28.0	...	3.42	ml	...	8km NE of Aguanga, CA	...	1539475062610	M 3.4 - 8km NE of Aguanga, CA	0	...	1539536756176	https...
3	NaN	...	0.026180	NaN	...	0.44	ml	...	9km NE of Aguanga, CA	...	1539474978070	M 0.4 - 9km NE of Aguanga, CA	0	...	1539475196167	https...
4	NaN	...	0.077990	NaN	...	2.16	md	...	10km NW of Avenal, CA	...	1539474716050	M 2.2 - 10km NW of Avenal, CA	0	...	1539477547926	https...

Figure 2.11 – Examining the top five rows of a dataframe

To get the last two rows, we use the `tail()` method and pass 2 as the number of rows:

```
>>> df.tail(2)
```

The following is the result:

	alert	...	dmin	felt	...	mag	magType	...	place	...	time	title	tsunami	...	updated	url
9330	NaN	...	0.01865	NaN	...	1.10	ml	...	9km NE of Aguanga, CA	...	1537229545350	M 1.1 - 9km NE of Aguanga, CA	0	...	1537230211640	https...
9331	NaN	...	0.01698	NaN	...	0.66	ml	...	9km NE of Aguanga, CA	...	1537228864470	M 0.7 - 9km NE of Aguanga, CA	0	...	1537305830770	https...

Figure 2.12 – Examining the bottom two rows of a dataframe

Tip

By default, when we print dataframes with many columns in a Jupyter Notebook, only a subset of them will be displayed. This is because pandas has a limit on the number of columns it will show. We can modify this behavior using `pd.set_option('display.max_columns', <new_value>)`. Consult the documentation at https://pandas.pydata.org/pandas-docs/stable/user_guide/options.html for additional information. The notebook also contains a few example commands.

We can use the `dtypes` attribute to see the data types of the columns, which makes it easy to see when columns are being stored as the wrong type. (Remember that strings will be stored as `object`.) Here, the `time` column is stored as an integer, which is something we will learn how to fix in *Chapter 3, Data Wrangling with Pandas*:

```
>>> df.dtypes
alert          object
...
mag           float64
magType       object
...
time          int64
title         object
tsunami      int64
...
tz            float64
updated      int64
url          object
dtype: object
```

Lastly, we can use the `info()` method to see how many non-null entries of each column we have and get information on our index. **Null** values are missing values, which, in pandas, will typically be represented as `None` for objects and `NaN` (**Not a Number**) for non-numeric values in a `float` or `integer` column:

```
>>> df.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 9332 entries, 0 to 9331
Data columns (total 26 columns):
 #   Column    Non-Null Count  Dtype  
---  --  
 0   alert      59 non-null    object 
  ...
 8   mag        9331 non-null  float64
 9   magType   9331 non-null  object 
  ...
 18  time       9332 non-null  int64  
 19  title      9332 non-null  object 
 20  tsunami    9332 non-null  int64  
  ...
 23  tz         9331 non-null  float64
 24  updated    9332 non-null  int64  
 25  url        9332 non-null  object 
dtypes: float64(9), int64(4), object(13)
memory usage: 1.9+ MB
```

After this initial inspection, we know a lot about the structure of our data and can now begin to try and make sense of it.

Describing and summarizing the data

So far, we've examined the structure of the `DataFrame` object we created from the earthquake data, but we don't know anything about the data other than what a couple of rows look like. The next step is to calculate summary statistics, which will help us get to know our data better. Pandas provides several methods for easily doing so; one such method is `describe()`, which also works on `Series` objects if we are only interested in a particular column. Let's get a summary of the numeric columns in our data:

```
>>> df.describe()
```

This gives us the 5-number summary, along with the count, mean, and standard deviation of the numeric columns:

	cdi	dmin	felt	gap	mag	...	sig	time	tsunami	tz	updated
count	329.000000	6139.000000	329.000000	6164.000000	9331.000000	...	9332.000000	9.332000e+03	9332.000000	9331.000000	9.332000e+03
mean	2.754711	0.544925	12.310030	121.506588	1.497345	...	56.899914	1.538284e+12	0.006537	-451.990140	1.538537e+12
std	1.010637	2.214305	48.954944	72.962363	1.203347	...	91.872163	6.080306e+08	0.080589	231.752571	6.564135e+08
min	0.000000	0.000648	0.000000	12.000000	-1.260000	...	0.000000	1.537229e+12	0.000000	-720.000000	1.537230e+12
25%	2.000000	0.020425	1.000000	66.142500	0.720000	...	8.000000	1.537793e+12	0.000000	-540.000000	1.537996e+12
50%	2.700000	0.059050	2.000000	105.000000	1.300000	...	26.000000	1.538245e+12	0.000000	-480.000000	1.538621e+12
75%	3.300000	0.177250	5.000000	159.000000	1.900000	...	56.000000	1.538766e+12	0.000000	-480.000000	1.539110e+12
max	8.400000	53.737000	580.000000	355.910000	7.500000	...	2015.000000	1.539475e+12	1.000000	720.000000	1.539537e+12

Figure 2.13 – Calculating summary statistics

Tip

If we want different percentiles, we can pass them in with the `percentiles` argument. For example, if we wanted only the 5th and 95th percentiles, we would run `df.describe(percentiles=[0.05, 0.95])`. Note we will still get the 50th percentile back because that is the median.

By default, `describe()` won't give us any information about the columns of type `object`, but we can either provide `include='all'` as an argument or run it separately for the data of type `np.object`:

```
>>> df.describe(include=np.object)
```

When describing non-numeric data, we still get the count of non-null occurrences (`count`); however, instead of the other summary statistics, we get the number of unique values (`unique`), the mode (`top`), and the number of times the mode was observed (`freq`):

	alert	code	detail	ids	magType	net	place	sources	status	title	type	types	url
count	59	9332	9332	9332	9331	9332	9332	9332	9332	9332	9332	9332	9332
unique	2	9332	9332	9332	10	14	5433	52	2	7807	5	42	9332
top	green	70628507	https://ear...	pr201827...	ml	ak	10km NE of Aguanga, CA	,ak,	reviewed	M 0.4 - 10km NE of Aguanga, CA	earthquake	,geoserve, origin, phase- data,	https://ear...
freq	58	1	1	1	6803	3166	306	2981	7797	55	9081	5301	1

Figure 2.14 – Summary statistics for categorical columns

Important note

The `describe()` method only gives us summary statistics for non-null values. This means that, if we had 100 rows and half of our data was null, then the average would be calculated as the sum of the 50 non-null rows divided by 50.

It is easy to get a snapshot of our data using the `describe()` method, but sometimes, we just want a particular statistic, either for a specific column or for all the columns. Pandas makes this a cinch as well. The following table includes methods that will work for both `Series` and `DataFrame` objects:

Method	Description	Data types
<code>count()</code>	The number of non-null observations	Any
<code>nunique()</code>	The number of unique values	Any
<code>sum()</code>	The total of the values	Numerical or Boolean
<code>mean()</code>	The average of the values	Numerical or Boolean
<code>median()</code>	The median of the values	Numerical
<code>min()</code>	The minimum of the values	Numerical
<code>idxmin()</code>	The index where the minimum values occurs	Numerical
<code>max()</code>	The maximum of the values	Numerical
<code>idxmax()</code>	The index where the maximum value occurs	Numerical
<code>abs()</code>	The absolute values of the data	Numerical
<code>std()</code>	The standard deviation	Numerical
<code>var()</code>	The variance	Numerical
<code>cov()</code>	The covariance between two <code>Series</code> , or a covariance matrix for all column combinations in a <code>DataFrame</code>	Numerical
<code>corr()</code>	The correlation between two <code>Series</code> , or a correlation matrix for all column combinations in a <code>DataFrame</code>	Numerical
<code>quantile()</code>	Calculates a specific quantile	Numerical
<code>cumsum()</code>	The cumulative sum	Numerical or Boolean
<code>cummin()</code>	The cumulative minimum	Numerical
<code>cummax()</code>	The cumulative maximum	Numerical

Figure 2.15 – Helpful calculation methods for series and dataframes

Tip

Python makes it easy to count how many times something is True. Under the hood, True evaluates to 1 and False evaluates to 0. Therefore, we can run the sum() method on a series of Booleans and get the count of True outputs.

With Series objects, we have some additional methods for describing our data:

- unique(): Returns the distinct values of the column.
- value_counts(): Returns a frequency table of the number of times each unique value in a given column appears, or, alternatively, the percentage of times each unique value appears when passed normalize=True.
- mode(): Returns the most common value of the column.

Consulting the USGS API documentation for the alert field (which can be found at <https://earthquake.usgs.gov/data/comcat/data-eventterms.php#alert>) tells us that it can be 'green', 'yellow', 'orange', or 'red' (when populated), and that it is the alert level from the **Prompt Assessment of Global Earthquakes for Response (PAGER)** earthquake impact scale. According to the USGS (<https://earthquake.usgs.gov/data/pager/>), "*the PAGER system provides fatality and economic loss impact estimates following significant earthquakes worldwide.*" From our initial inspection of the data, we know that the alert column is a string of two unique values and that the most common value is 'green', with many null values. What is the other unique value, though?

```
>>> df.alert.unique()
array([nan, 'green', 'red'], dtype=object)
```

Now that we understand what this field means and the values we have in our data, we expect there to be far more 'green' than 'red'; we can check our intuition with a frequency table by using value_counts(). Notice that we only get counts for the non-null entries:

```
>>> df.alert.value_counts()
green      58
red        1
Name: alert, dtype: int64
```

Note that `Index` objects also have several methods that can help us describe and summarize our data:

Method	Description
<code>argmax()</code> / <code>argmin()</code>	Find the location of the maximum/minimum value in the index
<code>equals()</code>	Compare the index to another <code>Index</code> object for equality
<code>isin()</code>	Check if the index values are in a list of values and return an array of Booleans
<code>max()</code> / <code>min()</code>	Find the maximum/minimum value in the index
<code>nunique()</code>	Get the number of unique values in the index
<code>to_series()</code>	Create a <code>Series</code> object from the index
<code>unique()</code>	Find the unique values of the index
<code>value_counts()</code>	Create a frequency table for the unique values in the index

Figure 2.16 – Helpful methods for the index

When we used `unique()` and `value_counts()`, we got a preview of how to select subsets of our data. Now, let's go into more detail and cover selection, slicing, indexing, and filtering.

Grabbing subsets of the data

So far, we have learned how to work with and summarize the data as a whole; however, we will often be interested in performing operations and/or analyses on subsets of our data. There are many types of subsets we may look to isolate from our data, such as selecting only specific columns or rows as a whole or when a specific criterion is met. In order to obtain subsets of the data, we need to be familiar with selection, slicing, indexing, and filtering.

For this section, we will work in the `5 - subsetting_data.ipynb` notebook. Our setup is as follows:

```
>>> import pandas as pd  
  
>>> df = pd.read_csv('data/earthquakes.csv')
```

Selecting columns

In the previous section, we saw an example of column selection when we looked at the unique values in the `alert` column; we accessed the column as an attribute of the dataframe. Remember that a column is a `Series` object, so, for example, selecting the `mag` column in the earthquake data gives us the magnitudes of the earthquakes as a `Series` object:

```
>>> df.mag  
0      1.35  
1      1.29  
2      3.42  
3      0.44  
4      2.16  
     ...  
9327    0.62  
9328    1.00  
9329    2.40  
9330    1.10  
9331    0.66  
Name: mag, Length: 9332, dtype: float64
```

Pandas provides us with a few ways to select columns. An alternative to using attribute notation to select a column is to access it with a dictionary-like notation:

```
>>> df['mag']  
0      1.35  
1      1.29  
2      3.42  
3      0.44  
4      2.16  
     ...  
9327    0.62  
9328    1.00  
9329    2.40  
9330    1.10  
9331    0.66  
Name: mag, Length: 9332, dtype: float64
```

Tip

We can also select columns using the `get()` method. This has the benefits of not raising an error if the column doesn't exist and allowing us to provide a backup value—the default is `None`. For example, if we call `df.get('event', False)`, it will return `False` since we don't have an `event` column.

Note that we aren't limited to selecting one column at a time. By passing a list to the dictionary lookup, we can select many columns, giving us a `DataFrame` object that is a subset of our original dataframe:

```
>>> df[['mag', 'title']]
```

This gives us the full `mag` and `title` columns from the original dataframe:

	mag	title
0	1.35	M 1.4 - 9km NE of Aguanga, CA
1	1.29	M 1.3 - 9km NE of Aguanga, CA
2	3.42	M 3.4 - 8km NE of Aguanga, CA
3	0.44	M 0.4 - 9km NE of Aguanga, CA
4	2.16	M 2.2 - 10km NW of Avenal, CA
...
9327	0.62	M 0.6 - 9km ENE of Mammoth Lakes, CA
9328	1.00	M 1.0 - 3km W of Julian, CA
9329	2.40	M 2.4 - 35km NNE of Hatillo, Puerto Rico
9330	1.10	M 1.1 - 9km NE of Aguanga, CA
9331	0.66	M 0.7 - 9km NE of Aguanga, CA

Figure 2.17 – Selecting multiple columns of a dataframe

String methods are a very powerful way to select columns. For example, if we wanted to select all the columns that start with `mag`, along with the `title` and `time` columns, we would do the following:

```
>>> df[
...      ['title', 'time']
...      + [col for col in df.columns if col.startswith('mag')]
... ]
```

We get back a dataframe composed of the four columns that matched our criteria. Notice how the columns were returned in the order we requested, which is not the order they originally appeared in. This means that if we want to reorder our columns, all we have to do is select them in the order we want them to appear:

		title	time	mag	magType
0		M 1.4 - 9km NE of Aguanga, CA	1539475168010	1.35	ml
1		M 1.3 - 9km NE of Aguanga, CA	1539475129610	1.29	ml
2		M 3.4 - 8km NE of Aguanga, CA	1539475062610	3.42	ml
3		M 0.4 - 9km NE of Aguanga, CA	1539474978070	0.44	ml
4		M 2.2 - 10km NW of Avenal, CA	1539474716050	2.16	md

9327		M 0.6 - 9km ENE of Mammoth Lakes, CA	1537230228060	0.62	md
9328		M 1.0 - 3km W of Julian, CA	1537230135130	1.00	ml
9329		M 2.4 - 35km NNE of Hatillo, Puerto Rico	1537229908180	2.40	md
9330		M 1.1 - 9km NE of Aguanga, CA	1537229545350	1.10	ml
9331		M 0.7 - 9km NE of Aguanga, CA	1537228864470	0.66	ml

Figure 2.18 – Selecting columns based on names

Let's break this example down. We used a list comprehension to go through each of the columns in the dataframe and only keep the ones whose names started with mag:

```
>>> [col for col in df.columns if col.startswith('mag')]  
['mag', 'magType']
```

Then, we added this result to the other two columns we wanted to keep (title and time):

```
>>> ['title', 'time'] \  
... + [col for col in df.columns if col.startswith('mag')]  
['title', 'time', 'mag', 'magType']
```

Finally, we were able to use this list to run the actual column selection on the dataframe, resulting in the dataframe in *Figure 2.18*:

```
>>> df [
...     ['title', 'time']
...     + [col for col in df.columns if col.startswith('mag')]
... ]
```

Tip

A complete list of string methods can be found in the Python 3 documentation at <https://docs.python.org/3/library/stdtypes.html#string-methods>.

Slicing

When we want to extract certain rows (slices) from our dataframe, we use **slicing**. DataFrame slicing works similarly to slicing with other Python objects, such as lists and tuples, with the first index being inclusive and the last index being exclusive:

```
>>> df[100:103]
```

When specifying a slice of 100:103, we get back rows 100, 101, and 102:

	alert	...	dmin	felt	...	mag	magType	...	place	...	time	title	tsunami	...	updated	url
100	NaN	...	NaN	NaN	...	1.20	ml	...	25km NW of Ester, Alaska	...	1539435449480	M 1.2 - 25km NW of Ester, Alaska	0	...	1539443551010	https...
101	NaN	...	0.01355	NaN	...	0.59	md	...	8km ESE of Mammoth Lakes, CA	...	1539435391320	M 0.6 - 8km ESE of Mammoth Lakes, CA	0	...	1539439802162	https...
102	NaN	...	0.02987	NaN	...	1.33	ml	...	8km ENE of Aguanga, CA	...	1539435293090	M 1.3 - 8km ENE of Aguanga, CA	0	...	1539435940470	https...

Figure 2.19 – Slicing a dataframe to extract specific rows

We can combine our row and column selections by using what is known as **chaining**:

```
>>> df[['title', 'time']][100:103]
```

First, we selected the `title` and `time` columns for all the rows, and then we pulled out rows with indices 100, 101, and 102:

		<code>title</code>	<code>time</code>
100		M 1.2 - 25km NW of Ester, Alaska	1539435449480
101		M 0.6 - 8km ESE of Mammoth Lakes, CA	1539435391320
102		M 1.3 - 8km ENE of Aguanga, CA	1539435293090

Figure 2.20 – Selecting specific rows and columns with chaining

In the preceding example, we selected the columns and then sliced the rows, but the order doesn't matter:

```
>>> df[100:103][['title', 'time']].equals(  
...     df[['title', 'time']][100:103]  
... )  
True
```

Tip

Note that we can slice on whatever is in our index; however, it would be difficult to determine the string or date after the last one we want, so with pandas, slicing dates and strings is different from integer slicing and is inclusive of both endpoints. Date slicing will work as long as the strings we provide can be parsed into a `datetime` object. In *Chapter 3, Data Wrangling with Pandas*, we'll see some examples of this and also learn how to change what we use as the index, thus making this type of slicing possible.

If we decide to use chaining to update the values in our data, we will find pandas complaining that we aren't doing so correctly (even if it works). This is to warn us that setting data with a sequential selection may not give us the result we anticipate. (More information can be found at https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy.)

Let's trigger this warning to understand it better. We will try to update the entries in the `title` column for a few earthquakes so that they're in lowercase:

```
>>> df[110:113]['title'] = df[110:113]['title'].str.lower()  
/.../book_env/lib/python3.7/.../:1: SettingWithCopyWarning:  
A value is trying to be set on a copy of a slice from a  
DataFrame.  
Try using .loc[row_indexer,col_indexer] = value instead
```

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy

```
"""Entry point for launching an IPython kernel.
```

As indicated by the warning, to be an effective pandas user, it's not enough to know selection and slicing—we must also master **indexing**. Since this is just a warning, our values have been updated, but this may not always be the case:

```
>>> df[110:113]['title']
110          m 1.1 - 35km s of ester, alaska
111      m 1.9 - 93km wnw of arctic village, alaska
112      m 0.9 - 20km wsw of smith valley, nevada
Name: title, dtype: object
```

Now, let's discuss how to use indexing to set values properly.

Indexing

Pandas indexing operations provide us with a one-method way to select both the rows and the columns we want. We can use `loc []` and `iloc []` to subset our dataframe using label-based or integer-based lookups, respectively. A good way to remember the difference is to think of them as **location** versus **integer location**. For all indexing methods, we provide the row indexer first and then the column indexer, with a comma separating them:

```
df.loc[row_indexer, column_indexer]
```

Note that by using `loc []`, as indicated in the warning message, we no longer trigger any warnings from pandas for this operation. We also changed the end index from 113 to 112 because `loc []` is inclusive of endpoints:

```
>>> df.loc[110:112, 'title'] = \
...     df.loc[110:112, 'title'].str.lower()
>>> df.loc[110:112, 'title']
110          m 1.1 - 35km s of ester, alaska
111      m 1.9 - 93km wnw of arctic village, alaska
112      m 0.9 - 20km wsw of smith valley, nevada
Name: title, dtype: object
```

We can select all the rows (columns) if we use `:` as the row (column) indexer, just like with regular Python slicing. Let's grab all the rows of the `title` column with `loc []`:

```
>>> df.loc[:, 'title']
0                  M 1.4 - 9km NE of Aguanga, CA
1                  M 1.3 - 9km NE of Aguanga, CA
2                  M 3.4 - 8km NE of Aguanga, CA
3                  M 0.4 - 9km NE of Aguanga, CA
4                  M 2.2 - 10km NW of Avenal, CA
...
9327      M 0.6 - 9km ENE of Mammoth Lakes, CA
9328          M 1.0 - 3km W of Julian, CA
9329      M 2.4 - 35km NNE of Hatillo, Puerto Rico
9330          M 1.1 - 9km NE of Aguanga, CA
9331          M 0.7 - 9km NE of Aguanga, CA
Name: title, Length: 9332, dtype: object
```

We can select multiple rows and columns at the same time with `loc []`:

```
>>> df.loc[10:15, ['title', 'mag']]
```

This leaves us with rows 10 through 15 for the `title` and `mag` columns only:

		title	mag
10		M 0.5 - 10km NE of Aguanga, CA	0.50
11	M 2.8 - 53km SE of Punta Cana, Dominican Republic		2.77
12		M 0.5 - 9km NE of Aguanga, CA	0.50
13	M 4.5 - 120km SSW of Banda Aceh, Indonesia		4.50
14		M 2.1 - 14km NW of Parkfield, CA	2.13
15	M 2.0 - 156km WNW of Haines Junction, Canada		2.00

Figure 2.21 – Selecting specific rows and columns with indexing

As we have seen, when using `loc []`, our end index is inclusive. This isn't the case with `iloc []`:

```
>>> df.iloc[10:15, [19, 8]]
```

Observe how we had to provide a list of integers to select the same columns; these are the column numbers (starting from 0). Using `iloc []`, we lost the row at index 15; this is because the integer slicing that `iloc []` employs is exclusive of the end index, as with Python slicing syntax:

	title	mag
10	M 0.5 - 10km NE of Aguanga, CA	0.50
11	M 2.8 - 53km SE of Punta Cana, Dominican Republic	2.77
12	M 0.5 - 9km NE of Aguanga, CA	0.50
13	M 4.5 - 120km SSW of Banda Aceh, Indonesia	4.50
14	M 2.1 - 14km NW of Parkfield, CA	2.13

Figure 2.22 – Selecting specific rows and columns by position

We aren't limited to using the slicing syntax for the rows, though; columns work as well:

```
>>> df.iloc[10:15, 6:10]
```

By using slicing, we can easily grab adjacent rows and columns:

	gap	ids	mag	magType
10	57.0	,ci37389162,	0.50	ml
11	186.0	,pr2018286010,	2.77	md
12	76.0	,ci37389146,	0.50	ml
13	157.0	,us1000hbti,	4.50	mb
14	71.0	,nc73096921,	2.13	md

Figure 2.23 – Selecting ranges of adjacent rows and columns by position

When using `loc []`, this slicing can be done on the column names as well. This gives us many ways to achieve the same result:

```
>>> df.iloc[10:15, 6:10].equals(df.loc[10:14, 'gap':'magType'])  
True
```

To look up scalar values, we use `at []` and `iat []`, which are faster. Let's select the magnitude (the `mag` column) of the earthquake that was recorded in the row at index 10:

```
>>> df.at[10, 'mag']  
0.5
```

The magnitude column has a column index of 8; therefore, we can also look up the magnitude with `iat []`:

```
>>> df.iat[10, 8]  
0.5
```

So far, we have seen how to get subsets of our data using row/column names and ranges, but how do we only take the data that meets some criteria? For this, we need to learn how to filter our data.

Filtering

Pandas gives us a few options for filtering our data, including **Boolean masks** and some special methods. With Boolean masks, we test our data against some value and get a structure of the same shape back, except it is filled with `True/False` values; pandas can use this to select the appropriate rows/columns for us. There are endless possibilities for creating Boolean masks—all we need is some code that returns one Boolean value for each row. For example, we can see which entries in the `mag` column had a magnitude greater than two:

```
>>> df.mag > 2  
0      False  
1      False  
2      True  
3     False  
...  
9328    False  
9329    True  
9330    False  
9331    False  
Name: mag, Length: 9332, dtype: bool
```

While we can run this on the entire dataframe, it wouldn't be too useful with our earthquake data since we have columns of various data types. However, we can use this strategy to get the subset of the data where the magnitude of the earthquake was greater than or equal to 7.0:

```
>>> df[df.mag >= 7.0]
```

Our resulting dataframe has just two rows:

	alert	...	dmin	felt	...	mag	magType	...	place	...	time	title	tsunami	...	updated	url
837	green	...	1.763	3.0	...	7.0	mww	...	117km E of Kimbe, Papua New Guinea	...	1539204500290	M 7.0 - 117km E of Kimbe, Papua New Guinea	1	...	1539378744253	https...
5263	red	...	1.589	18.0	...	7.5	mww	...	78km N of Palu, Indonesia	...	1538128963480	M 7.5 - 78km N of Palu, Indonesia	1	...	1539123134531	https...

Figure 2.24 – Filtering with Boolean masks

We got back a lot of columns we didn't need, though. We could have chained a column selection to the end of the last code snippet; however, `loc []` can handle Boolean masks as well:

```
>>> df.loc[
...     df.mag >= 7.0,
...     ['alert', 'mag', 'magType', 'title', 'tsunami', 'type']
... ]
```

The following dataframe has been filtered so that it only contains relevant columns:

	alert	mag	magType	title	tsunami	type
837	green	7.0	mww	M 7.0 - 117km E of Kimbe, Papua New Guinea	1	earthquake
5263	red	7.5	mww	M 7.5 - 78km N of Palu, Indonesia	1	earthquake

Figure 2.25 – Indexing with Boolean masks

We aren't limited to just one criterion, either. Let's grab the earthquakes with a red alert and a tsunami. To combine masks, we need to surround each of our conditions with parentheses and use the **bitwise AND operator** (`&`) to require *both* to be true:

```
>>> df.loc[
...     (df.tsunami == 1) & (df.alert == 'red'),
...     ['alert', 'mag', 'magType', 'title', 'tsunami', 'type']
... ]
```

There was only a single earthquake in the data that met our criteria:

	alert	mag	magType		title	tsunami	type
5263	red	7.5	mww	M 7.5 - 78km N of Palu, Indonesia		1	earthquake

Figure 2.26 – Combining filters with AND

If, instead, we want *at least one* of our conditions to be true, we can use the **bitwise OR operator** (|):

```
>>> df.loc[
...     (df.tsunami == 1) | (df.alert == 'red'),
...     ['alert', 'mag', 'magType', 'title', 'tsunami', 'type']
... ]
```

Notice that this filter is much less restrictive since, while both conditions can be true, we only require that one of them is:

	alert	mag	magType		title	tsunami	type
36	NaN	5.0	mww	M 5.0 - 165km NNW of Flying Fish Cove, Christm...		1	earthquake
118	green	6.7	mww	M 6.7 - 262km NW of Ozernovskiy, Russia		1	earthquake
501	green	5.6	mww	M 5.6 - 128km SE of Kimbe, Papua New Guinea		1	earthquake
799	green	6.5	mww	M 6.5 - 148km S of Severo-Kuril'sk, Russia		1	earthquake
816	green	6.2	mww	M 6.2 - 94km SW of Kokopo, Papua New Guinea		1	earthquake
...
8561	NaN	5.4	mb	M 5.4 - 228km S of Taron, Papua New Guinea		1	earthquake
8624	NaN	5.1	mb	M 5.1 - 278km SE of Pondaguitan, Philippines		1	earthquake
9133	green	5.1	ml	M 5.1 - 64km SSW of Kaktovik, Alaska		1	earthquake
9175	NaN	5.2	mb	M 5.2 - 126km N of Dili, East Timor		1	earthquake
9304	NaN	5.1	mb	M 5.1 - 34km NW of Finschhafen, Papua New Guinea		1	earthquake

Figure 2.27 – Combining filters with OR

Important note

When creating Boolean masks, we must use bitwise operators (`&`, `|`, `~`) instead of logical operators (`and`, `or`, `not`). A good way to remember this is that we want a Boolean for each item in the series we are testing rather than a single Boolean. For example, with the earthquake data, if we want to select the rows where the magnitude is greater than 1.5, then we want one Boolean value for each row, indicating whether the row should be selected. In cases where we want a single value for the data, perhaps to summarize it, we can use `any()` / `all()` to condense a Boolean series into a single Boolean value that can be used with logical operators. We will work with the `any()` and `all()` methods in *Chapter 4, Aggregating Pandas DataFrames*.

In the previous two examples, our conditions involved equality; however, we are by no means limited to this. Let's select all the earthquakes in Alaska where we have a non-null value for the `alert` column:

```
>>> df.loc[
...     (df.place.str.contains('Alaska'))
...     & (df.alert.notnull()),
...     ['alert', 'mag', 'magType', 'title', 'tsunami', 'type']
... ]
```

All the earthquakes in Alaska that have a value for `alert` are green, and some were accompanied by tsunamis, with the highest magnitude being 5.1:

	alert	mag	magType		title	tsunami	type
1015	green	5.0	ml	M 5.0 - 61km SSW of Chignik Lake, Alaska	1	earthquake	
1273	green	4.0	ml	M 4.0 - 71km SW of Kaktovik, Alaska	1	earthquake	
1795	green	4.0	ml	M 4.0 - 60km WNW of Valdez, Alaska	1	earthquake	
2752	green	4.0	ml	M 4.0 - 67km SSW of Kaktovik, Alaska	1	earthquake	
3260	green	3.9	ml	M 3.9 - 44km N of North Nenana, Alaska	0	earthquake	
4101	green	4.2	ml	M 4.2 - 131km NNW of Arctic Village, Alaska	0	earthquake	
6897	green	3.8	ml	M 3.8 - 80km SSW of Kaktovik, Alaska	0	earthquake	
8524	green	3.8	ml	M 3.8 - 69km SSW of Kaktovik, Alaska	0	earthquake	
9133	green	5.1	ml	M 5.1 - 64km SSW of Kaktovik, Alaska	1	earthquake	

Figure 2.28 – Creating Boolean masks with non-numeric columns

Let's break down how we got this. `Series` objects have some string methods that can be accessed via the `str` attribute. Using this, we can create a Boolean mask of all the rows where the `place` column contained the word `Alaska`:

```
df.place.str.contains('Alaska')
```

To get all the rows where the `alert` column was not null, we used the `Series` object's `notnull()` method (this works for `DataFrame` objects as well) to create a Boolean mask of all the rows where the `alert` column was not null:

```
df.alert.notnull()
```

Tip

We can use the **bitwise negation operator** (`~`), also called **NOT**, to negate all the Boolean values, which makes all `True` values `False` and vice versa. So, `df.alert.notnull()` and `~df.alert.isnull()` are equivalent.

Then, like we did previously, we combine the two conditions with the `&` operator to complete our mask:

```
(df.place.str.contains('Alaska')) & (df.alert.notnull())
```

Note that we aren't limited to checking if each row contains text; we can use regular expressions as well. **Regular expressions** (often called *regex*, for short) are very powerful because they allow us to define a search pattern rather than the exact content we want to find. This means that we can do things such as find all the words or digits in a string without having to know what all the words or digits are beforehand (or go through one character at a time). To do so, we simply pass in a string preceded by an `r` character outside the quotes; this lets Python know it is a **raw string**, which means that we can include backslash (\) characters in the string without Python thinking we are trying to escape the character immediately following it (such as when we use `\n` to mean a new line character instead of the letter `n`). This makes it perfect for use with regular expressions. The `re` module in the Python standard library (<https://docs.python.org/3/library/re.html>) handles regular expression operations; however, pandas lets us use regular expressions directly.

Using a regular expression, let's select all the earthquakes in California that have magnitudes of at least 3.8. We need to select entries in the `place` column that end in `CA` or `California` because the data isn't consistent (we will look at how to fix this in the next section). The `$` character means *end* and `'CA$'` gives us entries that end in `CA`, so we can use `'CA|California$'` to get entries that end in either:

```
>>> df.loc[
...     (df.place.str.contains(r'CA|California$'))
...     & (df.mag > 3.8),
...     ['alert', 'mag', 'magType', 'title', 'tsunami', 'type']
... ]
```

There were only two earthquakes in California with magnitudes greater than 3.8 during the time period we are studying:

	alert	mag	magType		title	tsunami	type
1465	green	3.83	mw	M 3.8 - 109km WNW of Trinidad, CA		0	earthquake
2414	green	3.83	mw	M 3.8 - 5km SW of Tres Pinos, CA		1	earthquake

Figure 2.29 – Filtering with regular expressions

Tip

Regular expressions are extremely powerful, but unfortunately, also difficult to get right. It is often helpful to grab some sample lines for parsing and use a website to test them. Note that regular expressions come in many flavors, so be sure to select Python. This website supports Python flavor regular expressions, and also provides a nice cheat sheet on the side: <https://regex101.com/>.

What if we want to get all earthquakes with magnitudes between 6.5 and 7.5? We could use two Boolean masks—one to check for magnitudes greater than or equal to 6.5, and another to check for magnitudes less than or equal to 7.5—and then combine them with the `&` operator. Thankfully, `pandas` makes this type of mask much easier to create by providing us with the `between()` method:

```
>>> df.loc[
...     df.mag.between(6.5, 7.5),
...     ['alert', 'mag', 'magType', 'title', 'tsunami', 'type']
... ]
```

The result contains all the earthquakes with magnitudes in the range [6.5, 7.5]—it's inclusive of both ends by default, but we can pass in `inclusive=False` to change this:

	alert	mag	magType		title	tsunami	type
118	green	6.7	mww	M 6.7 - 262km NW of Ozernovskiy, Russia	1	earthquake	
799	green	6.5	mww	M 6.5 - 148km S of Severo-Kuril'sk, Russia	1	earthquake	
837	green	7.0	mww	M 7.0 - 117km E of Kimbe, Papua New Guinea	1	earthquake	
4363	green	6.7	mww	M 6.7 - 263km NNE of Ndoi Island, Fiji	1	earthquake	
5263	red	7.5	mww	M 7.5 - 78km N of Palu, Indonesia	1	earthquake	

Figure 2.30 – Filtering using a range of values

We can use the `isin()` method to create a Boolean mask for values that match one of a list of values. This means that we don't have to write one mask for each of the values that we could match and then use `|` to join them. Let's utilize this to filter on the `magType` column, which indicates the measurement technique that was used to quantify the earthquake's magnitude. We will take a look at earthquakes measured with either the `mw` or `mwb` magnitude type:

```
>>> df.loc[
...     df.magType.isin(['mw', 'mwb']),
...     ['alert', 'mag', 'magType', 'title', 'tsunami', 'type']
... ]
```

We have two earthquakes that were measured with the `mwb` magnitude type and four that were measured with the `mw` magnitude type:

	alert	mag	magType		title	tsunami	type
995	NaN	3.35	mw	M 3.4 - 9km WNW of Cobb, CA	0	earthquake	
1465	green	3.83	mw	M 3.8 - 109km WNW of Trinidad, CA	0	earthquake	
2414	green	3.83	mw	M 3.8 - 5km SW of Tres Pinos, CA	1	earthquake	
4988	green	4.41	mw	M 4.4 - 1km SE of Delta, B.C., MX	1	earthquake	
6307	green	5.80	mwb	M 5.8 - 297km NNE of Ndoi Island, Fiji	0	earthquake	
8257	green	5.70	mwb	M 5.7 - 175km SSE of Lambasa, Fiji	0	earthquake	

Figure 2.31 – Filtering using membership in a list

So far, we have been filtering on specific values, but suppose we wanted to see all the data for the lowest-magnitude and highest-magnitude earthquakes. Rather than finding the minimum and maximum of the `mag` column first and then creating a Boolean mask, we can ask `pandas` to give us the index where these values occur, and easily filter to grab the full rows. We can use `idxmin()` and `idxmax()` for the indices of the minimum and maximum, respectively. Let's grab the row numbers for the lowest-magnitude and highest-magnitude earthquakes:

```
>>> [df.mag.idxmin(), df.mag.idxmax()]
[2409, 5263]
```

We can use these indices to grab the rows themselves:

```
>>> df.loc[
...     [df.mag.idxmin(), df.mag.idxmax()],
...     ['alert', 'mag', 'magType', 'title', 'tsunami', 'type']
... ]
```

The minimum magnitude earthquake occurred in Alaska and the highest magnitude earthquake occurred in Indonesia, accompanied by a tsunami. We will discuss the earthquake in Indonesia in *Chapter 5, Visualizing Data with Pandas and Matplotlib*, and *Chapter 6, Plotting with Seaborn and Customization Techniques*:

	alert	mag	magType		title	tsunami	type
2409	NaN	-1.26	ml	M -1.3 - 41km ENE of Adak, Alaska		0	earthquake
5263	red	7.50	mww	M 7.5 - 78km N of Palu, Indonesia		1	earthquake

Figure 2.32 – Filtering to isolate the rows containing the minimum and maximum of a column

Important note

Be advised that the `filter()` method does not filter the data according to its values, as we did in this section; rather, it can be used to subset rows or columns based on their names. Examples with `DataFrame` and `Series` objects can be found in the notebook.

Adding and removing data

In the previous sections, we frequently selected a subset of the columns, but if columns/rows aren't useful to us, we should just get rid of them. We also frequently selected data based on the value of the `mag` column; however, if we had made a new column holding the Boolean values for later selection, we would have only needed to calculate the mask once. Very rarely will we get data where we neither want to add nor remove something.

Before we begin adding and removing data, it's important to understand that while most methods will return a new `DataFrame` object, some will be in-place and change our data. If we write a function where we pass in a dataframe and change it, it will change our original dataframe as well. Should we find ourselves in a situation where we don't want to change the original data, but rather want to return a new copy of the data that has been modified, we must be sure to copy our dataframe before making any changes:

```
df_to_modify = df.copy()
```

Important note

By default, `df.copy()` makes a **deep copy** of the dataframe, which allows us to make changes to either the copy or the original without repercussions. If we pass in `deep=False`, we can obtain a **shallow copy**—changes to the shallow copy affect the original and vice versa. We will almost always want the deep copy, since we can change it without affecting the original. More information can be found in the documentation at <https://pandas.pydata.org/pandas-docs/stable/reference/api/pandas.DataFrame.copy.html>.

Now, let's turn to the final notebook, `6-adding_and_removing_data.ipynb`, and get set up for the remainder of this chapter. We will once again be working with the earthquake data, but this time, we will only read in a subset of the columns:

```
>>> import pandas as pd

>>> df = pd.read_csv(
...     'data/earthquakes.csv',
...     usecols=[
...         'time', 'title', 'place', 'magType',
...         'mag', 'alert', 'tsunami'
...     ]
... )
```

Creating new data

Creating new columns can be achieved in the same fashion as variable assignment. For example, we can create a column to indicate the source of our data; since all our data came from the same source, we can take advantage of **broadcasting** to set every row of this column to the same value:

```
>>> df ['source'] = 'USGS API'
>>> df.head()
```

The new column is created to the right of the original columns, with a value of `USGS API` for every row:

	alert	mag	magType	place	time	title	tsunami	source
0	NaN	1.35	ml	9km NE of Aguanga, CA	1539475168010	M 1.4 - 9km NE of Aguanga, CA	0	USGS API
1	NaN	1.29	ml	9km NE of Aguanga, CA	1539475129610	M 1.3 - 9km NE of Aguanga, CA	0	USGS API
2	NaN	3.42	ml	8km NE of Aguanga, CA	1539475062610	M 3.4 - 8km NE of Aguanga, CA	0	USGS API
3	NaN	0.44	ml	9km NE of Aguanga, CA	1539474978070	M 0.4 - 9km NE of Aguanga, CA	0	USGS API
4	NaN	2.16	md	10km NW of Avenal, CA	1539474716050	M 2.2 - 10km NW of Avenal, CA	0	USGS API

Figure 2.33 – Adding a new column

Important note

We cannot create the column with attribute notation (`df . source`) because the dataframe doesn't have that attribute yet, so we must use dictionary notation (`df ['source']`).

We aren't limited to broadcasting one value to the entire column; we can have the column hold the result of Boolean logic or a mathematical equation. For example, if we had data on distance and time, we could create a speed column that is the result of dividing the distance column by the time column. With our earthquake data, let's create a column that tells us whether the earthquake's magnitude was negative:

```
>>> df ['mag_negative'] = df.mag < 0
>>> df.head()
```

Note that the new column has been added to the right:

	alert	mag	magType	place	time	title	tsunami	source	mag_negative
0	NaN	1.35	ml	9km NE of Aguanga, CA	1539475168010	M 1.4 - 9km NE of Aguanga, CA	0	USGS API	False
1	NaN	1.29	ml	9km NE of Aguanga, CA	1539475129610	M 1.3 - 9km NE of Aguanga, CA	0	USGS API	False
2	NaN	3.42	ml	8km NE of Aguanga, CA	1539475062610	M 3.4 - 8km NE of Aguanga, CA	0	USGS API	False
3	NaN	0.44	ml	9km NE of Aguanga, CA	1539474978070	M 0.4 - 9km NE of Aguanga, CA	0	USGS API	False
4	NaN	2.16	md	10km NW of Avenal, CA	1539474716050	M 2.2 - 10km NW of Avenal, CA	0	USGS API	False

Figure 2.34 – Storing a Boolean mask in a new column

In the previous section, we saw that the `place` column has some data consistency issues—we have multiple names for the same entity. In some cases, earthquakes occurring in California are marked as CA and as California in others. Needless to say, this is confusing and can easily cause issues for us if we don't carefully inspect our data beforehand. For example, by just selecting CA, we miss out on 124 earthquakes marked as California. This isn't the only place with an issue either (Nevada and NV are also both present). By using a regular expression to extract everything in the `place` column after the comma, we can see some of the issues firsthand:

```
>>> df.place.str.extract(r',\s*(.*$)')[0].sort_values().unique()
array(['Afghanistan', 'Alaska', 'Argentina', 'Arizona',
       'Arkansas', 'Australia', 'Azerbaijan', 'B.C., MX',
       'Barbuda', 'Bolivia', ..., 'CA', 'California', 'Canada',
       'Chile', ..., 'East Timor', 'Ecuador', 'Ecuador region',
       ..., 'Mexico', 'Missouri', 'Montana', 'NV', 'Nevada',
       ..., 'Yemen', nan], dtype=object)
```

If we want to treat countries and anything near them as a single entity, we have some additional work to do (see Ecuador and Ecuador region). In addition, our naive attempt at parsing the location by looking at the information after the comma appears to have failed; this is because, in some cases, we don't have a comma. We will need to change our approach to parsing.

This is an **entity recognition problem**, and it's not trivial to solve. With a relatively small list of unique values (which we can view with `df.place.unique()`), we can simply look through and infer how to properly match up these names. Then, we can use the `replace()` method to replace patterns in the `place` column as we see fit:

```
>>> df['parsed_place'] = df.place.str.replace(
...     r'.* of ', '', regex=True # remove <x> of <x>
... ).str.replace(
...     'the ', '' # remove "the "
... ).str.replace(
...     r'CA$', 'California', regex=True # fix California
... ).str.replace(
...     r'NV$', 'Nevada', regex=True # fix Nevada
... ).str.replace(
...     r'MX$', 'Mexico', regex=True # fix Mexico
... ).str.replace(
...     r'region$', '', regex=True # fix "region" endings
... ).str.replace(
...     'northern ', '' # remove "northern "
... ).str.replace(
...     'Fiji Islands', 'Fiji' # line up the Fiji places
... ).str.replace( # remove anything else extraneous from start
...     r'^.*, ', '', regex=True
... ).str.strip() # remove any extra spaces
```

Now, we can check the parsed places we are left with. Notice that there is arguably still more to fix here with South Georgia and South Sandwich Islands and South Sandwich Islands. We could address this with another call to `replace()`; however, this goes to show that entity recognition can be quite challenging:

```
>>> df.parsed_place.sort_values().unique()
array([..., 'California', 'Canada', 'Carlsberg Ridge', ...,
       'Dominican Republic', 'East Timor', 'Ecuador',
       'El Salvador', 'Fiji', 'Greece', ...,
       'Mexico', 'Mid-Indian Ridge', 'Missouri', 'Montana',
       'Nevada', 'New Caledonia', ...,
       'South Georgia and South Sandwich Islands',
       'South Sandwich Islands', ..., 'Yemen'], dtype=object)
```

Important note

In practice, entity recognition can be an extremely difficult problem, where we may look to employ **natural language processing (NLP)** algorithms to help us. While this is well beyond the scope of this book, more information can be found at <https://www.kdnuggets.com/2018/12/introduction-named-entity-recognition.html>.

Pandas also provides us with a way to make many new columns at once in one method call. With the `assign()` method, the arguments are the names of the columns we want to create (or overwrite), and the values are the data for the columns. Let's create two new columns; one will tell us if the earthquake happened in California, and the other will tell us if it happened in Alaska. Rather than just show the first five entries (which are all in California), we will use `sample()` to randomly select five rows:

```
>>> df.assign(
...     in_ca=df.parsed_place.str.endswith('California'),
...     in_alaska=df.parsed_place.str.endswith('Alaska')
... ).sample(5, random_state=0)
```

Note that `assign()` doesn't change our original dataframe; instead, it returns a new `DataFrame` object with these columns added. If we want to replace our original dataframe with this, we just use variable assignment to store the result of `assign()` in `df` (for example, `df = df.assign(...)`):

	alert	mag	magType	place	time	title	tsunami	source	mag_negative	parsed_place	in_ca	in_alaska
7207	NaN	4.80	mwr	73km SSW of Masachapa, Nicaragua	1537749595210	M 4.8 - 73km SSW of Masachapa, Nicaragua	0	USGS API	False	Nicaragua	False	False
4755	NaN	1.09	ml	28km NNW of Packwood, Washington	1538227540460	M 1.1 - 28km NNW of Packwood, Washington	0	USGS API	False	Washington	False	False
4595	NaN	1.80	ml	77km SSW of Kaktovik, Alaska	1538259609862	M 1.8 - 77km SSW of Kaktovik, Alaska	0	USGS API	False	Alaska	False	True
3566	NaN	1.50	ml	102km NW of Arctic Village, Alaska	1538464751822	M 1.5 - 102km NW of Arctic Village, Alaska	0	USGS API	False	Alaska	False	True
2182	NaN	0.90	ml	26km ENE of Pine Valley, CA	1538801713880	M 0.9 - 26km ENE of Pine Valley, CA	0	USGS API	False	California	True	False

Figure 2.35 – Creating multiple new columns at once

The `assign()` method also accepts **lambda functions** (anonymous functions usually defined in one line and for single use); `assign()` will pass the dataframe into the lambda function as `x`, and we can work from there. This makes it possible for us to use the columns we are creating in `assign()` to calculate others. For example, let's once again create the `in_ca` and `in_alaska` columns, but this time also create a new column, `neither`, which is True if both `in_ca` and `in_alaska` are False:

```
>>> df.assign(
...     in_ca=df.parsed_place == 'California',
...     in_alaska=df.parsed_place == 'Alaska',
...     neither=lambda x: ~x.in_ca & ~x.in_alaska
... ).sample(5, random_state=0)
```

Remember that `~` is the bitwise negation operator, so this allows us to create a column with the result of NOT `in_ca` AND NOT `in_alaska` per row:

	alert	mag	magType	place	time	title	tsunami	source	mag_negative	parsed_place	in_ca	in_alaska	neither
7207	NaN	4.80	mwr	73km SSW of Masachapa, Nicaragua	1537749595210	M 4.8 - 73km SSW of Masachapa, Nicaragua	0	USGS API	False	Nicaragua	False	False	True
4755	NaN	1.09	ml	28km NNW of Packwood, Washington	1538227540460	M 1.1 - 28km NNW of Packwood, Washington	0	USGS API	False	Washington	False	False	True
4595	NaN	1.80	ml	77km SSW of Kaktovik, Alaska	1538259609862	M 1.8 - 77km SSW of Kaktovik, Alaska	0	USGS API	False	Alaska	False	True	False
3566	NaN	1.50	ml	102km NW of Arctic Village, Alaska	1538464751822	M 1.5 - 102km NW of Arctic Village, Alaska	0	USGS API	False	Alaska	False	True	False
2182	NaN	0.90	ml	26km ENE of Pine Valley, CA	1538801713880	M 0.9 - 26km ENE of Pine Valley, CA	0	USGS API	False	California	True	False	False

Figure 2.36 – Creating multiple new columns at once with lambda functions

Tip

When working with `pandas`, it's crucial to get comfortable with `lambda` functions, as they can be used with much of the functionality available and will dramatically improve the quality and readability of the code. Throughout this book, we will see various places where `lambda` functions can be used.

Now that we have seen how to add new columns, let's take a look at adding new rows. Say we were working with two separate dataframes; one with earthquakes accompanied by tsunamis and the other with earthquakes without tsunamis:

```
>>> tsunami = df[df.tsunami == 1]
>>> no_tsunami = df[df.tsunami == 0]

>>> tsunami.shape, no_tsunami.shape
((61, 10), (9271, 10))
```

If we wanted to look at earthquakes as a whole, we would want to concatenate the dataframes into a single one. To append rows to the bottom of our dataframe, we can either use `pd.concat()` or the `append()` method of the dataframe itself. The `concat()` function allows us to specify the axis that the operation will be performed along—0 for appending rows to the bottom of the dataframe, and 1 for appending to the right of the last column with respect to the leftmost pandas object in the concatenation list. Let's use `pd.concat()` with the default `axis` of 0 for rows:

```
>>> pd.concat([tsunami, no_tsunami]).shape
(9332, 10) # 61 rows + 9271 rows
```

Note that the previous result is equivalent to running the `append()` method on the dataframe. This still returns a new `DataFrame` object, but it saves us from having to remember which axis is which, since `append()` is actually a wrapper around the `concat()` function:

```
>>> tsunami.append(no_tsunami).shape
(9332, 10) # 61 rows + 9271 rows
```

So far, we have been working with a subset of the columns from the CSV file, but suppose that we now want to work with some of the columns we ignored when we read in the data. Since we have added new columns in this notebook, we won't want to read in the file and perform those operations again. Instead, we will concatenate along the columns (`axis=1`) to add back what we are missing:

```
>>> additional_columns = pd.read_csv(
...     'data/earthquakes.csv', usecols=['tz', 'felt', 'ids']
... )
>>> pd.concat([df.head(2), additional_columns.head(2)], axis=1)
```

Since the indices of the dataframes align, the additional columns are placed to the right of our original columns:

	alert	mag	magType	place	time	title	tsunami	source	mag_negative	parsed_place	felt	ids	tz
0	NaN	1.35	ml	9km NE of Aguanga, CA	1539475168010	M 1.4 - 9km NE of Aguanga, CA	0	USGS API	False	California	NaN	,ci37389218,	-480.0
1	NaN	1.29	ml	9km NE of Aguanga, CA	1539475129610	M 1.3 - 9km NE of Aguanga, CA	0	USGS API	False	California	NaN	,ci37389202,	-480.0

Figure 2.37 – Concatenating columns with matching indices

The `concat()` function uses the index to determine how to concatenate the values. If they don't align, this will generate additional rows because pandas won't know how to align them. Say we forgot that our original dataframe had the row numbers as the index, and we read in the additional columns by setting the `time` column as the index:

```
>>> additional_columns = pd.read_csv(
...     'data/earthquakes.csv',
...     usecols=['tz', 'felt', 'ids', 'time'],
...     index_col='time'
... )
>>> pd.concat([df.head(2), additional_columns.head(2)], axis=1)
```

Despite the additional columns containing data for the first two rows, pandas creates a new row for them because the index doesn't match. In *Chapter 3, Data Wrangling with Pandas*, we will see how to reset the index and set the index, both of which could resolve this issue:

	alert	mag	magType	place	time	title	tsunami	source	mag_negative	parsed_place	felt	ids	tz
0	NaN	1.35	ml	9km NE of Aguanga, CA	1.539475e+12	M 1.4 - 9km NE of Aguanga, CA	0.0	USGS API	False	California	NaN	NaN	NaN
1	NaN	1.29	ml	9km NE of Aguanga, CA	1.539475e+12	M 1.3 - 9km NE of Aguanga, CA	0.0	USGS API	False	California	NaN	NaN	NaN
1539475129610	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	,ci37389202,	-480.0
1539475168010	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	,ci37389218,	-480.0

Figure 2.38 – Concatenating columns with mismatching indices

Important note

In *Chapter 4, Aggregating Pandas DataFrames*, we will discuss merging, which will also handle some of these issues when we're augmenting the columns in the dataframe. Often, we will use `concat()` or `append()` to add rows, but `merge()` or `join()` to add columns.

Say we want to concatenate the `tsunami` and `no_tsunami` dataframes, but the `no_tsunami` dataframe has an additional column (suppose we added a new column to it called `type`). The `join` parameter specifies how to handle any overlap in column names (when appending to the bottom) or in row names (when concatenating to the right). By default, this is `outer`, so we keep everything; however, if we use `inner`, we will only keep what they have in common:

```
>>> pd.concat(
...     [
...         tsunami.head(2),
...         no_tsunami.head(2).assign(type='earthquake')
...     ],
...     join='inner'
... )
```

Notice that the `type` column from the `no_tsunami` dataframe doesn't show up because it wasn't present in the `tsunami` dataframe. Take a look at the index, though; these were the row numbers from the original dataframe before we divided it into `tsunami` and `no_tsunami`:

	alert	mag	magType	place	time	title	tsunami	source	mag_negative	parsed_place
36	NaN	5.00	mww	165km NNW of Flying Fish Cove, Christmas Island	1539459504090	M 5.0 - 165km NNW of Flying Fish Cove, Christm...	1	USGS API	False	Christmas Island
118	green	6.70	mww	262km NW of Ozernovskiy, Russia	1539429023560	M 6.7 - 262km NW of Ozernovskiy, Russia	1	USGS API	False	Russia
0	NaN	1.35	ml	9km NE of Aguanga, CA	1539475168010	M 1.4 - 9km NE of Aguanga, CA	0	USGS API	False	California
1	NaN	1.29	ml	9km NE of Aguanga, CA	1539475129610	M 1.3 - 9km NE of Aguanga, CA	0	USGS API	False	California

Figure 2.39 – Appending rows and keeping only shared columns

If the index is not meaningful, we can also pass in `ignore_index` to get sequential values in the index:

```
>>> pd.concat(
...     [
...         tsunami.head(2),
...         no_tsunami.head(2).assign(type='earthquake')
...     ],
...     join='inner', ignore_index=True
... )
```

The index is now sequential, and the row numbers no longer match the original dataframe:

	alert	mag	magType	place	time	title	tsunami	source	mag_negative	parsed_place
0	NaN	5.00	mww	165km NNW of Flying Fish Cove, Christmas Island	1539459504090	M 5.0 - 165km NNW of Flying Fish Cove, Christm...	1	USGS API	False	Christmas Island
1	green	6.70	mww	262km NW of Ozernovskiy, Russia	1539429023560	M 6.7 - 262km NW of Ozernovskiy, Russia	1	USGS API	False	Russia
2	NaN	1.35	ml	9km NE of Aguanga, CA	1539475168010	M 1.4 - 9km NE of Aguanga, CA	0	USGS API	False	California
3	NaN	1.29	ml	9km NE of Aguanga, CA	1539475129610	M 1.3 - 9km NE of Aguanga, CA	0	USGS API	False	California

Figure 2.40 – Appending rows and resetting the index

Be sure to consult the pandas documentation for more information on the concat() function and other operations for combining data, which we will discuss in *Chapter 4, Aggregating Pandas DataFrames*: http://pandas.pydata.org/pandas-docs/stable/user_guide/merging.html#concatenating-objects.

Deleting unwanted data

After adding that data to our dataframe, we can see the need to delete unwanted data. We need a way to undo our mistakes and get rid of data that we aren't going to use. Like adding data, we can use dictionary syntax to delete unwanted columns, just as we would when removing keys from a dictionary. Both del df['<column_name>'] and df.pop('<column_name>') will work, provided that there is indeed a column with that name; otherwise, we will get a KeyError. The difference here is that while del removes it right away, pop() will return the column that we are removing. Remember that both of these operations will change our original dataframe, so use them with care.

Let's use dictionary notation to delete the source column. Notice that it no longer appears in the result of df.columns:

```
>>> del df['source']
>>> df.columns
Index(['alert', 'mag', 'magType', 'place', 'time', 'title',
       'tsunami', 'mag_negative', 'parsed_place'],
      dtype='object')
```

Note that if we aren't sure whether the column exists, we should put our column deletion code in a try...except block:

```
try:
    del df['source']
except KeyError:
    pass # handle the error here
```

Earlier, we created the `mag_negative` column for filtering our dataframe; however, we no longer want this column as part of our dataframe. We can use `pop()` to grab the series for the `mag_negative` column, which we can use as a Boolean mask later without having it in our dataframe:

```
>>> mag_negative = df.pop('mag_negative')
>>> df.columns
Index(['alert', 'mag', 'magType', 'place', 'time', 'title',
       'tsunami', 'parsed_place'],
      dtype='object')
```

We now have a Boolean mask in the `mag_negative` variable that used to be a column in `df`:

```
>>> mag_negative.value_counts()
False    8841
True     491
Name: mag_negative, dtype: int64
```

Since we used `pop()` to remove the `mag_negative` series rather than deleting it, we can still use it to filter our dataframe:

```
>>> df[mag_negative].head()
```

This leaves us with the earthquakes that had negative magnitudes. Since we also called `head()`, we get back the first five such earthquakes:

	alert	mag	magType	place	time	title	tsunami	parsed_place
39	NaN	-0.10	ml	6km NW of Lemmon Valley, Nevada	1539458844506	M -0.1 - 6km NW of Lemmon Valley, Nevada	0	Nevada
49	NaN	-0.10	ml	6km NW of Lemmon Valley, Nevada	1539455017464	M -0.1 - 6km NW of Lemmon Valley, Nevada	0	Nevada
135	NaN	-0.40	ml	10km SSE of Beatty, Nevada	1539422175717	M -0.4 - 10km SSE of Beatty, Nevada	0	Nevada
161	NaN	-0.02	md	20km SSE of Ronan, Montana	1539412475360	M -0.0 - 20km SSE of Ronan, Montana	0	Montana
198	NaN	-0.20	ml	60km N of Pahrump, Nevada	1539398340822	M -0.2 - 60km N of Pahrump, Nevada	0	Nevada

Figure 2.41 – Using a popped column as a Boolean mask

DataFrame objects have a `drop()` method for removing multiple rows or columns either in-place (overwriting the original dataframe without having to reassign it) or returning a new DataFrame object. To remove rows, we pass the list of indices. Let's remove the first two rows:

```
>>> df.drop([0, 1]).head(2)
```

Notice that the index starts at 2 because we dropped 0 and 1:

	alert	mag	magType	place	time	title	tsunami	parsed_place
2	NaN	3.42	ml	8km NE of Aguanga, CA	1539475062610	M 3.4 - 8km NE of Aguanga, CA	0	California
3	NaN	0.44	ml	9km NE of Aguanga, CA	1539474978070	M 0.4 - 9km NE of Aguanga, CA	0	California

Figure 2.42 – Dropping specific rows

By default, `drop()` assumes that we want to delete rows (`axis=0`). If we want to drop columns, we can either pass `axis=1` or specify our list of column names using the `columns` argument. Let's delete some more columns:

```
>>> cols_to_drop = [
...     col for col in df.columns
...     if col not in [
...         'alert', 'mag', 'title', 'time', 'tsunami'
...     ]
... ]
>>> df.drop(columns=cols_to_drop).head()
```

This drops all the columns that aren't in the list we wanted to keep:

	alert	mag	time	title	tsunami
0	NaN	1.35	1539475168010	M 1.4 - 9km NE of Aguanga, CA	0
1	NaN	1.29	1539475129610	M 1.3 - 9km NE of Aguanga, CA	0
2	NaN	3.42	1539475062610	M 3.4 - 8km NE of Aguanga, CA	0
3	NaN	0.44	1539474978070	M 0.4 - 9km NE of Aguanga, CA	0
4	NaN	2.16	1539474716050	M 2.2 - 10km NW of Avenal, CA	0

Figure 2.43 – Dropping specific columns

Whether we decide to pass `axis=1` to `drop()` or use the `columns` argument, our result will be equivalent:

```
>>> df.drop(columns=cols_to_drop).equals(  
...     df.drop(cols_to_drop, axis=1)  
... )  
True
```

By default, `drop()` will return a new `DataFrame` object; however, if we really want to remove the data from our original dataframe, we can pass in `inplace=True`, which will save us from having to reassign the result back to our dataframe. The result is the same as in *Figure 2.43*:

```
>>> df.drop(columns=cols_to_drop, inplace=True)  
>>> df.head()
```

Always be careful with in-place operations. In some cases, it may be possible to undo them; however, in others, it may require starting over from the beginning and recreating the dataframe.

Summary

In this chapter, we learned how to use `pandas` for the data collection portion of data analysis and to describe our data with statistics, which will be helpful when we get to the drawing conclusions phase. We learned the main data structures of the `pandas` library, along with some of the operations we can perform on them. Next, we learned how to create `DataFrame` objects from a variety of sources, including flat files and API requests. Using earthquake data, we discussed how to summarize our data and calculate statistics from it. Subsequently, we addressed how to take subsets of data via selection, slicing, indexing, and filtering. Finally, we practiced adding and removing both columns and rows from our dataframe.

These tasks also form the backbone of our `pandas` workflow and the foundation for the new topics we will cover in the next few chapters on data wrangling, aggregation, and data visualization. Be sure to complete the exercises provided in the next section before moving on.

Exercises

Using the `data/parsed.csv` file and the material from this chapter, complete the following exercises to practice your pandas skills:

1. Find the 95th percentile of earthquake magnitude in Japan using the `mb` magnitude type.
2. Find the percentage of earthquakes in Indonesia that were coupled with tsunamis.
3. Calculate summary statistics for earthquakes in Nevada.
4. Add a column indicating whether the earthquake happened in a country or US state that is on the Ring of Fire. Use Alaska, Antarctica (look for Antarctic), Bolivia, California, Canada, Chile, Costa Rica, Ecuador, Fiji, Guatemala, Indonesia, Japan, Kermadec Islands, Mexico (be careful not to select New Mexico), New Zealand, Peru, Philippines, Russia, Taiwan, Tonga, and Washington.
5. Calculate the number of earthquakes in the Ring of Fire locations and the number outside of them.
6. Find the tsunami count along the Ring of Fire.

Further reading

Those with an R and/or SQL background may find it helpful to see how the pandas syntax compares:

- *Comparison with R / R Libraries*: https://pandas.pydata.org/pandas-docs/stable/getting_started/comparison/comparison_with_r.html
- *Comparison with SQL*: https://pandas.pydata.org/pandas-docs/stable/comparison_with_sql.html
- *SQL Queries*: https://pandas.pydata.org/pandas-docs/stable/getting_started/comparison/comparison_with_sql.html

The following are some resources on working with serialized data:

- *Pickle in Python: Object Serialization*: <https://www.datacamp.com/community/tutorials/pickle-python-tutorial>
- *Read RData/RDS files into pandas.DataFrame objects (pyreader)*: <https://github.com/ofajardo/pyreadr>

Additional resources for working with APIs are as follows:

- *Documentation for the requests package*: <https://requests.readthedocs.io/en/master/>
- *HTTP Methods*: <https://restfulapi.net/http-methods/>
- *HTTP Status Codes*: <https://restfulapi.net/http-status-codes/>

To learn more about regular expressions, consult the following resources:

- *Mastering Python Regular Expressions by Félix López, Victor Romero*: <https://www.packtpub.com/application-development/mastering-python-regular-expressions>
- *Regular Expression Tutorial — Learn How to Use Regular Expressions*: <https://www.regular-expressions.info/tutorial.html>

Section 2: Using Pandas for Data Analysis

Now that we have some exposure to the `pandas` library, understand what data analysis entails, and know various ways to collect data, we will focus on the skills we need to perform data wrangling and exploratory data analysis. This section will give us the tools we need to manipulate, reshape, summarize, aggregate, and visualize data in Python.

This section comprises the following chapters:

- *Chapter 3, Data Wrangling with Pandas*
- *Chapter 4, Aggregating Pandas DataFrames*
- *Chapter 5, Visualizing Data with Pandas and Matplotlib*
- *Chapter 6, Plotting with Seaborn and Customization Techniques*

3

Data Wrangling with Pandas

In the previous chapter, we learned about the main pandas data structures, how to create DataFrame objects with our collected data, and various ways to inspect, summarize, filter, select, and work with DataFrame objects. Now that we are well versed in the initial data collection and inspection stage, we can begin our foray into the world of data wrangling.

As mentioned in *Chapter 1, Introduction to Data Analysis*, preparing data for analysis is often the largest portion of the job time-wise for those working with data, and often the least enjoyable. On the bright side, pandas is well equipped to help with these tasks, and, by mastering the skills presented in this book, we will be able to get to the more interesting parts sooner.

It should be noted that data wrangling isn't something we do merely once in our analysis; it is highly likely that we will do some data wrangling and move on to another analysis task, such as data visualization, only to find that we need to do additional data wrangling. The more familiar we are with the data, the better we will be able to prepare the data for our analysis. It's crucial to form an intuition of what types our data should be, what format we need our data to be in for the visualization that would best convey what we are looking to show, and the data points we should collect for our analysis. This comes with experience, so we must practice the skills that will be covered in this chapter on our own data every chance we get.

Since this is a very large topic, our coverage of data wrangling will be split between this chapter and *Chapter 4, Aggregating Pandas DataFrames*. In this chapter, we will get an overview of data wrangling before exploring the **National Centers for Environmental Information (NCEI)** API for climate data and walking through the process of collecting temperature data from it using the `requests` library. Then, we will discuss data wrangling tasks that deal with preparing data for some initial analyses and visualizations (which we will learn about in *Chapter 5, Visualizing Data with Pandas and Matplotlib*, and *Chapter 6, Plotting with Seaborn and Customization Techniques*). We will address some more advanced aspects of data wrangling that relate to aggregations and combining datasets in *Chapter 4, Aggregating Pandas DataFrames*.

In this chapter, we will cover the following topics:

- Understanding data wrangling
- Exploring an API to find and collect temperature data
- Cleaning data
- Reshaping data
- Handling duplicate, missing, or invalid data

Chapter materials

The materials for this chapter can be found on GitHub at https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_03. There are five notebooks that we will work through, each numbered according to when they will be used, and two directories, `data/` and `exercises/`, which contain all the CSV files necessary for the aforementioned notebooks and end-of-chapter exercises, respectively. The following files are in the `data/` directory:

File	Description	Source
<code>bitcoin.csv</code>	Daily opening, high, low, and closing price of bitcoin, along with volume traded and market capitalization for 2017 through 2018.	CoinMarketCap
<code>dirty_data.csv</code>	2018 weather data for New York City, manipulated to introduce data issues.	Modified version of the data from the NCEI API's GHCND dataset.
<code>long_data.csv</code>	Long format temperature data for New York City in October 2018 from the Boonton 1 station, containing daily temperature at time of observation, minimum temperature, and maximum temperature.	The NCEI API's GHCND dataset
<code>nyc_temperatures.csv</code>	Temperature data for New York City in October 2018 measured from LaGuardia airport, containing daily minimum, maximum, and average temperature.	The NCEI API's GHCND dataset
<code>sp500.csv</code>	Daily opening, high, low, and closing price of the S&P 500 stock index, along with volume traded and adjusted close for 2017 through 2018.	The <code>stock_analysis</code> package (see <i>Chapter 7, Financial Analysis – Bitcoin and the Stock Market</i>).
<code>wide_data.csv</code>	Wide format temperature data for New York City in October 2018 from the Boonton 1 station, containing daily temperature at time of observation, minimum temperature, and maximum temperature.	The NCEI API's GHCND dataset

Figure 3.1 – Breakdown of the datasets used in this chapter

We will begin in the `1-wide_vs_long.ipynb` notebook by discussing wide versus long format data. Then, we will collect daily temperature data from the NCEI API, which can be found at <https://www.ncdc.noaa.gov/cdo-web/webservices/v2>, in the `2-using_the_weather_api.ipynb` notebook. The documentation for the **Global Historical Climatology Network – Daily (GHCND)** dataset we will be using can be found at https://www1.ncdc.noaa.gov/pub/data/cdo/documentation/GHCND_documentation.pdf.

Important note

The NCEI is part of the **National Oceanic and Atmospheric Administration (NOAA)**. As indicated by the URL for the API, this resource was created when the NCEI was called the NCDC. Should the URL for this resource change in the future, search for *NCEI weather API* to find the updated one.

In the `3-cleaning_data.ipynb` notebook, we will learn how to perform an initial round of cleaning on the temperature data and some financial data, which was collected using the `stock_analysis` package that we will build in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*. Afterward, we will walk through ways to reshape our data in the `4-reshaping_data.ipynb` notebook. Finally, in the `5-handling_data_issues.ipynb` notebook, we will learn about some strategies for dealing with duplicate, missing, or invalid data using some dirty data that can be found in `data/dirty_data.csv`. The text will indicate when it's time to switch between notebooks.

Understanding data wrangling

Like any professional field, data analysis is filled with buzzwords, and it can often be difficult for newcomers to understand the lingo—the topic of this chapter is no exception. When we perform **data wrangling**, we are taking our input data from its original state and putting it in a format where we can perform meaningful analysis on it. **Data manipulation** is another way to refer to this process. There is no set list of operations; the only goal is that the data post-wrangling is more useful to us than when we started. In practice, there are three common tasks involved in the data wrangling process:

- Data cleaning
- Data transformation
- Data enrichment

It should be noted that there is no inherent order to these tasks, and it is highly probable that we will perform each many times throughout the data wrangling process. This idea brings up an interesting conundrum: if we need to wrangle our data to prepare it for our analysis, isn't it possible to wrangle it in such a way that we tell the data what to say instead of us learning what it is saying?

"If you torture the data long enough, it will confess to anything."

— Ronald Coase, winner of a Nobel Prize in Economics

Those working with data will find it is very easy to distort the truth by manipulating the data. However, it is our duty to do our best to avoid deceit by keeping the effect our actions have on the data's integrity in mind, and by explaining the process we took to draw our conclusions to the people who consume our analyses, so that they too may make their own judgments.

Data cleaning

Once we have collected our data, brought it into a `DataFrame` object, and used the skills we discussed in *Chapter 2, Working with Pandas DataFrames*, to familiarize ourselves with the data, we will need to perform some data cleaning. An initial round of data cleaning will often give us the bare minimum we need to start exploring our data. Some essential data cleaning tasks to master include the following:

- Renaming
- Sorting and reordering
- Data type conversions

- Handling duplicate data
- Addressing missing or invalid data
- Filtering to the desired subset of data

Data cleaning is the best starting point for data wrangling, since having the data stored as the correct data types and easy-to-reference names will open up many avenues for exploration, such as summary statistics, sorting, and filtering. Since we covered filtering in *Chapter 2, Working with Pandas DataFrames*, we will focus on the other topics from the preceding list in this chapter.

Data transformation

Frequently, we will reach the data transformation stage after some initial data cleaning, but it is entirely possible that our dataset is unusable in its current shape, and we must restructure it before attempting to do any data cleaning. In **data transformation**, we focus on changing our data's structure to facilitate our downstream analyses; this usually involves changing which data goes along the rows and which goes down the columns.

Most data we will find is either **wide format** or **long format**; each of these formats has its merits, and it's important to know which one we will need for our analysis. Often, people will record and present data in wide format, but there are certain visualizations that require the data to be in long format:

	variables				
	date	TMAX	TMIN	TOBS	
observations	0	2018-10-01	21.1	8.9	13.9
	1	2018-10-02	23.9	13.9	17.2
	2	2018-10-03	25.0	15.6	16.1
	3	2018-10-04	22.8	11.7	11.7
	4	2018-10-05	23.3	11.7	18.9
	5	2018-10-06	20.0	13.3	16.1

	date	datatype	variable names	variable values
observations	0	2018-10-01	TMAX	21.1
	1	2018-10-01	TMIN	8.9
	2	2018-10-01	TOBS	13.9
	3	2018-10-02	TMAX	23.9
	4	2018-10-02	TMIN	13.9
	5	2018-10-02	TOBS	17.2

Figure 3.2 – (Left) wide format versus (right) long format

Wide format is preferred for analysis and database design, while long format is considered poor design because each column should be its own data type and have a singular meaning. However, in cases where new fields will be added (or old ones removed) from a table in a relational database, rather than having to alter all the tables each time, the database's maintainers may decide to use the long format. This allows them to provide a fixed schema for users of the database, while being able to update the data it contains as needed. When building an API, the long format may be chosen if flexibility is required. Perhaps the API will provide a generic response format (for instance, date, field name, and field value) that can support various tables from a database. This may also have to do with making the response easier to form, depending on how the data is stored in the database the API uses. Since we will find data in both of these formats, it's important we understand how to work with both of them and go from one to the other.

Now, let's navigate to the `1-wide_vs_long.ipynb` notebook to see some examples. First, we will import `pandas` and `matplotlib` (to help illustrate the strengths and weaknesses of each format when it comes to visualizations, which we will discuss in *Chapter 5, Visualizing Data with Pandas and Matplotlib*, and *Chapter 6, Plotting with Seaborn and Customization Techniques*) and read in the CSV files containing wide and long format data:

```
>>> import matplotlib.pyplot as plt
>>> import pandas as pd

>>> wide_df = \
...     pd.read_csv('data/wide_data.csv', parse_dates=['date'])
>>> long_df = pd.read_csv(
...     'data/long_data.csv',
...     usecols=['date', 'datatype', 'value'],
...     parse_dates=['date']
... )[['date', 'datatype', 'value']] # sort columns
```

The wide data format

With wide format data, we represent measurements of variables with their own columns, and each row represents an observation of those variables. This makes it easy for us to compare variables across observations, get summary statistics, perform operations, and present our data; however, some visualizations don't work with this data format because they may rely on the long format to split, size, and/or color the plot content.

Let's look at the top six observations from the wide format data in `wide_df`:

```
>>> wide_df.head(6)
```

Each column contains the top six observations of a specific class of temperature data in degrees Celsius—maximum temperature (**TMAX**), minimum temperature (**TMIN**), and temperature at the time of observation (**TOBS**)—at a daily frequency:

	date	TMAX	TMIN	TOBS
0	2018-10-01	21.1	8.9	13.9
1	2018-10-02	23.9	13.9	17.2
2	2018-10-03	25.0	15.6	16.1
3	2018-10-04	22.8	11.7	11.7
4	2018-10-05	23.3	11.7	18.9
5	2018-10-06	20.0	13.3	16.1

Figure 3.3 – Wide format temperature data

When working with wide format data, we can easily grab summary statistics on this data by using the `describe()` method. Note that while older versions of pandas treated datetimes as categorical, pandas is moving toward treating them as numeric, so we pass `datetime_is_numeric=True` to suppress the warning:

```
>>> wide_df.describe(include='all', datetime_is_numeric=True)
```

With hardly any effort on our part, we get summary statistics for the dates, maximum temperature, minimum temperature, and temperature at the time of observation:

	date	TMAX	TMIN	TOBS
count	31	31.000000	31.000000	31.000000
mean	2018-10-16 00:00:00	16.829032	7.561290	10.022581
min	2018-10-01 00:00:00	7.800000	-1.100000	-1.100000
25%	2018-10-08 12:00:00	12.750000	2.500000	5.550000
50%	2018-10-16 00:00:00	16.100000	6.700000	8.300000
75%	2018-10-23 12:00:00	21.950000	13.600000	16.100000
max	2018-10-31 00:00:00	26.700000	17.800000	21.700000
std	NaN	5.714962	6.513252	6.596550

Figure 3.4 – Summary statistics for the wide format temperature data

As we discussed previously, the summary data in the preceding table is easy to obtain and is informative. This format can easily be plotted with pandas as well, provided we tell it exactly what we want to plot:

```
>>> wide_df.plot(
...     x='date', y=['TMAX', 'TMIN', 'TOBS'], figsize=(15, 5),
...     title='Temperature in NYC in October 2018'
... ).set_ylabel('Temperature in Celsius')
>>> plt.show()
```

Pandas plots the daily maximum temperature, minimum temperature, and temperature at the time of observation as their own lines on a single line plot:

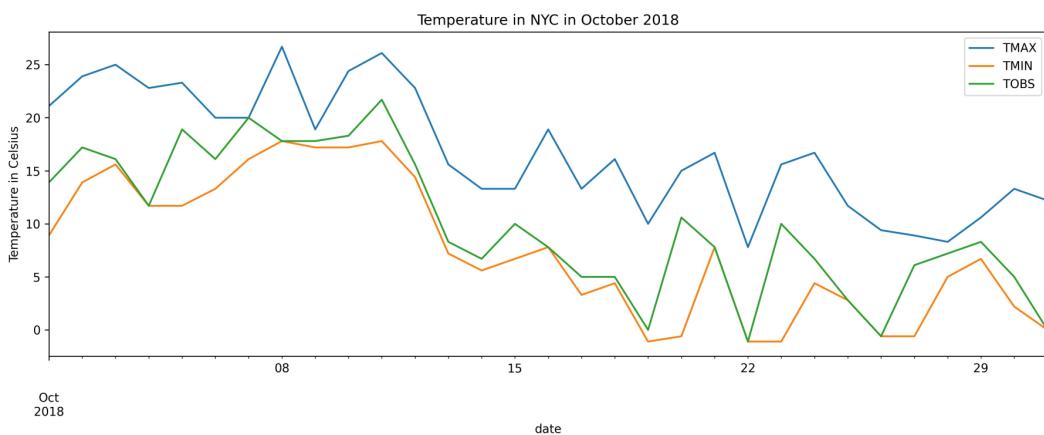


Figure 3.5 – Plotting the wide format temperature data

Important note

Don't worry about understanding the visualization code right now; it's here just to illustrate how each of these data formats can make certain tasks easier or harder. We will cover visualizations with pandas and matplotlib in *Chapter 5, Visualizing Data with Pandas and Matplotlib*.

The long data format

Long format data will have a row for each observation of a variable; this means that, if we have three variables being measured daily, we will have three rows for each day we record observations. The long format setup can be achieved by turning the variable column names into a single column, where the data is the variable name, and putting their values in a separate column.

We can look at the top six rows of the long format data in `long_df` to see the difference between wide format and long format data:

```
>>> long_df.head(6)
```

Notice that we now have three entries for each date, and the **datatype** column tells us what the data in the **value** column is for that row:

	date	datatype	value
0	2018-10-01	TMAX	21.1
1	2018-10-01	TMIN	8.9
2	2018-10-01	TOBS	13.9
3	2018-10-02	TMAX	23.9
4	2018-10-02	TMIN	13.9
5	2018-10-02	TOBS	17.2

Figure 3.6 – Long format temperature data

If we try to get summary statistics, like we did with the wide format data, the result isn't as helpful:

```
>>> long_df.describe(include='all', datetime_is_numeric=True)
```

The **value** column shows us summary statistics, but this is summarizing the daily maximum temperatures, minimum temperatures, and temperatures at the time of observation. The maximum will be the maximum of the daily maximum temperatures and the minimum will be the minimum of the daily minimum temperatures. This means that this summary data is not very helpful:

	date	datatype	value
count	93	93	93.000000
unique	NaN	3	NaN
top	NaN	TOBS	NaN
freq	NaN	31	NaN
mean	2018-10-16 00:00:00	NaN	11.470968
min	2018-10-01 00:00:00	NaN	-1.100000
25%	2018-10-08 00:00:00	NaN	6.700000
50%	2018-10-16 00:00:00	NaN	11.700000
75%	2018-10-24 00:00:00	NaN	17.200000
max	2018-10-31 00:00:00	NaN	26.700000
std	NaN	NaN	7.362354

Figure 3.7 – Summary statistics for the long format temperature data

This format is not very easy to digest and certainly shouldn't be how we present data; however, it makes it easy to create visualizations where our plotting library can color lines by the name of the variable, size the points by the values of a certain variable, and perform splits for faceting. Pandas expects its data for plotting to be in wide format, so, to easily make the same plot that we did with the wide format data, we must use another plotting library, called `seaborn`, which we will cover in *Chapter 6, Plotting with Seaborn and Customization Techniques*:

```
>>> import seaborn as sns

>>> sns.set(rc={'figure.figsize': (15, 5)}, style='white')

>>> ax = sns.lineplot(
...     data=long_df, x='date', y='value', hue='datatype'
... )
```

```
>>> ax.set_ylabel('Temperature in Celsius')
>>> ax.set_title('Temperature in NYC in October 2018')
>>> plt.show()
```

Seaborn can subset based on the `datatype` column to give us individual lines for the daily maximum temperature, minimum temperature, and temperature at the time of observation:

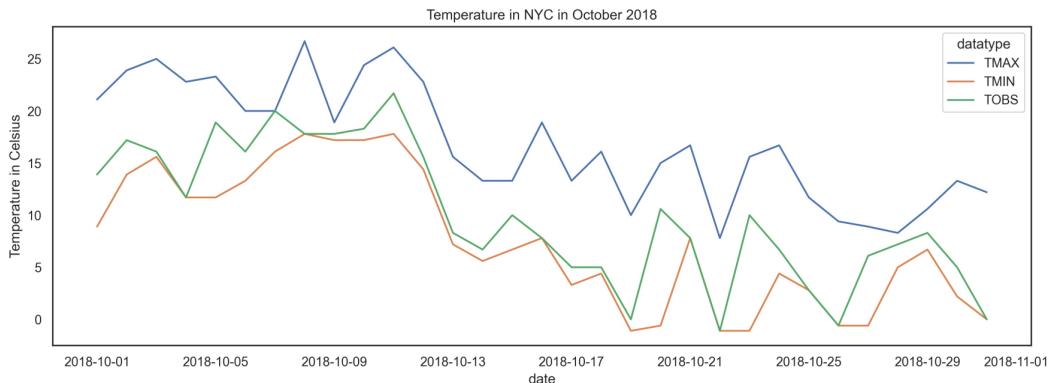


Figure 3.8 – Plotting the long format temperature data

Seaborn lets us specify the column to use for hue, which colored the lines in *Figure 3.8* by the temperature type. We aren't limited to this, though; with long format data, we can easily facet our plots:

```
>>> sns.set(
...     rc={'figure.figsize': (20, 10)},
...     style='white', font_scale=2
... )
>>> g = sns.FacetGrid(long_df, col='datatype', height=10)
>>> g = g.map(plt.plot, 'date', 'value')
>>> g.set_titles(size=25)
>>> g.set_xticklabels(rotation=45)
>>> plt.show()
```

Seaborn can use long format data to create subplots for each distinct value in the `datatype` column:

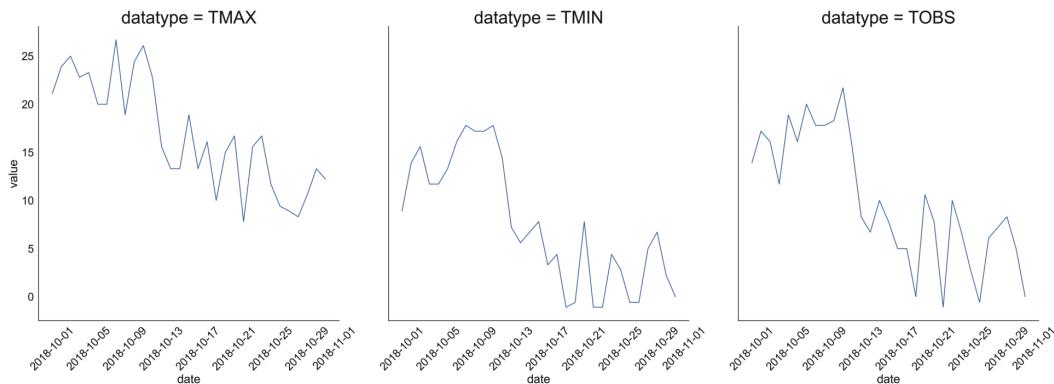


Figure 3.9 – Plotting subsets of the long format temperature data

Important note

While it is possible to create a plot similar to the preceding one with pandas and matplotlib using subplots, more complicated combinations of facets will make using seaborn infinitely easier. We will cover seaborn in *Chapter 6, Plotting with Seaborn and Customization Techniques*.

In the *Reshaping data* section, we will cover how to transform our data from wide to long format by melting, and from long to wide format by pivoting. Additionally, we will learn how to transpose data, which flips the columns and the rows.

Data enrichment

Once we have our cleaned data in the format we need for our analysis, we may find the need to enrich the data a bit. **Data enrichment** improves the quality of the data by adding to it in one way or another. This process becomes very important in modeling and in machine learning, where it forms part of the **feature engineering** process (which we will touch on in *Chapter 10, Making Better Predictions – Optimizing Models*).

When we're looking to enrich our data, we can either **merge** new data with the original data (by appending new rows or columns) or use the original data to create new data. The following are ways to enhance our data using the original data:

- **Adding new columns:** Using functions on the data from existing columns to create new values.

- **Binning:** Turning continuous data or discrete data with many distinct values into buckets, which makes the column discrete while letting us control the number of possible values in the column.
- **Aggregating:** Rolling up the data and summarizing it.
- **Resampling:** Aggregating time series data at specific intervals.

Now that we understand what data wrangling is, let's collect some data to work with. Note that we will cover data cleaning and transformation in this chapter, while data enrichment will be covered in *Chapter 4, Aggregating Pandas DataFrames*.

Exploring an API to find and collect temperature data

In *Chapter 2, Working with Pandas DataFrames*, we worked on data collection and how to perform an initial inspection and filtering of the data; this usually gives us ideas of things that need to be addressed before we move further in our analysis. Since this chapter builds on those skills, we will get to practice some of them here as well. To begin, we will start by exploring the weather API that's provided by the NCEI. Then, in the next section, we will learn about data wrangling using temperature data that was previously obtained from this API.

Important note

To use the NCEI API, you will have to request a token by filling out this form with your email address: <https://www.ncdc.noaa.gov/cdo-web/token>.

For this section, we will be working in the `2-using_the_weather_api.ipynb` notebook to request temperature data from the NCEI API. As we learned in *Chapter 2, Working with Pandas DataFrames*, we can use the `requests` library to interact with APIs. In the following code block, we import the `requests` library and create a convenience function for making the requests to a specific endpoint, sending our token along. To use this function, we need to provide a token, as indicated in bold:

```
>>> import requests

>>> def make_request(endpoint, payload=None):
...     """
...     Make a request to a specific endpoint on the
...     weather API passing headers and optional payload.
```

```
...     Parameters:
...         - endpoint: The endpoint of the API you want to
...                     make a GET request to.
...         - payload: A dictionary of data to pass along
...                     with the request.
...
...     Returns:
...         A response object.
"""
...
    return requests.get(
        'https://www.ncdc.noaa.gov/cdo-web/'
        f'api/v2/{endpoint}',
        headers={'token': 'PASTE_YOUR_TOKEN_HERE'},
        params=payload
    )
```

Tip

This function is making use of **f-strings**, which were introduced in Python 3.6; they improve code readability and reduce verbosity compared to using the `format()` method: `'api/v2/{}'.format(endpoint)`.

To use the `make_request()` function, we need to learn how to form our request. The NCEI has a helpful getting started page (<https://www.ncdc.noaa.gov/cdo-web/webservices/v2#gettingStarted>) that shows us how to form requests; we can progress through the tabs on the page to figure out what filters we want on our query. The `requests` library takes care of turning our dictionary of search parameters (passed in as `payload`) into a **query string** that gets appended to the end URL (for example, if we pass `2018-08-28` for `start` and `2019-04-15` for `end`, we will get `?start=2018-08-28&end=2019-04-15`), just like the examples on the website. This API provides many different endpoints for exploring what is offered and building up our ultimate request for the actual dataset. We will start by figuring out the ID of the dataset we want to query for (`datasetid`) using the `datasets` endpoint. Let's check which datasets have data within the date range of October 1, 2018 through today:

```
>>> response = \
...     make_request('datasets', {'startdate': '2018-10-01'})
```

Remember that we check the `status_code` attribute to make sure the request was successful. Alternatively, we can use the `ok` attribute to get a Boolean indicator if everything went as expected:

```
>>> response.status_code  
200  
>>> response.ok  
True
```

Tip

The API limits us to 5 requests per second and 10,000 requests per day. If we exceed these limits, the status code will indicate a client error (meaning that the error appears to have been caused by us). Client errors have status codes in the 400s; for example, 404, if the requested resource can't be found, or 400, if the server can't understand our request (or refuses to process it). Sometimes, the server has an issue on its side when processing our request, in which case we see status codes in the 500s. You can find a listing of common status codes and their meanings at <https://restfulapi.net/http-status-codes/>.

Once we have our response, we can use the `json()` method to get the payload. Then, we can use dictionary methods to determine which part we want to look at:

```
>>> payload = response.json()  
>>> payload.keys()  
dict_keys(['metadata', 'results'])
```

The `metadata` portion of the JSON payload tells us information about the result, while the `results` section contains the actual results. Let's see how much data we got back, so that we know whether we can print the results or whether we should try to limit the output:

```
>>> payload['metadata']  
{'resultset': {'offset': 1, 'count': 11, 'limit': 25}}
```

We got back 11 rows, so let's see what fields are in the `results` portion of the JSON payload. The `results` key contains a list of dictionaries. If we select the first one, we can look at the keys to see what fields the data contains. We can then reduce the output to the fields we care about:

```
>>> payload['results'][0].keys()  
dict_keys(['uid', 'mindate', 'maxdate', 'name',  
          'datacoverage', 'id'])
```

For our purposes, we want to look at the IDs and names of the datasets, so let's use a list comprehension to look at those only:

```
>>> [(data['id'], data['name']) for data in payload['results']]  
[('GHCND', 'Daily Summaries'),  
 ('GSOM', 'Global Summary of the Month'),  
 ('GSOY', 'Global Summary of the Year'),  
 ('NEXRAD2', 'Weather Radar (Level II)'),  
 ('NEXRAD3', 'Weather Radar (Level III)'),  
 ('NORMAL_ANN', 'Normals Annual/Seasonal'),  
 ('NORMAL_DLY', 'Normals Daily'),  
 ('NORMAL_HLY', 'Normals Hourly'),  
 ('NORMAL_MLY', 'Normals Monthly'),  
 ('PRECIP_15', 'Precipitation 15 Minute'),  
 ('PRECIP_HLY', 'Precipitation Hourly')]
```

The first entry in the result is what we are looking for. Now that we have a value for `datasetid` (GHCND), we proceed to identify one for `datacategoryid`, which we need to request temperature data. We do so using the `datacategories` endpoint. Here, we can print the JSON payload since it isn't that large (only nine entries):

```
>>> response = make_request(  
...     'datacategories', payload={'datasetid': 'GHCND'}  
... )  
>>> response.status_code  
200  
>>> response.json()['results']  
[{'name': 'Evaporation', 'id': 'EVAP'},  
 {'name': 'Land', 'id': 'LAND'},  
 {'name': 'Precipitation', 'id': 'PRCP'},  
 {'name': 'Sky cover & clouds', 'id': 'SKY'},  
 {'name': 'Sunshine', 'id': 'SUN'},  
 {'name': 'Air Temperature', 'id': 'TEMP'},  
 {'name': 'Water', 'id': 'WATER'},  
 {'name': 'Wind', 'id': 'WIND'},  
 {'name': 'Weather Type', 'id': 'WXTYPE'}]
```

Based on the previous result, we know that we want a value of TEMP for datacategoryid. Next, we use this to identify the data types we want by using the datatypes endpoint. We will use a list comprehension once again to only print the names and IDs; this is still a rather large list, so the output has been abbreviated:

```
>>> response = make_request(  
...     'datatypes',  
...     payload={'datacategoryid': 'TEMP', 'limit': 100}  
... )  
>>> response.status_code  
200  
>>> [(datatype['id'], datatype['name'])  
...     for datatype in response.json()['results']]  
[('CDSD', 'Cooling Degree Days Season to Date'),  
 ...,  
 ('TAVG', 'Average Temperature.'),  
 ('TMAX', 'Maximum temperature'),  
 ('TMIN', 'Minimum temperature'),  
 ('TOBS', 'Temperature at the time of observation')]
```

We are looking for the TAVG, TMAX, and TMIN data types. Now that we have everything we need to request temperature data for all locations, we need to narrow it down to a specific location. To determine a value for locationcategoryid, we must use the locationcategories endpoint:

```
>>> response = make_request(  
...     'locationcategories', payload={'datasetid': 'GHCND'}  
... )  
>>> response.status_code  
200
```

Note that we can use pprint from the Python standard library (<https://docs.python.org/3/library/pprint.html>) to print our JSON payload in an easier-to-read format:

```
>>> import pprint  
>>> pprint.pprint(response.json())  
{'metadata': {  
     'resultset': {'count': 12, 'limit': 25, 'offset': 1}},  
 'results': [{  
     'id': 'CITY', 'name': 'City'},  
     {'id': 'CLIM_DIV', 'name': 'Climate Division'},  
     {'id': 'CLIM_REG', 'name': 'Climate Region'},  
     {'id': 'CNTRY', 'name': 'Country'},
```

```
{'id': 'CNTY', 'name': 'County'},  
...,  
'id': 'ST', 'name': 'State'},  
'id': 'US_TERR', 'name': 'US Territory'},  
'id': 'ZIP', 'name': 'Zip Code'}}}
```

We want to look at New York City, so, for the `locationcategoryid` filter, `CITY` is the proper value. The notebook we are working in has a function to search for a field by name using **binary search** on the API; binary search is a more efficient way of searching through an ordered list. Since we know that the fields can be sorted alphabetically, and the API gives us metadata about the request, we know how many items the API has for a given field and can tell whether we have passed the one we are looking for.

With each request, we grab the middle entry and compare its location in the alphabet with our target; if the result comes before our target, we look at the half of the data that's greater than what we just got; otherwise, we look at the smaller half. Each time, we are slicing the data in half, so when we grab the middle entry to test, we are moving closer to the value we seek (see *Figure 3.10*):

```
>>> def get_item(name, what, endpoint, start=1, end=None):  
...     """  
...     Grab the JSON payload using binary search.  
...  
...     Parameters:  
...         - name: The item to look for.  
...         - what: Dictionary specifying what item `name` is.  
...         - endpoint: Where to look for the item.  
...         - start: The position to start at. We don't need  
...                 to touch this, but the function will manipulate  
...                 this with recursion.  
...         - end: The last position of the items. Used to  
...                 find the midpoint, but like `start` this is not  
...                 something we need to worry about.  
...  
...     Returns: Dictionary of the information for the item  
...             if found, otherwise an empty dictionary.  
...     """  
...     # find the midpoint to cut the data in half each time  
...     mid = (start + (end or 1)) // 2  
...  
...     # lowercase the name so this is not case-sensitive  
...     name = name.lower()
```

```
...     # define the payload we will send with each request
...     payload = {
...         'datasetid': 'GHCND', 'sortfield': 'name',
...         'offset': mid, # we'll change the offset each time
...         'limit': 1 # we only want one value back
...     }
...
...     # make request adding additional filters from `what`
...     response = make_request(endpoint, {**payload, **what})
...
...     if response.ok:
...         payload = response.json()
...
...         # if ok, grab the end index from the response
...         # metadata the first time through
...         end = end or \
...             payload['metadata']['resultset']['count']
...
...         # grab the lowercase version of the current name
...         current_name = \
...             payload['results'][0]['name'].lower()
...
...         # if what we are searching for is in the current
...         # name, we have found our item
...         if name in current_name:
...             # return the found item
...             return payload['results'][0]
...         else:
...             if start >= end:
...                 # if start index is greater than or equal
...                 # to end index, we couldn't find it
...                 return {}
...             elif name < current_name:
...                 # name comes before the current name in the
...                 # alphabet => search further to the left
...                 return get_item(name, what, endpoint,
...                                 start, mid - 1)
...             elif name > current_name:
...                 # name comes after the current name in the
...                 # alphabet => search further to the right
...                 return get_item(name, what, endpoint,
...                                 mid + 1, end)
```

```
...     else:
...         # response wasn't ok, use code to determine why
...         print('Response not OK, '
...               f'status: {response.status_code}')
```

This is a **recursive** implementation of the algorithm, meaning that we call the function itself from inside; we must be very careful when we do this to define a **base condition** so that it will eventually stop and not enter an infinite loop. It is possible to implement this iteratively. See the *Further reading* section at the end of this chapter for additional reading on binary search and **recursion**.

Important note

In a traditional implementation of binary search, it is trivial to find the length of the list that we are searching. With the API, we have to make one request to get the count; therefore, we must ask for the first entry (offset of 1) to orient ourselves. This means that we make an extra request here compared to what we would have needed if we knew how many locations were in the list before starting.

Now, let's use the binary search implementation to find the ID for New York City, which will be the value we will use for `locationid` in subsequent queries:

```
>>> nyc = get_item(
...     'New York', {'locationcategoryid': 'CITY'}, 'locations'
... )
>>> nyc
{'mindate': '1869-01-01',
 'maxdate': '2021-01-14',
 'name': 'New York, NY US',
 'datacoverage': 1,
 'id': 'CITY:US360019'}
```

By using binary search here, we find **New York** in **8** requests, despite it being close to the middle of 1,983 entries! For comparison, using linear search, we would have looked at 1,254 entries before finding it. In the following diagram, we can see how binary search eliminates sections of the list of locations systematically, which is represented by black on the number line (white means it is still possible that the desired value is in that section):

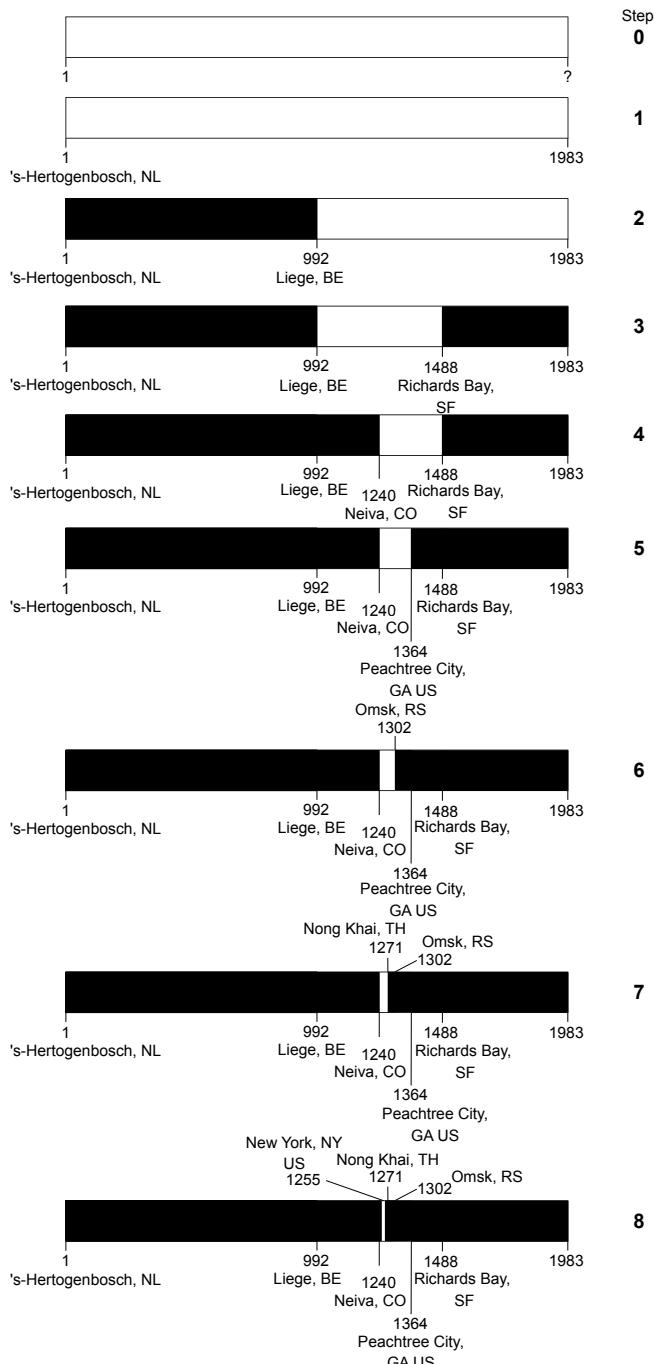


Figure 3.10 – Binary search to find New York City

Tip

Some APIs (such as the NCEI API) restrict the number of requests we can make within certain periods of time, so it's important to be smart about our requests. When searching a very long ordered list, think of binary search.

Optionally, we can drill down to the ID of the station that is collecting the data. This is the most granular level. Using binary search again, we can grab the station ID for the Central Park station:

```
>>> central_park = get_item(
...     'NY City Central Park',
...     {'locationid': nyc['id']}, 'stations'
... )
>>> central_park
{'elevation': 42.7,
'mindate': '1869-01-01',
'maxdate': '2020-01-13',
'latitude': 40.77898,
'name': 'NY CITY CENTRAL PARK, NY US',
'datacoverage': 1,
'id': 'GHCND:USW00094728',
'elevationUnit': 'METERS',
'longitude': -73.96925}
```

Now, let's request NYC's temperature data in Celsius for October 2018, recorded from Central Park. For this, we will use the `data` endpoint and provide all the parameters we picked up throughout our exploration of the API:

```
>>> response = make_request(
...     'data',
...     {'datasetid': 'GHCND',
...      'stationid': central_park['id'],
...      'locationid': nyc['id'],
...      'startdate': '2018-10-01',
...      'enddate': '2018-10-31',
...      'datatypeid': ['TAVG', 'TMAX', 'TMIN'],
...      'units': 'metric',
...      'limit': 1000}
... )
>>> response.status_code
200
```

Lastly, we will create a `DataFrame` object; since the `results` portion of the JSON payload is a list of dictionaries, we can pass it directly to `pd.DataFrame()`:

```
>>> import pandas as pd
>>> df = pd.DataFrame(response.json()['results'])
>>> df.head()
```

We get back long format data. The **datatype** column is the temperature variable being measured, and the **value** column contains the measured temperature:

	date	datatype	station	attributes	value
0	2018-10-01T00:00:00	TMAX	GHCND:USW00094728	,,W,2400	24.4
1	2018-10-01T00:00:00	TMIN	GHCND:USW00094728	,,W,2400	17.2
2	2018-10-02T00:00:00	TMAX	GHCND:USW00094728	,,W,2400	25.0
3	2018-10-02T00:00:00	TMIN	GHCND:USW00094728	,,W,2400	18.3
4	2018-10-03T00:00:00	TMAX	GHCND:USW00094728	,,W,2400	23.3

Figure 3.11 – Data retrieved from the NCEI API

Tip

We can use the previous code to turn any of the JSON responses we worked with in this section into a `DataFrame` object, if we find that easier to work with. However, it should be stressed that JSON payloads are pretty much ubiquitous when it comes to APIs (and, as Python users, we should be familiar with dictionary-like objects), so it won't hurt to get comfortable with them.

We asked for TAVG, TMAX, and TMIN, but notice that we didn't get TAVG. This is because the Central Park station isn't recording average temperature, despite being listed in the API as offering it—real-world data is dirty:

```
>>> df.datatype.unique()
array(['TMAX', 'TMIN'], dtype=object)

>>> if get_item(
...     'NY City Central Park',
...     {'locationid': nyc['id'], 'datatypeid': 'TAVG'},
...     'stations'
... ):
...     print('Found!')
Found!
```

Time for plan B: let's use LaGuardia Airport as the station instead of Central Park for the remainder of this chapter. Alternatively, we could have grabbed data for all the stations that cover New York City; however, since this would give us multiple entries per day for some of the temperature measurements, we won't do so here—we would need skills that will be covered in *Chapter 4, Aggregating Pandas DataFrames*, to work with that data.

The process of collecting the weather data from the LaGuardia Airport station is the same as with the Central Park station, but in the interest of brevity, we will read in the data for LaGuardia in the next notebook when we discuss cleaning the data. Note that the bottom cells of the current notebook contain the code that's used to collect this data.

Cleaning data

Let's move on to the `3-cleaning_data.ipynb` notebook for our discussion of data cleaning. As usual, we will begin by importing `pandas` and reading in our data. For this section, we will be using the `nyc_temperatures.csv` file, which contains the maximum daily temperature (`TMAX`), minimum daily temperature (`TMIN`), and the average daily temperature (`TAVG`) from the LaGuardia Airport station in New York City for October 2018:

```
>>> import pandas as pd  
>>> df = pd.read_csv('data/nyc_temperatures.csv')  
>>> df.head()
```

We retrieved long format data from the API; for our analysis, we want wide format data, but we will address that in the *Pivoting DataFrames* section, later in this chapter:

	date	datatype	station	attributes	value
0	2018-10-01T00:00:00	TAVG	GHCND:USW00014732	H,S,	21.2
1	2018-10-01T00:00:00	TMAX	GHCND:USW00014732	,W,2400	25.6
2	2018-10-01T00:00:00	TMIN	GHCND:USW00014732	,W,2400	18.3
3	2018-10-02T00:00:00	TAVG	GHCND:USW00014732	H,,S,	22.7
4	2018-10-02T00:00:00	TMAX	GHCND:USW00014732	,W,2400	26.1

Figure 3.12 – NYC temperature data

For now, we will focus on making little tweaks to the data that will make it easier for us to use: renaming columns, converting each column into the most appropriate data type, sorting, and reindexing. Often, this will be the time to filter the data down, but we did that when we worked on requesting data from the API; for a review of filtering with `pandas`, refer to *Chapter 2, Working with Pandas DataFrames*.

Renaming columns

Since the API endpoint we used could return data of any units and category, it had to call that column value. We only pulled temperature data in Celsius, so all our observations have the same units. This means that we can rename the value column so that it's clear what data we are working with:

```
>>> df.columns  
Index(['date', 'datatype', 'station', 'attributes', 'value'],  
      dtype='object')
```

The DataFrame class has a `rename()` method that takes a dictionary mapping the old column name to the new column name. In addition to renaming the value column, let's rename the attributes column to flags since the API documentation mentions that that column contains flags for information about data collection:

```
>>> df.rename(  
...     columns={'value': 'temp_C', 'attributes': 'flags'},  
...     inplace=True  
... )
```

Most of the time, pandas will return a new DataFrame object; however, since we passed in `inplace=True`, our original dataframe was updated instead. Always be careful with in-place operations, as they might be difficult or impossible to undo. Our columns now have their new names:

```
>>> df.columns  
Index(['date', 'datatype', 'station', 'flags', 'temp_C'],  
      dtype='object')
```

Tip

Both Series and Index objects can also be renamed using their `rename()` methods. Simply pass in the new name. For example, if we have a Series object called `temperature` and we want to rename it `temp_C`, we can run `temperature.rename('temp_C')`. The variable will still be called `temperature`, but the name of the data in the series itself will now be `temp_C`.

We can also do transformations on the column names with `rename()`. For instance, we can put all the column names in uppercase:

```
>>> df.rename(str.upper, axis='columns').columns  
Index(['DATE', 'DATATYPE', 'STATION', 'FLAGS', 'TEMP_C'],  
      dtype='object')
```

This method even lets us rename the values of the index, although this is something we don't have use for now since our index is just numbers. However, for reference, we would simply change `axis='columns'` in the preceding code to `axis='rows'`.

Type conversion

Now that the column names are indicative of the data they contain, we can check what types of data they hold. We should have formed an intuition as to what the data types should be after looking at the first few rows when we inspected the dataframe with the `head()` method previously. With type conversion, we aim to reconcile what the current data types are with what we believe they should be; we will be changing how our data is represented.

Note that, sometimes, we may have data that we believe should be a certain type, such as a date, but it is stored as a string; this could be for a very valid reason—data could be missing. In the case of missing data encoded as text (for example, ? or N/A), pandas will store it as a string when reading it in to allow for this data. It will be marked as `object` when we use the `dtypes` attribute on our dataframe. If we try to convert (or `cast`) these columns, we will either get an error or our result won't be what we expected. For example, if we have strings of decimal numbers, but try to convert the column into integers, we will get an error since Python knows they aren't integers; however, if we try to convert decimal numbers into integers, we will lose any information after the decimal point.

That being said, let's examine the data types in our temperature data. Note that the `date` column isn't actually being stored as a datetime:

```
>>> df.dtypes  
date          object  
datatype      object  
station       object  
flags         object  
temp_C        float64  
dtype: object
```

We can use the `pd.to_datetime()` function to convert it into a datetime:

```
>>> df.loc[:, 'date'] = pd.to_datetime(df.date)
>>> df.dtypes
date        datetime64[ns]
datatype      object
station       object
flags         object
temp_C        float64
dtype: object
```

This is much better. Now, we can get useful information when we summarize the `date` column:

```
>>> df.date.describe(datetime_is_numeric=True)
count                93
mean    2018-10-16 00:00:00
min     2018-10-01 00:00:00
25%     2018-10-08 00:00:00
50%     2018-10-16 00:00:00
75%     2018-10-24 00:00:00
max     2018-10-31 00:00:00
Name: date, dtype: object
```

Dealing with dates can be tricky since they come in many different formats and time zones; fortunately, pandas has more methods we can use for dealing with converting datetime objects. For example, when working with a `DatetimeIndex` object, if we need to keep track of time zones, we can use the `tz_localize()` method to associate our datetimes with a time zone:

```
>>> pd.date_range(start='2018-10-25', periods=2, freq='D') \
...      .tz_localize('EST')
DatetimeIndex(['2018-10-25 00:00:00-05:00',
               '2018-10-26 00:00:00-05:00'],
              dtype='datetime64[ns, EST]', freq=None)
```

This also works with `Series` and `DataFrame` objects that have an index of type `DatetimeIndex`. We can read in the CSV file again and, this time, specify that the `date` column will be our index and that we should parse any dates in the CSV file into datetimes:

```
>>> eastern = pd.read_csv(  
...      'data/nyc_temperatures.csv',  
...      index_col='date', parse_dates=True  
... ).tz_localize('EST')  
>>> eastern.head()
```

We had to read the file in again for this example because we haven't learned how to change the index of our data yet (covered in the *Reordering, reindexing, and sorting data* section, later this chapter). Note that we have added the Eastern Standard Time offset (-05:00 from UTC) to the datetimes in the index:

	datatype	station	attributes	value
date				
2018-10-01 00:00:00-05:00	TAVG	GHCND:USW00014732	H,S,	21.2
2018-10-01 00:00:00-05:00	TMAX	GHCND:USW00014732	,W,2400	25.6
2018-10-01 00:00:00-05:00	TMIN	GHCND:USW00014732	,W,2400	18.3
2018-10-02 00:00:00-05:00	TAVG	GHCND:USW00014732	H,S,	22.7
2018-10-02 00:00:00-05:00	TMAX	GHCND:USW00014732	,W,2400	26.1

Figure 3.13 – Time zone-aware dates in the index

We can use the `tz_convert()` method to change the time zone into a different one. Let's change our data into UTC:

```
>>> eastern.tz_convert('UTC').head()
```

Now, the offset is UTC (+00:00), but note that the time portion of the date is now 5 AM; this conversion took into account the -05:00 offset:

	datatype	station	attributes	value
date				
2018-10-01 05:00:00+00:00	TAVG	GHCND:USW00014732	H,S,	21.2
2018-10-01 05:00:00+00:00	TMAX	GHCND:USW00014732	,W,2400	25.6
2018-10-01 05:00:00+00:00	TMIN	GHCND:USW00014732	,W,2400	18.3
2018-10-02 05:00:00+00:00	TAVG	GHCND:USW00014732	H,S,	22.7
2018-10-02 05:00:00+00:00	TMAX	GHCND:USW00014732	,W,2400	26.1

Figure 3.14 – Converting data into another time zone

We can also truncate datetimes with the `to_period()` method, which comes in handy if we don't care about the full date. For example, if we wanted to aggregate our data by month, we could truncate our index to just the month and year and then perform the aggregation. Since we will cover aggregation in *Chapter 4, Aggregating Pandas DataFrames*, we will just do the truncation here. Note that we first remove the time zone information to avoid a warning from pandas that the `PeriodArray` class doesn't have time zone information, and therefore it will be lost. This is because the underlying data for a `PeriodIndex` object is stored as a `PeriodArray` object:

```
>>> eastern.tz_localize(None).to_period('M').index
PeriodIndex(['2018-10', '2018-10', ..., '2018-10', '2018-10'],
            dtype='period[M]', name='date', freq='M')
```

We can use the `to_timestamp()` method to convert our `PeriodIndex` object into a `DatetimeIndex` object; however, the datetimes all start at the first of the month now:

```
>>> eastern.tz_localize(None) \
...     .to_period('M').to_timestamp().index
DatetimeIndex(['2018-10-01', '2018-10-01', '2018-10-01', ...,
               '2018-10-01', '2018-10-01', '2018-10-01'],
              dtype='datetime64[ns]', name='date', freq=None)
```

Alternatively, we can use the `assign()` method to handle any type conversions by passing the column names as named parameters and their new values as the value for that argument to the method call. In practice, this will be more beneficial since we can perform many tasks in one call and use the columns we create in that call to calculate additional columns. For example, let's cast the `date` column to a datetime and add a new column for the temperature in Fahrenheit (`temp_F`). The `assign()` method returns a new `DataFrame` object, so we must remember to assign it to a variable if we want to keep it. Here, we will create a new one. Note that our original conversion of the dates modified the column, so, in order to illustrate that we can use `assign()`, we need to read our data in once more:

```
>>> df = pd.read_csv('data/nyc_temperatures.csv').rename(
...     columns={'value': 'temp_C', 'attributes': 'flags'}
... )

>>> new_df = df.assign(
...     date=pd.to_datetime(df.date),
...     temp_F=(df.temp_C * 9/5) + 32
... )
```

```
>>> new_df.dtypes
date          datetime64[ns]
datatype      object
station       object
flags         object
temp_C        float64
temp_F        float64
dtype: object

>>> new_df.head()
```

We now have datetimes in the date column and a new column, temp_F:

	date	datatype	station	flags	temp_C	temp_F
0	2018-10-01	TAVG	GHCND:USW00014732	H,,S,	21.2	70.16
1	2018-10-01	TMAX	GHCND:USW00014732	,,W,2400	25.6	78.08
2	2018-10-01	TMIN	GHCND:USW00014732	,,W,2400	18.3	64.94
3	2018-10-02	TAVG	GHCND:USW00014732	H,,S,	22.7	72.86
4	2018-10-02	TMAX	GHCND:USW00014732	,,W,2400	26.1	78.98

Figure 3.15 – Simultaneous type conversion and column creation

Additionally, we can use the `astype()` method to convert one column at a time. As an example, let's say we only cared about the temperatures at every whole number, but we don't want to round. In this case, we simply want to chop off the information after the decimal. To accomplish this, we can cast the floats as integers. This time, we will use **lambda functions** (first introduced in *Chapter 2, Working with Pandas DataFrames*), which make it possible to access the temp_F column to create the temp_F_whole column, even though df doesn't have this column before we call `assign()`. It is very common (and useful) to use lambda functions with `assign()`:

```
>>> df = df.assign(
...     date=lambda x: pd.to_datetime(x.date),
...     temp_C_whole=lambda x: x.temp_C.astype('int'),
...     temp_F=lambda x: (x.temp_C * 9/5) + 32,
...     temp_F_whole=lambda x: x.temp_F.astype('int')
... )
>>> df.head()
```

Note that we can refer to columns we've just created if we use a lambda function. It's also important to mention that we don't have to know whether to convert the column into a float or an integer: we can use `pd.to_numeric()`, which will convert the data into floats if it sees decimals. If all the numbers are whole, they will be converted into integers (obviously, we will still get errors if the data isn't numeric at all):

	date	datatype	station	flags	temp_C	temp_C_whole	temp_F	temp_F_whole
0	2018-10-01	TAVG	GHCND:USW00014732	H,,S,	21.2	21	70.16	70
1	2018-10-01	TMAX	GHCND:USW00014732	„W,2400	25.6	25	78.08	78
2	2018-10-01	TMIN	GHCND:USW00014732	„W,2400	18.3	18	64.94	64
3	2018-10-02	TAVG	GHCND:USW00014732	H,,S,	22.7	22	72.86	72
4	2018-10-02	TMAX	GHCND:USW00014732	„W,2400	26.1	26	78.98	78

Figure 3.16 – Creating columns with lambda functions

Lastly, we have two columns with data currently being stored as strings that can be represented in a better way for this dataset. The `station` and `datatype` columns only have one and three distinct values, respectively, meaning that we aren't being efficient with our memory use since we are storing them as strings. We could potentially have issues with analyses further down the line. Pandas has the ability to define columns as **categorical**; certain statistical operations both within pandas and other packages will be able to handle this data, provide meaningful statistics on them, and use them properly. Categorical variables can take on one of a few values; for example, blood type would be a categorical variable—people can only have one of A, B, AB, or O.

Going back to the temperature data, we only have one value for the `station` column and only three distinct values for the `datatype` column (TAVG, TMAX, TMIN). We can use the `astype()` method to cast these into categories and look at the summary statistics:

```
>>> df_with_categories = df.assign(
...     station=df.station.astype('category'),
...     datatype=df.datatype.astype('category')
... )

>>> df_with_categories.dtypes
date           datetime64[ns]
datatype      category
station       category
flags          object
temp_C        float64
temp_C_whole   int64
```

```
temp_F           float64
temp_F_whole      int64
dtype: object

>>> df_with_categories.describe(include='category')
```

The summary statistics for categories are just like those for strings. We can see the number of non-null entries (**count**), the number of unique values (**unique**), the mode (**top**), and the number of occurrences of the mode (**freq**):

	datatype	station
count	93	93
unique	3	1
top	TAVG	GHCND:USW00014732
freq	31	93

Figure 3.17 – Summary statistics for the categorical columns

The categories we just made don't have any order to them, but pandas does support this:

```
>>> pd.Categorical(
...     ['med', 'med', 'low', 'high'],
...     categories=['low', 'med', 'high'],
...     ordered=True
... )
['med', 'med', 'low', 'high']
Categories (3, object): ['low' < 'med' < 'high']
```

When the columns in our dataframe are stored in the appropriate type, it opens up additional avenues for exploration, such as calculating statistics, aggregating the data, and sorting the values. For example, depending on our data source, it's possible that the numeric data is represented as a string, in which case attempting to sort on the values will reorder the contents lexically, meaning the result could be 1, 10, 11, 2, rather than 1, 2, 10, 11 (numerical sort). Similarly, if we have dates represented as strings in a format other than YYYY-MM-DD, sorting on this information may result in non-chronological order; however, by converting the date strings with `pd.to_datetime()`, we can chronologically sort dates that are provided in any format. Type conversion makes it possible to reorder both the numeric data and the dates according to their values, rather than their initial string representations.

Reordering, reindexing, and sorting data

We will often find the need to sort our data by the values of one or many columns. Say we wanted to find the days that reached the highest temperatures in New York City during October 2018; we could sort our values by the `temp_C` (or `temp_F`) column in descending order and use `head()` to select the number of days we wanted to see. To accomplish this, we can use the `sort_values()` method. Let's look at the top 10 days:

```
>>> df[df.datatype == 'TMAX'] \
...     .sort_values(by='temp_C', ascending=False).head(10)
```

This shows us that on October 7th and October 10th the temperature reached its highest value during the month of October 2018, according to the LaGuardia station. We also have ties between October 2nd and 4th, October 1st and 9th, and October 5th and 8th, but notice that the dates aren't always sorted—the 10th is after the 7th, but the 4th comes before the 2nd:

	date	datatype	station	flags	temp_C	temp_C_whole	temp_F	temp_F_whole
19	2018-10-07	TMAX	GHCND:USW00014732	,W,2400	27.8	27	82.04	82
28	2018-10-10	TMAX	GHCND:USW00014732	,W,2400	27.8	27	82.04	82
31	2018-10-11	TMAX	GHCND:USW00014732	,W,2400	26.7	26	80.06	80
10	2018-10-04	TMAX	GHCND:USW00014732	,W,2400	26.1	26	78.98	78
4	2018-10-02	TMAX	GHCND:USW00014732	,W,2400	26.1	26	78.98	78
1	2018-10-01	TMAX	GHCND:USW00014732	,W,2400	25.6	25	78.08	78
25	2018-10-09	TMAX	GHCND:USW00014732	,W,2400	25.6	25	78.08	78
7	2018-10-03	TMAX	GHCND:USW00014732	,W,2400	25.0	25	77.00	77
13	2018-10-05	TMAX	GHCND:USW00014732	,W,2400	22.8	22	73.04	73
22	2018-10-08	TMAX	GHCND:USW00014732	,W,2400	22.8	22	73.04	73

Figure 3.18 – Sorting the data to find the warmest days

The `sort_values()` method can be used with a list of column names to break ties. The order in which the columns are provided will determine the sort order, with each subsequent column being used to break ties. As an example, let's make sure the dates are sorted in ascending order when breaking ties:

```
>>> df[df.datatype == 'TMAX'].sort_values(
...     by=['temp_C', 'date'], ascending=[False, True]
... ).head(10)
```

Since we are sorting in ascending order, in the case of a tie, the date that comes earlier in the year will be above the later one. Notice how October 2nd is now above October 4th, despite both having the same temperature reading:

	date	datatype	station	flags	temp_C	temp_C_whole	temp_F	temp_F_whole
19	2018-10-07	TMAX	GHCND:USW00014732	,,W,2400	27.8	27	82.04	82
28	2018-10-10	TMAX	GHCND:USW00014732	,,W,2400	27.8	27	82.04	82
31	2018-10-11	TMAX	GHCND:USW00014732	,,W,2400	26.7	26	80.06	80
4	2018-10-02	TMAX	GHCND:USW00014732	,,W,2400	26.1	26	78.98	78
10	2018-10-04	TMAX	GHCND:USW00014732	,,W,2400	26.1	26	78.98	78
1	2018-10-01	TMAX	GHCND:USW00014732	,,W,2400	25.6	25	78.08	78
25	2018-10-09	TMAX	GHCND:USW00014732	,,W,2400	25.6	25	78.08	78
7	2018-10-03	TMAX	GHCND:USW00014732	,,W,2400	25.0	25	77.00	77
13	2018-10-05	TMAX	GHCND:USW00014732	,,W,2400	22.8	22	73.04	73
22	2018-10-08	TMAX	GHCND:USW00014732	,,W,2400	22.8	22	73.04	73

Figure 3.19 – Sorting the data with multiple columns to break ties

Tip

In pandas, the index is tied to the rows—when we drop rows, filter, or do anything that returns only some of the rows, our index may look out of order (as we saw in the previous examples). At the moment, the index just represents the row number in our data, so we may be interested in changing the values so that we have the first entry at index 0. To have pandas do so automatically, we can pass `ignore_index=True` to `sort_values()`.

Pandas also provides an additional way to look at a subset of the sorted values; we can use `nlargest()` to grab the n rows with the largest values according to specific criteria and `nsmallest()` to grab the n smallest rows, without the need to sort the data beforehand. Both accept a list of column names or a string for a single column. Let's grab the top 10 days by average temperature this time:

```
>>> df[df.datatype == 'TAVG'].nlargest(n=10, columns='temp_C')
```

We get the warmest days (on average) in October:

	date	datatype	station	flags	temp_C	temp_C_whole	temp_F	temp_F_whole
27	2018-10-10	TAVG	GHCND:USW00014732	H,,S,	23.8	23	74.84	74
30	2018-10-11	TAVG	GHCND:USW00014732	H,,S,	23.4	23	74.12	74
18	2018-10-07	TAVG	GHCND:USW00014732	H,,S,	22.8	22	73.04	73
3	2018-10-02	TAVG	GHCND:USW00014732	H,,S,	22.7	22	72.86	72
6	2018-10-03	TAVG	GHCND:USW00014732	H,,S,	21.8	21	71.24	71
24	2018-10-09	TAVG	GHCND:USW00014732	H,,S,	21.8	21	71.24	71
9	2018-10-04	TAVG	GHCND:USW00014732	H,,S,	21.3	21	70.34	70
0	2018-10-01	TAVG	GHCND:USW00014732	H,,S,	21.2	21	70.16	70
21	2018-10-08	TAVG	GHCND:USW00014732	H,,S,	20.9	20	69.62	69
12	2018-10-05	TAVG	GHCND:USW00014732	H,,S,	20.3	20	68.54	68

Figure 3.20 – Sorting to find the 10 warmest days on average

We aren't limited to sorting values; if we wish, we can even order the columns alphabetically and sort the rows by their index values. For these tasks, we can use the `sort_index()` method. By default, `sort_index()` will target the rows so that we can do things such as order the index after performing an operation that shuffles it. For instance, the `sample()` method will give us randomly selected rows, which will lead to a jumbled index, so we can use `sort_index()` to order them afterward:

```
>>> df.sample(5, random_state=0).index
Int64Index([2, 30, 55, 16, 13], dtype='int64')
>>> df.sample(5, random_state=0).sort_index().index
Int64Index([2, 13, 16, 30, 55], dtype='int64')
```

Tip

If we need the result of `sample()` to be reproducible, we can pass in a **seed**, set to a number of our choosing (using the `random_state` argument). The seed initializes a pseudorandom number generator, so, provided that the same seed is used, the results will be the same.

When we want to target columns, we must pass in `axis=1`; rows will be the default (`axis=0`). Note that this argument is present in many pandas methods and functions (including `sample()`), so it's important to understand what it means. Let's use this knowledge to sort the columns of our dataframe alphabetically:

```
>>> df.sort_index(axis=1).head()
```

Having our columns in alphabetical order can come in handy when using `loc[]` because we can specify a range of columns with similar names; for example, we could now use `df.loc[:, 'station':'temp_F_whole']` to easily grab all of our temperature columns, along with the station information:

	datatype	date	flags	station	temp_C	temp_C_whole	temp_F	temp_F_whole
0	TAVG	2018-10-01	H,,S,	GHCND:USW00014732	21.2	21	70.16	70
1	TMAX	2018-10-01	,,W,2400	GHCND:USW00014732	25.6	25	78.08	78
2	TMIN	2018-10-01	,,W,2400	GHCND:USW00014732	18.3	18	64.94	64
3	TAVG	2018-10-02	H,,S,	GHCND:USW00014732	22.7	22	72.86	72
4	TMAX	2018-10-02	,,W,2400	GHCND:USW00014732	26.1	26	78.98	78

Figure 3.21 – Sorting the columns by name

Important note

Both `sort_index()` and `sort_values()` return new `DataFrame` objects. We must pass in `inplace=True` to update the dataframe we are working with.

The `sort_index()` method can also help us get an accurate answer when we're testing two dataframes for equality. Pandas will check that, in addition to having the same data, both have the same values for the index when it compares the rows. If we sort our dataframe by temperature in Celsius and check whether it is equal to the original dataframe, pandas tells us that it isn't. We must sort the index to see that they are the same:

```
>>> df.equals(df.sort_values(by='temp_C'))
False
>>> df.equals(df.sort_values(by='temp_C').sort_index())
True
```

Sometimes, we don't care too much about the numeric index, but we would like to use one (or more) of the other columns as the index instead. In this case, we can use the `set_index()` method. Let's set the `date` column as our index:

```
>>> df.set_index('date', inplace=True)
>>> df.head()
```

Notice that the `date` column has moved to the far left where the index goes, and we no longer have the numeric index:

	datatype	station	flags	temp_C	temp_C_whole	temp_F	temp_F_whole
date							
2018-10-01	TAVG	GHCND:USW00014732	H,,S,	21.2	21	70.16	70
2018-10-01	TMAX	GHCND:USW00014732	,,W,2400	25.6	25	78.08	78
2018-10-01	TMIN	GHCND:USW00014732	,,W,2400	18.3	18	64.94	64
2018-10-02	TAVG	GHCND:USW00014732	H,,S,	22.7	22	72.86	72
2018-10-02	TMAX	GHCND:USW00014732	,,W,2400	26.1	26	78.98	78

Figure 3.22 – Setting the date column as the index

Tip

We can also provide a list of columns to use as the index. This will create a `MultiIndex` object, where the first element in the list is the outermost level and the last is the innermost. We will discuss this further in the *Pivoting DataFrames* section.

Setting the index to a datetime lets us take advantage of datetime slicing and indexing, which we briefly discussed in *Chapter 2, Working with Pandas DataFrames*. As long as we provide a date format that pandas understands, we can grab the data. To select all of 2018, we can use `df.loc['2018']`; for the fourth quarter of 2018, we can use `df.loc['2018-Q4']`; and for October, we can use `df.loc['2018-10']`. These can also be combined to build ranges. Note that `loc[]` is optional when using ranges:

```
>>> df['2018-10-11':'2018-10-12']
```

This gives us the data from October 11, 2018 through October 12, 2018 (inclusive of both endpoints):

	datatype	station	flags	temp_C	temp_C_whole	temp_F	temp_F_whole
date							
2018-10-11	TAVG	GHCND:USW00014732	H,,S,	23.4	23	74.12	74
2018-10-11	TMAX	GHCND:USW00014732	,,W,2400	26.7	26	80.06	80
2018-10-11	TMIN	GHCND:USW00014732	,,W,2400	21.7	21	71.06	71
2018-10-12	TAVG	GHCND:USW00014732	H,,S,	18.3	18	64.94	64
2018-10-12	TMAX	GHCND:USW00014732	,,W,2400	22.2	22	71.96	71
2018-10-12	TMIN	GHCND:USW00014732	,,W,2400	12.2	12	53.96	53

Figure 3.23 – Selecting date ranges

We can use the `reset_index()` method to restore the date column:

```
>>> df['2018-10-11':'2018-10-12'].reset_index()
```

Our index now starts at 0, and the dates are now in a column called `date`. This is especially useful if we have data that we don't want to lose in the index, such as the date, but need to perform an operation as if it weren't in the index:

	date	datatype	station	flags	temp_C	temp_C_whole	temp_F	temp_F_whole
0	2018-10-11	TAVG	GHCND:USW00014732	H,,S,	23.4	23	74.12	74
1	2018-10-11	TMAX	GHCND:USW00014732	,,W,2400	26.7	26	80.06	80
2	2018-10-11	TMIN	GHCND:USW00014732	,,W,2400	21.7	21	71.06	71
3	2018-10-12	TAVG	GHCND:USW00014732	H,,S,	18.3	18	64.94	64
4	2018-10-12	TMAX	GHCND:USW00014732	,,W,2400	22.2	22	71.96	71
5	2018-10-12	TMIN	GHCND:USW00014732	,,W,2400	12.2	12	53.96	53

Figure 3.24 – Resetting the index

In some cases, we may have an index we want to continue to use, but we need to align it to certain values. For this purpose, we have the `reindex()` method. We provide it with an index to align our data to, and it adjusts the index accordingly. Note that this new index isn't necessarily part of the data—we simply have an index and want to match the current data up to it.

As an example, we will turn to the S&P 500 stock data in the `sp500.csv` file. It contains the **opening**, **high**, **low**, and **closing** (also called **OHLC**) prices daily for the S&P 500 from 2017 through the end of 2018, along with volume traded and the adjusted close (which we won't use). Let's read it in, setting the `date` column as the index and parsing the dates:

```
>>> sp = pd.read_csv(  
...     'data/sp500.csv', index_col='date', parse_dates=True  
... ).drop(columns=['adj_close']) # not using this column
```

Let's see what our data looks like and mark the day of the week for each row in order to understand what the index contains. We can easily isolate the date part from an index of type `DatetimeIndex`. When isolating date parts, pandas will give us the numeric representation of what we are looking for; if we are looking for the string version, we should look to see whether there is already a method before writing our own conversion function. In this case, it's `day_name()`:

```
>>> sp.head(10) \  
...     .assign(day_of_week=lambda x: x.index.day_name())
```

Tip

We can also do this with a series, but first, we need to access the `dt` attribute. For example, if we had a `date` column in the `sp` dataframe, we could grab the month with `sp.date.dt.month`. You can find the full list of what can be accessed at <https://pandas.pydata.org/pandas-docs/stable/reference/series.html#datetimelike-properties>.

Since the stock market is closed on the weekend (and holidays), we only have data for weekdays:

	high	low	open	close	volume	day_of_week
date						
2017-01-03	2263.879883	2245.129883	2251.570068	2257.830078	3770530000	Tuesday
2017-01-04	2272.820068	2261.600098	2261.600098	2270.750000	3764890000	Wednesday
2017-01-05	2271.500000	2260.449951	2268.179932	2269.000000	3761820000	Thursday
2017-01-06	2282.100098	2264.060059	2271.139893	2276.979980	3339890000	Friday
2017-01-09	2275.489990	2268.899902	2273.590088	2268.899902	3217610000	Monday
2017-01-10	2279.270020	2265.270020	2269.719971	2268.899902	3638790000	Tuesday
2017-01-11	2275.320068	2260.830078	2268.600098	2275.320068	3620410000	Wednesday
2017-01-12	2271.780029	2254.250000	2271.139893	2270.439941	3462130000	Thursday
2017-01-13	2278.679932	2271.510010	2272.739990	2274.639893	3081270000	Friday
2017-01-17	2272.080078	2262.810059	2269.139893	2267.889893	3584990000	Tuesday

Figure 3.25 – S&P 500 OHLC data

If we were analyzing the performance of a group of assets in a portfolio that included the S&P 500 and something that trades on the weekend, such as bitcoin, we would need to have values for every day of the year for the S&P 500. Otherwise, when looking at the daily value of our portfolio we would see huge drops every day the market was closed. To illustrate this, let's read in the bitcoin data from the `bitcoin.csv` file and combine the S&P 500 and bitcoin data into a portfolio. The bitcoin data also contains OHLC data and volume traded, but it comes with a column called `market_cap` that we don't need, so we have to drop that first:

```
>>> bitcoin = pd.read_csv(
...     'data/bitcoin.csv', index_col='date', parse_dates=True
... ).drop(columns=['market_cap'])
```

To analyze the portfolio, we will need to aggregate the data by day; this is a topic for *Chapter 4, Aggregating Pandas DataFrames*, so, for now, don't worry too much about how this aggregation is being performed—just know that we are summing up the data by day. For example, each day's closing price will be the sum of the closing price of the S&P 500 and the closing price of bitcoin:

```
# every day's closing price = S&P 500 close + Bitcoin close
# (same for other metrics)
>>> portfolio = pd.concat([sp, bitcoin], sort=False) \
...     .groupby(level='date').sum()

>>> portfolio.head(10).assign(
...     day_of_week=lambda x: x.index.day_name()
... )
```

Now, if we examine our portfolio, we will see that we have values for every day of the week; so far, so good:

	high	low	open	close	volume	day_of_week
date						
2017-01-01	1003.080000	958.700000	963.660000	998.330000	147775008	Sunday
2017-01-02	1031.390000	996.700000	998.620000	1021.750000	222184992	Monday
2017-01-03	3307.959883	3266.729883	3273.170068	3301.670078	3955698000	Tuesday
2017-01-04	3432.240068	3306.000098	3306.000098	3425.480000	4109835984	Wednesday
2017-01-05	3462.600000	3170.869951	3424.909932	3282.380000	4272019008	Thursday
2017-01-06	3328.910098	3148.000059	3285.379893	3179.179980	3691766000	Friday
2017-01-07	908.590000	823.560000	903.490000	908.590000	279550016	Saturday
2017-01-08	942.720000	887.250000	908.170000	911.200000	158715008	Sunday
2017-01-09	3189.179990	3148.709902	3186.830088	3171.729902	3359486992	Monday
2017-01-10	3194.140020	3166.330020	3172.159971	3176.579902	3754598000	Tuesday

Figure 3.26 – Portfolio of the S&P 500 and bitcoin

However, there is a problem with this approach, which is much easier to see with a visualization. Plotting will be covered in depth in *Chapter 5, Visualizing Data with Pandas and Matplotlib*, and *Chapter 6, Plotting with Seaborn and Customization Techniques*, so don't worry about the details for now:

```
>>> import matplotlib.pyplot as plt # module for plotting
>>> from matplotlib.ticker import StrMethodFormatter

# plot the closing price from Q4 2017 through Q2 2018
>>> ax = portfolio['2017-Q4':'2018-Q2'].plot(
...     y='close', figsize=(15, 5), legend=False,
...     title='Bitcoin + S&P 500 value without accounting '
...           'for different indices'
... )

# formatting
>>> ax.set_ylabel('price')
>>> ax.yaxis\
...     .set_major_formatter(StrMethodFormatter('${x:, .0f}'))
>>> for spine in ['top', 'right']:
...     ax.spines[spine].set_visible(False)

# show the plot
>>> plt.show()
```

Notice how there is a cyclical pattern here? It is dropping every day the market is closed because the aggregation only had bitcoin data to sum for those days:

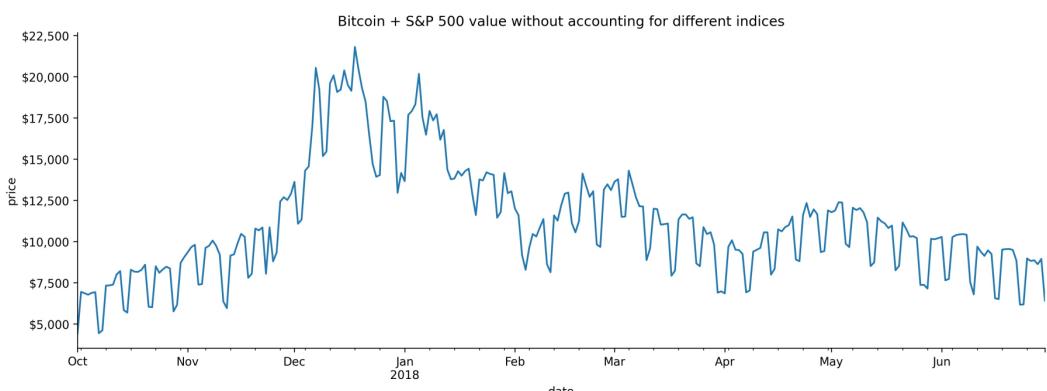


Figure 3.27 – Portfolio closing price without accounting for stock market closures

Clearly, this is a problem; an asset's value doesn't drop to zero whenever the market is closed. If we want pandas to fill the missing data in for us, we will need to reindex the S&P 500 data with bitcoin's index using the `reindex()` method, passing one of the following strategies to the `method` parameter:

- '`ffill`': This method brings values forward. In the previous example, this fills the days the market was closed with the data for the last time the market was open before those days.
- '`bfill`': This method backpropagates the values, which will result in carrying future results to past dates, meaning that this isn't the right option here.
- '`nearest`': This method fills according to the rows closest to the missing ones, which in this case will result in Sundays getting the data for the following Mondays, and Saturdays getting the data from the previous Fridays.

Forward-filling seems to be the best option, but since we aren't sure, we will see how this works on a few rows of the data first:

```
>>> sp.reindex(bitcoin.index, method='ffill').head(10) \
...     .assign(day_of_week=lambda x: x.index.day_name())
```

Notice any issues with this? Well, the volume traded (`volume`) column makes it seem like the days we used forward-filling for are actually days when the market is open:

	high	low	open	close	volume	day_of_week
date						
2017-01-01	NaN	NaN	NaN	NaN	NaN	Sunday
2017-01-02	NaN	NaN	NaN	NaN	NaN	Monday
2017-01-03	2263.879883	2245.129883	2251.570068	2257.830078	3.770530e+09	Tuesday
2017-01-04	2272.820068	2261.600098	2261.600098	2270.750000	3.764890e+09	Wednesday
2017-01-05	2271.500000	2260.449951	2268.179932	2269.000000	3.761820e+09	Thursday
2017-01-06	2282.100098	2264.060059	2271.139893	2276.979980	3.339890e+09	Friday
2017-01-07	2282.100098	2264.060059	2271.139893	2276.979980	3.339890e+09	Saturday
2017-01-08	2282.100098	2264.060059	2271.139893	2276.979980	3.339890e+09	Sunday
2017-01-09	2275.489990	2268.899902	2273.590088	2268.899902	3.217610e+09	Monday
2017-01-10	2279.270020	2265.270020	2269.719971	2268.899902	3.638790e+09	Tuesday

Figure 3.28 – Forward-filling dates with missing values

Tip

The `compare()` method will show us the values that differ across identically-labeled dataframes (same index and columns); we can use it to isolate the changes in our data when forward-filling here. There is an example in the notebook.

Ideally, we only want to maintain the value of the stock when the stock market is closed—the volume traded should be zero. In order to handle the `NaN` values in a different manner for each column, we will turn to the `assign()` method. To fill any `NaN` values in the `volume` column with 0, we will use the `fillna()` method, which we will see more of in the *Handling duplicate, missing, or invalid data* section, later in this chapter. The `fillna()` method also allows us to pass in a method instead of a value, so we can forward-fill the `close` column, which was the only column that made sense from our previous attempt. Lastly, we can use the `np.where()` function for the remaining columns, which allows us to build a vectorized `if...else`. It takes the following form:

```
np.where(boolean condition, value if True, value if False)
```

Vectorized operations are performed on all the elements in the array at once; since each element has the same data type, these calculations can be run rather quickly. As a general rule of thumb, with pandas, we should avoid writing loops in favor of vectorized operations for better performance. NumPy functions are designed to work on arrays, so they are perfect candidates for high-performance pandas code. This will make it easy for us to set any `NaN` values in the `open`, `high`, or `low` columns to the value in the `close` column for the same day. Since these come after the `close` column gets worked on, we will have the forward-filled value for `close` to use for the other columns where necessary:

```
>>> import numpy as np

>>> sp_reindexed = sp.reindex(bitcoin.index).assign(
...     # volume is 0 when the market is closed
...     volume=lambda x: x.volume.fillna(0),
...     # carry this forward
...     close=lambda x: x.close.fillna(method='ffill'),
...     # take the closing price if these aren't available
...     open=lambda x: \
...         np.where(x.open.isnull(), x.close, x.open),
...     high=lambda x: \
...         np.where(x.high.isnull(), x.close, x.high),
...     low=lambda x: np.where(x.low.isnull(), x.close, x.low)
... )
```

```
>>> sp_reindexed.head(10).assign(
...     day_of_week=lambda x: x.index.day_name()
... )
```

On Saturday, January 7th and Sunday, January 8th, we now have volume traded at zero. The OHLC prices are all equal to the closing price on Friday, the 6th:

	high	low	open	close	volume	day_of_week
date						
2017-01-01	NaN	NaN	NaN	NaN	0.000000e+00	Sunday
2017-01-02	NaN	NaN	NaN	NaN	0.000000e+00	Monday
2017-01-03	2263.879883	2245.129883	2251.570068	2257.830078	3.770530e+09	Tuesday
2017-01-04	2272.820068	2261.600098	2261.600098	2270.750000	3.764890e+09	Wednesday
2017-01-05	2271.500000	2260.449951	2268.179932	2269.000000	3.761820e+09	Thursday
2017-01-06	2282.100098	2264.060059	2271.139893	2276.979980	3.339890e+09	Friday
2017-01-07	2276.979980	2276.979980	2276.979980	2276.979980	0.000000e+00	Saturday
2017-01-08	2276.979980	2276.979980	2276.979980	2276.979980	0.000000e+00	Sunday
2017-01-09	2275.489990	2268.899902	2273.590088	2268.899902	3.217610e+09	Monday
2017-01-10	2279.270020	2265.270020	2269.719971	2268.899902	3.638790e+09	Tuesday

Figure 3.29 – Reindexing the S&P 500 data with specific strategies per column

Tip

Here, we use `np.where()` to both introduce a function we will see throughout this book and to make it easier to understand what is going on, but note that `np.where(x.open.isnull(), x.close, x.open)` can be replaced with the `combine_first()` method, which (for this use case) is equivalent to `x.open.combine_first(x.close)`. We will use the `combine_first()` method in the *Handling duplicate, missing, or invalid data* section, later this chapter.

Now, let's recreate the portfolio with the reindexed S&P 500 data and use a visualization to compare it with the previous attempt (again, don't worry about the plotting code, which will be covered in *Chapter 5, Visualizing Data with Pandas and Matplotlib*, and *Chapter 6, Plotting with Seaborn and Customization Techniques*):

```
# every day's closing price = S&P 500 close adjusted for
# market closure + Bitcoin close (same for other metrics)
>>> fixed_portfolio = sp_reindexed + bitcoin

# plot the reindexed portfolio's close (Q4 2017 - Q2 2018)
>>> ax = fixed_portfolio['2017-Q4':'2018-Q2'].plot(
...     y='close', figsize=(15, 5), linewidth=2,
...     label='reindexed portfolio of S&P 500 + Bitcoin',
...     title='Reindexed portfolio vs.'
...         'portfolio with mismatched indices'
... )

# add line for original portfolio for comparison
>>> portfolio['2017-Q4':'2018-Q2'].plot(
...     y='close', ax=ax, linestyle='--',
...     label='portfolio of S&P 500 + Bitcoin w/o reindexing'
... )

# formatting
>>> ax.set_ylabel('price')
>>> ax.yaxis\
...     .set_major_formatter(StrMethodFormatter('${x:.0f}'))
>>> for spine in ['top', 'right']:
...     ax.spines[spine].set_visible(False)

# show the plot
>>> plt.show()
```

The orange dashed line is our original attempt at studying the portfolio (without reindexing), while the blue solid line is the portfolio we just built with reindexing and different filling strategies per column. Keep this strategy in mind for the exercises in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*:

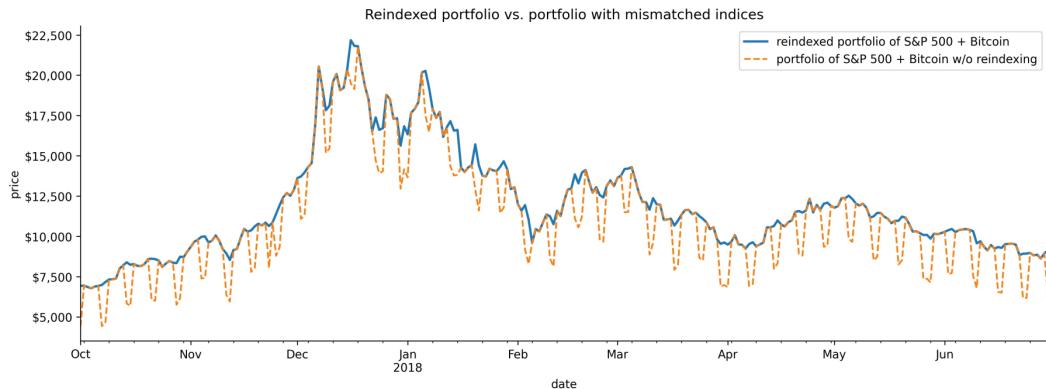


Figure 3.30 – Visualizing the effect of reindexing

Tip

We can also use the `reindex()` method to reorder the rows. For example, if our data is stored in `x`, then `x.reindex([32, 20, 11])` will return a new `DataFrame` object of three rows: 32, 20, and 11 (in that order). This can be done along the columns with `axis=1` (the default is `axis=0` for rows).

Now, let's turn our attention to reshaping data. Recall that we had to first filter the temperature data by the `datatype` column and then sort to find the warmest days; reshaping the data will make this easier, and also make it possible for us to aggregate and summarize the data.

Reshaping data

Data isn't always given to us in the format that's most convenient for our analysis. Therefore, we need to be able to restructure data into both wide and long formats, depending on the analysis we want to perform. For many analyses, we will want wide format data so that we can look at the summary statistics easily and share our results in that format.

However, this isn't always as black and white as going from long format to wide format or vice versa. Consider the following data from the *Exercises* section:

	ticker	date	high	low	open	close	volume
0	AAPL	2018-01-02	43.075001	42.314999	42.540001	43.064999	102223600
0	AMZN	2018-01-02	1190.000000	1170.510010	1172.000000	1189.010010	2694500
0	FB	2018-01-02	181.580002	177.550003	177.679993	181.419998	18151900
0	GOOG	2018-01-02	1066.939941	1045.229980	1048.339966	1065.000000	1237600
0	NFLX	2018-01-02	201.649994	195.419998	196.100006	201.070007	10966900

Figure 3.31 – Data with some long and some wide format columns

It's possible to have data where some of the columns are in wide format (**open**, **high**, **low**, **close**, **volume**), but others are in long format (**ticker**). Summary statistics using `describe()` on this data aren't helpful unless we first filter on **ticker**. This format makes it easy to compare the stocks; however, as we briefly discussed when we learned about wide and long formats, we wouldn't be able to easily plot the closing price for each stock using pandas—we would need seaborn. Alternatively, we could restructure the data for that visualization.

Now that we understand the motivation for restructuring data, let's move to the next notebook, `4 - reshaping_data.ipynb`. We will begin by importing pandas and reading in the `long_data.csv` file, adding the temperature in Fahrenheit column (`temp_F`), and performing some of the data cleaning we just learned about:

```
>>> import pandas as pd

>>> long_df = pd.read_csv(
...     'data/long_data.csv',
...     usecols=['date', 'datatype', 'value']
... ).rename(columns={'value': 'temp_C'}).assign(
...     date=lambda x: pd.to_datetime(x.date),
...     temp_F=lambda x: (x.temp_C * 9/5) + 32
... )
```

Our long format data looks like this:

	datatype	date	temp_C	temp_F
0	TMAX	2018-10-01	21.1	69.98
1	TMIN	2018-10-01	8.9	48.02
2	TOBS	2018-10-01	13.9	57.02
3	TMAX	2018-10-02	23.9	75.02
4	TMIN	2018-10-02	13.9	57.02

Figure 3.32 – Long format temperature data

In this section, we will discuss transposing, pivoting, and melting our data. Note that after reshaping the data, we will often revisit the data cleaning tasks as things may have changed, or we may need to change things we couldn't access easily before. For example, we will want to perform some type conversion if the values were all turned into strings in long format, but in wide format some columns are clearly numeric.

Transposing DataFrames

While we will be pretty much only working with wide or long formats, pandas provides ways to restructure our data as we see fit, including taking the **transpose** (flipping the rows with the columns), which we may find useful to make better use of our display area when we're printing parts of our dataframe:

```
>>> long_df.set_index('date').head(6).T
```

Notice that the index is now in the columns, and that the column names are in the index:

date	2018-10-01	2018-10-01	2018-10-01	2018-10-02	2018-10-02	2018-10-02
datatype	TMAX	TMIN	TOBS	TMAX	TMIN	TOBS
temp_C	21.10	8.90	13.90	23.90	13.90	17.20
temp_F	69.98	48.02	57.02	75.02	57.02	62.96

Figure 3.33 – Transposed temperature data

It may not be immediately apparent how useful this can be, but we will see this a quite few times throughout this book; for example, to make content easier to display in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*, and to build a particular visualization for machine learning in *Chapter 9, Getting Started with Machine Learning in Python*.

Pivoting DataFrames

We **pivot** our data to go from long format to wide format. The `pivot()` method performs this restructuring of our `DataFrame` object. To pivot, we need to tell pandas which column currently holds the values (with the `values` argument) and the column that contains what will become the column names in wide format (the `columns` argument). Optionally, we can provide a new index (the `index` argument). Let's pivot into wide format, where we have a column for each of the temperature measurements in Celsius and use the dates as the index:

```
>>> pivoted_df = long_df.pivot(
...     index='date', columns='datatype', values='temp_C'
... )
>>> pivoted_df.head()
```

In our starting dataframe, there was a `datatype` column that contained only `TMAX`, `TMIN`, or `TOBS` as strings. Now, these are column names because we passed in `columns='datatype'`. By passing in `index='date'`, the date column became our index, without needing to run `set_index()`. Finally, the values for each combination of date and datatype are the corresponding temperatures in Celsius since we passed in `values='temp_C'`:

datatype	TMAX	TMIN	TOBS
date			
2018-10-01	21.1	8.9	13.9
2018-10-02	23.9	13.9	17.2
2018-10-03	25.0	15.6	16.1
2018-10-04	22.8	11.7	11.7
2018-10-05	23.3	11.7	18.9

Figure 3.34 – Pivoting the long format temperature data into wide format

As we discussed at the beginning of this chapter, with the data in wide format, we can easily get meaningful summary statistics with the `describe()` method:

```
>>> pivoted_df.describe()
```

We can see that we have 31 observations for all three temperature measurements and that this month has a wide range of temperatures (highest daily maximum of 26.7°C and lowest daily minimum of -1.1°C):

datatype	TMAX	TMIN	TOBS
count	31.000000	31.000000	31.000000
mean	16.829032	7.561290	10.022581
std	5.714962	6.513252	6.596550
min	7.800000	-1.100000	-1.100000
25%	12.750000	2.500000	5.550000
50%	16.100000	6.700000	8.300000
75%	21.950000	13.600000	16.100000
max	26.700000	17.800000	21.700000

Figure 3.35 – Summary statistics on the pivoted temperature data

We lost the temperature in Fahrenheit, though. If we want to keep it, we can provide multiple columns to `values`:

```
>>> pivoted_df = long_df.pivot(  
...     index='date', columns='datatype',  
...     values=['temp_C', 'temp_F'])  
... )  
>>> pivoted_df.head()
```

However, we now get an extra level above the column names. This is called a **hierarchical index**:

	temp_C			temp_F		
datatype	TMAX	TMIN	TOBS	TMAX	TMIN	TOBS
date						
2018-10-01	21.1	8.9	13.9	69.98	48.02	57.02
2018-10-02	23.9	13.9	17.2	75.02	57.02	62.96
2018-10-03	25.0	15.6	16.1	77.00	60.08	60.98
2018-10-04	22.8	11.7	11.7	73.04	53.06	53.06
2018-10-05	23.3	11.7	18.9	73.94	53.06	66.02

Figure 3.36 – Pivoting with multiple value columns

With this hierarchical index, if we want to select TMIN in Fahrenheit, we will first need to select temp_F and then TMIN:

```
>>> pivoted_df['temp_F']['TMIN'].head()
date
2018-10-01    48.02
2018-10-02    57.02
2018-10-03    60.08
2018-10-04    53.06
2018-10-05    53.06
Name: TMIN, dtype: float64
```

Important note

In cases where we need to perform an aggregation as we pivot (due to duplicate values in the index), we can use the `pivot_table()` method, which we will discuss in *Chapter 4, Aggregating Pandas DataFrames*.

We have been working with a single index throughout this chapter; however, we can create an index from any number of columns with `set_index()`. This gives us an index of type `MultiIndex`, where the outermost level corresponds to the first element in the list provided to `set_index()`:

```
>>> multi_index_df = long_df.set_index(['date', 'datatype'])

>>> multi_index_df.head().index
MultiIndex([('2018-10-01', 'TMAX'),
            ('2018-10-01', 'TMIN'),
            ('2018-10-01', 'TOBS'),
            ('2018-10-02', 'TMAX'),
            ('2018-10-02', 'TMIN')],
           names=['date', 'datatype'])

>>> multi_index_df.head()
```

Notice that we now have two levels in the index—date is the outermost level and datatype is the innermost:

		temp_C temp_F	
date	datatype		
2018-10-01	TMAX	21.1	69.98
	TMIN	8.9	48.02
	TOBS	13.9	57.02
2018-10-02	TMAX	23.9	75.02
	TMIN	13.9	57.02

Figure 3.37 – Working with a multi-level index

The `pivot()` method expects the data to only have one column to set as the index; if we have a multi-level index, we should use the `unstack()` method instead. We can use `unstack()` on `multi_index_df` and get a similar result to what we had previously. Order matters here because, by default, `unstack()` will move the innermost level of the index to the columns; in this case, that means we will keep the `date` level in the index and move the `datatype` level to the column names. To unstack a different level, simply pass in the index of the level to `unstack`, where 0 is the leftmost and -1 is the rightmost, or the name of the level (if it has one). Here, we will use the default:

```
>>> unstacked_df = multi_index_df.unstack()  
>>> unstacked_df.head()
```

With `multi_index_df`, we had `datatype` as the innermost level of the index, so, after using `unstack()`, it is along the columns. Note that we once again have a hierarchical index in the columns. In *Chapter 4, Aggregating Pandas DataFrames*, we will discuss a way to squash this back into a single level of columns:

		temp_C		temp_F			
datatype	date	TMAX	TMIN	TOBS	TMAX	TMIN	TOBS
	2018-10-01	21.1	8.9	13.9	69.98	48.02	57.02
	2018-10-02	23.9	13.9	17.2	75.02	57.02	62.96
	2018-10-03	25.0	15.6	16.1	77.00	60.08	60.98
	2018-10-04	22.8	11.7	11.7	73.04	53.06	53.06
	2018-10-05	23.3	11.7	18.9	73.94	53.06	66.02

Figure 3.38 – Unstacking a multi-level index to pivot data

The `unstack()` method has the added benefit of allowing us to specify how to fill in missing values that come into existence upon reshaping the data. To do so, we can use the `fill_value` parameter. Imagine a case where we have been given the data for TAVG for October 1, 2018 only. We could append this to `long_df` and set our index to the `date` and `datatype` columns, as we did previously:

```
>>> extra_data = long_df.append([{
...     'datatype': 'TAVG',
...     'date': '2018-10-01',
...     'temp_C': 10,
...     'temp_F': 50
... }]).set_index(['date', 'datatype']).sort_index()

>>> extra_data['2018-10-01':'2018-10-02']
```

We now have four temperature measurements for October 1, 2018, but only three for the remaining days:

		temp_C	temp_F
	date	datatype	
2018-10-01		TAVG	10.0 50.00
		TMAX	21.1 69.98
		TMIN	8.9 48.02
		TOBS	13.9 57.02
2018-10-02		TMAX	23.9 75.02
		TMIN	13.9 57.02
		TOBS	17.2 62.96

Figure 3.39 – Introducing an additional temperature measurement into the data

Using `unstack()`, as we did previously, will result in `NaN` values for most of the TAVG data:

```
>>> extra_data.unstack().head()
```

Take a look at the TAVG columns after we unstack:

datatype	temp_C				temp_F			
	TAVG	TMAX	TMIN	TOBS	TAVG	TMAX	TMIN	TOBS
date								
2018-10-01	10.0	21.1	8.9	13.9	50.0	69.98	48.02	57.02
2018-10-02	NaN	23.9	13.9	17.2	NaN	75.02	57.02	62.96
2018-10-03	NaN	25.0	15.6	16.1	NaN	77.00	60.08	60.98
2018-10-04	NaN	22.8	11.7	11.7	NaN	73.04	53.06	53.06
2018-10-05	NaN	23.3	11.7	18.9	NaN	73.94	53.06	66.02

Figure 3.40 – Unstacking can lead to null values

To address this, we can pass in an appropriate `fill_value`. However, we are restricted to passing in a value for this, not a strategy (as we saw when we discussed reindexing), so while there is no good value for this case, we can use `-40` to illustrate how this works:

```
>>> extra_data.unstack(fill_value=-40).head()
```

The `NaN` values have now been replaced with `-40.0`. However, note that now both `temp_C` and `temp_F` have the same temperature reading. Actually, this is the reason we picked `-40` for `fill_value`; it is the temperature at which both Fahrenheit and Celsius are equal, so we won't confuse people with them both being the same number; for example, `0` (since $0^{\circ}\text{C} = 32^{\circ}\text{F}$ and $0^{\circ}\text{F} = -17.78^{\circ}\text{C}$). Since this temperature is also much colder than the temperatures measured in New York City and is below `TMIN` for all the data we have, it is more likely to be deemed a data entry error or a signal that data is missing compared to if we had used `0`. Note that, in practice, it is better to be explicit about the missing data if we are sharing this with others and leave the `NaN` values:

datatype	temp_C				temp_F			
	TAVG	TMAX	TMIN	TOBS	TAVG	TMAX	TMIN	TOBS
date								
2018-10-01	10.0	21.1	8.9	13.9	50.0	69.98	48.02	57.02
2018-10-02	-40.0	23.9	13.9	17.2	-40.0	75.02	57.02	62.96
2018-10-03	-40.0	25.0	15.6	16.1	-40.0	77.00	60.08	60.98
2018-10-04	-40.0	22.8	11.7	11.7	-40.0	73.04	53.06	53.06
2018-10-05	-40.0	23.3	11.7	18.9	-40.0	73.94	53.06	66.02

Figure 3.41 – Unstacking with a default value for missing combinations

To summarize, `unstack()` should be our method of choice when we have a multi-level index and would like to move one or more of the levels to the columns; however, if we are simply using a single index, the `pivot()` method's syntax is likely to be easier to specify correctly since it's more apparent which data will end up where.

Melting DataFrames

To go from wide format to long format, we need to **melt** the data. Melting undoes a pivot. For this example, we will read in the data from the `wide_data.csv` file:

```
>>> wide_df = pd.read_csv('data/wide_data.csv')
>>> wide_df.head()
```

Our wide data contains a column for the date and a column for each temperature measurement we have been working with:

	date	TMAX	TMIN	TOBS
0	2018-10-01	21.1	8.9	13.9
1	2018-10-02	23.9	13.9	17.2
2	2018-10-03	25.0	15.6	16.1
3	2018-10-04	22.8	11.7	11.7
4	2018-10-05	23.3	11.7	18.9

Figure 3.42 – Wide format temperature data

We can use the `melt()` method for flexible reshaping—allowing us to turn this into long format, similar to what we got from the API. Melting requires that we specify the following:

- Which column(s) uniquely identify a row in the wide format data with the `id_vars` argument
- Which column(s) contain(s) the variable(s) with the `value_vars` argument

Optionally, we can also specify how to name the column containing the variable names in the long format data (`var_name`) and the name for the column containing their values (`value_name`). By default, these will be `variable` and `value`, respectively.

Now, let's use the `melt()` method to turn the wide format data into long format:

```
>>> melted_df = wide_df.melt(  
...      id_vars='date', value_vars=['TMAX', 'TMIN', 'TOBS'],  
...      value_name='temp_C', var_name='measurement'  
... )  
>>> melted_df.head()
```

The date column was the identifier for our rows, so we provided that as `id_vars`. We turned the values in the TMAX, TMIN, and TOBS columns into a single column with the temperatures (`value_vars`) and used their column names as the values for a measurement column (`var_name='measurement'`). Lastly, we named the values column (`value_name='temp_C'`). We now have just three columns; the date, the temperature reading in Celsius (`temp_C`), and a column indicating which temperature measurement is in that row's `temp_C` cell (`measurement`):

	date	measurement	temp_C
0	2018-10-01	TMAX	21.1
1	2018-10-02	TMAX	23.9
2	2018-10-03	TMAX	25.0
3	2018-10-04	TMAX	22.8
4	2018-10-05	TMAX	23.3

Figure 3.43 – Melting the wide format temperature data

Just as we had an alternative way of pivoting data with the `unstack()` method, we also have another way of melting data with the `stack()` method. This method will pivot the columns into the innermost level of the index (resulting in an index of type `MultiIndex`), so we need to double-check our index before calling it. It also lets us drop row/column combinations that result in no data, if we choose. We can do the following to get a similar output to the `melt()` method:

```
>>> wide_df.set_index('date', inplace=True)  
>>> stacked_series = wide_df.stack() # put datatypes in index  
>>> stacked_series.head()  
date  
2018-10-01    TMAX    21.1  
                  TMIN    8.9  
                  TOBS   13.9
```

```
2018-10-02    TMAX      23.9
              TMIN      13.9
dtype: float64
```

Notice that the result came back as a `Series` object, so we will need to create the `DataFrame` object once more. We can use the `to_frame()` method and pass in a name to use for the column once it is a dataframe:

```
>>> stacked_df = stacked_series.to_frame('values')
>>> stacked_df.head()
```

Now, we have a dataframe with a multi-level index, containing date and datatype, with values as the only column. Notice, however, that only the `date` portion of our index has a name:

values		
date		
2018-10-01	TMAX	21.1
	TMIN	8.9
	TOBS	13.9
2018-10-02	TMAX	23.9
	TMIN	13.9

Figure 3.44 – Stacking to melt the temperature data into long format

Initially, we used `set_index()` to set the index to the `date` column because we didn't want to melt that; this formed the first level of the multi-level index. Then, the `stack()` method moved the `TMAX`, `TMIN`, and `TOBS` columns into the second level of the index. However, this level was never named, so it shows up as `None`, but we know that the level should be called `datatype`:

```
>>> stacked_df.head().index
MultiIndex([('2018-10-01', 'TMAX'),
            ('2018-10-01', 'TMIN'),
            ('2018-10-01', 'TOBS'),
            ('2018-10-02', 'TMAX'),
            ('2018-10-02', 'TMIN')],
           names=['date', None])
```

We can use the `set_names()` method to address this:

```
>>> stacked_df.index\  
...     .set_names(['date', 'datatype'], inplace=True)  
>>> stacked_df.index.names  
FrozenList(['date', 'datatype'])
```

Now that we understand the basics of data cleaning and reshaping, we will walk through an example of how these techniques can be combined when working with data that contains various issues.

Handling duplicate, missing, or invalid data

So far, we have discussed things we could change with the way the data was represented with zero ramifications. However, we didn't discuss a very important part of data cleaning: how to deal with data that appears to be duplicated, invalid, or missing. This is separated from the rest of the data cleaning discussion because it is an example where we will do some initial data cleaning, then reshape our data, and finally look to handle these potential issues; it is also a rather hefty topic.

We will be working in the `5-handling_data_issues.ipynb` notebook and using the `dirty_data.csv` file. Let's start by importing pandas and reading in the data:

```
>>> import pandas as pd  
>>> df = pd.read_csv('data/dirty_data.csv')
```

The `dirty_data.csv` file contains wide format data from the weather API that has been altered to introduce many common data issues that we will encounter in the wild. It contains the following fields:

- PRCP: Precipitation in millimeters
- SNOW: Snowfall in millimeters
- SNWD: Snow depth in millimeters
- TMAX: Maximum daily temperature in Celsius
- TMIN: Minimum daily temperature in Celsius
- TOBS: Temperature at the time of observation in Celsius
- WESF: Water equivalent of snow in millimeters

This section is divided into two parts. In the first part, we will discuss some tactics to uncover issues within a dataset, and in the second part, we will learn how to mitigate some of the issues present in this dataset.

Finding the problematic data

In *Chapter 2, Working with Pandas DataFrames*, we learned the importance of examining our data when we get it; it's not a coincidence that many of the ways to inspect the data will help us find these issues. Examining the results of calling `head()` and `tail()` on the data is always a good first step:

```
>>> df.head()
```

In practice, `head()` and `tail()` aren't as robust as the rest of what we will discuss in this section, but we can still get some useful information by starting here. Our data is in wide format, and at a quick glance, we can see that we have some potential issues. Sometimes, the `station` field is recorded as `?`, while other times, it has a station ID. We have values of negative infinity (`-inf`) for snow depth (`SNWD`), along with some very hot temperatures for `TMAX`. Lastly, we can observe many `NaN` values in several columns, including the `inclement_weather` column, which appears to also contain Boolean values:

	date	station	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
0	2018-01-01T00:00:00	?	0.0	0.0	-inf	5505.0	-40.0	NaN	NaN	NaN
1	2018-01-01T00:00:00	?	0.0	0.0	-inf	5505.0	-40.0	NaN	NaN	NaN
2	2018-01-01T00:00:00	?	0.0	0.0	-inf	5505.0	-40.0	NaN	NaN	NaN
3	2018-01-02T00:00:00	GHCND:USC00280907	0.0	0.0	-inf	-8.3	-16.1	-12.2	NaN	False
4	2018-01-03T00:00:00	GHCND:USC00280907	0.0	0.0	-inf	-4.4	-13.9	-13.3	NaN	False

Figure 3.45 – Dirty data

Using `describe()`, we can see if we have any missing data and look at the 5-number summary to spot potential issues:

```
>>> df.describe()
```

The SNWD column appears to be useless, and the TMAX column seems unreliable. For perspective, the temperature of the Sun's photosphere is around 5,505°C, so we certainly wouldn't expect to observe those air temperatures in New York City (or anywhere on Earth, for that matter). This likely means that the TMAX column was set to a nonsensical, large number when it wasn't available. The fact that it is so large is actually what helps identify it using the summary statistics we get from `describe()`. If unknowns were encoded with another value, say 40°C, we couldn't be sure it wasn't actual data:

	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF
count	765.000000	577.000000	577.0	765.000000	765.000000	398.000000	11.000000
mean	5.360392	4.202773	NaN	2649.175294	-15.914379	8.632161	16.290909
std	10.002138	25.086077	NaN	2744.156281	24.242849	9.815054	9.489832
min	0.000000	0.000000	-inf	-11.700000	-40.000000	-16.100000	1.800000
25%	0.000000	0.000000	NaN	13.300000	-40.000000	0.150000	8.600000
50%	0.000000	0.000000	NaN	32.800000	-11.100000	8.300000	19.300000
75%	5.800000	0.000000	NaN	5505.000000	6.700000	18.300000	24.900000
max	61.700000	229.000000	inf	5505.000000	23.900000	26.100000	28.700000

Figure 3.46 – Summary statistics for the dirty data

We can use the `info()` method to see if we have any missing values and check that our columns have the expected data types. In doing so, we immediately see two issues: we have 765 rows, but for five of the columns, we have many fewer non-null entries. This output also shows us that the data type of the `inclement_weather` column is not Boolean, though we may have thought so from the name. Notice that the ? value that we saw for the `station` column when we used `head()` doesn't show up here—it's important to inspect our data from many different angles:

```
>>> df.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 765 entries, 0 to 764
Data columns (total 10 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   date             765 non-null    object  
 1   station          765 non-null    object  
 2   PRCP             765 non-null    float64 
 3   SNOW             577 non-null    float64 
 4   SNWD             577 non-null    float64 
 5   TMAX             765 non-null    float64 
```

```

6   TMIN                765 non-null      float64
7   TOBS                398 non-null      float64
8   WESF                 11 non-null      float64
9   inclement_weather   408 non-null    object
dtypes: float64(7), object(3)
memory usage: 59.9+ KB

```

Now, let's track down those null values. Both `Series` and `DataFrame` objects provide two methods to do so: `isnull()` and `isna()`. Note that if we use the method on the `DataFrame` object, the result will tell us which rows have all null values, which isn't what we want in this case. Here, we want to examine the rows that have null values in the `SNOW`, `SNWD`, `TOBS`, `WESF`, or `inclement_weather` columns. This means that we will need to combine checks for each of the columns with the `|` (bitwise OR) operator:

```

>>> contain_nulls = df[
...     df.SNOW.isna() | df.SNWD.isna() | df.TOBS.isna()
...     | df.WESF.isna() | df.inclement_weather.isna()
... ]
>>> contain_nulls.shape[0]
765
>>> contain_nulls.head(10)

```

If we look at the `shape` attribute of our `contain_nulls` dataframe, we will see that every single row contains some null data. Looking at the top 10 rows, we can see some `NaN` values in each of these rows:

	date	station	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
0	2018-01-01T00:00:00		?	0.0	0.0	-inf	5505.0	-40.0	NaN	NaN
1	2018-01-01T00:00:00		?	0.0	0.0	-inf	5505.0	-40.0	NaN	NaN
2	2018-01-01T00:00:00		?	0.0	0.0	-inf	5505.0	-40.0	NaN	NaN
3	2018-01-02T00:00:00	GHCND:USC00280907	0.0	0.0	-inf	-8.3	-16.1	-12.2	NaN	False
4	2018-01-03T00:00:00	GHCND:USC00280907	0.0	0.0	-inf	-4.4	-13.9	-13.3	NaN	False
5	2018-01-03T00:00:00	GHCND:USC00280907	0.0	0.0	-inf	-4.4	-13.9	-13.3	NaN	False
6	2018-01-03T00:00:00	GHCND:USC00280907	0.0	0.0	-inf	-4.4	-13.9	-13.3	NaN	False
7	2018-01-04T00:00:00		?	20.6	229.0	inf	5505.0	-40.0	NaN	19.3
8	2018-01-04T00:00:00		?	20.6	229.0	inf	5505.0	-40.0	NaN	19.3
9	2018-01-05T00:00:00		?	0.3	NaN	NaN	5505.0	-40.0	NaN	NaN

Figure 3.47 – Rows in the dirty data with nulls

Tip

By default, the `sort_values()` method that we discussed earlier in this chapter will put any `Nan` values last. We can change this behavior (to put them first) by passing in `na_position='first'`, which can also be helpful when looking for patterns in the data when the sort columns have null values.

Note that we can't check whether the value of the column is equal to `Nan` because `Nan` is not equal to anything:

```
>>> import numpy as np
>>> df[df.inclement_weather == 'NaN'].shape[0] # doesn't work
0
>>> df[df.inclement_weather == np.nan].shape[0] # doesn't work
0
```

We must use the aforementioned options (`isna() / isnull()`):

```
>>> df[df.inclement_weather.isna()].shape[0] # works
357
```

Note that `inf` and `-inf` are actually `np.inf` and `-np.inf`. Therefore, we can find the number of rows with `inf` or `-inf` values by doing the following:

```
>>> df[df.SNWD.isin([-np.inf, np.inf])].shape[0]
577
```

This only tells us about a single column, though, so we could write a function that will use a dictionary comprehension to return the number of infinite values per column in our dataframe:

```
>>> def get_inf_count(df):
...     """Find the number of inf/-inf values per column"""
...     return {
...         col: df[
...             df[col].isin([np.inf, -np.inf])
...         ].shape[0] for col in df.columns
...     }
```

Using our function, we find that the SNWD column is the only column with infinite values, but the majority of the values in the column are infinite:

```
>>> get_inf_count(df)
{'date': 0, 'station': 0, 'PRCP': 0, 'SNOW': 0, 'SNWD': 577,
'TMAX': 0, 'TMIN': 0, 'TOBS': 0, 'WESF': 0,
'inclement_weather': 0}
```

Before we can decide on how to handle the infinite values of snow depth, we should look at the summary statistics for snowfall (SNOW), which forms a big part of determining the snow depth (SNWD). To do so, we can make a dataframe with two series, where one contains the summary statistics for the snowfall column when the snow depth is `np.inf`, and the other for when it is `-np.inf`. In addition, we will use the `T` attribute to transpose the data for easier viewing:

```
>>> pd.DataFrame({
...     'np.inf Snow Depth':
...         df[df.SNWD == np.inf].SNOW.describe(),
...     '-np.inf Snow Depth':
...         df[df.SNWD == -np.inf].SNOW.describe()
... }).T
```

The snow depth was recorded as negative infinity when there was no snowfall; however, we can't be sure this isn't just a coincidence going forward. If we are just going to be working with this fixed date range, we can treat that as having a depth of 0 or NaN because it didn't snow. Unfortunately, we can't really make any assumptions with the positive infinity entries. They most certainly aren't that, but we can't decide what they should be, so it's probably best to leave them alone or not look at this column:

	count	mean	std	min	25%	50%	75%	max
np.inf Snow Depth	24.0	101.041667	74.498018	13.0	25.0	120.5	152.0	229.0
-np.inf Snow Depth	553.0	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0

Figure 3.48 – Summary statistics for snowfall when snow depth is infinite

We are working with a year of data, but somehow, we have 765 rows, so we should check why. The only columns we have yet to inspect are the `date` and `station` columns. We can use the `describe()` method to see the summary statistics for them:

```
>>> df.describe(include='object')
```

In 765 rows of data, the `date` column only has 324 unique values (meaning that some dates are missing), with some dates being present as many as eight times (`freq`). There are only two unique values for the `station` column, with the most frequent being **GHCND:USC00280907**. Since we saw some station IDs with the value of `?` when we used `head()` earlier (Figure 3.45), we know that is the other value; however, we can use `unique()` to see all the unique values if we hadn't. We also know that `?` occurs 367 times (765 - 398), without the need to use `value_counts()`:

	<code>date</code>	<code>station</code>	<code>inclement_weather</code>
<code>count</code>	765	765	408
<code>unique</code>	324	2	2
<code>top</code>	2018-07-05T00:00:00	GHCND:USC00280907	False
<code>freq</code>	8	398	384

Figure 3.49 – Summary statistics for the non-numeric columns in the dirty data

In practice, we may not know why the station is sometimes recorded as `?`—it could be intentional to show that they don't have the station, an error in the recording software, or an accidental omission that got encoded as `?`. How we deal with this would be a judgment call, as we will discuss in the next section.

Upon seeing that we had 765 rows of data and two distinct values for the station ID, we might have assumed that each day had two entries—one per station. However, this would only account for 730 rows, and we also now know that we are missing some dates. Let's see whether we can find any duplicate data that could account for this. We can use the result of the `duplicated()` method as a Boolean mask to find the duplicate rows:

```
>>> df[df.duplicated()].shape[0]  
284
```

Depending on what we are trying to achieve, we may handle duplicates differently. The rows that are returned can be modified with the `keep` argument. By default, it is '`first`', and, for each row that is present more than once, we will get only the additional rows (besides the first). However, if we pass in `keep=False`, we will get all the rows that are present more than once, not just each additional appearance they make:

```
>>> df[df.duplicated(keep=False)].shape[0]  
482
```

There is also a subset argument (first positional argument), which allows us to focus just on the duplicates of certain columns. Using this, we can see that when the `date` and `station` columns are duplicated, so is the rest of the data because we get the same result as before. However, we don't know if this is actually a problem:

```
>>> df[df.duplicated(['date', 'station'])].shape[0]
284
```

Now, let's examine a few of the duplicated rows:

```
>>> df[df.duplicated()].head()
```

Just looking at the first five rows shows us that some rows are repeated at least three times. Remember that the default behavior of `duplicated()` is to not show the first occurrence, which means that rows **1** and **2** have another matching value in the data (same for rows **5** and **6**):

	date	station	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
1	2018-01-01T00:00:00		?	0.0	0.0	-inf	5505.0	-40.0	NaN	NaN
2	2018-01-01T00:00:00		?	0.0	0.0	-inf	5505.0	-40.0	NaN	NaN
5	2018-01-03T00:00:00	GHCND:USC00280907	0.0	0.0	-inf	-4.4	-13.9	-13.3	NaN	False
6	2018-01-03T00:00:00	GHCND:USC00280907	0.0	0.0	-inf	-4.4	-13.9	-13.3	NaN	False
8	2018-01-04T00:00:00		?	20.6	229.0	inf	5505.0	-40.0	NaN	19.3

Figure 3.50 – Examining the duplicate data

Now that we know how to find problems in our data, let's learn about some ways we can try to address them. Note that there is no panacea here, and it will often come down to knowing the data we are working with and making judgment calls.

Mitigating the issues

We are in an unsatisfactory state with our data, and while we can work to make it better, the best plan of action isn't always evident. Perhaps the easiest thing we can do when faced with this class of data issues is to remove the duplicate rows. However, it is crucial that we evaluate the ramifications such a decision may have on our analysis. Even in cases where it appears that the data we are working with was collected from a larger dataset that had additional columns, thus making all our data distinct, we can't be sure that removing these columns is the reason the remaining data was duplicated—we would need to consult the source of the data and any available documentation.

Since we know that both stations will be for New York City, we may decide to drop the `station` column—they may have just been collecting different data. If we then decide to remove duplicate rows using the `date` column and keep the data for the station that wasn't ?, in the case of duplicates, we will lose all data we have for the `WESF` column because the ? station is the only one reporting `WESF` measurements:

```
>>> df[df.WESF.notna()].station.unique()
array(['?'], dtype=object)
```

One satisfactory solution in this case may be to carry out the following actions:

1. Perform type conversion on the `date` column:

```
>>> df.date = pd.to_datetime(df.date)
```

2. Save the `WESF` column as a series:

```
>>> station_qm_wesf = df[df.station == '?'] \
...      .drop_duplicates('date').set_index('date').WESF
```

3. Sort the dataframe by the `station` column in descending order to put the station with no ID (?) last:

```
>>> df.sort_values(
...     'station', ascending=False, inplace=True
... )
```

4. Remove rows that are duplicated based on the `date`, keeping the first occurrences, which will be ones where the `station` column has an ID (if that station has measurements). Note that `drop_duplicates()` can be done in-place, but if what we are trying to do is complicated, it's best not to start out with the in-place operation:

```
>>> df_deduped = df.drop_duplicates('date')
```

5. Drop the `station` column and set the index to the `date` column (so that it matches the `WESF` data):

```
>>> df_deduped = df_deduped.drop(columns='station') \
...      .set_index('date').sort_index()
```

6. Update the `WESF` column using the `combine_first()` method to `coalesce` (just as in SQL for those coming from a SQL background) the values to the first non-null entry; this means that if we had data from both stations, we would first take the value provided by the station with an ID, and if (and only if) that station was null would we take the value from the station without an ID (?). Since both `df_deduped` and `station_qm_wesf` are using the date as the index, the values are properly matched to the appropriate date:

```
>>> df_deduped = df_deduped.assign(WESF=
...     lambda x: x.WESF.combine_first(station_qm_wesf)
... )
```

This may sound a little complicated, but that's largely because we haven't learned about aggregation yet. In *Chapter 4, Aggregating Pandas DataFrames*, we will look at another way to go about this. Let's take a look at the result using the aforementioned implementation:

```
>>> df_deduped.shape
(324, 8)
>>> df_deduped.head()
```

We are now left with 324 rows—one for each unique date in our data. We were able to save the `WESF` column by putting it alongside the data from the other station:

	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
date								
2018-01-01	0.0	0.0	-inf	5505.0	-40.0	NaN	NaN	NaN
2018-01-02	0.0	0.0	-inf	-8.3	-16.1	-12.2	NaN	False
2018-01-03	0.0	0.0	-inf	-4.4	-13.9	-13.3	NaN	False
2018-01-04	20.6	229.0	inf	5505.0	-40.0	NaN	19.3	True
2018-01-05	14.2	127.0	inf	-4.4	-13.9	-13.9	NaN	True

Figure 3.51 – Using data wrangling to keep the information in the WESF column

Tip

We could have also specified to keep the last entry instead of the first or drop all duplicates with the `keep` argument, just like when we checked for duplicates with `duplicated()`. Keep this in mind as the `duplicated()` method can be useful in giving the results of a dry run on a deduplication task.

Now, let's deal with the null data. We can choose to drop it, replace it with some arbitrary value, or impute it using surrounding data. Each of these options has its ramifications. If we drop the data, we are going about our analysis with only part of the data; if we end up dropping half the rows, this is going to have a big impact. When changing the values of the data, we may be affecting the outcome of our analysis.

To drop all the rows with any null data (this doesn't have to be true for all the columns of the row, so be careful), we use the `dropna()` method; in our case, this leaves us with just 4 rows:

```
>>> df_deduped.dropna().shape  
(4, 8)
```

We can change the default behavior to only drop a row if all the columns are null with the `how` argument, except this doesn't get rid of anything:

```
>>> df_deduped.dropna(how='all').shape # default is 'any'  
(324, 8)
```

Thankfully, we can also use a subset of columns to determine what to drop. Say we wanted to look at snow data; we would most likely want to make sure that our data had values for `SNOW`, `SNWD`, and `inclement_weather`. This can be achieved with the `subset` argument:

```
>>> df_deduped.dropna(  
...     how='all', subset=['inclement_weather', 'SNOW', 'SNWD'])  
... ).shape  
(293, 8)
```

Note that this operation can also be performed along the columns, and that we can provide a threshold for the number of null values that must be observed to drop the data with the `thresh` argument. For example, if we say that at least 75% of the rows must be null to drop the column, we will drop the `WESF` column:

```
>>> df_deduped.dropna(  
...     axis='columns',  
...     thresh=df_deduped.shape[0] * .75 # 75% of rows  
... ).columns  
Index(['PRCP', 'SNOW', 'SNWD', 'TMAX', 'TMIN', 'TOBS',  
      'inclement_weather'],  
      dtype='object')
```

Since we have a lot of null values, we will likely be more interested in keeping these values, and perhaps finding a better way to represent them. If we replace the null data, we must exercise caution when deciding what to fill in instead; filling in all the values we don't have with some other value may yield strange results later on, so we must think about how we will use this data first.

To fill in null values with other data, we use the `fillna()` method, which gives us the option of specifying a value or a strategy for how to perform the filling. We will discuss filling with a single value first. The `WESF` column contains mostly null values, but since it is a measurement in milliliters that takes on the value of `NaN` when there is no water equivalent of snowfall, we can fill in the nulls with zeros. Note that this can be done in-place (again, as a general rule of thumb, we should use caution with in-place operations):

```
>>> df_deduped.loc[:, 'WESF'].fillna(0, inplace=True)
>>> df_deduped.head()
```

The `WESF` column no longer contains `NaN` values:

	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
date								
2018-01-01	0.0	0.0	-inf	5505.0	-40.0	NaN	0.0	NaN
2018-01-02	0.0	0.0	-inf	-8.3	-16.1	-12.2	0.0	False
2018-01-03	0.0	0.0	-inf	-4.4	-13.9	-13.3	0.0	False
2018-01-04	20.6	229.0	inf	5505.0	-40.0	NaN	19.3	True
2018-01-05	14.2	127.0	inf	-4.4	-13.9	-13.9	0.0	True

Figure 3.52 – Filling in null values in the `WESF` column

At this point, we have done everything we can without distorting the data. We know that we are missing dates, but if we reindex, we don't know how to fill in the resulting `NaN` values. With the weather data, we can't assume that because it snowed one day that it will snow the next, or that the temperature will be the same. For this reason, note that the following examples are just for illustrative purposes only—just because we can do something doesn't mean we should. The right solution will most likely depend on the domain and the problem we are looking to solve.

That being said, let's try to address some of the remaining issues with the temperature data. We know that when TMAX is the temperature of the Sun, it must be because there was no measured value, so let's replace it with NaN. We will also do so for TMIN, which currently uses -40°C for its placeholder, despite the coldest temperature ever recorded in NYC being -15°F (-26.1°C) on February 9, 1934 (<https://www.weather.gov/media/okx/Climate/CentralPark/extremes.pdf>):

```
>>> df_deduped = df_deduped.assign(  
...     TMAX=lambda x: x.TMAX.replace(5505, np.nan),  
...     TMIN=lambda x: x.TMIN.replace(-40, np.nan)  
... )
```

We will also make an assumption that the temperature won't change drastically from day to day. Note that this is actually a big assumption, but it will allow us to understand how the `fillna()` method works when we provide a strategy through the `method` parameter: '`ffill`' to forward-fill or '`bfill`' to back-fill. Notice we don't have the '`nearest`' option, like we did when we were reindexing, which would have been the best option; so, to illustrate how this works, let's use forward-filling:

```
>>> df_deduped.assign(  
...     TMAX=lambda x: x.TMAX.fillna(method='ffill'),  
...     TMIN=lambda x: x.TMIN.fillna(method='ffill')  
... ).head()
```

Take a look at the TMAX and TMIN columns on January 1st and 4th. Both are NaN on the 1st because we don't have data before then to bring forward, but the 4th now has the same values as the 3rd:

	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
date								
2018-01-01	0.0	0.0	-inf	NaN	NaN	NaN	0.0	NaN
2018-01-02	0.0	0.0	-inf	-8.3	-16.1	-12.2	0.0	False
2018-01-03	0.0	0.0	-inf	-4.4	-13.9	-13.3	0.0	False
2018-01-04	20.6	229.0	inf	-4.4	-13.9	NaN	19.3	True
2018-01-05	14.2	127.0	inf	-4.4	-13.9	-13.9	0.0	True

Figure 3.53 – Forward-filling null values

If we want to handle the nulls and infinite values in the `SNWD` column, we can use the `np.nan_to_num()` function; it turns `NaN` into 0 and `inf/-inf` into very large positive/negative finite numbers, making it possible for machine learning models (discussed in *Chapter 9, Getting Started with Machine Learning in Python*) to learn from this data:

```
>>> df_deduped.assign(
...     SNWD=lambda x: np.nan_to_num(x.SNWD)
... ).head()
```

This doesn't make much sense for our use case though. For instances of `-np.inf`, we may choose to set `SNWD` to 0 since we saw there was no snowfall on those days. However, we don't know what to do with `np.inf`, and the large positive numbers, arguably, make this more confusing to interpret:

	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
date								
2018-01-01	0.0	0.0	-1.797693e+308	NaN	NaN	NaN	0.0	NaN
2018-01-02	0.0	0.0	-1.797693e+308	-8.3	-16.1	-12.2	0.0	False
2018-01-03	0.0	0.0	-1.797693e+308	-4.4	-13.9	-13.3	0.0	False
2018-01-04	20.6	229.0	1.797693e+308	NaN	NaN	NaN	19.3	True
2018-01-05	14.2	127.0	1.797693e+308	-4.4	-13.9	-13.9	0.0	True

Figure 3.54 – Replacing infinite values

Depending on the data we are working with, we may choose to use the `clip()` method as an alternative to the `np.nan_to_num()` function. The `clip()` method makes it possible to cap values at a specific minimum and/or maximum threshold. Since the snow depth can't be negative, let's use `clip()` to enforce a lower bound of zero. To show how the upper bound works, we will use the snowfall (`SNOW`) as an estimate:

```
>>> df_deduped.assign(
...     SNWD=lambda x: x.SNWD.clip(0, x.SNOW)
... ).head()
```

The values of SNWD for January 1st through 3rd are now 0 instead of -inf, while the values of SNWD for January 4th and 5th went from inf to that day's value for SNOW:

	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
date								
2018-01-01	0.0	0.0	0.0	NaN	NaN	NaN	0.0	NaN
2018-01-02	0.0	0.0	0.0	-8.3	-16.1	-12.2	0.0	False
2018-01-03	0.0	0.0	0.0	-4.4	-13.9	-13.3	0.0	False
2018-01-04	20.6	229.0	229.0	NaN	NaN	NaN	19.3	True
2018-01-05	14.2	127.0	127.0	-4.4	-13.9	-13.9	0.0	True

Figure 3.55 – Capping values at thresholds

Our last strategy is imputation. When we replace a missing value with a new value derived from the data, using summary statistics or data from other observations, it is called **imputation**. For example, we can impute with the mean to replace temperature values. Unfortunately, if we are only missing values for the end of the month of October, and we replace them with the mean of the values from the rest of the month, this is likely to be skewed toward the extreme values, which are the warmer temperatures at the beginning of October, in this case. Like everything else that was discussed in this section, we must exercise caution and think about any potential consequences or side effects of our actions.

We can combine imputation with the `fillna()` method. As an example, let's fill in the NaN values for TMAX and TMIN with their medians and TOBS with the average of TMIN and TMAX (after imputing them):

```
>>> df_deduped.assign(  
...     TMAX=lambda x: x.TMAX.fillna(x.TMAX.median()),  
...     TMIN=lambda x: x.TMIN.fillna(x.TMIN.median()),  
...     # average of TMAX and TMIN  
...     TOBS=lambda x: x.TOBS.fillna((x.TMAX + x.TMIN) / 2)  
... ).head()
```

Notice from the changes to the data for January 1st and 4th that the median maximum and minimum temperatures were 14.4°C and 5.6°C, respectively. This means that when we impute TOBS and also don't have TMAX and TMIN in the data, we get 10°C:

	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
date								
2018-01-01	0.0	0.0	-inf	14.4	5.6	10.0	0.0	NaN
2018-01-02	0.0	0.0	-inf	-8.3	-16.1	-12.2	0.0	False
2018-01-03	0.0	0.0	-inf	-4.4	-13.9	-13.3	0.0	False
2018-01-04	20.6	229.0	inf	14.4	5.6	10.0	19.3	True
2018-01-05	14.2	127.0	inf	-4.4	-13.9	-13.9	0.0	True

Figure 3.56 – Imputing missing values with summary statistics

If we want to run the same calculation on all the columns, we should use the `apply()` method instead of `assign()`, since it saves us the redundancy of having to write the same calculation for each of the columns. For example, let's fill in all the missing values with the rolling 7-day median of their values, setting the number of periods required for the calculation to zero to ensure that we don't introduce extra null values. We will cover rolling calculations and `apply()` in *Chapter 4, Aggregating Pandas DataFrames*, so this is just a preview:

```
>>> df_deduped.apply(lambda x:
...     # Rolling 7-day median (covered in chapter 4).
...     # we set min_periods (# of periods required for
...     # calculation) to 0 so we always get a result
...     x.fillna(x.rolling(7, min_periods=0).median())
... ).head(10)
```

It's kind of hard to tell where our imputed values are here—temperatures can fluctuate quite a bit day to day. We know that January 4th had missing data from our previous attempt; our imputed temperatures are colder than those around it with this strategy. In reality, it was slightly warmer that day (around -3°C):

	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
date								
2018-01-01	0.0	0.0	-inf	NaN	NaN	NaN	0.0	NaN
2018-01-02	0.0	0.0	-inf	-8.30	-16.1	-12.20	0.0	False
2018-01-03	0.0	0.0	-inf	-4.40	-13.9	-13.30	0.0	False
2018-01-04	20.6	229.0	inf	-6.35	-15.0	-12.75	19.3	True
2018-01-05	14.2	127.0	inf	-4.40	-13.9	-13.90	0.0	True
2018-01-06	0.0	0.0	-inf	-10.00	-15.6	-15.00	0.0	False
2018-01-07	0.0	0.0	-inf	-11.70	-17.2	-16.10	0.0	False
2018-01-08	0.0	0.0	-inf	-7.80	-16.7	-8.30	0.0	False
2018-01-10	0.0	0.0	-inf	5.00	-7.8	-7.80	0.0	False
2018-01-11	0.0	0.0	-inf	4.40	-7.8	1.10	0.0	False

Figure 3.57 – Imputing missing values with the rolling median

Important note

It's important to exercise caution when imputing. If we pick the wrong strategy for the data, we can make a real mess of things.

Another way of imputing missing data is to have pandas calculate what the values should be with the `interpolate()` method. By default, it will perform linear interpolation, making the assumption that all the rows are evenly spaced. Our data is daily data, although some days are missing, so it is just a matter of reindexing first. Let's combine this with the `apply()` method to interpolate all of our columns at once:

```
>>> df_deduped.reindex(  
...     pd.date_range('2018-01-01', '2018-12-31', freq='D')  
... ).apply(lambda x: x.interpolate()).head(10)
```

Check out January 9th, which we didn't have previously—the values for TMAX, TMIN, and TOBS are the average of the values for the day prior (January 8th) and the day after (January 10th):

	PRCP	SNOW	SNWD	TMAX	TMIN	TOBS	WESF	inclement_weather
2018-01-01	0.0	0.0	-inf	NaN	NaN	NaN	0.0	NaN
2018-01-02	0.0	0.0	-inf	-8.3	-16.10	-12.20	0.0	False
2018-01-03	0.0	0.0	-inf	-4.4	-13.90	-13.30	0.0	False
2018-01-04	20.6	229.0	inf	-4.4	-13.90	-13.60	19.3	True
2018-01-05	14.2	127.0	inf	-4.4	-13.90	-13.90	0.0	True
2018-01-06	0.0	0.0	-inf	-10.0	-15.60	-15.00	0.0	False
2018-01-07	0.0	0.0	-inf	-11.7	-17.20	-16.10	0.0	False
2018-01-08	0.0	0.0	-inf	-7.8	-16.70	-8.30	0.0	False
2018-01-09	0.0	0.0	-inf	-1.4	-12.25	-8.05	0.0	NaN
2018-01-10	0.0	0.0	-inf	5.0	-7.80	-7.80	0.0	False

Figure 3.58 – Interpolating missing values

Different strategies for interpolation can be specified via the `method` argument; be sure to check out the `interpolate()` method documentation to view the available options.

Summary

Congratulations on making it through this chapter! Data wrangling may not be the most exciting part of the analytics workflow, but we will spend a lot of time on it, so it's best to be well versed in what pandas has to offer.

In this chapter, we learned more about what data wrangling is (aside from a data science buzzword) and got some firsthand experience with cleaning and reshaping our data. Utilizing the `requests` library, we once again practiced working with APIs to extract data of interest; then, we used `pandas` to begin our introduction to data wrangling, which we will continue in the next chapter. Finally, we learned how to deal with duplicate, missing, and invalid data points in various ways and discussed the ramifications of those decisions.

Building on these concepts, in the next chapter, we will learn how to aggregate dataframes and work with time series data. Be sure to complete the end-of-chapter exercises before moving on.

Exercises

Complete the following exercises using what we have learned so far in this book and the data in the `exercises` / directory:

1. We want to look at data for the **Facebook, Apple, Amazon, Netflix, and Google (FAANG)** stocks, but we were given each as a separate CSV file (obtained using the `stock_analysis` package we will build in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*). Combine them into a single file and store the dataframe of the FAANG data as `faang` for the rest of the exercises:
 - a) Read in the `aapl.csv`, `amzn.csv`, `fb.csv`, `goog.csv`, and `nflx.csv` files.
 - b) Add a column to each dataframe, called `ticker`, indicating the ticker symbol it is for (Apple's is AAPL, for example); this is how you look up a stock. In this case, the filenames happen to be the ticker symbols.
 - c) Append them together into a single dataframe.
 - d) Save the result in a CSV file called `faang.csv`.
2. With `faang`, use type conversion to cast the values of the `date` column into datetimes and the `volume` column into integers. Then, sort by `date` and `ticker`.
3. Find the seven rows in `faang` with the lowest value for `volume`.
4. Right now, the data is somewhere between long and wide format. Use `melt()` to make it completely long format. Hint: `date` and `ticker` are our ID variables (they uniquely identify each row). We need to melt the rest so that we don't have separate columns for `open`, `high`, `low`, `close`, and `volume`.
5. Suppose we found out that on July 26, 2018 there was a glitch in how the data was recorded. How should we handle this? Note that there is no coding required for this exercise.
6. The **European Centre for Disease Prevention and Control (ECDC)** provides an open dataset on COVID-19 cases called *daily number of new reported cases of COVID-19 by country worldwide* (<https://www.ecdc.europa.eu/en/publications-data/download-todays-data-geographic-distribution-covid-19-cases-worldwide>). This dataset is updated daily, but we will use a snapshot that contains data from January 1, 2020 through September 18, 2020. Clean and pivot the data so that it is in wide format:
 - a) Read in the `covid19_cases.csv` file.
 - b) Create a `date` column using the data in the `dateRep` column and the `pd.to_datetime()` function.

- c) Set the date column as the index and sort the index.
- d) Replace all occurrences of United_States_of_America and United_Kingdom with USA and UK, respectively. Hint: the replace() method can be run on the dataframe as a whole.
- e) Using the countriesAndTerritories column, filter the cleaned COVID-19 cases data down to Argentina, Brazil, China, Colombia, India, Italy, Mexico, Peru, Russia, Spain, Turkey, the UK, and the USA.
- f) Pivot the data so that the index contains the dates, the columns contain the country names, and the values are the case counts (the cases column). Be sure to fill in NaN values with 0.
7. In order to determine the case totals per country efficiently, we need the aggregation skills we will learn about in *Chapter 4, Aggregating Pandas DataFrames*, so the ECDC data in the covid19_cases.csv file has been aggregated for us and saved in the covid19_total_cases.csv file. It contains the total number of cases per country. Use this data to find the 20 countries with the largest COVID-19 case totals. Hints: when reading in the CSV file, pass in `index_col='cases'`, and note that it will be helpful to transpose the data before isolating the countries.

Further reading

Check out the following resources for more information on the topics that were covered in this chapter:

- *A Quick-Start Tutorial on Relational Database Design*: https://www.ntu.edu.sg/home/ehchua/programming/sql/relational_database_design.html
- *Binary search*: <https://www.khanacademy.org/computing/computer-science/algorithms/binary-search/a/binary-search>
- *How Recursion Works—explained with flowcharts and a video*: <https://www.freecodecamp.org/news/how-recursion-works-explained-with-flowcharts-and-a-video-de61f40cb7f9/>
- *Python f-strings*: <https://realpython.com/python-f-strings/>
- *Tidy Data (article by Hadley Wickham)*: <https://www.jstatsoft.org/article/view/v059i10>
- *5 Golden Rules for Great Web API Design*: <https://www.toptal.com/api-developers/5-golden-rules-for-designing-a-great-web-api>

4

Aggregating Pandas DataFrames

In this chapter, we will continue our discussion of data wrangling from *Chapter 3, Data Wrangling with Pandas*, by addressing the enrichment and aggregation of data. This includes essential skills, such as merging dataframes, creating new columns, performing window calculations, and aggregating by group membership. Calculating aggregations and summaries will help us draw conclusions about our data.

We will also take a look at the additional functionality pandas has for working with time series data, beyond the time series slicing we introduced in previous chapters, including how we can roll up the data with aggregation and select it based on the time of day. Much of the data we will encounter is time series data, so being able to effectively work with time series is paramount. Of course, performing these operations efficiently is important, so we will also review how to write efficient pandas code.

This chapter will get us comfortable with performing analyses using DataFrame objects. Consequently, these topics are more advanced compared to the prior content and may require a few rereads, so be sure to follow along with the notebooks, which contain additional examples.

The following topics will be covered in this chapter:

- Performing database-style operations on DataFrames
- Using DataFrame operations to enrich data
- Aggregating data
- Working with time series data

Chapter materials

The materials for this chapter can be found on GitHub at https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_04. There are four notebooks that we will work through, each numbered according to when they will be used. The text will prompt you to switch. We will begin with the `1-querying_and_merging.ipynb` notebook to learn about querying and merging dataframes. Then, we will move on to the `2-dataframe_operations.ipynb` notebook to discuss data enrichment through operations such as binning, window functions, and pipes. For this section, we will also use the `window_calc.py` Python file, which contains a function for performing window calculations using pipes.

Tip

The `understanding_window_calculations.ipynb` notebook contains some interactive visualizations for understanding window functions. This may require some additional setup, but the instructions are in the notebook.

Next, in the `3-aggregations.ipynb` notebook, we will discuss aggregations, pivot tables, and crosstabs. Finally, we will focus on additional capabilities pandas provides when working with time series data in the `4-time_series.ipynb` notebook. Note that we will not go over the `0-weather_data_collection.ipynb` notebook; however, for those interested, it contains the code that was used to collect the data from the **National Centers for Environmental Information (NCEI)** API, which can be found at <https://www.ncdc.noaa.gov/cdo-web/webservices/v2>.

Throughout this chapter, we will use a variety of datasets, which can be found in the `data/` directory:

File	Description	Source
<code>dirty_data.csv</code>	Dirty weather data from the <i>Handling duplicate, missing, or invalid data</i> section in <i>Chapter 3, Data Wrangling with Pandas</i>	Adapted from the NCEI API's GHCND dataset
<code>fb_2018.csv</code>	Facebook stock's opening, high, low, and closing price daily, along with volume traded for 2018.	The <code>stock_analysis</code> package (see <i>Chapter 7, Financial Analysis – Bitcoin and the Stock Market</i>).
<code>fb_week_of_may_20_per_minute.csv</code>	Facebook stock's opening, high, low, and closing price per minute, along with volume traded for May 20, 2019 through May 24, 2019.	Nasdaq
<code>melted_stock_data.csv</code>	The contents of <code>fb_week_of_may_20_per_minute.csv</code> melted into a single column for the price and another for the timestamp.	Adapted from Nasdaq
<code>nyc_weather_2018.csv</code>	Long format weather data for New York City across various stations.	The NCEI API's GHCND dataset.
<code>stocks.db</code>	The <code>fb_prices</code> and <code>aapl_prices</code> tables contain the stock prices for Facebook and Apple, respectively, for May 20, 2019 through May 24, 2019. Facebook is at a minute granularity, whereas Apple has timestamps that include (fictitious) seconds.	Adapted from Nasdaq
<code>weather_by_station.csv</code>	Long format weather data for New York City across various stations, along with station information.	The NCEI API's GHCND dataset and the <code>stations</code> endpoint.
<code>weather_stations.csv</code>	Information on all the stations providing weather data for New York City.	The NCEI API's <code>stations</code> endpoint.
<code>weather.db</code>	The <code>weather</code> table contains New York City weather data, while the <code>stations</code> table contains information on the stations.	The NCEI API's GHCND dataset and the <code>stations</code> endpoint.

Figure 4.1 – Datasets used in this chapter

Note that the `exercises/` directory contains the CSV files that are required to complete the end-of-chapter exercises. More information on these datasets can be found in the `exercises/README.md` file.

Performing database-style operations on DataFrames

DataFrame objects are analogous to tables in a database: each has a name we refer to it by, is composed of rows, and contains columns of specific data types. Consequently, pandas allows us to carry out database-style operations on them. Traditionally, databases support a minimum of four operations, called **CRUD: Create, Read, Update, and Delete**.

A database query language—most commonly **SQL** (pronounced *sequel* or *S-Q-L*), which stands for **Structured Query Language**—is used to ask the database to perform these operations. Knowledge of SQL is not required for this book; however, we will look at the SQL equivalent for the pandas operations that will be discussed in this section since it may aid the understanding of those familiar with SQL. Many data professionals have some familiarity with basic SQL, so consult the *Further reading* section for resources that provide a more formal introduction.

For this section, we will be working in the `1-querying_and_merging.ipynb` notebook. We will begin with our imports and read in the NYC weather data CSV file:

```
>>> import pandas as pd  
>>> weather = pd.read_csv('data/nyc_weather_2018.csv')  
>>> weather.head()
```

This is long format data—we have several different weather observations per day for various stations covering NYC in 2018:

	date	datatype	station	attributes	value
0	2018-01-01T00:00:00	PRCP	GHCND:US1CTFR0039	,,N,	0.0
1	2018-01-01T00:00:00	PRCP	GHCND:US1NJBG0015	,,N,	0.0
2	2018-01-01T00:00:00	SNOW	GHCND:US1NJBG0015	,,N,	0.0
3	2018-01-01T00:00:00	PRCP	GHCND:US1NJBG0017	,,N,	0.0
4	2018-01-01T00:00:00	SNOW	GHCND:US1NJBG0017	,,N,	0.0

Figure 4.2 – NYC weather data

In *Chapter 2, Working with Pandas DataFrames*, we covered how to create dataframes; this was the pandas equivalent of a "CREATE TABLE ..." SQL statement. When we discussed selection and filtering in *Chapter 2, Working with Pandas DataFrames*, and *Chapter 3, Data Wrangling with Pandas*, we were focusing on reading from dataframes, which equated to the SELECT (picking columns) and WHERE (filtering by Boolean criteria) SQL clauses. We carried out update (UPDATE in SQL) and delete (DELETE FROM in SQL) operations when we discussed working with missing data in *Chapter 3, Data Wrangling with Pandas*. In addition to those basic CRUD operations, the concept of a **join** or **merge** of tables exists. We will discuss the pandas implementation in this section, along with the idea of querying a DataFrame object.

Querying DataFrames

Pandas provides the `query()` method so that we can easily write complicated filters instead of using a Boolean mask. The syntax is similar to the `WHERE` clause in a SQL statement. To illustrate this, let's query the weather data for all the rows where the value of the `SNOW` column was greater than zero for stations with `US1NY` in their station ID:

```
>>> snow_data = weather.query(
...     'datatype == "SNOW" and value > 0 '
...     'and station.str.contains("US1NY")'
... )
>>> snow_data.head()
```

Each row is a snow observation for a given combination of date and station. Notice that the values vary quite a bit for January 4th—some stations received more snow than others:

	date	datatype	station	attributes	value
114	2018-01-01T00:00:00	SNOW	GHCND:US1NYWC0019	,N,	25.0
789	2018-01-04T00:00:00	SNOW	GHCND:US1NYNS0007	,N,	41.0
794	2018-01-04T00:00:00	SNOW	GHCND:US1NYNS0018	,N,	10.0
798	2018-01-04T00:00:00	SNOW	GHCND:US1NYNS0024	,N,	89.0
800	2018-01-04T00:00:00	SNOW	GHCND:US1NYNS0030	,N,	102.0

Figure 4.3 – Querying the weather data for observations of snow

This query is equivalent to the following in SQL. Note that `SELECT *` selects all the columns in the table (our dataframe, in this case):

```
SELECT * FROM weather
WHERE
    datatype == "SNOW" AND value > 0 AND station LIKE "%US1NY%";
```

In *Chapter 2, Working with Pandas DataFrames*, we learned how to use a Boolean mask to get the same result:

```
>>> weather[
...     (weather.datatype == 'SNOW') & (weather.value > 0)
...     & weather.station.str.contains('US1NY')
... ].equals(snow_data)
True
```

For the most part, which one we use is a matter of preference; however, if we have a long name for our dataframe, we will probably prefer the `query()` method. In the previous example, we had to type the dataframe's name an additional three times in order to use the mask.

Tip

When using Boolean logic with the `query()` method, we can use both logical operators (`and`, `or`, `not`) and bitwise operators (`&`, `|`, `~`).

Merging DataFrames

When we discussed stacking dataframes one on top of the other with the `pd.concat()` function and the `append()` method in *Chapter 2, Working with Pandas DataFrames*, we were performing the equivalent of the SQL `UNION ALL` statement (or just `UNION`, if we also removed the duplicates, as we saw in *Chapter 3, Data Wrangling with Pandas*). Merging dataframes deals with how to line them up by row.

When referring to databases, merging is traditionally called a **join**. There are four types of joins: full (outer), left, right, and inner. These join types let us know how the result will be affected by values that are only present on one side of the join. This is a concept that's much more easily understood visually, so let's look at some Venn diagrams and then do some sample joins on the weather data. Here, the darker regions represent the data we are left with after performing the join:

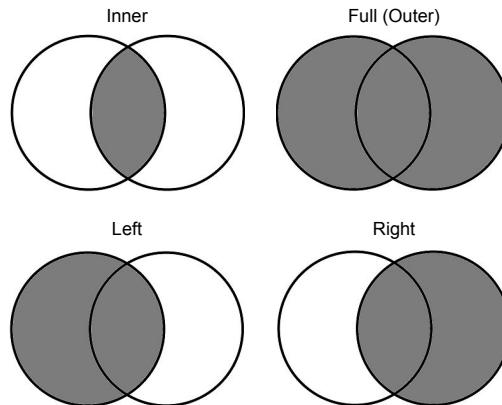


Figure 4.4 – Understanding join types

We have been working with data from numerous weather stations, but we don't know anything about them besides their IDs. It would be helpful to know exactly where each of the stations is located to better understand discrepancies between weather readings for the same day in NYC. When we queried for the snow data, we saw quite a bit of variation in the readings for January 4th (see *Figure 4.3*). This is most likely due to the location of the station. Stations at higher elevations or farther north may record more snow. Depending on how far they actually are from NYC, they may have been experiencing a snowstorm that was heavier somewhere else, such as Connecticut or Northern New Jersey.

The NCEI API's `stations` endpoint gives us all the information we need for the stations. This is in the `weather_stations.csv` file, as well as in the `stations` table in the SQLite database. Let's read this data into a dataframe:

```
>>> station_info = pd.read_csv('data/weather_stations.csv')
>>> station_info.head()
```

For reference, Central Park in NYC is at 40.7829° N, 73.9654° W (latitude 40.7829 and longitude -73.9654), and NYC has an elevation of 10 meters. The first five stations that record NYC data are not in New York. The ones in New Jersey are southwest of NYC, while the ones in Connecticut are northeast of NYC:

	id	name	latitude	longitude	elevation
0	GHCND:US1CTFR0022	STAMFORD 2.6 SSW, CT US	41.064100	-73.577000	36.6
1	GHCND:US1CTFR0039	STAMFORD 4.2 S, CT US	41.037788	-73.568176	6.4
2	GHCND:US1NJBG0001	BERGENFIELD 0.3 SW, NJ US	40.921298	-74.001983	20.1
3	GHCND:US1NJBG0002	SADDLE BROOK TWP 0.6 E, NJ US	40.902694	-74.083358	16.8
4	GHCND:US1NJBG0003	TENAFLY 1.3 W, NJ US	40.914670	-73.977500	21.6

Figure 4.5 – Weather stations dataset

Joins require us to specify how to match the data up. The only data the `weather` dataframe has in common with the `station_info` dataframe is the station ID. However, the columns containing this information are not named the same: in the `weather` dataframe, this column is called `station`, while in the `station_info` dataframe, it is called `id`. Before we join the data, let's get some information on how many distinct stations we have and how many entries are in each dataframe:

```
>>> station_info.id.describe()
```

```
count          279
unique         279
top           GHCND:US1NJBG0029
freq            1
Name: id, dtype: object

>>> weather.station.describe()
count          78780
unique         110
top           GHCND:USW00094789
freq           4270
Name: station, dtype: object
```

The difference in the number of unique stations across the dataframes tells us they don't contain all the same stations. Depending on the type of join we pick, we may lose some data. Therefore, it's important to look at the row count before and after the join. We can see this in the `count` entry from the output of `describe()`, but we don't need to run that just to get the row count. Instead, we can use the `shape` attribute, which gives us a tuple of the form `(number of rows, number of columns)`. To select the rows, we just grab the value at index 0 (1 for columns):

```
>>> station_info.shape[0], weather.shape[0] # 0=rows, 1=cols
(279, 78780)
```

Since we will be checking the row count often, it makes more sense to write a function that will give us the row count for any number of dataframes. The `*dfs` argument collects all the input to this function in a tuple, which we can iterate over in a list comprehension to get the row count:

```
>>> def get_row_count(*dfs):
...     return [df.shape[0] for df in dfs]
>>> get_row_count(station_info, weather)
[279, 78780]
```

Now that we know that we have 78,780 rows of weather data and 279 rows of station information data, we can begin looking at the types of joins. We'll begin with the inner join, which will result in the least amount of rows (unless the two dataframes have all the same values for the column being joined on, in which case all the joins will be equivalent). The `inner join` will return the columns from both dataframes where they have a match on the specified key column. Since we will be joining on the `weather.station` column and the `station_info.id` column, we will only get weather data for stations that are in `station_info`.

We will use the `merge()` method to perform the join (which is an inner join by default) by providing the left and right dataframes, along with specifying which columns to join on. Since the station ID column is named differently across dataframes, we must specify the names with `left_on` and `right_on`. The left dataframe is the one we call `merge()` on, while the right one is the dataframe that gets passed in as an argument:

```
>>> inner_join = weather.merge(
...     station_info, left_on='station', right_on='id'
... )
>>> inner_join.sample(5, random_state=0)
```

Notice that we have five additional columns, which have been added to the right. These came from the `station_info` dataframe. This operation also kept both the `station` and `id` columns, which are identical:

	date	datatype	station	attributes	value	id	name	latitude	longitude	elevation
10739	2018-08-07T00:00:00	SNOW	GHCND:US1NJMN0069	,N,	0.0	GHCND:US1NJMN0069	LONG BRANCH 1.7 SSW, NJ US	40.275368	-74.006027	9.4
45188	2018-12-21T00:00:00	TMAX	GHCND:USW00014732	,W,2400	16.7	GHCND:USW00014732	LAGUARDIA AIRPORT, NY US	40.779440	-73.880350	3.4
59823	2018-01-15T00:00:00	WDF5	GHCND:USW00094741	,W,	40.0	GHCND:USW00094741	TETERBORO AIRPORT, NJ US	40.850000	-74.061390	2.7
10852	2018-10-31T00:00:00	PRCP	GHCND:US1NJMN0069	T,N,	0.0	GHCND:US1NJMN0069	LONG BRANCH 1.7 SSW, NJ US	40.275368	-74.006027	9.4
46755	2018-05-05T00:00:00	SNOW	GHCND:USW00014734	,W,	0.0	GHCND:USW00014734	NEWARK LIBERTY INTERNATIONAL AIRPORT, NJ US	40.682500	-74.169400	2.1

Figure 4.6 – Results of an inner join between the weather and stations datasets

In order to remove the duplicate information in the `station` and `id` columns, we can rename one of them before the join. Consequently, we will only have to supply a value for the `on` parameter because the columns will share the same name:

```
>>> weather.merge(
...     station_info.rename(dict(id='station'), axis=1),
...     on='station'
... ).sample(5, random_state=0)
```

Since the columns shared the name, we only get one back after joining on them:

		date	datatype	station	attributes	value	name	latitude	longitude	elevation
10739		2018-08-07T00:00:00	SNOW	GHCND:US1NJMN0069	,,N,	0.0	LONG BRANCH 1.7 SSW, NJ US	40.275368	-74.006027	9.4
45188		2018-12-21T00:00:00	TMAX	GHCND:USW00014732	,,W,2400	16.7	LAGUARDIA AIRPORT, NY US	40.779440	-73.880350	3.4
59823		2018-01-15T00:00:00	WDF5	GHCND:USW00094741	,,W,	40.0	TEREBORO AIRPORT, NJ US	40.850000	-74.061390	2.7
10852		2018-10-31T00:00:00	PRCP	GHCND:US1NJMN0069	T,,N,	0.0	LONG BRANCH 1.7 SSW, NJ US	40.275368	-74.006027	9.4
46755		2018-05-05T00:00:00	SNOW	GHCND:USW00014734	,,W,	0.0	NEWARK LIBERTY INTERNATIONAL AIRPORT, NJ US	40.682500	-74.169400	2.1

Figure 4.7 – Matching the names of the joining column to prevent duplicate data in the result

Tip

We can join on multiple columns by passing the list of column names to the `on` parameter or to the `left_on` and `right_on` parameters.

Remember that we had 279 unique stations in the `station_info` dataframe, but only 110 unique stations for the weather data. When we performed the inner join, we lost all the stations that didn't have weather observations associated with them. If we don't want to lose rows on a particular side of the join, we can perform a left or right join instead. A **left join** requires us to list the dataframe with the rows that we want to keep (even if they don't exist in the other dataframe) on the left and the other dataframe on the right; a **right join** is the inverse:

```
>>> left_join = station_info.merge(
...     weather, left_on='id', right_on='station', how='left'
... )
>>> right_join = weather.merge(
...     station_info, left_on='station', right_on='id',
...     how='right'
... )
>>> right_join[right_join.datatype.isna()].head() # see nulls
```

Wherever the other dataframe contains no data, we will get null values. We may want to investigate why we don't have any weather data associated with these stations.

Alternatively, our analysis may involve determining the availability of data per station, so getting null values isn't necessarily an issue:

	date	datatype	station	attributes	value		id	name	latitude	longitude	elevation
0	NaN	NaN	NaN	NaN	NaN	GHCND:US1CTFR0022	STAMFORD 2.6 SSW, CT US	41.064100	-73.577000	36.6	
344	NaN	NaN	NaN	NaN	NaN	GHCND:US1NJBG0001	BERGENFIELD 0.3 SW, NJ US	40.921298	-74.001983	20.1	
345	NaN	NaN	NaN	NaN	NaN	GHCND:US1NJBG0002	SADDLE BROOK TWP 0.6 E, NJ US	40.902694	-74.083358	16.8	
718	NaN	NaN	NaN	NaN	NaN	GHCND:US1NJBG0005	WESTWOOD 0.8 ESE, NJ US	40.983041	-74.015858	15.8	
719	NaN	NaN	NaN	NaN	NaN	GHCND:US1NJBG0006	RAMSEY 0.6 E, NJ US	41.058611	-74.134068	112.2	

Figure 4.8 – Null values may be introduced when not using an inner join

Since we placed the `station_info` dataframe on the left for the left join and on the right for the right join, the results here are equivalent. In both cases, we chose to keep all the stations present in the `station_info` dataframe, accepting null values for the weather observations. To prove they are equivalent, we need to put the columns in the same order, reset the index, and sort the data:

```
>>> left_join.sort_index(axis=1) \
...     .sort_values(['date', 'station'], ignore_index=True) \
...     .equals(right_join.sort_index(axis=1).sort_values(
...         ['date', 'station'], ignore_index=True
...     ))
True
```

Note that we have additional rows in the left and right joins because we kept all the stations that didn't have weather observations:

```
>>> get_row_count(inner_join, left_join, right_join)
[78780, 78949, 78949]
```

The final type of join is a **full outer join**, which will keep all the values, regardless of whether or not they exist in both dataframes. For instance, say we queried for stations with US1NY in their station ID because we believed that stations measuring NYC weather would have to be labeled as such. This means that an inner join would result in losing observations from the stations in Connecticut and New Jersey, while a left/right join would result in either lost station information or lost weather data. The outer join will preserve all the data. We will also pass in `indicator=True` to add an additional column to the resulting dataframe, which will indicate which dataframe each row came from:

```
>>> outer_join = weather.merge(
...     station_info[station_info.id.str.contains('US1NY')], 
...     left_on='station', right_on='id',
...     how='outer', indicator=True
... )
# view effect of outer join
>>> pd.concat([
...     outer_join.query(f'_merge == "{kind}"') \
...         .sample(2, random_state=0)
...     for kind in outer_join._merge.unique()
... ]).sort_index()
```

Indices **23634** and **25742** come from stations located in New York, and the match gives us information about the station. Indices **60645** and **70764** are for stations that don't have US1NY in their station ID, causing nulls for the station information columns. The bottom two rows are stations in New York that aren't providing weather observations for NYC. This join keeps all the data and will often introduce null values, unlike inner joins, which won't:

	date	datatype	station	attributes	value		id	name	latitude	longitude	elevation	_merge
23634	2018-04-12T00:00:00	PRCP	GHCND:US1NYNS0043	„N,	0.0	GHCND:US1NYNS0043		PLAINVIEW 0.4 ENE, NY US	40.785919	-73.466873	56.7	both
25742	2018-03-25T00:00:00	PRCP	GHCND:US1NYSF0061	„N,	0.0	GHCND:US1NYSF0061		CENTERPORT 0.9 SW, NY US	40.891689	-73.383133	53.6	both
60645	2018-04-16T00:00:00	TMIN	GHCND:USW00094741	„W,	3.9		NaN	NaN	NaN	NaN	NaN	left_only
70764	2018-03-23T00:00:00	SNWD	GHCND:US1NJHD0002	„N,	203.0		NaN	NaN	NaN	NaN	NaN	left_only
78790		NaN	NaN	NaN	NaN	GHCND:US1NYQN0033		HOWARD BEACH 0.4 NNW, NY US	40.662099	-73.841345	2.1	right_only
78800		NaN	NaN	NaN	NaN	GHCND:US1NYWC0009		NEW ROCHELLE 1.3 S, NY US	40.904000	-73.777000	21.9	right_only

Figure 4.9 – An outer join keeps all the data

The aforementioned joins are equivalent to SQL statements of the following form, where we simply change <JOIN_TYPE> to (INNER) JOIN, LEFT JOIN, RIGHT JOIN, or FULL OUTER JOIN for the appropriate join:

```
SELECT *
FROM left_table
<JOIN_TYPE> right_table
ON left_table.<col> == right_table.<col>;
```

Joining dataframes makes working with the dirty data in *Chapter 3, Data Wrangling with Pandas*, easier. Remember, we had data from two distinct stations: one had a valid station ID and the other was ?. The ? station was the only one recording the water equivalent of snow (WESF). Now that we know about joining dataframes, we can join the data from the valid station ID to the data from the ? station that we are missing by date. First, we will need to read in the CSV file, setting the date column as the index. We will drop the duplicates and the SNWD column (snow depth), which we found to be uninformative since most of the values were infinite (both in the presence and absence of snow):

```
>>> dirty_data = pd.read_csv(
...     'data/dirty_data.csv', index_col='date'
... ).drop_duplicates().drop(columns='SNWD')
>>> dirty_data.head()
```

Our starting data looks like this:

	station	PRCP	SNOW	TMAX	TMIN	TOBS	WESF	inclement_weather
date								
2018-01-01T00:00:00		?	0.0	0.0	5505.0	-40.0	NaN	NaN
2018-01-02T00:00:00	GHCND:USC00280907	0.0	0.0	-8.3	-16.1	-12.2	NaN	False
2018-01-03T00:00:00	GHCND:USC00280907	0.0	0.0	-4.4	-13.9	-13.3	NaN	False
2018-01-04T00:00:00		?	20.6	229.0	5505.0	-40.0	NaN	19.3
2018-01-05T00:00:00		?	0.3	NaN	5505.0	-40.0	NaN	NaN

Figure 4.10 – Dirty data from the previous chapter

Now, we need to create a dataframe for each station. To reduce output, we will drop some additional columns:

```
>>> valid_station = dirty_data.query('station != "?"') \
...     .drop(columns=['WESF', 'station'])
>>> station_with_wesf = dirty_data.query('station == "?"') \
...     .drop(columns=['station', 'TOBS', 'TMIN', 'TMAX'])
```

This time, the column we want to join on (the date) is actually the index, so we will pass in `left_index` to indicate that the column to use from the left dataframe is the index, and then `right_index` to indicate the same for the right dataframe. We will perform a left join to make sure we don't lose any rows from our valid station, and, where possible, augment them with the observations from the ? station:

```
>>> valid_station.merge(  
...     station_with_wesf, how='left',  
...     left_index=True, right_index=True  
... ).query('WESF > 0').head()
```

For all the columns that the dataframes had in common, but weren't part of the join, we have two versions now. The versions coming from the left dataframe have the `_x` suffix appended to the column names, and those coming from the right dataframe have `_y` as the suffix:

	PRCP_x	SNOW_x	TMAX	TMIN	TOBS	inclement_weather_x	PRCP_y	SNOW_y	WESF	inclement_weather_y
date										
2018-01-30T00:00:00	0.0	0.0	6.7	-1.7	-0.6	False	1.5	13.0	1.8	True
2018-03-08T00:00:00	48.8	NaN	1.1	-0.6	1.1	False	28.4	NaN	28.7	NaN
2018-03-13T00:00:00	4.1	51.0	5.6	-3.9	0.0	True	3.0	13.0	3.0	True
2018-03-21T00:00:00	0.0	0.0	2.8	-2.8	0.6	False	6.6	114.0	8.6	True
2018-04-02T00:00:00	9.1	127.0	12.8	-1.1	-1.1	True	14.0	152.0	15.2	True

Figure 4.11 – Merging weather data from different stations

We can provide our own suffixes with the `suffixes` parameter. Let's use a suffix for the ? station only:

```
>>> valid_station.merge(  
...     station_with_wesf, how='left',  
...     left_index=True, right_index=True,  
...     suffixes=('', '_?')  
... ).query('WESF > 0').head()
```

Since we specified an empty string for the left suffix, the columns coming from the left dataframe have their original names. However, the right suffix of `_?` was added to the names of the columns that came from the right dataframe:

	PRCP	SNOW	TMAX	TMIN	TOBS	inclement_weather	PRCP_?	SNOW_?	WESF	inclement_weather_?
date										
2018-01-30T00:00:00	0.0	0.0	6.7	-1.7	-0.6		False	1.5	13.0	1.8
2018-03-08T00:00:00	48.8	NaN	1.1	-0.6	1.1		False	28.4	NaN	28.7
2018-03-13T00:00:00	4.1	51.0	5.6	-3.9	0.0		True	3.0	13.0	3.0
2018-03-21T00:00:00	0.0	0.0	2.8	-2.8	0.6		False	6.6	114.0	8.6
2018-04-02T00:00:00	9.1	127.0	12.8	-1.1	-1.1		True	14.0	152.0	15.2

Figure 4.12 – Specifying the suffix for shared columns not being used in the join

When we are joining on the index, an easier way to do this is to use the `join()` method instead of `merge()`. It also defaults to an inner join, but this behavior can be changed with the `how` parameter, just like with `merge()`. The `join()` method will always use the index of the left dataframe to join, but it can use a column in the right dataframe if its name is passed to the `on` parameter. Note that suffixes are now specified using `lsuffix` for the left dataframe's suffix and `rsuffix` for the right one. This yields the same result as the previous example (*Figure 4.12*):

```
>>> valid_station.join(
...     station_with_wesf, how='left', rsuffix='_?'
... ).query('WESF > 0').head()
```

One important thing to keep in mind is that joins can be rather resource-intensive, so it is often beneficial to figure out what will happen to the rows before going through with it. If we don't already know what type of join we want, this can help give us an idea. We can use **set operations** on the index we plan to join on to figure this out.

Remember that the mathematical definition of a **set** is a collection of distinct objects. By definition, the index is a set. Set operations are often explained with Venn diagrams:

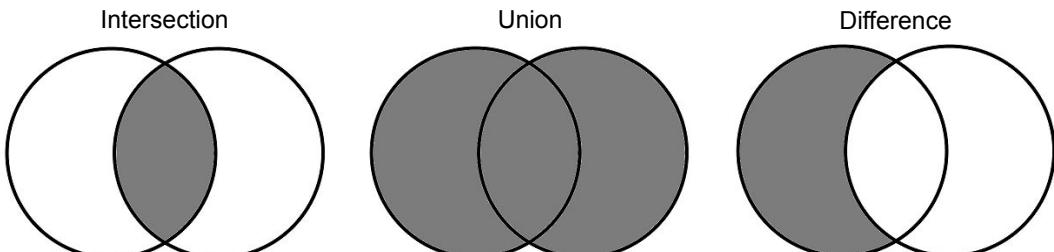


Figure 4.13 – Set operations

Important note

Note that `set` is also a Python type that's available in the standard library. A common use of sets is to remove duplicates from a list. More information on sets in Python can be found in the documentation at <https://docs.python.org/3/library/stdtypes.html#set-types-set-frozenset>.

Let's use the `weather` and `station_info` dataframes to illustrate set operations. First, we must set the index to the column(s) that will be used for the join operation:

```
>>> weather.set_index('station', inplace=True)
>>> station_info.set_index('id', inplace=True)
```

To see what will remain with an inner join, we can take the **intersection** of the indices, which shows us the overlapping stations:

```
>>> weather.index.intersection(station_info.index)
Index(['GHCND:US1CTFR0039', ..., 'GHCND:USW1NYQN0029'],
      dtype='object', length=110)
```

As we saw when we ran the inner join, we only got station information for the stations with weather observations. This doesn't tell us what we lost, though; for this, we need to find the **set difference**, which will subtract the sets and give us the values of the first index that aren't in the second. With the set difference, we can easily see that, when performing an inner join, we don't lose any rows from the weather data, but we lose 169 stations that don't have weather observations:

```
>>> weather.index.difference(station_info.index)
Index([], dtype='object')

>>> station_info.index.difference(weather.index)
Index(['GHCND:US1CTFR0022', ..., 'GHCND:USW00014786'],
      dtype='object', length=169)
```

Note that this output also tells us how left and right joins will turn out. To avoid losing rows, we want to put the `station_info` dataframe on the same side as the join (on the left for a left join and on the right for a right join).

Tip

We can use the `symmetric_difference()` method on the indices of the dataframes involved in the join to see what will be lost from both sides: `index_1.symmetric_difference(index_2)`. The result will be the values that are only in one of the indices. An example is in the notebook.

Lastly, we can use the `union` to view all the values we will keep if we run a full outer join. Remember, the `weather` dataframe contains the stations repeated throughout because they provide daily measurements, so we call the `unique()` method before taking the union to see the number of stations we will keep:

```
>>> weather.index.unique().union(station_info.index)
Index(['GHCND:US1CTFR0022', ..., 'GHCND:USW00094789'],
      dtype='object', length=279)
```

The *Further reading* section at the end of this chapter contains some resources on set operations and how pandas compares to SQL. For now, let's move on to data enrichment.

Using DataFrame operations to enrich data

Now that we've discussed how to query and merge DataFrame objects, let's learn how to perform complex operations on them to create and modify columns and rows. For this section, we will be working in the `2-dataframe_operations.ipynb` notebook using the weather data, along with Facebook stock's volume traded and opening, high, low, and closing prices daily for 2018. Let's import what we will need and read in the data:

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

>>> weather = pd.read_csv(
...     'data/nyc_weather_2018.csv', parse_dates=['date']
... )
>>> fb = pd.read_csv(
...     'data/fb_2018.csv', index_col='date', parse_dates=True
... )
```

We will begin by reviewing operations that summarize entire rows and columns before moving on to binning, applying functions across rows and columns, and window calculations, which summarize data along a certain number of observations at a time (such as moving averages).

Arithmetic and statistics

Pandas has several methods for calculating statistics and performing mathematical operations, including comparisons, floor division, and the modulo operation. These methods give us more flexibility in how we define the calculation by allowing us to specify the axis to perform the calculation on (when performing it on a DataFrame object). By default, the calculation will be performed along the columns (`axis=1` or `axis='columns'`), which generally contain observations of a single variable of a single data type; however, we can pass in `axis=0` or `axis='index'` to perform the calculation along the rows instead.

In this section, we are going to use a few of these methods to create new columns and modify our data to see how we can use new data to draw some initial conclusions. Note that the complete list can be found at <https://pandas.pydata.org/pandas-docs/stable/reference/series.html#binary-operator-functions>.

To start off, let's create a column with the Z-score for the volume traded in Facebook stock and use it to find the days where the Z-score is greater than three in absolute value. These values are more than three standard deviations from the mean, which may be abnormal (depending on the data). Remember from our discussion of Z-scores in *Chapter 1, Introduction to Data Analysis*, that we calculate them by subtracting the mean and dividing by the standard deviation. Rather than using mathematical operators for subtraction and division, we will use the `sub()` and `div()` methods, respectively:

```
>>> fb.assign(
...     abs_z_score_volume=lambda x: x.volume \
...         .sub(x.volume.mean()).div(x.volume.std()).abs()
... ).query('abs_z_score_volume > 3')
```

Five days in 2018 had Z-scores for volume traded greater than three in absolute value. These dates in particular will come up often in the rest of this chapter as they mark some trouble points for Facebook's stock price:

	open	high	low	close	volume	abs_z_score_volume
date						
2018-03-19	177.01	177.17	170.06	172.56	88140060	3.145078
2018-03-20	167.47	170.20	161.95	168.15	129851768	5.315169
2018-03-21	164.80	173.40	163.30	169.39	106598834	4.105413
2018-03-26	160.82	161.10	149.02	160.06	126116634	5.120845
2018-07-26	174.89	180.13	173.75	176.26	169803668	7.393705

Figure 4.14 – Adding a Z-score column

Two other very useful methods are `rank()` and `pct_change()`, which let us rank the values of a column (and store them in a new column) and calculate the percentage change between periods, respectively. By combining these, we can see which five days had the largest percentage change of volume traded in Facebook stock from the day prior:

```
>>> fb.assign(
...     volume_pct_change=fb.volume.pct_change(),
...     pct_change_rank=lambda x: \
...         x.volume_pct_change.abs().rank(ascending=False)
... ).nsmallest(5, 'pct_change_rank')
```

The day with the largest percentage change in volume traded was January 12, 2018, which happens to coincide with one of the many Facebook scandals that shook the stock in 2018 (<https://www.cnbc.com/2018/11/20/facebook-scandals-in-2018-effect-on-stock.html>). This was when they announced changes to the news feed to prioritize content from a user's friends over brands they follow. Given that a large component of Facebook's revenue comes from advertising (nearly 89% in 2017, *source: https://www.investopedia.com/ask/answers/120114/how-does-facebook-fb-make-money.asp*), this caused panic as many sold the stock, driving up the volume traded drastically and dropping the stock price:

	open	high	low	close	volume	volume_pct_change	pct_change_rank
date							
2018-01-12	178.06	181.48	177.40	179.37	77551299	7.087876	1.0
2018-03-19	177.01	177.17	170.06	172.56	88140060	2.611789	2.0
2018-07-26	174.89	180.13	173.75	176.26	169803668	1.628841	3.0
2018-09-21	166.64	167.25	162.81	162.93	45994800	1.428956	4.0
2018-03-26	160.82	161.10	149.02	160.06	126116634	1.352496	5.0

Figure 4.15 – Ranking trading days by percentage change in volume traded

We can use slicing to look at the change around this announcement:

```
>>> fb['2018-01-11':'2018-01-12']
```

Notice how we are able to combine everything we learned in the last few chapters to get interesting insights from our data. We were able to sift through a year's worth of stock data and find some days that had large effects on Facebook stock (good or bad):

	open	high	low	close	volume
date					
2018-01-11	188.40	188.40	187.38	187.77	9588587
2018-01-12	178.06	181.48	177.40	179.37	77551299

Figure 4.16 – Facebook stock data before and after announcing changes to the news feed

Lastly, we can inspect the dataframe with aggregated Boolean operations. For example, we can see that Facebook stock never had a daily low price greater than \$215 in 2018 with the `any()` method:

```
>>> (fb > 215).any()
open          True
high          True
low          False
close          True
volume         True
dtype: bool
```

If we want to see if all the rows in a column meet the criteria, we can use the `all()` method. This tells us that Facebook has at least one day for the opening, high, low, and closing prices with a value less than or equal to \$215:

```
>>> (fb > 215).all()
open          False
high          False
low          False
close          False
volume         True
dtype: bool
```

Now, let's take a look at how we can use binning to divide up our data rather than a specific value, such as \$215 in the `any()` and `all()` examples.

Binning

Sometimes, it's more convenient to work with categories rather than the specific values. A common example is working with ages—most likely, we don't want to look at the data for each age, such as 25 compared to 26; however, we may very well be interested in how the group of individuals aged 25-34 compares to the group of those aged 35-44. This is called **binning** or **discretizing** (going from continuous to discrete); we take our data and place the observations into bins (or buckets) matching the range they fall into. By doing so, we can drastically reduce the number of distinct values our data can take on and make it easier to analyze.

Important note

While binning our data can make certain parts of the analysis easier, keep in mind that it will reduce the information in that field since the granularity is reduced.

One interesting thing we could do with the volume traded would be to see which days had high trade volume and look for news about Facebook on those days or large swings in price. Unfortunately, it is highly unlikely that the volume will be the same any two days; in fact, we can confirm that, in the data, no two days have the same volume traded:

```
>>> (fb.volume.value_counts() > 1).sum()  
0
```

Remember that `fb.volume.value_counts()` gives us the number of occurrences for each unique value for `volume`. We can then create a Boolean mask for whether the count is greater than 1 and sum it up (`True` evaluates to 1 and `False` evaluates to 0). Alternatively, we can use `any()` instead of `sum()`, which, rather than telling us the number of unique values of `volume` that had more than one occurrence, would give us `True` if at least one volume traded amount occurred more than once and `False` otherwise.

Clearly, we will need to create some ranges for the volume traded in order to look at the days of high trading volume, but how do we decide which range is a good range? One way is to use the `pd.cut()` function for binning based on value. First, we should decide how many bins we want to create—three seems like a good split, since we can label the bins low, medium, and high. Next, we need to determine the width of each bin; pandas tries to make this process as painless as possible, so if we want equally-sized bins, all we have to do is specify the number of bins we want (otherwise, we must specify the upper bound for each bin as a list):

```
>>> volume_binned = pd.cut(  
...     fb.volume, bins=3, labels=['low', 'med', 'high']  
... )  
>>> volume_binned.value_counts()  
low      240  
med       8  
high      3  
Name: volume, dtype: int64
```

Tip

Note that we provided labels for each bin here; if we don't do this, each bin will be labeled by the interval of values it includes, which may or may not be helpful for us, depending on our application. If we want to both label the values and see the bins afterward, we can pass in `retbins=True` when we call `pd.cut()`. Then, we can access the binned data as the first element of the tuple that is returned, and the bin ranges themselves as the second element.

It looks like an overwhelming majority of the trading days were in the low-volume bin; keep in mind that this is all relative because we evenly divided the range between the minimum and maximum trading volumes. Let's look at the data for the three days of high volume:

```
>>> fb[volume_binned == 'high'] \  
...     .sort_values('volume', ascending=False)
```

Even among the high-volume days, we can see that July 26, 2018 had a much higher trade volume compared to the other two dates in March (nearly 40 million additional shares were traded):

	open	high	low	close	volume
date					
2018-07-26	174.89	180.13	173.75	176.26	169803668
2018-03-20	167.47	170.20	161.95	168.15	129851768
2018-03-26	160.82	161.10	149.02	160.06	126116634

Figure 4.17 – Facebook stock data on days in the high-volume traded bucket

In fact, querying a search engine for *Facebook stock price July 26, 2018* reveals that Facebook had announced their earnings and disappointing user growth after market close on July 25th, which was followed by lots of after-hours selling. When the market opened the next morning, the stock had dropped from \$217.50 at close on the 25th to \$174.89 at market open on the 26th. Let's pull out this data:

```
>>> fb['2018-07-25':'2018-07-26']
```

Not only was there a huge drop in stock price, but the volume traded also skyrocketed, increasing by more than 100 million. All of this resulted in a loss of about \$120 billion in Facebook's market capitalization (<https://www.marketwatch.com/story/facebook-stock-crushed-after-revenue-user-growth-miss-2018-07-25>):

	open	high	low	close	volume
date					
2018-07-25	215.715	218.62	214.27	217.50	64592585
2018-07-26	174.890	180.13	173.75	176.26	169803668

Figure 4.18 – Facebook stock data leading up to the day with the highest volume traded in 2018

If we look at the other two days marked as high-volume trading days, we will find a plethora of information as to why. Both of these days were marked by scandal for Facebook. The Cambridge Analytica political data privacy scandal broke on Saturday, March 17, 2018, so trading with this information didn't commence until Monday the 19th (<https://www.nytimes.com/2018/03/19/technology/facebook-cambridge-analytica-explained.html>):

```
>>> fb['2018-03-16':'2018-03-20']
```

Things only got worse once more information was revealed in the following days with regards to the severity of the incident:

	open	high	low	close	volume
date					
2018-03-16	184.49	185.33	183.41	185.09	24403438
2018-03-19	177.01	177.17	170.06	172.56	88140060
2018-03-20	167.47	170.20	161.95	168.15	129851768

Figure 4.19 – Facebook stock data when the Cambridge Analytica scandal broke

As for the third day of high trading volume (March 26, 2018), the FTC launched an investigation into the Cambridge Analytica scandal, so Facebook's woes continued (<https://www.cnbc.com/2018/03/26/ftc-confirms-facebook-data-breach-investigation.html>).

If we look at some of the dates within the medium trading volume group, we can see that many are part of the three trading events we just discussed. This forces us to reexamine how we created the bins in the first place. Perhaps equal-width bins wasn't the answer? Most days were pretty close in volume traded; however, a few days caused the bin width to be rather large, which left us with a large imbalance of days per bin:

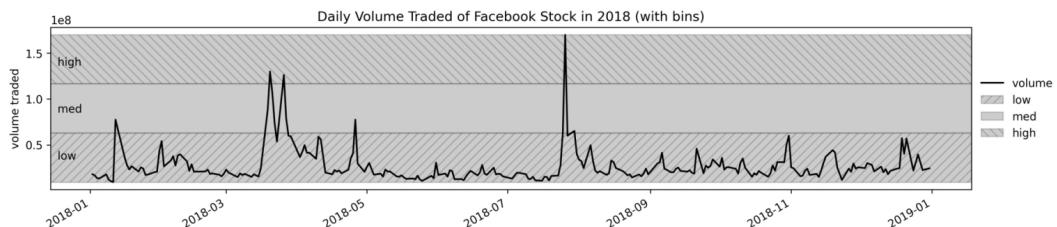


Figure 4.20 – Visualizing the equal-width bins

If we want each bin to have an equal number of observations, we can split the bins based on evenly-spaced quantiles using the `pd.qcut()` function. We can bin the volumes into quartiles to evenly bucket the observations into bins of varying width, giving us the 63 highest trading volume days in the `q4` bin:

```
>>> volume_qbinned = pd.qcut(
...     fb.volume, q=4, labels=['q1', 'q2', 'q3', 'q4']
... )
>>> volume_qbinned.value_counts()
```

```

q1      63
q2      63
q4      63
q3      62
Name: volume, dtype: int64

```

Notice that the bins don't cover the same range of volume traded anymore:

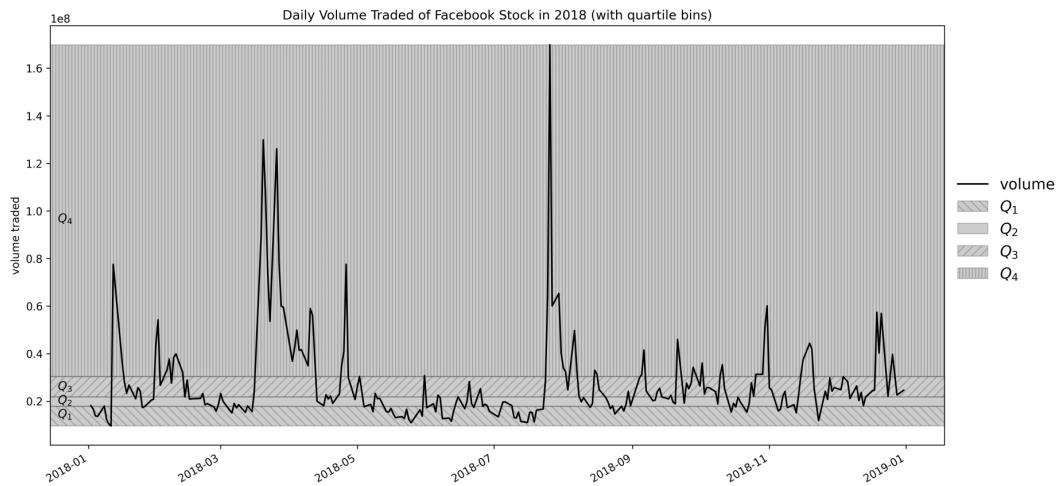


Figure 4.21 – Visualizing the bins based on quartiles

Tip

In both of these examples, we let pandas calculate the bin ranges; however, both `pd.cut()` and `pd.qcut()` allow us to specify the upper bounds for each bin as a list.

Applying functions

So far, most of the actions we have taken on our data have been column-specific. When we want to run the same code on all the columns in our dataframe, we can use the `apply()` method for more succinct code. Note that this will not be done in-place.

Before we get started, let's isolate the weather observations from the Central Park station and pivot the data:

```

>>> central_park_weather = weather.query(
...     'station == "GHCND:USW00094728"'
... ).pivot(index='date', columns='datatype', values='value')

```

Let's calculate the Z-scores of the TMIN (minimum temperature), TMAX (maximum temperature), and PRCP (precipitation) observations in Central Park in October 2018. It's important that we don't try to take the Z-scores across the full year. NYC has four seasons, and what is considered normal weather will depend on which season we are looking at. By isolating our calculation to October, we can see if October had any days with very different weather:

```
>>> oct_weather_z_scores = central_park_weather\  
...     .loc['2018-10', ['TMIN', 'TMAX', 'PRCP']]\  
...     .apply(lambda x: x.sub(x.mean()).div(x.std()))  
>>> oct_weather_z_scores.describe().T
```

TMIN and TMAX don't appear to have any values that differ much from the rest of October, but PRCP does:

datatype	count	mean	std	min	25%	50%	75%	max
TMIN	31.0	-1.790682e-16	1.0	-1.339112	-0.751019	-0.474269	1.065152	1.843511
TMAX	31.0	1.951844e-16	1.0	-1.305582	-0.870013	-0.138258	1.011643	1.604016
PRCP	31.0	4.655774e-17	1.0	-0.394438	-0.394438	-0.394438	-0.240253	3.936167

Figure 4.22 – Calculating Z-scores for multiple columns at once

We can use `query()` to extract the value for this date:

```
>>> oct_weather_z_scores.query('PRCP > 3').PRCP  
date  
2018-10-27      3.936167  
Name: PRCP, dtype: float64
```

If we look at the summary statistics for precipitation in October, we can see that this day had much more precipitation than the rest:

```
>>> central_park_weather.loc['2018-10', 'PRCP'].describe()  
count      31.000000  
mean       2.941935  
std        7.458542  
min       0.000000  
25%      0.000000  
50%      0.000000  
75%      1.150000  
max      32.300000  
Name: PRCP, dtype: float64
```

The `apply()` method lets us run vectorized operations on entire columns or rows at once. We can apply pretty much any function we can think of as long as those operations are valid on all the columns (or rows) in our data. For example, we can use the `pd.cut()` and `pd.qcut()` binning functions we discussed in the previous section to divide each column into bins (provided we want the same number of bins or value ranges). Note that there is also an `applymap()` method if the function we want to apply isn't vectorized. Alternatively, we can use `np.vectorize()` to vectorize our functions for use with `apply()`. Consult the notebook for an example.

Pandas does provide some functionality for iterating over the dataframe, including the `iteritems()`, `itertuples()`, and `iterrows()` methods; however, we should avoid using these unless we absolutely can't find another solution. Pandas and NumPy are designed for vectorized operations, which are much faster because they are written in efficient C code; by writing a loop to iterate one element at a time, we are making it more computationally intensive due to the way Python implements integers and floats. For instance, look at how the time to complete the simple operation of adding the number 10 to each value in a series of floats grows linearly with the number of rows when using `iteritems()`, but stays near zero, regardless of size, when using a vectorized operation:

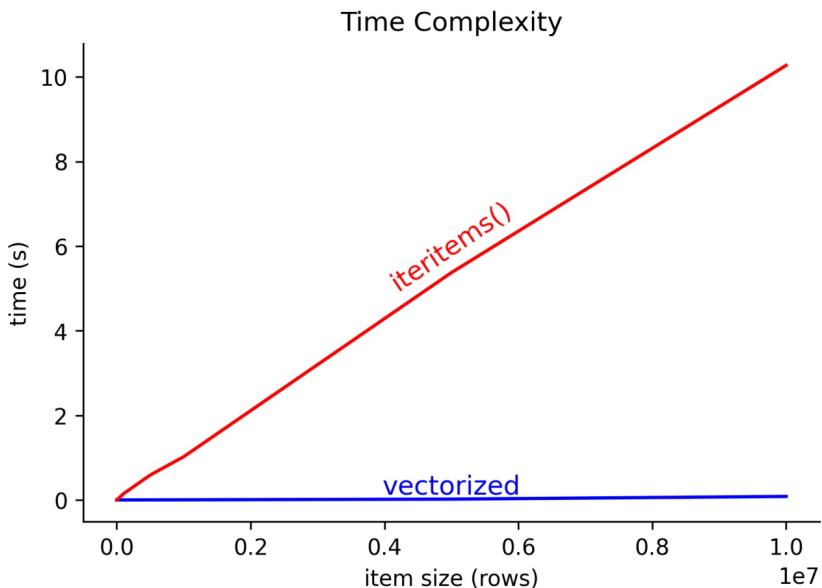


Figure 4.23 – Vectorized versus iterative operations

All the functions and methods we have used so far have involved the full row or column; however, sometimes, we are more interested in performing window calculations, which use a section of the data.

Window calculations

Pandas makes it possible to perform calculations over a window or range of rows/columns. In this section, we will discuss a few ways of constructing these windows. Depending on the type of window, we get a different look at our data.

Rolling windows

When our index is of type `DatetimeIndex`, we can specify the window in day parts (such as `2H` for two hours or `3D` for three days); otherwise, we can specify the number of periods as an integer. Say we are interested in the amount of rain that has fallen in a rolling 3-day window; it would be quite tedious (and probably inefficient) to implement this with what we have learned so far. Fortunately, we can use the `rolling()` method to get this information easily:

```
>>> central_park_weather.loc['2018-10'].assign(  
...     rolling_PRCP=lambda x: x.PRCP.rolling('3D').sum()  
... )[['PRCP', 'rolling_PRCP']].head(7).T
```

After performing the rolling 3-day sum, each date will show the sum of that day's and the previous two days' precipitation:

date	2018-10-01	2018-10-02	2018-10-03	2018-10-04	2018-10-05	2018-10-06	2018-10-07
datatype							
PRCP	0.0	17.5	0.0	1.0	0.0	0.0	0.0
rolling_PRCP	0.0	17.5	17.5	18.5	1.0	1.0	0.0

Figure 4.24 – Rolling 3-day total precipitation

Tip

If we want to use dates for the rolling calculation, but don't have dates in the index, we can pass the name of our date column to the `on` parameter in the call to `rolling()`. Conversely, if we want to use an integer index of row numbers, we can simply pass in an integer as the window; for example, `rolling(3)` for a 3-row window.

To change the aggregation, all we have to do is call a different method on the result of `rolling()`; for example, `mean()` for the average and `max()` for the maximum. The rolling calculation can also be applied to all the columns at once:

```
>>> central_park_weather.loc['2018-10'] \
...     .rolling('3D').mean().head(7).iloc[:, :6]
```

This gives us the 3-day rolling average for all the weather observations from Central Park:

datatype	AWND	PRCP	SNOW	SNWD	TMAX	TMIN
date						
2018-10-01	0.900000	0.000000	0.0	0.0	24.400000	17.200000
2018-10-02	0.900000	8.750000	0.0	0.0	24.700000	17.750000
2018-10-03	0.966667	5.833333	0.0	0.0	24.233333	17.566667
2018-10-04	0.800000	6.166667	0.0	0.0	24.233333	17.200000
2018-10-05	1.033333	0.333333	0.0	0.0	23.133333	16.300000
2018-10-06	0.833333	0.333333	0.0	0.0	22.033333	16.300000
2018-10-07	1.066667	0.000000	0.0	0.0	22.600000	17.400000

Figure 4.25 – Rolling 3-day average for all weather observations

To apply different aggregations across columns, we can use the `agg()` method instead; it allows us to specify the aggregations to perform per column as a predefined or custom function. We simply pass in a dictionary mapping the columns to the aggregation to perform on them. Let's find the rolling 3-day maximum temperature (TMAX), minimum temperature (TMIN), average wind speed (AWND), and total precipitation (PRCP). Then, we will join it to the original data so that we can compare the results:

```
>>> central_park_weather \
...     ['2018-10-01':'2018-10-07'].rolling('3D').agg({
...     'TMAX': 'max', 'TMIN': 'min',
...     'AWND': 'mean', 'PRCP': 'sum'
... }).join( # join with original data for comparison
...         central_park_weather[['TMAX', 'TMIN', 'AWND', 'PRCP']],
...         lsuffix='_rolling'
... ).sort_index(axis=1) # put rolling calcs next to originals
```

Using `agg()`, we were able to calculate different rolling aggregations for each column:

	AWND	AWND_rolling	PRCP	PRCP_rolling	TMAX	TMAX_rolling	TMIN	TMIN_rolling
date								
2018-10-01	0.9	0.900000	0.0	0.0	24.4	24.4	17.2	17.2
2018-10-02	0.9	0.900000	17.5	17.5	25.0	25.0	18.3	17.2
2018-10-03	1.1	0.966667	0.0	17.5	23.3	25.0	17.2	17.2
2018-10-04	0.4	0.800000	1.0	18.5	24.4	25.0	16.1	16.1
2018-10-05	1.6	1.033333	0.0	1.0	21.7	24.4	15.6	15.6
2018-10-06	0.5	0.833333	0.0	1.0	20.0	24.4	17.2	15.6
2018-10-07	1.1	1.066667	0.0	0.0	26.1	26.1	19.4	15.6

Figure 4.26 – Using different rolling calculations per column

Tip

We can also use variable-width windows with a little extra effort: we can either create a subclass of `BaseIndexer` and provide the logic for determining the window bounds in the `get_window_bounds()` method (more information can be found at https://pandas.pydata.org/pandas-docs/stable/user_guide/computation.html#custom-window-rolling), or we can use one of the predefined classes in the `pandas.api.indexers` module. The notebook we are currently working in contains an example of using the `VariableOffsetWindowIndexer` class to perform a 3-business day rolling calculation.

With rolling calculations, we have a sliding window over which we calculate our functions; however, in some cases, we are more interested in the output of a function on all the data up to that point, in which case we use an expanding window.

Expanding windows

Expanding calculations will give us the cumulative value of our aggregation function. We use the `expanding()` method to perform a calculation with an expanding window; methods such as `cumsum()` and `cummax()` use expanding windows for their calculations. The advantage of using `expanding()` directly is additional flexibility: we aren't limited to predefined aggregations, and we can specify the minimum number of periods before the calculation starts with the `min_periods` parameter (defaults to 1). With the Central Park weather data, let's use the `expanding()` method to calculate the month-to-date average precipitation:

```
>>> central_park_weather.loc['2018-06'].assign(
...     TOTAL_PRCP=lambda x: x.PRCP.cumsum(),
...     AVG_PRCP=lambda x: x.PRCP.expanding().mean()
... ).head(10)[['PRCP', 'TOTAL_PRCP', 'AVG_PRCP']].T
```

Note that while there is no method for the cumulative mean, we are able to use the `expanding()` method to calculate it. The values in the `AVG_PRCP` column are the values in the `TOTAL_PRCP` column divided by the number of days processed:

	date	2018-06-01	2018-06-02	2018-06-03	2018-06-04	2018-06-05	2018-06-06	2018-06-07	2018-06-08	2018-06-09	2018-06-10
datatype											
PRCP		6.9	2.00	6.4	4.10	0.00	0.000000	0.000000	0.000	0.000000	0.30
TOTAL_PRCP		6.9	8.90	15.3	19.40	19.40	19.400000	19.400000	19.400	19.400000	19.70
AVG_PRCP		6.9	4.45	5.1	4.85	3.88	3.233333	2.771429	2.425	2.155556	1.97

Figure 4.27 – Calculating the month-to-date average precipitation

As we did with `rolling()`, we can provide column-specific aggregations with the `agg()` method. Let's find the expanding maximum temperature, minimum temperature, average wind speed, and total precipitation. Note that we can also pass in NumPy functions to `agg()`:

```
>>> central_park_weather[
...     ['2018-10-01':'2018-10-07'].expanding().agg({
...         'TMAX': np.max, 'TMIN': np.min,
...         'AWND': np.mean, 'PRCP': np.sum
... }).join(
...     central_park_weather[['TMAX', 'TMIN', 'AWND', 'PRCP']],
...     lsuffix='_expanding'
... ).sort_index(axis=1)
```

Once again, we joined the window calculations with the original data for comparison:

	AWND	AWND_expanding	PRCP	PRCP_expanding	TMAX	TMAX_expanding	TMIN	TMIN_expanding
date								
2018-10-01	0.9	0.900000	0.0		24.4		17.2	
2018-10-02	0.9	0.900000	17.5		25.0		18.3	
2018-10-03	1.1	0.966667	0.0		23.3		17.2	
2018-10-04	0.4	0.825000	1.0		24.4		16.1	
2018-10-05	1.6	0.980000	0.0		21.7		15.6	
2018-10-06	0.5	0.900000	0.0		20.0		17.2	
2018-10-07	1.1	0.928571	0.0		26.1		19.4	

Figure 4.28 – Performing different expanding window calculations per column

Both rolling and expanding windows equally weight all the observations in the window when performing calculations, but sometimes, we want to place more emphasis on more recent values. One option is to exponentially weight the observations.

Exponentially weighted moving windows

Pandas also provides the `ewm()` method for exponentially weighted moving calculations. As discussed in *Chapter 1, Introduction to Data Analysis*, we can use the **exponentially weighted moving average (EWMA)** to smooth our data. Let's compare the rolling 30-day average to the 30-day EWMA of the maximum daily temperature. Note that we use the `span` argument to specify the number of periods to use for the EWMA calculation:

```
>>> central_park_weather.assign(
...     AVG=lambda x: x.TMAX.rolling('30D').mean(),
...     EWMA=lambda x: x.TMAX.ewm(span=30).mean()
... ).loc['2018-09-29':'2018-10-08', ['TMAX', 'EWMA', 'AVG']].T
```

Unlike the rolling average, the EWMA places higher importance on more recent observations, so the jump in temperature on October 7th has a larger effect on the EWMA than the rolling average:

date	2018-09-29	2018-09-30	2018-10-01	2018-10-02	2018-10-03	2018-10-04	2018-10-05	2018-10-06	2018-10-07	2018-10-08
datatype										
TMAX	22.200000	21.100000	24.400000	25.000000	23.300000	24.400000	21.700000	20.000000	26.100000	23.300000
EWMA	24.410887	24.197281	24.210360	24.261304	24.199285	24.212234	24.050154	23.788854	23.937960	23.896802
AVG	24.723333	24.573333	24.533333	24.460000	24.163333	23.866667	23.533333	23.070000	23.143333	23.196667

Figure 4.29 – Smoothing the data with moving averages

Tip

Check out the `understanding_window_calculations.ipynb` notebook, which contains some interactive visualizations for understanding window functions. This may require some additional setup, but the instructions are in the notebook.

Pipes

Pipes facilitate chaining together operations that expect pandas data structures as their first argument. By using pipes, we can build up complex workflows without needing to write highly nested and hard-to-read code. In general, pipes let us turn something like `f(g(h(data), 20), x=True)` into the following, making it much easier to read:

```
data.pipe(h)\ # first call h(data)
    .pipe(g, 20)\ # call g on the result with positional arg 20
    .pipe(f, x=True) # call f on result with keyword arg x=True
```

Say we wanted to print the dimensions of a subset of the Facebook dataframe with some formatting by calling this function:

```
>>> def get_info(df):
...     return '%d rows, %d cols and max closing Z-score: %d'
...             % (*df.shape, df.close.max())
```

Before we call the function, however, we want to calculate the Z-scores for all the columns. One approach is the following:

```
>>> get_info(fb.loc['2018-Q1']\
...           .apply(lambda x: (x - x.mean())/x.std()))
```

Alternatively, we could pipe the dataframe after calculating the Z-scores to this function:

```
>>> fb.loc['2018-Q1'].apply(lambda x: (x - x.mean())/x.std())\
...           .pipe(get_info)
```

Pipes can also make it easier to write reusable code. In several of the code snippets in this book, we have seen the idea of passing a function into another function, such as when we pass a NumPy function to `apply()` and it gets executed on each column. We can use pipes to extend that functionality to methods of pandas data structures:

```
>>> fb.pipe(pd.DataFrame.rolling, '20D').mean().equals(
...         fb.rolling('20D').mean()
... ) # the pipe is calling pd.DataFrame.rolling(fb, '20D')
True
```

To illustrate how this can benefit us, let's look at a function that will give us the result of a window calculation of our choice. The function is in the `window_calc.py` file. We will import the function and use ?? from IPython to view the function definition:

```
>>> from window_calc import window_calc
>>> window_calc??
Signature: window_calc(df, func, agg_dict, *args, **kwargs)
Source:
def window_calc(df, func, agg_dict, *args, **kwargs):
    """
    Run a window calculation of your choice on the data.

    Parameters:
        - df: The `DataFrame` object to run the calculation on.
        - func: The window calculation method that takes `df` as the first argument.
        - agg_dict: Information to pass to `agg()`, could be a dictionary mapping the columns to the aggregation function to use, a string name for the function, or the function itself.
        - args: Positional arguments to pass to `func`.
        - kwargs: Keyword arguments to pass to `func`.

    Returns:
        A new `DataFrame` object.
    """
    return df.pipe(func, *args, **kwargs).agg(agg_dict)
File:      ~/.../ch_04/window_calc.py
Type:      function
```

Our `window_calc()` function takes the dataframe, the function to execute (as long as it takes a dataframe as its first argument), and information on how to aggregate the result, along with any optional parameters, and gives us back a new dataframe with the results of the window calculations. Let's use this function to find the expanding median of the Facebook stock data:

```
>>> window_calc(fb, pd.DataFrame.expanding, np.median).head()
```

Note that the `expanding()` method doesn't require us to specify any parameters, so all we had to do was pass in `pd.DataFrame.expanding` (no parentheses), along with the aggregation to perform as the window calculation on the dataframe:

	open	high	low	close	volume
date					
2018-01-02	177.68	181.580	177.5500	181.420	18151903.0
2018-01-03	179.78	183.180	179.4400	183.045	17519233.0
2018-01-04	181.88	184.780	181.3300	184.330	16886563.0
2018-01-05	183.39	185.495	182.7148	184.500	15383729.5
2018-01-08	184.90	186.210	184.0996	184.670	16886563.0

Figure 4.30 – Using pipes to perform expanding window calculations

The `window_calc()` function also takes `*args` and `**kwargs`; these are optional parameters that, if supplied, will be collected by Python into `kwargs` when they are passed by name (such as `span=20`) and into `args` if not (passed by position). These can then be **unpacked** and passed to another function or method call by using `*` for `args` and `**` for `kwargs`. We need this behavior in order to use the `ewm()` method for the EWMA of the closing price of Facebook stock:

```
>>> window_calc(fb, pd.DataFrame.ewm, 'mean', span=3).head()
```

In the previous example, we had to use `**kwargs` because the `span` argument is not the first argument that `ewm()` receives, and we didn't want to pass the ones before it:

	open	high	low	close	volume
date					
2018-01-02	177.680000	181.580000	177.550000	181.420000	1.815190e+07
2018-01-03	180.480000	183.713333	180.070000	183.586667	1.730834e+07
2018-01-04	183.005714	185.140000	182.372629	184.011429	1.534980e+07
2018-01-05	184.384000	186.078667	183.736560	185.525333	1.440299e+07
2018-01-08	185.837419	187.534839	185.075110	186.947097	1.625679e+07

Figure 4.31 – Using pipes to perform exponentially weighted window calculations

To calculate the rolling 3-day weather aggregations for Central Park, we take advantage of `*args` since we know that the window is the first argument to `rolling()`:

```
>>> window_calc(  
...     central_park_weather.loc['2018-10'],  
...     pd.DataFrame.rolling,  
...     {'TMAX': 'max', 'TMIN': 'min',  
...      'AWND': 'mean', 'PRCP': 'sum'},  
...     '3D'  
... ) .head()
```

We were able to aggregate each of the columns differently since we passed in a dictionary instead of a single value:

		TMAX	TMIN	AWND	PRCP
	date				
	2018-10-01	24.4	17.2	0.900000	0.0
	2018-10-02	25.0	17.2	0.900000	17.5
	2018-10-03	25.0	17.2	0.966667	17.5
	2018-10-04	25.0	16.1	0.800000	18.5
	2018-10-05	24.4	15.6	1.033333	1.0

Figure 4.32 – Using pipes to perform rolling window calculations

Notice how we were able to create a consistent API for the window calculations, without the caller needing to figure out which aggregation method to call after the window function. This hides some of the implementation details, while making it easier to use. We will be using this function as the base for some of the functionality in the `StockVisualizer` class we will build in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*.

Aggregating data

We already got a sneak peek at aggregation when we discussed window calculations and pipes in the previous section. Here, we will focus on summarizing the dataframe through aggregation, which will change the shape of our dataframe (often through row reduction). We also saw how easy it is to take advantage of vectorized NumPy functions on pandas data structures, especially to perform aggregations. This is what NumPy does best: it performs computationally efficient mathematical operations on numeric arrays.

NumPy pairs well with aggregating dataframes since it gives us an easy way to summarize data with different pre-written functions; often, when aggregating, we just need the NumPy function, since most of what we would want to write ourselves has previously been built. We have already seen some NumPy functions commonly used for aggregations, such as `np.sum()`, `np.mean()`, `np.min()`, and `np.max()`; however, we aren't limited to numeric operations—we can use things such as `np.unique()` on strings. Always check whether NumPy already has a function before implementing one yourself.

For this section, we will be working in the `3-aggregations.ipynb` notebook. Let's import `pandas` and `numpy` and read in the data we will be working with:

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

>>> fb = pd.read_csv(
...     'data/fb_2018.csv', index_col='date', parse_dates=True
... ).assign(trading_volume=lambda x: pd.cut(
...     x.volume, bins=3, labels=['low', 'med', 'high']
... ))
>>> weather = pd.read_csv(
...     'data/weather_by_station.csv',
...     index_col='date', parse_dates=True
... )
```

Note that the weather data for this section has been merged with some of the station data:

	datatype		station	value		station_name
		date				
2018-01-01	PRCP	GHCND:US1CTFR0039	0.0		STAMFORD	4.2 S, CT US
2018-01-01	PRCP	GHCND:US1NJBG0015	0.0	NORTH ARLINGTON	0.7 WNW, NJ US	
2018-01-01	SNOW	GHCND:US1NJBG0015	0.0	NORTH ARLINGTON	0.7 WNW, NJ US	
2018-01-01	PRCP	GHCND:US1NJBG0017	0.0	GLEN ROCK	0.7 SSE, NJ US	
2018-01-01	SNOW	GHCND:US1NJBG0017	0.0	GLEN ROCK	0.7 SSE, NJ US	

Figure 4.33 – Merged weather and station data for this section

Before we dive into any calculations, let's make sure that our data won't be displayed in scientific notation. We will modify how floats are formatted for displaying. The format we will apply is `.2f`, which will provide the float with two digits after the decimal point:

```
>>> pd.set_option('display.float_format', lambda x: '%.2f' % x)
```

First, we will take a look at summarizing the full dataset before moving on to summarizing by groups and building pivot tables and crosstabs.

Summarizing DataFrames

When we discussed window calculations, we saw that we could run the `agg()` method on the result of `rolling()`, `expanding()`, or `ewm()`; however, we can also call it directly on the dataframe in the same fashion. The only difference is that the aggregations done this way will be performed on all the data, meaning that we will only get a series back that contains the overall result. Let's aggregate the Facebook stock data the same way we did with the window calculations. Note that we won't get anything back for the `trading_volume` column, which contains the volume traded bins from `pd.cut()`; this is because we aren't specifying an aggregation to run on that column:

```
>>> fb.agg({
...     'open': np.mean, 'high': np.max, 'low': np.min,
...     'close': np.mean, 'volume': np.sum
... })
open          171.45
high          218.62
low           123.02
close          171.51
volume    6949682394.00
dtype: float64
```

We can use aggregations to easily find the total snowfall and precipitation for 2018 in Central Park. In this case, since we will be performing the sum on both, we can either use `agg('sum')` or call `sum()` directly:

```
>>> weather.query('station == "GHCND:USW00094728"') \
...     .pivot(columns='datatype', values='value') \
...     [['SNOW', 'PRCP']].sum()
datatype
SNOW    1007.00
PRCP   1665.30
dtype: float64
```

Additionally, we can provide multiple functions to run on each of the columns we want to aggregate. As we have already seen, we get a `Series` object when each column has a single aggregation. To distinguish between the aggregations in the case of multiple ones per column, pandas will return a `DataFrame` object instead. The index of this dataframe will tell us which metric is being calculated for which column:

```
>>> fb.agg({
...     'open': 'mean',
...     'high': ['min', 'max'],
...     'low': ['min', 'max'],
...     'close': 'mean'
... })
```

This results in a dataframe where the rows indicate the aggregation function being applied to the data columns. Note that we get nulls for any combination of aggregation and column that we didn't explicitly ask for:

	open	high	low	close
mean	171.45	NaN	NaN	171.51
min	NaN	129.74	123.02	NaN
max	NaN	218.62	214.27	NaN

Figure 4.34 – Performing multiple aggregations per column

So far, we have learned how to aggregate over specific windows and over the entire dataframe; however, the real power comes with the ability to aggregate by group membership. This lets us calculate things such as the total precipitation per month, per station and average OHLC stock prices for each volume traded bin we've created.

Aggregating by group

To calculate the aggregations per group, we must first call the `groupby()` method on the dataframe and provide the column(s) we want to use to determine distinct groups. Let's look at the average of our stock data points for each of the volume traded bins we created with `pd.cut()`; remember, these are three equal-width bins:

```
>>> fb.groupby('trading_volume').mean()
```

The average OHLC prices are smaller for larger trading volumes, which was to be expected given that the three dates in the high-volume traded bin were selloffs:

	open	high	low	close	volume
trading_volume					
low	171.36	173.46	169.31	171.43	24547207.71
med	175.82	179.42	172.11	175.14	79072559.12
high	167.73	170.48	161.57	168.16	141924023.33

Figure 4.35 – Aggregating by group

After running `groupby()`, we can also select specific columns for aggregation:

```
>>> fb.groupby('trading_volume')\n...     ['close'].agg(['min', 'max', 'mean'])
```

This gives us the aggregations for the closing price in each volume traded bucket:

	min	max	mean
trading_volume			
low	124.06	214.67	171.43
med	152.22	217.50	175.14
high	160.06	176.26	168.16

Figure 4.36 – Aggregating a specific column per group

If we need more fine-tuned control over how each column gets aggregated, we use the `agg()` method again with a dictionary that maps the columns to their aggregation function. As we did previously, we can provide lists of functions per column; the result, however, will look a little different:

```
>>> fb_agg = fb.groupby('trading_volume').agg({\n...     'open': 'mean', 'high': ['min', 'max'],\n...     'low': ['min', 'max'], 'close': 'mean'\n... })\n>>> fb_agg
```

We now have a hierarchical index in the columns. Remember, this means that if we want to select the minimum low price for the medium volume traded bucket, we need to use `fb_agg.loc['med', 'low']['min']`:

	open		high		low	close
	mean	min	max	min	max	mean
trading_volume						
low	171.36	129.74	216.20	123.02	212.60	171.43
med	175.82	162.85	218.62	150.75	214.27	175.14
high	167.73	161.10	180.13	149.02	173.75	168.16

Figure 4.37 – Performing multiple aggregations per column with groups

The columns are stored in a `MultiIndex` object:

```
>>> fb_agg.columns
MultiIndex([( 'open', 'mean'),
            ( 'high', 'min'),
            ( 'high', 'max'),
            ( 'low', 'min'),
            ( 'low', 'max'),
            ('close', 'mean')],
           )
```

We can use a list comprehension to remove this hierarchy and instead have our column names in the form of `<column>_<agg>`. At each iteration, we will get a tuple of the levels from the `MultiIndex` object, which we can combine into a single string to remove the hierarchy:

```
>>> fb_agg.columns = ['_'.join(col_agg)
...                     for col_agg in fb_agg.columns]
>>> fb_agg.head()
```

This replaces the hierarchy in the columns with a single level:

	open_mean	high_min	high_max	low_min	low_max	close_mean
trading_volume						
low	171.36	129.74	216.20	123.02	212.60	171.43
med	175.82	162.85	218.62	150.75	214.27	175.14
high	167.73	161.10	180.13	149.02	173.75	168.16

Figure 4.38 – Flattening out the hierarchical index

Say we want to see the average observed precipitation across all the stations per day. We would need to group by the date, but it is in the index. In this case, we have a few options:

- Resampling, which we will cover in the *Working with time series data* section, later in this chapter.
- Resetting the index and using the date column that gets created from the index.
- Passing `level=0` to `groupby()` to indicate that the grouping should be performed on the outermost level of the index.
- Using a `Grouper` object.

Here, we will pass `level=0` to `groupby()`, but note that we can also pass in `level='date'` because our index is named. This gives us the average precipitation observations across the stations, which may give us a better idea of the weather than simply picking a station to look at. Since the result is a single-column `DataFrame` object, we call `squeeze()` to turn it into a `Series` object:

```
>>> weather.loc['2018-10'].query('datatype == "PRCP"') \
...     .groupby(level=0).mean().head().squeeze()
date
2018-10-01    0.01
2018-10-02    2.23
2018-10-03   19.69
2018-10-04    0.32
2018-10-05    0.96
Name: value, dtype: float64
```

We can also group by many categories at once. Let's find the quarterly total recorded precipitation per station. Here, rather than pass in `level=0` to `groupby()`, we need to use a `Grouper` object to aggregate from daily to quarterly frequency. Since this will create a multi-level index, we will also use `unstack()` to put the inner level (the quarter) along the columns after the aggregation is performed:

```
>>> weather.query('datatype == "PRCP"').groupby(
...     ['station_name', pd.Grouper(freq='Q')])
... ).sum().unstack().sample(5, random_state=1)
```

There are many possible follow-ups for this result. We could look at which stations receive the most/least precipitation. We could go back to the location and elevation information we had for each station to see if that affects precipitation. We could also see which quarter has the most/least precipitation across the stations:

		value			
	date	2018-03-31	2018-06-30	2018-09-30	2018-12-31
station_name					
WANTAGH 1.1 NNE, NY US		279.90	216.80	472.50	277.20
STATEN ISLAND 1.4 SE, NY US		379.40	295.30	438.80	409.90
SYOSSET 2.0 SSW, NY US		323.50	263.30	355.50	459.90
STAMFORD 4.2 S, CT US		338.00	272.10	424.70	390.00
WAYNE TWP 0.8 SSW, NJ US		246.20	295.30	620.90	422.00

Figure 4.39 – Aggregating by a column with dates in the index

Tip

The `DataFrameGroupBy` objects returned by the `groupby()` method have a `filter()` method, which allows us to filter groups. We can use this to exclude certain groups from the aggregation. Simply pass a function that returns a Boolean for each group's subset of the dataframe (`True` to include the group and `False` to exclude it). An example is in the notebook.

Let's see which months have the most precipitation. First, we need to group by day and average the precipitation across the stations. Then, we can group by month and sum the resulting precipitation. Finally, we will use `nlargest()` to get the five months with the most precipitation:

```
>>> weather.query('datatype == "PRCP"') \
...      .groupby(level=0).mean() \
...      .groupby(pd.Grouper(freq='M')).sum().value.nlargest()
date
2018-11-30    210.59
2018-09-30    193.09
2018-08-31    192.45
2018-07-31    160.98
2018-02-28    158.11
Name: value, dtype: float64
```

Perhaps the previous result was surprising. The saying goes *April showers bring May flowers*; however, April wasn't in the top five (neither was May, for that matter). Snow will count toward precipitation, but that doesn't explain why summer months are higher than April. Let's look for days that accounted for a large percentage of the precipitation in a given month to see if April shows up there.

To do so, we need to calculate the average daily precipitation across stations and then find the total per month; this will be the denominator. However, in order to divide the daily values by the total for their month, we will need a `Series` object of equal dimensions. This means that we will need to use the `transform()` method, which will perform the specified calculation on the data while always returning an object of equal dimensions to what we started with. Therefore, we can call it on a `Series` object and always get a `Series` object back, regardless of what the aggregation function itself would return:

```
>>> weather.query('datatype == "PRCP"') \
...     .rename(dict(value='prcp'), axis=1) \
...     .groupby(level=0).mean() \
...     .groupby(pd.Grouper(freq='M')) \
...     .transform(np.sum) ['2018-01-28':'2018-02-03']
```

Rather than getting a single sum for January and another for February, notice that we have the same value being repeated for the January entries and a different one for the February ones. Note that the value for February is the value we found in the previous result:

prcp	date
69.31	2018-01-28
69.31	2018-01-29
69.31	2018-01-30
69.31	2018-01-31
158.11	2018-02-01
158.11	2018-02-02
158.11	2018-02-03

Figure 4.40 – The denominator for calculating the percentage of monthly precipitation

We can make this a column in our dataframe to easily calculate the percentage of the monthly precipitation that occurred each day. Then, we can use `nlargest()` to pull out the largest values:

```
>>> weather.query('datatype == "PRCP"') \
...     .rename(dict(value='prcp'), axis=1) \
...     .groupby(level=0).mean()
```

```

...     .assign(
...         total_prcp_in_month=lambda x: x.groupby(
...             pd.Grouper(freq='M')).transform(np.sum),
...         pct_monthly_prcp=lambda x: \
...             x.prcp.div(x.total_prcp_in_month)
...     ).nlargest(5, 'pct_monthly_prcp')

```

Together, the 4th- and 5th-place days in terms of the amount of monthly precipitation they accounted for make up more than 50% of the rain in April. They were also consecutive days:

	prcp	total_prcp_in_month	pct_monthly_prcp
date			
2018-10-12	34.77	105.63	0.33
2018-01-13	21.66	69.31	0.31
2018-03-02	38.77	137.46	0.28
2018-04-16	39.34	140.57	0.28
2018-04-17	37.30	140.57	0.27

Figure 4.41 – Calculating the percentage of monthly precipitation that occurred each day

Important note

The `transform()` method also works on `DataFrame` objects, in which case it will return a `DataFrame` object. We can use it to easily standardize all the columns at once. An example is in the notebook.

Pivot tables and crosstabs

To wrap up this section, we will discuss some `pandas` functions that will aggregate our data into some common formats. The aggregation methods we discussed previously will give us the highest level of customization; however, `pandas` provides some functions to quickly generate a pivot table and a crosstab in a common format.

In order to generate a pivot table, we must specify what to group on and, optionally, which subset of columns we want to aggregate and/or how to aggregate (average, by default). Let's create a pivot table of averaged OHLC data for Facebook per volume traded bin:

```
>>> fb.pivot_table(columns='trading_volume')
```

Since we passed in `columns='trading_volume'`, the distinct values in the `trading_volume` column were placed along the columns. The columns from the original dataframe then went to the index. Notice that the index for the columns has a name (`trading_volume`):

<code>trading_volume</code>	<code>low</code>	<code>med</code>	<code>high</code>
<code>close</code>	171.43	175.14	168.16
<code>high</code>	173.46	179.42	170.48
<code>low</code>	169.31	172.11	161.57
<code>open</code>	171.36	175.82	167.73
<code>volume</code>	24547207.71	79072559.12	141924023.33

Figure 4.42 – Pivot table of column averages per volume traded bin

Tip

If we pass `trading_volume` as the `index` argument instead, we get the transpose of *Figure 4.42*, which is also the exact same output as *Figure 4.35* when we used `groupby()`.

With the `pivot()` method, we weren't able to handle multi-level indices or indices with repeated values. For this reason, we haven't been able to put the weather data in wide format. The `pivot_table()` method solves this issue. To do so, we need to put the date and station information in the index and the distinct values of the datatype column along the columns. The values will come from the value column. We will use the median to aggregate any overlapping combinations (if any):

```
>>> weather.reset_index().pivot_table(  
...     index=['date', 'station', 'station_name'],  
...     columns='datatype',  
...     values='value',  
...     aggfunc='median'  
... ).reset_index().tail()
```

After resetting the index, we have our data in wide format. One final step would be to rename the index:

datatype	date	station	station_name	AWND	DAPR	MDPR	PGTM	PRCP	SNOW	SNWD	...
28740	2018-12-31	GHCND:USW00054787	FARMINGDALE REPUBLIC AIRPORT, NY US	5.00	NaN	NaN	2052.00	28.70	NaN	NaN	...
28741	2018-12-31	GHCND:USW00094728	NY CITY CENTRAL PARK, NY US	NaN	NaN	NaN	NaN	25.90	0.00	0.00	...
28742	2018-12-31	GHCND:USW00094741	TETERBORO AIRPORT, NJ US	1.70	NaN	NaN	1954.00	29.20	NaN	NaN	...
28743	2018-12-31	GHCND:USW00094745	WESTCHESTER CO AIRPORT, NY US	2.70	NaN	NaN	2212.00	24.40	NaN	NaN	...
28744	2018-12-31	GHCND:USW00094789	JFK INTERNATIONAL AIRPORT, NY US	4.10	NaN	NaN	NaN	31.20	0.00	0.00	...

Figure 4.43 – Pivot table with median values per datatype, station, and date

We can use the `pd.crosstab()` function to create a frequency table. For example, if we want to see how many low-, medium-, and high-volume trading days Facebook stock had each month, we can use a crosstab. The syntax is pretty straightforward; we pass the row and column labels to the `index` and `columns` parameters, respectively. By default, the values in the cells will be the count:

```
>>> pd.crosstab(
...     index=fb.trading_volume, columns=fb.index.month,
...     colnames=['month'] # name the columns index
... )
```

This makes it easy to see the months when high volumes of Facebook stock were traded:

month	1	2	3	4	5	6	7	8	9	10	11	12	
trading_volume	low	20	19	15	20	22	21	18	23	19	23	21	19
	med	1	0	4	1	0	0	2	0	0	0	0	0
	high	0	0	2	0	0	0	1	0	0	0	0	0

Figure 4.44 – Crosstab showing the number of trading days per month, per volume traded bin

Tip

We can normalize the output to percentages of the row/column totals by passing in `normalize='rows'`/`normalize='columns'`. An example is in the notebook.

To change the aggregation function, we can provide an argument to `values` and then specify `aggfunc`. To illustrate this, let's find the average closing price of each trading volume bucket per month instead of the count in the previous example:

```
>>> pd.crosstab(
...     index=fb.trading_volume, columns=fb.index.month,
...     colnames=['month'], values=fb.close, aggfunc=np.mean
... )
```

We now get the average closing price per month, per volume traded bin, with null values when that combination wasn't present in the data:

month	1	2	3	4	5	6	7	8	9	10	11	12
trading_volume												
low	185.24	180.27	177.07	163.29	182.93	195.27	201.92	177.49	164.38	154.19	141.64	137.16
med	179.37	NaN	164.76	174.16	NaN	NaN	194.28	NaN	NaN	NaN	NaN	NaN
high	NaN	NaN	164.11	NaN	NaN	NaN	176.26	NaN	NaN	NaN	NaN	NaN

Figure 4.45 – Crosstab using averages instead of counts

We can also get row and column subtotals with the `margins` parameter. Let's count the number of times each station recorded snow per month and include the subtotals:

```
>>> snow_data = weather.query('datatype == "SNOW"')
>>> pd.crosstab(
...     index=snow_data.station_name,
...     columns=snow_data.index.month,
...     colnames=['month'],
...     values=snow_data.value,
...     aggfunc=lambda x: (x > 0).sum(),
...     margins=True, # show row and column subtotals
...     margins_name='total observations of snow' # subtotals
... )
```

Along the bottom row, we have the total snow observations per month, while down the rightmost column, we have the total snow observations in 2018 per station:

month	1	2	3	4	5	6	7	8	9	10	11	12	total observations of snow
station_name													
ALBERTSON 0.2 SSE, NY US	3.00	1.00	3.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	9.00
AMITYVILLE 0.1 WSW, NY US	1.00	0.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00
AMITYVILLE 0.6 NNE, NY US	3.00	1.00	3.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8.00
ARMONK 0.3 SE, NY US	6.00	4.00	6.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	3.00	23.00
BLOOMINGDALE 0.7 SSE, NJ US	2.00	1.00	3.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	8.00
...
WESTFIELD 0.6 NE, NJ US	3.00	0.00	4.00	1.00	0.00	NaN	0.00	0.00	0.00	NaN	1.00	NaN	9.00
WOODBRIDGE TWP 1.1 ESE, NJ US	4.00	1.00	3.00	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	11.00
WOODBRIDGE TWP 1.1 NNE, NJ US	2.00	1.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	7.00
WOODBRIDGE TWP 3.0 NNW, NJ US	NaN	0.00	0.00	NaN	NaN	0.00	NaN	NaN	NaN	0.00	0.00	NaN	0.00
total observations of snow	190.00	97.00	237.00	81.00	0.00	0.00	0.00	0.00	0.00	49.00	13.00		667.00

Figure 4.46 – Crosstab counting the number of days with snow per month, per station

Just by looking at a few stations, we can see that, despite all of them supplying weather information for NYC, they don't share every facet of the weather. Depending on which stations we choose to look at, we could be adding/subtracting snow from what really happened in NYC.

Working with time series data

With time series data, we have some additional operations we can use, for anything from selection and filtering to aggregation. We will be exploring some of this functionality in the `4-time_series.ipynb` notebook. Let's start off by reading in the Facebook data from the previous sections:

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

>>> fb = pd.read_csv(
...     'data/fb_2018.csv', index_col='date', parse_dates=True
... ).assign(trading_volume=lambda x: pd.cut(
...     x.volume, bins=3, labels=['low', 'med', 'high']
... ))
```

We will begin this section by discussing the selection and filtering of time series data before moving on to shifting, differencing, resampling, and finally merging based on time. Note that it's important to set the index to our date (or datetime) column, which will allow us to take advantage of the additional functionality we will be discussing. Some operations may work without doing this, but for a smooth process throughout our analysis, using an index of type `DatetimeIndex` is recommended.

Time-based selection and filtering

Let's start with a quick recap of datetime slicing and indexing. We can easily isolate data for the year by indexing on it: `fb.loc['2018']`. In the case of our stock data, the full dataframe would be returned because we only have 2018 data; however, we can filter to a month (`fb.loc['2018-10']`) or to a range of dates. Note that using `loc []` is optional with ranges:

```
>>> fb['2018-10-11':'2018-10-15']
```

We only get three days back because the stock market is closed on the weekends:

	<code>open</code>	<code>high</code>	<code>low</code>	<code>close</code>	<code>volume</code>	<code>trading_volume</code>
<code>date</code>						
2018-10-11	150.13	154.81	149.1600	153.35	35338901	low
2018-10-12	156.73	156.89	151.2998	153.74	25293492	low
2018-10-15	153.32	155.57	152.5500	153.52	15433521	low

Figure 4.47 – Selecting data based on a date range

Keep in mind that the date range can also be supplied using other frequencies, such as month or the quarter of the year:

```
>>> fb.loc['2018-q1'].equals(fb['2018-01':'2018-03'])  
True
```

When targeting the beginning or end of a date range, pandas has some additional methods for selecting the first or last rows within a specified unit of time. We can select the first week of stock prices in 2018 using the `first ()` method and an offset of `1W`:

```
>>> fb.first('1W')
```

January 1, 2018 was a holiday, meaning that the market was closed. It was also a Monday, so the week here is only four days long:

	open	high	low	close	volume	trading_volume
date						
2018-01-02	177.68	181.58	177.5500	181.42	18151903	low
2018-01-03	181.88	184.78	181.3300	184.67	16886563	low
2018-01-04	184.90	186.21	184.0996	184.33	13880896	low
2018-01-05	185.59	186.90	184.9300	186.85	13574535	low

Figure 4.48 – Facebook stock data during the first week of trading in 2018

We can perform a similar operation for the most recent dates as well. Selecting the last week in the data is as simple as switching the `first()` method with the `last()` method:

```
>>> fb.last('1W')
```

Since December 31, 2018 was a Monday, the last week only consists of one day:

	open	high	low	close	volume	trading_volume
date						
2018-12-31	134.45	134.64	129.95	131.09	24625308	low

Figure 4.49 – Facebook stock data during the last week of trading in 2018

When working with daily stock data, we only have data for the dates the stock market was open. Suppose that we reindexed the data to include rows for each day of the year:

```
>>> fb_reindexed = fb.reindex(
...     pd.date_range('2018-01-01', '2018-12-31', freq='D')
... )
```

The reindexed data would have all nulls for January 1st and any other days the market was closed. We can combine the `first()`, `isna()`, and `all()` methods to confirm this. Here, we will also use the `squeeze()` method to turn the 1-row DataFrame object resulting from the call to `first('1D').isna()` into a Series object so that calling `all()` yields a single value:

```
>>> fb_reindexed.first('1D').isna().squeeze().all()
True
```

We can use the `first_valid_index()` method to obtain the index of the first non-null entry in our data, which will be the first day of trading in the data. To obtain the last day of trading, we can use the `last_valid_index()` method. For the first quarter of 2018, the first day of trading was January 2nd and the last was March 29th:

```
>>> fb_reindexed.loc['2018-Q1'].first_valid_index()
Timestamp('2018-01-02 00:00:00', freq='D')
>>> fb_reindexed.loc['2018-Q1'].last_valid_index()
Timestamp('2018-03-29 00:00:00', freq='D')
```

If we wanted to know what Facebook's stock price looked like as of March 31, 2018, our initial idea may be to use indexing to retrieve it. However, if we try to do so with `loc[]` (`fb_reindexed.loc['2018-03-31']`), we will get null values because the stock market wasn't open that day. If we use the `asof()` method instead, it will give us the closest non-null data that precedes the date we ask for, which in this case is March 29th. Therefore, if we wanted to see how Facebook performed on the last day in each month, we could use `asof()`, and avoid having to first check if the market was open that day:

```
>>> fb_reindexed.asof('2018-03-31')
open                  155.15
high                 161.42
low                  154.14
close                 159.79
volume                59434293.00
trading_volume          low
Name: 2018-03-31 00:00:00, dtype: object
```

For the next few examples, we will need time information in addition to the date. The datasets we have been working with thus far lack a time component, so we will switch to the Facebook stock data by the minute from May 20, 2019 through May 24, 2019 from Nasdaq.com. In order to properly parse the datetimes, we need to pass in a lambda function as the `date_parser` argument since they are not in a standard format (for instance, May 20, 2019 at 9:30 AM is represented as `2019-05-20 09-30`); the lambda function will specify how to convert the data in the `date` field into datetimes:

```
>>> stock_data_per_minute = pd.read_csv(
...     'data/fb_week_of_may_20_per_minute.csv',
...     index_col='date', parse_dates=True,
...     date_parser=lambda x: \
...         pd.to_datetime(x, format='%Y-%m-%d %H-%M')
... )
>>> stock_data_per_minute.head()
```

We have the OHLC data per minute, along with the volume traded per minute:

	open	high	low	close	volume
date					
2019-05-20 09:30:00	181.6200	181.6200	181.6200	181.6200	159049.0
2019-05-20 09:31:00	182.6100	182.6100	182.6100	182.6100	468017.0
2019-05-20 09:32:00	182.7458	182.7458	182.7458	182.7458	97258.0
2019-05-20 09:33:00	182.9500	182.9500	182.9500	182.9500	43961.0
2019-05-20 09:34:00	183.0600	183.0600	183.0600	183.0600	79562.0

Figure 4.50 – Facebook stock data by the minute

Important note

In order to properly parse datetimes in a non-standard format, we need to specify the format it is in. For a reference on the available codes, consult the Python documentation at <https://docs.python.org/3/library/datetime.html#strftime-strptime-behavior>.

We can use `first()` and `last()` with `agg()` to bring this data to a daily granularity. To get the true open value, we need to take the first observation per day; conversely, for the true closing value, we need to take the last observation per day. The high and low will be the maximum and minimum of their respective columns per day. Volume traded will be the daily sum:

```
>>> stock_data_per_minute.groupby(pd.Grouper(freq='1D')).agg({
...     'open': 'first',
...     'high': 'max',
...     'low': 'min',
...     'close': 'last',
...     'volume': 'sum'
... })
```

This rolls the data up to a daily frequency:

	open	high	low	close	volume
date					
2019-05-20	181.62	184.1800	181.6200	182.72	10044838.0
2019-05-21	184.53	185.5800	183.9700	184.82	7198405.0
2019-05-22	184.81	186.5603	184.0120	185.32	8412433.0
2019-05-23	182.50	183.7300	179.7559	180.87	12479171.0
2019-05-24	182.33	183.5227	181.0400	181.06	7686030.0

Figure 4.51 – Rolling up the data from the minute level to the daily level

The next two methods we will discuss help us select data based on the time part of the datetime. The `at_time()` method allows us to isolate rows where the time part of the datetime is the time we specify. By running `at_time('9:30')`, we can grab all the market open prices (the stock market opens at 9:30 AM):

```
>>> stock_data_per_minute.at_time('9:30')
```

This tells us what the stock data looked like at the opening bell each day:

	open	high	low	close	volume
date					
2019-05-20 09:30:00	181.62	181.62	181.62	181.62	159049.0
2019-05-21 09:30:00	184.53	184.53	184.53	184.53	58171.0
2019-05-22 09:30:00	184.81	184.81	184.81	184.81	41585.0
2019-05-23 09:30:00	182.50	182.50	182.50	182.50	121930.0
2019-05-24 09:30:00	182.33	182.33	182.33	182.33	52681.0

Figure 4.52 – Grabbing the stock data at market open each day

We can use the `between_time()` method to grab all the rows where the time portion of the datetime is between two times (inclusive of the endpoints by default). This method can be very useful if we want to look at data within a certain time range, day over day. Let's grab all the rows within the last two minutes of trading each day (15:59 - 16:00):

```
>>> stock_data_per_minute.between_time('15:59', '16:00')
```

It looks like the last minute (16:00) has significantly more volume traded each day compared to the previous minute (15:59). Perhaps people rush to make trades before close:

date	open	high	low	close	volume
2019-05-20 15:59:00	182.915	182.915	182.915	182.915	134569.0
2019-05-20 16:00:00	182.720	182.720	182.720	182.720	1113672.0
2019-05-21 15:59:00	184.840	184.840	184.840	184.840	61606.0
2019-05-21 16:00:00	184.820	184.820	184.820	184.820	801080.0
2019-05-22 15:59:00	185.290	185.290	185.290	185.290	96099.0
2019-05-22 16:00:00	185.320	185.320	185.320	185.320	1220993.0
2019-05-23 15:59:00	180.720	180.720	180.720	180.720	109648.0
2019-05-23 16:00:00	180.870	180.870	180.870	180.870	1329217.0
2019-05-24 15:59:00	181.070	181.070	181.070	181.070	52994.0
2019-05-24 16:00:00	181.060	181.060	181.060	181.060	764906.0

Figure 4.53 – Stock data in the last two minutes of trading per day

We may wonder if this also happens in the first two minutes. Do people put their trades in the night before, and they execute when the market opens? It is trivial to change the previous code to answer that question. Instead, let's see if, on average, more shares were traded within the first 30 minutes of trading or in the last 30 minutes for the week in question. We can combine `between_time()` with `groupby()` to answer this question. In addition, we need to use `filter()` to exclude groups from the aggregation. The excluded groups are times that aren't in the time range we want:

```
>>> shares_traded_in_first_30_min = stock_data_per_minute\
...     .between_time('9:30', '10:00')\
...     .groupby(pd.Grouper(freq='1D'))\
...     .filter(lambda x: (x.volume > 0).all())\
...     .volume.mean()
```

```
>>> shares_traded_in_last_30_min = stock_data_per_minute\  
...     .between_time('15:30', '16:00')\  
...     .groupby(pd.Grouper(freq='1D'))\  
...     .filter(lambda x: (x.volume > 0).all())\  
...     .volume.mean()
```

For the week in question, there were 18,593 more trades on average around the opening time than the closing time:

```
>>> shares_traded_in_first_30_min \  
... - shares_traded_in_last_30_min  
18592.967741935485
```

Tip

We can use the `normalize()` method on `DatetimeIndex` objects or after first accessing the `dt` attribute of a `Series` object to normalize all the datetimes to midnight. This is helpful when the time isn't adding value to our data. There are examples of this in the notebook.

With the stock data, we have a snapshot of the price for each minute or day (depending on the granularity), but we may be interested in seeing the change between time periods as a time series rather than aggregating the data. For this, we need to learn how to create lagged data.

Shifting for lagged data

We can use the `shift()` method to create lagged data. By default, the shift will be by one period, but this can be any integer (positive or negative). Let's use `shift()` to create a new column that indicates the previous day's closing price for the daily Facebook stock data. From this new column, we can calculate the price change due to after-hours trading (after the market close one day right up to the market open the following day):

```
>>> fb.assign(  
...     prior_close=lambda x: x.close.shift(),  
...     after_hours_change_in_price=lambda x: \  
...         x.open - x.prior_close,  
...     abs_change=lambda x: \  
...         x.after_hours_change_in_price.abs()  
... ).nlargest(5, 'abs_change')
```

This gives us the days that were most affected by after-hours trading:

	open	high	low	close	volume	trading_volume	prior_close	after_hours_change_in_price	abs_change
date									
2018-07-26	174.89	180.13	173.75	176.26	169803668	high	217.50	-42.61	42.61
2018-04-26	173.22	176.27	170.80	174.16	77556934	med	159.69	13.53	13.53
2018-01-12	178.06	181.48	177.40	179.37	77551299	med	187.77	-9.71	9.71
2018-10-31	155.00	156.40	148.96	151.79	60101251	low	146.22	8.78	8.78
2018-03-19	177.01	177.17	170.06	172.56	88140060	med	185.09	-8.08	8.08

Figure 4.54 – Using lagged data to calculate after-hours changes in stock price

Tip

To add/subtract time from the datetimes in the index, consider using `Timedelta` objects instead. There is an example of this in the notebook.

In the previous example, we used the shifted data to calculate the change across columns. However, if, rather than the after-hours trading, we were interested in the change in Facebook's stock price each day, we would calculate the difference between the closing price and the shifted closing price. Pandas makes it a little easier than this, as we will see next.

Differenced data

We've already discussed creating lagged data with the `shift()` method. However, often, we are interested in how the values change from one time period to the next. For this, pandas has the `diff()` method. By default, this will calculate the change from time period $t-1$ to time period t :

$$x_{\text{diff}} = x_t - x_{t-1}$$

Note that this is equivalent to subtracting the result of `shift()` from the original data:

```
>>> (fb.drop(columns='trading_volume')
... - fb.drop(columns='trading_volume').shift())
... ).equals(fb.drop(columns='trading_volume').diff())
True
```

We can use `diff()` to easily calculate the day-over-day change in the Facebook stock data:

```
>>> fb.drop(columns='trading_volume').diff().head()
```

For the first few trading days of the year, we can see that the stock price increased, and that the volume traded decreased daily:

	open	high	low	close	volume
date					
2018-01-02	NaN	NaN	NaN	NaN	NaN
2018-01-03	4.20	3.20	3.7800	3.25	-1265340.0
2018-01-04	3.02	1.43	2.7696	-0.34	-3005667.0
2018-01-05	0.69	0.69	0.8304	2.52	-306361.0
2018-01-08	1.61	2.00	1.4000	1.43	4420191.0

Figure 4.55 – Calculating day-over-day changes

Tip

To specify the number of periods that are used for the difference, simply pass in an integer to `diff()`. Note that this number can be negative. An example of this is in the notebook.

Resampling

Sometimes, the data is at a granularity that isn't conducive to our analysis. Consider the case where we have data per minute for the full year of 2018. The level of granularity and nature of the data may render plotting useless. Therefore, we will need to aggregate the data to a less granular frequency:

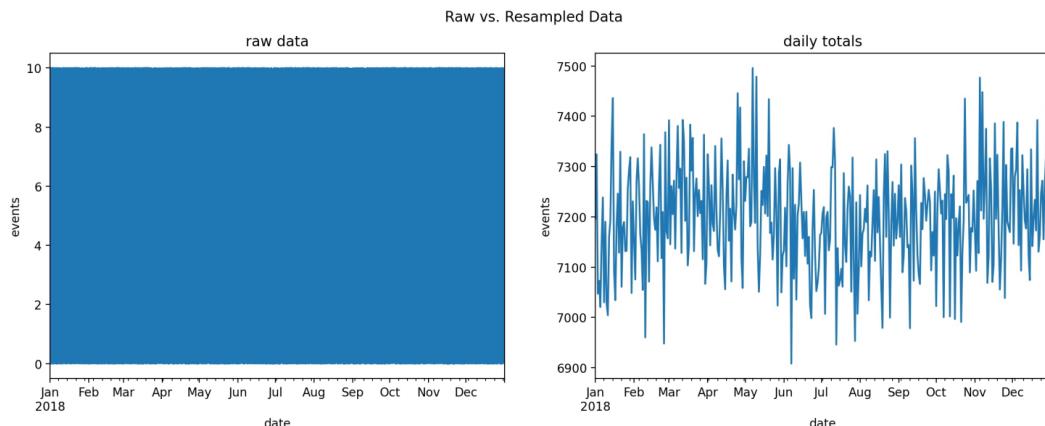


Figure 4.56 – Resampling can be used to roll up granular data

Suppose we had a full year of the data in *Figure 4.50* (Facebook stock data by the minute). It's possible that this level of granularity is beyond what is useful for us, in which case we can use the `resample()` method to aggregate our time series data to a different granularity. To use `resample()`, all we have to do is say how we want to roll up the data and tack on an optional call to an aggregation method. For example, we can resample this minute-by-minute data to a daily frequency and specify how to aggregate each column:

```
>>> stock_data_per_minute.resample('1D').agg({
...     'open': 'first',
...     'high': 'max',
...     'low': 'min',
...     'close': 'last',
...     'volume': 'sum'
... })
```

This is equivalent to the result we got back in the *Time-based selection and filtering* section (*Figure 4.51*):

	open	high	low	close	volume
date					
2019-05-20	181.62	184.1800	181.6200	182.72	10044838.0
2019-05-21	184.53	185.5800	183.9700	184.82	7198405.0
2019-05-22	184.81	186.5603	184.0120	185.32	8412433.0
2019-05-23	182.50	183.7300	179.7559	180.87	12479171.0
2019-05-24	182.33	183.5227	181.0400	181.06	7686030.0

Figure 4.57 – Per-minute data resampled into daily data

We can resample to any frequency supported by pandas (more information can be found in the documentation at http://pandas.pydata.org/pandas-docs/stable/user_guide/timeseries.html). Let's resample the daily Facebook stock data to the quarterly average:

```
>>> fb.resample('Q').mean()
```

This gives us the average quarterly performance of the stock. The fourth quarter of 2018 was clearly troublesome:

	open	high	low	close	volume
date					
2018-03-31	179.472295	181.794659	177.040428	179.551148	3.292640e+07
2018-06-30	180.373770	182.277689	178.595964	180.704687	2.405532e+07
2018-09-30	180.812130	182.890886	178.955229	181.028492	2.701982e+07
2018-12-31	145.272460	147.620121	142.718943	144.868730	2.697433e+07

Figure 4.58 – Resampling to quarterly averages

To look further into this, we can use the `apply()` method to look at the difference between how the quarter began and how it ended. We will also need the `first()` and `last()` methods from the *Time-based selection and filtering* section:

```
>>> fb.drop(columns='trading_volume').resample('Q').apply(  
...     lambda x: x.last('1D').values - x.first('1D').values  
... )
```

Facebook's stock price declined in all but the second quarter:

	open	high	low	close	volume
date					
2018-03-31	-22.53	-20.1600	-23.410	-21.63	41282390
2018-06-30	39.51	38.3997	39.844	38.93	-20984389
2018-09-30	-25.04	-28.6600	-29.660	-32.90	20304060
2018-12-31	-28.58	-31.2400	-31.310	-31.35	-1782369

Figure 4.59 – Summarizing Facebook stock's performance per quarter in 2018

Consider the melted minute-by-minute stock data in `melted_stock_data.csv`:

```
>>> melted_stock_data = pd.read_csv(  
...     'data/melted_stock_data.csv',  
...     index_col='date', parse_dates=True  
... )  
>>> melted_stock_data.head()
```

The OHLC format makes it easy to analyze the stock data, but a single column is trickier:

	price
date	
2019-05-20 09:30:00	181.6200
2019-05-20 09:31:00	182.6100
2019-05-20 09:32:00	182.7458
2019-05-20 09:33:00	182.9500
2019-05-20 09:34:00	183.0600

Figure 4.60 – Stock prices by the minute

The `Resampler` object we get back after calling `resample()` has an `ohlc()` method, which we can use to retrieve the OHLC data we are used to seeing:

```
>>> melted_stock_data.resample('1D').ohlc()['price']
```

Since the column in the original data was called `price`, we select it after calling `ohlc()`, which is pivoting our data. Otherwise, we will have a hierarchical index in the columns:

	open	high	low	close
date				
2019-05-20	181.62	184.1800	181.6200	182.72
2019-05-21	184.53	185.5800	183.9700	184.82
2019-05-22	184.81	186.5603	184.0120	185.32
2019-05-23	182.50	183.7300	179.7559	180.87
2019-05-24	182.33	183.5227	181.0400	181.06

Figure 4.61 – Resampling the stock prices per minute to form daily OHLC data

In the previous examples, we **downsampled** to reduce the granularity of the data; however, we can also **upsample** to increase the granularity of the data. We can even call `asfreq()` after to not aggregate the result:

```
>>> fb.resample('6H').asfreq().head()
```

Note that when we resample at a granularity that's finer than the data we have, it will introduce NaN values:

	open	high	low	close	volume	trading_volume
date						
2018-01-02 00:00:00	177.68	181.58	177.55	181.42	18151903.0	low
2018-01-02 06:00:00	NaN	NaN	NaN	NaN	NaN	NaN
2018-01-02 12:00:00	NaN	NaN	NaN	NaN	NaN	NaN
2018-01-02 18:00:00	NaN	NaN	NaN	NaN	NaN	NaN
2018-01-03 00:00:00	181.88	184.78	181.33	184.67	16886563.0	low

Figure 4.62 – Upsampling increases the granularity of the data and will introduce null values

The following are a few ways we can handle the NaN values. In the interest of brevity, examples of these are in the notebook:

- Use `pad()` after `resample()` to forward fill.
- Call `fillna()` after `resample()`, as we saw in *Chapter 3, Data Wrangling with Pandas*, when we handled missing values.
- Use `asfreq()` followed by `assign()` to handle each column individually.

So far, we have been working with time series data stored in a single DataFrame object, but we may want to combine time series. While the techniques discussed in the *Merging DataFrames* section will work for time series, pandas provides additional functionality for merging time series so that we can merge on close matches rather than requiring an exact match. We will discuss these next.

Merging time series

Time series often go down to the second or are even more granular, meaning that it can be difficult to merge if the entries don't have the same datetime. Pandas solves this problem with two additional merging functions. When we want to pair up observations that are close in time, we can use `pd.merge_asof()` to match on nearby keys rather than on equal keys, like we did with joins. On the other hand, if we want to match up the equal keys and interleave the keys without matches, we can use `pd.merge_ordered()`.

To illustrate how these work, we are going to use the `fb_prices` and `aapl_prices` tables in the `stocks.db` SQLite database. These contain the prices of Facebook and Apple stock, respectively, along with a timestamp of when the price was recorded. Note that the Apple data was collected before the stock split in August 2020 (<https://www.marketwatch.com/story/3-things-to-know-about-apples-stock-split-2020-08-28>). Let's read these tables from the database:

```
>>> import sqlite3

>>> with sqlite3.connect('data/stocks.db') as connection:
...     fb_prices = pd.read_sql(
...         'SELECT * FROM fb_prices', connection,
...         index_col='date', parse_dates=['date']
...     )
...     aapl_prices = pd.read_sql(
...         'SELECT * FROM aapl_prices', connection,
...         index_col='date', parse_dates=['date']
...     )
```

The Facebook data is at the minute granularity; however, we have (fictitious) seconds for the Apple data:

```
>>> fb_prices.index.second.unique()
Int64Index([0], dtype='int64', name='date')
>>> aapl_prices.index.second.unique()
Int64Index([ 0, 52, ..., 37, 28], dtype='int64', name='date')
```

If we use `merge()` or `join()`, we will only have values for both Apple and Facebook when the Apple price was at the top of the minute. Instead, to try and line these up, we can perform an *as of* merge. In order to handle the mismatch, we will specify to merge with the nearest minute (`direction='nearest'`) and require that a match can only occur between times that are within 30 seconds of each other (`tolerance`). This will place the Apple data with the minute that it is closest to, so `9:31:52` will go with `9:32` and `9:37:07` will go with `9:37`. Since the times are on the index, we pass in `left_index` and `right_index`, just like we did with `merge()`:

```
>>> pd.merge_asof(
...     fb_prices, aapl_prices,
...     left_index=True, right_index=True,
...     # merge with nearest minute
...     direction='nearest',
...     tolerance=pd.Timedelta(30, unit='s')
... ).head()
```

This is similar to a left join; however, we are more lenient when matching the keys. Note that in the case where multiple entries in the Apple data match the same minute, this function will only keep the closest one. We get a null value for 9 : 31 because the entry for Apple at 9 : 31 was 9 : 31 : 52, which gets placed at 9 : 32 when using nearest:

	FB	AAPL
date		
2019-05-20 09:30:00	181.6200	183.5200
2019-05-20 09:31:00	182.6100	NaN
2019-05-20 09:32:00	182.7458	182.8710
2019-05-20 09:33:00	182.9500	182.5000
2019-05-20 09:34:00	183.0600	182.1067

Figure 4.63 – Merging time series data with a 30-second tolerance

If we don't want the behavior of a left join, we can use the `pd.merge_ordered()` function instead. This will allow us to specify our join type, which will be 'outer' by default. We will have to reset our index to be able to join on the datetimes, however:

```
>>> pd.merge_ordered(  
...     fb_prices.reset_index(), aapl_prices.reset_index()  
... ).set_index('date').head()
```

This strategy will give us null values whenever the times don't match exactly, but it will at least sort them for us:

	FB	AAPL
date		
2019-05-20 09:30:00	181.6200	183.520
2019-05-20 09:31:00	182.6100	NaN
2019-05-20 09:31:52	NaN	182.871
2019-05-20 09:32:00	182.7458	NaN
2019-05-20 09:32:36	NaN	182.500

Figure 4.64 – Performing a strict merge on time series data and ordering it

Tip

We can pass `fill_method='ffill'` to `pd.merge_ordered()` to forward-fill the first `NaN` after a value, but it does not propagate beyond that; alternatively, we can chain a call to `fillna()`. There is an example of this in the notebook.

The `pd.merge_ordered()` function also makes it possible to perform a group-wise merge, so be sure to check out the documentation for more information.

Summary

In this chapter, we discussed how to join dataframes, how to determine the data we will lose for each type of join using set operations, and how to query dataframes as we would a database. We then went over some more involved transformations on our columns, such as binning and ranking, and how to do so efficiently with the `apply()` method. We also learned the importance of vectorized operations in writing efficient pandas code. Then, we explored window calculations and using pipes for cleaner code. Our discussion of window calculations served as a primer for aggregating across whole dataframes and by groups. We also went over how to generate pivot tables and crosstabs. Finally, we looked at some time series-specific functionality in pandas for everything from selection and aggregation to merging.

In the next chapter, we will cover visualization, which pandas implements by providing a wrapper around `matplotlib`. Data wrangling will play a key role in prepping our data for visualization, so be sure to complete the exercises that are provided in the following section before moving on.

Exercises

Using the CSV files in the `exercises/` folder and what we have learned so far in this book, complete the following exercises:

1. With the `earthquakes.csv` file, select all the earthquakes in Japan with a magnitude of 4.9 or greater using the `mb` magnitude type.
2. Create bins for each full number of earthquake magnitude (for instance, the first bin is $(0, 1]$, the second is $(1, 2]$, and so on) with the `ml` magnitude type and count how many are in each bin.

3. Using the `faang.csv` file, group by the ticker and resample to monthly frequency. Make the following aggregations:
 - a) Mean of the opening price
 - b) Maximum of the high price
 - c) Minimum of the low price
 - d) Mean of the closing price
 - e) Sum of the volume traded
4. Build a crosstab with the earthquake data between the `tsunami` column and the `magType` column. Rather than showing the frequency count, show the maximum magnitude that was observed for each combination. Put the magnitude type along the columns.
5. Calculate the rolling 60-day aggregations of the OHLC data by ticker for the FAANG data. Use the same aggregations as exercise 3.
6. Create a pivot table of the FAANG data that compares the stocks. Put the ticker in the rows and show the averages of the OHLC and volume traded data.
7. Calculate the Z-scores for each numeric column of Amazon's data (`ticker` is `AMZN`) in Q4 2018 using `apply()`.
8. Add event descriptions:
 - a) Create a dataframe with the following three columns: `ticker`, `date`, and `event`. The columns should have the following values:
 - i) `ticker: 'FB'`
 - ii) `date: ['2018-07-25', '2018-03-19', '2018-03-20']`
 - iii) `event: ['Disappointing user growth announced after close.', 'Cambridge Analytica story', 'FTC investigation']`
 - b) Set the index to `['date', 'ticker']`.
 - c) Merge this data with the FAANG data using an outer join.

9. Use the `transform()` method on the FAANG data to represent all the values in terms of the first date in the data. To do so, divide all the values for each ticker by the values for the first date in the data for that ticker. This is referred to as an **index**, and the data for the first date is the **base** (https://ec.europa.eu/eurostat/statistics-explained/index.php/Beginners:Statistical_concept_-_Index_and_base_year). When data is in this format, we can easily see growth over time. Hint: `transform()` can take a function name.
10. The **European Centre for Disease Prevention and Control (ECDC)** provides an open dataset on COVID-19 cases called *daily number of new reported cases of COVID-19 by country worldwide* (<https://www.ecdc.europa.eu/en/publications-data/download-todays-data-geographic-distribution-covid-19-cases-worldwide>). This dataset is updated daily, but we will use a snapshot that contains data through September 18, 2020. Complete the following tasks to practice the skills you've learned up to this point in the book:
 - a) Prepare the data:
 - i) Read in the data in the `covid19_cases.csv` file.
 - ii) Create a `date` column by parsing the `dateRep` column into a datetime.
 - iii) Set the `date` column as the index.
 - iv) Use the `replace()` method to update all occurrences of `United_States_of_America` and `United_Kingdom` to `USA` and `UK`, respectively.
 - v) Sort the index.
 - b) For the five countries with the most cases (cumulative), find the day with the largest number of cases.
 - c) Find the 7-day average change in COVID-19 cases for the last week in the data for the five countries with the most cases.
 - d) Find the first date that each country other than China had cases.
 - e) Rank the countries by cumulative cases using percentiles.

Further reading

Check out the following resources for more information on the topics that were covered in this chapter:

- *Intro to SQL: Querying and managing data:* <https://www.khanacademy.org/computing/computer-programming/sql>
- *(Pandas) Comparison with SQL:* https://pandas.pydata.org/pandas-docs/stable/getting_started/comparison/comparison_with_sql.html
- *Set Operations:* https://www.probabilitycourse.com/chapter1/1_2_2_set_operations.php
- **args and **kwargs in Python explained:* <https://pythontips.com/2013/08/04/args-and-kwargs-in-python-explained/>

5

Visualizing Data with Pandas and Matplotlib

So far, we have been working with data strictly in a tabular format. However, the human brain excels at picking out visual patterns; hence, our natural next step is learning how to visualize our data. Visualizations make it much easier to spot aberrations in our data and explain our findings to others. However, we should not reserve data visualizations exclusively for those we present our conclusions to, as visualizations will be crucial in helping us understand our data quickly and more completely in our exploratory data analysis.

There are numerous types of visualizations that go way beyond what we may have seen in the past. In this chapter, we will cover the most common plot types, such as line plots, histograms, scatter plots, and bar plots, along with several other plot types that build upon these. We won't be covering pie charts—they are notorious for being difficult to read properly, and there are better ways to get our point across.

Python has many libraries for creating visualizations, but the main one for data analysis (and other purposes) is `matplotlib`. The `matplotlib` library can be a little tricky to learn at first, but thankfully, `pandas` has its own wrappers around some of the `matplotlib` functionality, allowing us to create many different types of visualizations without needing to write a single line with `matplotlib` (or, at least, very few). For more complicated plot types that aren't built into `pandas` or `matplotlib`, we have the `seaborn` library, which we will discuss in the next chapter. With these three at our disposal, we should be able to create most (if not all) of the visualizations we desire. Animations and interactive plots are beyond the scope of this book, but you can check out the *Further reading* section for more information.

In this chapter, we will cover the following topics:

- An introduction to `matplotlib`
- Plotting with `pandas`
- The `pandas.plotting` module

Chapter materials

The materials for this chapter can be found on GitHub at https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_05. We will be working with three datasets, all of which can be found in the `data/` directory. In the `fb_stock_prices_2018.csv` file, we have the daily opening, high, low, and closing prices of Facebook stock from January through December 2018, along with the volume traded. This was obtained using the `stock_analysis` package, which we will build in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*. The stock market is closed on the weekends, so we only have data for the trading days.

The `earthquakes.csv` file contains earthquake data collected from the **United States Geological Survey (USGS)** API (<https://earthquake.usgs.gov/fdsnws/event/1/>) for September 18, 2018 through October 13, 2018. For each earthquake, we have the value of the magnitude (the `mag` column), the scale it was measured on (the `magType` column), when (the `time` column) and where (the `place` column) it occurred, and the `parsed_place` column for the state or country where the earthquake occurred (we added this column back in *Chapter 2, Working with Pandas DataFrames*). Other unnecessary columns have been removed.

In the `covid19_cases.csv` file, we have an export from the *daily number of new reported cases of COVID-19 by country worldwide* dataset provided by the **European Centre for Disease Prevention and Control (ECDC)**, which can be found at <https://www.ecdc.europa.eu/en/publications-data/download-todays-data-geographic-distribution-covid-19-cases-worldwide>. For scripted or automated collection of this data, the ECDC makes the current day's CSV file available via <https://opendata.ecdc.europa.eu/covid19/casedistribution/csv>. The snapshot we will be using was collected on September 19, 2020 and contains the number of new COVID-19 cases per country from December 31, 2019 through September 18, 2020, with partial data for September 19, 2020. For this chapter, we will look at the 8-month span from January 18, 2020 through September 18, 2020.

Throughout this chapter, we will be working through three notebooks. These are numbered in the order they will be used—one for each of the main sections of this chapter. We will begin our discussion of plotting in Python with an introduction to `matplotlib` in the `1-introducing_matplotlib.ipynb` notebook. Then, we will learn how to create visualizations using `pandas` in the `2-plotting_with_pandas.ipynb` notebook. Finally, we will explore some additional plotting options that `pandas` provides in the `3-pandas_plotting_module.ipynb` notebook. You will be prompted when it is time to switch between the notebooks.

An introduction to matplotlib

The plotting capabilities in `pandas` and `seaborn` are powered by `matplotlib`: both of these packages provide wrappers around the lower-level functionality in `matplotlib`. Consequently, we have many visualization options at our fingertips with minimal code to write; however, this comes at a price: reduced flexibility in what we can create.

We may find that the `pandas` or `seaborn` implementation isn't quite meeting our needs, and, indeed, it may be impossible to override a particular setting after creating the plot with them, meaning we will have to do some of the legwork with `matplotlib`. Additionally, many of the tweaks that will be made to the final appearance of the visualization will be handled with `matplotlib` commands, which we will discuss in the next chapter. Therefore, it would greatly benefit us to have some understanding of how `matplotlib` works.

The basics

The `matplotlib` package is rather large since it encompasses quite a bit of functionality. Fortunately for us, for most of our plotting tasks, all we need is the `pyplot` module, which provides a MATLAB-like plotting framework. Occasionally, we will need to import additional modules for other tasks, such as animations, changing the style, or altering the default parameters; we will see some examples of this in the next chapter.

Rather than importing the whole `matplotlib` package, we will only import the `pyplot` module using the dot (.) notation; this reduces the amount of typing we need to do in order to access what we need, and we don't take up more space in memory with code we won't use. Note that `pyplot` is traditionally aliased as `plt`:

```
import matplotlib.pyplot as plt
```

Before we look at our first plots, let's cover how to actually view them. Matplotlib will create our visualizations with the plot commands; however, we won't see the visualization until we request to see it. It is done in this fashion so that we can continually tweak the visualization with additional code, until we are ready to finalize it. Unless we save a reference to our plot, once it is displayed, we will have to recreate it to change something. This is because the reference to the last plot will have been destroyed to free up resources in memory.

Matplotlib uses the `plt.show()` function to display the visualization. It must be called after each visualization we create. When using the Python shell, it will also prevent additional code from being executed until the window is closed because it is a blocking function. In Jupyter Notebooks, we can simply use the `%matplotlib inline` **magic command** (a special IPython command preceded by a % sign) once, and our visualizations will be automatically displayed when the cell with our visualization code is executed. Magic commands (or *magics* for short) are run as regular code within a Jupyter Notebook cell. If, up to this point in the book, you haven't been keen on using Jupyter Notebooks and would like to get that set up now, you can refer to *Chapter 1, Introduction to Data Analysis*.

Important note

The `%matplotlib inline` magic embeds static images of the plot into our notebook. Another common option is the `%matplotlib notebook` magic. It provides a small level of interactivity to the plot by allowing actions such as resizing and zooming, though note that this requires some additional setup if you're using JupyterLab and can lead to some confusing bugs, depending on the code that's running in the notebook. Check out this article for more information: <https://medium.com/@1522933668924/using-matplotlib-in-jupyter-notebooks-comparing-methods-and-some-tips-python-c38e85b40ba1>.

Let's create our first plot in the `1-introducing_matplotlib.ipynb` notebook, using the Facebook stock prices data from the `fb_stock_prices_2018.csv` file in the repository for this chapter. First, we need to import `pyplot` and `pandas` (in this example, we will use `plt.show()`, so we don't need to run the magic here):

```
>>> import matplotlib.pyplot as plt  
>>> import pandas as pd
```

Next, we read in the CSV file and specify the index as the `date` column, since we know what the data looks like from previous chapters:

```
>>> fb = pd.read_csv(  
...     'data/fb_stock_prices_2018.csv',  
...     index_col='date',  
...     parse_dates=True  
... )
```

To understand how Facebook's stock has evolved over time, we can create a line plot of the daily opening price. For this task, we will use the `plt.plot()` function, providing the data to be used on the *x*-axis and *y*-axis, respectively. We will then follow up with a call to `plt.show()` to display it:

```
>>> plt.plot(fb.index, fb.open)  
>>> plt.show()
```

The result is the following plot:



Figure 5.1 – Our first plot with matplotlib

If we want to present this visualization, we would have to go back and add our axis labels, plot title, legend (if applicable), and possibly fix the *y*-axis range; this will be covered in the next chapter when we discuss formatting and customizing the appearance of our plots. Pandas and seaborn will take care of some of this for us, at least.

For the remainder of this book, we will be using the `%matplotlib inline` magic command (remember, this needs to be used in a Jupyter Notebook to work), so we won't be calling `plt.show()` after our plotting code. The following code gives the same output as the preceding block:

```
>>> %matplotlib inline
>>> import matplotlib.pyplot as plt
>>> import pandas as pd

>>> fb = pd.read_csv(
...     'data/fb_stock_prices_2018.csv',
...     index_col='date',
...     parse_dates=True
... )
>>> plt.plot(fb.index, fb.open)
```

Important note

Be sure to run the `%matplotlib inline` magic command now if you are using a Jupyter Notebook. This ensures that the plotting code in the rest of this chapter displays the output automatically.

We can also use the `plt.plot()` function to generate scatter plots, provided that we specify a format string for the plot as the third argument. A format string is of the form '`[marker] [linestyle] [color]`'; for example, '`--k`' for a black dashed line. Since we don't want a line for the scatter plot, we omit the `linestyle` component. We can make a scatter plot of red circles with the '`or`' format string; here, `o` is for circles and `r` is for the color red. The following code generates a scatter plot of high price versus low price. Notice that we can pass our dataframe in the `data` argument and then use the string names for the columns, instead of passing the series as `x` and `y`:

```
>>> plt.plot('high', 'low', 'or', data=fb.head(20))
```

Barring days of large fluctuations, we would expect the points to be in the form of a line, since the high and low prices won't be far from each other. This is true for the most part, but be careful of the scale that was generated automatically—the *x*-axis and the *y*-axis don't line up perfectly:

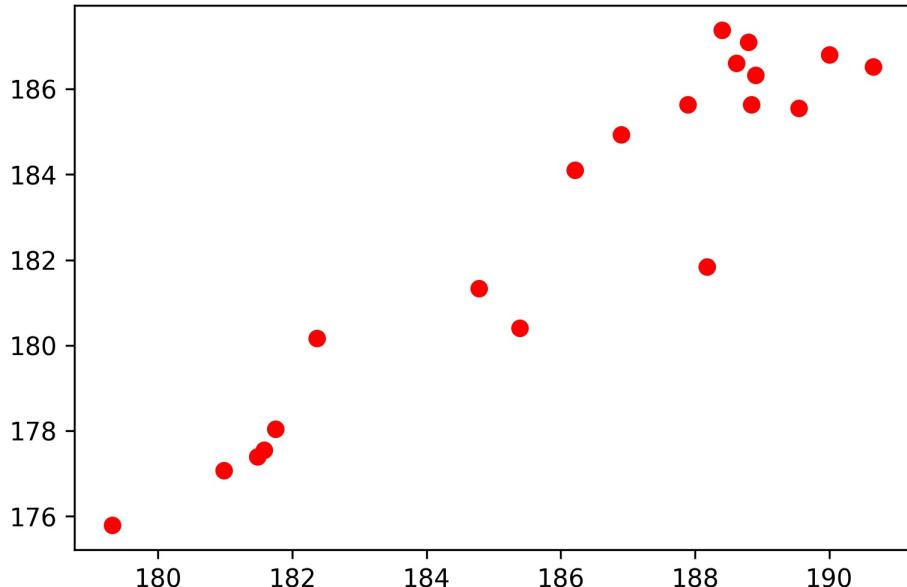


Figure 5.2 – Making a scatter plot with matplotlib

Note that there is some flexibility in specifying the format string. For instance, a format string of the form '`[color] [marker] [linestyle]`' will work unless it is ambiguous. The following table shows some examples of how to formulate a format string for a variety of plot styles; the complete list of options can be found in the **Notes** section in the documentation at https://matplotlib.org/api/_as_gen/matplotlib.pyplot.plot.html:

Marker	Linestyle	Color	Format String	Result
	-	b	-b	blue solid line
.		k	.k	black points
	--	r	--r	red dashed line
o	-	g	o-g	green solid line with circles
:		m	:m	magenta dotted line
x	-.	c	x-.c	cyan dot-dashed line with x's

Figure 5.3 – Styling shortcuts for matplotlib

The format string is a handy way of specifying many options at once, and the good news, as we will see in the *Plotting with pandas* section, is that it works with the `plot()` method in pandas as well. However, if we would rather specify each option separately, we can use the `color`, `linestyle`, and `marker` arguments; check out the values we can pass as keyword arguments to `plt.plot()` in the documentation—pandas will also pass these down to matplotlib for us.

Tip

As an alternative to defining styles per variable being plotted, consider trying out `cycler` from the matplotlib team to specify which combinations matplotlib should cycle between (https://matplotlib.org/gallery/color/color_cycler.html). We will see an example of this in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*.

To create histograms with `matplotlib`, we use the `hist()` function instead. Let's make a histogram of the earthquake magnitudes in the `earthquakes.csv` file, using those measured with the `ml` magnitude type:

```
>>> quakes = pd.read_csv('data/earthquakes.csv')
>>> plt.hist(quakes.query('magType == "ml"').mag)
```

The resulting histogram gives us an idea of the range of earthquake magnitudes we can expect using the `ml` measurement technique:

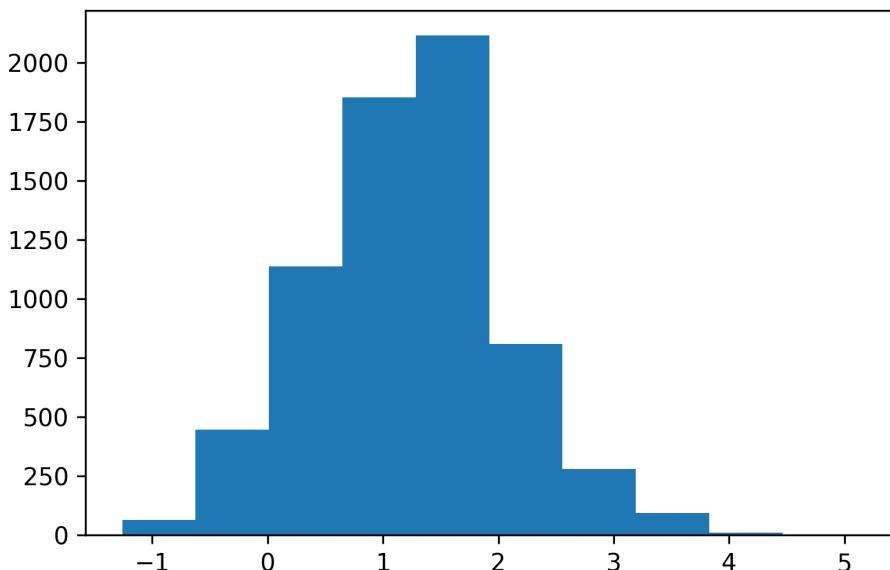


Figure 5.4 – Making a histogram with matplotlib

As we could have guessed, the magnitudes tend to be small, and the distribution appears to be somewhat normal. However, a word of caution regarding histograms—bin size matters. There are cases where we can change the number of bins the data is divided into and change what the histogram indicates the distribution to be. For example, if we make two histograms for this data using different numbers of bins, the distributions look different:

```
>>> x = quakes.query('magType == "ml"').mag
>>> fig, axes = plt.subplots(1, 2, figsize=(10, 3))
>>> for ax, bins in zip(axes, [7, 35]):
...     ax.hist(x, bins=bins)
...     ax.set_title(f'bins param: {bins}')
```

Notice how the distribution appears unimodal in the left subplot, but seems bimodal in the right subplot:

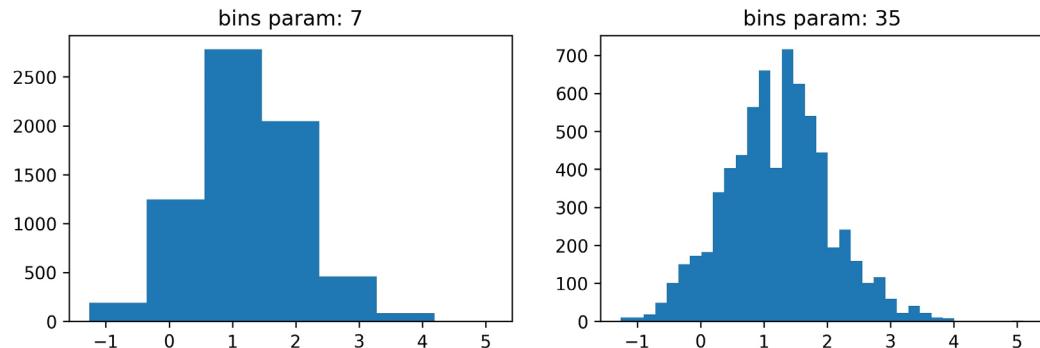


Figure 5.5 – Different bin sizes can drastically change a histogram

Tip

Some common rules of thumb for selecting the number of bins can be found at https://en.wikipedia.org/wiki/Histogram#Number_of_bins_and_width. However, note that, in some cases, a bee swarm plot can be easier to interpret than a histogram; this can be created with `seaborn`, as we will see in *Chapter 6, Plotting with Seaborn and Customization Techniques*.

There are a couple of additional things to note from this example, which we will address in the next section on plot components:

- We can make subplots.
- Plotting functions in `pyplot` can also be used as methods of `matplotlib` objects, such as `Figure` and `Axes` objects.

One last thing regarding basic usage that we will find handy is saving plots as images—we shouldn't be limited to showing the figures in Python only. We can save the last figure with the `plt.savefig()` function by passing in the path to save the image at; for example, `plt.savefig('my_plot.png')`. Note that, if `plt.show()` was called prior to saving, the file will be empty, since the reference to the last plot will be gone after the call to `plt.show()` (`matplotlib` closes the `Figure` object to free up resources in memory). With the `%matplotlib inline` magic command, we can both see and save our image in the same cell.

Plot components

In the prior examples using `plt.plot()`, we didn't have to create a `Figure` object—`matplotlib` took care of creating it for us in the background. However, as we saw when creating *Figure 5.5*, anything beyond a basic plot will require a little more legwork, including creating a `Figure` object ourselves. The `Figure` class is the top level for `matplotlib` visualizations. It contains the `Axes` objects, which themselves contain additional plot objects, such as lines and ticks. In the case of subplots, the `Figure` object contains `Axes` objects with additional functionality.

We use the `plt.figure()` function to create `Figure` objects; these will have zero `Axes` objects until a plot is added:

```
>>> fig = plt.figure()  
<Figure size 432x288 with 0 Axes>
```

The `plt.subplots()` function creates a `Figure` object with `Axes` objects for subplots in the arrangement specified. If we ask `plt.subplots()` for one row and one column, a `Figure` object with one `Axes` object will be returned. This can be useful when writing functions that generate subplot layouts based on the input, since we don't need to worry about needing a special case to handle a single subplot. Here, we will specify an arrangement of one row and two columns; this returns a (`Figure`, `Axes`) tuple, which we can unpack:

```
>>> fig, axes = plt.subplots(1, 2)
```

When using the `%matplotlib inline` magic command, we will see the figure that was created:

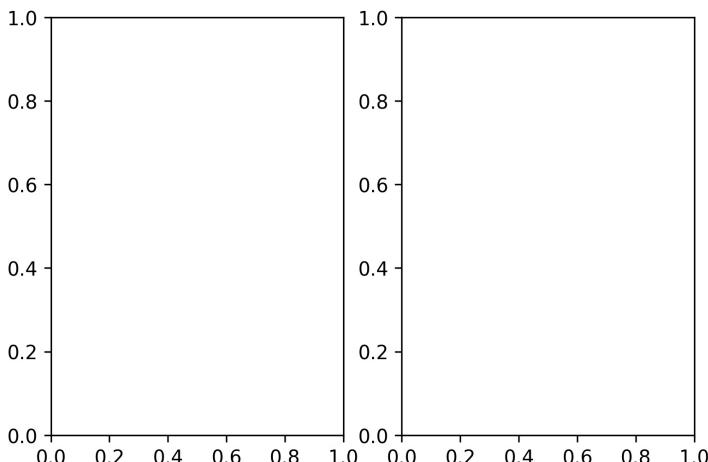


Figure 5.6 – Creating subplots

The alternative to using `plt.subplots()` would be to use the `add_axes()` method on the `Figure` object that we get after running `plt.figure()`. The `add_axes()` method takes a list in the form of `[left, bottom, width, height]` as proportions of the figure dimensions, representing the area in the figure this subplot should occupy:

```
>>> fig = plt.figure(figsize=(3, 3))
>>> outside = fig.add_axes([0.1, 0.1, 0.9, 0.9])
>>> inside = fig.add_axes([0.7, 0.7, 0.25, 0.25])
```

This enables the creation of plots inside of plots:

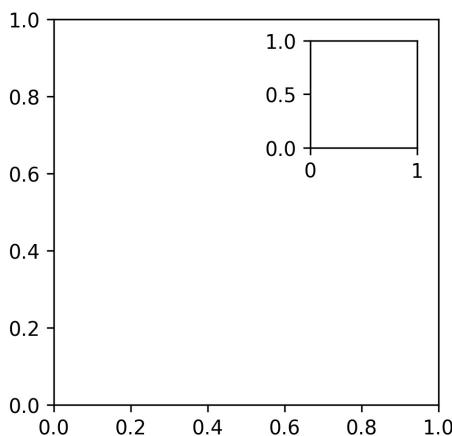


Figure 5.7 – Plot with an inset plot using matplotlib

If our goal is to keep all the plots separate but not all equally sized, we can use the `add_gridspec()` method on a `Figure` object to create a grid for the subplots. Then, we can run `add_subplot()`, passing in the area(s) from the grid that the given subplot should occupy:

```
>>> fig = plt.figure(figsize=(8, 8))
>>> gs = fig.add_gridspec(3, 3)
>>> top_left = fig.add_subplot(gs[0, 0])
>>> mid_left = fig.add_subplot(gs[1, 0])
>>> top_right = fig.add_subplot(gs[:2, 1:])
>>> bottom = fig.add_subplot(gs[2, :])
```

This results in the following layout:

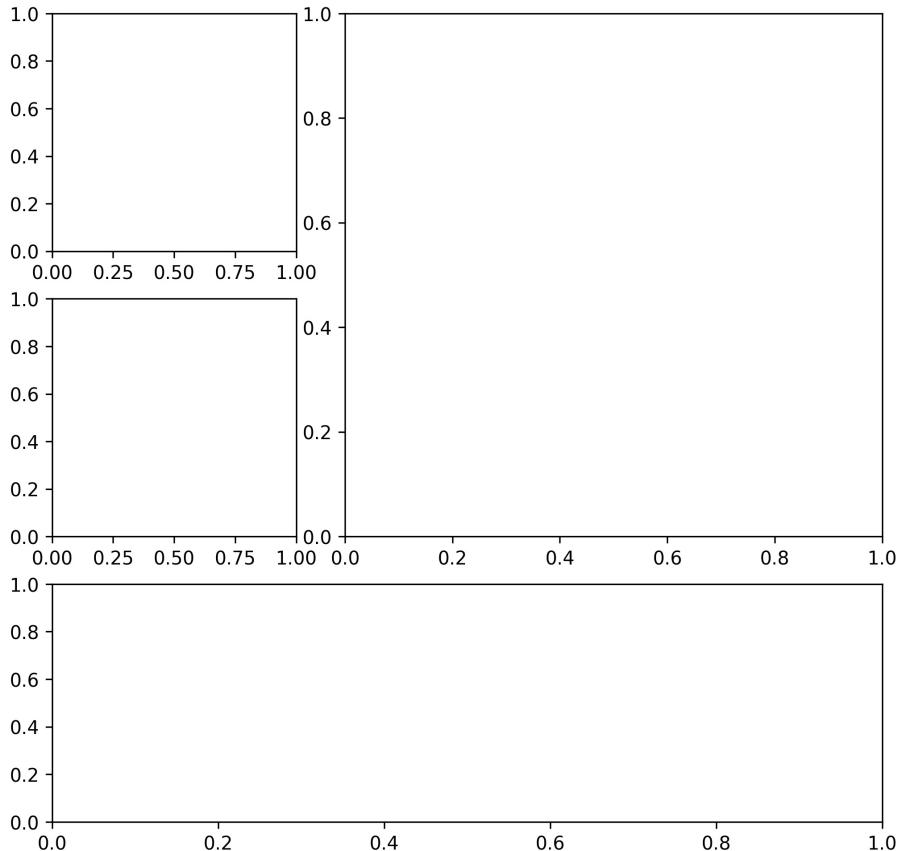


Figure 5.8 – Building custom plot layouts with matplotlib

In the previous section, we discussed how to save visualizations using `plt.savefig()` but we also can use the `savefig()` method on `Figure` objects:

```
>>> fig.savefig('empty.png')
```

This is very useful to remember since with `plt.<func>()`, we only have access to the last `Figure` object; however, if we save the references to our `Figure` objects, we can work with any of them, regardless of when they were created. Additionally, this foreshadows an important concept that you will notice throughout this chapter: `Figure` and `Axes` objects have methods with similar or identical names to their `pyplot` function counterparts.

While it's convenient to have references to all of the `Figure` objects we create, it is good practice to close them when we are done with them so that we don't waste any resources. This can be accomplished with the `plt.close()` function. If we don't pass in anything, it will close the last `Figure` object; however, we can pass in a specific `Figure` object to close only that one or '`'all'`' to close all of the `Figure` objects we have open:

```
>>> plt.close('all')
```

It's important to get comfortable working with `Figure` and `Axes` objects directly as it enables more fine-grained control of the resulting visualizations. This will become evident in the next chapter.

Additional options

A few of our visualizations looked a little squished. To remedy this, we can pass in a value for `figsize` in our call to `plt.figure()` or `plt.subplots()`. We specify the dimensions with a `(width, height)` tuple in inches. The `plot()` method we will see with `pandas` also accepts the `figsize` parameter, so bear this in mind:

```
>>> fig = plt.figure(figsize=(10, 4))
<Figure size 720x288 with 0 Axes>
>>> fig, axes = plt.subplots(1, 2, figsize=(10, 4))
```

Notice that these subplots are more square-shaped than the subplots in *Figure 5.6* when we didn't specify `figsize`:

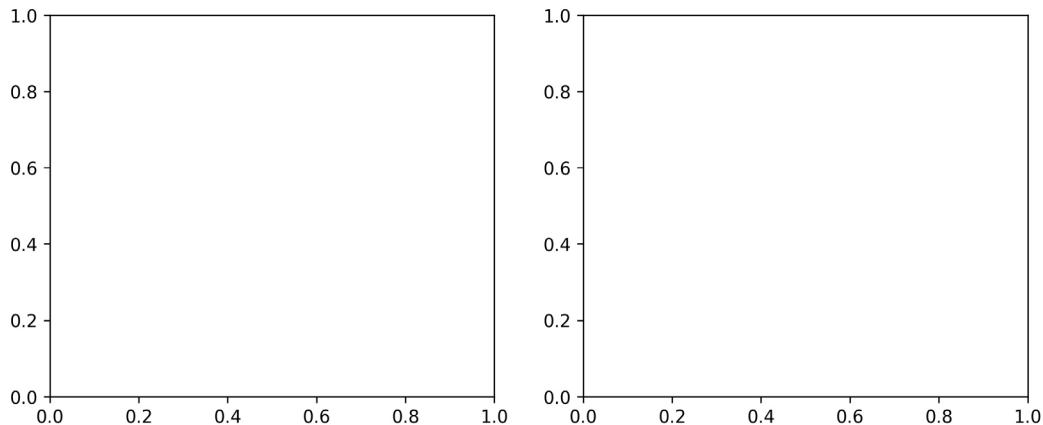


Figure 5.9 – Specifying plot size

It's not too bad specifying the `figsize` parameter for our plots one by one. However, if we find that we are resizing everything to the same size, there's a better alternative. Matplotlib houses its defaults in `rcParams`, which acts like a dictionary, meaning we can easily overwrite what we wish for our session and get the defaults back when we restart our Python session. Since there are many options in this dictionary (over 300 at the time of writing), let's randomly select a few of them to get an idea of what is available:

```
>>> import random
>>> import matplotlib as mpl

>>> rcpParams_list = list(mpl.rcParams.keys())
>>> random.seed(20) # make this repeatable
>>> random.shuffle(rcparams_list)

>>> sorted(rcparams_list[:20])
['axes.axisbelow',
 'axes.formatter.limits',
 'boxplot.vertical',
 'contour.corner_mask',
 'date.autoformatter.month',
 'legend.labelspacing',
 'lines.dashed_pattern',
 'lines.dotted_pattern',
 'lines.scale_dashes',
 'lines.solid_capstyle',
 'lines.solid_joinstyle',
 'mathtext.tt',
 'patch.linewidth',
 'pdf.fonttype',
 'savefig.jpeg_quality',
 'svg.fonttype',
 'text.latex.preview',
 'toolbar',
 'ytick.labelright',
 'ytick.minor.size']
```

As you can see, there are many options we can tinker with here. Let's check what the current default value for `figsize` is:

```
>>> mpl.rcParams['figure.figsize']
[6.0, 4.0]
```

To change this for our current session, simply set it equal to a new value:

```
>>> mpl.rcParams['figure.figsize'] = (300, 10)
>>> mpl.rcParams['figure.figsize']
[300.0, 10.0]
```

Before we move on, let's restore the default settings by using the `mpl.rcdefaults()` function. The default value for `figsize` is actually different than what we had previously; this is because `%matplotlib inline` sets different values for a few of the plot-related parameters when it is first run (<https://github.com/ipython/ipykernel/blob/master/ipykernel/pylab/config.py#L42-L56>):

```
>>> mpl.rcdefaults()
>>> mpl.rcParams['figure.figsize']
[6.8, 4.8]
```

Note that we can also use the `plt.rc()` function to update a particular setting if we know its group (`figure`, in this case) and parameter name (`figsize`). As we did previously, we can use `plt.rcdefaults()` to reset the defaults:

```
# change `figsize` default to (20, 20)
>>> plt.rc('figure', figsize=(20, 20))
>>> plt.rcdefaults() # reset the default
```

Tip

If we find ourselves making the same changes every time we start Python, we should look into reading our configuration in rather than updating the default values each time. Consult the `mpl.rc_file()` function for more information.

Plotting with pandas

Both `Series` and `DataFrame` objects have a `plot()` method that allows us to create several different plots and control some aspects of their formatting, such as subplot layout, figure size, titles, and whether to share an axis across subplots. This makes plotting our data much more convenient, as the bulk of the work to create presentable plots is achieved with a single method call. Under the hood, `pandas` is making several calls to `matplotlib` to produce our plot. Some of the most frequently used arguments to the `plot()` method include the following:

Parameter	Purpose	Data Type
<code>kind</code>	Determines the plot type	String
<code>x / y</code>	Column(s) to plot on the x-axis/y-axis	String or list
<code>ax</code>	Draws the plot on the <code>Axes</code> object provided	<code>Axes</code>
<code>subplots</code>	Determines whether to make subplots	Boolean
<code>layout</code>	Specifies how to arrange the subplots	Tuple of <code>(rows, columns)</code>
<code>figsize</code>	Size to make the <code>Figure</code> object	Tuple of <code>(width, height)</code>
<code>title</code>	The title of the plot or subplots	String for the plot title or a list of strings for subplot titles
<code>legend</code>	Determines whether to show the legend	Boolean
<code>label</code>	What to call an item in the legend	String if a single column is being plotted; otherwise, a list of strings
<code>style</code>	<code>matplotlib</code> style strings for each item being plotted	String if a single column is being plotted; otherwise, a list of strings
<code>color</code>	The color to plot the item in	String or red, green, blue tuple if a single column is being plotted; otherwise, a list
<code>colormap</code>	The colormap to use	String or <code>matplotlib</code> colormap object
<code>logx / logy / loglog</code>	Determines whether to use a logarithmic scale for the x-axis, y-axis, or both	Boolean
<code>xticks / yticks</code>	Determines where to draw the ticks on the x-axis/y-axis	List of values
<code>xlim / ylim</code>	The axis limits for the x-axis/y-axis	Tuple of the form <code>(min, max)</code>
<code>rot</code>	The angle to write the tick labels at	Integer
<code>sharex / sharey</code>	Determines whether to have subplots share the x-axis/y-axis	Boolean
<code>fontsize</code>	Controls the size of the tick labels	Integer
<code>grid</code>	Turns on/off the grid lines	Boolean

Figure 5.10 – Frequently used pandas plotting arguments

Rather than having separate functions for each plot type, as we saw during our discussion of `matplotlib`, the `plot()` method from `pandas` allows us to specify the type of plot we want using the `kind` argument. The choice of plot will determine which other arguments are required. We can use the `Axes` object that's returned by the `plot()` method to further modify our plot.

Let's explore this functionality in the `2-plotting_with_pandas.ipynb` notebook. Before we begin, we need to handle our imports for this section and read in the data we will be using (Facebook stock prices, earthquakes, and COVID-19 cases):

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

>>> fb = pd.read_csv(
...     'data/fb_stock_prices_2018.csv',
...     index_col='date',
...     parse_dates=True
... )
>>> quakes = pd.read_csv('data/earthquakes.csv')
>>> covid = pd.read_csv('data/covid19_cases.csv').assign(
...     date=lambda x: \
...         pd.to_datetime(x.dateRep, format='%d/%m/%Y')
... ).set_index('date').replace(
...     'United_States_of_America', 'USA'
... ).sort_index()['2020-01-18':'2020-09-18']
```

In the next few sections, we will discuss how to generate an appropriate visualization for a specific analysis goal, such as showing the evolution over time or the relationship between the variables in the data. Note that, wherever possible, the plots have been styled so that they can be interpreted in black and white for this book.

Evolution over time

When working with time series data (such as the Facebook stock data stored in the `fb` variable), we often want to show how the data has changed over time. To do this, we use line plots and, in some cases, bar plots (covered in the *Counts and frequencies* section). In the case of a line plot, we simply provide `kind='line'` to `plot()`, indicating which columns will be `x` and `y`. Note that we actually don't need to provide a column for `x` because pandas, by default, will use the index (this also makes it possible to generate the line plot of a `Series` object). Additionally, notice that we can provide a format string to the `style` argument, just like we did with the `matplotlib` plots:

```
>>> fb.plot(
...     kind='line', y='open', figsize=(10, 5), style='-b',
...     legend=False, title='Evolution of Facebook Open Price'
... )
```

This gives us a plot similar to what we achieved with `matplotlib`; however, in this single method call, we specified the figure size for this plot only, turned off the legend, and gave it a title:

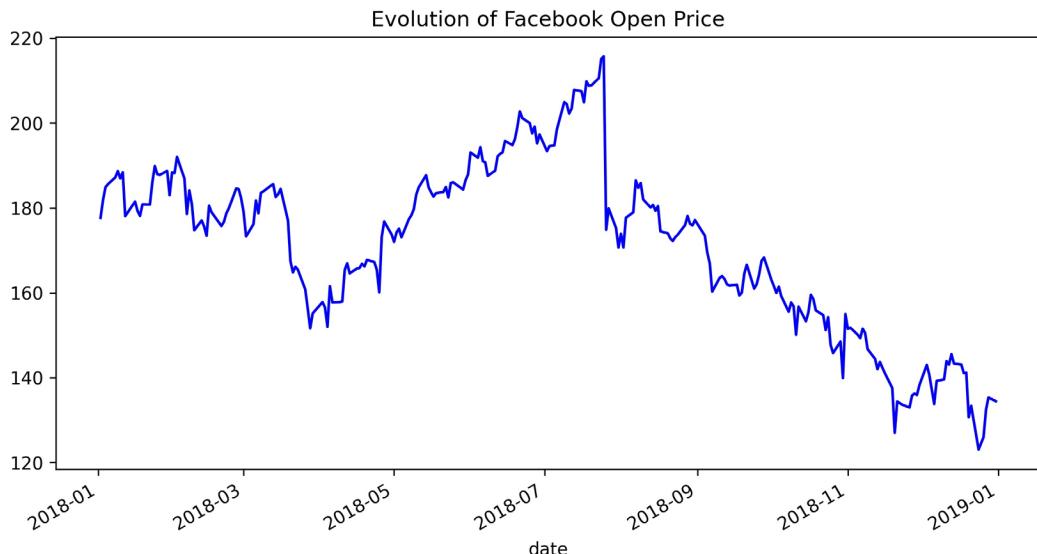


Figure 5.11 – Our first plot with pandas

As with `matplotlib`, we don't have to use the style format strings—instead, we can pass each component separately with its associated keyword. For example, the following code gives us the same result as the previous one:

```
fb.plot(
    kind='line', y='open', figsize=(10, 5),
    color='blue', linestyle='solid',
    legend=False, title='Evolution of Facebook Open Price'
)
```

We aren't limited to plotting one line at a time with the `plot()` method; we can also pass in a list of columns to plot and style them individually. Note that we actually don't need to specify `kind='line'` because that is the default:

```
>>> fb.first('1W').plot(
...     y=['open', 'high', 'low', 'close'],
...     style=['o-b', '--r', ':k', '-g'],
...     title='Facebook OHLC Prices during '
...         '1st Week of Trading 2018'
... ).autoscale() # add space between data and axes
```

This results in the following plot, where each line is styled differently:

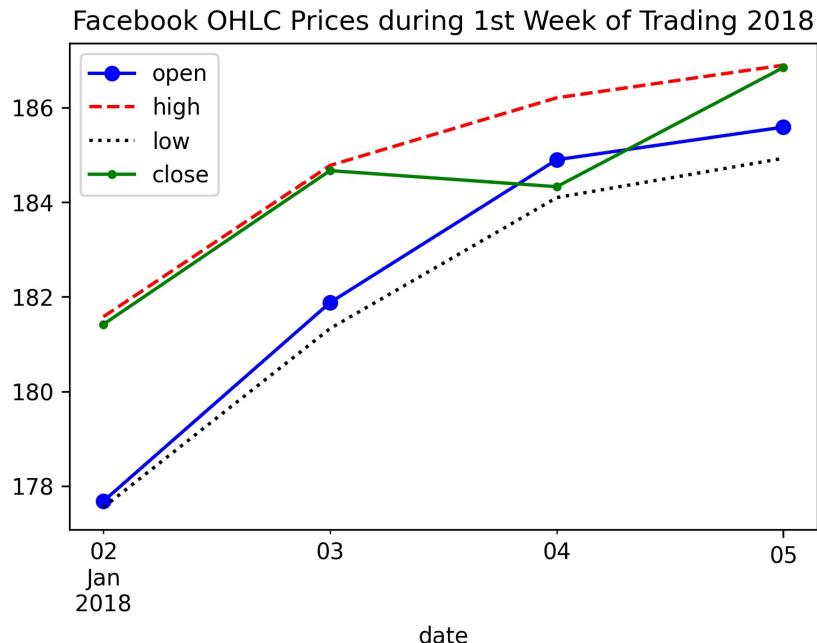


Figure 5.12 – Plotting multiple columns

Additionally, we can easily have pandas plot all our columns in that same call. The `x` and `y` arguments can take a single column name or a list of them; if we provide nothing, pandas will use all of them. Note that the columns must be passed as the `y` argument when `kind='line'`; however, other plot types support passing lists of columns to `x` as well. In this case, it may be helpful to ask for subplots instead of having all the lines on the same plot. Let's visualize all the columns in the Facebook data as line plots:

```
>>> fb.plot(  
...     kind='line', subplots=True, layout=(3, 2),  
...     figsize=(15, 10), title='Facebook Stock 2018'  
... )
```

Using the `layout` argument, we told pandas how to arrange our subplots (three rows and two columns):

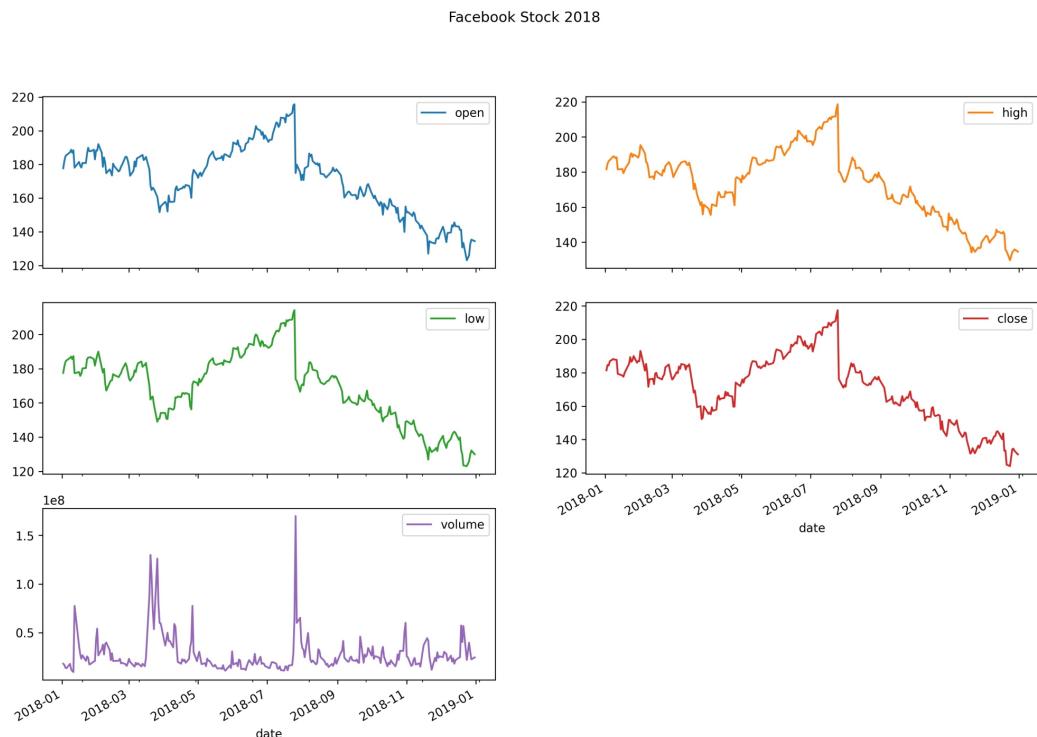


Figure 5.13 – Creating subplots with pandas

Notice that the subplots automatically share the *x*-axis, since they share an index. The *y*-axis is not shared because the `volume` time series is on a different scale. We can alter this behavior in some plot types by passing the `sharex` or `sharey` argument with a Boolean to `plot()`. The legend will be rendered by default, so, for each subplot, we have a single item in the legend indicating which data it contains. We didn't provide a list of subplot titles with the `title` argument in this case, since the legend served that purpose; however, we passed a single string for the title of the plot as a whole. To summarize, when working with subplots, we have two options when it comes to the title:

- Passing a single string for the title of the figure as a whole.
- Passing a list of strings to use as the title for each subplot.

Sometimes, we want to make subplots where each has a few variables in them for comparison. This can be achieved by first creating the subplots with `plt.subplots()` and then providing the `Axes` objects to the `ax` parameter. To illustrate this, let's take a look at daily new cases of COVID-19 in China, Spain, Italy, the USA, Brazil, and India. This is long format data, so we must first pivot it so that the dates (which we set as the index when we read in the CSV file) are in the index of the pivot table and the countries (`countriesAndTerritories`) are in the columns. Since there is a lot of fluctuation in these values, we will plot the 7-day moving average of new cases using the `rolling()` method introduced in *Chapter 4, Aggregating Pandas DataFrames*:

```
>>> new_cases_rolling_average = covid.pivot_table(  
...     index=covid.index,  
...     columns='countriesAndTerritories',  
...     values='cases'  
... ).rolling(7).mean()
```

Rather than create a separate plot for each country (which makes it harder to compare) or plot them all together (which will make it difficult to see the smaller values), we will plot countries that have had a similar number of cases in the same subplot. We will also use different line styles in order to distinguish between them in black and white:

```
>>> fig, axes = plt.subplots(1, 3, figsize=(15, 5))  
  
>>> new_cases_rolling_average[['China']]\  
...     .plot(ax=axes[0], style='-.c')  
>>> new_cases_rolling_average[['Italy', 'Spain']].plot(  
...     ax=axes[1], style=['--', '--'],  
...     title='7-day rolling average of new '  
...         'COVID-19 cases\n(source: ECDC)'  
... )  
>>> new_cases_rolling_average[['Brazil', 'India', 'USA']]\  
...     .plot(ax=axes[2], style=['---', ':', '-'])
```

By directly using `matplotlib` to generate the `Axes` objects for each subplot, we gained a lot more flexibility in the resulting layout:

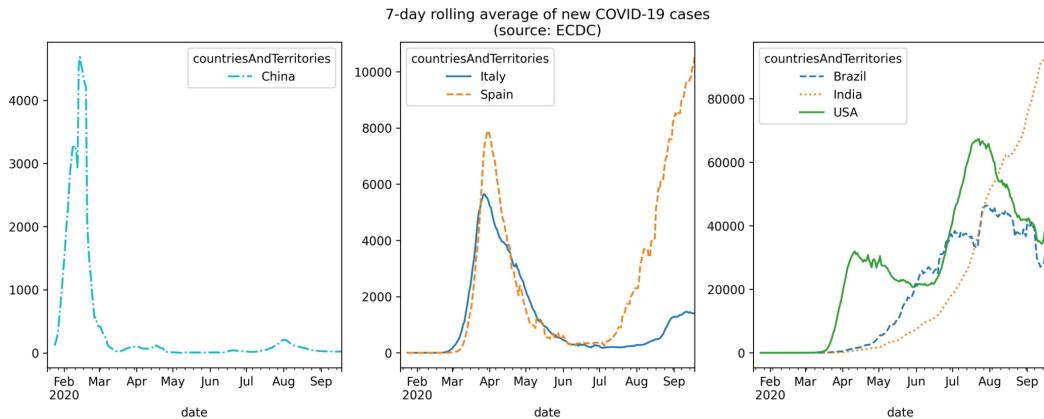


Figure 5.14 – Controlling which data gets plotted in each of the subplots

In the previous plot, we were able to compare countries with similar levels of daily new COVID-19 cases, but we couldn't compare all of them in the same subplot due to scale. One way to get around this is to use an **area plot**, which makes it possible for us to visualize the overall 7-day rolling average of new COVID-19 cases and, at the same time, how much each country is contributing to the total. In the interest of readability, we will group Italy and Spain together and create another category for countries other than the USA, Brazil, and India:

```
>>> cols = [
...     col for col in new_cases_rolling_average.columns
...     if col not in [
...         'USA', 'Brazil', 'India', 'Italy & Spain'
...     ]
... ]
>>> new_cases_rolling_average.assign(
...     **{'Italy & Spain': lambda x: x.Italy + x.Spain}
... ).sort_index(axis=1).assign(
...     Other=lambda x: x[cols].sum(axis=1)
... ).drop(columns=cols).plot(
...     kind='area', figsize=(15, 5),
...     title='7-day rolling average of new '
...           'COVID-19 cases\n(source: ECDC)'
... )
```

For those viewing the resulting plot in black and white, Brazil is the bottom layer, with India on top of it and so on. The combined height of the plot areas is the overall value, and the height of a given shaded region is the value for that country. This shows us that more than half of the daily new cases are in Brazil, India, Italy, Spain, and the USA combined:

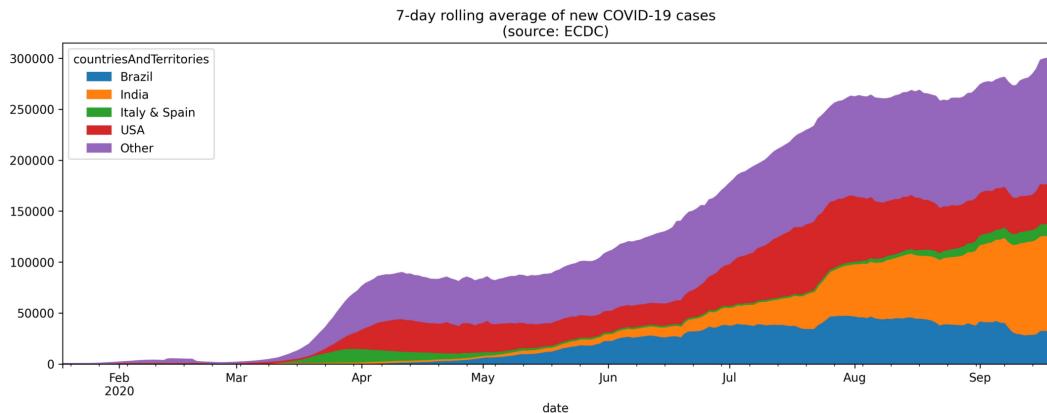


Figure 5.15 – Creating an area plot

Another way to visualize evolution over time is to look at the cumulative sum over time. Let's plot the cumulative number of COVID-19 cases in China, Spain, Italy, the USA, Brazil, and India, using the `ax` parameter to once again to create subplots. To calculate the cumulative sum over time, we group by the location (`countriesAndTerritories`) and the date, which is our index, so we use `pd.Grouper()`; this time, we will use `groupby()` and `unstack()` to pivot our data into wide format for the plot:

```
>>> fig, axes = plt.subplots(1, 3, figsize=(15, 3))

>>> cumulative_covid_cases = covid.groupby(
...     ['countriesAndTerritories', pd.Grouper(freq='1D')]
... ).cases.sum().unstack(0).apply('cumsum')

>>> cumulative_covid_cases[['China']] \
...     .plot(ax=axes[0], style='-.c')
>>> cumulative_covid_cases[['Italy', 'Spain']].plot(
...     ax=axes[1], style=['--', '---'],
...     title='Cumulative COVID-19 Cases\n(source: ECDC)'
... )
>>> cumulative_covid_cases[['Brazil', 'India', 'USA']] \
...     .plot(ax=axes[2], style=['---', ':', '-'])
```

Viewing the cumulative COVID-19 cases shows that while China and Italy appear to have COVID-19 cases under control, Spain, the USA, Brazil, and India are struggling:

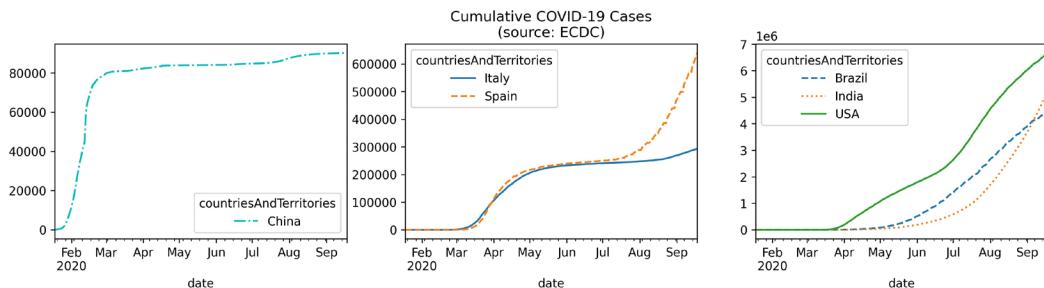


Figure 5.16 – Plotting the cumulative sum over time

Important note

We used dotted and dashed lines multiple times in this section to ensure that the resulting plots could be interpreted in black and white; note, however, that accepting the default colors and line styles will suffice when presenting these plots in color. Often, different line styles signify a difference in the data types—for example, we could use a solid line for the evolution over time and a dashed line to represent the rolling average.

Relationships between variables

When we want to visualize the relationship between variables, we often begin with scatter plots, which show us the value of the y variable at different values of the x variable. This makes it very easy for us to spot correlations and possible non-linear relationships. In the previous chapter, when we looked at the Facebook stock data, we saw that the days of high volume traded appeared to be correlated with large drops in stock price. We can use a scatter plot to visualize this relationship:

```
>>> fb.assign(
...     max_abs_change=fb.high - fb.low
... ).plot(
...     kind='scatter', x='volume', y='max_abs_change',
...     title='Facebook Daily High - Low vs. Volume Traded'
... )
```

There appears to be a relationship, but it does not seem linear:

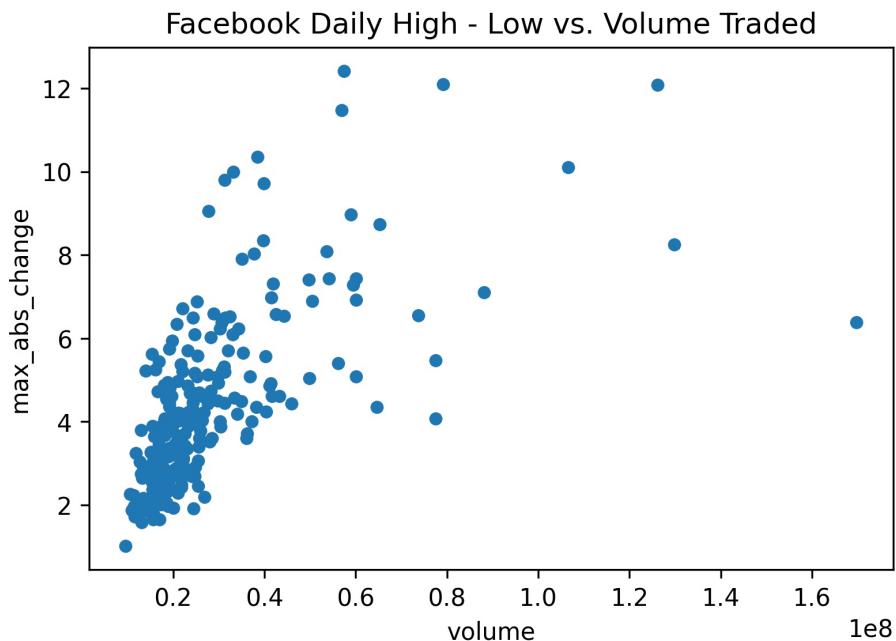


Figure 5.17 – Making scatter plots with pandas

Let's try taking the logarithm (log) of the volume. To do so, we have a couple of options:

- Create a new column that is the log of the volume using `np.log()`.
- Use a logarithmic scale for the x -axis by passing in `logx=True` to the `plot()` method or calling `plt.xscale('log')`.

In this case, it makes the most sense to simply change how we display our data, since we aren't going to use the new column:

```
>>> fb.assign(
...     max_abs_change=fb.high - fb.low
... ).plot(
...     kind='scatter', x='volume', y='max_abs_change',
...     title='Facebook Daily High - '
...         'Low vs. log(Volume Traded)',
...     logx=True
... )
```

After modifying the x -axis scale, we get the following scatter plot:

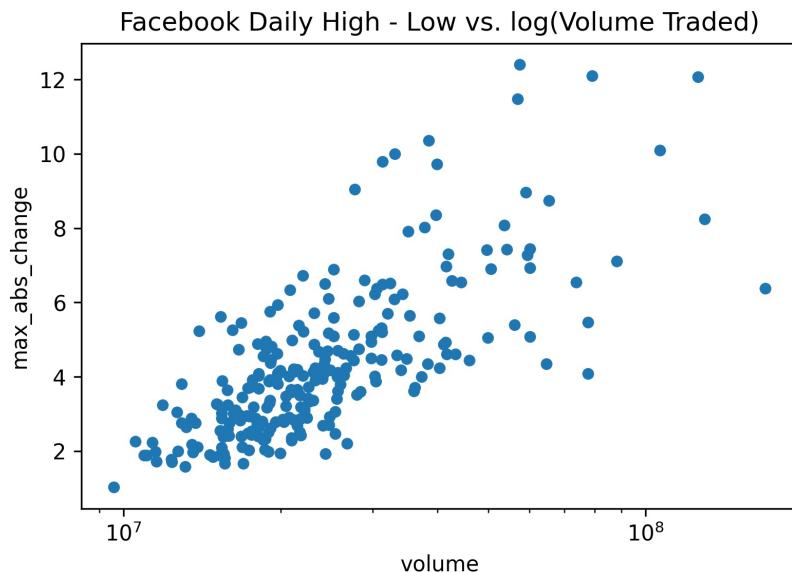


Figure 5.18 – Applying a logarithmic scale to the x -axis

Tip

The `plot()` method from `pandas` has three arguments for logarithmic scales: `logx`/`logy` for single axis adjustments and `loglog` for setting both to the logarithmic scale.

One problem with scatter plots is that it can be very difficult to discern the concentration of points in a given area, since they are simply plotted one on top of the other. We can use the `alpha` argument to control the transparency of the points; this argument takes values from 0 to 1, where 0 is entirely transparent and 1 is completely opaque. By default, they are opaque (value of 1); however, if we make them more transparent, we should be able to see some of the overlap:

```
>>> fb.assign(
...     max_abs_change=fb.high - fb.low
... ).plot(
...     kind='scatter', x='volume', y='max_abs_change',
...     title='Facebook Daily High - '
...         'Low vs. log(Volume Traded)',
...     logx=True, alpha=0.25
... )
```

We can now begin to make out the density of points in the lower-left region of the plot, but it's still relatively difficult:

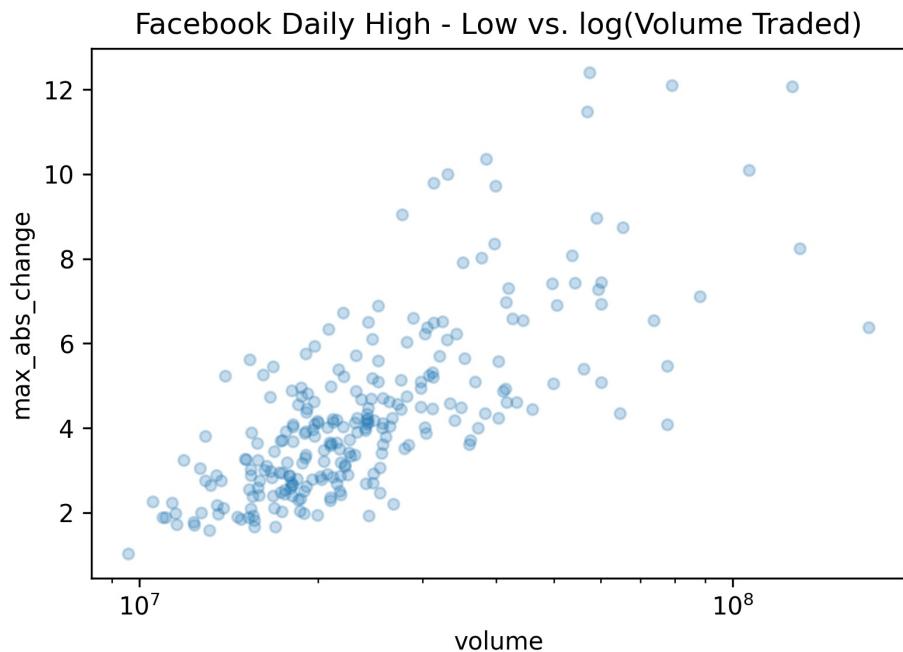


Figure 5.19 – Modifying transparency to visualize overlap

Thankfully, we have another plot type at our disposal: `hexbin`. **Hexbins** form a two-dimensional histogram by dividing the plot into a grid of hexagons and shading them based on the concentration of points in each bin. Let's view this data as hexbins:

```
>>> fb.assign(
...     log_volume=np.log(fb.volume),
...     max_abs_change=fb.high - fb.low
... ).plot(
...     kind='hexbin',
...     x='log_volume',
...     y='max_abs_change',
...     title='Facebook Daily High - '
...         'Low vs. log(Volume Traded)',
...     colormap='gray_r',
...     gridsize=20,
...     sharex=False # bug fix to keep the x-axis label
... )
```

The colorbar on the side indicates the relationship between color and the number of points in that bin. The colormap we chose (`gray_r`) shades the bins darker (toward black) for high density, and lighter (toward white) for low density. By passing in `gridsize=20`, we are specifying that 20 hexagons should be used across the x -axis, and then having pandas determine how many to use along the y -axis so that they are approximately regular in shape; we can, however, pass a tuple to choose the number in both directions. A larger value for `gridsize` will make the bins harder to see, while a smaller one will result in fuller bins that take up more space on the plot—we must strike a balance:

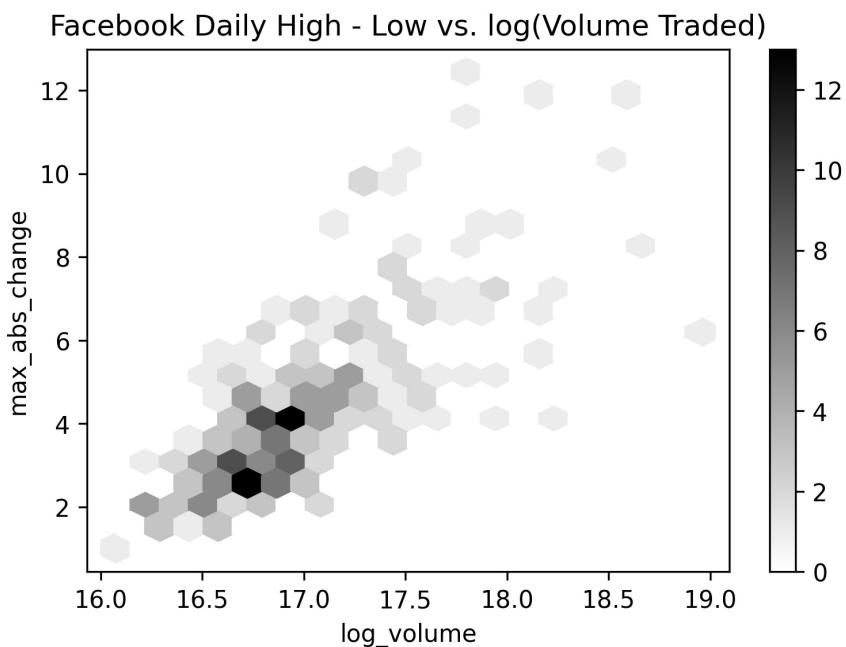


Figure 5.20 – Plotting hexbins with pandas

Finally, if we simply want to visualize the correlation between variables, we can plot a correlation matrix. A **correlation matrix** depicts the magnitude and direction (positive or negative) of the correlation. Let's take a look at the correlation matrix for the Facebook data we have been working with. To do so, we can use a combination of pandas and either the `plt.matshow()` or `plt.imshow()` function from `matplotlib`. Since there is a lot of code that needs to be run in the same cell, we will discuss the purpose of each section immediately after this code block:

```
>>> fig, ax = plt.subplots(figsize=(20, 10))

# calculate the correlation matrix
>>> fb_corr = fb.assign(
...     log_volume=np.log(fb.volume),
...     max_abs_change=fb.high - fb.low
... ).corr()

# create the heatmap and colorbar
>>> im = ax.matshow(fb_corr, cmap='seismic')
>>> im.set_clim(-1, 1)
>>> fig.colorbar(im)

# label the ticks with the column names
>>> labels = [col.lower() for col in fb_corr.columns]
>>> ax.set_xticks(ax.get_xticks()[1:-1])
>>> ax.set_xticklabels(labels, rotation=45)
>>> ax.set_yticks(ax.get_yticks()[1:-1])
>>> ax.set_yticklabels(labels)

# include the value of the correlation coefficient in the boxes
>>> for (i, j), coef in np.ndenumerate(fb_corr):
...     ax.text(
...         i, j, fr'$\rho$ = {coef:.2f}',
...         ha='center', va='center',
...         color='white', fontsize=14
...     )
```

A **heatmap** lets us easily visualize the correlation coefficients, provided we choose a diverging colormap—we will discuss the different types of colormaps when we discuss customizing plots in *Chapter 6, Plotting with Seaborn and Customization Techniques*. Essentially, for this plot, we want red for correlation coefficients greater than zero and blue for those below; correlation coefficients near zero will be devoid of color, and stronger correlations will be darker shades of their respective colors. This can be achieved by selecting the `seismic` colormap and then setting the limits of the color scale to [-1, 1], since the correlation coefficient has those bounds:

```
im = ax.matshow(fb_corr, cmap='seismic')
im.set_clim(-1, 1) # set the bounds of the color scale
fig.colorbar(im) # add the colorbar to the figure
```

To be able to read the resulting heatmap, we need to label the rows and columns with the names of the variables in our data:

```
labels = [col.lower() for col in fb_corr.columns]
ax.set_xticks(ax.get_xticks()[1:-1]) # to handle matplotlib bug
ax.set_xticklabels(labels, rotation=45)
ax.set_yticks(ax.get_yticks()[1:-1]) # to handle matplotlib bug
ax.set_yticklabels(labels)
```

While the color scale will make it easy for us to differentiate between weak and strong correlations, it is often helpful to annotate the heatmap with the actual correlation coefficients. This can be accomplished by using the `text()` method on the `Axes` object containing the plot. For this plot, we placed white, center-aligned text indicating the value of the Pearson correlation coefficient for each variable combination:

```
# iterate over the matrix
for (i, j), coef in np.ndenumerate(fb_corr):
    ax.text(
        i, j,
        fr'$\rho$ = {coef:.2f}', # raw (r), format (f) string
        ha='center', va='center',
        color='white', fontsize=14
    )
```

This results in an annotated heatmap showing the correlations between the variables in the Facebook dataset:

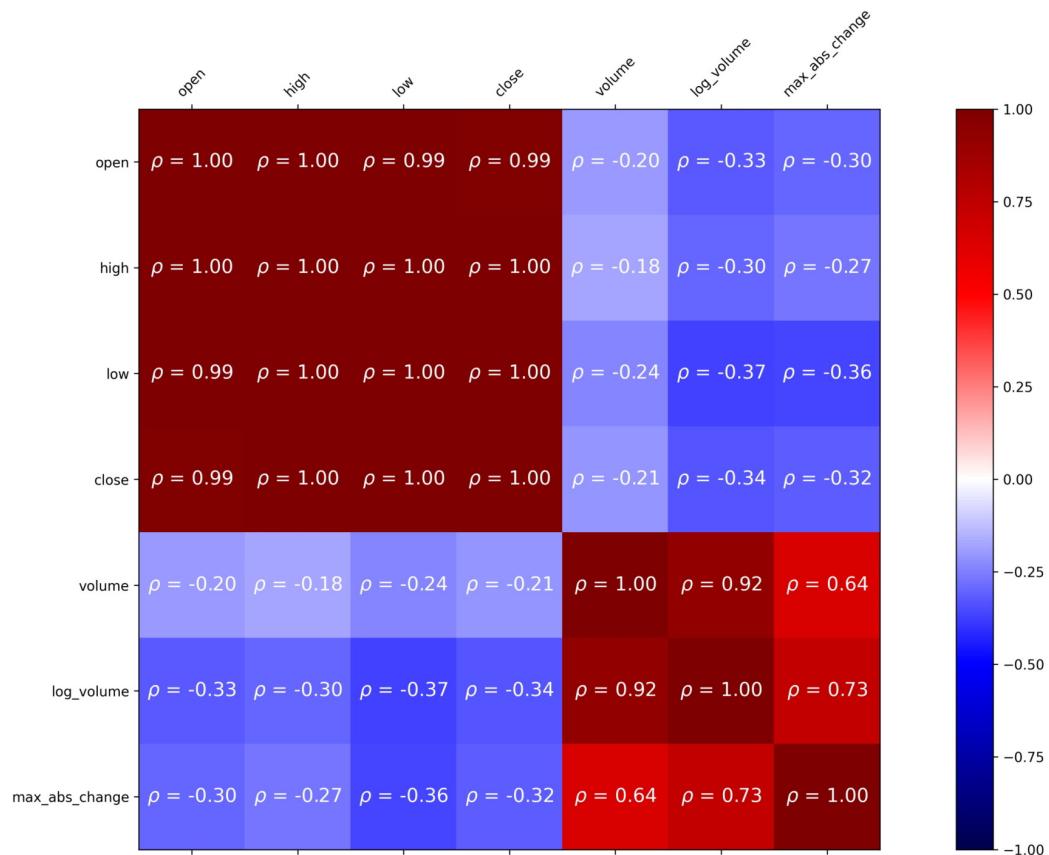


Figure 5.21 – Visualizing correlations as a heatmap

In *Figure 5.21*, we can easily see strong positive correlations among the OHLC time series, as well as among the volume traded and maximum absolute value of change. However, there are weak negative correlations between these groups. Furthermore, we can see that taking the logarithm of the volume does indeed increase the coefficient of correlation with `max_abs_change` from 0.64 to 0.73. When we discuss `seaborn` in the next chapter, we will learn an easier way to generate a heatmap, and also cover annotations in more detail.

Distributions

Often, we want to visualize the distribution of our data to see what values it takes on. Depending on the type of data we have, we may choose to use histograms, **kernel density estimates (KDEs)**, box plots, or **empirical cumulative distribution functions (ECDFs)**. When working with discrete data, histograms are a good place to start. Let's take a look at the histogram of daily volume traded in Facebook stock:

```
>>> fb.volume.plot(  
...     kind='hist',  
...     title='Histogram of Daily Volume Traded '  
...             'in Facebook Stock'  
...     )  
>>> plt.xlabel('Volume traded') # label x-axis (see ch 6)
```

This is a great example of real-world data that is, most definitely, not normally distributed. The volume traded is right skewed, with a long tail to the right. Recall that in *Chapter 4, Aggregating Pandas DataFrames*, when we discussed binning and looked at low, medium, and high volume traded, almost all of the data fell in the low bucket, which aligns with what we see in this histogram:

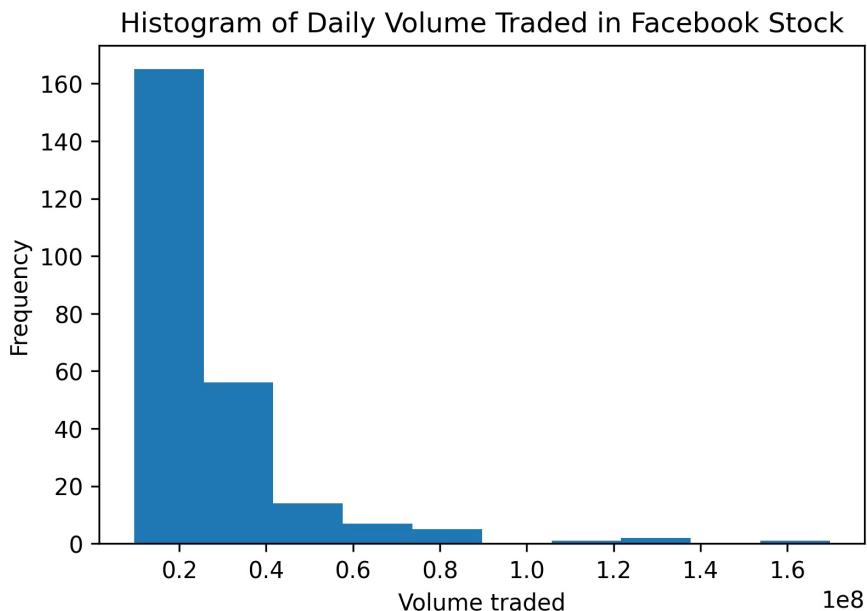


Figure 5.22 – Creating a histogram with pandas

Tip

As with the `plt.hist()` function from `matplotlib`, we can provide a custom value for the number of bins with the `bins` argument. However, we must be careful that we don't misrepresent the distribution.

We can also create multiple histograms on the same plot to compare distributions by using the `ax` parameter to specify the same `Axes` object for each plot. In this case, we must use the `alpha` parameter to see any overlaps. Given that we have many different measurement techniques for earthquakes (the `magType` column), we may be interested in comparing the different ranges of magnitudes they yield:

```
>>> fig, axes = plt.subplots(figsize=(8, 5))

>>> for magtype in quakes.magType.unique():
...     data = quakes.query(f'magType == "{magtype}"').mag
...     if not data.empty:
...         data.plot(
...             kind='hist',
...             ax=axes,
...             alpha=0.4,
...             label=magtype,
...             legend=True,
...             title='Comparing histograms '
...                   'of earthquake magnitude by magType'
...         )

>>> plt.xlabel('magnitude') # label x-axis (discussed in ch 6)
```

This shows us that `m1` is the most common `magType`, followed by `md`, and that they yield similar ranges of magnitudes; however, `mb`, which is the third-most common, yields higher magnitudes:

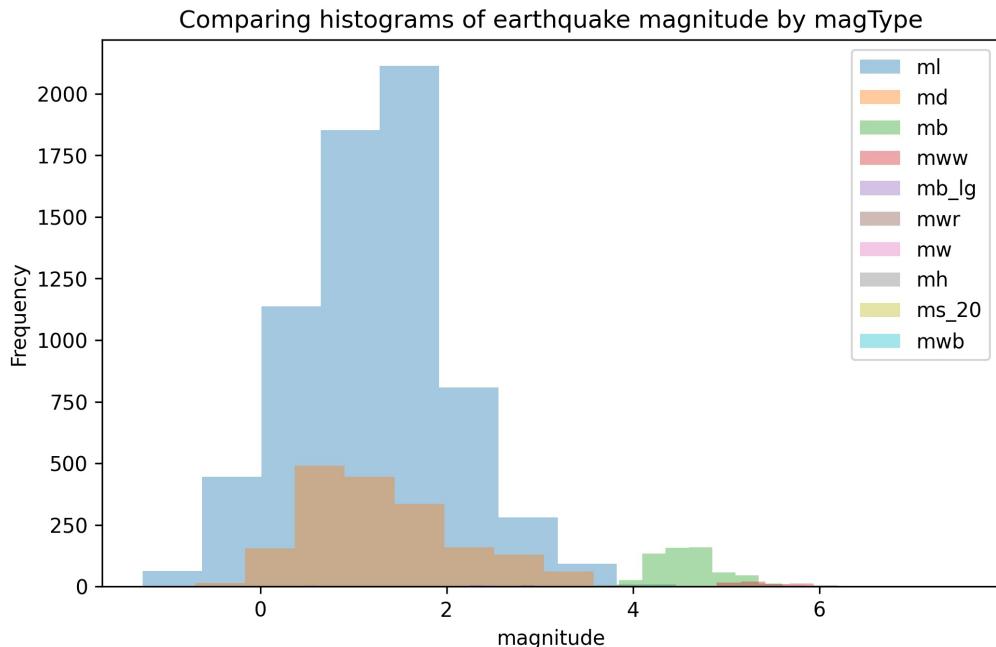


Figure 5.23 – Plotting overlapping histograms with pandas

When working with continuous data (such as stock prices), we can use KDEs. Let's take a look at the KDE of the daily high price for Facebook stock. Note that we can pass either `kind='kde'` or `kind='density'`:

```
>>> fb.high.plot(
...     kind='kde',
...     title='KDE of Daily High Price for Facebook Stock'
... )
>>> plt.xlabel('Price ($)') # label x-axis (discussed in ch 6)
```

The resulting density curve has some left skew:

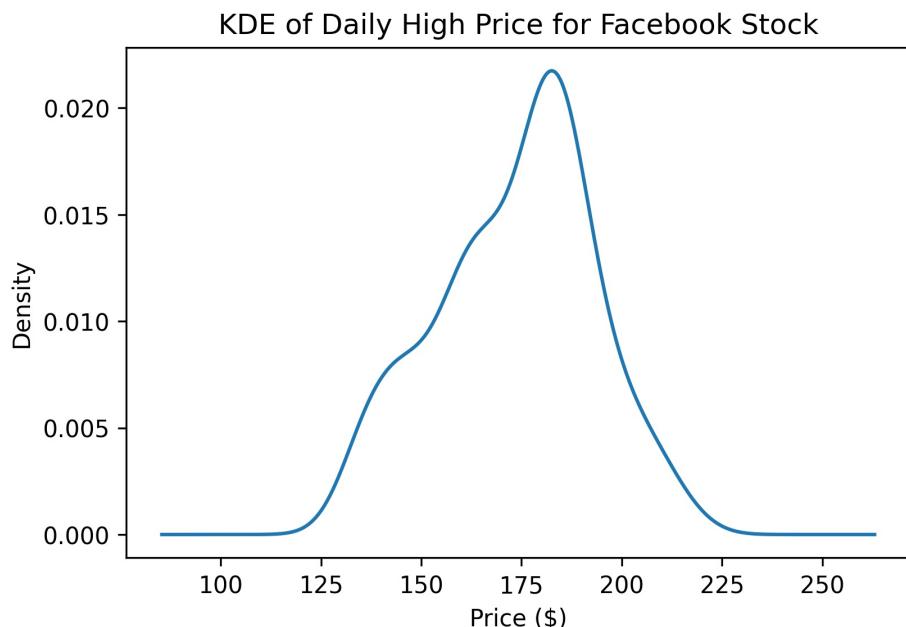


Figure 5.24 – Visualizing the KDE with pandas

We may also want to visualize the KDE superimposed on top of the histogram. Pandas allows us to pass the `Axes` object we want to plot on, and also returns one after creating the visualization, which makes this a cinch:

```
>>> ax = fb.high.plot(kind='hist', density=True, alpha=0.5)
>>> fb.high.plot(
...     ax=ax, kind='kde', color='blue',
...     title='Distribution of Facebook Stock\'s '
...           'Daily High Price in 2018'
... )
>>> plt.xlabel('Price ($)') # label x-axis (discussed in ch 6)
```

Notice that we had to pass `density=True` when we generated the histogram to make sure that the y -axis for the histogram and KDE were on the same scale. Otherwise, the KDE would have been too small to see. The histogram then gets plotted with density on the y -axis so that we can better understand how the KDE got its shape. We also increased the transparency of the histogram so that we could see the KDE line on top. Note that if we remove the `color='blue'` part of the KDE call, we don't need to change the value of `alpha` in the histogram call because the KDE and histogram will be different colors; we are plotting them both in blue since they represent the same data:

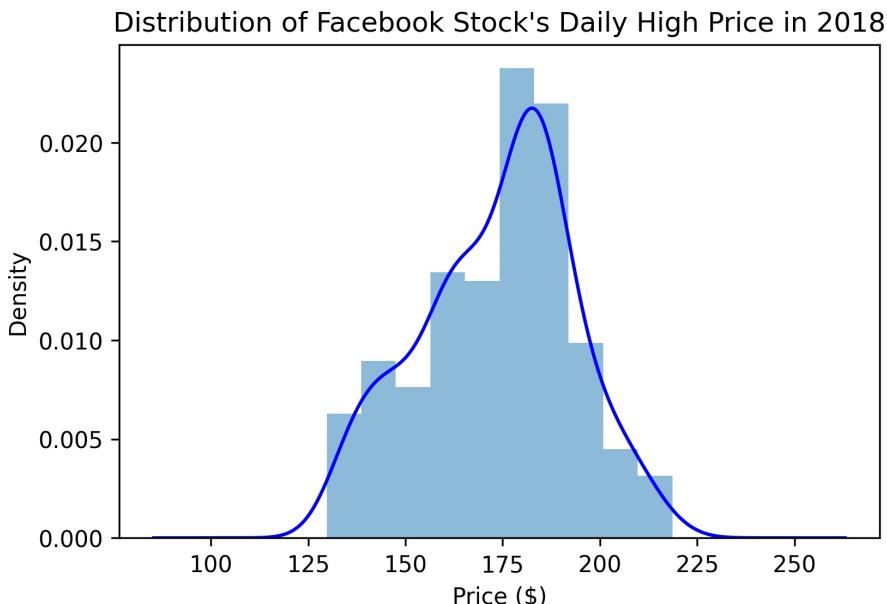


Figure 5.25 – Combining a KDE and a histogram with pandas

The KDE shows us an estimated **probability density function (PDF)**, which tells us how probability is distributed over the values of the data. However, in some cases, we are more interested in the probability of getting less than or equal to (or greater than or equal to) some value, which we can see with the **cumulative distribution function (CDF)**.

Important note

With a CDF, the values for the x variable go along the x -axis, while the cumulative probability of getting, at most, a given x goes along the y -axis. This cumulative probability is between 0 and 1 and is written as $P(X \leq x)$, where the lowercase (x) is the value for comparison and the uppercase (X) is the random variable, X . More information can be found at <https://www.itl.nist.gov/div898/handbook/eda/section3/eda362.htm>.

Using the `statsmodels` package, we can estimate the CDF giving us the **empirical cumulative distribution function (ECDF)**. Let's use this to understand the distribution of magnitudes for earthquakes measured with the `ml` magnitude type:

```
>>> from statsmodels.distributions.empirical_distribution \
...      import ECDF
>>> ecdf = ECDF(quakes.query('magType == "ml"]').mag)
>>> plt.plot(ecdf.x, ecdf.y)

# axis labels (we will cover this in chapter 6)
>>> plt.xlabel('mag') # add x-axis label
>>> plt.ylabel('cumulative probability') # add y-axis label

# add title (we will cover this in chapter 6)
>>> plt.title('ECDF of earthquake magnitude with magType ml')
```

This yields the following ECDF:

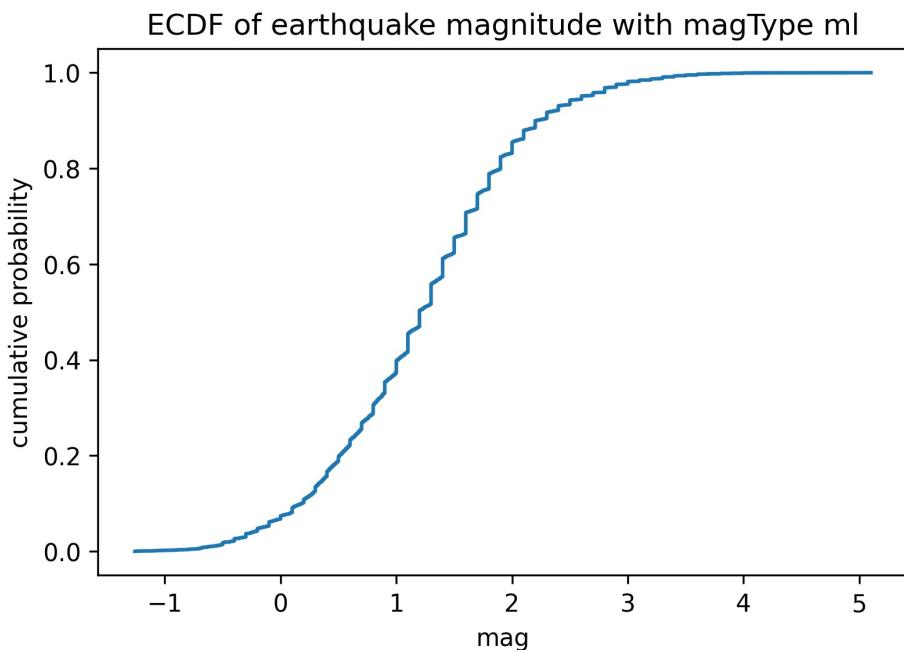


Figure 5.26 – Visualizing the ECDF

This can be very useful in gaining a better understanding of our data when we conduct our EDA. However, we must be careful how we interpret this and how we explain it to others, if we choose to do so. Here, we can see that if this distribution is indeed representative of the population, the probability of the m_1 magnitude of the earthquake being less than or equal to 3 is **98%** for earthquakes measured with that measurement technique:

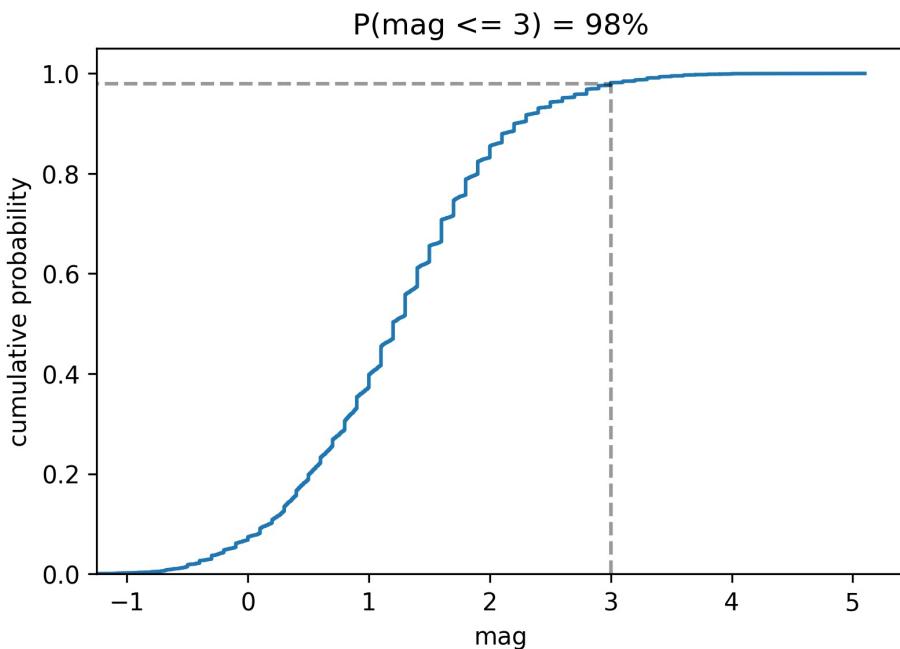


Figure 5.27 – Interpreting the ECDF

Finally, we can use box plots to visualize potential outliers and the distribution using quartiles. As an example, let's visualize the OHLC prices for Facebook stock across the whole dataset:

```
>>> fb.iloc[:, :4].plot(
...     kind='box',
...     title='Facebook OHLC Prices Box Plot'
... )
>>> plt.ylabel('price ($)') # label x-axis (discussed in ch 6)
```

Notice that we do lose some information we had in the other plots. We no longer have an idea of the density of points throughout the distribution; with the box plot, we focus on the 5-number summary instead:

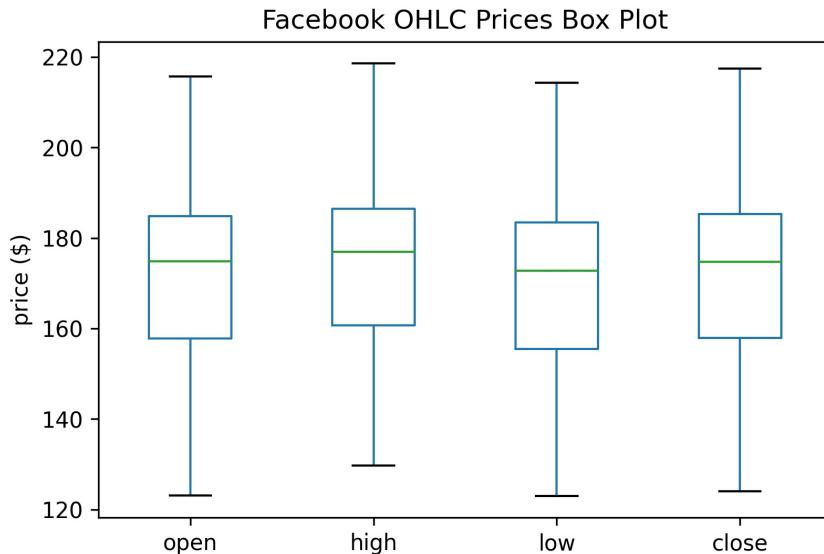


Figure 5.28 – Creating box plots with pandas

Tip

We can create a notched box plot by passing in `notch=True`. The notch marks a 95% confidence interval around the median, which can be helpful when comparing differences between groups. There is an example in the notebook.

We can also call the `boxplot()` method after calling `groupby()`. Let's examine how the box plots change when we calculate them based on the volume traded:

```
>>> fb.assign(
...     volume_bin=\
...         pd.cut(fb.volume, 3, labels=['low', 'med', 'high'])
... ).groupby('volume_bin').boxplot(
...     column=['open', 'high', 'low', 'close'],
...     layout=(1, 3), figsize=(12, 3)
... )
>>> plt.suptitle(
...     'Facebook OHLC Box Plots by Volume Traded', y=1.1
... )
```

Remember from *Chapter 4, Aggregating Pandas DataFrames*, that most of the days fell in the low volume traded bucket, so we would expect to see more variation there because of what the stock data looked like over time:

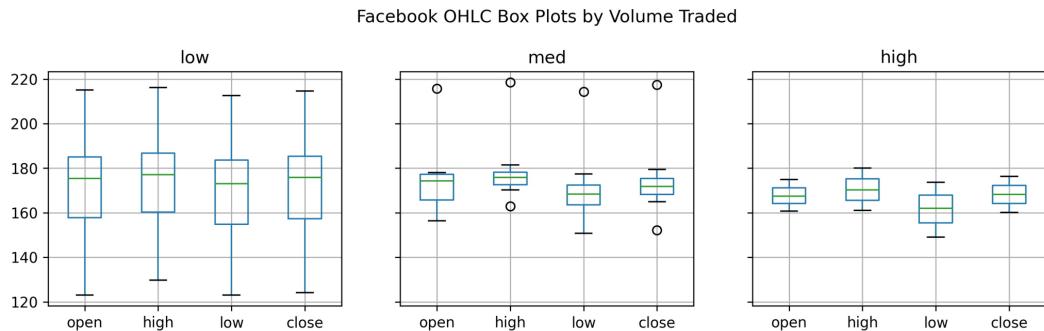


Figure 5.29 – Box plots per group with pandas

We can also use this technique to see the distribution of earthquake magnitudes based on which `magType` was used and compare it with the expected ranges on the USGS website (<https://www.usgs.gov/natural-hazards/earthquake-hazards/science/magnitude-types>):

```
>>> quakes[['mag', 'magType']] \
...      .groupby('magType') \
...      .boxplot(figsize=(15, 8), subplots=False)

# formatting (covered in chapter 6)
>>> plt.title('Earthquake Magnitude Box Plots by magType')
>>> plt.ylabel('magnitude')
```

The USGS website mentions situations in which certain measurement techniques can't be used and the range of magnitudes each measurement technique is authoritative for (when outside that range, other techniques are used). Here, we can see that, together, the techniques cover a wide spectrum of magnitudes, while none of them cover everything:

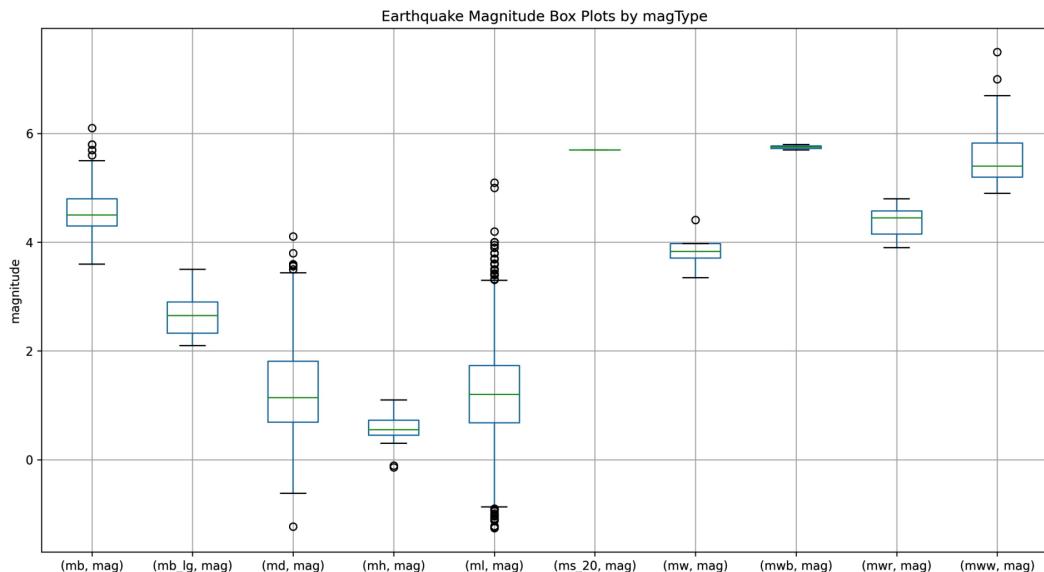


Figure 5.30 – Box plots per group in a single plot

Important note

While histograms, KDEs, ECDFs, and box plots are all ways of looking at the distribution of the data, we saw that each visualization showed us a different aspect of it. It's important to visualize the data from many angles before drawing any conclusions.

Counts and frequencies

When working with categorical data, we can create bar plots for displaying counts of our data or frequencies of particular values. The bars can be vertical (`kind='bar'`) or horizontal (`kind='barh'`). Vertical bar plots are useful when we have many categories or there is some order to the categories (for example, an evolution over time). Horizontal bar plots make it easy to compare the size of each category while allowing sufficient space on the margin for long category names (without the need to rotate them).

We can use a horizontal bar plot to see which places in the `quakes` dataframe have had the most earthquakes. First, we call the `value_counts()` method on the `parsed_place` series and take the top 15 places for earthquakes. Next, we reverse the order so that the smallest ones in this list are on top, which will sort the highest to the top of the bar plot that we will make. Note that we could reverse the sort order as an argument to `value_counts()`, but since we would still have to grab the top 15, we are doing both in a single `iloc` call:

```
>>> quakes.parsed_place.value_counts().iloc[14::-1].plot(
...     kind='barh', figsize=(10, 5),
...     title='Top 15 Places for Earthquakes '
...         '(September 18, 2018 - October 13, 2018)'
... )
>>> plt.xlabel('earthquakes') # label x-axis (see ch 6)
```

Remember, slicing notation is `[start:stop:step]`, and in this case, since the step is negative, the order is reversed; we start at index 14 (the 15th entry) and get closer to index 0 each time. By passing `kind='barh'`, we get a horizontal bar plot that shows that most of the earthquakes in this dataset occur in Alaska. Perhaps it is surprising to see the number of earthquakes over such a short time period, but many of these earthquakes are so small in magnitude that people don't even feel them:

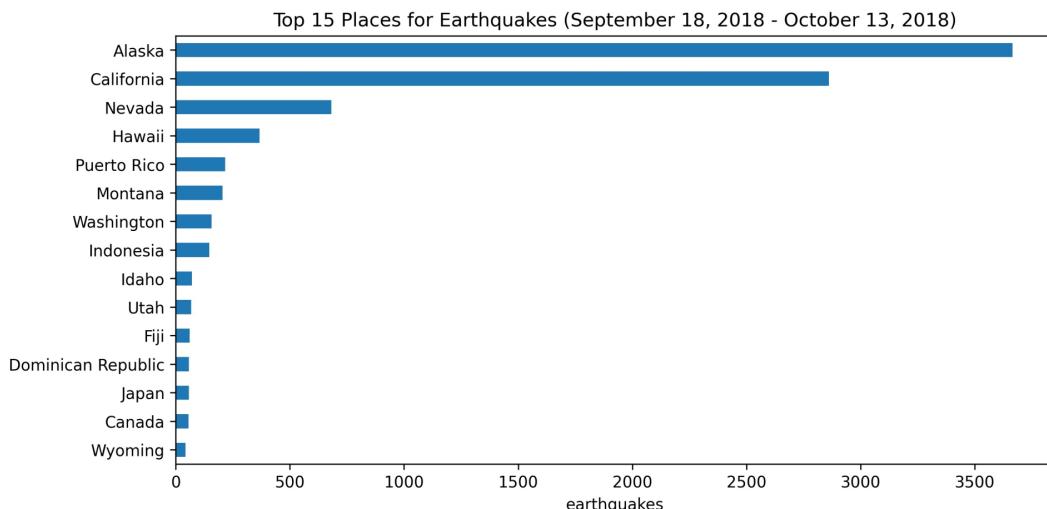


Figure 5.31 – Plotting horizontal bars with pandas

Our data also contains information about whether the earthquake was accompanied by a tsunami. Let's use `groupby()` to make a bar plot of the top 10 places that were hit by tsunamis during the time period we have in our data:

```
>>> quakes.groupby(  
...     'parsed_place'  
... ).tsunami.sum().sort_values().iloc[-10:,].plot(  
...     kind='barh', figsize=(10, 5),  
...     title='Top 10 Places for Tsunamis '  
...             '(September 18, 2018 - October 13, 2018)'  
... )  
>>> plt.xlabel('tsunamis') # label x-axis (discussed in ch 6)
```

Notice that this time, we used `iloc[-10:,]`, which starts at the 10th largest value (since `sort_values()` sorts in ascending order by default) and goes to the largest value, giving us the top 10. Here, we can see that Indonesia had many more tsunamis than the other places during this time period:

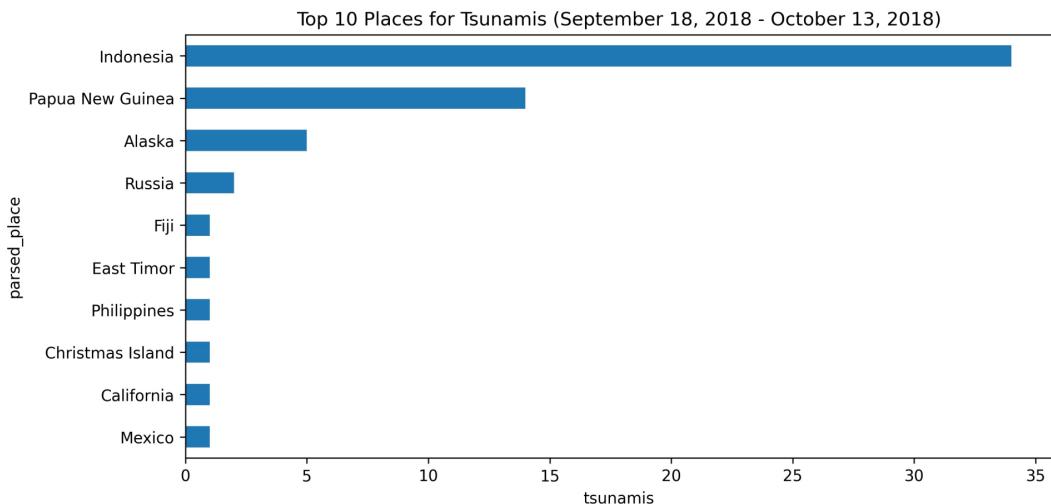


Figure 5.32 – Plotting the result of a group by calculation

After seeing something like this, we may be prompted to look further into the number of tsunamis in Indonesia each day. We can visualize this evolution over time as a line plot or with a vertical bar plot by using `kind='bar'`. Here, we will use bars to avoid interpolating the points:

```
>>> indonesia_quakes = quakes.query(
...     'parsed_place == "Indonesia"'
... ).assign(
...     time=lambda x: pd.to_datetime(x.time, unit='ms'),
...     earthquake=1
... ).set_index('time').resample('1D').sum()

# format the datetimes in the index for the x-axis
>>> indonesia_quakes.index = \
...     indonesia_quakes.index.strftime('%b\n%d')

>>> indonesia_quakes.plot(
...     y=['earthquake', 'tsunami'], kind='bar', rot=0,
...     figsize=(15, 3), label=['earthquakes', 'tsunamis'],
...     title='Earthquakes and Tsunamis in Indonesia '
...     '(September 18, 2018 - October 13, 2018)'
... )

# label the axes (discussed in chapter 6)
>>> plt.xlabel('date')
>>> plt.ylabel('count')
```

On September 28, 2018, we can see a spike in both earthquakes and tsunamis in Indonesia; on this date a 7.5 magnitude earthquake occurred, causing a devastating tsunami:

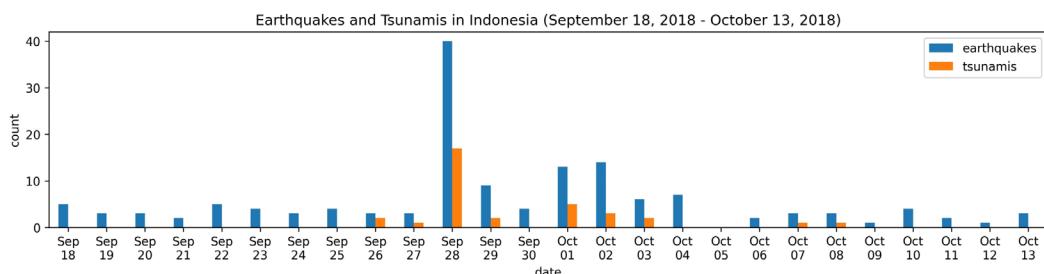


Figure 5.33 – Comparing counts over time

We can also create grouped bars from a single column's values by using `groupby()` and `unstack()`. This makes it possible for us to generate bars for each distinct value in the column. Let's use this strategy to take a look at the frequency of a tsunami accompanying an earthquake, as a percentage. We can handle this using the `apply()` method, as we learned in *Chapter 4, Aggregating Pandas DataFrames*, along `axis=1` (to apply row by row). For illustration purposes, we will look at the seven places with the highest percentage of earthquakes accompanied by a tsunami:

```
>>> quakes.groupby(['parsed_place', 'tsunami']).mag.count() \
...     .unstack().apply(lambda x: x / x.sum(), axis=1) \
...     .rename(columns={0: 'no', 1: 'yes'}) \
...     .sort_values('yes', ascending=False)[7:-1] \
...     .plot.bah(
...         title='Frequency of a tsunami accompanying ' \
...               'an earthquake'
...     )
# move legend to the right of the plot; label axes
>>> plt.legend(title='tsunami?', bbox_to_anchor=(1, 0.65))
>>> plt.xlabel('percentage of earthquakes')
>>> plt.ylabel('')
```

Christmas Island had one earthquake during this time period, but it was accompanied by a tsunami. Papua New Guinea, on the other hand, had tsunamis alongside roughly 40% of its earthquakes:

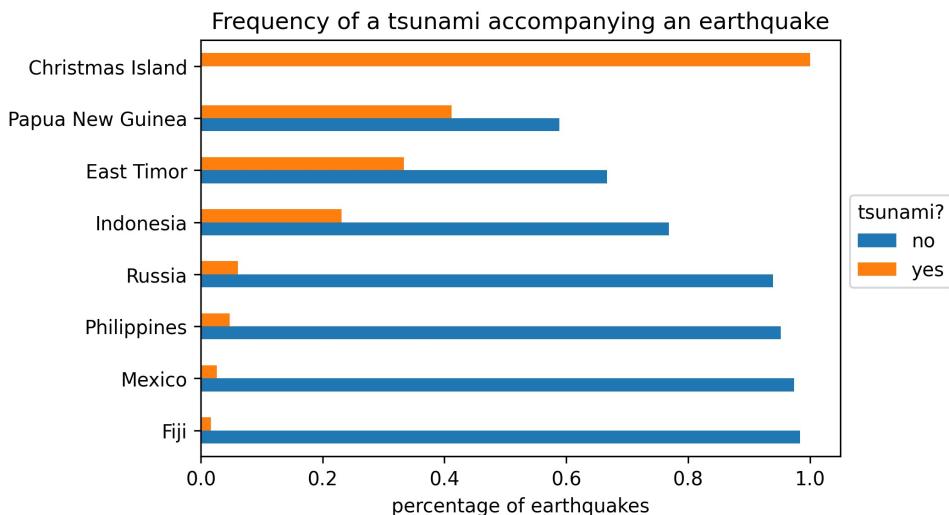


Figure 5.34 – Bar plot with a group by

Tip

When saving the preceding plots, long category names may get cut off; if that's the case, try running `plt.tight_layout()` before saving.

Now, let's use vertical bars to see which methods of measuring earthquake magnitude are most prevalent by using `kind='bar'`:

```
>>> quakes.magType.value_counts().plot(
...     kind='bar', rot=0,
...     title='Earthquakes Recorded per magType'
... )

# label the axes (discussed in ch 6)
>>> plt.xlabel('magType')
>>> plt.ylabel('earthquakes')
```

It appears that `ml` is, by far, the most common method for measuring earthquake magnitudes. This makes sense since it is the *original magnitude relationship defined by Richter and Gutenberg in 1935 for local earthquakes*, according to the USGS page explaining the `magType` field in the dataset we are using (<https://www.usgs.gov/natural-hazards/earthquake-hazards/science/magnitude-types>):

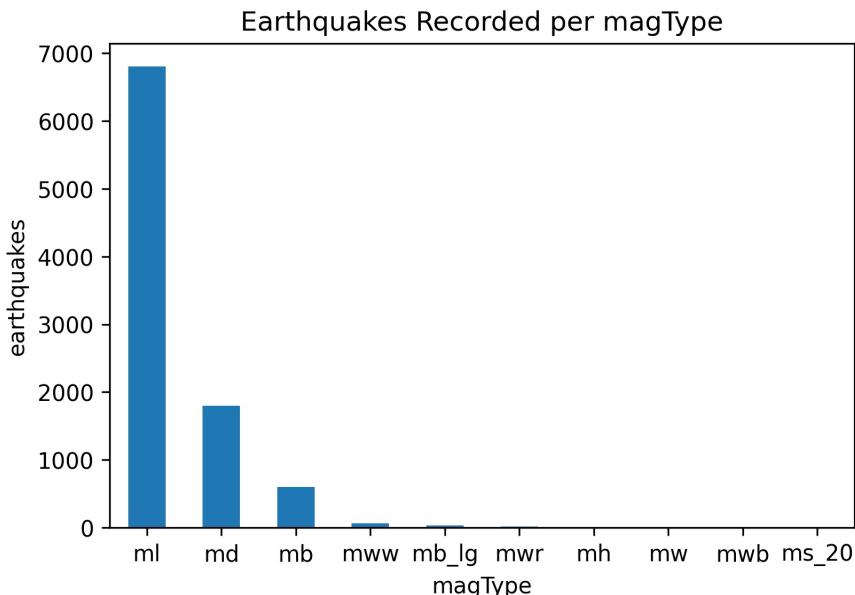


Figure 5.35 – Comparing category counts

Say we want to see how many earthquakes of a given magnitude there were and to distinguish them by `magType`. This shows us a few things in a single plot:

- Which magnitudes occur most often across `magType`.
- The relative ranges of magnitude that each `magType` yields.
- The most common values for `magType`.

To do so, we can make a stacked bar plot. First, we will round all magnitudes down to the nearest integer. This means that all earthquakes will be marked as the part of the magnitude before the decimal point (for example, 5.5 gets marked as 5, just like 5.7, 5.2, and 5.0). Next, we will need to create a pivot table with the magnitude in the index and the magnitude type along the columns; we will count the number of earthquakes for the values:

```
>>> pivot = quakes.assign(  
...     mag_bin=lambda x: np.floor(x.mag)  
... ).pivot_table(  
...     index='mag_bin',  
...     columns='magType',  
...     values='mag',  
...     aggfunc='count'  
... )
```

Once we have the pivot table, we can create a stacked bar plot by passing in `stacked=True` when plotting:

```
>>> pivot.plot.bar(  
...     stacked=True,  
...     rot=0,  
...     title='Earthquakes by integer magnitude and magType'  
... )  
>>> plt.ylabel('earthquakes') # label axes (discussed in ch 6)
```

This results in the following plot, which shows that most of the earthquakes are measured with the `m1` magnitude type and have magnitudes below four:

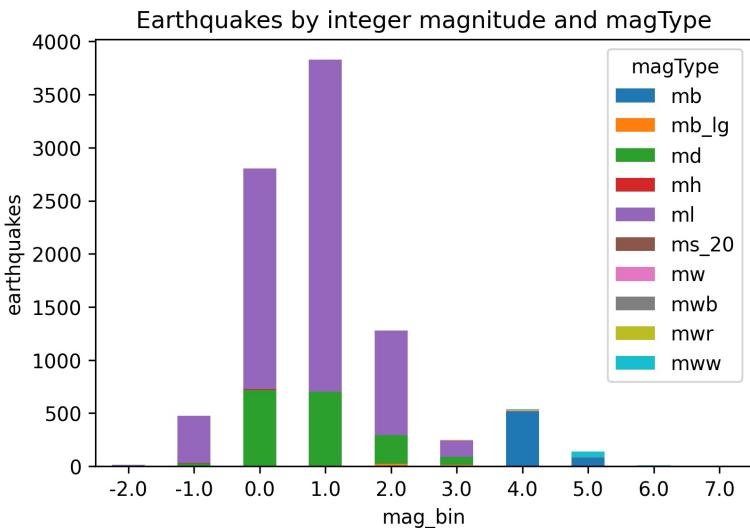


Figure 5.36 – Stacked bar plot

The other bars are dwarfed in comparison to `m1`, which makes it difficult for us to see which magnitude types assign higher magnitudes to earthquakes. To address this, we can make a normalized stacked bar plot. Rather than showing the count of earthquakes for each combination of magnitude and `magType`, we will show what percentage of earthquakes of a given magnitude used each `magType`:

```
>>> normalized_pivot = \
...     pivot.fillna(0).apply(lambda x: x / x.sum(), axis=1)
...
>>> ax = normalized_pivot.plot.bar(
...     stacked=True, rot=0, figsize=(10, 5),
...     title='Percentage of earthquakes by integer magnitude ' +
...           'for each magType'
... )
>>> ax.legend(bbox_to_anchor=(1, 0.8)) # move legend
>>> plt.ylabel('percentage') # label axes (discussed in ch 6)
```

Now, we can easily see that `mww` yields higher magnitudes and that `ml` appears to be spread across the lower end of the spectrum:

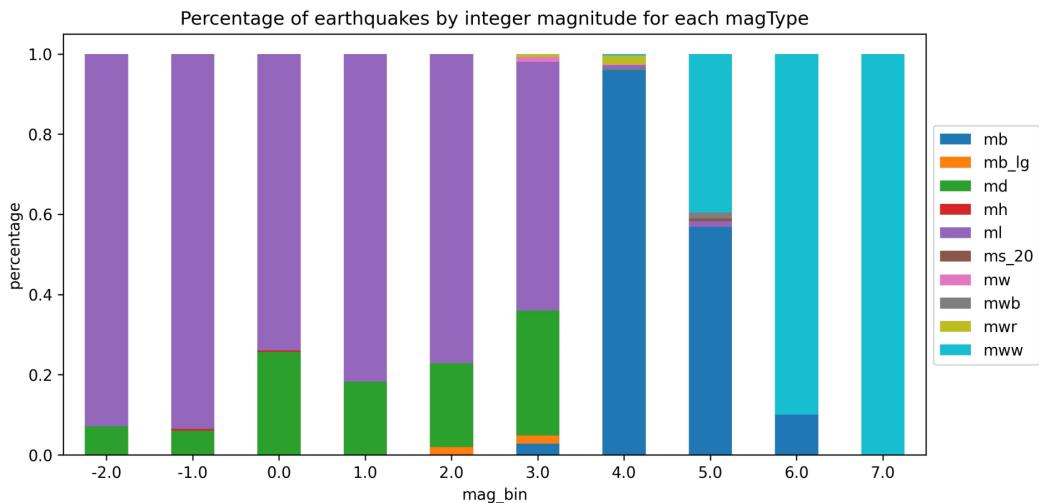


Figure 5.37 – Normalized stacked bar plot

Note that we can also use this strategy with a call to the `groupby()` and then `unstack()` methods. Let's revisit the frequency of a tsunami accompanying an earthquake plot, but rather than use grouped bars, we will stack them:

```
>>> quakes.groupby(['parsed_place', 'tsunami']).mag.count() \
...     .unstack().apply(lambda x: x / x.sum(), axis=1) \
...     .rename(columns={0: 'no', 1: 'yes'}) \
...     .sort_values('yes', ascending=False)[7::-1] \
...     .plot.barh(
...         title='Frequency of a tsunami accompanying ' \
...               'an earthquake',
...         stacked=True
...     )

# move legend to the right of the plot
>>> plt.legend(title='tsunami?', bbox_to_anchor=(1, 0.65))

# label the axes (discussed in chapter 6)
>>> plt.xlabel('percentage of earthquakes')
>>> plt.ylabel('')
```

This stacked bar plot makes it very easy for us to compare the frequencies of tsunamis across different places:

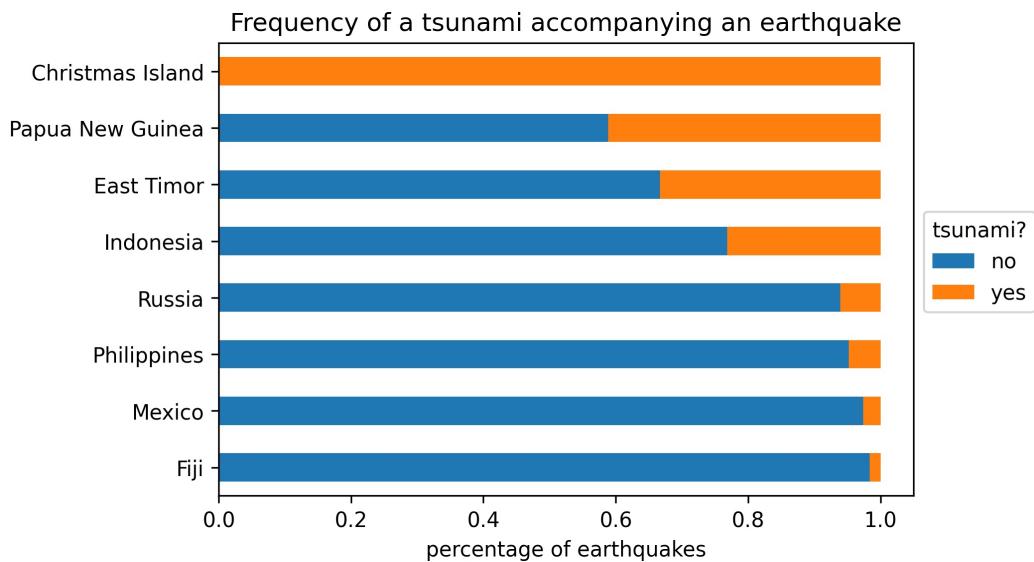


Figure 5.38 – Normalized stacked bar plot with a group by

Categorical data limits us in terms of the types of plots we can use, but there are some alternatives to the bar plot. We will take a look at them in the *Utilizing seaborn for advanced plotting* section in the next chapter; for now, let's take a look at the `pandas.plotting` module.

The `pandas.plotting` module

In the *Plotting with pandas* section, we covered standard plots that pandas has provided easier implementations for. However, pandas also has a module (which is appropriately named `plotting`) with special plots that we can use on our data. Note that the customization options of these may be more limited because of how they are composed and returned to us.

We will be working in the `3-pandas_plotting_module.ipynb` notebook for this section. As usual, we will begin with our imports and reading in the data; we will only be using the Facebook data here:

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

>>> fb = pd.read_csv(
...     'data/fb_stock_prices_2018.csv',
...     index_col='date',
...     parse_dates=True
... )
```

Now, let's take a tour of some of the plots available in the `pandas.plotting` module and learn how we can utilize the resulting visualizations in our EDA.

Scatter matrices

Earlier in this chapter, we discussed using scatter plots to show relationships among variables. Often, we want to see these for each combination of variables in the data, which can be tedious to execute. The `pandas.plotting` module contains the `scatter_matrix()` function, which makes this much easier. Let's use it to view the scatter plots for each combination of columns in our Facebook stock prices data:

```
>>> from pandas.plotting import scatter_matrix
>>> scatter_matrix(fb, figsize=(10, 10))
```

This results in the following plot matrix, which is often used in machine learning to see which variables could be useful in building a model. We can easily see that we have strong positive correlations between the opening, high, low, and closing prices:

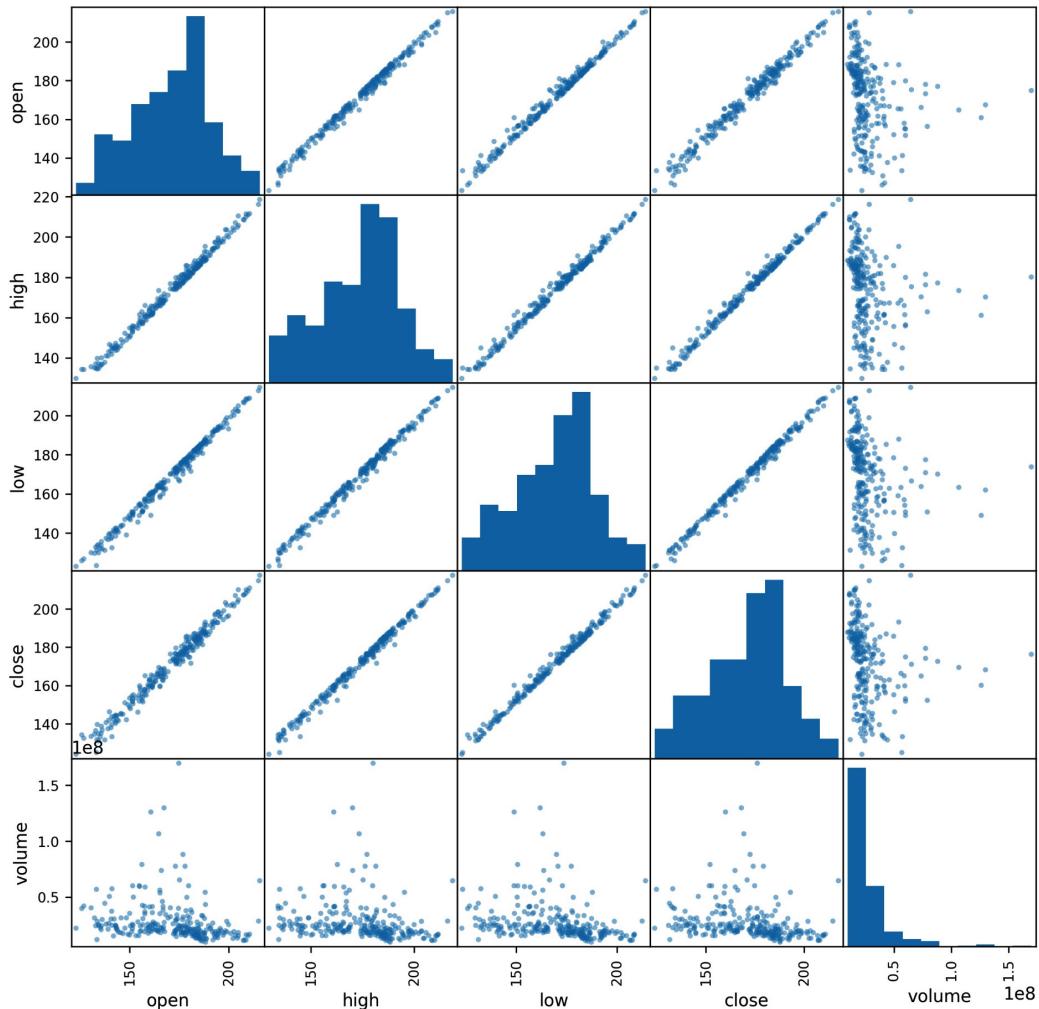


Figure 5.39 – Pandas scatter matrix

By default, on the diagonal, where the column is paired with itself, we get its histogram. Alternatively, we can ask for the KDE by passing in `diagonal='kde'`:

```
>>> scatter_matrix(fb, figsize=(10, 10), diagonal='kde')
```

This results in a scatter matrix with KDEs along the diagonal instead of histograms:

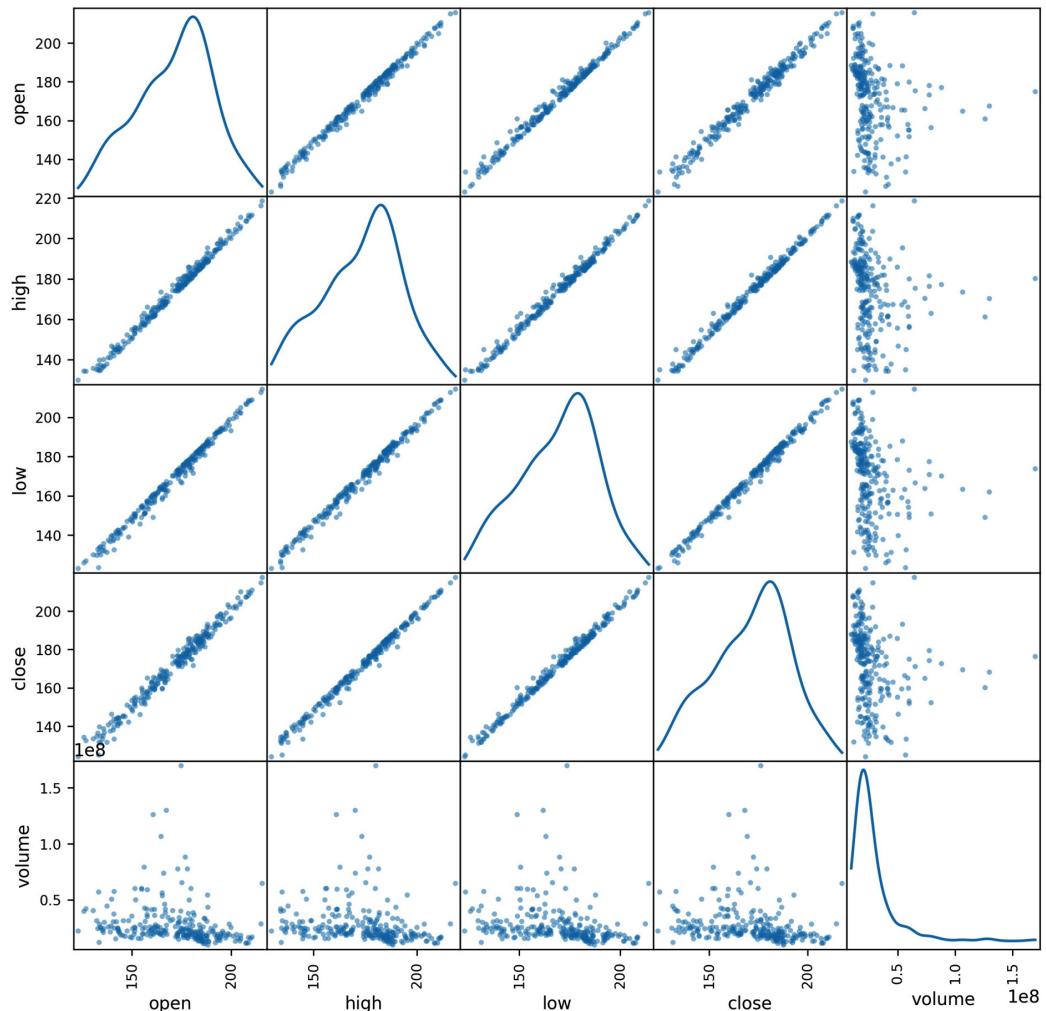


Figure 5.40 – Scatter matrix with KDEs

While a scatter matrix makes it easy to examine the relationships between our variables, sometimes, we are interested in **autocorrelation**, which means that the time series is correlated with a lagged version of itself. One way to visualize this is with a lag plot.

Lag plots

We can use a **lag plot** to check for relationships among values at a given time to those a certain number of periods before that time; that is, for a 1-period lag, we create a scatter plot of `data[:-1]` (all but the last entry) and `data[1:]` (from the second entry to the last one).

If our data is random, this plot will have no pattern. Let's test this with some random data generated with NumPy:

```
>>> from pandas.plotting import lag_plot
>>> np.random.seed(0) # make this repeatable
>>> lag_plot(pd.Series(np.random(size=200)))
```

The random data points don't indicate any pattern, just random noise:

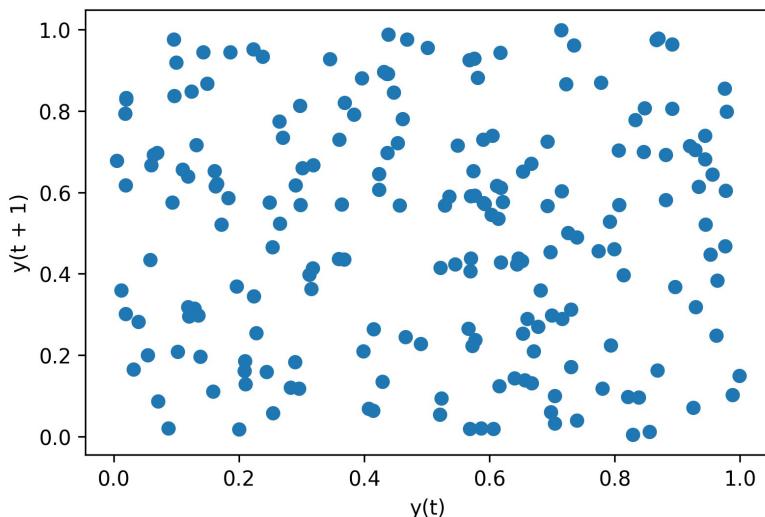


Figure 5.41 – Lag plot of random noise

With our stock data, we know that the prices on a given day are determined by what happened the day before; therefore, we would expect to see a pattern in the lag plot. Let's use the closing price of Facebook's stock to test whether our intuition is correct:

```
>>> lag_plot(fb.close)
```

As expected, this results in a linear pattern:

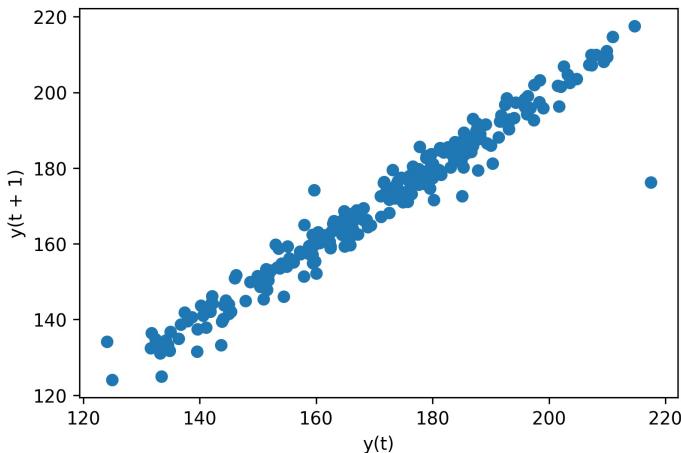


Figure 5.42 – Lag plot of Facebook stock prices

We can also specify the number of periods to use for the lag. The default lag is one, but we can change this with the `lag` parameter. For example, we can compare each value to the value of the week prior with `lag=5` (remember that the stock data only contains data for weekdays since the market is closed on the weekends):

```
>>> lag_plot(fb.close, lag=5)
```

This still yields a strong correlation, but, compared to *Figure 5.42*, it definitely looks weaker:

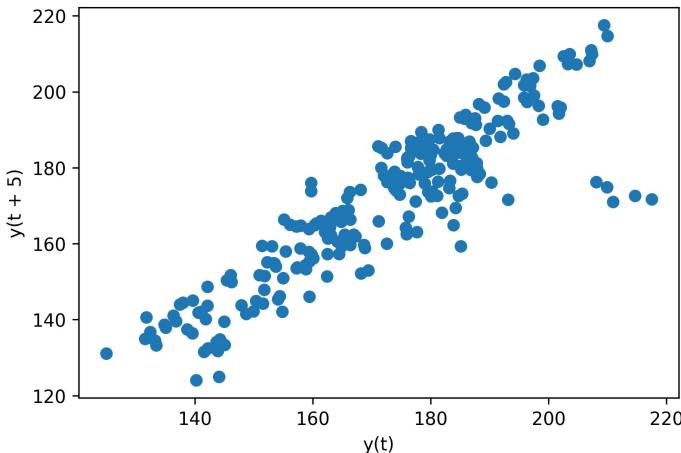


Figure 5.43 – Customizing the number of periods for the lag plot

While lag plots help us visualize autocorrelation, they don't show us how many periods of autocorrelation our data contains. For this purpose, we can use autocorrelation plots.

Autocorrelation plots

Pandas provides an additional way for us to look for autocorrelation in our data with the `autocorrelation_plot()` function, which shows the autocorrelation by the number of lags. Random data will be near an autocorrelation of zero.

As we did when discussing lag plots, let's first examine what this looks like for random data generated with NumPy:

```
>>> from pandas.plotting import autocorrelation_plot  
>>> np.random.seed(0) # make this repeatable  
>>> autocorrelation_plot(pd.Series(np.random.random(size=200)))
```

Indeed, the autocorrelation is near zero, and the line is within the confidence bands (99% is dashed; 95% is solid):

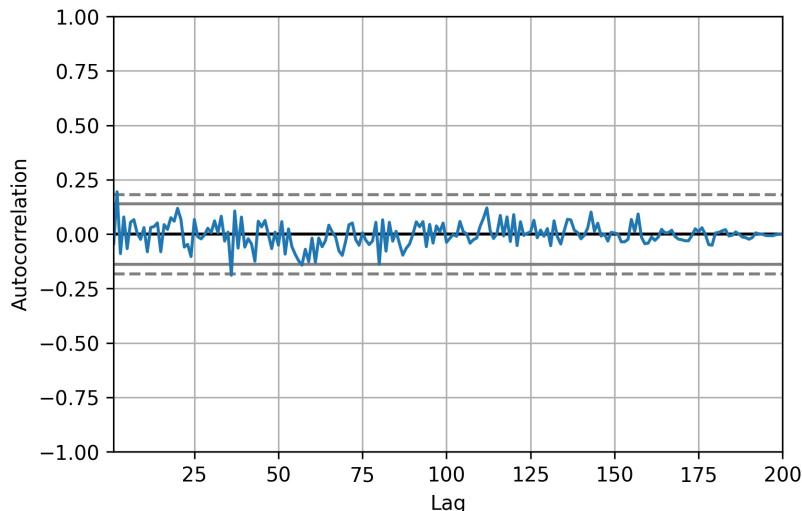


Figure 5.44 – Autocorrelation plot of random data

Let's explore what the autocorrelation plot looks like for the closing price of Facebook's stock, since the lag plots indicated several periods of autocorrelation:

```
>>> autocorrelation_plot(fb.close)
```

Here, we can see that there is autocorrelation for many lag periods before it becomes noise:

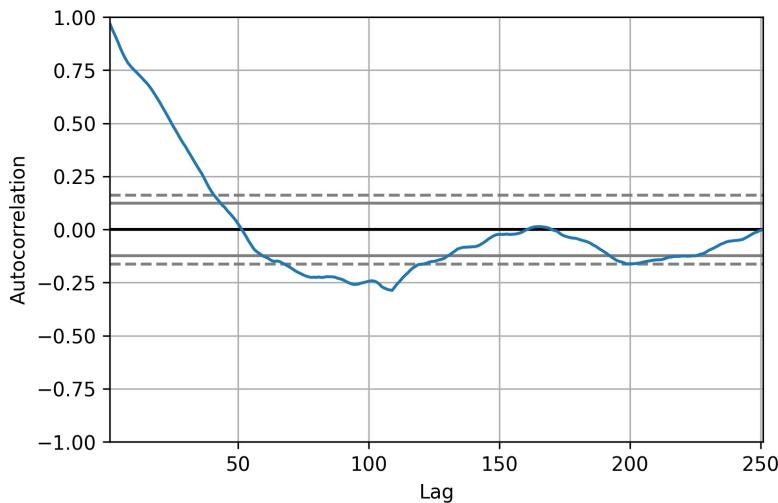


Figure 5.45 – Autocorrelation plot of Facebook stock prices

Tip

Recall from *Chapter 1, Introduction to Data Analysis*, that one of the components in an ARIMA model is the autoregressive component. The autocorrelation plot can be used to help determine the number of time lags to use. We will build an ARIMA model in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*.

Bootstrap plots

Pandas also provides a plotting function for assessing the uncertainty of common summary statistics via **bootstrapping**. The function will take the specified number of random samples of a given size (with replacement) from the variable in question (the `samples` and `size` parameters, respectively) and calculate the summary statistics. Then, it will return a visualization of the results.

Let's see what the uncertainty for the summary statistics of the volume traded data looks like:

```
>>> from pandas.plotting import bootstrap_plot
>>> fig = bootstrap_plot(
...     fb.volume, fig=plt.figure(figsize=(10, 6))
... )
```

This results in the following subplots, which we can use to assess the uncertainty in the mean, median, and midrange (the midpoint of the range):

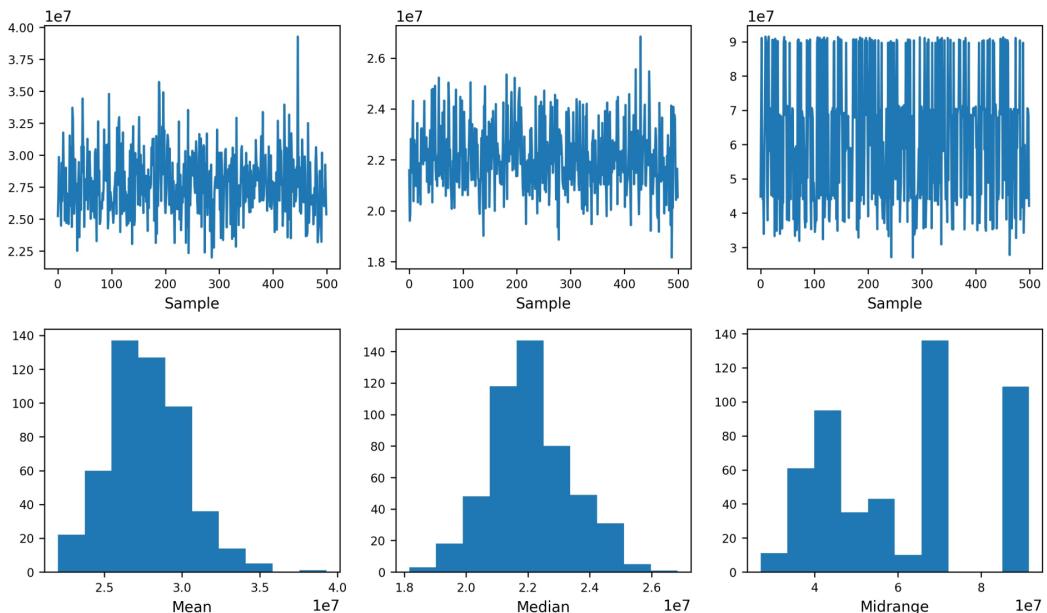


Figure 5.46 – Pandas bootstrap plot

This was a sample of a few of the functions in the `pandas.plotting` module. For the full list, check out <https://pandas.pydata.org/pandas-docs/stable/reference/plotting.html>.

Summary

Now that we've completed this chapter, we are well-equipped to quickly create a variety of visualizations in Python using `pandas` and `matplotlib`. We now understand the basics of how `matplotlib` works and the main components of a plot. Additionally, we discussed various plot types and the situations in which to use them—a crucial component of data visualization is choosing the appropriate plot. Be sure to check out the *Choosing the appropriate visualization* section in the *Appendix* for future reference.

Note that the best practices for visualization don't just apply to the plot type, but also to the formatting of the plot, which we will discuss in the next chapter. In addition to this, we will build upon the foundation we laid here to discuss additional plots using `seaborn` and how to customize our plots using `matplotlib`. Be sure to complete the end-of-chapter exercises to practice plotting before moving on, as we will be building on this chapter's material.

Exercises

Create the following visualizations using what you have learned up to this point in this book. Use the data from this chapter's `data/` directory:

1. Plot the rolling 20-day minimum of the Facebook closing price using `pandas`.
2. Create a histogram and KDE of the change from open to close in the price of Facebook stock.
3. Using the earthquake data, create box plots for the magnitudes of each `magType` used in Indonesia.
4. Make a line plot of the difference between the weekly maximum high price and the weekly minimum low price for Facebook. This should be a single line.
5. Plot the 14-day moving average of the daily change in new COVID-19 cases in Brazil, China, India, Italy, Spain, and the USA:
 - a) First, use the `diff()` method that was introduced in the *Working with time series data* section of *Chapter 4, Aggregating Pandas DataFrames*, to calculate the day-over-day change in new cases. Then, use `rolling()` to calculate the 14-day moving average.
 - b) Make three subplots: one for China; one for Spain and Italy; and one for Brazil, India, and the USA.
6. Using `matplotlib` and `pandas`, create two subplots side-by-side showing the effect that after-hours trading has had on Facebook's stock prices:
 - a) The first subplot will contain a line plot of the daily difference between that day's opening price and the prior day's closing price (be sure to review the *Working with time series data* section of *Chapter 4, Aggregating Pandas DataFrames*, for an easy way to do this).
 - b) The second subplot will be a bar plot showing the net effect this had monthly, using `resample()`.

- c) Bonus #1: Color the bars according to whether there are gains in the stock price (green) or drops in the stock price (red).
- d) Bonus #2: Modify the x -axis of the bar plot to show the three-letter abbreviation for the month.

Further reading

Take a look at the following resources for additional information on the concepts that were discussed in this chapter:

- *Bootstrapping (statistics)*: [https://en.wikipedia.org/wiki/Bootstrapping_\(statistics\)](https://en.wikipedia.org/wiki/Bootstrapping_(statistics))
- *Data Visualization - Best Practices and Foundations*: <https://www.toptal.com/designers/data-visualization/data-visualization-best-practices>
- *How to Create Animated Graphs in Python (with matplotlib)*: <https://towardsdatascience.com/how-to-create-animated-graphs-in-python-bb619cc2dec1>
- *Interactive Plots with JavaScript (D3.js)*: <https://d3js.org/>
- *Intro to Animations in Python (with plotly)*: <https://plot.ly/python/animations/>
- *IPython: Built-in magic commands*: <https://ipython.readthedocs.io/en/stable/interactive/magics.html>
- *The Importance of Integrity: How Plot Parameters Influence Interpretation*: <https://www.t4g.com/insights/plot-parameters-influence-interpretation/>
- *5 Python Libraries for Creating Interactive Plots*: <https://mode.com/blog/python-interactive-plot-libraries/>

6

Plotting with Seaborn and Customization Techniques

In the previous chapter, we learned how to create many different visualizations using `matplotlib` and `pandas` on wide-format data. In this chapter, we will see how we can make visualizations from long-format data, using `seaborn`, and how to customize our plots to improve their interpretability. Remember that the human brain excels at finding patterns in visual representations; by making clear and meaningful data visualizations, we can help others (not to mention ourselves) understand what the data is trying to say.

Seaborn is capable of making many of the same plots we created in the previous chapter; however, it also makes quick work of long-format data, allowing us to use subsets of our data to encode additional information into our visualizations, such as facets and/or colors for different categories. We will walk through some implementations of what we did in the previous chapter that are easier (or just more aesthetically pleasing) using `seaborn`, such as heatmaps and pair plots (the `seaborn` equivalent of the scatter plot matrix). In addition, we will explore some new plot types that `seaborn` provides to address issues that other plot types may be susceptible to.

Afterward, we will change gears and begin our discussion on customizing the appearance of our data visualizations. We will walk through the process of creating annotations, adding reference lines, properly labeling our plots, controlling the color palette used, and tailoring the axes to meet our needs. This is the final piece we need to make our visualizations ready to present to others.

In this chapter, we will cover the following topics:

- Utilizing `seaborn` for more advanced plot types
- Formatting plots with `matplotlib`
- Customizing visualizations

Chapter materials

The materials for this chapter can be found on GitHub at https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_06. We will be working with three datasets once again, all of which can be found in the `data/` directory. In the `fb_stock_prices_2018.csv` file, we have Facebook's stock price for all trading days in 2018. This data is the OHLC data (opening, high, low, and closing price), along with the volume traded. It was gathered using the `stock_analysis` package, which we will build in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*. The stock market is closed on the weekends, so we only have data for the trading days.

The `earthquakes.csv` file contains earthquake data pulled from the **United States Geological Survey (USGS)** API (<https://earthquake.usgs.gov/fdsnws/event/1/>) for September 18, 2018, through October 13, 2018. For each earthquake, we have the magnitude (the `mag` column), the scale it was measured on (the `magType` column), when (the `time` column), and where (the `place` column) it occurred; we also have the `parsed_place` column, which indicates the state or country in which the earthquake occurred (we added this column back in *Chapter 2, Working with Pandas DataFrames*). Other unnecessary columns have been removed.

In the `covid19_cases.csv` file, we have an export from the *daily number of new reported cases of COVID-19 by country worldwide* dataset provided by the **European Centre for Disease Prevention and Control (ECDC)**, which can be found at <https://www.ecdc.europa.eu/en/publications-data/download-todays-data-geographic-distribution-covid-19-cases-worldwide>. For scripted or automated collection of this data, the ECDC makes the current day's CSV file available via this link: <https://opendata.ecdc.europa.eu/covid19/casedistribution/csv>. The snapshot we will be using was collected on September 19, 2020 and contains the number of new COVID-19 cases per country from December 31, 2019 through September 18, 2020 with partial data for September 19, 2020. For this chapter, we will look at the 8-month span from January 18, 2020 through September 18, 2020.

Throughout this chapter, we will be working through three Jupyter Notebooks. These are all numbered according to their order of use. We will begin exploring the capabilities of `seaborn` in the `1-introduction_to_seaborn.ipynb` notebook. Next, we will move on to the `2-formatting_plots.ipynb` notebook as we discuss formatting and labeling our plots. Finally, in the `3-customizing_visualizations.ipynb` notebook, we will learn how to add reference lines, shade regions, include annotations, and customize our visualizations. The text will prompt us when to switch notebooks.

Tip

The supplementary `covid19_cases_map.ipynb` notebook walks through an example of plotting data on a map using COVID-19 cases worldwide. It can be used to get started with maps in Python and also builds upon some of the formatting we will discuss in this chapter.

In addition, we have two Python (`.py`) files that contain functions we will use throughout the chapter: `viz.py` and `color_utils.py`. Let's get started by exploring `seaborn`.

Utilizing seaborn for advanced plotting

As we saw in the previous chapter, `pandas` provides implementations for most visualizations we would want to create; however, there is another library, `seaborn`, that provides additional functionality for more involved visualizations and makes creating visualizations with long-format data much easier than `pandas`. These also tend to look much nicer than standard visualizations generated by `matplotlib`.

For this section, we will be working with the `1-introduction_to_seaborn.ipynb` notebook. First, we must import `seaborn`, which is traditionally aliased as `sns`:

```
>>> import seaborn as sns
```

Let's also import `numpy`, `matplotlib.pyplot`, and `pandas`, and then read in the CSV files for the Facebook stock prices and earthquake data:

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

>>> fb = pd.read_csv(
...     'data/fb_stock_prices_2018.csv',
...     index_col='date',
...     parse_dates=True
... )
>>> quakes = pd.read_csv('data/earthquakes.csv')
```

While `seaborn` offers alternatives to many of the plot types we covered in the previous chapter, for the most part, we will only cover new types that `seaborn` makes possible and leave learning about the rest as an exercise. Additional available functions using the `seaborn` API can be found at <https://seaborn.pydata.org/api.html>.

Categorical data

There was a devastating tsunami in Indonesia on September 28, 2018; it came after a 7.5 magnitude earthquake occurred near Palu, Indonesia (<https://www.livescience.com/63721-tsunami-earthquake-indonesia.html>). Let's create a visualization to understand which magnitude types are used in Indonesia, the range of magnitudes recorded, and how many of the earthquakes were accompanied by a tsunami. To do this, we need a way to plot relationships in which one of the variables is categorical (`magType`) and the other is numeric (`mag`).

Important note

Information on the different magnitude types can be found at <https://www.usgs.gov/natural-hazards/earthquake-hazards/science/magnitude-types>.

When we discussed scatter plots in *Chapter 5, Visualizing Data with Pandas and Matplotlib*, we were limited to both variables being numeric; however, with `seaborn`, we have two additional plot types at our disposal that allow us to have one categorical and one numeric variable. The first is the `stripplot()` function, which plots the points in strips that denote each category. The second is the `swarmplot()` function, which we will see later.

Let's create this visualization with `stripplot()`. We pass the subset of earthquakes occurring in Indonesia to the `data` parameter, and specify that we want to put `magType` on the `x`-axis (`x`), magnitudes on the `y`-axis (`y`), and color the points by whether the earthquake was accompanied by a tsunami (`hue`):

```
>>> sns.stripplot(
...     x='magType',
...     y='mag',
...     hue='tsunami',
...     data=quakes.query('parsed_place == "Indonesia"')
... )
```

Using the resulting plot, we can see that the earthquake in question is the highest orange point in the `mww` column (don't forget to call `plt.show()` if not using the Jupyter Notebook provided):

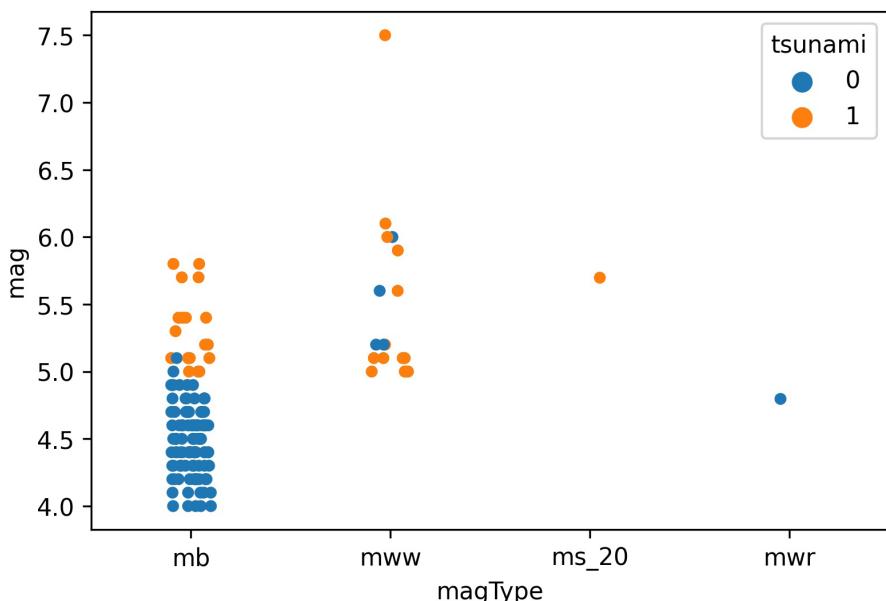


Figure 6.1 – Seaborn's strip plot

For the most part, the tsunamis occurred with higher magnitude earthquakes, as we would expect; however, due to the high concentration of points at lower magnitudes, we can't really see all the points. We could try to adjust the `jitter` argument, which controls how much random noise to add to the point in an attempt to reduce overlaps, or the `alpha` argument for transparency, as we did in the previous chapter; fortunately, there is another function, `swarmplot()`, that will reduce the overlap as much as possible, so we will use that instead:

```
>>> sns.swarmplot(
...     x='magType',
...     y='mag',
...     hue='tsunami',
...     data=quakes.query('parsed_place == "Indonesia")',
...     size=3.5 # point size
... )
```

The **swarm plot** (or bee swarm plot) also has the bonus of giving us a glimpse of what the distribution might be. We can now see many more earthquakes in the lower section of the `mb` column:

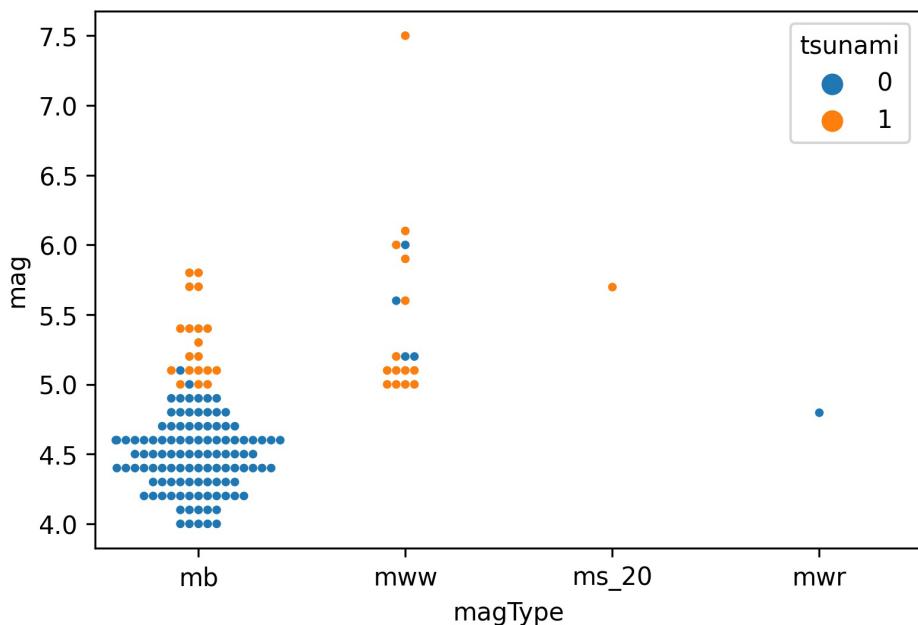


Figure 6.2 – Seaborn's swarm plot

In the *Plotting with pandas* section in the previous chapter, when we discussed how to visualize distributions, we discussed the box plot. Seaborn provides an enhanced box plot for large datasets, which shows additional quantiles for more information on the shape of the distribution, particularly in the tails. Let's use the enhanced box plot to compare earthquake magnitudes across different magnitude types, as we did in *Chapter 5, Visualizing Data with Pandas and Matplotlib*:

```
>>> sns.boxenplot(
...     x='magType', y='mag', data=quakes[['magType', 'mag']])
... )
>>> plt.title('Comparing earthquake magnitude by magType')
```

This results in the following plot:

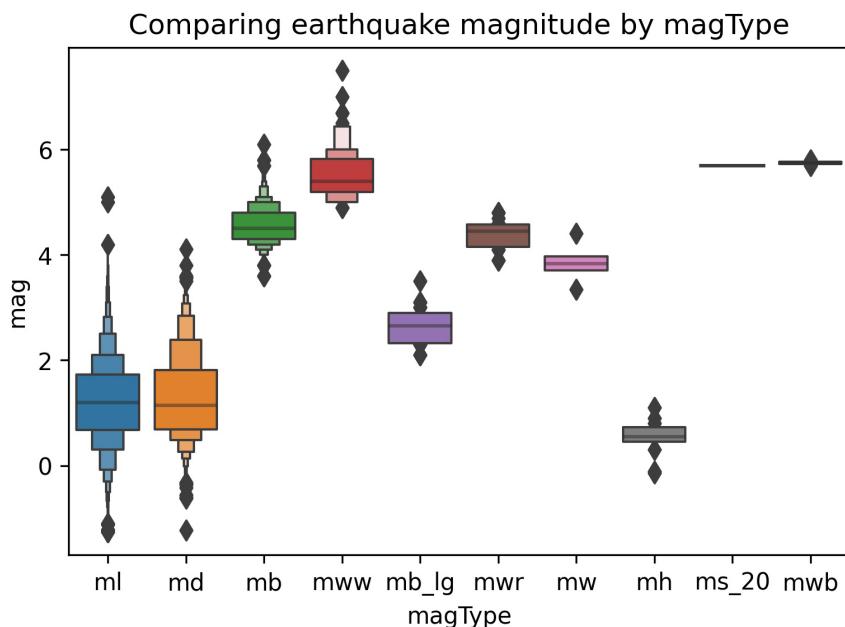


Figure 6.3 – Seaborn's enhanced box plot

Tip

The enhanced box plot was introduced in the paper *Letter-value plots: Boxplots for large data*, by Heike Hofmann, Karen Kafadar, and Hadley Wickham, which can be found at <https://vita.had.co.nz/papers/letter-value-plot.html>.

Box plots are great for visualizing the quantiles of our data, but we lose information about the distribution. As we saw, an enhanced box plot is one way to address this—another strategy is to use a violin plot, which combines a kernel density estimate (estimation of the underlying distribution) and a box plot:

```
>>> fig, axes = plt.subplots(figsize=(10, 5))
>>> sns.violinplot(
...     x='magType', y='mag', data=quakes[['magType', 'mag']],
...     ax=axes, scale='width' # all violins have same width
... )
>>> plt.title('Comparing earthquake magnitude by magType')
```

The box plot portion runs through the center of each violin plot; the **kernel density estimate (KDE)** is then drawn on both sides using the box plot as its *x*-axis. We can read the KDE from either side of the box plot since it is symmetrical:

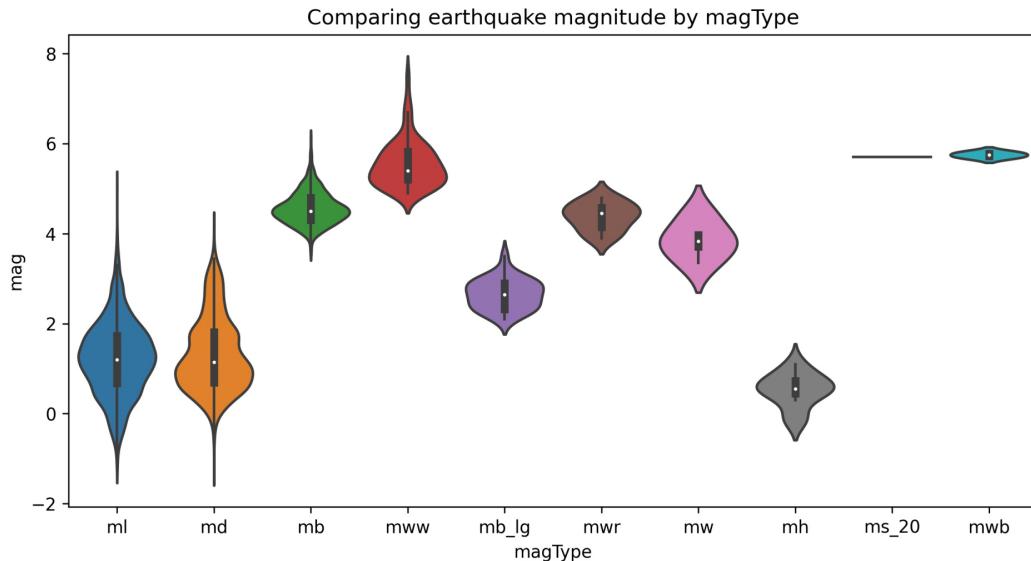


Figure 6.4 – Seaborn's violin plot

The seaborn documentation also lists out the plotting functions by the type of data being plotted; the full offering of categorical plots is available at <https://seaborn.pydata.org/api.html#categorical-plots>. Be sure to check out the `countplot()` and `barplot()` functions for variations on the bar plots we created with pandas in the previous chapter.

Correlations and heatmaps

As promised, let's learn an easier way to generate heatmaps compared to what we had to do in *Chapter 5, Visualizing Data with Pandas and Matplotlib*. Once again, we will make a heatmap of the correlations between the OHLC stock prices, the log of volume traded, and the daily difference between the highest and lowest prices (`max_abs_change`); however, this time, we will use `seaborn`, which gives us the `heatmap()` function for an easier way to produce this visualization:

```
>>> sns.heatmap(  
...     fb.sort_index().assign(  
...         log_volume=np.log(fb.volume),  
...         max_abs_change=fb.high - fb.low  
...     ).corr(),  
...     annot=True,  
...     center=0,  
...     vmin=-1,  
...     vmax=1  
... )
```

Tip

When using `seaborn`, we can still use functions from `matplotlib`, such as `plt.savefig()` and `plt.tight_layout()`. Note that if there are issues with `plt.tight_layout()`, pass `bbox_inches='tight'` to `plt.savefig()` instead.

We pass in `center=0` so that `seaborn` puts values of 0 (no correlation) at the center of the colormap it uses. In order to set the bounds of the color scale to that of the correlation coefficient, we need to provide `vmin=-1` and `vmax=1` as well. Notice that we also passed in `annot=True` to write the correlation coefficients in each box—we get the benefit of the numerical data and the visual data all in one plot with a single function call:

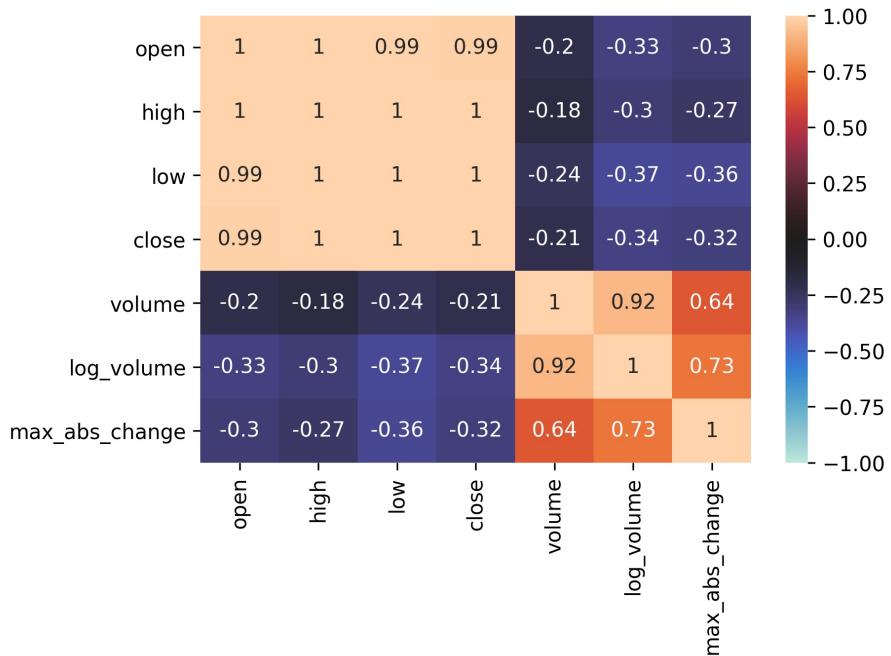


Figure 6.5 – Seaborn's heatmap

Seaborn also provides us with an alternative to the `scatter_matrix()` function provided in the `pandas.plotting` module, called `pairplot()`. We can use this to see the correlations between the columns in the Facebook data as scatter plots instead of the heatmap:

```
>>> sns.pairplot(fb)
```

This result makes it easy to understand the near-perfect positive correlation between the OHLC columns shown in the heatmap, while also showing us histograms for each column along the diagonal:

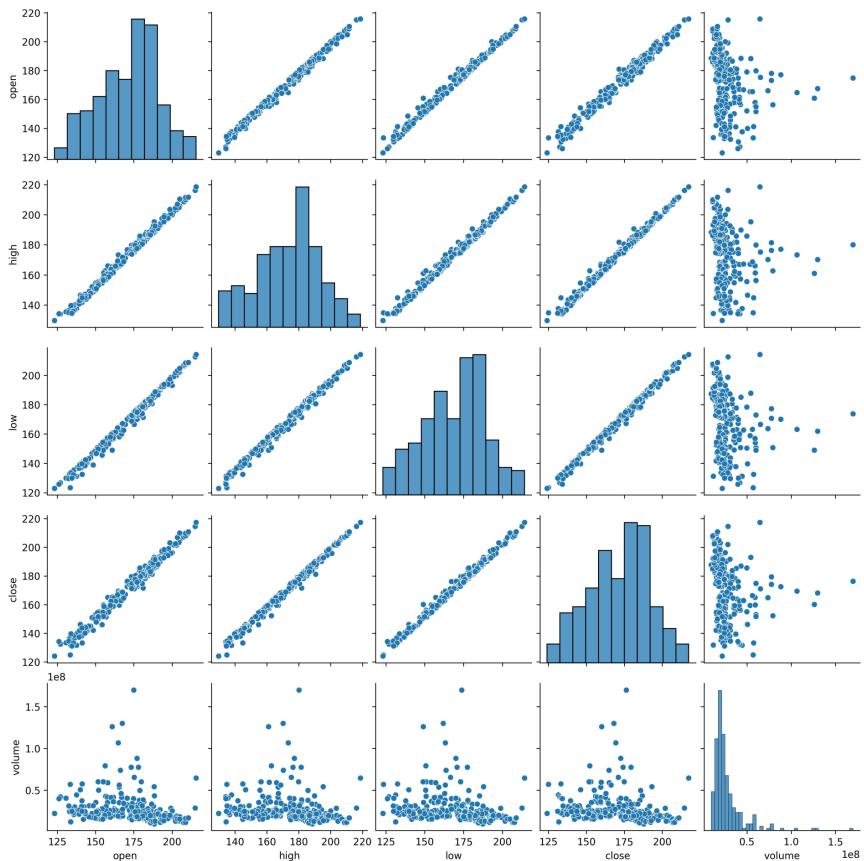


Figure 6.6 – Seaborn's pair plot

Facebook's performance in the latter half of 2018 was markedly worse than in the first half, so we may be interested to see how the distribution of the data changed each quarter of the year. As with the `pandas.plotting.scatter_matrix()` function, we can specify what to do along the diagonal with the `diag_kind` argument; however, unlike `pandas`, we can easily color everything based on other data with the `hue` argument. To do so, we just add the `quarter` column and then provide it to the `hue` argument:

```
>>> sns.pairplot(
...     fb.assign(quarter=lambda x: x.index.quarter),
...     diag_kind='kde', hue='quarter'
... )
```

We can now see how the distributions of the OHLC columns had lower standard deviations (and, subsequently, lower variances) in the first quarter and how the stock price lost a lot of ground in the fourth quarter (the distribution shifts to the left):

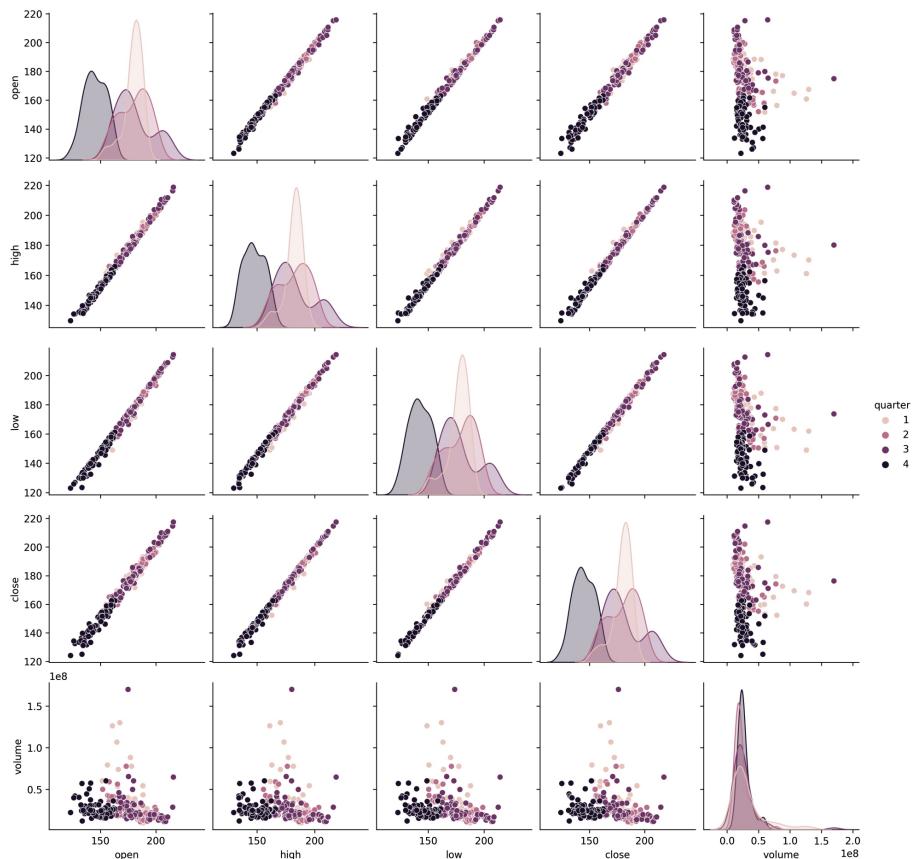


Figure 6.7 – Utilizing the data to determine plot colors

Tip

We can also pass `kind='reg'` to `pairplot()` to show regression lines.

If we only want to compare two variables, we can use `jointplot()`, which will give us a scatter plot along with the distribution of each variable along the side. Let's look once again at how the log of volume traded correlates with the difference between the daily high and low prices in Facebook stock, as we did in *Chapter 5, Visualizing Data with Pandas and Matplotlib*:

```
>>> sns.jointplot(
...     x='log_volume',
...     y='max_abs_change',
...     data=fb.assign(
...         log_volume=np.log(fb.volume),
...         max_abs_change=fb.high - fb.low
...     )
... )
```

Using the default value for the `kind` argument, we get histograms for the distributions and a plain scatter plot in the center:

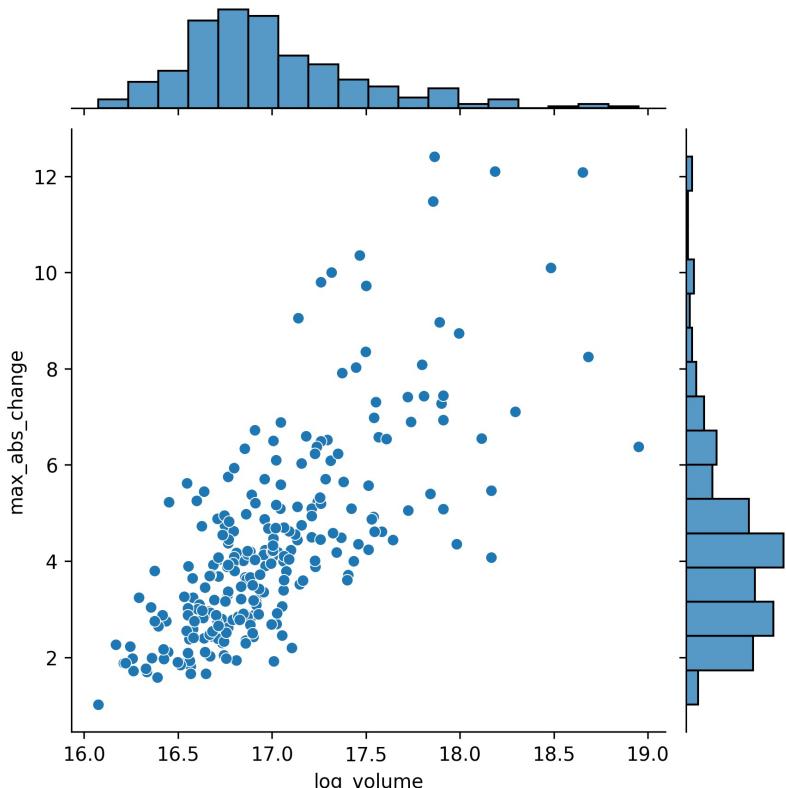


Figure 6.8 – Seaborn's joint plot

Seaborn gives us plenty of alternatives for the `kind` argument. For example, we can use `hexbins` because there is a significant overlap when we use the scatter plot:

```
>>> sns.jointplot(  
...     x='log_volume',  
...     y='max_abs_change',  
...     kind='hex',  
...     data=fb.assign(  
...         log_volume=np.log(fb.volume),  
...         max_abs_change=fb.high - fb.low  
...     )  
... )
```

We can now see the large concentration of points in the lower-left corner:

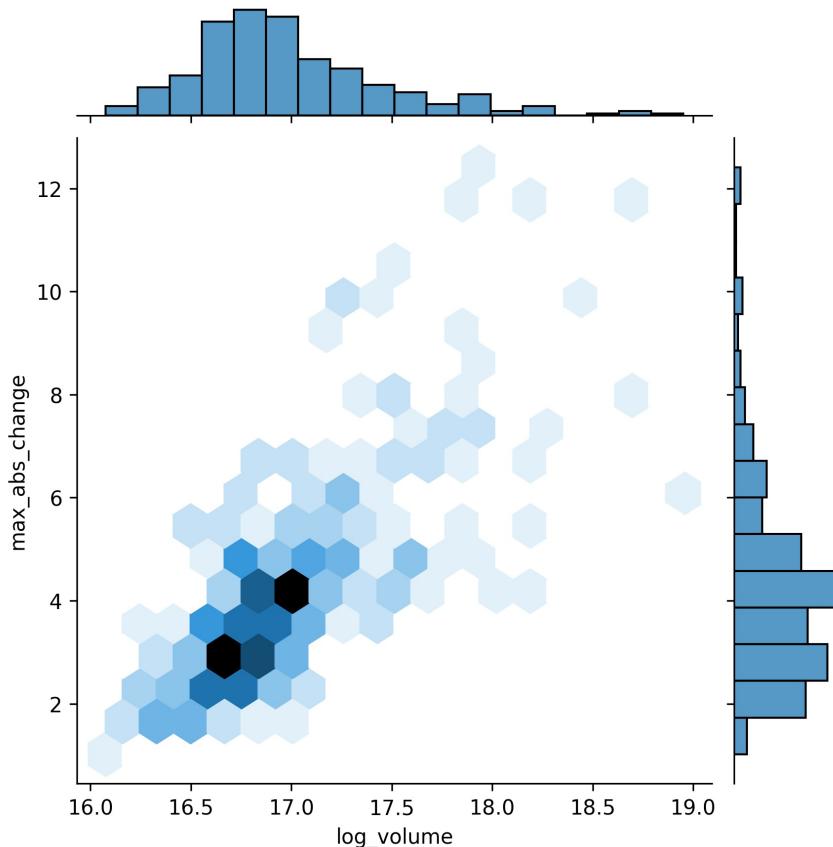


Figure 6.9 – Joint plot using hexbins

Another way of viewing the concentration of values is to use `kind='kde'`, which gives us a **contour plot** to represent the joint density estimate along with KDEs for each of the variables:

```
>>> sns.jointplot(  
...     x='log_volume',  
...     y='max_abs_change',  
...     kind='kde',  
...     data=fb.assign(  
...         log_volume=np.log(fb.volume),  
...         max_abs_change=fb.high - fb.low  
...     )  
... )
```

Each curve in the contour plot contains points of a given density:

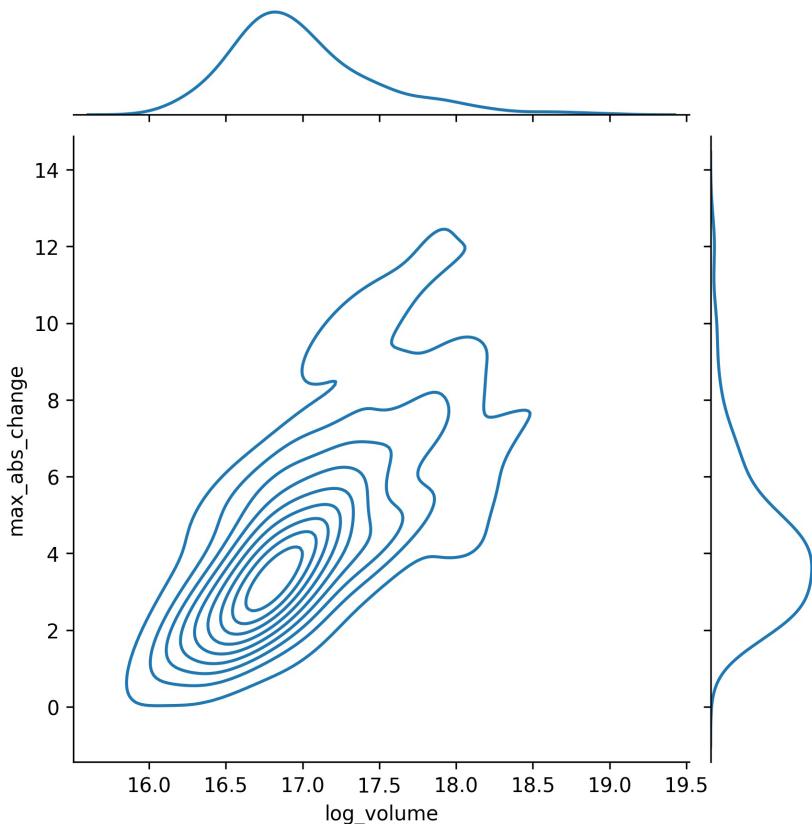


Figure 6.10 – Joint distribution plot

Furthermore, we can plot a regression in the center and get KDEs in addition to histograms along the sides:

```
>>> sns.jointplot(  
...     x='log_volume',  
...     y='max_abs_change',  
...     kind='reg',  
...     data=fb.assign(  
...         log_volume=np.log(fb.volume),  
...         max_abs_change=fb.high - fb.low  
...     )  
... )
```

This results in a linear regression line being drawn through the scatter plot, along with a confidence band surrounding the line in a lighter color:

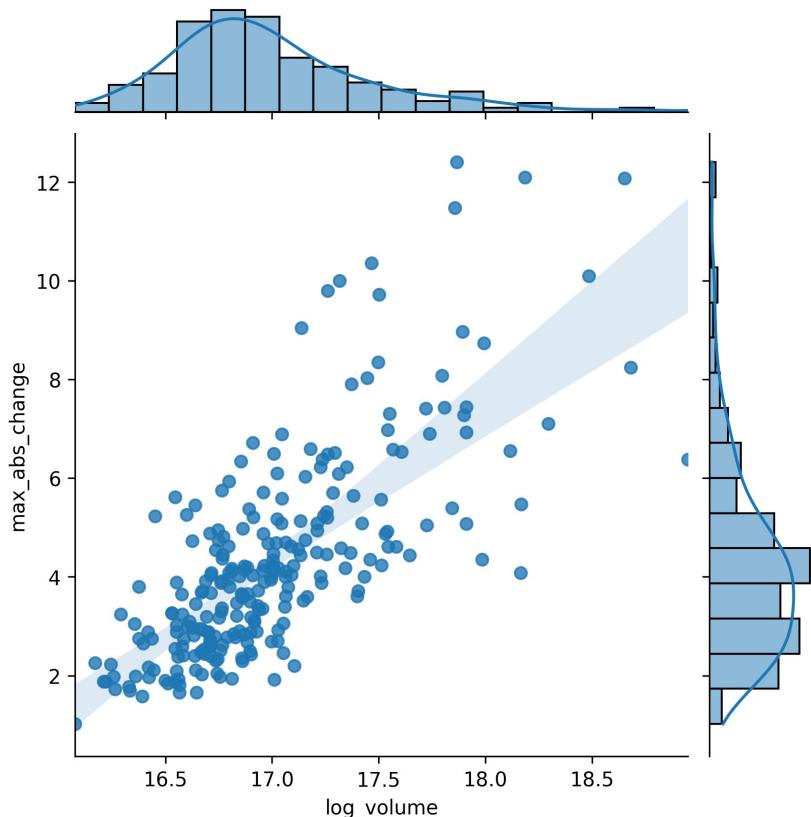


Figure 6.11 – Joint plot with linear regression and KDEs

The relationship appears to be linear, but we should look at the **residuals** to check. Residuals are the observed values minus the values predicted using the regression line. We can look directly at the residuals that would result from the previous regression with `kind='resid'`:

```
>>> sns.jointplot(
...     x='log_volume',
...     y='max_abs_change',
...     kind='resid',
...     data=fb.assign(
...         log_volume=np.log(fb.volume),
...         max_abs_change=fb.high - fb.low
...     )
... )
# update y-axis label (discussed next section)
>>> plt.ylabel('residuals')
```

Notice that the residuals appear to be getting further away from zero at higher quantities of volume traded, which could mean this isn't the right way to model this relationship:

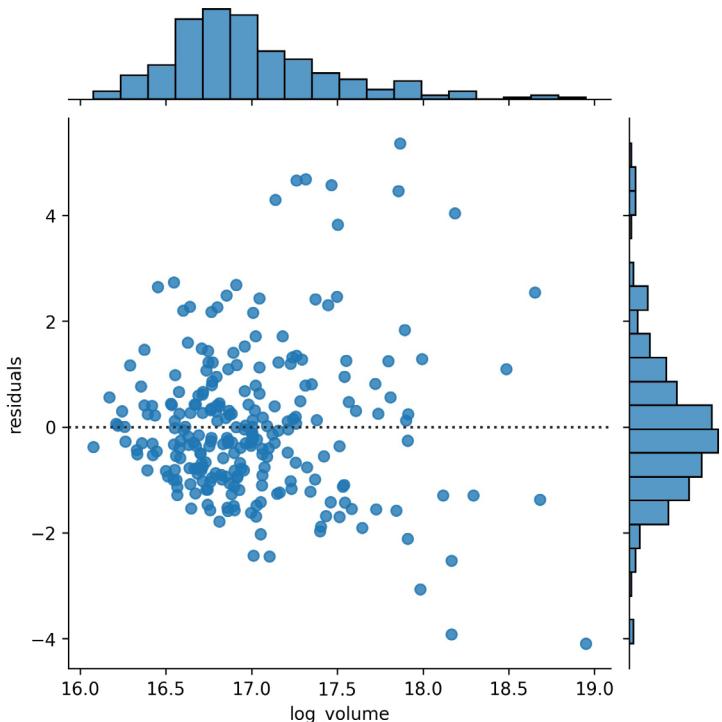


Figure 6.12 – Joint plot showing linear regression residuals

We just saw that we can use `jointplot()` to get a regression plot or a residuals plot; naturally, `seaborn` exposes functions to make these directly without the overhead of creating the entire joint plot. Let's discuss those next.

Regression plots

The `regplot()` function will calculate a regression line and plot it, while the `residplot()` function will calculate the regression and plot only the residuals. We can write a function to combine these for us, but first, some setup.

Our function will plot all permutations of any two columns (as opposed to combinations; order matters with permutations, for example, `(open, close)` is not equivalent to `(close, open)`). This allows us to see each column as the regressor and as the dependent variable; since we don't know the direction of the relationship, we let the viewer decide after calling the function. This generates many subplots, so we will create a new dataframe with just a few columns from our Facebook data.

We'll be looking at the logarithm of the volume traded (`log_volume`) and the daily difference between the highest and lowest price of Facebook stock (`max_abs_change`). Let's use `assign()` to create these new columns and save them in a new dataframe called `fb_reg_data`:

```
>>> fb_reg_data = fb.assign(  
...     log_volume=np.log(fb.volume),  
...     max_abs_change=fb.high - fb.low  
... ).iloc[:, -2:]
```

Next, we need to import `itertools`, which is part of the Python standard library (<https://docs.python.org/3/library/itertools.html>). When writing plotting functions, `itertools` can be extremely helpful; it makes it very easy to create efficient iterators for things such as permutations, combinations, and infinite cycles or repeats:

```
>>> import itertools
```

Iterables are objects that can be iterated over. When we start a loop, an **iterator** is created from the iterable. At each iteration, the iterator provides its next value, until it is exhausted; this means that once we complete a single iteration through all its items, there is nothing left, and it can't be reused. Iterators are iterables, but not all iterables are iterators. Iterables that aren't iterators can be used repeatedly.

The iterators we get back when using `itertools` can only be used once through:

```
>>> iterator = itertools.repeat("I'm an iterator", 1)

>>> for i in iterator:
...     print(f'-->{i}')
-->I'm an iterator

>>> print(
...     'This printed once because the iterator '
...     'has been exhausted'
... )
This printed once because the iterator has been exhausted

>>> for i in iterator:
...     print(f'-->{i}')
```

A list, on the other hand, is an iterable; we can write something that loops over all the elements in the list, and we will still have a list for later reuse:

```
>>> iterable = list(itertools.repeat("I'm an iterable", 1))

>>> for i in iterable:
...     print(f'-->{i}')
-->I'm an iterable

>>> print('This prints again because it\'s an iterable:')
This prints again because it's an iterable:

>>> for i in iterable:
...     print(f'-->{i}')
-->I'm an iterable
```

Now that we have some background on `itertools` and iterators, let's write the function for our regression and residuals permutation plots:

```
def reg_resid_plots(data):
    """
    Using `seaborn`, plot the regression and residuals plots
    side-by-side for every permutation of 2 columns in data.

    Parameters:
        - data: A `pandas.DataFrame` object

    Returns:
        A matplotlib `Axes` object.
    """
    num_cols = data.shape[1]
    permutation_count = num_cols * (num_cols - 1)

    fig, ax = \
        plt.subplots(permutation_count, 2, figsize=(15, 8))

    for (x, y), axes, color in zip(
            itertools.permutations(data.columns, 2),
            ax,
            itertools.cycle(['royalblue', 'darkorange']))
    ) :
        for subplot, func in zip(
                axes, (sns.regplot, sns.residplot))
        :
            func(x=x, y=y, data=data, ax=subplot, color=color)
            if func == sns.residplot:
                subplot.set_ylabel('residuals')
    return fig.axes
```

In this function, we can see that all the material covered so far in this chapter and from the previous chapter is coming together; we calculate how many subplots we need, and since we will have two plots for each permutation, we just need the number of permutations to determine the row count. We take advantage of the `zip()` function, which gives us values from multiple iterables at once in tuples, and tuple unpacking to easily iterate over the permutation tuples and the 2D NumPy array of `Axes` objects. Take some time to make sure you understand what is going on here; there are also resources on `zip()` and tuple unpacking in the *Further reading* section at the end of this chapter.

Important note

If we provide different length iterables to `zip()`, we will only get a number of tuples equal to the shortest length. For this reason, we can use infinite iterators, such as those we get when using `itertools.repeat()`, which repeats the same value infinitely (when we don't specify the number of times to repeat the value), and `itertools.cycle()`, which cycles between all the values provided infinitely.

Calling our function is effortless, with only a single parameter:

```
>>> from viz import reg_resid_plots
>>> reg_resid_plots(fb_reg_data)
```

The first row of subsets is what we saw earlier with the joint plots, and the second row is the regression when flipping the x and y variables:

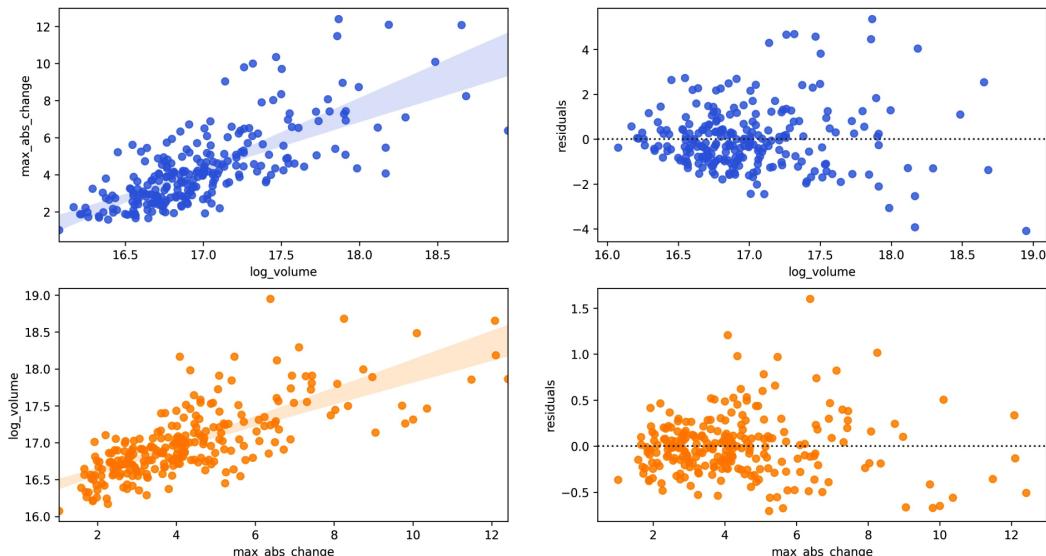


Figure 6.13 – Seaborn linear regression and residual plots

Tip

The `regplot()` function supports polynomial and logistic regression through the `order` and `logistic` parameters, respectively.

Seaborn also makes it easy to plot regressions across different subsets of our data with `lmplot()`. We can split our regression plots with `hue`, `col`, and `row`, which will color by values in a given column, make a new column for each value, and make a new row for each value, respectively.

We saw that Facebook's performance was different across each quarter of the year, so let's calculate a regression per quarter with the Facebook stock data, using the volume traded and the daily difference between the highest and lowest price, to see whether this relationship also changes:

```
>>> sns.lmplot(  
...     x='log_volume',  
...     y='max_abs_change',  
...     col='quarter',  
...     data=fb.assign(  
...         log_volume=np.log(fb.volume),  
...         max_abs_change=fb.high - fb.low,  
...         quarter=lambda x: x.index.quarter  
...     )  
... )
```

Notice that the regression line in the fourth quarter has a much steeper slope than previous quarters:

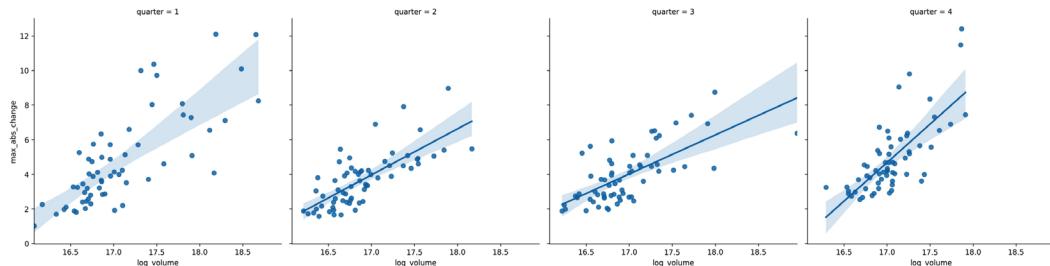


Figure 6.14 – Seaborn linear regression plots with subsets

Note that the result of running `lmplot()` is a `FacetGrid` object, which is a powerful feature of `seaborn`. Let's now discuss how we can make these directly with any plot inside.

Faceting

Faceting allows us to plot subsets (facets) of our data across subplots. We already saw a few as a result of some `seaborn` functions; however, we can easily make them for ourselves for use with any plotting function. Let's create a visualization that will allow us to compare the distributions of earthquake magnitudes in Indonesia and Papua New Guinea depending on whether there was a tsunami.

First, we create a `FacetGrid` object with the data we will be using and define how it will be subset with the `row` and `col` arguments:

```
>>> g = sns.FacetGrid(  
...     quakes.query(  
...         'parsed_place.isin(''  
...             ["Indonesia", "Papua New Guinea"] ) ' '  
...         'and magType == "mb" '  
...     ),  
...     row='tsunami',  
...     col='parsed_place',  
...     height=4  
... )
```

Then, we use the `FacetGrid.map()` method to run a plotting function on each of the subsets, passing along any necessary arguments. We will make histograms with KDEs for the location and tsunami data subsets using the `sns.histplot()` function:

```
>>> g = g.map(sns.histplot, 'mag', kde=True)
```

For both locations, we can see that tsunamis occurred when the earthquake magnitude was 5.0 or greater:

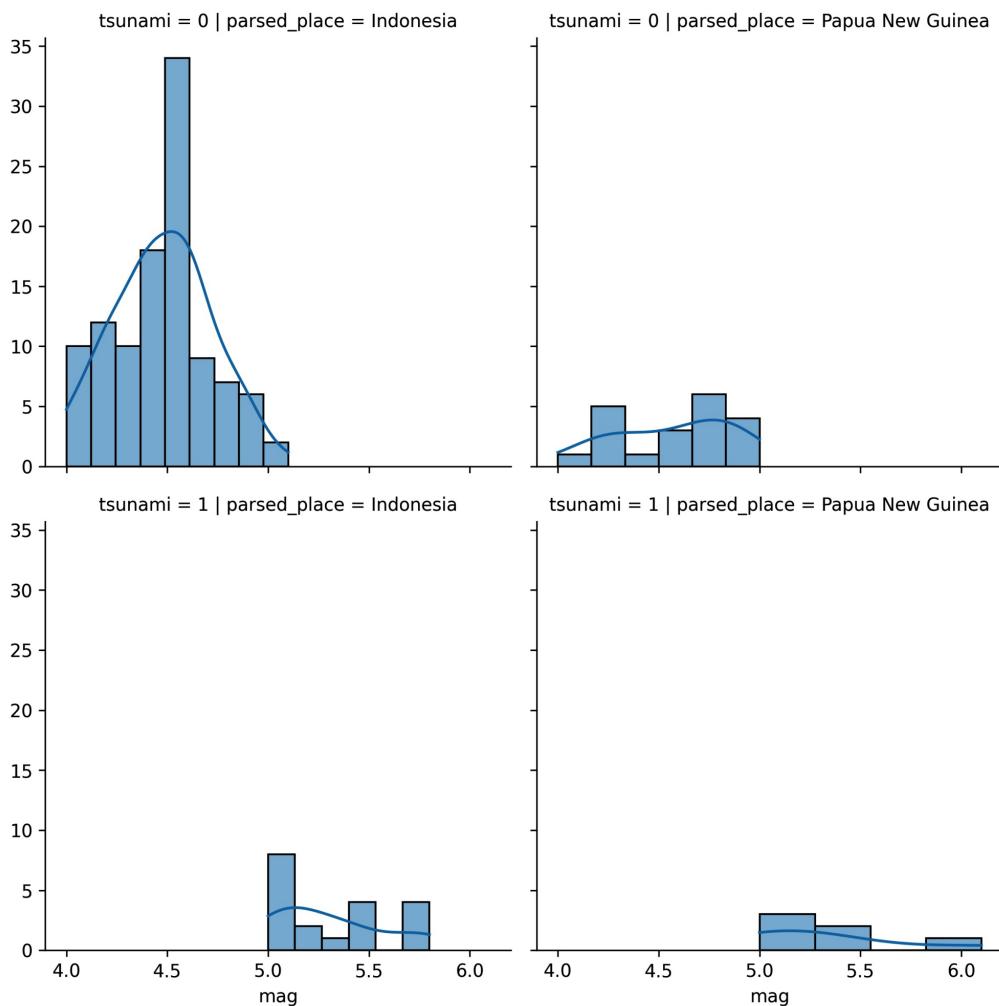


Figure 6.15 – Plotting with facet grids

This concludes our discussion of the plotting capabilities of seaborn; however, I encourage you to check out the API (<https://seaborn.pydata.org/api.html>) to see additional functionality. Also, be sure to consult the *Choosing the appropriate visualization* section in the *Appendix* as a reference when looking to plot some data.

Formatting plots with matplotlib

A big part of making our visualizations presentable is choosing the right plot type and having them well labeled so they are easy to interpret. By carefully tuning the final appearance of our visualizations, we make them easier to read and understand.

Let's now move to the `2-formatting_plots.ipynb` notebook, run the setup code to import the packages we need, and read in the Facebook stock data and COVID-19 daily new cases data:

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

>>> fb = pd.read_csv(
...     'data/fb_stock_prices_2018.csv',
...     index_col='date',
...     parse_dates=True
... )
>>> covid = pd.read_csv('data/covid19_cases.csv').assign(
...     date=lambda x: \
...         pd.to_datetime(x.dateRep, format='%d/%m/%Y')
... ).set_index('date').replace(
...     'United_States_of_America', 'USA'
... ).sort_index()['2020-01-18':'2020-09-18']
```

In the next few sections, we will discuss how to add titles, axis labels, and legends to our plots, as well as how to customize the axes. Note that everything in this section needs to be called before running `plt.show()` or within the same Jupyter Notebook cell if using the `%matplotlib inline` magic command.

Titles and labels

Some of the visualizations we have created thus far didn't have titles or axis labels. We know what is going on in the figure, but if we were to present them to others, there could be some confusion. It's good practice to be explicit with our labels and titles.

We saw that, when plotting with pandas, we could add a title by passing the `title` argument to the `plot()` method, but we can also do this with `matplotlib` using `plt.title()`. Note that we can pass x/y values to `plt.title()` to control the placement of our text. We can also change the font and its size. Labeling our axes is just as easy; we can use `plt.xlabel()` and `plt.ylabel()`. Let's plot the Facebook closing price and label everything using `matplotlib`:

```
>>> fb.close.plot()
>>> plt.title('FB Closing Price')
>>> plt.xlabel('date')
>>> plt.ylabel('price ($)')
```

This results in the following plot:

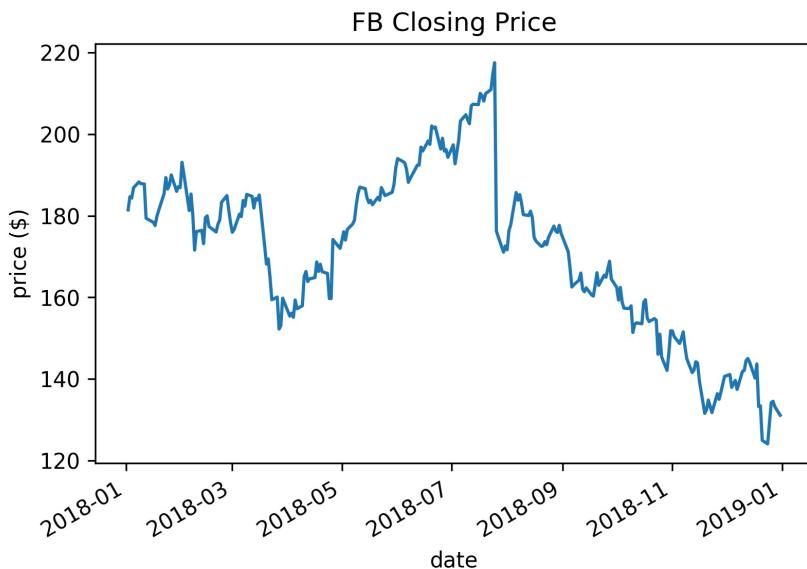


Figure 6.16 – Labeling plots with matplotlib

When working with subplots, we have to take a different approach. To see this firsthand, let's make subplots of Facebook stock's OHLC data and use `plt.title()` to give the entire plot a title, along with `plt.ylabel()` to give each subplot's *y*-axis a label:

```
>>> fb.iloc[:, :4] \
...     .plot(subplots=True, layout=(2, 2), figsize=(12, 5))
>>> plt.title('Facebook 2018 Stock Data')
>>> plt.ylabel('price ($)')
```

Using `plt.title()` puts the title on the last subplot, instead of being the title for the plots as a whole, as we intended. The same thing happens to the *y*-axis label:

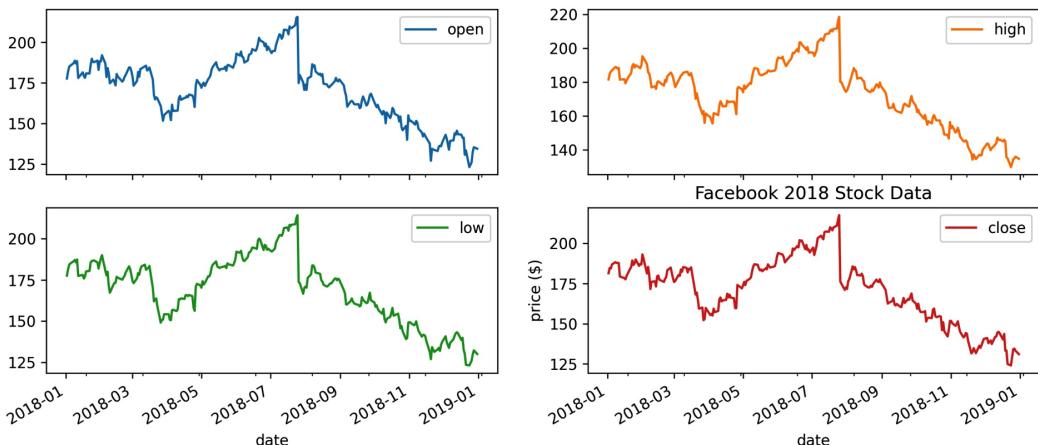


Figure 6.17 – Labeling subplots can be confusing

In the case of subplots, we want to give the entire figure a title; therefore, we use `plt.suptitle()` instead. Conversely, we want to give each subplot a *y*-axis label, so we use the `set_ylabel()` method on each of the `Axes` objects returned by the call to `plot()`. Note that the `Axes` objects are returned in a NumPy array of the same dimensions as the subplot layout, so for easier iteration, we call `flatten()`:

```
>>> axes = fb.iloc[:, :4] \
...     .plot(subplots=True, layout=(2, 2), figsize=(12, 5))
>>> plt.suptitle('Facebook 2018 Stock Data')
>>> for ax in axes.flatten():
...     ax.set_ylabel('price ($)')
```

This results in a title for the plot as a whole and *y*-axis labels for each of the subplots:

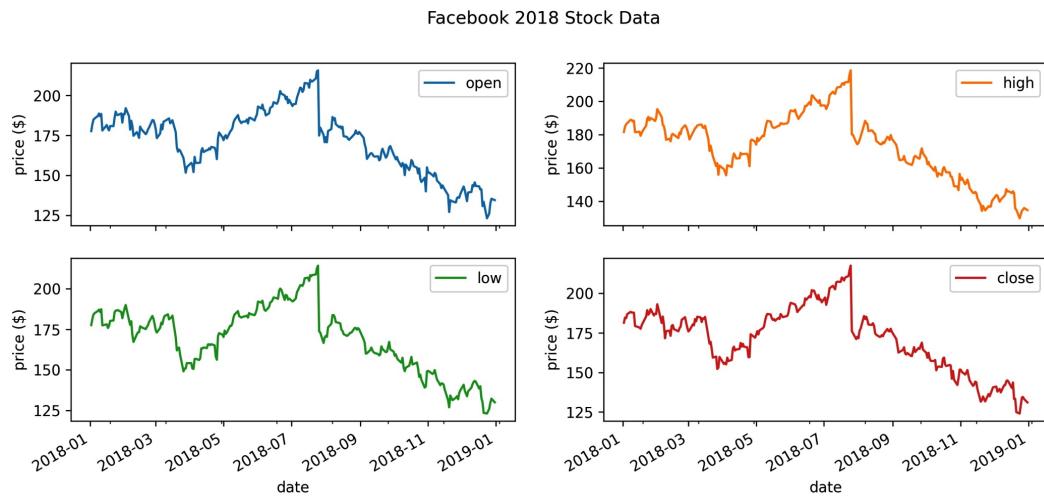


Figure 6.18 – Labeling subplots

Note that the `Figure` class also has a `suptitle()` method and that the `Axes` class's `set()` method lets us label the axes, title the plot, and much more in a single call, for example, `set(xlabel='...', ylabel='...', title='...', ...)`. Depending on what we are trying to do, we may need to call methods on `Figure` or `Axes` objects directly, so it's important to be aware of them.

Legends

Matplotlib makes it possible to control many aspects of the legend through the `plt.legend()` function and the `Axes.legend()` method. For example, we can specify the legend's location and format how the legend looks, including customizing the fonts, colors, and much more. Both the `plt.legend()` function and the `Axes.legend()` method can also be used to show a legend when the plot doesn't have one initially. Here is a sampling of some commonly used parameters:

Parameter	Purpose
<code>loc</code>	Specify the location of the legend
<code>bbox_to_anchor</code>	Used in conjunction with <code>loc</code> to specify legend location
<code>ncol</code>	Set the number of columns the labels will be broken into, default is 1
<code>framealpha</code>	Control the transparency of the legend's background
<code>title</code>	Give the legend a title

Figure 6.19 – Helpful parameters for legend formatting

The legend will use the label of each object that was plotted. If we don't want something to show up, we can make its label an empty string. However, if we simply want to alter how something shows up, we can pass its display name through the `label` argument. Let's plot Facebook stock's closing price and the 20-day moving average, using the `label` argument to provide a descriptive name for the legend:

```
>>> fb.assign(
...     ma=lambda x: x.close.rolling(20).mean()
... ).plot(
...     y=['close', 'ma'],
...     title='FB closing price in 2018',
...     label=['closing price', '20D moving average'],
...     style=['-', '--']
... )
>>> plt.legend(loc='lower left')
>>> plt.ylabel('price ($)')
```

By default, `matplotlib` tries to find the best location for the plot, but sometimes it covers up parts of the plot as in this case. Therefore, we chose to place the legend in the lower-left corner of the plot. Note that the text in the legend is what we provided in the `label` argument to `plot()`:

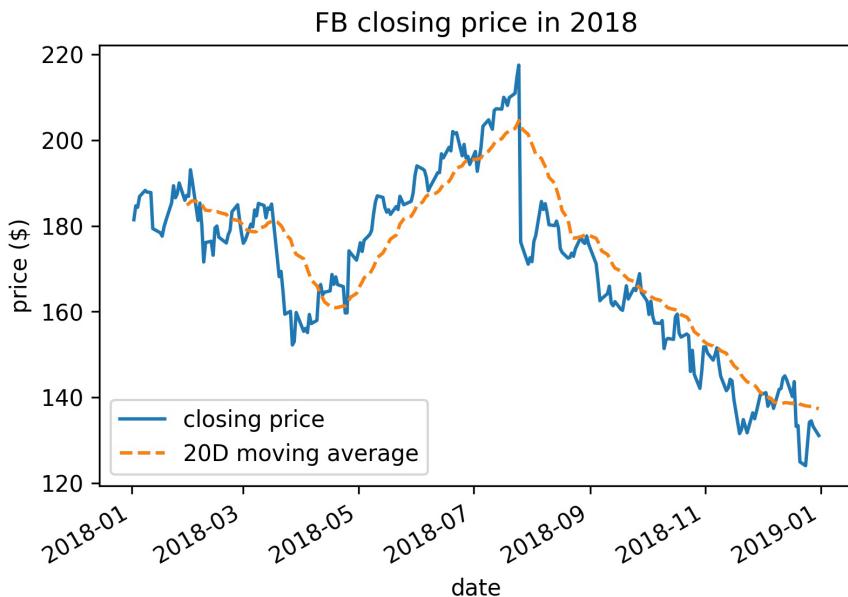


Figure 6.20 – Moving the legend

Notice that we passed a string to the `loc` argument to specify the legend location; we also have the option of passing the code as an integer or a tuple for the (x, y) coordinates to draw the lower-left corner of the legend box. The following table contains the possible location strings:

Location String	Location Code
'best'	0
'upper right'	1
'upper left'	2
'lower left'	3
'lower right'	4
'right'	5
'center left'	6
'center right'	7
'lower center'	8
'upper center'	9
'center'	10

Figure 6.21 – Common legend locations

Let's now take a look at styling the legend with the `framealpha`, `ncol`, and `title` arguments. We will plot the percentage of the world's daily new COVID-19 cases that occurred in Brazil, China, Italy, Spain, and the USA over the 8-month period from January 18, 2020 through September 18, 2020. In addition, we will remove the top and right spines of the plot to make it look cleaner:

```
>>> new_cases = covid.reset_index().pivot(
...     index='date',
...     columns='countriesAndTerritories',
...     values='cases'
... ).fillna(0)

>>> pct_new_cases = new_cases.apply(
...     lambda x: x / new_cases.apply('sum', axis=1), axis=0
... )[
...     ['Italy', 'China', 'Spain', 'USA', 'India', 'Brazil']
... ].sort_index(axis=1).fillna(0)
```

```
>>> ax = pct_new_cases.plot(
...     figsize=(12, 7),
...     style=['-' * 3 + [ '--', ':', '-.'],
...     title='Percentage of the World\'s New COVID-19 Cases'
...         '\n(source: ECDC)'
... )

>>> ax.legend(title='Country', framealpha=0.5, ncol=2)
>>> ax.set_xlabel('')
>>> ax.set_ylabel('percentage of the world\'s COVID-19 cases')

>>> for spine in ['top', 'right']:
...     ax.spines[spine].set_visible(False)
```

Our legend is neatly arranged in two columns and contains a title. We also increased the transparency of the legend's border:

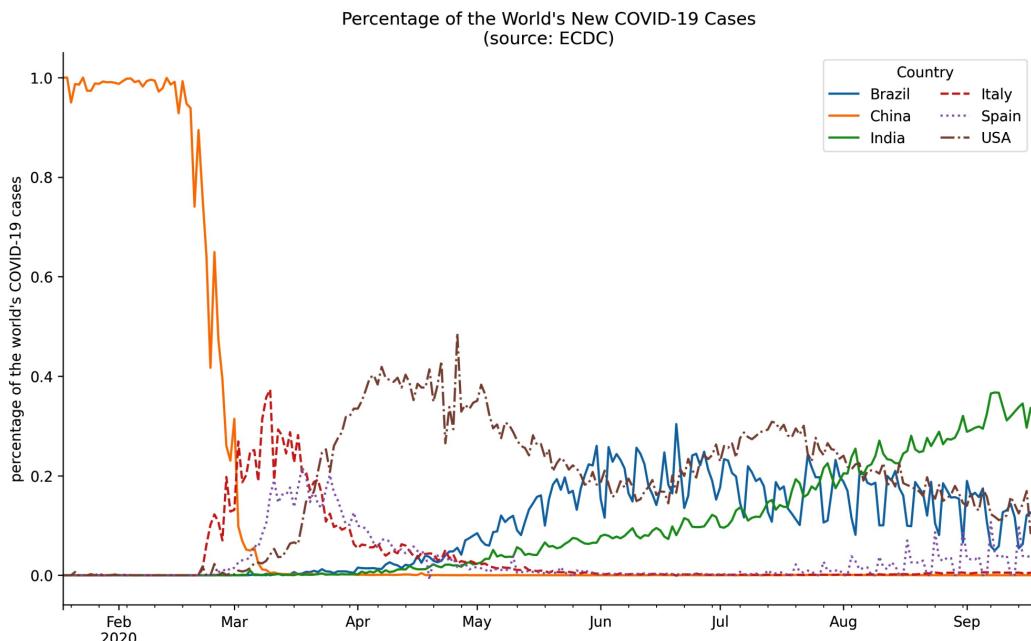


Figure 6.22 – Formatting the legend

Tip

Don't get overwhelmed trying to memorize all of the available options. It is easier if we don't try to learn every possible customization, but rather look up the functionality that matches what we have in mind for our visualization when needed.

Formatting axes

Back in *Chapter 1, Introduction to Data Analysis*, we discussed how our axis limits can make for misleading plots if we aren't careful. We have the option of passing this as a tuple to the `xlim/ylim` arguments when using the `plot()` method from `pandas`. Alternatively, with `matplotlib`, we can adjust the limits of each axis with the `plt.xlim()/plt.ylim()` function or the `set_xlim()/set_ylim()` method on an `Axes` object. We pass values for the minimum and maximum, separately; if we want to keep what was automatically generated, we can pass in `None`. Let's modify the previous plot of the percentage of the world's daily new COVID-19 cases per country to start the *y*-axis at zero:

```
>>> ax = pct_new_cases.plot(
...     figsize=(12, 7),
...     style=['-' * 3 + [ '--', ':', '-.'],
...     title='Percentage of the World\'s New COVID-19 Cases'
...         '\n(source: ECDC)'
... )

>>> ax.legend(framealpha=0.5, ncol=2)
>>> ax.set_xlabel('')
>>> ax.set_ylabel('percentage of the world\'s COVID-19 cases')
>>> ax.set_ylim(0, None)

>>> for spine in ['top', 'right']:
...     ax.spines[spine].set_visible(False)
```

Notice that the *y*-axis now begins at zero:

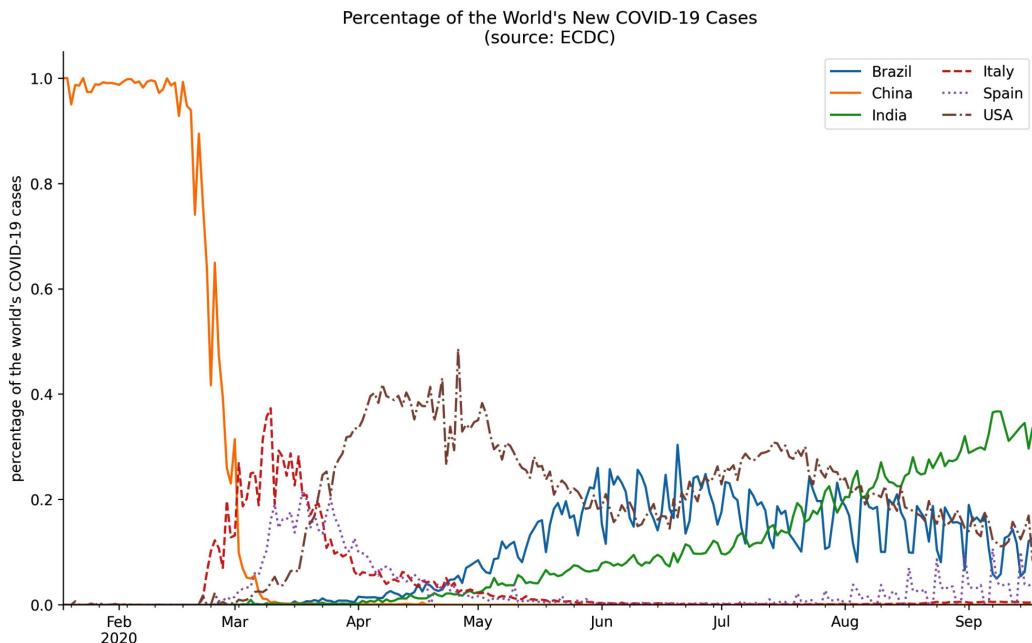


Figure 6.23 – Updating axis limits with matplotlib

If we instead want to change the scale of the axis, we can use `plt.xscale()`/
`plt.yscale()` and pass the type of scale we want. So, `plt.yscale('log')`,
for example, will use the log scale for the *y*-axis; we saw how to do this with pandas
in the previous chapter.

We can also control which tick marks show up and what they are labeled as by passing
in the tick locations and labels to `plt.xticks()` or `plt.yticks()`. Note that we
can also call these functions to obtain the tick locations and labels. For example, since our
data starts and ends on the 18th of the month, let's move the tick marks in the previous
plot to the 18th of each month and then label the ticks accordingly:

```
>>> ax = pct_new_cases.plot(  
...     figsize=(12, 7),  
...     style=['-' * 3 + [ '--', ':', '-.'],  
...     title='Percentage of the World\\\'s New COVID-19 Cases'  
...         '\n(source: ECDC)'  
... )
```

```
>>> tick_locs = covid.index[covid.index.day == 18].unique()
>>> tick_labels = \
...     [loc.strftime('%b %d\n%Y') for loc in tick_locs]
>>> plt.xticks(tick_locs, tick_labels)

>>> ax.legend(framealpha=0.5, ncol=2)
>>> ax.set_xlabel('')
>>> ax.set_ylabel('percentage of the world\'s COVID-19 cases')
>>> ax.set_ylimit(0, None)

>>> for spine in ['top', 'right']:
...     ax.spines[spine].set_visible(False)
```

After moving the tick marks, we have a tick label on the first data point in the plot (January 18, 2020) and on the last (September 18, 2020):

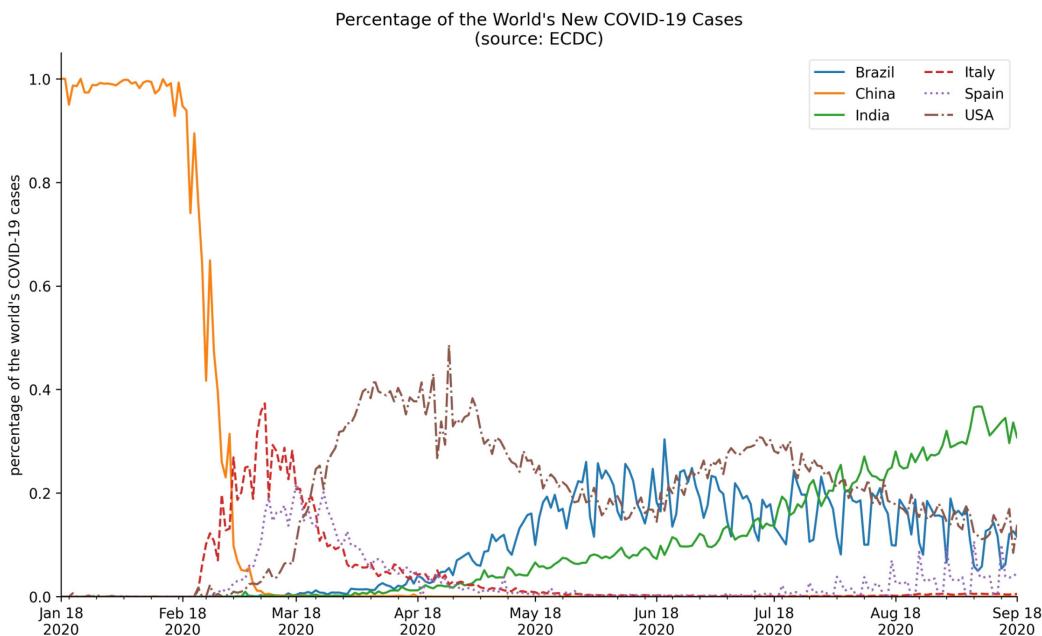


Figure 6.24 – Editing tick labels

We are currently representing the percentages as decimals, but we may wish to format the labels to be written using the percent sign. Note that there is no need to use the `plt.yticks()` function to do so; instead, we can use the `PercentFormatter` class from the `matplotlib.ticker` module:

```
>>> from matplotlib.ticker import PercentFormatter

>>> ax = pct_new_cases.plot(
...     figsize=(12, 7),
...     style=['-' * 3 + [ '--', ':', '-.'],
...     title='Percentage of the World\'s New COVID-19 Cases'
...         '\n(source: ECDC)'
... )

>>> tick_locs = covid.index[covid.index.day == 18].unique()
>>> tick_labels = \
...     [loc.strftime('%b %d\n%Y') for loc in tick_locs]
>>> plt.xticks(tick_locs, tick_labels)

>>> ax.legend(framealpha=0.5, ncol=2)
>>> ax.set_xlabel('')
>>> ax.set_ylabel('percentage of the world\'s COVID-19 cases')
>>> ax.set_ylim(0, None)
>>> ax.xaxis.set_major_formatter(PercentFormatter(xmax=1))

>>> for spine in ['top', 'right']:
...     ax.spines[spine].set_visible(False)
```

By specifying `xmax=1`, we are indicating that our values should be divided by 1 (since they are already percentages), before multiplying by 100 and appending the percent sign. This results in percentages along the *y*-axis:

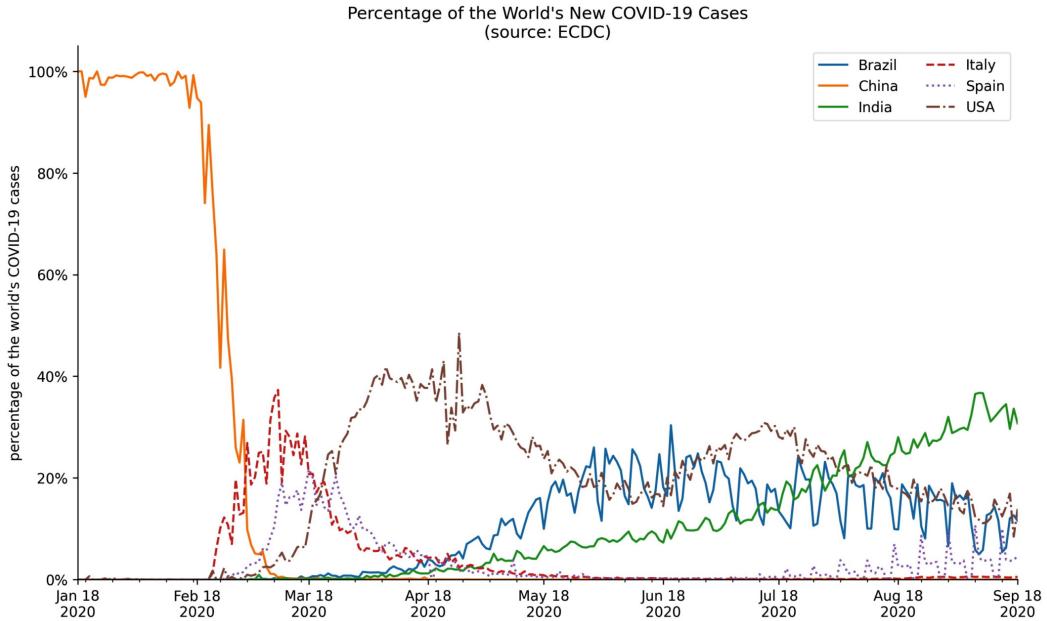


Figure 6.25 – Formatting tick labels as percentages

Another useful formatter is the `EngFormatter` class, which will automatically handle formatting numbers as thousands, millions, and so on using **engineering notation**. Let's use this to plot the cumulative COVID-19 cases per continent in millions:

```
>>> from matplotlib.ticker import EngFormatter

>>> ax = covid.query('continentExp != "Other"').groupby([
...     'continentExp', pd.Grouper(freq='1D')
... ]).cases.sum().unstack(0).apply('cumsum').plot(
...     style=['-', '--', '-.', ':', '-.'],
...     title='Cumulative COVID-19 Cases per Continent'
...         '\n(source: ECDC)'
... )

>>> ax.legend(title='', loc='center left')
>>> ax.set(xlabel='', ylabel='total COVID-19 cases')
>>> ax.yaxis.set_major_formatter(EngFormatter())

>>> for spine in ['top', 'right']:
...     ax.spines[spine].set_visible(False)
```

Notice that we didn't need to divide the cumulative case counts by 1 million to get these numbers—the `EngFormatter` object that we passed to `set_major_formatter()` automatically figured out that it should use millions (M) based on the data:

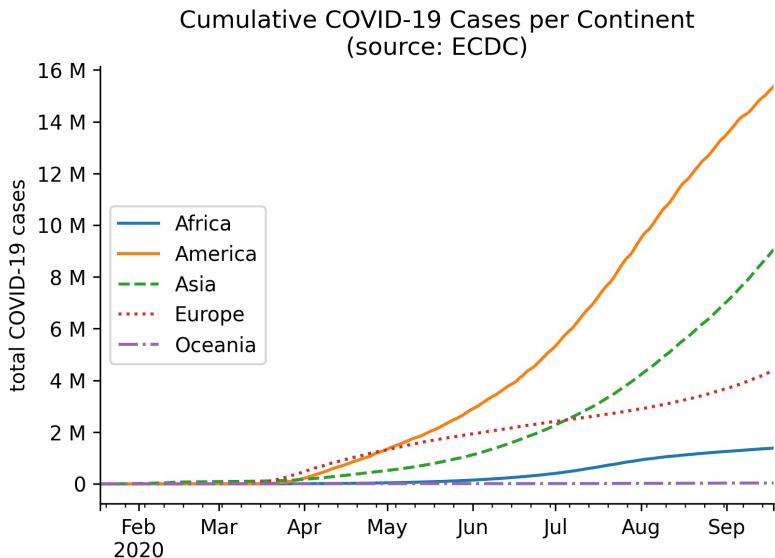


Figure 6.26 – Formatting tick labels with engineering notation

Both the `PercentFormatter` and `EngFormatter` classes format the tick labels, but sometimes we want to change the location of the ticks rather than format them. One way of doing so is with the `MultipleLocator` class, which makes it easy for us to place the ticks at multiples of a number of our choosing. To illustrate how we could use this, let's take a look at the daily new COVID-19 cases in New Zealand from April 18, 2020 through September 18, 2020:

```
>>> ax = new_cases.New_Zealand['2020-04-18':'2020-09-18'].plot(  
...      title='Daily new COVID-19 cases in New Zealand'  
...      '\n(source: ECDC)'  
... )  
>>> ax.set(xlabel='', ylabel='new COVID-19 cases')  
  
>>> for spine in ['top', 'right']:  
...     ax.spines[spine].set_visible(False)
```

Without us intervening with the tick locations, `matplotlib` is showing the ticks in increments of 2.5. We know that there is no such thing as half of a case, so it makes more sense to show this data with only integer ticks:

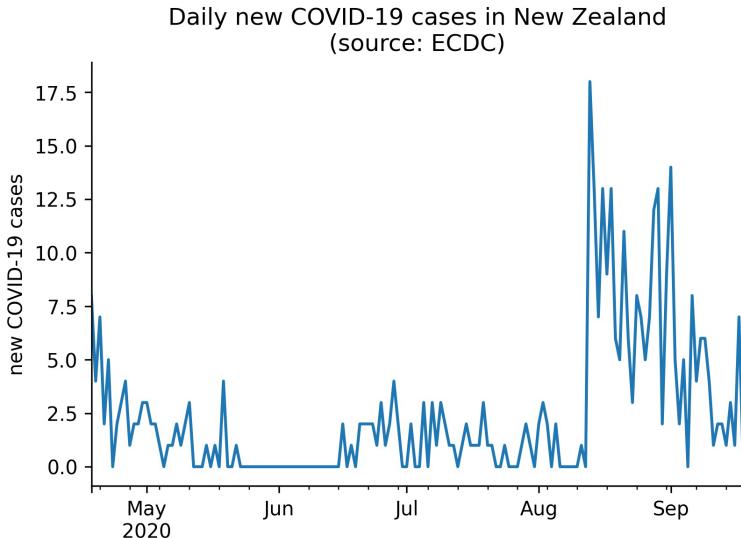


Figure 6.27 – Default tick locations

Let's fix this by using the `MultipleLocator` class. Here, we aren't formatting the axis labels, but rather controlling which ones are shown; for this reason, we have to call the `set_major_locator()` method instead of `set_major_formatter()`:

```
>>> from matplotlib.ticker import MultipleLocator

>>> ax = new_cases.New_Zealand['2020-04-18':'2020-09-18'].plot(
...     title='Daily new COVID-19 cases in New Zealand'
...     '\n(source: ECDC)'
... )
>>> ax.set(xlabel='', ylabel='new COVID-19 cases')
>>> ax.yaxis.set_major_locator(MultipleLocator(base=3))

>>> for spine in ['top', 'right']:
...     ax.spines[spine].set_visible(False)
```

Since we passed in `base=3`, our *y*-axis now contains integers in increments of three:

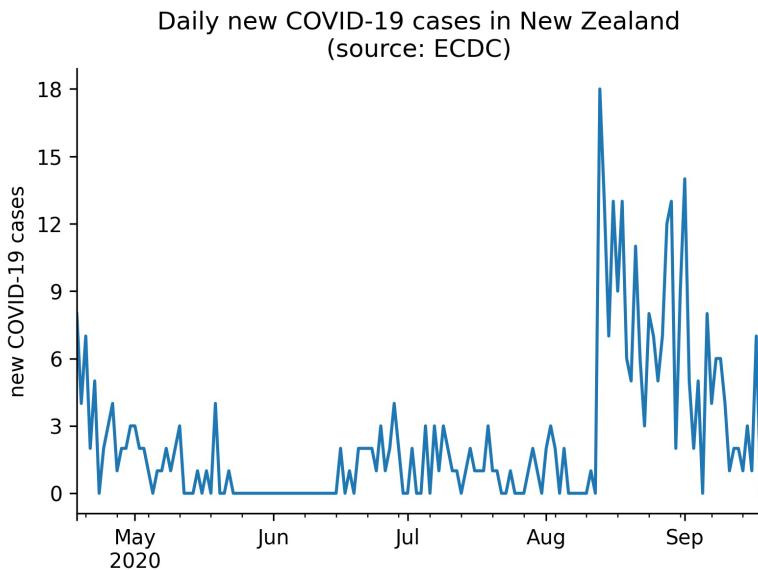


Figure 6.28 – Using integer tick locations

These were only three of the features provided with the `matplotlib.ticker` module, so I highly recommend you check out the documentation for more information. There is also a link in the *Further reading* section at the end of this chapter.

Customizing visualizations

So far, all of the code we've learned for creating data visualizations has been for making the visualization itself. Now that we have a strong foundation, we are ready to learn how to add reference lines, control colors and textures, and include annotations.

In the `3 - customizing_visualizations.ipynb` notebook, let's handle our imports and read in the Facebook stock prices and earthquake datasets:

```
>>> %matplotlib inline
>>> import matplotlib.pyplot as plt
>>> import pandas as pd
```

```
>>> fb = pd.read_csv(  
...     'data/fb_stock_prices_2018.csv',  
...     index_col='date',  
...     parse_dates=True  
... )  
>>> quakes = pd.read_csv('data/earthquakes.csv')
```

Tip

Changing the style in which the plots are created is an easy way to change their look and feel without setting each aspect separately. To set the style for `seaborn`, use `sns.set_style()`. With `matplotlib`, we can use `plt.style.use()` to specify the stylesheet(s) we want to use. These will be used for all visualizations created in that session. If, instead, we only want it for a single plot, we can use `sns.set_context()` or `plt.style.context()`. Available styles for `seaborn` can be found in the documentation of the aforementioned functions and in `matplotlib` by taking a look at the values in `plt.style.available`.

Adding reference lines

Quite often, we want to draw attention to a specific value on our plot, perhaps as a boundary or turning point. We may be interested in whether the line gets crossed or serves as a partition. In finance, horizontal reference lines may be drawn on top of the line plot of a stock's price, marking the support and resistance.

The **support** is a price level at which a downward trend is expected to reverse because the stock is now at a price level at which buyers are more enticed to purchase, driving the price up and away from this point. On the flip side, the **resistance** is the price level at which an upward trend is expected to reverse since the price is an attractive selling point; thus, the price falls down and away from this point. Of course, this is not to say these levels don't get surpassed. Since we have Facebook stock data, let's add the support and resistance reference lines to our line plot of the closing price.

Important note

Going over how support and resistance are calculated is beyond the scope of this chapter, but *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*, will include some code for calculating these using pivot points. Also, be sure to check out the *Further reading* section for a more in-depth introduction to support and resistance.

Our two horizontal reference lines will be at the support of \$124.46 and the resistance of \$138.53. Both these numbers were derived using the `stock_analysis` package, which we will build in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*. We simply need to create an instance of the `StockAnalyzer` class to calculate these metrics:

```
>>> from stock_analysis import StockAnalyzer

>>> fb_analyzer = StockAnalyzer(fb)
>>> support, resistance = (
...     getattr(fb_analyzer, stat)(level=3)
...     for stat in ['support', 'resistance']
... )
>>> support, resistance
(124.45666666666667, 138.52666666666667)
```

We will use the `plt.axhline()` function for this task, but note that this will also work on the `Axes` object. Remember that the text we provide to the `label` arguments will be populated in the legend:

```
>>> fb.close['2018-12'] \
...     .plot(title='FB Closing Price December 2018')
>>> plt.axhline(
...     y=resistance, color='r', linestyle='--',
...     label=f'resistance (${resistance:.2f})'
... )
>>> plt.axhline(
...     y=support, color='g', linestyle='--',
...     label=f'support (${support:.2f})'
... )
>>> plt.ylabel('price ($)')
>>> plt.legend()
```

We should already be familiar with the f-string format from earlier chapters, but notice the additional text after the variable name here (`: .2f`). The support and resistance are stored as floats in the `support` and `resistance` variables, respectively. The colon (`:`) precedes the **format specifier** (commonly written as `format_spec`), which tells Python how to format that variable; in this case, we are formatting it as a decimal (`f`) with a comma as the thousands separator (`,`) and two digits of precision after the decimal (`.2`). This will also work with the `format()` method, in which case it would look like `'{:,.2f}'.format(resistance)`. This formatting makes for an informative legend in our plot:

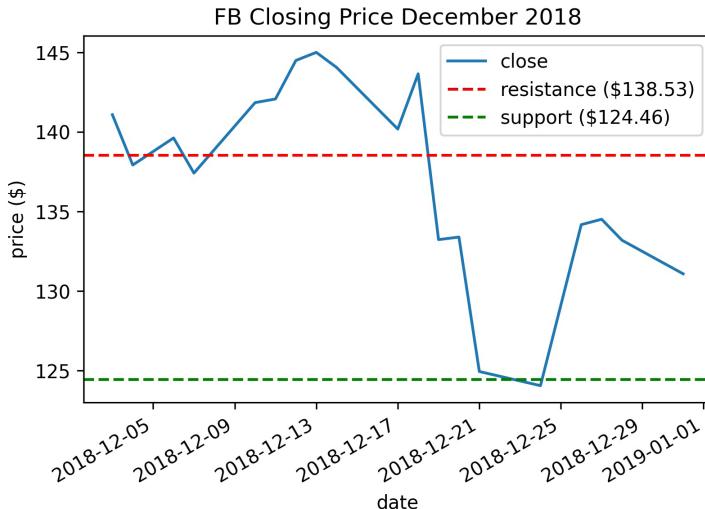


Figure 6.29 – Creating horizontal reference lines with matplotlib

Important note

Those with personal investment accounts will likely find some literature there on support and resistance when looking to place limit orders or stop losses based on the stock hitting a certain price point since these can help inform the feasibility of the target price. In addition, these reference lines may be used by traders to analyze the stock's momentum and decide whether it is time to buy/sell the stock.

Turning back to the earthquake data, let's use `plt.axvline()` to draw vertical reference lines for the number of standard deviations from the mean on the distribution of earthquake magnitudes in Indonesia. The `std_from_mean_kde()` function located in the `viz.py` module in the GitHub repository uses `itertools` to easily make the combinations of the colors and values we need to plot:

```
import itertools

def std_from_mean_kde(data):
    """
    Plot the KDE along with vertical reference lines
    for each standard deviation from the mean.

    Parameters:
        - data: `pandas.Series` with numeric data
    """
    # ... (rest of the function code)
```

```
    Returns:
        Matplotlib `Axes` object.
    """
mean_mag, std_mean = data.mean(), data.std()

    ax = data.plot(kind='kde')
    ax.axvline(mean_mag, color='b', alpha=0.2, label='mean')

    colors = ['green', 'orange', 'red']
    multipliers = [1, 2, 3]
    signs = ['-', '+']
    linestyles = [':', '-.', '--']

    for sign, (color, multiplier, style) in itertools.product(
        signs, zip(colors, multipliers, linestyles)
    ):
        adjustment = multiplier * std_mean
        if sign == '-':
            value = mean_mag - adjustment
            label = '{} {}{}{}{}'.format(
                r'$\mu$', r'$\pm$', multiplier, r'$\sigma$'
            )
        else:
            value = mean_mag + adjustment
            label = None # label each color only once

        ax.axvline(
            value, color=color, linestyle=style,
            label=label, alpha=0.5
        )

    ax.legend()
    return ax
```

The `product()` function from `itertools` will give us all combinations of items from any number of iterables. Here, we have zipped the colors, multipliers, and line styles since we always want a green dotted line for a multiplier of 1; an orange dot-dashed line for a multiplier of 2; and a red dashed line for a multiplier of 3. When `product()` uses these tuples, we get positive- and negative-signed combinations for everything. To keep our legend from getting too crowded, we only label each color once using the \pm sign. Since we have combinations between a string and a tuple at each iteration, we unpack the tuple in our `for` statement for easier use.

Tip

We can use LaTeX math symbols (<https://www.latex-project.org/>) to label our plots if we follow a certain pattern. First, we must mark the string as `raw` by preceding it with the `r` character. Then, we must surround the LaTeX with \$ symbols. For example, we used `r'μ'` for the Greek letter μ in the preceding code.

Let's use the `std_from_mean_kde()` function to see which parts of the estimated distribution of earthquake magnitudes in Indonesia are within one, two, or three standard deviations from the mean:

```
>>> from viz import std_from_mean_kde

>>> ax = std_from_mean_kde(
...     quakes.query(
...         'magType == "mb" and parsed_place == "Indonesia"'
...     ).mag
... )
>>> ax.set_title('mb magnitude distribution in Indonesia')
>>> ax.set_xlabel('mb earthquake magnitude')
```

Notice the KDE is right-skewed—it has a longer tail on the right side, and the mean is to the right of the mode:

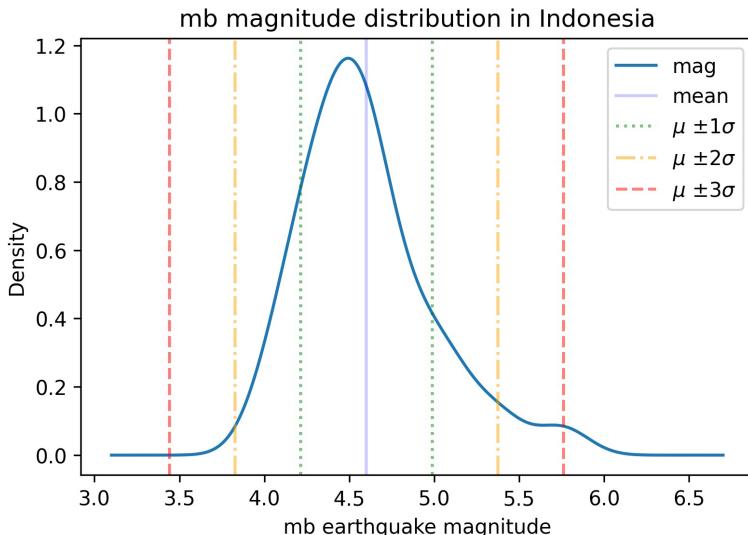


Figure 6.30 – Including vertical reference lines

Tip

To make a straight line of arbitrary slope, simply pass the endpoints of the line as two `x` values and two `y` values (for example, `[0, 2]` and `[2, 0]`) to `plt.plot()` using the same `Axes` object. For lines that aren't straight, `np.linspace()` can be used to create a range of evenly-spaced points on `[start, stop]`, which can be used for the `x` values and to calculate the `y` values. As a reminder, when specifying a range, square brackets mean inclusive of both endpoints and round brackets are exclusive, so `[0, 1)` goes from 0 to as close to 1 as possible without being 1. We see these when using `pd.cut()` and `pd.qcut()` if we don't name the buckets.

Shading regions

In some cases, the reference line itself isn't so interesting, but the area between two of them is; for this purpose, we have `axvspan()` and `axhspan()`. Let's revisit the support and resistance of Facebook stock's closing price. We can use `axhspan()` to shade the area that falls between the two:

```
>>> ax = fb.close.plot(title='FB Closing Price')
>>> ax.axhspan(support, resistance, alpha=0.2)
>>> plt.ylabel('Price ($)')
```

Note that the color of the shaded region is determined by the `facecolor` argument. For this example, we accepted the default:

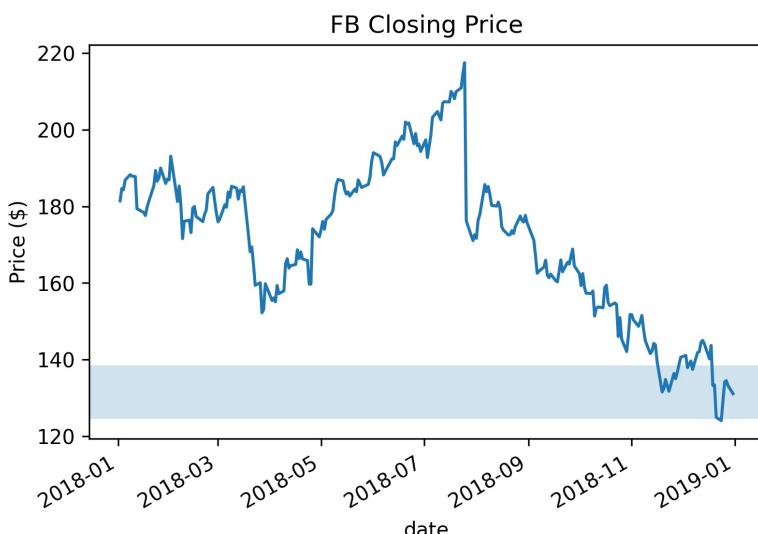


Figure 6.31 – Adding a horizontal shaded region

When we are interested in shading the area between two curves, we can use the `plt.fill_between()` and `plt.fill_betweenx()` functions. The `plt.fill_between()` function accepts one set of x values and two sets of y values; we can use `plt.fill_betweenx()` if we require the opposite. Let's shade the area between Facebook's high price and low price each day of the fourth quarter using `plt.fill_between()`:

```
>>> fb_q4 = fb.loc['2018-Q4']
>>> plt.fill_between(fb_q4.index, fb_q4.high, fb_q4.low)
>>> plt.xticks([
...     '2018-10-01', '2018-11-01', '2018-12-01', '2019-01-01'
... ])
>>> plt.xlabel('date')
>>> plt.ylabel('price ($)')
>>> plt.title(
...     'FB differential between high and low price Q4 2018'
... )
```

This gives us a better idea of the variation in price on a given day; the taller the vertical distance, the higher the fluctuation:

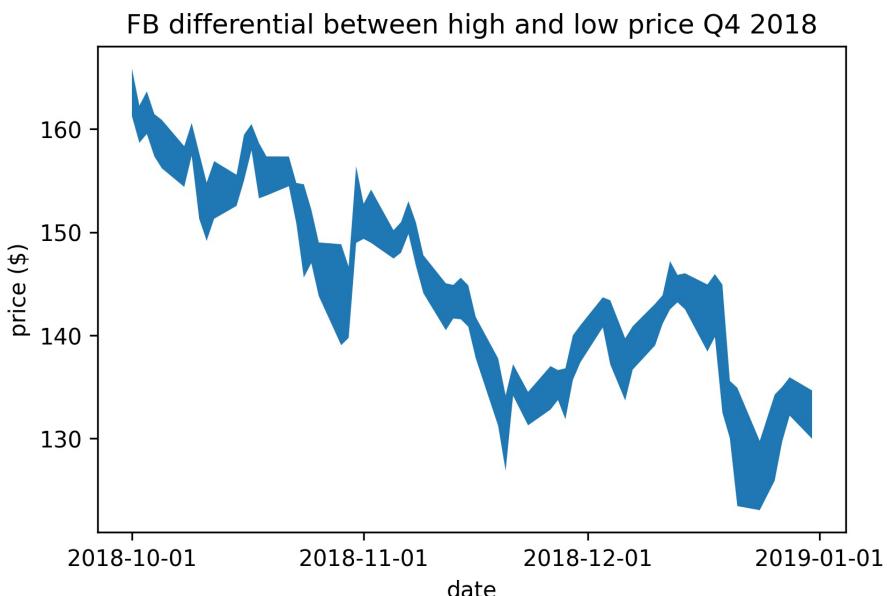


Figure 6.32 – Shading between two curves

By providing a Boolean mask to the `where` argument, we can specify when to fill the area between the curves. Let's fill in only December from the previous example. We will add dashed lines for the high price curve and the low price curve throughout the time period to see what is happening:

```
>>> fb_q4 = fb.loc['2018-Q4']
>>> plt.fill_between(
...     fb_q4.index, fb_q4.high, fb_q4.low,
...     where=fb_q4.index.month == 12,
...     color='khaki', label='December differential'
... )
>>> plt.plot(fb_q4.index, fb_q4.high, '--', label='daily high')
>>> plt.plot(fb_q4.index, fb_q4.low, '--', label='daily low')
>>> plt.xticks([
...     '2018-10-01', '2018-11-01', '2018-12-01', '2019-01-01'
... ])
>>> plt.xlabel('date')
>>> plt.ylabel('price ($)')
>>> plt.legend()
>>> plt.title(
...     'FB differential between high and low price Q4 2018'
... )
```

This results in the following plot:

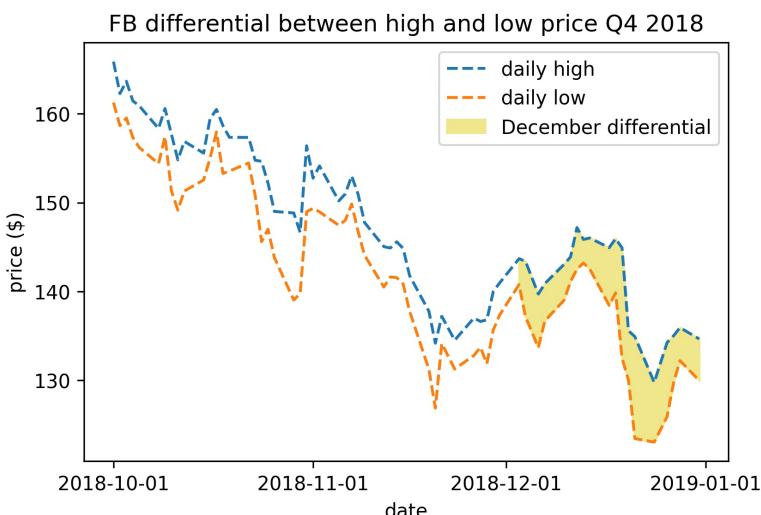


Figure 6.33 – Selectively shading between two curves

With reference lines and shaded regions, we are able to draw attention to certain areas, and can even label them in the legend, but we are limited in the text we can use to explain them. Let's now discuss how to annotate our plot for additional context.

Annotations

We will often find the need to annotate specific points in our visualizations either to point out events, such as the days on which Facebook's stock price dropped due to certain news stories breaking, or to label values that are important for comparisons. For example, let's use the `plt.annotate()` function to label the support and resistance:

```
>>> ax = fb.close.plot(
...     title='FB Closing Price 2018',
...     figsize=(15, 3)
... )
>>> ax.set_ylabel('price ($)')
>>> ax.axhspan(support, resistance, alpha=0.2)
>>> plt.annotate(
...     f'support\nn(${support:.2f})',
...     xy=('2018-12-31', support),
...     xytext=('2019-01-21', support),
...     arrowprops={'arrowstyle': '->'}
... )
>>> plt.annotate(
...     f'resistance\nn(${resistance:.2f})',
...     xy=('2018-12-23', resistance)
... )
>>> for spine in ['top', 'right']:
...     ax.spines[spine].set_visible(False)
```

Notice the annotations are different; when we annotated the resistance, we only provided the text for the annotation and the coordinates of the point being annotated with the `xy` argument. However, when we annotated the support, we also provided values for the `xytext` and `arrowprops` arguments; this allowed us to put the text somewhere other than where the value occurred and add an arrow indicating where it occurred. By doing so, we avoid obscuring the last few days of data with our label:

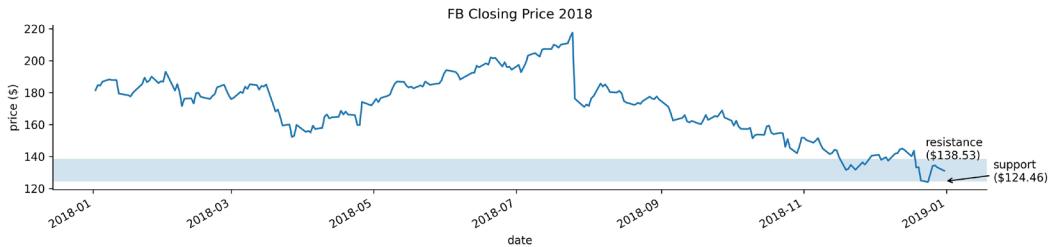


Figure 6.34 – Including annotations

The `arrowprops` argument gives us quite a bit of customization over the type of arrow we want, although it might be difficult to get it perfect. As an example, let's annotate the big decline in the price of Facebook in July with the percentage drop:

```
>>> close_price = fb.loc['2018-07-25', 'close']
>>> open_price = fb.loc['2018-07-26', 'open']
>>> pct_drop = (open_price - close_price) / close_price
>>> fb.close.plot(title='FB Closing Price 2018', alpha=0.5)
>>> plt.annotate(
...     f'{pct_drop:.2%}', va='center',
...     xy=('2018-07-27', (open_price + close_price) / 2),
...     xytext=('2018-08-20', (open_price + close_price) / 2),
...     arrowprops=dict(arrowstyle='->', widthB=4.0, lengthB=0.2)
... )
>>> plt.ylabel('price ($)')
```

Notice that we were able to format the `pct_drop` variable as a percentage with two digits of precision by using `.2%` in the format specifier of the f-string. In addition, by specifying `va='center'`, we tell `matplotlib` to vertically center our annotation in the middle of the arrow:

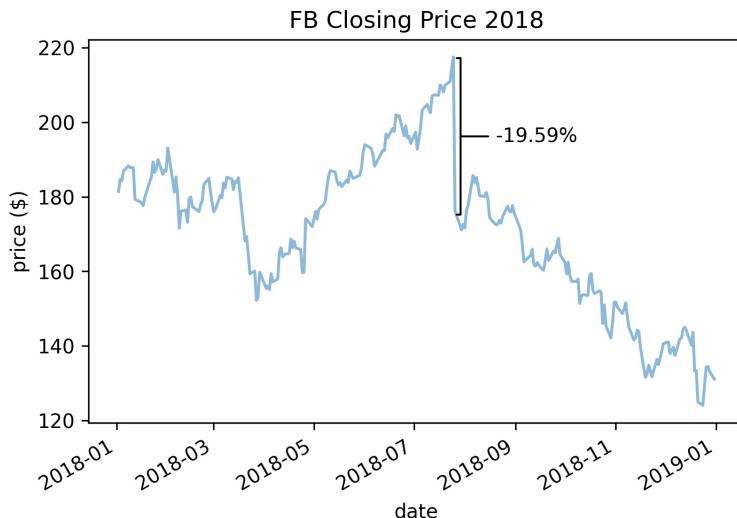


Figure 6.35 – Customizing the annotation's arrow

Matplotlib provides a lot of flexibility to customize these annotations—we can pass any option that the `Text` class in `matplotlib` supports (https://matplotlib.org/api/text_api.html#matplotlib.text.Text). To change colors, simply pass the desired color in the `color` argument. We can also control font size, weight, family, and style through the `fontsize`, `fontweight`, `fontfamily`, and `fontstyle` arguments, respectively.

Colors

For the sake of consistency, the visualizations we produce should stick to a color scheme. Companies and academic institutions alike often have custom color palettes for presentations. We can easily adopt the same color palette in our visualizations too.

So far, we have either been providing colors to the `color` argument with their single character names, such as '`b`' for blue and '`k`' for black, or their names ('`blue`' or '`black`'). We have also seen that `matplotlib` has many colors that can be specified by name; the full list can be found in the documentation at https://matplotlib.org/examples/color/named_colors.html.

Important note

Remember that if we are providing a color with the `style` argument, we are limited to the colors that have a single-character abbreviation.

In addition, we can provide a hex code for the color we want; those who have worked with HTML or CSS in the past will no doubt be familiar with these as a way to specify the exact color (regardless of what different places call it). For those unfamiliar with a hex color code, it specifies the amount of red, green, and blue used to make the color in question in the #RRGGBB format. Black is #000000 and white is #FFFFFF (case-insensitive). This may be confusing because F is most definitely not a number; however, these are hexadecimal numbers (base 16, not the base 10 we traditionally use), where 0–9 still represents 0–9, but A–F represents 10–15.

Matplotlib accepts hex codes as a string to the `color` argument. To illustrate this, let's plot Facebook's opening price in #8000FF:

```
>>> fb.plot(  
...     y='open',  
...     figsize=(5, 3),  
...     color='#8000FF',  
...     legend=False,  
...     title='Evolution of FB Opening Price in 2018'  
... )  
>>> plt.ylabel('price ($)')
```

This results in a purple line plot:

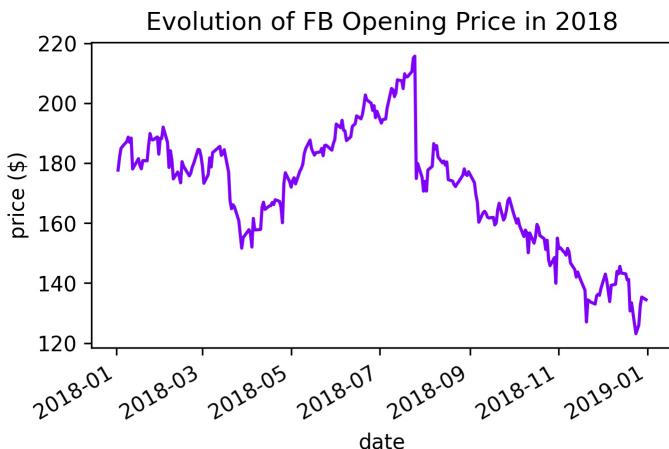


Figure 6.36 – Changing line color

Alternatively, we may be given the values in RGB or **red, green, blue, alpha (RGBA)** values, in which case we can pass them to the `color` argument as a tuple. If we don't provide the alpha, it will default to 1 for opaque. One thing to note here is that, while we will find these numbers presented in the range [0, 255], `matplotlib` requires them to be in the range [0, 1], so we must divide each by 255. The following code is equivalent to the preceding example, except we use the RGB tuple instead of the hex code:

```
fb.plot(
    y='open',
    figsize=(5, 3),
    color=(128 / 255, 0, 1),
    legend=False,
    title='Evolution of FB Opening Price in 2018'
)
plt.ylabel('price ($)')
```

In the previous chapter, we saw several examples in which we needed many different colors for the varying data we were plotting, but where do these colors come from? Well, `matplotlib` has numerous colormaps that are used for this purpose.

Colormaps

Rather than having to specify all the colors we want to use upfront, `matplotlib` can take a colormap and cycle through the colors there. When we discussed heatmaps in the previous chapter, we considered the importance of using the proper class of colormap for the given task. There are three types of colormaps, each with its own purpose, as shown in the following table:

Class	Purpose
Qualitative	No ordering or relationship between colors; just used to distinguish between groups
Sequential	For information with ordering, such as temperature
Diverging	There is a middle value between two extremes that has meaning; for example, correlation coefficients are bounded in the range [-1, 1], and 0 has meaning (no correlation)

Figure 6.37 – Types of colormaps

Tip

Browse colors by name, hex, and RGB values at <https://www.colorhex.com/>, and find the full color spectrum for the colormaps at https://matplotlib.org/gallery/color/colormap_reference.html.

In Python, we can obtain a list of all the available colormaps by running the following:

```
>>> from matplotlib import cm
>>> cm.datad.keys()
dict_keys(['Blues', 'BrBG', 'BuGn', 'BuPu', 'CMRmap', 'GnBu',
          'Greens', 'Greys', 'OrRd', 'Oranges', 'PRGn',
          'PiYG', 'PuBu', 'PuBuGn', 'PuOr', 'PuRd', 'Purples',
          'RdBu', 'RdGy', 'RdPu', 'RdYlBu', 'RdYlGn',
          'Reds', ..., 'Blues_r', 'BrBG_r', 'BuGn_r', ...])
```

Notice that some of the colormaps are present twice where one is in the reverse order, signified by the `_r` suffix on the name. This is very helpful since we don't have to invert our data to map the values to the colors we want. Pandas accepts these colormaps as strings or matplotlib colormaps with the `colormap` argument of the `plot()` method, meaning we can pass in `'coolwarm_r'`, `cm.get_cmap('coolwarm_r')`, or `cm.coolwarm_r` and get the same result.

Let's use the `coolwarm_r` colormap to show how Facebook stock's closing price oscillates between the 20-day rolling minimum and maximum prices:

```
>>> ax = fb.assign(
...     rolling_min=lambda x: x.low.rolling(20).min(),
...     rolling_max=lambda x: x.high.rolling(20).max()
... ).plot(
...     y=['rolling_max', 'rolling_min'],
...     colormap='coolwarm_r',
...     label=['20D rolling max', '20D rolling min'],
...     style=[':', '--'],
...     figsize=(12, 3),
...     title='FB closing price in 2018 oscillating between '
...           '20-day rolling minimum and maximum price'
... )
```

```
>>> ax.plot(
...     fb.close, 'purple', alpha=0.25, label='closing price'
... )
>>> plt.legend()
>>> plt.ylabel('price ($)')
```

Notice how easy it was to get red to represent hot performance (rolling maximum) and blue for cold (rolling minimum), by using the reversed colormap, rather than trying to make sure pandas plotted the rolling minimum first:

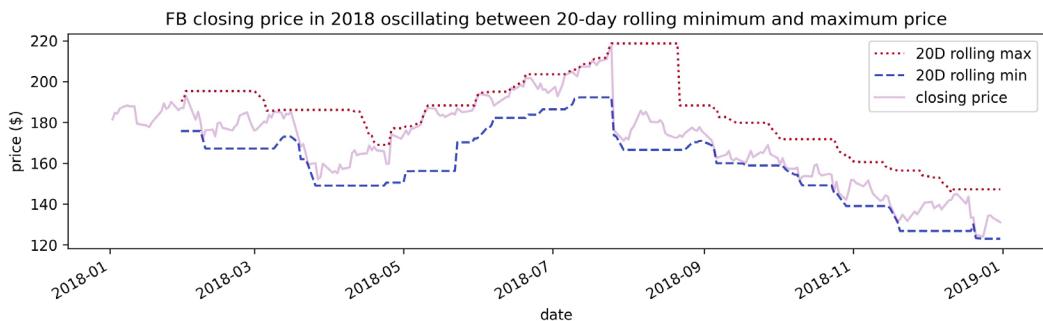


Figure 6.38 – Working with colormaps

The `colormap` object is a callable, meaning we can pass it values in the range [0, 1] and it will tell us the RGBA value for that point on the colormap, which we can use for the `color` argument. This gives us more fine-tuned control over the colors that we use from the colormap. We can use this technique to control how we spread the colormap across our data. For example, we can ask for the midpoint of the `ocean` colormap to use with the `color` argument:

```
>>> cm.get_cmap('ocean')(.5)
(0.0, 0.2529411764705882, 0.5019607843137255, 1.0)
```

Tip

There's an example of using a colormap as a callable in the `covid19_cases_map.ipynb` notebook, where COVID-19 case counts are mapped to colors, with darker colors indicating more cases.

Despite the wealth of colormaps available, we may find the need to create our own. Perhaps we have a color palette we like to work with or have some requirement that we use a specific color scheme. We can make our own colormaps with `matplotlib`. Let's make a blended colormap that goes from purple (#800080) to yellow (#FFFF00) with orange (#FFA500) in the center. All the functions we need for this are in `color_utils.py`. We can import the functions like this if we are running Python from the same directory as the file:

```
>>> import color_utils
```

First, we need to translate these hex colors to their RGB equivalents, which is what the `hex_to_rgb_color_list()` function will do. Note that this function can also handle the shorthand hex codes of three digits when the RGB values use the same hexadecimal digit for both of the digits (for example, #F1D is the shorthand equivalent of #FF11DD):

```
import re

def hex_to_rgb_color_list(colors):
    """
    Take color or list of hex code colors and convert them
    to RGB colors in the range [0,1].

    Parameters:
        - colors: Color or list of color strings as hex codes

    Returns:
        The color or list of colors in RGB representation.
    """
    if isinstance(colors, str):
        colors = [colors]

    for i, color in enumerate(
        [color.replace('#', '') for color in colors]
    ):
        hex_length = len(color)

        if hex_length not in [3, 6]:
            raise ValueError(
                'Colors must be of the form #FFFFFF or #FFF'
            )
        regex = '.' * (hex_length // 3)
```

```

    colors[i] = [
        int(val * (6 // hex_length), 16) / 255
        for val in re.findall(regex, color)
    ]
return colors[0] if len(colors) == 1 else colors

```

Tip

Take a look at the `enumerate()` function; this lets us grab the index and the value at that index when we iterate, rather than looking up the value in the loop. Also, notice how easy it is for Python to convert base 10 numbers to hexadecimal numbers with the `int()` function by specifying the base. (Remember that `//` is integer division—we have to do this since `int()` expects an integer and not a float.)

The next function we need is one to take those RGB colors and create the values for the colormap. This function will need to do the following:

1. Create a 4D NumPy array with 256 slots for color definitions. Note that we don't want to change the transparency, so we will leave the fourth dimension (alpha) alone.
2. For each dimension (red, green, and blue), use the `np.linspace()` function to create even transitions between the target colors (that is, transition from the red component of color 1 to the red component of color 2, then to the red component of color 3, and so on, before repeating this process with the green components and finally the blue components).
3. Return a `ListedColormap` object that we can use when plotting.

This is what the `blended_cmap()` function does:

```

from matplotlib.colors import ListedColormap
import numpy as np

def blended_cmap(rgb_color_list):
    """
    Create a colormap blending from one color to the other.

    Parameters:
    - rgb_color_list: List of colors represented as
        [R, G, B] values in the range [0, 1], like
        [[0, 0, 0], [1, 1, 1]], for black and white.
    """

```

```
Returns:
    A matplotlib `ListedColormap` object
"""

if not isinstance(rgb_color_list, list):
    raise ValueError('Colors must be passed as a list.')
elif len(rgb_color_list) < 2:
    raise ValueError('Must specify at least 2 colors.')
elif (
    not isinstance(rgb_color_list[0], list)
    or not isinstance(rgb_color_list[1], list)
) or (
    (len(rgb_color_list[0]) != 3
     or len(rgb_color_list[1]) != 3)
):
    raise ValueError(
        'Each color should be a list of size 3.'
)

N, entries = 256, 4 # red, green, blue, alpha
rgbas = np.ones((N, entries))

segment_count = len(rgb_color_list) - 1
segment_size = N // segment_count
remainder = N % segment_count # need to add this back later

for i in range(entries - 1): # we don't alter alphas
    updates = []
    for seg in range(1, segment_count + 1):
        # handle uneven splits due to remainder
        offset = 0 if not remainder or seg > 1 \
                  else remainder

        updates.append(np.linspace(
            start=rgb_color_list[seg - 1][i],
            stop=rgb_color_list[seg][i],
            num=segment_size + offset
        ))
    rgbas[:,i] = np.concatenate(updates)
return ListedColormap(rgbas)
```

We can use the `draw_cmap()` function to draw a colorbar, which allows us to visualize our colormap:

```
import matplotlib.pyplot as plt

def draw_cmap(cmap, values=np.array([[0, 1]]), **kwargs):
    """
    Draw a colorbar for visualizing a colormap.

    Parameters:
    - cmap: A matplotlib colormap
    - values: Values to use for the colormap
    - kwargs: Keyword arguments to pass to `plt.colorbar()`

    Returns:
    A matplotlib `Colorbar` object, which you can save
    with: `plt.savefig(<file_name>, bbox_inches='tight')`
    """
    img = plt.imshow(values, cmap=cmap)
    cbar = plt.colorbar(**kwargs)
    img.axes.remove()
    return cbar
```

This function makes it easy for us to add a colorbar with a custom colormap for any visualization we choose; the `covid19_cases_map.ipynb` notebook has an example using COVID-19 cases plotted on a world map. For now, let's use these functions to create and visualize our colormap. We will be using them by importing the module (which we did earlier):

```
>>> my_colors = ['#800080', '#FFA500', '#FFFF00']
>>> rgbs = color_utils.hex_to_rgb_color_list(my_colors)
>>> my_cmap = color_utils.blended_cmap(rgbs)
>>> color_utils.draw_cmap(my_cmap, orientation='horizontal')
```

This results in the following colorbar showing our colormap:



Figure 6.39 – Custom blended colormap

Tip

Seaborn also provides additional color palettes, along with handy utilities for picking colormaps and making custom ones for use with `matplotlib` interactively in a Jupyter Notebook. Check out the *Choosing color palettes* tutorial (https://seaborn.pydata.org/tutorial/color_palettes.html) for more information. The notebook also contains a short example.

As we have seen in the colorbar we created, these colormaps have the ability to show different gradients of the colors to capture values on a continuum. If we merely want each line in our line plot to be a different color, we most likely want to cycle between different colors. For that, we can use `itertools.cycle()` with a list of colors; they won't be blended, but we can cycle through them endlessly because it will be an infinite iterator. We used this technique earlier in the chapter to define our own colors for the regression residuals plots:

```
>>> import itertools
>>> colors = itertools.cycle(['#ffffff', '#f0f0f0', '#000000'])
>>> colors
<itertools.cycle at 0x1fe4f300>
>>> next(colors)
'#ffffff'
```

Even simpler would be the case where we have a list of colors somewhere, but rather than putting that in our plotting code and storing another copy in memory, we can write a simple **generator** that just *yields* from that master list. By using generators, we are being efficient with memory without crowding our plotting code with the color logic. Note that a generator is defined as a function, but instead of using `return`, it uses `yield`. The following snippet shows a mock-up for this scenario, which is similar to the `itertools` solution; however, it is not infinite. This just goes to show that we can find many ways to do something in Python; we have to find the implementation that best meets our needs:

```
from my_plotting_module import master_color_list

def color_generator():
    yield from master_color_list
```

Using `matplotlib`, the alternative would be to instantiate a `ListedColormap` object with the color list and define a large value for `N` so that it repeats for long enough (if we don't provide it, it will only go through the colors once):

```
>>> from matplotlib.colors import ListedColormap
>>> red_black = ListedColormap(['red', 'black'], N=2000)
>>> [red_black(i) for i in range(3)]
[(1.0, 0.0, 0.0, 1.0),
 (0.0, 0.0, 0.0, 1.0),
 (1.0, 0.0, 0.0, 1.0)]
```

Note that we can also use `cycler` from the `matplotlib` team, which adds additional flexibility by allowing us to define combinations of colors, line styles, markers, line widths, and more to cycle through. The API details the available functionality and can be found at <https://matplotlib.org/cycler/>. We will see an example of this in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*.

Conditional coloring

Colormaps make it easy to vary color according to the values in our data, but what happens if we only want to use a specific color when certain conditions are met? In that case, we need to build a function around color selection.

We can write a generator to determine plot color based on our data and only calculate it when it is asked for. Let's say we wanted to assign colors to years from 1992 to 200018 (no, that's not a typo) based on whether they are leap years, and distinguish why they aren't leap years (for example, we want a special color for years divisible by 100 but not 400, which aren't leap years). We certainly don't want to keep a list this size in memory, so we create a generator to calculate the color on demand:

```
def color_generator():
    for year in range(1992, 200019): # integers [1992, 200019)
        if year % 100 == 0 and year % 400 != 0:
            # special case (divisible by 100 but not 400)
            color = '#f0f0f0'
        elif year % 4 == 0:
            # leap year (divisible by 4)
            color = '#000000'
        else:
            color = '#ffffff'
    yield color
```

Important note

The **modulo operator** (%) returns the remainder of a division operation. For example, $4 \% 2$ equals 0 because 4 is divisible by 2. However, since 4 is not divisible by 3, $4 \% 3$ is non-zero; it is 1 because we can fit 3 into 4 once and will have 1 left over ($4 - 3$). The modulo operator can be used to check the divisibility of one number by another and is often used to check whether a number is odd or even. Here, we are using it to see whether the conditions for being a leap year (which depend on divisibility) are met.

Since we defined `year_colors` as a generator, Python will remember where we are in this function and resume when `next()` is called:

```
>>> year_colors = color_generator()
>>> year_colors
<generator object color_generator at 0x7bef148dfed0>
>>> next(year_colors)
'#000000'
```

Simpler generators can be written with **generator expressions**. For example, if we don't care about the special case anymore, we can use the following:

```
>>> year_colors = (
...     '#ffffff'
...     if (not year % 100 and year % 400) or year % 4
...     else '#000000' for year in range(1992, 200019)
... )
>>> year_colors
<generator object <genexpr> at 0x7bef14415138>
>>> next(year_colors)
'#000000'
```

Those not coming from Python might find it strange that our Boolean conditions in the previous code snippet are actually numbers (`year % 400` results in an integer). This is taking advantage of Python's *truthy/falsey* values; values that have zero value (such as the number 0) or are empty (such as [] or '') are *falsey*. Therefore, while in the first generator, we wrote `year % 400 != 0` to show exactly what was going on, the more **Pythonic** way is `year % 400`, since if there is no remainder (evaluates to 0), the statement will be evaluated as `False`, and vice versa. Obviously, we will have times where we must choose between readability and being Pythonic, but it's good to be aware of how to write Pythonic code, as it will often be more efficient.

Tip

Run `import this` in Python to see the **Zen of Python**, which gives some ideas of what it means to be Pythonic.

Now that we have some exposure to working with colors in `matplotlib`, let's consider another way we can make our data stand out. Depending on what we are plotting or how our visualization will be used (for example, in black and white), it might make sense to use textures along with, or instead of, colors.

Textures

In addition to customizing the colors used in our visualizations, `matplotlib` also makes it possible to include textures with a variety of plotting functions. This is achieved via the `hatch` argument, which `pandas` will pass down for us. Let's create a bar plot of weekly volume traded in Facebook stock during Q4 2018 with textured bars:

```
>>> weekly_volume_traded = fb.loc['2018-Q4'] \
...     .groupby(pd.Grouper(freq='W')).volume.sum()

>>> weekly_volume_traded.index = \
...     weekly_volume_traded.index.strftime('W %W')

>>> ax = weekly_volume_traded.plot(
...     kind='bar',
...     hatch='*',
...     color='lightgray',
...     title='Volume traded per week in Q4 2018'
... )
>>> ax.set(
...     xlabel='week number',
...     ylabel='volume traded'
... )
```

With `hatch='*' , our bars are filled with stars. Notice that we also set the color for each of the bars, so there is a lot of flexibility here:`

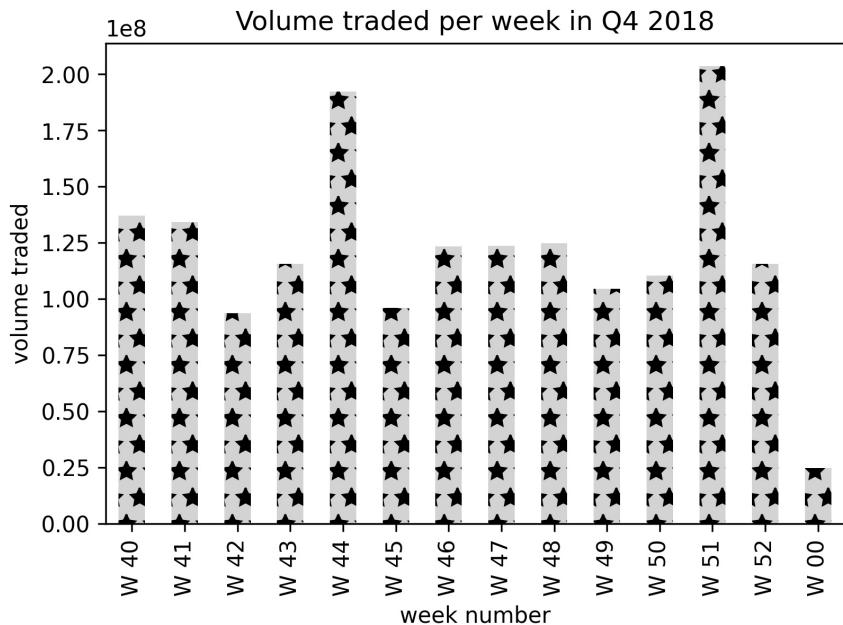


Figure 6.40 – Using textured bars

Textures can also be combined to make new patterns and repeated to intensify the effect. Let's revisit the `plt.fill_between()` example where we colored the December section only (*Figure 6.33*). This time we will use textures to distinguish between each month, rather than only shading December; we will fill October with rings, November with slashes, and December with small dots:

```
>>> import calendar

>>> fb_q4 = fb.loc['2018-Q4']
>>> for texture, month in zip(
...     ['oo', '/\\/\\"\\', '...', [10, 11, 12]
... ) :
...     plt.fill_between(
...         fb_q4.index, fb_q4.high, fb_q4.low,
...         hatch=texture, facecolor='white',
...         where=fb_q4.index.month == month,
...         label=f'{calendar.month_name[month]} differential'
...     )
```

```

>>> plt.plot(fb_q4.index, fb_q4.high, '--', label='daily high')
>>> plt.plot(fb_q4.index, fb_q4.low, '--', label='daily low')
>>> plt.xticks([
...     '2018-10-01', '2018-11-01', '2018-12-01', '2019-01-01'
... ])
>>> plt.xlabel('date')
>>> plt.ylabel('price ($)')
>>> plt.title(
...     'FB differential between high and low price Q4 2018'
... )
>>> plt.legend()

```

Using `hatch='o'` would yield thin rings, so we used '`oo`' to get thicker rings for October. For November, we wanted a crisscross pattern, so we combined two forward slashes and two backslashes (we actually have four backslashes because they must be escaped). To achieve the small dots for December, we used three periods—the more we add, the denser the texture becomes:

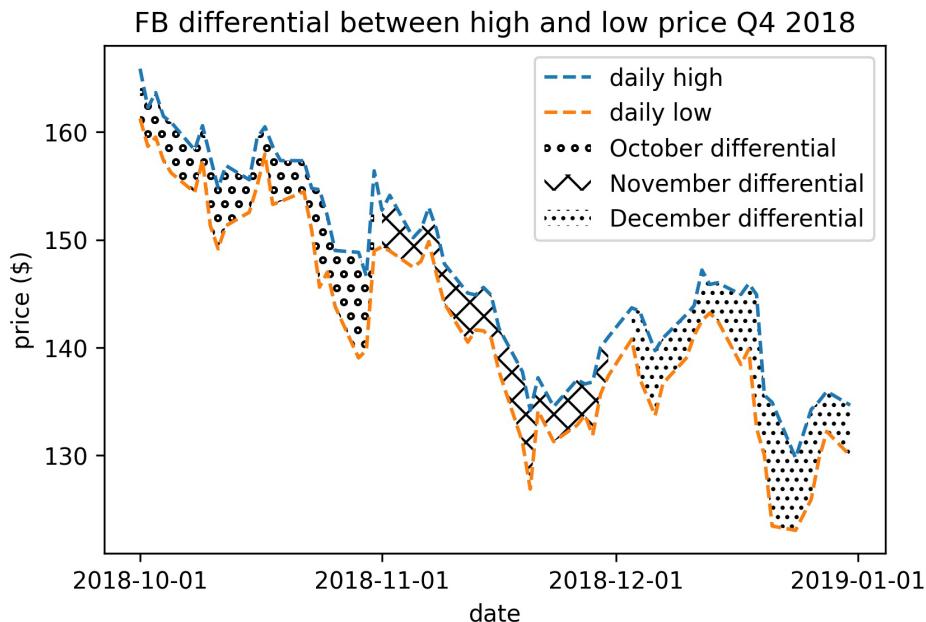


Figure 6.41 – Combining textures

This concludes our discussion of plot customizations. By no means was this meant to be complete, so be sure to explore the `matplotlib` API for more.

Summary

Whew, that was a lot! We learned how to create impressive and customized visualizations using `matplotlib`, `pandas`, and `seaborn`. We discussed how we can use `seaborn` for additional plotting types and cleaner versions of some familiar ones. Now we can easily make our own colormaps, annotate our plots, add reference lines and shaded regions, finesse the axes/legends/titles, and control most aspects of how our visualizations will appear. We also got a taste of working with `itertools` and creating our own generators.

Take some time to practice what we've discussed with the end-of-chapter exercises. In the next chapter, we will apply all that we have learned to finance, as we build our own Python package and compare bitcoin to the stock market.

Exercises

Create the following visualizations using what we have learned so far in this book and the data from this chapter. Be sure to add titles, axis labels, and legends (where appropriate) to the plots:

1. Using `seaborn`, create a heatmap to visualize the correlation coefficients between earthquake magnitude and whether there was a tsunami for earthquakes measured with the `mb` magnitude type.
2. Create a box plot of Facebook volume traded and closing prices, and draw reference lines for the bounds of a Tukey fence with a multiplier of 1.5. The bounds will be at $Q_1 - 1.5 \times IQR$ and $Q_3 + 1.5 \times IQR$. Be sure to use the `quantile()` method on the data to make this easier. (Pick whichever orientation you prefer for the plot, but make sure to use subplots.)
3. Plot the evolution of cumulative COVID-19 cases worldwide, and add a dashed vertical line on the date that it surpassed 1 million. Be sure to format the tick labels on the y -axis accordingly.
4. Use `axvspan()` to shade a rectangle from '`2018-07-25`' to '`2018-07-31`', which marks the large decline in Facebook price on a line plot of the closing price.
5. Using the Facebook stock price data, annotate the following three events on a line plot of the closing price:
 - a) **Disappointing user growth announced after close** on July 25, 2018
 - b) **Cambridge Analytica story breaks** on March 19, 2018 (when it affected the market)
 - c) **FTC launches investigation** on March 20, 2018

6. Modify the `reg_resid_plots()` function to use a `matplotlib` colormap instead of cycling between two colors. Remember, for this use case, we should pick a qualitative colormap or make our own.

Further reading

Check out the following resources for more information on the topics covered in this chapter:

- *Choosing Colormaps*: <https://matplotlib.org/tutorials/colors/colormaps.html>
- *Controlling figure aesthetics (seaborn)*: <https://seaborn.pydata.org/tutorial/aesthetics.html>
- *Customizing Matplotlib with style sheets and rcParams*: <https://matplotlib.org/tutorials/introductory/customizing.html>
- *Format String Syntax*: <https://docs.python.org/3/library/string.html#format-string-syntax>
- *Generator Expressions (PEP 289)*: <https://www.python.org/dev/peps/pep-0289/>
- *Information Dashboard Design: Displaying Data for At-a-Glance Monitoring, Second Edition, by Stephen Few*: <https://www.amazon.com/Information-Dashboard-Design-At-Glance/dp/1938377001/>
- *Matplotlib Named Colors*: https://matplotlib.org/examples/color/named_colors.html
- *Multiple assignment and tuple unpacking improve Python code readability*: <https://treyhunner.com/2018/03/tuple-unpacking-improves-python-code-readability/>
- *Python: range is not an iterator!*: <https://treyhunner.com/2018/02/python-range-is-not-an-iterator/>
- *Python zip() function*: <https://www.journaldev.com/15891/python-zip-function>
- *Seaborn API reference*: <https://seaborn.pydata.org/api.html>
- *Show Me the Numbers: Designing Tables and Graphs to Enlighten, by Stephen Few*: <https://www.amazon.com/gp/product/0970601972/>

- *Style sheets reference (Matplotlib):* https://matplotlib.org/gallery/style_sheets/style_sheets_reference.html
- *Support and Resistance Basics:* <https://www.investopedia.com/trading/support-and-resistance-basics/>
- *The Iterator Protocol: How "For Loops" Work in Python:* <https://treyhunner.com/2016/12/python-iterator-protocol-how-for-loops-work/>
- *The Visual Display of Quantitative Information, by Edward R. Tufte:* <https://www.amazon.com/Visual-Display-Quantitative-Information/dp/1930824130>
- *Tick formatters:* https://matplotlib.org/gallery/ticks_and_spines/tick-formatters.html
- *What does Pythonic mean?:* <https://stackoverflow.com/questions/25011078/what-does-pythonic-mean>

Section 3: Applications – Real-World Analyses Using Pandas

It's time to see how to bring together everything we have learned so far. In this section, we will take some real-world datasets and run through analyses from start to finish, combining all the concepts covered in the previous chapters and introducing some new material along the way.

This section comprises the following chapters:

- *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*
- *Chapter 8, Rule-Based Anomaly Detection*

7

Financial Analysis – Bitcoin and the Stock Market

It's time to switch gears and work on an application. In this chapter, we will explore a financial application by performing an analysis of bitcoin and the stock market. This chapter builds upon everything we have learned so far—we will extract data from the Internet; perform some exploratory data analysis; create visualizations with pandas, seaborn, and matplotlib; calculate important metrics for analyzing the performance of financial instruments using pandas; and get a taste of building some models. Note that we are not trying to learn financial analysis here, but rather walk through an introduction of how the skills we have learned in this book can be applied to financial analysis.

This chapter is also a departure from the standard workflow in this book. Up until this point, we have been working with Python as more of a functional programming language. However, Python also supports **object-oriented programming (OOP)**. This means we can build classes that will carry out the major tasks we need to perform, which in this chapter are the following: collecting data from the Internet (with the `StockReader` class), visualizing financial assets (with the `Visualizer` classes), calculating financial metrics (with the `StockAnalyzer` class), and modeling financial data (with the `StockModeler` class). Since we will need a lot of code to make the analysis process clean and easy to reproduce, we will build a Python package to house these classes. The code will be reproduced in the text and explained as usual; however, we don't need to type/run it on our own—be sure to read the *Chapter materials* section for this chapter to get set up properly.

This chapter will be challenging and may require a few rereads; however, it will teach best practices, and the skills acquired here will dramatically improve your coding skills, which will quickly pay off. One main takeaway should be that OOP can be very helpful in packaging up analysis tasks. Each class should have a single purpose and be well documented. If we have many classes, we should spread them across separate files and make a package. This makes it very easy for others to install/use them and for us to standardize the way certain tasks are performed across a project. As an example, we shouldn't have each of our collaborators on a project writing their own functions to connect to a database. Standardized, well-documented code will save lots of headaches down the road.

The following topics will be covered in this chapter:

- Building a Python package
- Collecting financial data
- Conducting exploratory data analysis
- Performing technical analysis of financial instruments
- Modeling performance using historical data

Chapter materials

For this chapter, we will be creating our own package for stock analysis. This makes it extremely easy for us to distribute our code and for others to use our code. The final product of this package is on GitHub at https://github.com/stefmolin/stock-analysis/tree/2nd_edition. Python's package manager, pip, is capable of installing packages from GitHub and also building them locally; this leaves us with either of the following choices as to how we want to proceed:

- Install from GitHub if we don't plan on editing the source code for our own use.
- Fork and clone the repository and then install it on our machine in order to modify the code.

If we wish to install from GitHub directly, we don't need to do anything here since this was installed when we set up our environment back in *Chapter 1, Introduction to Data Analysis*; however, for reference, we would do the following to install packages from GitHub:

```
(book_env) $ pip3 install \
git+https://github.com/stefmolin/stock-analysis.git@2nd_edition
```

Tip

The @2nd_edition portion of the URL tells pip to install the version that was tagged 2nd_edition. To install the version of the code on a particular branch instead, replace this with @<branch_name>. For example, if we want the code being developed on a branch called dev, we use @dev. Be sure to check that the branch exists first, of course. We can also use the commit hash in the same fashion to grab a specific commit. More information is available at https://pip.pypa.io/en/latest/reference/pip_install/#git.

To install locally in editable mode—meaning that any changes will automatically be reflected locally without having to reinstall—we use the -e flag. Run the following from the command line in the virtual environment we created in *Chapter 1, Introduction to Data Analysis*, to do so. Note that this will clone the latest version of the package, which may be different from the version in the text (the version with the 2nd_edition tag):

```
(book_env) $ git clone \
git@github.com:stefmolin/stock-analysis.git
(book_env) $ pip3 install -r stock-analysis/requirements.txt
(book_env) $ pip3 install -e stock-analysis
```

Important note

This example uses `git clone` over SSH; if SSH keys are not set up already, clone over HTTPS instead by using a variation of the URL: <https://github.com/stefmolin/stock-analysis.git>. Alternatively, follow the instructions on GitHub for generating SSH keys first. Consult this Stack Overflow post if you're interested in just cloning the version with the 2nd_edition tag: <https://stackoverflow.com/questions/20280726/how-to-git-clone-a-specific-tag>.

We will be using this package throughout this chapter. The directory for this chapter in this book's repository has the `financial_analysis.ipynb` notebook we will use for our actual analysis and can be found at https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_07. The `data/` folder contains backup files in case the data sources have changed since publication or there are any errors when collecting the data with the `StockReader` class; simply read in the CSV files and follow along with the rest of this chapter should this happen. Similarly, the `exercises/` folder contains backup files for the exercises.

Important note

If we change a file in a package installed in editable mode when working with Jupyter Notebooks, we will need to restart our kernel or open a new Python shell and reimport the package. This is because Python will cache it after import. Other options include using `importlib.reload()` or the IPython autoreload extension (<https://ipython.readthedocs.io/en/stable/config/extensions/autoreload.html>).

Building a Python package

Building packages is considered good coding practice since it allows for writing modular code and reuse. **Modular code** is code that is written in many smaller pieces for more pervasive use, without needing to know the underlying implementation details of everything involved in a task. For example, when we use `matplotlib` to plot something, we don't need to know what the code inside the functions we call is doing exactly—it suffices to simply know what the input and output will be to build on top of it.

Package structure

A **module** is a single file of Python code that can be imported; `window_calc.py` from *Chapter 4, Aggregating Pandas DataFrames*, and `viz.py` from *Chapter 6, Plotting with Seaborn and Customization Techniques*, were both modules. A **package** is a collection of modules organized into directories. Packages can also be imported, but when we import a package we have access to certain modules inside, so we don't have to import each one individually. This also allows us to build modules that import from each other without the need to maintain a single very large module.

To turn modules into a package, we follow these steps:

1. Create a directory with the name of the package (`stock_analysis` for this chapter).
2. Place the modules in the aforementioned directory.
3. Add an `__init__.py` file containing any Python code to run upon importing the package (this can be—and often is—empty).
4. Make a `setup.py` file at the same level as the package's top-level directory (`stock_analysis` here), which will give `pip` instructions on how to install the package. See the *Further reading* section for information on creating this.

Once the aforementioned steps are complete, the package can be installed with `pip`. Note that, while our package only contains a single directory, we can build a package with as many subpackages as we desire. These subpackages are created just as if we were creating a package, with the exception that they don't need a `setup.py` file:

1. Create a directory for the subpackage inside the main package directory (or inside some other subpackage).
2. Place the subpackage's modules in this directory.
3. Add the `__init__.py` file, with code that should be run when the subpackage is imported (this can be empty).

The directory hierarchy for a package with a single subpackage would look something like this:

```
repo_folder
| -- <package_name>
|   | -- __init__.py
|   | -- some_module.py
|   `-- <subpackage_name>
|       | -- __init__.py
|       | -- another_module.py
|       `-- last_module.py
`-- setup.py
```

Some other things to be aware of when building a package include the following:

- Writing a **README** file for the repository so that others know what it contains (see <https://www.makeareadme.com/>).
- **Linting** the code in order to conform to coding standards and analyze the code for possible errors (check out the `pylint` package at <https://www.pylint.org/>).
- Adding tests that will make sure changes to the code don't break anything and that the code does what it is meant to do (take a look at the `pytest` package at <https://docs.pytest.org/en/latest/>).

Overview of the stock_analysis package

In this chapter, we will be creating a Python package called `stock_analysis` using the various Python packages we have discussed so far, along with the Python standard library. This package is located in the `stock-analysis` repository (<https://github.com/stefmolin/stock-analysis>), which is arranged like this:

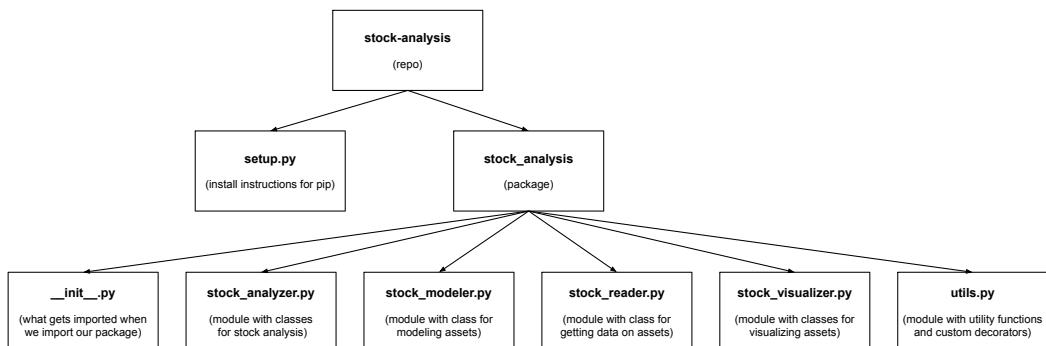


Figure 7.1 – Structure of the stock-analysis repository

The modules in our package will contain custom classes for conducting the technical analysis of an asset. **Classes** should be designed for a single purpose; this makes it easier to build, use, and debug if issues arise. Therefore, we will be building several classes in order to cover the various facets of our financial analysis. We will need a class for each of the following purposes:

Purpose	Class(es)	Module
Collecting the data from various sources	StockReader	stock_reader.py
Visualizing the data	Visualizer , StockVisualizer , AssetGroupVisualizer	stock_visualizer.py
Calculating financial metrics	StockAnalyzer , AssetGroupAnalyzer	stock_analyzer.py
Modeling the data	StockModeler	stock_modeler.py

Figure 7.2 – Main themes and classes for the stock_analysis package

It can be helpful to visualize the interaction between modules in a package and the functionality each class provides. For this purpose, we can build **Unified Modeling Language (UML)** diagrams.

UML diagrams

UML diagrams show information about which attributes and methods classes have and how classes are related to others. We can see in the following diagram that all the modules rely on `utils.py` for utility functions:

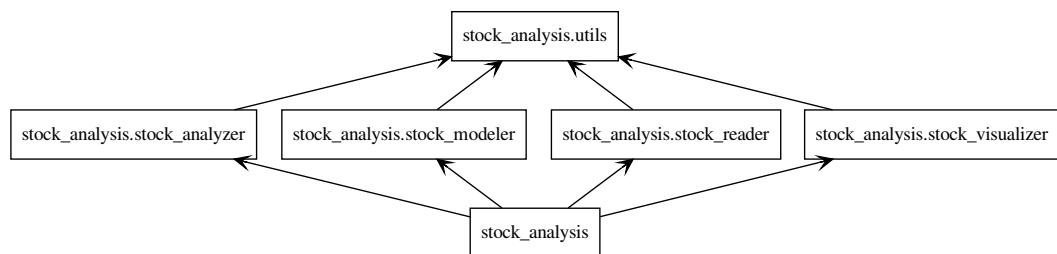


Figure 7.3 – Module dependencies in the stock_analysis package

Tip

The `pylint` package comes with `pyreverse`, which makes UML diagrams. If `graphviz` is installed (<http://www.graphviz.org/download/>), running the following from the command line generates a PNG file for the relationship between modules and a UML diagram for the classes (provided the repository was cloned and `pylint` is installed):

```
pyreverse -o png stock_analysis
```

The UML diagram for the classes in the `stock_analysis` package looks like this:

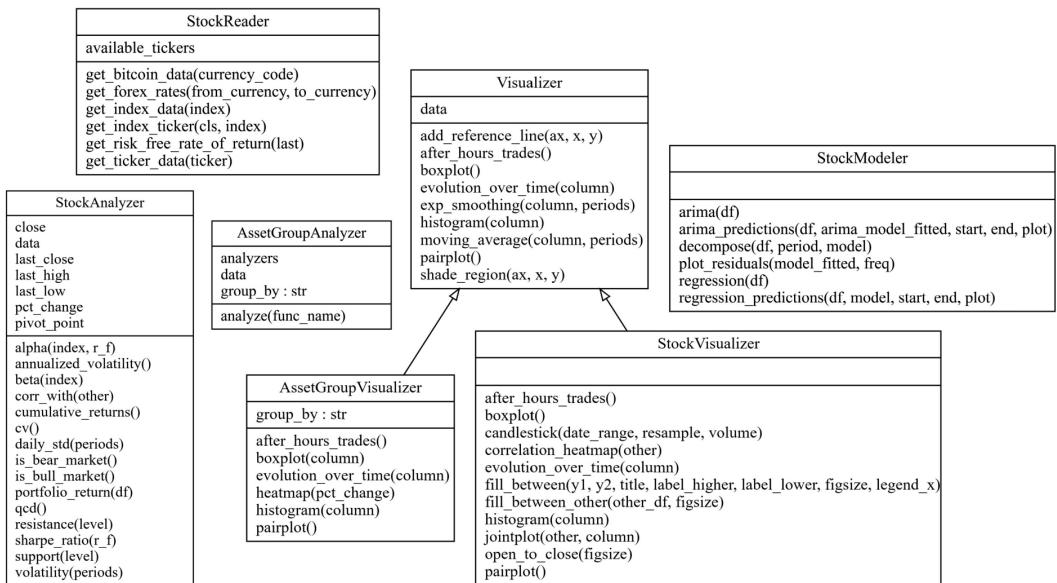


Figure 7.4 – UML diagrams for classes in the `stock_analysis` package

The top section in each box contains the class name; the middle section contains the attributes of that class; while the bottom section contains any methods defined in that class. Notice the arrows pointing from the `AssetGroupVisualizer` and `StockVisualizer` classes to the `Visualizer` class? This means that both are a type of `Visualizer`. The methods shown for the `AssetGroupVisualizer` and `StockVisualizer` classes are defined differently in those classes compared to the `Visualizer` class. We will cover this in more depth in the *Exploratory data analysis* section. Throughout the remaining sections of this chapter, we will be going over each of the classes in the `stock_analysis` package in more detail and using their functionality to perform technical analysis of financial assets.

Collecting financial data

Back in *Chapter 2, Working with Pandas DataFrames*, and *Chapter 3, Data Wrangling with Pandas*, we worked with APIs to gather data; however, there are other ways to collect data from the Internet. We can use **web scraping** to extract data from the HTML page itself, which pandas offers with the `pd.read_html()` function—it returns a dataframe for each of the HTML tables it finds on the page. For economic and financial data, an alternative is the `pandas_datareader` package, which the `StockReader` class in the `stock_analysis` package uses to collect financial data.

Important note

In case anything has changed with the data sources that are used in this chapter or you encounter errors when using the `StockReader` class to collect data, the CSV files in the `data/` folder can be read in as a replacement in order to follow along with the text; for example:

```
pd.read_csv('data/bitcoin.csv', index_col='date',  
            parse_dates=True)
```

The StockReader class

Since we will be collecting data for various assets across the same date range, it makes sense to create a class that hides all of the implementation details and, therefore, avoid lots of copying and pasting (and potential mistakes). For this purpose, we will build the `StockReader` class, which will make it easier to collect data for bitcoin, stocks, and stock market indices. We can simply create an instance of the `StockReader` class by providing the date range we want for our analysis, and then use the methods it provides to get whichever data we please. The following UML diagram provides a high-level overview of the implementation:

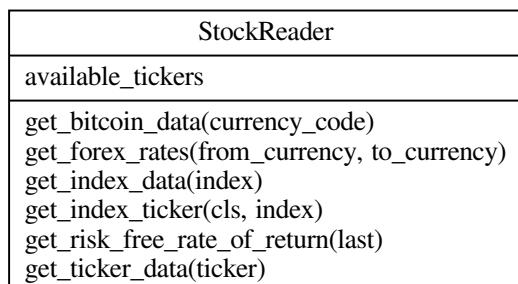


Figure 7.5 – UML diagram for the `StockReader` class

The UML diagram tells us that the `StockReader` class provides an attribute for the available tickers (`available_tickers`) and can perform the following actions:

- Pull bitcoin data in the desired currency with the `get_bitcoin_data()` method.
- Pull daily foreign exchange rates data with the `get_forex_rates()` method.
- Pull data for an index on the stock market (such as the S&P 500) with the `get_index_data()` method.
- Look up the ticker (stock market symbol) for a specific index (for instance, `^GSPC` for the S&P 500 ticker on Yahoo! Finance) with the `get_index_ticker()` method.
- Collect the risk-free rate of return with the `get_risk_free_rate_of_return()` method.
- Pull data for a ticker on the stock market (such as `NFLX` for Netflix) with the `get_ticker_data()` method.

Now that we understand why we need this class and have a high-level overview of its structure, we can proceed to looking at the code. Since there is a lot of code in the `stock_analysis/stock_reader.py` module to review, we will break down the file piece by piece. Note that this may change the indentation level, so please consult the file itself for the full version.

The first line of the module is the **docstring** for the module. If we run `help()` on the module itself, that will appear near the top. This describes the purpose of our module. This is immediately followed by any imports we will need:

```
"""Gather select stock data."""

import datetime as dt
import re

import pandas as pd
import pandas_datareader.data as web

from .utils import label_sanitizer
```

Notice that the import statements are organized in three groups, following **PEP 8** (Python style guidelines available at <https://www.python.org/dev/peps/pep-0008/>), which states that they should be in the following order:

1. Standard library imports (`datetime` and `re`)
2. Third-party libraries (`pandas` and `pandas_datareader`)
3. Relative import from another module in the `stock_analysis` package (`.utils`)

After our imports, we define the `StockReader` class. First, we create a dictionary mapping tickers for indices to a descriptive name in `_index_tickers`. Notice that our class also has a docstring, which defines its purpose. Here, we will only reproduce a few of the tickers available:

```
class StockReader:  
    """Class for reading financial data from websites."""  
  
    _index_tickers = {'S&P 500': '^GSPC', 'Dow Jones': '^DJI',  
                      'NASDAQ': '^IXIC'}
```

When building a class, there are many **special methods** (colloquially referred to as *dunder methods* because their names start and end with double underscores) that we can provide to customize the behavior of the class when it's used with language operators:

- Initialize an object (`__init__()`).
- Make an object comparable for sorting (`__eq__()`, `__lt__()`, `__gt__()`, and more).
- Perform arithmetic on the object (`__add__()`, `__sub__()`, `__mul__()`, and so on).
- Be able to use built-in Python functions such as `len()` on it (`__len__()`).
- Get a string representation of the object for use with the `print()` function (`__repr__()` and `__str__()`).
- Support iteration and indexing (`__getitem__()`, `__iter__()`, and `__next__()`).

Thankfully, we don't have to write all this functionality every time we make a class. In most cases, we just need the `__init__()` method, which is run when we create an object. (More information on special methods can be found at <https://dbader.org/blog/python-dunder-methods> and <https://docs.python.org/3/reference/datamodel.html#special-method-names>.)

Objects of the `StockReader` class hold on to the start and end dates that data will be gathered for, so we put this in the `__init__()` method. We parse the dates that are passed in by the caller to allow for the use of any date separator; for example, we will be able to handle inputs of Python `datetime` objects; strings in the form of '`YYYYMMDD`'; or strings representing dates using any separator that matches the non-digit regular expression (`\D`), such as '`YYYY|MM|DD`' or '`YYYY/MM/DD`'. The separator, if there is one, gets replaced with an empty string so that we can build our datetimes using the '`YYYYMMDD`' format in our method. In addition, we raise a `ValueError` if the caller gives us a start date equal to or after the end date:

```
def __init__(self, start, end=None):
    """
    Create a `StockReader` object for reading across
    a given date range.

    Parameters:
        - start: The first date to include, as a datetime
            object or a string in the format 'YYYYMMDD'.
        - end: The last date to include, as a datetime
            object or string in the format 'YYYYMMDD'.
            Defaults to today if not provided.
    """
    self.start, self.end = map(
        lambda x: x.strftime('%Y%m%d') \
            if isinstance(x, dt.date) \
            else re.sub(r'\D', '', x),
        [start, end or dt.date.today()])
    if self.start >= self.end:
        raise ValueError('`start` must be before `end`')
```

Note that we didn't define `_index_tickers` in the `__init__()` method, which is called upon creation of this object, because we only need one copy of this information for all the objects that are created from this class. The `_index_tickers` class attribute is private (signified, by convention, with a preceding underscore) in the sense that unless a user of this class knows the name of it, they won't find it easily (note that methods can also be private). This is done with the intention of protecting it (although it isn't guaranteed) and also because the user doesn't need it directly (it's for the internal workings of the class). Instead, we will provide a **property**, which we can access as an attribute, and a class method for getting the value mapped to a given key in that dictionary.

Tip

Class methods are methods that can be used on the class itself, without having to create an instance of the class beforehand. This contrasts with the instance methods we have seen so far. **Instance methods** are used with instances of a class for actions specific to that instance. We often don't need class methods, but if we have data that is shared across all instances of a class, it makes more sense to create a class method rather than an instance method.

Since `_index_tickers` is private, we want to provide an easy way for users of our class to see what is available. Therefore, we will create a property for the keys of `_index_tickers`. To do so, we use the `@property` decorator. **Decorators** are functions that wrap around other functions, allowing for the execution of extra code before and/or after the inner function executes. This class makes heavy use of decorators: we will use some already written ones (`@property` and `@classmethod`) and write one of our own to clean up and standardize the results across the methods that gather the data (`@label_sanitizer`). To use a decorator, we place it above the function or method definition:

```
@property
def available_tickers(self):
    """Indices whose tickers are supported."""
    return list(self._index_tickers.keys())
```

Furthermore, we provide a way of getting the ticker using a class method because our tickers are stored in a class variable. Class methods, by convention, receive `cls` as their first argument while instance methods receive `self`:

```
@classmethod
def get_index_ticker(cls, index):
    """
    Get the ticker of the specified index, if known.

    Parameters:
        - index: The name of the index; check
            `available_tickers` for full list which includes:
            - 'S&P 500' for S&P 500,
            - 'Dow Jones' for Dow Jones Industrial Average,
            - 'NASDAQ' for NASDAQ Composite Index

    Returns:
        The ticker as a string if known, otherwise `None`.
    """

    # Implementation logic here
```

```
try:  
    index = index.upper()  
except AttributeError:  
    raise ValueError(`index` must be a string)  
return cls._index_tickers.get(index, None)
```

Tip

If we want to prohibit certain actions within our code, we can check for them and `raise` errors as we see fit; this allows us to provide more informative error messages or simply accompany specific errors with some additional actions before reraising them (by using `raise` without an expression). If, instead, we wish to run certain code when something goes wrong, we use a `try...except` block: we surround the possibly troublesome code with `try` and put what to do if trouble occurs in the `except` clause.

When we get to the *Technical analysis of financial instruments* section, we will need the risk-free rate of return to calculate some of the metrics. This is the rate of return of an investment that has no risk of financial loss; in practice, we use the 10-year US Treasury bill. Since this rate will depend on the date range we are analyzing, we will add this functionality to the `StockReader` class and avoid having to look it up ourselves. We will use the `pandas_datareader` package to collect this data from the Federal Reserve Bank of St. Louis (<https://fred.stlouisfed.org/series/DGS10>), providing the option to return the daily rates for the date range we are studying (to analyze the data itself) or just the last one (if we need a single value for a calculation):

```
def get_risk_free_rate_of_return(self, last=True):  
    """  
        Get risk-free rate of return w/ 10-year US T-bill  
        from FRED (https://fred.stlouisfed.org/series/DGS10)  
  
    Parameter:  
        - last: If `True`, return the rate on the last  
            date in the date range else, return a `Series`  
            object for the rate each day in the date range.  
  
    Returns:  
        A single value or a `pandas.Series` object.  
    """
```

```
data = web.DataReader(  
    'DGS10', 'fred', start=self.start, end=self.end  
)  
data.index.rename('date', inplace=True)  
data = data.squeeze()  
return data.asof(self.end) \  
    if last and isinstance(data, pd.Series) else data
```

The remaining method code is replaced with `pass`, which tells Python to do nothing (and reminds us to update it later) so that the code can function as it was reproduced. We will write the following methods in the next section:

```
@label_sanitizer  
def get_ticker_data(self, ticker):  
    pass  
  
def get_index_data(self, index):  
    pass  
  
def get_bitcoin_data(self, currency_code):  
    pass  
  
@label_sanitizer  
def get_forex_rates(self, from_currency, to_currency,  
                    **kwargs):  
    pass
```

Important note

Since we aren't going to be looking at foreign exchange rates, we won't cover the `get_forex_rates()` method in this chapter; however, this method provides an additional example of how to use the `pandas_datareader` package, so I encourage you to take a look at it. Note that, in order to use this method, you will need to get a free API key from AlphaVantage at <https://www.alphavantage.co/support/#api-key>.

Both the `get_ticker_data()` and `get_forex_rates()` methods are decorated with `@label_sanitizer`, which aligns the data we receive from various sources to the same column names so that we don't have to clean them later. The `@label_sanitizer` decorator is defined in the `stock_analysis/utils.py` module. As we did previously, let's begin by looking at the docstring and imports of the `utils` module:

```
"""Utility functions for stock analysis."""

from functools import wraps
import re

import pandas as pd
```

Next, we have the `_sanitize_label()` function, which will clean up a single label. Note that we prefix the function name with an underscore because we don't intend for the users of our package to use this directly—it is for our decorator to use:

```
def _sanitize_label(label):
    """
    Clean up a label by removing non-letter, non-space
    characters and putting in all lowercase with underscores
    replacing spaces.

    Parameters:
        - label: The text you want to fix.

    Returns:
        The sanitized label.
    """
    return re.sub(r'[^w\s]', '', label)\n        .lower().replace(' ', '_')
```

Finally, we define the `@label_sanitizer` decorator, which is a function that cleans up the column and index names in the data we get from the Internet. Without this decorator, the column names in our collected data could have unexpected characters such as asterisks or spaces in them, making them unwieldy. By using the decorator, the methods will always return a dataframe with the names cleaned, saving us a step:

```
def label_sanitizer(method):
    """
    Decorator around a method that returns a dataframe to
    clean up all labels in said dataframe (column names and
    index name) by using `_sanitize_label()`.
```

```
Parameters:
    - method: The method to wrap.

Returns:
    A decorated method or function.

"""
@wraps(method) # keep original docstring for help()
def method_wrapper(self, *args, **kwargs):
    df = method(self, *args, **kwargs)

    # fix the column names
    df.columns = [
        _sanitize_label(col) for col in df.columns
    ]

    # fix the index name
    df.index.rename(
        _sanitize_label(df.index.name), inplace=True
    )

    return df
return method_wrapper
```

Note that there is also a decorator inside the definition of the `label_sanitizer()` function. The `@wraps` decorator from the `functools` module in the standard library gives the decorated function/method the same docstring it had beforehand; this is necessary because decoration actually creates a new function/method, thus rendering `help()` pretty useless unless we intervene.

Tip

Using the `@label_sanitizer` syntax is **syntactic sugar**, meaning that it makes it easier to express, compared to defining the method and then writing `method = label_sanitizer(method)`. However, both are valid.

Now that we understand decorators, we are ready to finish building the `StockReader` class. Note that we will be using and creating additional decorators for the other classes in the `stock_analysis` package as well, so make sure that you are comfortable with them before moving on.

Collecting historical data from Yahoo! Finance

The foundation of our data collection will be the `get_ticker_data()` method. It uses the `pandas_datareader` package to grab the data from Yahoo! Finance:

```
@label_sanitizer
def get_ticker_data(self, ticker):
    """
    Get historical OHLC data for given date range and ticker.

    Parameter:
        - ticker: The stock symbol to lookup as a string.

    Returns: A `pandas.DataFrame` object with the stock data.
    """
    return web.get_data_yahoo(ticker, self.start, self.end)
```

Important note

There have been issues with `pandas_datareader` and the Yahoo! Finance API in the past, causing the `pandas_datareader` developers to deprecate support for it via the `web.DataReader()` function (<https://pandas-datareader.readthedocs.io/en/latest/whatsnew.html#v0-6-0-january-24-2018>); instead, we have to use their workaround: `web.get_data_yahoo()`.

To collect data for a stock market index, we can use the `get_index_data()` method, which first looks up the index's ticker and then calls the `get_ticker_data()` method we just defined. Note that since the `get_ticker_data()` method is decorated with `@label_sanitizer`, the `get_index_data()` method doesn't need the `@label_sanitizer` decorator:

```
def get_index_data(self, index):
    """
    Get historical OHLC data from Yahoo! Finance
    for the chosen index for given date range.

    Parameter:
        - index: String representing the index you want
            data for, supported indices include:
            - 'S&P 500' for S&P 500,
            - 'Dow Jones' for Dow Jones Industrial Average,
            - 'NASDAQ' for NASDAQ Composite Index
```

```
Returns:  
    A `pandas.DataFrame` object with the index data.  
    """  
    if index not in self.available_tickers:  
        raise ValueError(  
            'Index not supported. Available tickers'  
            f"are: {', '.join(self.available_tickers)}"  
        )  
    return self.get_ticker_data(self.get_index_ticker(index))
```

Yahoo! Finance also provides data for bitcoin; however, we must pick a currency to use. The `get_bitcoin_data()` method accepts a currency code to create the symbol for the search on Yahoo! Finance (for instance, BTC-USD for bitcoin data in USD). The actual collection of the data is once again handled by the `get_ticker_data()` method:

```
def get_bitcoin_data(self, currency_code):  
    """  
    Get bitcoin historical OHLC data for given date range.  
  
    Parameter:  
        - currency_code: The currency to collect the bitcoin  
            data in, e.g. USD or GBP.  
  
    Returns:  
        A `pandas.DataFrame` object with the bitcoin data.  
    """  
    return self\  
        .get_ticker_data(f'BTC-{currency_code}')\  
        .loc[self.start:self.end] # clip dates
```

At this point, the `StockReader` class is ready for use, so let's get started in the `financial_analysis.ipynb` notebook and import the `stock_analysis` package that will be used for the rest of this chapter:

```
>>> import stock_analysis
```

Python runs the `stock_analysis/__init__.py` file when we import the `stock_analysis` package:

```
"""Classes for making technical stock analysis easier."""

from .stock_analyzer import StockAnalyzer, AssetGroupAnalyzer
from .stock_modeler import StockModeler
from .stock_reader import StockReader
from .stock_visualizer import \
    StockVisualizer, AssetGroupVisualizer
```

Important note

The code in the `stock_analysis/__init__.py` file makes it easier for us to access the package's classes—for example, rather than having to run `stock_analysis.stock_reader.StockReader()`, we only have to run `stock_analysis.StockReader()` to create a `StockReader` object.

Next, we will create an instance of the `StockReader` class by providing the start and (optionally) end dates for the data it will collect. We will work with 2019-2020 data. Note that when we run this code, Python is calling the `StockReader.__init__()` method:

```
>>> reader = \
...     stock_analysis.StockReader('2019-01-01', '2020-12-31')
```

Now, we will collect the **Facebook, Apple, Amazon, Netflix, and Google (FAANG)**, S&P 500, and bitcoin data. Since all the stocks we are working with are priced in USD, we will ask for the bitcoin data in USD. Note that we are using a generator expression and multiple assignment to get dataframes for each FAANG stock:

```
>>> fb, aapl, amzn, nflx, goog = (
...     reader.get_ticker_data(ticker)
...     for ticker in ['FB', 'AAPL', 'AMZN', 'NFLX', 'GOOG']
... )
>>> sp = reader.get_index_data('S&P 500')
>>> bitcoin = reader.get_bitcoin_data('USD')
```

Tip

Be sure to run `help(stock_analysis.StockReader)` or `help(reader)` to see all the methods and properties that are defined. The output clearly denotes which methods are class methods in a different section, and the properties will be listed at the bottom in the **data descriptors** section. This is an important step to take in order to get familiar with new code.

Exploratory data analysis

Now that we have our data, we want to get familiar with it. As we saw in *Chapter 5, Visualizing Data with Pandas and Matplotlib* and *Chapter 6, Plotting with Seaborn and Customization Techniques*, creating good visualizations requires knowledge of `matplotlib`, and—depending on the data format and the end goal for the visualization—`seaborn`. Just as we did with the `StockReader` class, we want to make it easier to visualize both individual assets and groups of assets, so rather than expecting users of our package (and, perhaps, our collaborators) to be proficient with `matplotlib` and `seaborn`, we will create wrappers around this functionality. This means that users of this package only have to be able to use the `stock_analysis` package to visualize their financial data. In addition, we are able to set a standard for how the visualizations look and avoid copying and pasting large amounts of code for each new analysis we want to conduct, which brings consistency and efficiency gains.

To make all of this possible, we have the `Visualizer` classes in `stock_analysis/stock_visualizer.py`. There are three classes in this file:

- `Visualizer`: This is the base class for defining the functionality of a `Visualizer` object. Most of the methods are **abstract**, meaning that the subclasses (children) that inherit from this superclass (parent) will need to override them and implement the code; these define what an object should do, without getting into the specifics.
- `StockVisualizer`: This is the subclass we will use to visualize a single asset.
- `AssetGroupVisualizer`: This is the subclass we will use to visualize multiple assets using `groupby()` operations.

Before we discuss the code for these classes, let's go over some additional functions in the `stock_analysis/utils.py` file, which will help create these asset groups and describe them for EDA purposes. For these functions, we need to import `pandas`:

```
import pandas as pd
```

The `group_stocks()` function takes in a dictionary that maps the name of the asset to the dataframe for that asset and outputs a new dataframe with all the data from the input dataframes and a new column, denoting which asset the data belongs to:

```
def group_stocks(mapping):
    """
    Create a new dataframe with many assets and a new column
    indicating the asset that row's data belongs to.

    Parameters:
        - mapping: A key-value mapping of the form
            {asset_name: asset_df}

    Returns:
        A new `pandas.DataFrame` object
    """
    group_df = pd.DataFrame()

    for stock, stock_data in mapping.items():
        df = stock_data.copy(deep=True)
        df['name'] = stock
        group_df = group_df.append(df, sort=True)

    group_df.index = pd.to_datetime(group_df.index)

    return group_df
```

Since we will have many methods and functions throughout the package that will expect their dataframes in a specific format, we will build a new decorator: `@validate_df`. This decorator checks that the input to a given method or function is an object of type `DataFrame` and that it has at least the columns specified with the `columns` argument of the decorator. We will provide the columns as a `set` object. This allows us to check the set difference between the columns we must have and the columns in the input data (see *Chapter 4, Aggregating Pandas DataFrames*, for a review of set operations). If the dataframe has the columns we request (at a minimum), the set difference will be empty, which means that the dataframe passes the test. This decorator will raise a `ValueError` if either of these conditions is violated.

Let's take a look at how this is defined in the `stock_analysis/utils.py` file:

```
def validate_df(columns, instance_method=True):
    """
    Decorator that raises a `ValueError` if input isn't a
    `DataFrame` or doesn't contain the proper columns. Note
    the `DataFrame` must be the first positional argument
    passed to this method.

    Parameters:
        - columns: A set of required column names.
            For example, {'open', 'high', 'low', 'close'}.
        - instance_method: Whether or not the item being
            decorated is an instance method. Pass `False` to
            decorate static methods and functions.

    Returns:
        A decorated method or function.
    """
    def method_wrapper(method):
        @wraps(method)
        def validate_wrapper(self, *args, **kwargs):
            # functions and static methods don't pass self so
            # self is the 1st positional argument in that case
            df = (self, *args)[0 if not instance_method else 1]
            if not isinstance(df, pd.DataFrame):
                raise ValueError(
                    'Must pass in a pandas `DataFrame`'
                )
            if columns.difference(df.columns):
                raise ValueError(
                    'Dataframe must contain the following'
                    f' columns: {columns}'
                )
            return method(self, *args, **kwargs)
        return validate_wrapper
    return method_wrapper
```

Groups made with the `group_stocks()` function can be described in a single output using the `describe_group()` function. The `group_stocks()` function adds a column called `name` that `describe_group()` looks for, so we use the `@validate_df` decorator to make sure that the format is correct before trying to run the function:

```
@validate_df(columns={'name'}, instance_method=False)
def describe_group(data):
    """
    Run `describe()` on the asset group.

    Parameters:
        - data: Grouped data resulting from `group_stocks()`

    Returns:
        The transpose of the grouped description statistics.
    """
    return data.groupby('name').describe().T
```

Let's use the `group_stocks()` function to make some asset groups for our analysis:

```
>>> from stock_analysis.utils import \
...     group_stocks, describe_group
>>> faang = group_stocks({
...     'Facebook': fb, 'Apple': aapl, 'Amazon': amzn,
...     'Netflix': nflx, 'Google': goog
... })
>>> faang_sp = group_stocks({
...     'Facebook': fb, 'Apple': aapl, 'Amazon': amzn,
...     'Netflix': nflx, 'Google': goog, 'S&P 500': sp
... })
>>> all_assets = group_stocks({
...     'Bitcoin': bitcoin, 'S&P 500': sp, 'Facebook': fb,
...     'Apple': aapl, 'Amazon': amzn, 'Netflix': nflx,
...     'Google': goog
... })
```

Using these groups, the output of `describe()` can be much more informative for comparison purposes compared to running it on each dataframe separately. The `describe_group()` function handles running `describe()` with `groupby()`. This makes it easier to look at the summary for the closing price across assets:

```
>>> describe_group(all_assets).loc['close', ]
```

At a glance, we can see that we have more data for bitcoin than the rest. This is because the prices change daily, whereas for stocks, we only see the data for trading days. Another thing we can glean from this is scale; bitcoin is not only much more volatile but is much higher in value than everything else:

name	Amazon	Apple	Bitcoin	Facebook	Google	Netflix	S&P 500
count	505.000000	505.000000	727.000000	505.000000	505.000000	505.000000	505.000000
mean	2235.904988	73.748386	9252.825408	208.146574	1335.188544	387.966593	3065.907599
std	594.306346	27.280933	4034.014685	39.665111	200.793911	78.931238	292.376435
min	1500.280029	35.547501	3399.471680	131.740005	1016.059998	254.589996	2237.399902
25%	1785.660034	50.782501	7218.593750	180.029999	1169.949951	329.089996	2870.719971
50%	1904.280029	66.730003	9137.993164	196.770004	1295.280029	364.369995	3005.469971
75%	2890.300049	91.632500	10570.513184	235.940002	1476.229980	469.959991	3276.020020
max	3531.449951	136.690002	29001.720703	303.910004	1827.989990	556.549988	3756.070068

Figure 7.6 – Summary statistics for the closing price per financial instrument

If we don't want to look at the assets individually, we can combine them into a portfolio, which we can treat as a single asset. The `make_portfolio()` function from `stock_analysis/utils.py` groups the data by date and sums all the columns, giving us the total stock price and volume traded of our portfolio:

```
@validate_df(columns=set(), instance_method=False)
def make_portfolio(data, date_level='date'):
    """
    Make a portfolio of assets by grouping by date and
    summing all columns.

    Note: the caller is responsible for making sure the
    dates line up across assets and handling when they don't.
    """
    return data.groupby(level=date_level).sum()
```

This function assumes that the assets are traded on the same frequency. Bitcoin trades every day of the week, while the stock market doesn't. For this reason, we would have to decide how to handle this difference before using this function if our portfolio was a mix of bitcoin and the stock market; consult our discussion of reindexing in *Chapter 3, Data Wrangling with Pandas*, for a possible strategy. We will use this function in the exercises at the end of this chapter to build a portfolio of the FAANG stocks, which all trade on the same frequency, in order to look at the effect of after-hours trading on the FAANG stocks as a whole.

The Visualizer class family

As we learned from previous chapters, visualization will make our analysis much easier, so let's begin our discussion of the `Visualizer` classes in `stock_analysis/stock_visualizer.py`. First, we will define our base class, `Visualizer`. The following UML diagram tells us this is our base class because it has arrows pointing to it. These arrows originate from the subclasses (`AssetGroupVisualizer` and `StockVisualizer`):

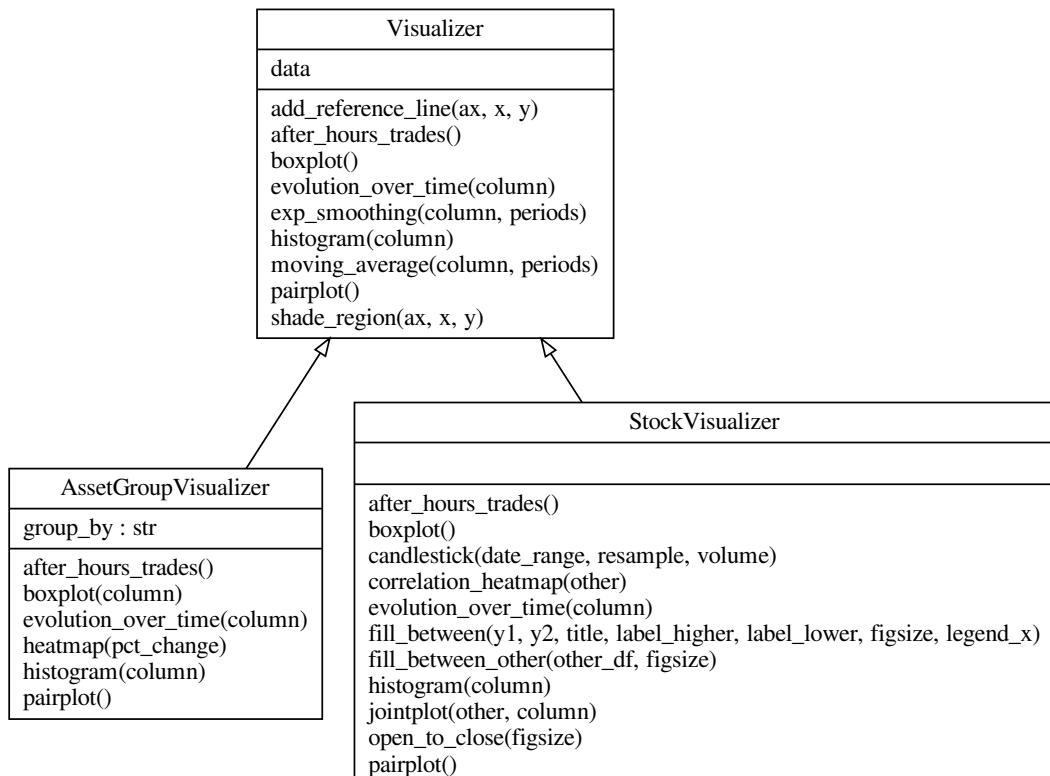


Figure 7.7 – Visualizer class hierarchy

Figure 7.7 also tells us the methods we will be defining for each of the classes in this section. This includes methods for visualizing the effect of after-hours trading (`after_hours_trades()`) and the evolution over time of an asset's price (`evolution_over_time()`), which we will use to compare assets visually.

We start the module with our docstring and imports. For our visualizations, we will need `matplotlib`, `numpy`, `pandas`, and `seaborn`, along with `mplfinance` (a `matplotlib` derivative package for financial visualizations):

```
"""Visualize financial instruments."""

import math

import matplotlib.pyplot as plt
import mplfinance as mpf
import numpy as np
import pandas as pd
import seaborn as sns

from .utils import validate_df
```

Next, we begin by defining the `Visualizer` class. This class will hold the data it will be used to visualize, so we put this in the `__init__()` method:

```
class Visualizer:
    """Base visualizer class not intended for direct use."""

    @validate_df(columns={'open', 'high', 'low', 'close'})
    def __init__(self, df):
        """Store the input data as an attribute."""
        self.data = df
```

This base class will provide us with **static methods** for adding reference lines to plots and also adding shaded regions, without needing to remember which `matplotlib` function we need to call for the orientation; static methods don't depend on the class for data. We define the `add_reference_line()` method for adding horizontal or vertical lines (and anything in between) using the `@staticmethod` decorator; notice we don't have `self` or `cls` as the first argument:

```
@staticmethod
def add_reference_line(ax, x=None, y=None, **kwargs):
    """
    Static method for adding reference lines to plots.
```

```
Parameters:
    - ax: `Axes` object to add the reference line to.
    - x, y: The x, y value to draw the line at as a
        single value or numpy array-like structure.
        - For horizontal: pass only `y`
        - For vertical: pass only `x`
        - For AB line: pass both `x` and `y`
    - kwargs: Additional keyword args. to pass down.

Returns:
    The matplotlib `Axes` object passed in.

"""
try:
    # numpy array-like structures -> AB line
    if x.shape and y.shape:
        ax.plot(x, y, **kwargs)
except:
    # error triggers if x or y isn't array-like
    try:
        if not x and not y:
            raise ValueError(
                'You must provide an `x` or a `y`'
            )
        elif x and not y:
            ax.axvline(x, **kwargs) # vertical line
        elif not x and y:
            ax.axhline(y, **kwargs) # horizontal line
    except:
        raise ValueError(
            'If providing only `x` or `y`, '
            'it must be a single value'
        )
    ax.legend()
return ax
```

Tip

See the *Further reading* section for more information on class methods, static methods, and abstract methods.

The `shade_region()` static method for adding shaded regions to a plot is similar to the `add_reference_line()` static method:

```
@staticmethod
def shade_region(ax, x=tuple(), y=tuple(), **kwargs):
    """
    Static method for shading a region on a plot.

    Parameters:
        - ax: `Axes` object to add the shaded region to.
        - x: Tuple with the `xmin` and `xmax` bounds for
            the rectangle drawn vertically.
        - y: Tuple with the `ymin` and `ymax` bounds for
            the rectangle drawn horizontally.
        - kwargs: Additional keyword args. to pass down.

    Returns:
        The matplotlib `Axes` object passed in.
    """
    if not x and not y:
        raise ValueError(
            'You must provide an x or a y min/max tuple'
        )
    elif x and y:
        raise ValueError('You can only provide x or y.')
    elif x and not y:
        ax.axvspan(*x, **kwargs) # vertical region
    elif not x and y:
        ax.axhspan(*y, **kwargs) # horizontal region
    return ax
```

Since we want our plotting capabilities to be flexible, we are going to define a static method that will make it easy for us to plot one or many items without needing to check the number of items beforehand. This will be utilized in the classes we build using the `Visualizer` class as our base:

```
@staticmethod
def _iter_handler(items):
    """
    Static method for making a list out of an item if
    it isn't a list or tuple already.
```

```
Parameters:
    - items: The variable to make sure it is a list.

    Returns: The input as a list or tuple.
"""
if not isinstance(items, (list, tuple)):
    items = [items]
return items
```

We want to support window functions for single assets and groups of them; however, the implementation of this will vary, so we will define an **abstract method** (a method without implementation) in the superclass, and the subclasses will override it to provide the implementation:

```
def _window_calc(self, column, periods, name, func,
                  named_arg, **kwargs):
"""
To be implemented by subclasses. Defines how to add
lines resulting from window calculations.
"""
raise NotImplementedError('To be implemented by '
                           'subclasses.')
```

This allows us to define functionality that depends on `_window_calc()` but doesn't need to know the exact implementation, just the result. The `moving_average()` method uses `_window_calc()` to add moving average lines to the plot:

```
def moving_average(self, column, periods, **kwargs):
"""
Add line(s) for the moving average of a column.

Parameters:
    - column: The name of the column to plot.
    - periods: The rule or list of rules for
        resampling, like '20D' for 20-day periods.
    - kwargs: Additional arguments to pass down.

    Returns: A matplotlib `Axes` object.
"""
return self._window_calc(
    column, periods, name='MA', named_arg='rule',
    func=pd.DataFrame.resample, **kwargs
)
```

In a similar fashion, we define the `exp_smoothing()` method, which will use `_window_calc()` to add exponentially smoothed moving average lines to the plot:

```
def exp_smoothing(self, column, periods, **kwargs):
    """
    Add line(s) for the exponentially smoothed moving
    average of a column.

    Parameters:
        - column: The name of the column to plot.
        - periods: The span or list of spans for,
            smoothing like 20 for 20-day periods.
        - kwargs: Additional arguments to pass down.

    Returns:
        A matplotlib `Axes` object.
    """
    return self._window_calc(
        column, periods, name='EWMA',
        func=pd.DataFrame.ewm, named_arg='span', **kwargs
    )
```

Note that while we have methods for adding the moving average and the exponentially smoothed moving average to a plot of a column, they both call `_window_calc()`, which isn't defined here. This is because each of the subclasses will have its own implementation of `_window_calc()`, while they will inherit the top-level method without the need to override `moving_average()` or `exp_smoothing()`.

Important note

Remember that methods preceded with a single underscore (`_`) are Python's version of **private methods**—they can still be accessed outside this class, but they don't show up when we run `help()` on objects of that class. We created `_window_calc()` as a private method because users of the `Visualizer` classes will only need to call `moving_average()` and `exp_smoothing()`.

Finally, we will add placeholders for the methods all subclasses will have. These are abstract methods that will be defined by each subclass individually because the implementation will be different depending on if we are visualizing a single asset or a group of them. For brevity, the following is a subset of the abstract methods defined in this class:

```
def evolution_over_time(self, column, **kwargs):
    """Creates line plots."""
    raise NotImplementedError('To be implemented by '
                             'subclasses.')

def after_hours_trades(self):
    """Show the effect of after-hours trading."""
    raise NotImplementedError('To be implemented by '
                             'subclasses.')

def pairplot(self, **kwargs):
    """Create pairplots."""
    raise NotImplementedError('To be implemented by '
                             'subclasses.'
```

The subclasses will also define any methods that are unique to them and/or override the implementation of the `Visualizer` class, if necessary. Anything they don't override, they will inherit. By using **inheritance**, we can define a broad class such as `Visualizer` by what all `Visualizers` should do and then have more specific versions, such as the `StockVisualizer` class, which handles single assets only.

Visualizing a stock

Let's start the `StockVisualizer` class by inheriting from `Visualizer`; we will choose not to override the `__init__()` method because the `StockVisualizer` class will only have a `dataframe` as an attribute. Instead, we will provide implementations for the methods that need to be added (which are unique to this class) or overridden.

Important note

We will only cover a subset of the functionality in the interest of brevity; however, I highly encourage you to both read through the full code base and test out the functionality in the notebook.

The first method we will override is `evolution_over_time()`, which will create a line plot of a column over time:

```
class StockVisualizer(Visualizer):
    """Visualizer for a single stock."""

    def evolution_over_time(self, column, **kwargs):
        """
        Visualize the evolution over time of a column.

        Parameters:
        - column: The name of the column to visualize.
        - kwargs: Additional arguments to pass down.

        Returns:
            A matplotlib `Axes` object.
        """
        return self.data.plot.line(y=column, **kwargs)
```

Next, we will use `mplfinance` to create a **candlestick plot**, which is a way to visualize the OHLC data together. Each row of the OHLC time series will be plotted as a candlestick. When the candlestick is black, the asset's closing price was smaller than the opening price (it lost value); when the candlestick is white, the asset's closing price was higher than its opening price, as illustrated in the following diagram:

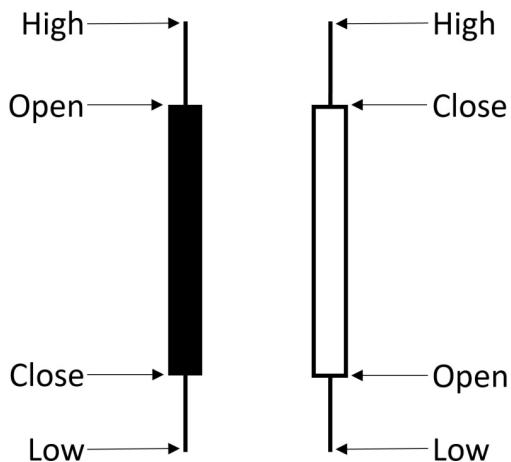


Figure 7.8 – Understanding a candlestick plot

The `candlestick()` method also provides options to resample the data, show volume traded, and plot a specific date range:

```
def candlestick(self, date_range=None, resample=None,
                volume=False, **kwargs):
    """
    Create a candlestick plot for the OHLC data.

    Parameters:
    - date_range: String or `slice()` of dates to
      pass to `loc[]`, if `None` the plot will be
      for the full range of the data.
    - resample: The offset to use for resampling
      the data, if desired.
    - volume: Whether to show a bar plot for volume
      traded under the candlesticks
    - kwargs: Keyword args for `mplfinance.plot()`
    """
    if not date_range:
        date_range = slice(
            self.data.index.min(), self.data.index.max()
        )
    plot_data = self.data.loc[date_range]

    if resample:
        agg_dict = {
            'open': 'first', 'close': 'last',
            'high': 'max', 'low': 'min', 'volume': 'sum'
        }
        plot_data = plot_data.resample(resample).agg({
            col: agg_dict[col] for col in plot_data.columns
            if col in agg_dict
        })

    mpf.plot(
        plot_data, type='candle', volume=volume, **kwargs
    )
```

Now, we add the `after_hours_trades()` method, which helps us visualize the effect after-hours trading had on an individual asset, with bars colored red for losses and green for gains:

```
def after_hours_trades(self):
    """
    Visualize the effect of after-hours trading.

    Returns: A matplotlib `Axes` object.
    """
    after_hours = self.data.open - self.data.close.shift()

    monthly_effect = after_hours.resample('1M').sum()
    fig, axes = plt.subplots(1, 2, figsize=(15, 3))

    after_hours.plot(
        ax=axes[0],
        title='After-hours trading\n' +
              '(Open Price - Prior Day\'s Close)'
    ).set_ylabel('price')

    monthly_effect.index = \
        monthly_effect.index.strftime('%Y-%b')
    monthly_effect.plot(
        ax=axes[1], kind='bar', rot=90,
        title='After-hours trading monthly effect',
        color=np.where(monthly_effect >= 0, 'g', 'r')
    ).axhline(0, color='black', linewidth=1)

    axes[1].set_ylabel('price')
    return axes
```

Next, we will add a static method that will allow us to fill the area between two curves of our choosing. The `fill_between()` method will use `plt.fill_between()` to color the area green or red depending on which curve is higher:

```
@staticmethod
def fill_between(y1, y2, title, label_higher, label_lower,
                 figsize, legend_x):
    """
    Visualize the difference between assets.
```

```
Parameters:
    - y1, y2: Data to plot, filling y2 - y1.
    - title: The title for the plot.
    - label_higher: Label for when y2 > y1.
    - label_lower: Label for when y2 <= y1.
    - figsize: (width, height) for the plot dimensions.
    - legend_x: Where to place legend below the plot.

Returns: A matplotlib `Axes` object.
"""
is_higher = y2 - y1 > 0
fig = plt.figure(figsize=figsize)

for exclude_mask, color, label in zip(
    (is_higher, np.invert(is_higher)),
    ('g', 'r'),
    (label_higher, label_lower)
):
    plt.fill_between(
        y2.index, y2, y1, figure=fig,
        where=exclude_mask, color=color, label=label
    )
plt.suptitle(title)
plt.legend(
    bbox_to_anchor=(legend_x, -0.1),
    framealpha=0, ncol=2
)
for spine in ['top', 'right']:
    fig.axes[0].spines[spine].set_visible(False)
return fig.axes[0]
```

The `open_to_close()` method will help us visualize the daily differential between opening and closing price via the `fill_between()` static method. We will color the area green if the closing price is higher than the opening price and red if the opposite is true:

```
def open_to_close(self, figsize=(10, 4)):
    """
    Visualize the daily change in price from open to close.

    Parameters:
        - figsize: (width, height) of plot
```

```

    Returns:
        A matplotlib `Axes` object.
    """
    ax = self.fill_between(
        self.data.open, self.data.close,
        figsize=figsize, legend_x=0.67,
        title='Daily price change (open to close)',
        label_higher='price rose', label_lower='price fell'
    )
    ax.set_ylabel('price')
    return ax

```

In addition to visualizing the differential between the opening and closing price of an individual asset, we will want to compare prices between assets. The `fill_between_other()` method will help us visualize the differential between the asset we created the visualizer for and another asset, using `fill_between()` again. We will color the differential green when the visualizer's asset is higher than the other asset and red for when it is lower:

```

def fill_between_other(self, other_df, figsize=(10, 4)):
    """
    Visualize difference in closing price between assets.

    Parameters:
        - other_df: The other asset's data.
        - figsize: (width, height) for the plot.

    Returns:
        A matplotlib `Axes` object.
    """
    ax = self.fill_between(
        other_df.open, self.data.close, figsize=figsize,
        legend_x=0.7, label_higher='asset is higher',
        label_lower='asset is lower',
        title='Differential between asset price '
              '(this - other)'
    )
    ax.set_ylabel('price')
    return ax

```

The time has finally come to override the `_window_calc()` method, which defines how to add reference lines based on window calculations for a single asset. Note how we are able to use the `pipe()` method (introduced in *Chapter 4, Aggregating Pandas DataFrames*) to make our window calculation plots work with different functions, and the `_iter_handler()` method to make our loop work without having to check if we have more than one reference line to plot:

```
def _window_calc(self, column, periods, name, func,
                 named_arg, **kwargs):
    """
    Helper method for plotting a series and adding
    reference lines using a window calculation.

    Parameters:
        - column: The name of the column to plot.
        - periods: The rule/span or list of them to pass
            to the resampling/smoothing function, like '20D'
            for 20-day periods (resampling) or 20 for a
            20-day span (smoothing)
        - name: The name of the window calculation (to
            show in the legend).
        - func: The window calculation function.
        - named_arg: The name of the argument `periods`
            is being passed as.
        - kwargs: Additional arguments to pass down.

    Returns:
        A matplotlib `Axes` object.
    """
    ax = self.data.plot(y=column, **kwargs)
    for period in self._iter_handler(periods):
        self.data[column].pipe(
            func, **{named_arg: period}
        ).mean().plot(
            ax=ax, linestyle='--',
            label=f"""{period if isinstance(
                period, str
            ) else str(period) + 'D'} {name}"""
        )
    plt.legend()
    return ax
```

So far, each visualization concerned data for a single asset; however, sometimes we want to be able to visualize the relationship between assets, so we will build a wrapper around the `jointplot()` function from `seaborn`:

```
def jointplot(self, other, column, **kwargs):
    """
    Generate a seaborn jointplot for given column in
    this asset compared to another asset.

    Parameters:
        - other: The other asset's dataframe.
        - column: Column to use for the comparison.
        - kwargs: Keyword arguments to pass down.

    Returns: A seaborn jointplot
    """
    return sns.jointplot(
        x=self.data[column], y=other[column], **kwargs
    )
```

Another way of viewing the relationship between assets is the correlation matrix. `DataFrame` objects have a `corrwith()` method that will calculate the correlation coefficient between each column and the same column (by name) in another `dataframe`. This doesn't fill the matrix that's needed for a heatmap, as we saw in previous chapters; rather, it is the diagonal. The `correlation_heatmap()` method creates a matrix for the `sns.heatmap()` function and fills in the diagonal with the correlation coefficients; then, it makes sure that only the diagonal is displayed using a mask. In addition, we will use the daily percentage change of each column when calculating the correlations to handle the difference in scale (for instance, between Apple's stock price and Amazon's stock price):

```
def correlation_heatmap(self, other):
    """
    Plot the correlations between this asset and another
    one with a heatmap.

    Parameters:
        - other: The other dataframe.

    Returns: A seaborn heatmap
    """

```

```
corrs = \
    self.data.pct_change().corrwith(other.pct_change())
corrs = corrs[~pd.isnull(corrs)]
size = len(corrs)
matrix = np.zeros((size, size), float)
for i, corr in zip(range(size), corrs):
    matrix[i][i] = corr

# create mask to only show diagonal
mask = np.ones_like(matrix)
np.fill_diagonal(mask, 0)

return sns.heatmap(
    matrix, annot=True, center=0, vmin=-1, vmax=1,
    mask=mask, xticklabels=self.data.columns,
    yticklabels=self.data.columns
)
```

Now that we understand some of the functionality available in the `StockVisualizer` class, we can begin our exploratory analysis. Let's create a `StockVisualizer` object to perform some EDA on the Netflix stock data:

```
>>> %matplotlib inline
>>> import matplotlib.pyplot as plt

>>> netflix_viz = stock_analysis.StockVisualizer(nflx)
```

Once we initialize our `StockVisualizer` object with the Netflix dataframe, we can generate many different plot types. We won't go over examples of everything this object lets us do (I will leave that up to you to experiment with), but let's take a look at the closing price over time with some moving averages to study the trend:

```
>>> ax = netflix_viz.moving_average('close', ['30D', '90D'])
>>> netflix_viz.shade_region(
...     ax, x=('2019-10-01', '2020-07-01'),
...     color='blue', alpha=0.1
... )
>>> ax.set(title='Netflix Closing Price', ylabel='price ($)')
```

These moving averages give us a smoothed version of the stock price curve. Notice that, in the shaded region, the 90-day moving average is acting like a ceiling for the stock price:

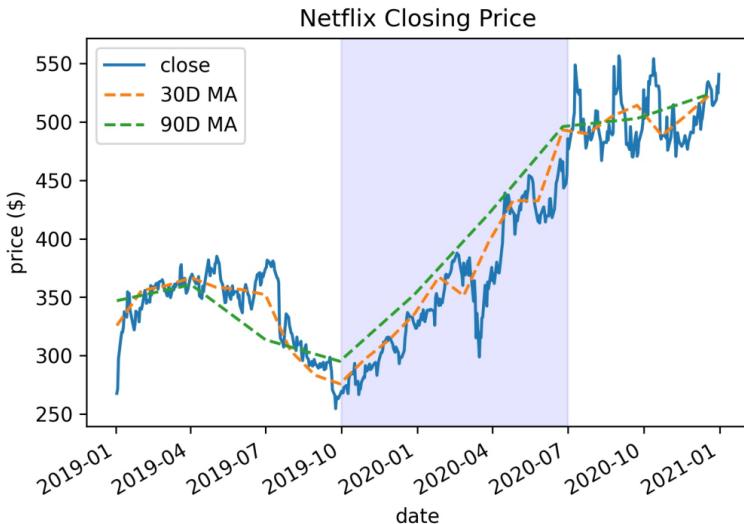


Figure 7.9 – Netflix stock price with moving averages

Traders experiment with different-period moving averages depending on the task at hand, such as anticipating upside moves (increases in stock price) and making planned exits before downside moves (decreases in stock price). Other uses include calculating automatic **support** and **resistance** levels (which we first saw in *Chapter 6, Plotting with Seaborn and Customization Techniques*) by finding the portion of the moving average line that props up the data from beneath or the one that acts as a ceiling for the data, respectively. When a stock price approaches the support, the price tends to be attractive enough that people buy, thus increasing the price (moving up from the support toward the resistance). However, when the stock reaches the resistance, it tends to encourage people to sell, bringing the stock price down (moving away from the resistance and toward the support).

Figure 7.10 shows an example of how support (green) and resistance (red) act as lower and upper bounds, respectively, for the stock price; once the price hits either of these bounds, it tends to bounce back in the opposite direction due to buyers/sellers of the stock taking action:

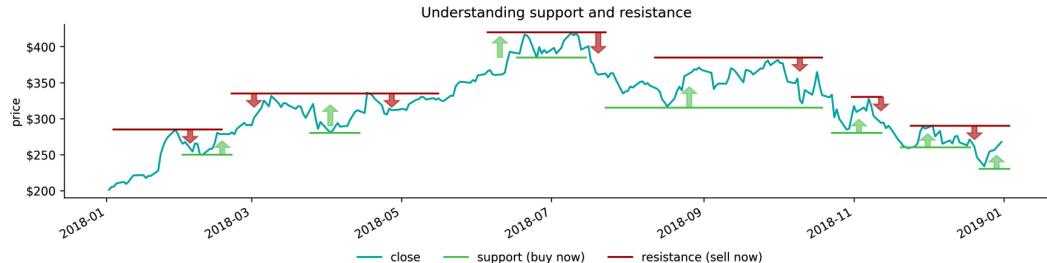


Figure 7.10 – Example support and resistance for Netflix stock in 2018

Often, the **exponentially weighted moving average (EWMA)** can provide a better trend since we can put additional emphasis on more recent values. Let's see how exponential smoothing looks for our data:

```
>>> ax = netflix_viz.exp_smoothing('close', [30, 90])
>>> netflix_viz.shade_region(
...     ax, x=('2020-04-01', '2020-10-01'),
...     color='blue', alpha=0.1
... )
>>> ax.set(title='Netflix Closing Price', ylabel='price ($)')
```

The 90-day EWMA appears to be acting as the support level in the shaded region:

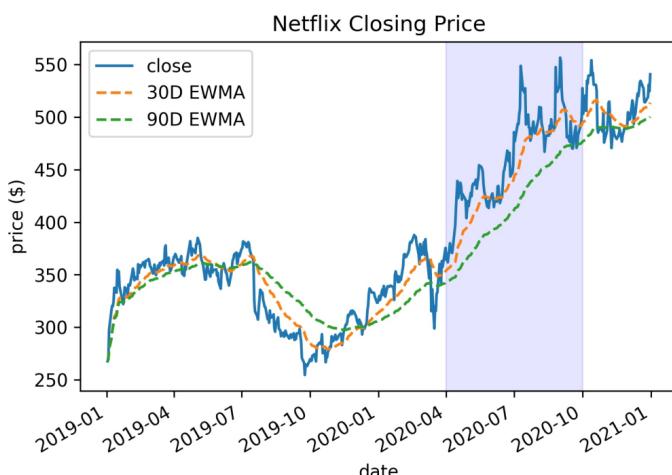


Figure 7.11 – Netflix stock price with EWMA

Tip

The notebook contains a cell for interactive visualization of the moving average and the EWMA using widgets. We can use these types of visualizations to determine the best window for the calculations. Note that using this cell may require some additional setup, but it is all noted right above the cell in the notebook.

In the exercises for *Chapter 5, Visualizing Data with Pandas and Matplotlib*, we wrote code for generating a visualization that represented the effect that after-hours trading had on Facebook; the `StockVisualizer` class also has this functionality. Let's use the `after_hours_trades()` method to see how Netflix fared:

```
>>> netflix_viz.after_hours_trades()
```

Netflix had a rough third quarter in 2019 in terms of after-hours trades:

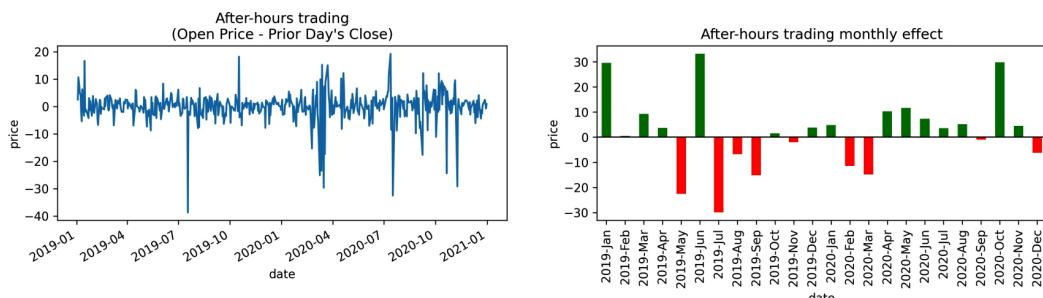


Figure 7.12 – Visualizing the effect of after-hours trading on Netflix stock

We can use candlestick plots to study the OHLC data. Let's create one for Netflix, along with a bar plot for volume traded, by using the `candlestick()` method. We will also resample the data into 2-week intervals to improve the visibility of the candlesticks:

```
>>> netflix_viz.candlestick(
...     resample='2W', volume=True, xrotation=90,
...     datetime_format='%Y-%b -'
... )
```

Remember from *Figure 7.8* that when the body of the candlestick is white, it means that the stock gained value. Note that, for the most part, the spikes in volume traded were accompanied by increases in stock value:

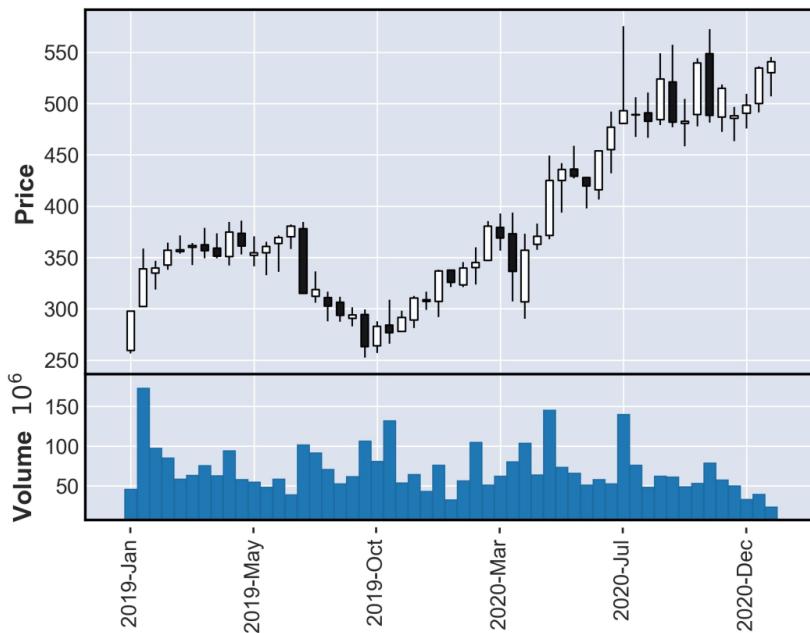


Figure 7.13 – Candlestick plot with trading volume

Tip

Traders use candlestick plots to look for and analyze patterns in an asset's performance, which can be used to make trading decisions. Check out this article for an introduction to candlestick plots and some common patterns traders look for: <https://www.investopedia.com/trading/candlestick-charts-what-is-it/>.

Before moving on, we need to reset our plot styles. The `mplfinance` package sets many of the available styling options for its plots, so let's return to the style we are familiar with for now:

```
>>> import matplotlib as mpl  
>>> mpl.rcParams()  
>>> %matplotlib inline
```

We have already taken a look at a stock in isolation (Facebook) in prior chapters, so let's take this in a different direction and compare Netflix to others. Let's use the `jointplot()` method to see how Netflix compares to the S&P 500:

```
>>> netflix_viz.jointplot(sp, 'close')
```

If we take a look at the plot, they appear to be weakly positively correlated. With financial analysis, we can calculate a metric called **beta** that indicates an asset's correlation to an index, such as the S&P 500. We will calculate beta in the *Technical analysis of financial instruments* section later in this chapter:

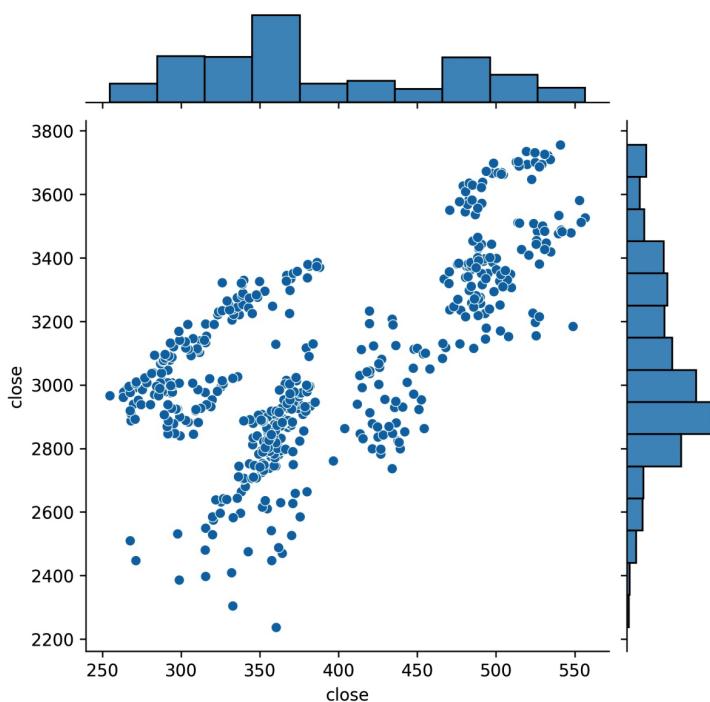


Figure 7.14 – Comparing Netflix to the S&P 500

We can use the `correlation_heatmap()` method to visualize the correlations between Netflix and Amazon as a heatmap, using the daily percentage change of each of the columns:

```
>>> netflix_viz.correlation_heatmap(amzn)
```

Netflix and Amazon are weakly positively correlated, but only on the OHLC data:

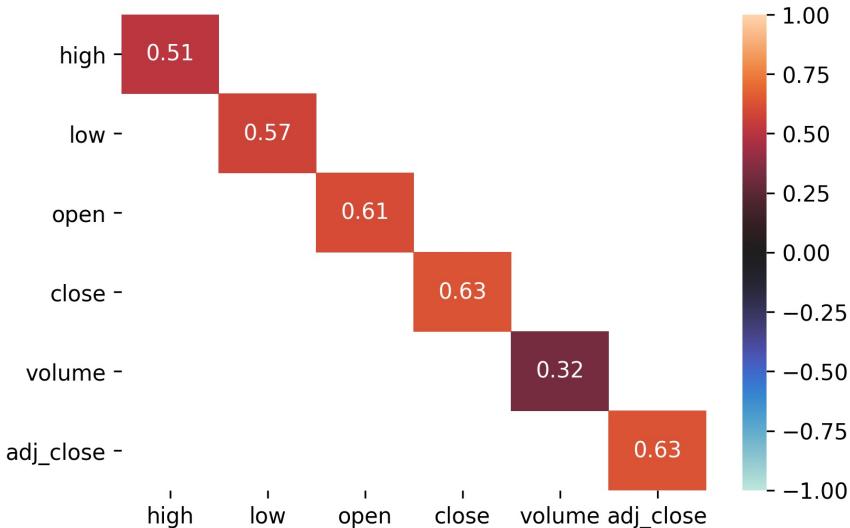


Figure 7.15 – Correlation heatmap between Netflix and Amazon

Lastly, we can use the `fill_between_other()` method to see how another asset grew (or fell) in price compared to Netflix. We will compare Netflix to Tesla here to see an example of one stock surpassing another:

```
>>> tsla = reader.get_ticker_data('TSLA')
>>> change_date = (tsla.close > nflx.close).idxmax()
>>> ax = netflix_viz.fill_between_other(tsla)
>>> netflix_viz.add_reference_line(
...     ax, x=change_date, color='k', linestyle=':', alpha=0.5,
...     label=f'TSLA > NFLX {change_date:%Y-%m-%d}'
... )
```

Notice that the shaded region shrinks in height as it approaches the reference line—this is the difference between the values in Netflix stock and Tesla stock decreasing over time. On November 11, 2020, as Tesla overtakes Netflix, the shaded region changes in color (from green to red) and begins to increase in height as Tesla widens the gap:

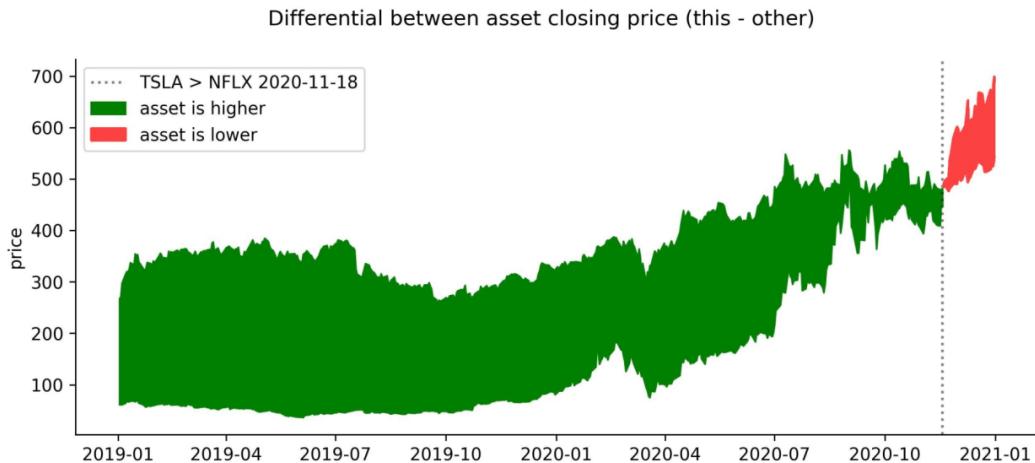


Figure 7.16 – Stock price differential between Netflix and Tesla

Up until this point, we have discussed visualizing a single asset—in this case, Netflix—so let's move on and see how we can perform some EDA across asset groups with the `AssetGroupVisualizer` class.

Visualizing multiple assets

As we did previously, we will start by inheriting from the `Visualizer` class and writing our docstring. Note that the `AssetGroupVisualizer` class also keeps track of the column to use for `groupby()` operations, so we override the `__init__()` method; since this change was meant to be in addition to what was already there, we call the `__init__()` method of the superclass as well:

```
class AssetGroupVisualizer(Visualizer):
    """Visualizes groups of assets in a single dataframe."""

    # override for group visuals
    def __init__(self, df, group_by='name'):
        """This object keeps track of the group by column."""
        super().__init__(df)
        self.group_by = group_by
```

Next, we define the `evolution_over_time()` method to plot the same column for all the assets in the group in a single plot for comparison purposes. Since our data is of a different shape, we will use `seaborn` this time:

```
def evolution_over_time(self, column, **kwargs):
    """
    Visualize the evolution over time for all assets.

    Parameters:
        - column: The name of the column to visualize.
        - kwargs: Additional arguments to pass down.

    Returns: A matplotlib `Axes` object.
    """
    if 'ax' not in kwargs:
        fig, ax = plt.subplots(1, 1, figsize=(10, 4))
    else:
        ax = kwargs.pop('ax')
    return sns.lineplot(
        x=self.data.index, y=column, hue=self.group_by,
        data=self.data, ax=ax, **kwargs
    )
```

When using `seaborn` or only plotting a single asset, we didn't have to worry about the layout of our subplots; however, for some of the other asset group visualizations, we need a way to automatically determine a reasonable subplot layout. For this, we will add the `_get_layout()` method, which will generate the `Figure` and `Axes` objects we need for a given number of subplots (determined by the number of unique assets in the group):

```
def _get_layout(self):
    """
    Helper method for getting an autolayout of subplots.

    Returns: `Figure` and `Axes` objects to plot with.
    """
    subplots_needed = self.data[self.group_by].nunique()
    rows = math.ceil(subplots_needed / 2)
    fig, axes = \
        plt.subplots(rows, 2, figsize=(15, 5 * rows))
    if rows > 1:
        axes = axes.flatten()
```

```

if subplots_needed < len(axes):
    # remove excess axes from autolayout
    for i in range(subplots_needed, len(axes)):
        # can't use comprehension here
        fig.delaxes(axes[i])
return fig, axes

```

Now, we need to define how `_window_calc()` will work with groups. We will need to use our `_get_layout()` method to build subplots for each of the assets in the group:

```

def _window_calc(self, column, periods, name, func,
                 named_arg, **kwargs):
    """
    Helper method for plotting a series and adding
    reference lines using a window calculation.

    Parameters:
    - column: The name of the column to plot.
    - periods: The rule/span or list of them to pass
      to the resampling/smoothing function, like '20D'
      for 20-day periods (resampling) or 20 for a
      20-day span (smoothing)
    - name: The name of the window calculation (to
      show in the legend).
    - func: The window calculation function.
    - named_arg: The name of the argument `periods`
      is being passed as.
    - kwargs: Additional arguments to pass down.

    Returns:
        A matplotlib `Axes` object.
    """
    fig, axes = self._get_layout()
    for ax, asset_name in zip(
        axes, self.data[self.group_by].unique()
    ):
        subset = self.data.query(
            f'{self.group_by} == "{asset_name}"'
        )
        ax = subset.plot(
            y=column, ax=ax, label=asset_name, **kwargs
        )

```

```
        for period in self._iter_handler(periods):
            subset[column].pipe(
                func, **{named_arg: period}
            ).mean().plot(
                ax=ax, linestyle='--',
                label=f""'{period if isinstance(
                    period, str
                ) else str(period) + 'D'} {name}''''
            )
        ax.legend()
    plt.tight_layout()
    return ax
```

We can override `after_hours_trades()` to visualize the effect of after-hours trading on a group of assets using subplots and iterating over the assets in the group:

```
def after_hours_trades(self):
    """
    Visualize the effect of after-hours trading.

    Returns: A matplotlib `Axes` object.
    """
    num_categories = self.data[self.group_by].nunique()
    fig, axes = plt.subplots(
        num_categories, 2, figsize=(15, 3 * num_categories)
    )

    for ax, (name, data) in zip(
        axes, self.data.groupby(self.group_by)
    ):
        after_hours = data.open - data.close.shift()
        monthly_effect = after_hours.resample('1M').sum()

        after_hours.plot(
            ax=ax[0],
            title=f'{name} Open Price - Prior Day\\'s Close'
        ).set_ylabel('price')

        monthly_effect.index = \
            monthly_effect.index.strftime('%Y-%b')
```

```

monthly_effect.plot(
    ax=ax[1], kind='bar', rot=90,
    color=np.where(monthly_effect >= 0, 'g', 'r'),
    title=f'{name} after-hours trading '
          'monthly effect'
).axhline(0, color='black', linewidth=1)
ax[1].set_ylabel('price')
plt.tight_layout()
return axes

```

With the `StockVisualizer` class, we were able to generate a joint plot between two assets' closing prices, but here we can override `pairplot()` to allow us to see the relationships between the closing prices across assets in the group:

```

def pairplot(self, **kwargs):
    """
    Generate a seaborn pairplot for this asset group.

    Parameters:
    - kwargs: Keyword arguments to pass down.

    Returns: A seaborn pairplot
    """
    return sns.pairplot(
        self.data.pivot_table(
            values='close', index=self.data.index,
            columns=self.group_by
        ), diag_kind='kde', **kwargs
    )

```

Finally, we add the `heatmap()` method, which generates a heatmap of the correlations between the closing prices of all the assets in the group:

```

def heatmap(self, pct_change=True, **kwargs):
    """
    Generate a heatmap for correlations between assets.

    Parameters:
    - pct_change: Whether to show the correlations
      of the daily percent change in price.
    - kwargs: Keyword arguments to pass down.
    """

```

```

    Returns: A seaborn heatmap
    """
    pivot = self.data.pivot_table(
        values='close', index=self.data.index,
        columns=self.group_by
    )
    if pct_change:
        pivot = pivot.pct_change()
    return sns.heatmap(
        pivot.corr(), annot=True, center=0,
        vmin=-1, vmax=1, **kwargs
    )

```

We can use the `heatmap()` method to see how the daily percentage change across assets compares. This will handle the difference in scale between the assets (Google and Amazon have much higher stock prices than Facebook and Apple, meaning that gains of a few dollars mean more to Facebook and Apple):

```

>>> all_assets_viz = \
...     stock_analysis.AssetGroupVisualizer(all_assets)
>>> all_assets_viz.heatmap()

```

Apple-S&P 500 and Facebook-Google have the strongest correlations, with bitcoin having no correlation with anything:

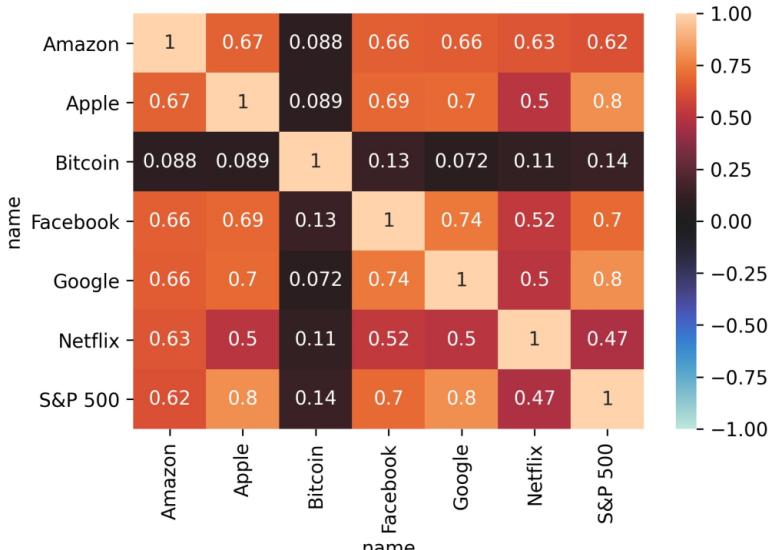


Figure 7.17 – Correlations between asset prices

In the interest of brevity, rather than show all the methods for visualizing an asset group, which will result in large plots, I will leave that to you to view and try out in the notebook. However, let's combine these `Visualizers` to see how all of our assets evolved over time:

```
>>> faang_sp_viz = \
...     stock_analysis.AssetGroupVisualizer(faang_sp)
>>> bitcoin_viz = stock_analysis.StockVisualizer(bitcoin)

>>> fig, axes = plt.subplots(1, 2, figsize=(15, 5))
>>> faang_sp_viz.evolution_over_time(
...     'close', ax=axes[0], style=faang_sp_viz.group_by
... )
>>> bitcoin_viz.evolution_over_time(
...     'close', ax=axes[1], label='Bitcoin'
... )
```

Note that bitcoin had huge gains to close out 2020 (check out the scale on the *y*-axis), and Amazon also saw a lot of growth in 2020:

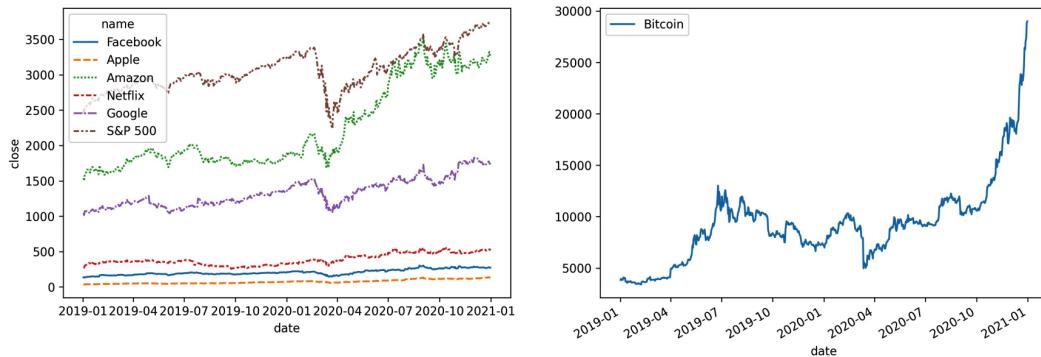


Figure 7.18 – Evolution of asset price over time

Now that we have a good feel for our data, we are ready to look at some metrics. Note that, while we only looked at and used a subset of the code, I encourage you to try out all the methods in the `Visualizer` classes using the notebook for this chapter; the exercises will also offer an additional occasion to use them.

Technical analysis of financial instruments

With technical analysis of assets, metrics (such as cumulative returns and volatility) are calculated to compare various assets to each other. As with the previous two sections in this chapter, we will be writing a module with classes to help us. We will need the `StockAnalyzer` class for technical analysis of a single asset and the `AssetGroupAnalyzer` class for technical analysis of a group of assets. These classes are in the `stock_analysis/stock_analyzer.py` file.

As with the other modules, we will start with our docstring and imports:

```
"""Classes for technical analysis of assets."""

import math

from .utils import validate_df
```

The StockAnalyzer class

For analyzing individual assets, we will build the `StockAnalyzer` class, which calculates metrics for a given asset. The following UML diagram shows all the metrics that it provides:

StockAnalyzer
close data last_close last_high last_low pct_change pivot_point alpha(index, r_f) annualized_volatility() beta(index) corr_with(other) cumulative_returns() cv() daily_std(periods) is_bear_market() is_bull_market() portfolio_return(df) qcd() resistance(level) sharpe_ratio(r_f) support(level) volatility(periods)

Figure 7.19 – Structure of the StockAnalyzer class

A `StockAnalyzer` instance will be initialized with the data for the asset on which we want to perform a technical analysis. This means that our `__init__()` method will need to accept the data as a parameter:

```
class StockAnalyzer:
    """Provides metrics for technical analysis of a stock."""

    @validate_df(columns=['open', 'high', 'low', 'close'])
    def __init__(self, df):
        """Create a `StockAnalyzer` object with OHLC data"""
        self.data = df
```

Most of the calculations for our technical analysis will rely on the closing price of the stock, so rather than needing to write `self.data.close` in all of our methods, we will create a property so that we can access it with `self.close` instead. This makes our code cleaner and easier to follow:

```
@property
def close(self):
    """Get the close column of the data."""
    return self.data.close
```

A few calculations will also need the percent change of the `close` column, so we will make a property for easier access to that as well:

```
@property
def pct_change(self):
    """Get the percent change of the close column."""
    return self.close.pct_change()
```

Since we will be calculating support and resistance levels using the **pivot point**, which is the average of the high, low, and close on the last day in the data, we will make a property for it, as well:

```
@property
def pivot_point(self):
    """Calculate the pivot point."""
    return (self.last_close + self.last_high
           + self.last_low) / 3
```

Note that we are also using other properties—`self.last_close`, `self.last_high`, and `self.last_low`—which we define using the `last()` method on the data, before selecting the column in question and using `iat[]` to get just the price:

```
@property
def last_close(self):
    """Get the value of the last close in the data."""
    return self.data.last('1D').close.iat[0]

@property
def last_high(self):
    """Get the value of the last high in the data."""
    return self.data.last('1D').high.iat[0]

@property
def last_low(self):
    """Get the value of the last low in the data."""
    return self.data.last('1D').low.iat[0]
```

Now, we have everything we need to calculate support and resistance. We will be calculating each at three different levels, where the first level is the closest to the closing price and the third level is the farthest. The first level will therefore be the most restrictive level, and the third will be the least restrictive. We define the `resistance()` method as follows, allowing the caller to specify the level to calculate:

```
def resistance(self, level=1):
    """Calculate the resistance at the given level."""
    if level == 1:
        res = (2 * self.pivot_point) - self.last_low
    elif level == 2:
        res = self.pivot_point \
              + (self.last_high - self.last_low)
    elif level == 3:
        res = self.last_high \
              + 2 * (self.pivot_point - self.last_low)
    else:
        raise ValueError('Not a valid level.')
    return res
```

The support () method is defined in a similar fashion:

```
def support(self, level=1):
    """Calculate the support at the given level."""
    if level == 1:
        sup = (2 * self.pivot_point) - self.last_high
    elif level == 2:
        sup = self.pivot_point \
              - (self.last_high - self.last_low)
    elif level == 3:
        sup = self.last_low \
              - 2 * (self.last_high - self.pivot_point)
    else:
        raise ValueError('Not a valid level.')
    return sup
```

Next, we will work on creating methods for analyzing asset volatility. First, we will calculate the daily standard deviation of the percent change in the closing price, for which we will need to specify the number of trading periods. In order to make sure that we can't use more trading periods than we have in the data, we will define a property with the maximum value we can use for this argument:

```
@property
def _max_periods(self):
    """Get the number of trading periods in the data."""
    return self.data.shape[0]
```

Now that we have our maximum, we can define the daily_std() method, which calculates the daily standard deviation of the daily percentage change:

```
def daily_std(self, periods=252):
    """
    Calculate daily standard deviation of percent change.

    Parameters:
        - periods: The number of periods to use for the
            calculation; default is 252 for the trading days
            in a year. Note if you provide a number greater
            than the number of trading periods in the data,
            `self._max_periods` will be used instead.

    Returns: The standard deviation
    """

```

```
        return self.pct_change\[  
            min(periods, self._max_periods) * -1:\].std()
```

While `daily_std()` is useful on its own, we can take this a step further and calculate annualized volatility by multiplying the daily standard deviation by the square root of the number of trading periods in the year, which we assume to be 252:

```
def annualized_volatility(self):  
    """Calculate the annualized volatility."""  
    return self.daily_std() * math.sqrt(252)
```

In addition, we can look at rolling volatility by using the `rolling()` method:

```
def volatility(self, periods=252):  
    """Calculate the rolling volatility.  
  
    Parameters:  
        - periods: The number of periods to use for the  
            calculation; default is 252 for the trading  
            days in a year. Note if you provide a number  
            greater than the number of trading periods in the  
            data, `self._max_periods` will be used instead.  
  
    Returns: A `pandas.Series` object.  
    """  
    periods = min(periods, self._max_periods)  
    return self.close.rolling(periods).std()\br/>           / math.sqrt(periods)
```

We often want to compare assets, so we provide the `corr_with()` method to calculate the correlations between them using daily percentage change:

```
def corr_with(self, other):  
    """Calculate the correlations between dataframes.  
  
    Parameters:  
        - other: The other dataframe.  
  
    Returns: A `pandas.Series` object  
    """  
    return \  
           self.data.pct_change().corrwith(other.pct_change())
```

Next, we define some metrics for comparing the level of dispersion of assets. In *Chapter 1, Introduction to Data Analysis*, we discussed the coefficient of variation (the `cv()` method) and the quantile coefficient of dispersion (the `qcd()` method), which we can use to achieve this, both of which we will add here:

```
def cv(self):
    """
    Calculate the coefficient of variation for the asset.
    The lower this is, the better the risk/return tradeoff.
    """
    return self.close.std() / self.close.mean()

def qcd(self):
    """Calculate the quantile coefficient of dispersion."""
    q1, q3 = self.close.quantile([0.25, 0.75])
    return (q3 - q1) / (q3 + q1)
```

In addition, we want a way to quantify the volatility of an asset compared to an index, such as the S&P 500, for which we calculate **beta**—the ratio of the covariance of the asset's return and the index's return to the variance of the asset's return. We add the `beta()` method, which allows the user to specify the index to use as a benchmark:

```
def beta(self, index):
    """
    Calculate the beta of the asset.

    Parameters:
        - index: The data for the index to compare to.

    Returns:
        Beta, a float.
    """
    index_change = index.close.pct_change()
    beta = self.pct_change.cov(index_change) \
        / index_change.var()
    return beta
```

Next, we define a method for calculating the cumulative returns of an asset as a series. This is defined as the cumulative product of one plus the percent change in closing price:

```
def cumulative_returns(self):
    """Calculate cumulative returns for plotting."""
    return (1 + self.pct_change).cumprod()
```

The next few metrics we want to support require calculating the return of the portfolio. To make things simpler, we will assume that there is no distribution per share so that the return of the portfolio is the percent change from the starting price to the ending price over the time period covered by the data. We will define this as a static method since we will need to calculate this for an index, and not just the data stored in `self.data`:

```
@staticmethod
def portfolio_return(df):
    """
    Calculate return assuming no distribution per share.

    Parameters:
        - df: The asset's dataframe.

    Returns: The return, as a float.
    """
    start, end = df.close[0], df.close[-1]
    return (end - start) / start
```

While beta allows us to compare an asset's volatility to an index, **alpha** allows us to compare the returns of the asset to those of an index. To do so, we also need the risk-free rate of return, which is the rate of return of an investment that has no risk of financial loss; in practice, we use US Treasury bills for this. Calculating alpha requires calculating the portfolio return of the index and the asset, along with beta:

```
def alpha(self, index, r_f):
    """
    Calculates the asset's alpha.

    Parameters:
        - index: The index to compare to.
        - r_f: The risk-free rate of return.

    Returns: Alpha, as a float.
    """

```

```
r_f /= 100
r_m = self.portfolio_return(index)
beta = self.beta(index)
r = self.portfolio_return(self.data)
alpha = r - r_f - beta * (r_m - r_f)
return alpha
```

Tip

`r_f /= 100` in the previous code snippet divides `r_f` by 100 before storing the result back in `r_f`. It's shorthand for `r_f = r_f / 100`. Python also has these operators for other arithmetic functions—for example, `+=`, `-=`, `*=`, and `%=`.

We also want to add methods that will tell us whether the asset is in a **bear market** or a **bull market**, meaning that it had a decline or increase in stock price of 20% or more in the last 2 months, respectively:

```
def is_bear_market(self):
    """
    Determine if a stock is in a bear market, meaning its
    return in the last 2 months is a decline of 20% or more
    """
    return \
        self.portfolio_return(self.data.last('2M')) <= -.2

def is_bull_market(self):
    """
    Determine if a stock is in a bull market, meaning its
    return in the last 2 months is an increase of >= 20%.
    """
    return \
        self.portfolio_return(self.data.last('2M')) >= .2
```

Lastly, we will add a method for calculating the **Sharpe ratio**, which tells us the return we receive in excess of the risk-free rate of return for the volatility we take on with the investment:

```
def sharpe_ratio(self, r_f):
    """
    Calculates the asset's Sharpe ratio.

    Parameters:
        - r_f: The risk-free rate of return.

    Returns:
        The Sharpe ratio, as a float.
    """
    return (
        self.cumulative_returns().last('1D').iat[0] - r_f
    ) / self.cumulative_returns().std()
```

Take some time to digest the code in this module as we are continuing to build upon what we have discussed. We won't be using all of these metrics for our technical analysis, but I encourage you to try them out in the notebook for this chapter.

The AssetGroupAnalyzer class

All the calculations we will work with in this section are defined on the `StockAnalyzer` class; however, rather than having to run these for each of the assets we want to compare, we will also create the `AssetGroupAnalyzer` class (in the same module) that's capable of providing these metrics for a group of assets.

The `StockAnalyzer` and `AssetGroupAnalyzer` classes will share much of their functionality, which makes a strong argument for designing them with inheritance; however, sometimes—as in this case—composition can make more sense. When objects contain instances of other classes, it is referred to as **composition**. This design decision leaves us with the following very simple UML diagram for the `AssetGroupAnalyzer` class:

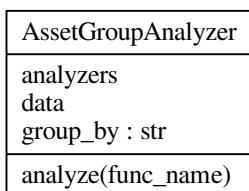


Figure 7.20 – Structure of the `AssetGroupAnalyzer` class

We create an `AssetGroupAnalyzer` instance by providing the dataframe for the assets and the name of the grouping column (if not `name`). Upon initialization, the `_composition_handler()` method is called to create a dictionary of `StockAnalyzer` objects (one for each asset):

```
class AssetGroupAnalyzer:
    """Analyzes many assets in a dataframe."""

    @validate_df(columns={'open', 'high', 'low', 'close'})
    def __init__(self, df, group_by='name'):
        """
        Create an `AssetGroupAnalyzer` object with a
        dataframe of OHLC data and column to group by.
        """

        self.data = df
        if group_by not in self.data.columns:
            raise ValueError(
                f'`group_by` column "{group_by}" not in df.'
            )
        self.group_by = group_by
        self.analyzers = self._composition_handler()

    def _composition_handler(self):
        """
        Create a dictionary mapping each group to its analyzer,
        taking advantage of composition instead of inheritance.
        """

        return {
            group: StockAnalyzer(data)
            for group, data in self.data.groupby(self.group_by)
        }
```

The `AssetGroupAnalyzer` class has only one public method, `analyze()`—all the actual calculations are delegated to the `StockAnalyzer` objects stored in the `analyzers` attribute:

```
def analyze(self, func_name, **kwargs):
    """
    Run a `StockAnalyzer` method on all assets.

    Parameters:
        - func_name: The name of the method to run.
        - kwargs: Additional arguments to pass down.

    Returns:
        A dictionary mapping each asset to the result
        of the calculation of that function.
    """
    if not hasattr(StockAnalyzer, func_name):
        raise ValueError(
            f'StockAnalyzer has no "{func_name}" method.'
        )

    if not kwargs:
        kwargs = {}

    return {
        group: getattr(analyzer, func_name)(**kwargs)
        for group, analyzer in self.analyzers.items()
    }
```

With inheritance, in this case, all the methods would have to be overridden because they can't handle the `groupby()` operation. Conversely, with composition, all that's necessary is to create `StockAnalyzer` objects for each asset and use dictionary comprehensions for the calculations. Another neat thing is that, by using `getattr()`, there is no need to mirror the methods in the `AssetGroupAnalyzer` class because `analyze()` can grab the method by name using the `StockAnalyzer` objects.

Comparing assets

Let's use the `AssetGroupAnalyzer` class to compare all the assets we have collected data for. As with prior sections, we won't use all the methods in the `StockAnalyzer` class here, so be sure to try them out on your own:

```
>>> all_assets_analyzer = \
...     stock_analysis.AssetGroupAnalyzer(all_assets)
```

Remember from *Chapter 1, Introduction to Data Analysis*, that the **coefficient of variation (CV)** is the ratio of the standard deviation to the mean; this helps us compare the variation of asset closing prices, even though their means are of different magnitudes (for instance, Amazon and Apple). The CV can also be used to compare the volatility to the expected return of an investment and quantify the risk-return trade-off. Let's use the CV to see which asset's closing price is the most widely dispersed:

```
>>> all_assets_analyzer.analyze('cv')
{'Amazon': 0.2658012522278963,
 'Apple': 0.36991905161737615,
 'Bitcoin0.43597652683008137,
 'Facebook': 0.19056336194852783,
 'Google': 0.15038618497328074,
 'Netflix': 0.20344854330432688,
 'S&P 500': 0.09536374658108937}
```

It's probably not a surprise that bitcoin has the widest spread. Rather than use the closing price, percent change daily can be used to calculate the annualized volatility. This involves calculating the standard deviations of percent change over the last year and multiplying it by the square root of the number of trading days in the year (the code assumes 252). By using percent change, large changes in price (relative to the asset's price) will be penalized more severely. Using annualized volatility, Facebook looks much more volatile compared to when we used the CV (although still not the most volatile):

```
>>> all_assets_analyzer.analyze('annualized_volatility')
{'Amazon': 0.3851099077041784,
 'Apple': 0.4670809643500882,
 'Bitcoin': 0.4635140114227397,
 'Facebook0.45943066572169544,
 'Google': 0.3833720603377728,
 'Netflix': 0.4626772090887299,
 'S&P 500': 0.34491195196047003}
```

Given that all the assets have gained value toward the end of our dataset, let's check if any of them have entered a **bull market**, meaning that the asset's return in the last 2 months is a 20% or greater gain:

```
>>> all_assets_analyzer.analyze('is_bull_market')
{'Amazon': False,
'Apple': True,
'Bitcoin': True,
'Facebook': False,
'Google': False,
'Netflix': False,
'S&P 500': False}
```

It looks like Apple and bitcoin had quite a November and December in 2020. The other assets appear to not have fared as well; however, none of them are in a bear market (we can confirm this by passing '`is_bear_market`' to `analyze()`). Yet another way to analyze volatility is to compare the assets to an index by calculating **beta**. Positive values greater than 1 indicate volatility higher than the index, while negative values less than -1 indicate inverse relationships to the index:

```
>>> all_assets_analyzer.analyze('beta', index=sp)
{'Amazon': 0.7563691182389207,
'Apple': 1.173273501105916,
'Bitcoin': 0.3716024282483362,
'Facebook': 1.024592821854751,
'Google': 0.98620762504024,
'Netflix': 0.7408228073823271,
'S&P 500': 1.0000000000000002}
```

Using the betas from the previous result, we can see that Apple is the most volatile compared to the S&P 500, meaning that if this was our portfolio (leaving out bitcoin for the moment), adding Apple would have increased the portfolio risk. However, we know that bitcoin is not correlated to the S&P 500 (see the correlation heatmap in *Figure 7.17*), so this low beta is misleading.

The last metric we will take a look at is **alpha**, which is used to compare the return of an investment to the market. Calculating alpha requires that we pass in the risk-free rate of return (`r_f`); we typically use the return of a US Treasury bill for this number. Rates can be looked up at <https://www.treasury.gov/resource-center/data-chart-center/interest-rates/pages/TextView.aspx?data=yield>; alternatively, we can use our `StockReader` object (`reader`) to collect this for us. Let's compare the alphas for the assets using the S&P 500 as our index:

```
>>> r_f = reader.get_risk_free_rate_of_return() # 0.93
>>> all_assets_analyzer.analyze('alpha', index=sp, r_f=r_f)
{'Amazon': 0.7383391908270172,
 'Apple': 1.7801122522388666,
 'Bitcoin': 6.355297988074054,
 'Facebook': 0.5048625273190841,
 'Google': 0.18537197824248092,
 'Netflix': 0.6500392764754642,
 'S&P 500': -1.1102230246251565e-16}
```

Everything beat the S&P 500, which essentially being a portfolio of 500 stocks has lower risk and lower returns due to **diversification**. This brings us to cumulative returns, which shows the return for each dollar we invested. To make this plot a little easier to interpret in the black and white text, we will create a custom `Cycler` object (<https://matplotlib.org/cycler/>) that varies the color and line styles:

```
>>> from cycler import cycler
>>> bw_viz_cycler = (
...     cycler(color=[plt.get_cmap('tab10')(x/10)
...                   for x in range(10)])
...     + cycler(linestyle=['dashed', 'solid', 'dashdot',
...                         'dotted', 'solid'] * 2))
>>> fig, axes = plt.subplots(1, 2, figsize=(15, 5))
>>> axes[0].set_prop_cycle(bw_viz_cycler)
>>> cumulative_returns = \
...     all_assets_analyzer.analyze('cumulative_returns')
>>> for name, data in cumulative_returns.items():
...     data.plot(
...         ax=axes[1] if name == 'Bitcoin' else axes[0],
...         label=name, legend=True
...     )
>>> fig.suptitle('Cumulative Returns')
```

Despite the struggles in early 2020, all of the assets gained value. Notice that the bitcoin subplot's y -axis goes from 0 to 7 (right subplot), while the stock market subplot (left) covers half of that range:

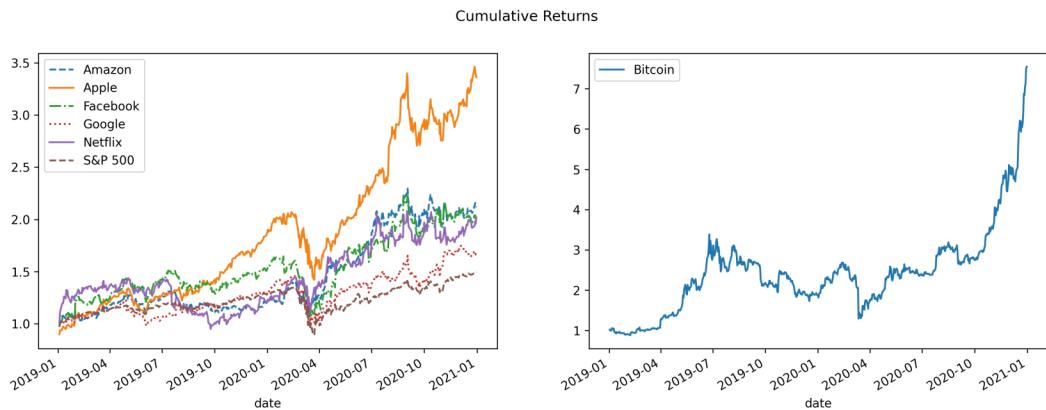


Figure 7.21 – Cumulative returns for all assets

Now that we have a good understanding of how to analyze financial instruments, let's try our hand at forecasting future performance.

Modeling performance using historical data

The goal of this section is to give us a taste of how to build some models; as such, the following examples are not meant to be the best possible model, but rather a simple and relatively quick implementation for learning purposes. Once again, the `stock_analysis` package has a class for this section's task: `StockModeler`.

Important note

To fully understand the statistical elements of this section and modeling in general, we need a solid understanding of statistics; however, the purpose of this discussion is to show how modeling techniques can be applied to financial data without dwelling on the underlying mathematics.

The StockModeler class

The `StockModeler` class will make it easier for us to build and evaluate some simple financial models without needing to interact directly with the `statsmodels` package. In addition, we will reduce the number of steps that are needed to generate a model with the methods we create. The following UML diagram shows that this is a rather simple class. Notice that we have no attributes because `StockModeler` is a **static class** (meaning that we don't instantiate it):

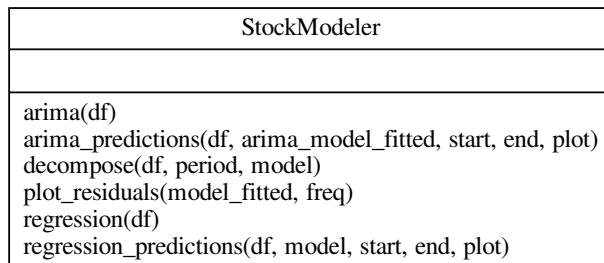


Figure 7.22 – Structure of the StockModeler class

The `StockModeler` class is defined in `stock_analysis/stock_modeler.py` and has methods for both building models and doing some preliminary analysis of their performance. As usual, we start the module with our docstring and imports:

```

"""Simple time series modeling for stocks."""

import matplotlib.pyplot as plt
import pandas as pd
from statsmodels.tsa.arima.model import ARIMA
from statsmodels.tsa.seasonal import seasonal_decompose
import statsmodels.api as sm

from .utils import validate_df
  
```

Next, we will start the `StockModeler` class and raise an error if someone tries to instantiate it:

```

class StockModeler:
    """Static methods for modeling stocks."""

    def __init__(self):
        raise NotImplementedError(
            "This class must be used statically: "
            "don't instantiate it."
        )
  
```

One of the tasks we want this class to support is time series decomposition, which we discussed back in *Chapter 1, Introduction to Data Analysis*. We imported the `seasonal_decompose()` function from `statsmodels`, so we just have to call it on the closing price in our `decompose()` method:

```
@staticmethod
@validate_df(columns={'close'}, instance_method=False)
def decompose(df, period, model='additive'):
    """
    Decompose the closing price of the stock into
    trend, seasonal, and remainder components.

    Parameters:
        - df: The dataframe containing the stock closing
              price as `close` and with a time index.
        - period: The number of periods in the frequency.
        - model: How to compute the decomposition
                 ('additive' or 'multiplicative')

    Returns:
        A `statsmodels` decomposition object.
    """
    return seasonal_decompose(
        df.close, model=model, period=period
    )
```

Notice that we have two decorators for the `decompose()` method. The topmost decorator is applied on the result of the ones below it. In this example, we have the following:

```
staticmethod(
    validate_df(
        decompose, columns={'close'}, instance_method=False
    )
)
```

In addition, we want to support creating ARIMA models, which we also discussed in *Chapter 1, Introduction to Data Analysis*. ARIMA models use the $ARIMA(p, d, q)$ notation, where p is the number of time lags (or order) of the AR model, d is the number of past values that were subtracted from the data (the I model), and q is the number of periods used in the MA model. So, an $ARIMA(1, 1, 1)$ is a model with one time lag for the autoregressive portion, data differenced once, and a 1-period moving average. If we have any zeros for the orders, we can eliminate those—for example, $ARIMA(1, 0, 1)$ is equivalent to $ARMA(1, 1)$, and $ARIMA(0, 0, 3)$ is equivalent to $MA(3)$. A seasonal ARIMA model is written as $ARIMA(p, d, q)(P, D, Q)_m$ where m is the number of periods in the seasonal model and P , D , and Q are the orders for the seasonal ARIMA model. The `StockModeler.arima()` method doesn't support the seasonal components (for simplicity) and takes p , d , and q as parameters, but to avoid confusion we will name them after the ARIMA feature they represent—for example, ar for autoregressive (p). In addition, we are going to have our static method provide the option of fitting the model before returning it:

```

@staticmethod
@validate_df(columns={'close'}, instance_method=False)
def arima(df, *, ar, i, ma, fit=True, freq='B'):
    """
    Create an ARIMA object for modeling time series.

    Parameters:
        - df: The dataframe containing the stock closing
              price as `close` and with a time index.
        - ar: The autoregressive order (p).
        - i: The differenced order (q).
        - ma: The moving average order (d).
        - fit: Whether to return the fitted model
        - freq: Frequency of the time series

    Returns:
        A `statsmodels` ARIMA object which you can use
        to fit and predict.
    """
    arima_model = ARIMA(
        df.close.asfreq(freq).fillna(method='ffill'),
        order=(ar, i, ma)
    )
    return arima_model.fit() if fit else arima_model

```

Tip

Note that the method signature (`df, *, ar, i, ma, ...`) has an asterisk (*) in it. This forces the parameters listed after it to be supplied as keyword arguments when calling the method. It's a nice way to make sure that whoever uses this is explicit about what they want.

To go along with this, we want a way to evaluate the ARIMA model's predictions, so we will add the `arima_predictions()` static method. We will also provide the option of getting back the predictions as a `Series` object or as a plot:

```
@staticmethod
@validate_df(columns={'close'}, instance_method=False)
def arima_predictions(df, arima_model_fitted, start, end,
                      plot=True, **kwargs):
    """
    Get ARIMA predictions as a `Series` object or plot.

    Parameters:
        - df: The dataframe for the stock.
        - arima_model_fitted: The fitted ARIMA model.
        - start: The start date for the predictions.
        - end: The end date for the predictions.
        - plot: Whether to plot the result, default is
            `True` meaning the plot is returned instead of
            the `Series` object containing the predictions.
        - kwargs: Additional arguments to pass down.

    Returns:
        A matplotlib `Axes` object or predictions
        depending on the value of the `plot` argument.
    """
    predictions = \
        arima_model_fitted.predict(start=start, end=end)

    if plot:
        ax = df.close.plot(**kwargs)
        predictions.plot(
            ax=ax, style='r:', label='arima predictions'
        )
        ax.legend()

    return ax if plot else predictions
```

Similar to what we built for ARIMA models, we will also provide the `regression()` method for building a linear regression model of the closing price with a lag of 1. For this, we will once again use `statsmodels` (in *Chapter 9, Getting Started with Machine Learning in Python*, we will use `scikit-learn` for linear regression instead):

```
@staticmethod
@validate_df(columns={'close'}, instance_method=False)
def regression(df):
    """
    Create linear regression of time series with lag=1.

    Parameters:
        - df: The dataframe with the stock data.

    Returns:
        X, Y, and the fitted model
    """
    X = df.close.shift().dropna()
    Y = df.close[1:]
    return X, Y, sm.OLS(Y, X).fit()
```

As with the `arima_predictions()` method, we want to provide a way to review the predictions from the model, either as a `Series` object or as a plot. Unlike the ARIMA model, it will only predict one value at a time. Therefore, we will start our predictions on the day after the last closing price and iteratively use the previous prediction to predict the next one. To handle all this, we will write the `regression_predictions()` method:

```
@staticmethod
@validate_df(columns={'close'}, instance_method=False)
def regression_predictions(df, model, start, end,
                           plot=True, **kwargs):
    """
    Get linear regression predictions as a `pandas.Series` object or plot.

    Parameters:
        - df: The dataframe for the stock.
        - model: The fitted linear regression model.
        - start: The start date for the predictions.
        - end: The end date for the predictions.
    """
    predictions = pd.Series(index=pd.date_range(start, end))
    predictions[0] = model.predict(df.loc[start].values.reshape(1, -1))
```

```
- plot: Whether to plot the result, default is
      `True` meaning the plot is returned instead of
      the `Series` object containing the predictions.
- kwargs: Additional arguments to pass down.

>Returns:
A matplotlib `Axes` object or predictions
depending on the value of the `plot` argument.

"""
predictions = pd.Series(
    index=pd.date_range(start, end), name='close'
)
last = df.last('1D').close
for i, date in enumerate(predictions.index):
    if not i:
        pred = model.predict(last)
    else:
        pred = model.predict(predictions.iloc[i - 1])
    predictions.loc[date] = pred[0]

if plot:
    ax = df.close.plot(**kwargs)
    predictions.plot(
        ax=ax, style='r:',
        label='regression predictions'
    )
    ax.legend()

return ax if plot else predictions
```

Lastly, for both the ARIMA and linear regression models, we want to visualize the errors in the predictions, or **residuals**. The fitted models both have a `resid` attribute, which will give us the residuals; we simply need to plot them as a scatter plot to check their variance and a KDE to check their mean. For this, we will add the `plot_residuals()` method:

```
@staticmethod
def plot_residuals(model_fitted, freq='B'):
    """
    Visualize the residuals from the model.
```

```

Parameters:
    - model_fitted: The fitted model
    - freq: Frequency that the predictions were
        made on. Default is 'B' (business day).

Returns:
    A matplotlib `Axes` object.

"""
fig, axes = plt.subplots(1, 2, figsize=(15, 5))
residuals = pd.Series(
    model_fitted.resid.asfreq(freq), name='residuals'
)
residuals.plot(
    style='bo', ax=axes[0], title='Residuals'
)
axes[0].set(xlabel='Date', ylabel='Residual')
residuals.plot(
    kind='kde', ax=axes[1], title='Residuals KDE'
)
axes[1].set_xlabel('Residual')
return axes

```

Now, let's take the `StockModeler` class for a spin, once again using the Netflix data.

Time series decomposition

As mentioned in *Chapter 1, Introduction to Data Analysis*, time series can be decomposed into trend, seasonal, and remainder components utilizing a specified frequency. This can be achieved with the `statsmodels` package, which `StockModeler.decompose()` is using:

```

>>> from stock_analysis import StockModeler
>>> decomposition = StockModeler.decompose(nflx, 20)
>>> fig = decomposition.plot()
>>> fig.suptitle(
...     'Netflix Stock Price Time Series Decomposition', y=1
... )
>>> fig.set_figheight(6)
>>> fig.set_figwidth(10)
>>> fig.tight_layout()

```

This returns the decomposition plot for Netflix with a frequency of 20 trading days:

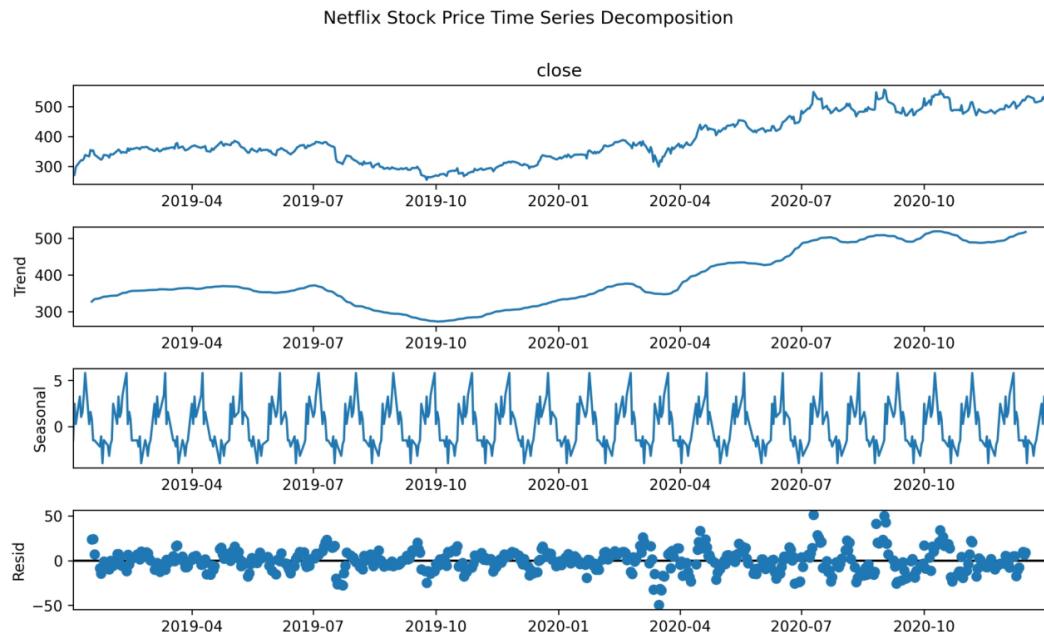


Figure 7.23 – Time series decomposition of Netflix's stock price over time

For more complicated models, we could decompose and then build our model around the components. That is beyond the scope of this chapter, however, so let's move on to ARIMA models.

ARIMA

As we discussed in *Chapter 1, Introduction to Data Analysis*, ARIMA models have autoregressive, difference, and moving average components. They can also be built using the `statsmodels` package, which the `StockModeler.arima()` method is using; this method returns a fitted ARIMA model for the stock according to the specifications provided. Here, we will use the `%%capture` magic to avoid printing any warnings triggered by the ARIMA model fitting, since we are making a simple model to explore functionality:

```
>>> %%capture
>>> arima_model = StockModeler.arima(nflx, ar=10, i=1, ma=5)
```

Tip

We're picking these values because they run in a reasonable amount of time. In practice, we can use the `autocorrelation_plot()` function from the `pandas.plotting` module that was introduced in *Chapter 5, Visualizing Data with Pandas and Matplotlib*, to help find a good value for `ar`.

Once the model is fitted, we can obtain information on it with the model's `summary()` method:

```
>>> print(arima_model.summary())
```

The summary is quite extensive, and we should read the documentation when looking to interpret it; however, this article is likely to be a more digestible introduction:

<https://medium.com/analytics-vidhya/interpreting-arma-model-results-in-statsmodels-for-absolute-beginners-a4d22253ad1c>. Be advised that interpreting this summary will require a solid understanding of statistics:

SARIMAX Results						
Dep. Variable:	close	No. Observations:	522			
Model:	ARIMA(10, 1, 5)	Log Likelihood	-1925.850			
Date:	Mon, 18 Jan 2021	AIC	3883.700			
Time:	19:02:23	BIC	3951.792			
Sample:	01-02-2019 - 12-31-2020	HQIC	3910.372			
Covariance Type:	opg					
	coef	std err	z	P> z	[0.025	0.975]
ar.L1	-0.1407	0.254	-0.554	0.580	-0.639	0.358
ar.L2	0.1384	0.178	0.777	0.437	-0.211	0.488
ar.L3	-0.3349	0.165	-2.033	0.042	-0.658	-0.012
ar.L4	0.6575	0.171	3.839	0.000	0.322	0.993
ar.L5	0.5988	0.215	2.787	0.005	0.178	1.020
ar.L6	-0.1005	0.076	-1.315	0.188	-0.250	0.049
ar.L7	0.0555	0.052	1.072	0.284	-0.046	0.157
ar.L8	-0.0522	0.042	-1.256	0.209	-0.134	0.029
ar.L9	-0.0722	0.051	-1.425	0.154	-0.172	0.027
ar.L10	0.1021	0.056	1.813	0.070	-0.008	0.212
ma.L1	-0.0084	0.257	-0.032	0.974	-0.513	0.496
ma.L2	-0.0854	0.196	-0.435	0.663	-0.470	0.299
ma.L3	0.3300	0.184	1.797	0.072	-0.030	0.690
ma.L4	-0.6166	0.174	-3.549	0.000	-0.957	-0.276
ma.L5	-0.5170	0.213	-2.425	0.015	-0.935	-0.099
sigma2	93.0293	3.711	25.071	0.000	85.756	100.302
Ljung-Box (Q):		33.12	Jarque-Bera (JB):		373.34	
Prob(Q):		0.77	Prob(JB):		0.00	
Heteroskedasticity (H):		2.46	Skew:		-0.10	
Prob(H) (two-sided):		0.00	Kurtosis:		7.14	

Warnings:
[1] Covariance matrix calculated using the outer product of gradients (complex-step).

Figure 7.24 – Summary of our ARIMA model

For our purposes, a simpler way of analyzing the model is to look at the **residuals**, or the discrepancy between the observed values and predictions made by the model. The residuals should have a mean of 0 and have equal variance throughout, meaning that they should not depend on the independent variable (which is the date, in this case). The latter requirement is referred to as **homoskedasticity**; when this assumption is not met, the estimates given by the model are not optimal. The `StockModeler.plot_residuals()` method helps check for this visually:

```
>>> StockModeler.plot_residuals(arima_model)
```

While the residuals are centered at 0 (right subplot), they are **heteroskedastic**—note how their variance appears to increase over time (left subplot):

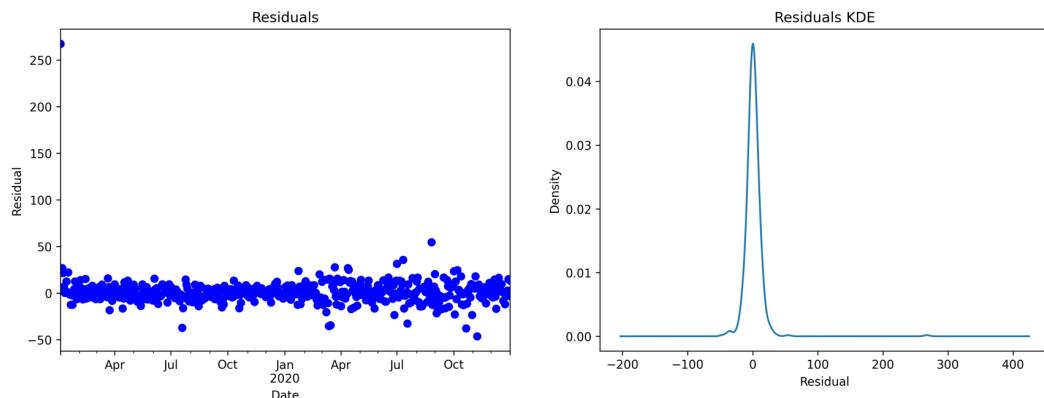


Figure 7.25 – Evaluating the residuals of our ARIMA model

Tip

When we looked at the model summary in *Figure 7.24*, `statsmodels` ran a statistical test for heteroskedasticity using the default significance level of 0.05. The value of the test statistic is labeled **Heteroskedasticity (H)** and the p-value is labeled **Prob(H) (two-sided)**. Note that the result was statistically significant (the p-value was less than or equal to the significance level), meaning it's very unlikely that our residuals are homoskedastic.

As an alternative to building an ARIMA model, the `StockModeler` class also gives us the option of using linear regression to model the closing price of a financial instrument.

Linear regression with statsmodels

The `StockModeler.regression()` method builds a linear regression model for closing price as a function of the prior day's closing price using `statsmodels`:

```
>>> X, Y, lm = StockModeler.regression(nflx)
>>> print(lm.summary())
```

Once again, the `summary()` method gives us statistics on the model's fit:

```
OLS Regression Results
=====
Dep. Variable:           close   R-squared (uncentered):      0.999
Model:                 OLS    Adj. R-squared (uncentered):  0.999
Method:                Least Squares   F-statistic:           7.470e+05
Date:      Mon, 18 Jan 2021   Prob (F-statistic):        0.00
Time:          19:15:40   Log-Likelihood:            -1889.3
No. Observations:      504    AIC:                  3781.
Df Residuals:         503    BIC:                  3785.
Df Model:                   1
Covariance Type:    nonrobust
=====
            coef    std err        t     P>|t|      [0.025    0.975]
-----
close    1.0011    0.001    864.291      0.000      0.999    1.003
=====
Omnibus:             50.714   Durbin-Watson:        2.317
Prob(Omnibus):       0.000    Jarque-Bera (JB):  307.035
Skew:                 -0.014   Prob(JB):            2.13e-67
Kurtosis:              6.824   Cond. No.             1.00
=====
```

Warnings:

[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

Figure 7.26 – Summary of our linear regression model

Tip

Take a look at this article for some guidance on how to interpret the summary: <https://medium.com/swlh/interpreting-linear-regression-through-statsmodels-summary-4796d359035a>.

The adjusted R² makes this model look very good since it is near 1 (in *Chapter 9, Getting Started with Machine Learning in Python*, we will discuss this metric further); however, we know that this is simply because stock data is highly autocorrelated, so let's look at the residuals again:

```
>>> StockModeler.plot_residuals(lm)
```

This model also suffers from heteroskedasticity:

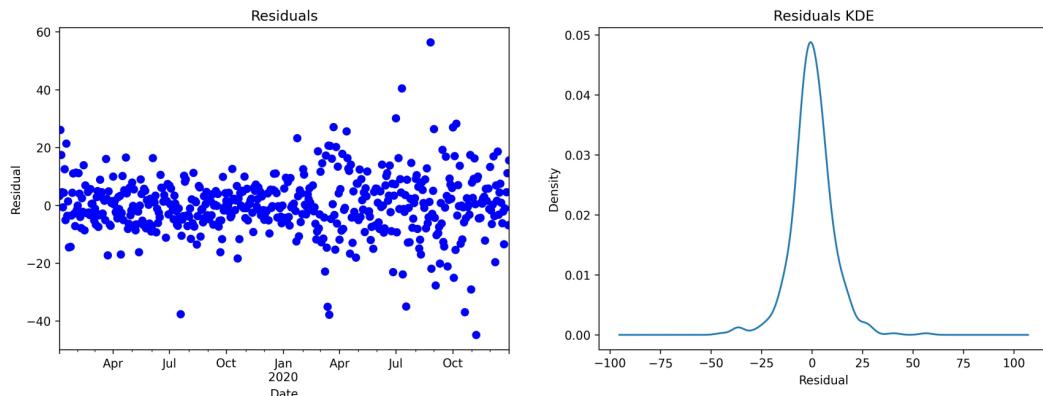


Figure 7.27 – Evaluating the residuals of our linear regression model

Let's now see whether the ARIMA model or the linear regression model performs better at forecasting Netflix stock's closing prices.

Comparing models

In order to compare our models, we need to test their predictions on some new data. Let's gather the daily closing price of Netflix stock for the first two weeks in January 2021 and use the prediction methods in the `StockModeler` class to visualize our model predictions versus reality:

```
>>> import datetime as dt

>>> start = dt.date(2021, 1, 1)
>>> end = dt.date(2021, 1, 14)

>>> jan = stock_analysis.StockReader(start, end) \
...     .get_ticker_data('NFLX')

>>> fig, axes = plt.subplots(1, 2, figsize=(15, 5))
```

```

>>> arima_ax = StockModeler.arima_predictions(
...     nflux, arima_model, start=start, end=end,
...     ax=axes[0], title='ARIMA', color='b'
... )
>>> jan.close.plot(
...     ax=arima_ax, style='b--', label='actual close'
... )
>>> arima_ax.legend()
>>> arima_ax.set_ylabel('price ($)')
>>>
>>> linear_reg = StockModeler.regression_predictions(
...     nflux, lm, start=start, end=end,
...     ax=axes[1], title='Linear Regression', color='b'
... )
>>> jan.close.plot(
...     ax=linear_reg, style='b--', label='actual close'
... )
>>> linear_reg.legend()
>>> linear_reg.set_ylabel('price ($)')

```

The ARIMA model's predictions look more in line with the pattern we would expect, but, given the unpredictable nature of the stock market, both models are far off from what actually happened in the first two weeks of January 2021:

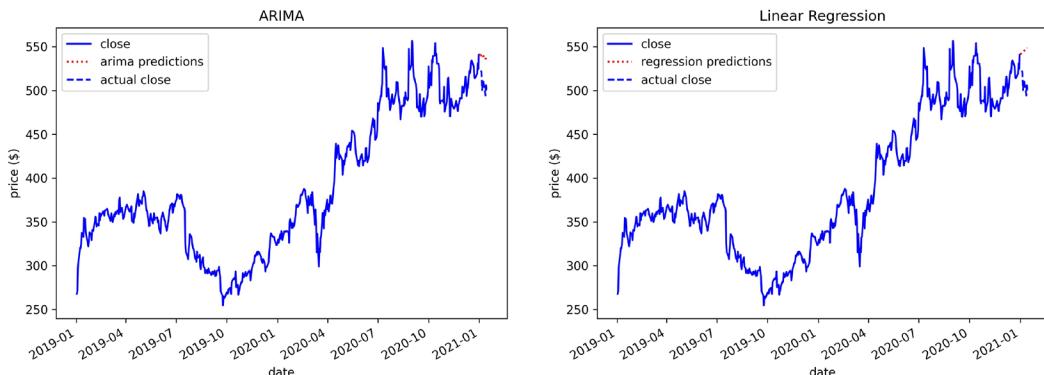


Figure 7.28 – Model predictions versus reality

As we can see, forecasting stock performance is not easy, even for a few days. There is a lot of data that is not being captured by these models, such as news stories, regulations, and changes in management, to name a few. No matter how well a model appears to fit, be weary of trusting predictions as these will be extrapolations, and there is a lot of randomness not being accounted for.

To further illustrate this, take a look at the following set of plots that have been generated using random walks and stock data. Only one is real data, but which one? The answer follows the plots, so be sure to take a guess before looking:

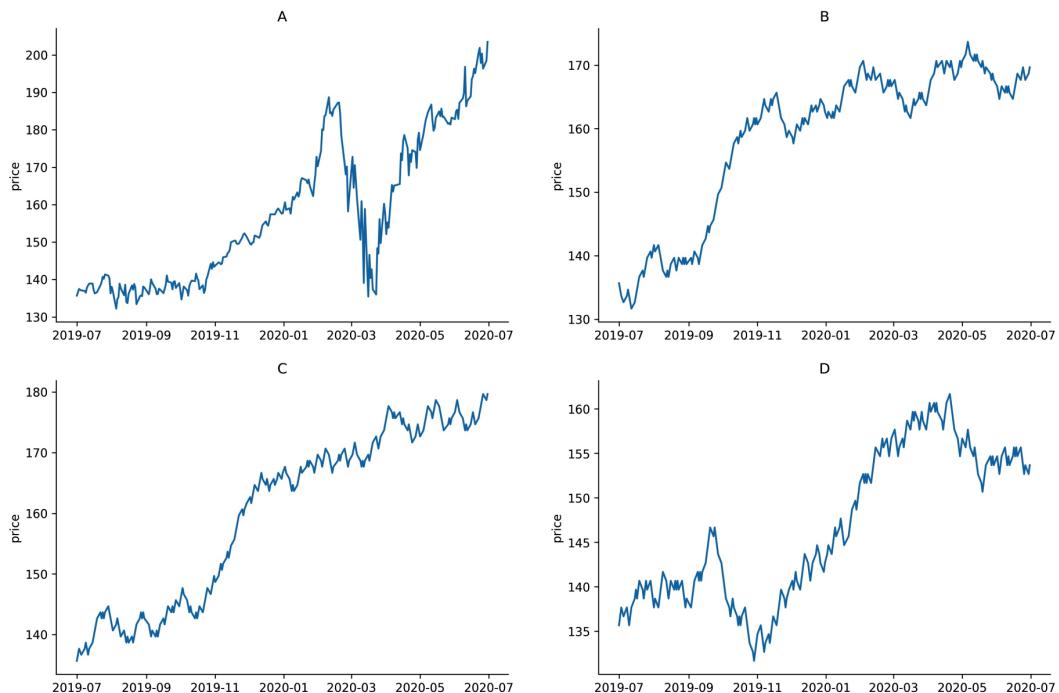


Figure 7.29 – Real or fake stock data?

Each of these time series originates at the same point (Microsoft's closing price on July 1, 2019), but only **A** is real stock data—**B**, **C**, and **D** are all random walks. Hard (or impossible) to tell, right?

Summary

In this chapter, we saw how building Python packages for our analysis applications can make it very easy for others to carry out their own analyses and reproduce ours, as well as for us to create repeatable workflows for future analyses.

The `stock_analysis` package we created in this chapter contained classes for gathering stock data from the Internet (`StockReader`); visualizing individual assets or groups of them (`Visualizer` family); calculating metrics for single assets or groups of them for comparisons (`StockAnalyzer` and `AssetGroupAnalyzer`, respectively); and time series modeling with decomposition, ARIMA, and linear regression (`StockModeler`). We also got our first look at using the `statsmodels` package in the `StockModeler` class. This chapter showed us how the `pandas`, `matplotlib`, `seaborn`, and `numpy` functionality that we've covered so far in this book has come together and how these libraries can work harmoniously with other packages for custom applications. I strongly encourage you to reread the code in the `stock_analysis` package and test out some of the methods we didn't cover in this chapter to make sure you have the concepts down.

In the next chapter, we will work on another application as we learn how to build a simulator for login attempts and try our hand at rule-based anomaly detection.

Exercises

Use the `stock_analysis` package to complete the following exercises. Unless otherwise noted, use data from 2019 through the end of 2020. In case there are any issues collecting the data with the `StockReader` class, backup CSV files are provided in the `exercises/` directory:

1. Using the `StockAnalyzer` and `StockVisualizer` classes, calculate and plot three levels of support and resistance for Netflix's closing price.
2. With the `StockVisualizer` class, look at the effect of after-hours trading on the FAANG stocks:
 - a) As individual stocks
 - b) As a portfolio using the `make_portfolio()` function from the `stock_analysis.utils` module

3. Using the `StockVisualizer.open_to_close()` method, create a plot that fills the area between the FAANG stocks' opening price (as a portfolio) and its closing price each day in red if the price declined and in green if the price increased. As a bonus, do the same for a portfolio of bitcoin and the S&P 500.
4. Mutual funds and **exchange-traded funds (ETFs)** are funds that are composed of many assets. They are built to mitigate risk, so volatility for the fund will be lower than that of the assets that compose it. (Information on how they differ can be found at <https://www.investopedia.com/articles/exchangetradedfunds/08/etf-mutual-fund-difference.asp>.) Compare a mutual fund or ETF of your choice to three of its largest stocks (by composition) using annualized volatility and the `AssetGroupAnalyzer` class.
5. Write a function that returns a dataframe of one row with columns for `alpha`, `beta`, `sharpe_ratio`, `annualized_volatility`, `is_bear_market`, and `is_bull_market`, which each contain the results of running the respective methods on a given stock using the `StockAnalyzer` class. Dictionary comprehensions and the `getattr()` function, as used in the `AssetGroupAnalyzer.analyze()` method, will be useful.
6. With the `StockModeler` class, build an ARIMA model fit on the S&P 500 data from January 1, 2019 through November 30, 2020 and use it to predict the performance in December 2020. Be sure to examine the residuals and compare the predicted performance to the actual performance.
7. Request an API key for AlphaVantage (<https://www.alphavantage.co/support/#api-key>) and collect the daily foreign exchange rate from USD to JPY using the `get_forex_rates()` method on the same `StockReader` object you created to collect the data for the previous exercises. Build a candlestick plot with the data from February 2019 through January 2020, resampled to 1-week intervals. Hint: take a look at the `slice()` function from the standard library (<https://docs.python.org/3/library/functions.html#slice>) in order to provide the date range.

Further reading

Check out the following resources for more information on the material covered in this chapter:

- *A guide to Python's function decorators*: <https://www.thecodeship.com/patterns/guide-to-python-function-decorators/>
- *Alpha*: <https://www.investopedia.com/terms/a/alpha.asp>
- *An Introduction to Classes and Inheritance (in Python)*: <http://www.jesshamrick.com/2011/05/18/an-introduction-to-classes-and-inheritance-in-python/>
- *Beta*: <https://www.investopedia.com/terms/b/beta.asp>
- *Coefficient of Variation (CV)*: <https://www.investopedia.com/terms/c/coefficientofvariation.asp>
- *Classes (Python Documentation)*: <https://docs.python.org/3/tutorial/classes.html>
- *How After-Hours Trading Affects Stock Prices*: <https://www.investopedia.com/ask/answers/05/saleafterhours.asp>
- *How to Create a Python Package*: <https://www.pythontutorial.net/python-basics/tutorials/python-package/>
- *How to Create an ARIMA Model for Time Series Forecasting in Python*: <https://machinelearningmastery.com/arima-for-time-series-forecasting-with-python/>
- *Linear Regression in Python using statsmodels*: <https://datatofish.com/statsmodels-linear-regression/>
- *Object-Oriented Programming*: <https://python.swaroopch.com/oop.html>
- *Random walk*: https://en.wikipedia.org/wiki/Random_walk
- *Stock Analysis*: <https://www.investopedia.com/terms/s/stock-analysis.asp>
- *Support and Resistance Basics*: <https://www.investopedia.com/trading/support-and-resistance-basics/>

- *Technical Analysis:* <https://www.investopedia.com/technical-analysis-4689657>
- *The definitive guide on how to use static, class or abstract methods in Python:* <https://julien.danjou.info/guide-python-static-class-abstract-methods/>
- *Writing the Setup Script:* <https://docs.python.org/3/distutils/setupscript.html>

8

Rule-Based Anomaly Detection

It's time to catch some hackers trying to gain access to a website using a **brute-force attack**—trying to log in with a bunch of username-password combinations until they gain access. This type of attack is very noisy, so it gives us plenty of data points for **anomaly detection**, which is the process of looking for data generated from a process other than the one we deem to be typical activity. The hackers will be simulated and won't be as crafty as they can be in real life, but it will give us great exposure to anomaly detection.

We will be creating a package that will handle the simulation of the login attempts in order to generate the data for this chapter. Knowing how to simulate is an essential skill to have in our toolbox. Sometimes, it's difficult to solve a problem with an exact mathematical solution; however, it might be easy to define how small components of the system work. In these cases, we can model the small components and simulate the behavior of the system as a whole. The result of the simulation gives us an approximation of the solution that may be sufficient for our purposes.

We will utilize rule-based anomaly detection to identify suspicious activity in the simulated data. By the end of this chapter, we will have an understanding of how to simulate data using random numbers generated from various probability distributions, get more exposure to the Python standard library, gain additional experience building Python packages, practice performing exploratory data analysis, and get an introduction to anomaly detection.

The following topics will be covered in this chapter:

- Simulating login attempts to create our dataset for the chapter
- Performing exploratory data analysis to understand the simulated data
- Using rules and baselines for anomaly detection

Chapter materials

We will be building a simulation package to generate the data for this chapter; it is on GitHub at https://github.com/stefmolin/login-attempt-simulator/tree/2nd_edition. This package was installed from GitHub when we set up our environment back in *Chapter 1, Introduction to Data Analysis*; however, you can follow the instructions in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*, to install a version of the package that you can edit.

The repository for this chapter, which can be found at https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_08, has the notebook we will use for our actual analysis (`anomaly_detection.ipynb`), the data files we will be working with in the `logs/` folder, the data used for the simulation in the `user_data/` folder, and the `simulate.py` file, which contains a Python script that we can run on the command line to simulate the data for the chapter.

Simulating login attempts

Since we can't easily find login attempt data from a breach (it's not typically shared due to its sensitive nature), we will be simulating it. Simulation requires a strong understanding of statistical modeling, estimating probabilities of certain events, and identifying appropriate assumptions to simplify where necessary. In order to run the simulation, we will build a Python package (`login_attempt_simulator`) to simulate a login process requiring a correct username and password (without any extra authentication measures, such as two-factor authentication) and a script (`simulate.py`) that can be run on the command line, both of which we will discuss in this section.

Assumptions

Before we jump into the code that handles the simulation, we need to understand the assumptions. It is impossible to control for every possible variable when we make a simulation, so we must identify some simplifying assumptions to get started.

The simulator makes the following assumptions regarding valid users of the website:

- Valid users come according to a **Poisson process** at an hourly rate that depends on the day of the week and the time of day. A Poisson process models arrivals per unit of time (our simulation will use an hour) as a Poisson distribution with mean λ (lambda). The interarrival times are exponentially distributed with mean $1/\lambda$.
- Valid users connect from 1-3 IP addresses (a unique identifier for each device using the Internet), which comprise 4 random integers in the range [0, 255] separated by periods. It is possible, although highly unlikely, that two valid users share an IP address.
- Valid users are unlikely to make many mistakes while entering their credentials.

Important note

The interarrival times have the **memoryless** property, meaning that the time between two consecutive arrivals has no bearing on when the subsequent arrival will happen.

The simulator makes the following assumptions about the hackers:

- The hackers try to avoid an account lockout by only testing a few username-password combinations, rather than a full-blown **dictionary attack** (for every user, trying every password the hacker has in a dictionary of possible passwords that they maintain). However, they don't add delays between their attempts.
- Since the hackers don't want to cause a denial of service, they limit the volume of their attacks and only make one attempt at a time.
- The hackers know the number of accounts that exist in the system and have a good idea of the format the usernames are in, but are guessing the exact usernames. They will choose to try to guess all 133 usernames, or some subset of them.
- Each attack is standalone, meaning there is a single hacker acting for each attack, and a hacker never attacks more than once.
- The hackers don't share information about which username-password combinations are correct.

- The attacks come at random times.
- Each hacker will use a single IP address, which is generated in the same way the valid user ones are. However, our simulator is capable of varying this IP address, a feature that we will look at in *Chapter 11, Machine Learning Anomaly Detection*, to make this scenario more challenging.
- Although highly unlikely, it is possible the hacker has the same IP address as a valid user. The hacker may even be a valid user.

We are abstracting away some of the complexity of password-guessing as well; instead, we are using random numbers to determine whether or not the password is guessed correctly—this means we aren't considering how the website stores passwords, perhaps as plaintext (hopefully not), hashes (the irreversible transformation of the plaintext password that allows verification without storing the actual password), or salted hashes (refer to the *Further reading* section for an article on this). In practice, a hacker could gain access to the stored passwords and figure out what they are offline (see the article on rainbow tables in the *Further reading* section at the end of this chapter), in which case the techniques discussed in this chapter wouldn't be as helpful, since the logs wouldn't have a record of their attempts. Keep in mind that the hackers in this simulation are very conspicuous.

The login_attempt_simulator package

This package is much more lightweight than the `stock_analysis` package from the previous chapter; we only have three files:

```
login_attempt_simulator
|-- __init__.py
|-- login_attempt_simulator.py
`-- utils.py
```

We will walk through each of these files in the following sections. Note that parts of the docstrings have been removed for brevity; check the files themselves for the full documentation.

Helper functions

Let's start our discussion with the `utils.py` functions, which are helpers for our simulator class. First, we create our docstring for the module and handle our imports:

```
"""Utility functions for the login attempt simulator."""
```

```
import ipaddress
import itertools
```

```
import json
import random
import string
```

Next, we define the `make_user_base()` function, which makes the user base for our web application. It creates a file of usernames by combining one lowercase letter from the English alphabet with each last name in the list inside the function, and adds a few administrative accounts as well; this results in a user base of 133 accounts. By writing to a file, we ensure we don't have to generate this every time we run our simulation and can simply read from it to simulate in the future:

```
def make_user_base(out_file):
    """Generate a user base and save it to a file."""
    with open(out_file, 'w') as user_base:
        for first, last in itertools.product(
            string.ascii_lowercase,
            ['smith', 'jones', 'kim', 'lopez', 'brown']
        ): # makes 130 accounts
            user_base.write(first + last + '\n')
        # adds 3 more accounts
        for account in ['admin', 'master', 'dba']:
            user_base.write(account + '\n')
```

Since we will need to use this user base in our simulator, we also write a function to read the user base file into a list. The `get_valid_users()` function reads the file written by the `make_user_base()` function back into a Python list:

```
def get_valid_users(user_base_file):
    """Read in users from the user base file."""
    with open(user_base_file, 'r') as file:
        return [user.strip() for user in file.readlines()]
```

The `random_ip_generator()` function creates IP addresses from random numbers of the form `xxx.xxx.xxx.xxx`, where `x` is an integer in the range `[0, 255]`. We are using the `ipaddress` module from the Python standard library (<https://docs.python.org/3/library/ipaddress.html>) to avoid assigning private IP addresses:

```
def random_ip_generator():
    """Randomly generate a fake IP address."""
    try:
        ip_address = ipaddress.IPv4Address('%d.%d.%d.%d' %
                                             tuple(random.randint(0, 255) for _ in range(4)))
    )
```

```

        except ipaddress.AddressValueError:
            ip_address = random_ip_generator()
        return str(ip_address) if ip_address.is_global \
            else random_ip_generator()
    
```

Each of our users will have a few IP addresses from which they attempt to log in. The `assign_ip_addresses()` function maps 1-3 random IP addresses to each user, creating a dictionary:

```

def assign_ip_addresses(user_list):
    """Assign users 1-3 fake IP addresses."""
    return {
        user: [
            random_ip_generator()
            for _ in range(random.randint(1, 3))
        ] for user in user_list
    }
    
```

The `save_user_ips()` and `read_user_ips()` functions save the user-IP address mapping to a JSON file and read it back into the dictionary file, respectively:

```

def save_user_ips(user_ip_dict, file):
    """Save the user-IP address mapping to a JSON file."""
    with open(file, 'w') as file:
        json.dump(user_ip_dict, file)

def read_user_ips(file):
    """Read in the JSON file of the user-IP address mapping."""
    with open(file, 'r') as file:
        return json.loads(file.read())
    
```

Tip

The Python standard library has lots of helpful modules that we might not find many occasions to use but are definitely worth knowing about. Here, we use the `json` module to save dictionaries to JSON files and read them back later. We are using the `ipaddress` module to work with IP addresses, and the `string` module to get the characters in the alphabet without having to type them all out.

The LoginAttemptSimulator class

The `LoginAttemptSimulator` class in the `login_attempt_simulator.py` file handles the heavy lifting of carrying out the simulation with all the random number generation logic. As usual, we start with our module docstring and imports:

```
"""Simulator of login attempts from valid users and hackers."""

import calendar
import datetime as dt
from functools import partial
import math
import random
import string

import numpy as np
import pandas as pd

from .utils import random_ip_generator, read_user_ips
```

Next, we begin defining the `LoginAttemptSimulator` class with its docstring, along with some class variables for storing constants. We do this to avoid magic numbers (numbers in the code that don't seem to have meaning) and spelling errors with strings we will use in multiple spots. Note that these messages are only for our logs; the web application doesn't show the end users why the authentication attempt failed (nor should it):

```
class LoginAttemptSimulator:
    """Simulate login attempts from valid users + attackers."""

    ATTEMPTS_BEFORE_LOCKOUT = 3
    ACCOUNT_LOCKED = 'error_account_locked'
    WRONG_USERNAME = 'error_wrong_username'
    WRONG_PASSWORD = 'error_wrong_password'
```

Important note

Take note of how we used class variables to store constants, such as error messages, so that we don't risk typos in the code. This means that every time we use these error messages, the text will be identical, which will keep the data clean. In Python, constants are typically written in all caps (<https://www.python.org/dev/peps/pep-0008/#constants>).

The `__init__()` method will handle the setup for the simulator, such as reading in the user base from the file indicated, initializing the logs, storing success probabilities, and determining the start and end dates for the simulation, as needed:

```
def __init__(self, user_base_json_file, start, end=None, *,
             attacker_success_probs=[.25, .45],
             valid_user_success_probs=[.87, .93, .95],
             seed=None):
    # user, ip address dictionary
    self.user_base = read_user_ips(user_base_json_file)
    self.users = [user for user in self.user_base.keys()]

    self.start = start
    self.end = end if end else self.start + \
        dt.timedelta(days=random.uniform(1, 50))

    self.hacker_success_likelihoods = \
        attacker_success_probs
    self.valid_user_success_likelihoods = \
        valid_user_success_probs

    self.log = pd.DataFrame(columns=[
        'datetime', 'source_ip', 'username',
        'success', 'failure_reason'
    ])
    self.hack_log = \
        pd.DataFrame(columns=['start', 'end', 'source_ip'])

    self.locked_accounts = []

    # set seeds for random numbers from random and numpy:
    random.seed(seed)
    np.random.seed(seed)
```

The `_record()` method appends the result of each attempt to the log, noting the IP address it came from, which username, at what time, whether it succeeded, and the reason for failure, if there was one:

```
def _record(self, when, source_ip, username, success,
           failure_reason):
    """
    Record the outcome of a login attempt.

    Parameters:
        - when: The datetime of the event.
        - source_ip: IP address the attempt came from.
        - username: The username used in the attempt.
        - success: Whether the attempt succeeded (Boolean).
        - failure_reason: Reason for the failure.

    Returns:
        None, the `log` attribute is updated.
    """
    self.log = self.log.append({
        'datetime': when,
        'source_ip': source_ip,
        'username': username,
        'success': success,
        'failure_reason': failure_reason
    }, ignore_index=True)
```

The `_attempt_login()` method handles the logic of determining whether the login attempt succeeds:

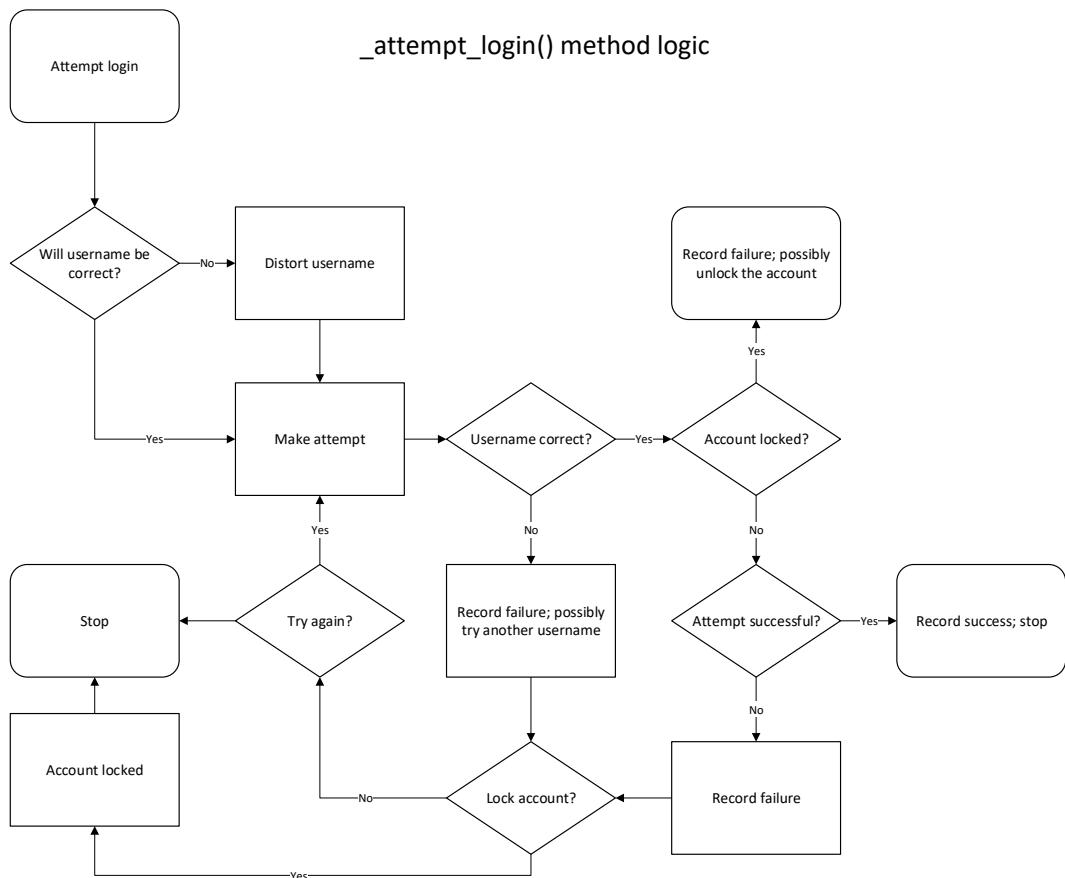


Figure 8.1 – Simulation logic

We provide the probability of entering a correct username (`username_accuracy`) and the probabilities of successfully entering the password for each attempt (`success_likelihoods`). The number of attempts is the minimum of the number of attempts allowed before an account lockout and the length of the list of success probabilities (`success_likelihoods`). The outcome of each attempt is passed to `_record()` using **partials** (from `functools`), which allow us to create functions that fix certain parameters to a specific value (so we don't have to pass the same value continuously):

```
def _attempt_login(self, when, source_ip, username,
                  username_accuracy, success_likelihoods):
    """
    Simulates a login attempt, allowing for account
    lockouts, and recording the results.

    Parameters:
        - when: The datetime to start trying.
        - source_ip: IP address the attempt came from.
        - username: The username being used in the attempt.
        - username_accuracy: Prob. username is correct.
        - success_likelihoods: List of probabilities that
            password is correct (one per attempt).

    Returns:
        The datetime after trying.
    """
    current = when
    recorder = partial(self._record, source_ip=source_ip)

    if random.random() > username_accuracy:
        correct_username = username
        username = self._distort_username(username)

    if username not in self.locked_accounts:
        tries = len(success_likelihoods)
        for i in range(
            min(tries, self.ATTEMPTS_BEFORE_LOCKOUT)
        ):
            current += dt.timedelta(seconds=1)
```

```
        if username not in self.users:
            recorder(
                when=current, username=username,
                success=False,
                failure_reason=self.WRONG_USERNAME
            )

            if random.random() <= username_accuracy:
                username = correct_username
                continue

            if random.random() <= success_likelihoods[i]:
                recorder(
                    when=current, username=username,
                    success=True, failure_reason=None
                )
                break
            else:
                recorder(
                    when=current, username=username,
                    success=False,
                    failure_reason=self.WRONG_PASSWORD
                )
        else:
            if tries >= self.ATTEMPTS_BEFORE_LOCKOUT \
            and username in self.users:
                self.locked_accounts.append(username)
        else:
            recorder(
                when=current, username=username, success=False,
                failure_reason=self.ACCOUNT_LOCKED
            )
            if random.random() >= .5: # unlock account randomly
                self.locked_accounts.remove(username)
    return current
```

The `_valid_user_attempts_login()` and `_hacker_attempts_login()` methods are wrappers around the `_attempt_login()` method that handle the adjustment in probabilities for valid users and hackers, respectively. Notice that while both use a Gaussian (normal) distribution to determine how accurate the username will be, the valid user's distribution has a higher mean and lower standard deviation, meaning they are more likely to provide the correct username when trying to log in. This is because, while valid users may make typos (infrequently), the hackers are guessing:

```
def _hacker_attempts_login(self, when, source_ip,
                           username):
    """Simulates a login attempt from an attacker."""
    return self._attempt_login(
        when=when, source_ip=source_ip, username=username,
        username_accuracy=random.gauss(mu=0.35, sigma=0.5),
        success_likelihoods=self.hacker_success_likelihoods
    )

def _valid_user_attempts_login(self, when, username):
    """Simulates a login attempt from a valid user."""
    return self._attempt_login(
        when=when, username=username,
        source_ip=random.choice(self.user_base[username]),
        username_accuracy=\n            random.gauss(mu=1.01, sigma=0.01),
        success_likelihoods=\n            self.valid_user_success_likelihoods
    )
```

When the simulator determines that the username will not be provided correctly, it calls the `_distort_username()` method, which randomly decides to omit a letter from the valid username or to replace one of the letters with another one. While hackers enter incorrect usernames because they are guessing (not due to typos), we abstract away this detail in order to use a single function for introducing username errors for both valid users and hackers:

```
@staticmethod
def _distort_username(username):
    """
    Alters the username to allow for wrong username login
    failures. Randomly removes a letter or replaces a
    letter in a valid username.
    """
```

```

username = list(username)
change_index = random.randint(0, len(username) - 1)
if random.random() < .5: # remove random letter
    username.pop(change_index)
else: # randomly replace a single letter
    username[change_index] = \
        random.choice(string.ascii_lowercase)
return ''.join(username)

```

We use the `_valid_user_arrivals()` method to generate the number of users that will arrive in a given hour and the interarrival times using Poisson and exponential distributions, respectively:

```

@staticmethod
def _valid_user_arrivals(when):
    """
    Static method for simulating Poisson process of
    arrivals (users wanting to log in). Lambda for the
    Poisson varies depending upon the day and time of week.
    """
    is_weekday = when.weekday() not in (
        calendar.SATURDAY, calendar.SUNDAY
    )
    late_night = when.hour < 5 or when.hour >= 11
    work_time = is_weekday \
        and (when.hour >= 9 or when.hour <= 17)

    if work_time:
        # hours 9-5 on work days get higher lambda
        poisson_lambda = random.triangular(1.5, 5, 2.75)
    elif late_night:
        # hours in middle of night get lower lambda
        poisson_lambda = random.uniform(0.0, 5.0)
    else:
        poisson_lambda = random.uniform(1.5, 4.25)

    hourly_arrivals = np.random.poisson(poisson_lambda)
    interarrival_times = np.random.exponential(
        1/poisson_lambda, size=hourly_arrivals
    )

    return hourly_arrivals, interarrival_times

```

Important note

We are using `numpy` instead of `random` to generate random numbers from the exponential distribution because we can ask for multiple values at once (one for each of the hourly arrivals determined by the Poisson process). Also, note that `random` doesn't provide a Poisson distribution, so we need `numpy`.

Our simulation uses many different distributions, so it can be helpful to see what they look like. The following subplots show examples for each of the distributions we are using. Notice that the Poisson distribution is drawn differently. This is because the Poisson distribution is discrete. For this reason, we often use it to model arrivals—here, we use it for modeling the arrivals of users attempting to log in. Discrete distributions have a **probability mass function (PMF)** instead of a **probability density function (PDF)**:

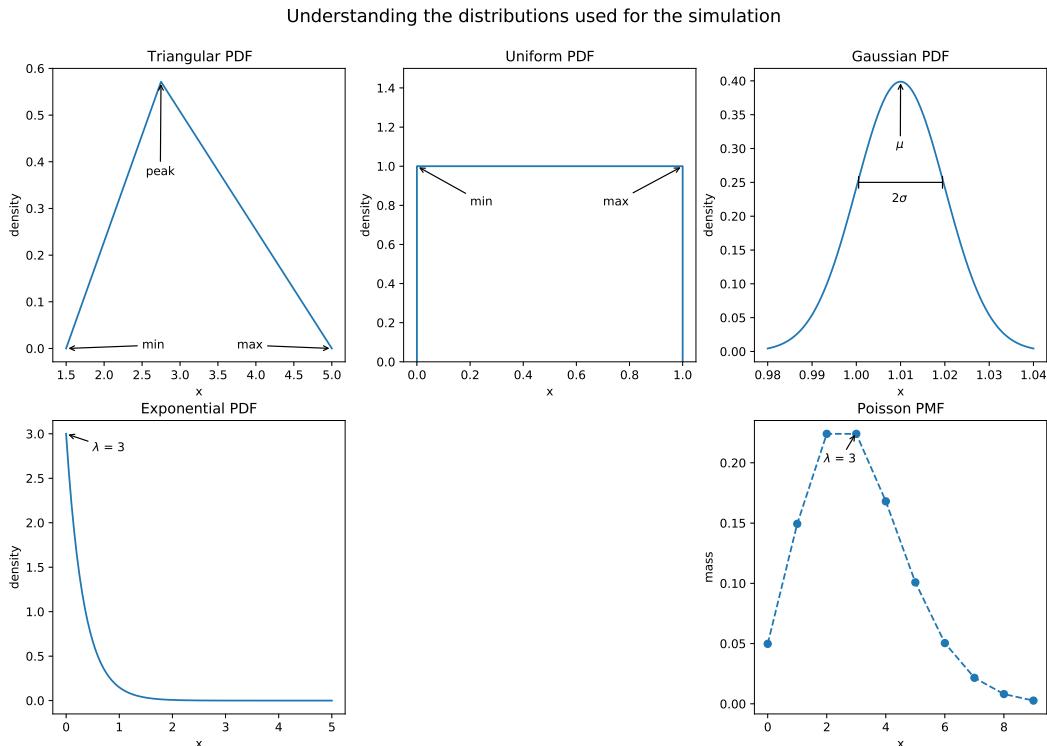


Figure 8.2 – Distributions used in the simulation

The `_hack()` method generates a random IP address for the hacker and carries out a brute-force attack on a given user list:

```
def _hack(self, when, user_list, vary_ips):
    """
    Simulate an attack by a random hacker.

    Parameters:
        - when: The datetime to start the attack.
        - user_list: The list of users to try to hack.
        - vary_ips: Whether or not to vary the IP address.

    Returns:
        Initial IP address and the end time for recording.
    """
    hacker_ip = random_ip_generator()
    random.shuffle(user_list)
    for user in user_list:
        when = self._hacker_attempts_login(
            when=when, username=user,
            source_ip=random_ip_generator() if vary_ips \
                else hacker_ip
        )
    return hacker_ip, when
```

Now that we have the functionality to carry out the main parts of the simulation, we write the `simulate()` method to put it all together:

```
def simulate(self, *, attack_prob, try_all_users_prob,
            vary_ips):
    """
    Simulate login attempts.

    Parameters:
        - attack_probs: Probability of attack in given hour
        - try_all_users_prob: Prob. hacker will try to
            guess credentials for all users vs random subset.
        - vary_ips: Whether to vary the IP address.

    """
    hours_in_date_range = math.floor(
        (self.end - self.start).total_seconds() / 60 / 60
    )
```

```
for offset in range(hours_in_date_range + 1):
    current = self.start + dt.timedelta(hours=offset)

    # simulate hacker
    if random.random() < attack_prob:
        attack_start = current \
            + dt.timedelta(hours=random.random())
        source_ip, end_time = self._hack(
            when=attack_start,
            user_list=self.users if \
                random.random() < try_all_users_prob \
            else random.sample(
                self.users,
                random.randint(0, len(self.users)))
        ),
        vary_ips=vary_ips
    )
    self.hack_log = self.hack_log.append(
        dict(
            start=attack_start, end=end_time,
            source_ip=source_ip
        ), ignore_index=True
    )

    # simulate valid users
    hourly_arrivals, interarrival_times = \
        self._valid_user_arrivals(current)
    random_user = random.choice(self.users)
    random_ip = \
        random.choice(self.user_base[random_user])
    for i in range(hourly_arrivals):
        current += \
            dt.timedelta(hours=interarrival_times[i])
        current = self._valid_user_attempts_login(
            current, random_user
        )
```

We want to save the logs to CSV files, so we add the `_save()` method as a static method to allow for less repetition in the code for the two save methods. The `save_log()` method will save the login attempts and the `save_hack_log()` method will save the record of the attacks:

```
@staticmethod
def _save(data, filename, sort_column):
    """Sort data by the datetime and save to a CSV file."""
    data.sort_values(sort_column)\n        .to_csv(filename, index=False)

def save_log(self, filename):
    """Save the login attempts log to a CSV file."""
    self._save(self.log, filename, 'datetime')

def save_hack_log(self, filename):
    """Save the record of the attacks to a CSV file."""
    self._save(self.hack_log, filename, 'start')
```

Notice that there were many private methods in this class; this is because users of this class only need to be able to create an instance of this class (`__init__()`), simulate by hour (`simulate()`), and save the output (`save_log()` and `save_hack_log()`)—all other methods are for internal use by objects of this class. The methods behind the scenes will handle the bulk of the work.

Lastly, we have the `__init__.py` file, which makes this a package, but also provides us with an easier way to import the main class:

```
"""Package for simulating login data."""

from .login_attempt_simulator import LoginAttemptSimulator
```

Now that we understand how the simulator works, we will discuss how to run the simulation to collect the login attempts data.

Simulating from the command line

Rather than writing the code to simulate the login attempts every time, we can package this up in a script that we can easily run from the command line. The Python standard library has the `argparse` module (<https://docs.python.org/3/library/argparse.html>), which allows us to specify arguments to our script that can be supplied from the command line.

Let's take a look at the `simulate.py` file to see how to do this. We start with our imports:

```
"""Script for simulating login attempts."""

import argparse
import datetime as dt
import os
import logging
import random

import login_attempt_simulator as sim
```

In order to provide status updates when using this from the command line, we are going to set up logging messages using the standard library's `logging` module (<https://docs.python.org/3/library/logging.html>):

```
# Logging configuration
FORMAT = '[%(levelname)s] [%(name)s] %(message)s'
logging.basicConfig(level=logging.INFO, format=FORMAT)
logger = logging.getLogger(os.path.basename(__file__))
```

Next, we define some utility functions for generating file paths that we will need for reading and writing data during the simulation:

```
def get_simulation_file_path(path_provided, directory,
                             default_file):
    """Get filepath, make directory if necessary."""
    if path_provided:
        file = path_provided
    else:
        if not os.path.exists(directory):
            os.mkdir(directory)
        file = os.path.join(directory, default_file)
    return file

def get_user_base_file_path(path_provided, default_file):
    """Get the path for a user_data directory file."""
    return get_simulation_file_path(
        path_provided, 'user_data', default_file
    )
```

```
def get_log_file_path(path_provided, default_file):
    """Get the path for a logs directory file."""
    return get_simulation_file_path(
        path_provided, 'logs', default_file
    )
```

The largest part of this script defines which command-line parameters can be passed—we will allow the user to specify whether they want to create a new user base, set a seed, when to start the simulation, how long to simulate, and where to save all the files. The actual simulation is taken care of in a few lines thanks to the package we built. This section will only run when this module is run, rather than imported:

```
if __name__ == '__main__':
    # command-line argument parsing
    parser = argparse.ArgumentParser()
    parser.add_argument(
        'days', type=float,
        help='number of days to simulate from start'
    )
    parser.add_argument(
        'start_date', type=str,
        help="datetime to start in the form 'YYYY-MM-DD(...)'"
    )
    parser.add_argument(
        '-m', '--make', action='store_true',
        help='make user base'
    )
    parser.add_argument(
        '-s', '--seed', type=int,
        help='set a seed for reproducibility'
    )
    parser.add_argument(
        '-u', '--userbase',
        help='file to write the user base to'
    )
    parser.add_argument(
        '-i', '--ip',
        help='file to write user-IP address map to'
    )
```

```
parser.add_argument(
    '-l', '--log', help='file to write the attempt log to'
)
parser.add_argument(
    '--hl', '--hacklog',
    help='file to write the hack log to'
)
```

Tip

The code placed in the `if __name__ == '__main__'` block will only be run when this module is run as a script. This makes it possible for us to import the functions defined in the module without running the simulation.

After defining the arguments, we need to parse them in order to use them:

```
args = parser.parse_args()
```

Once we have the command-line arguments parsed, we check to see whether we need to generate the user base or read it in:

```
user_ip_mapping_file = \
    get_user_base_file_path(args.ip, 'user_ips.json')

if args.make:
    logger.warning(
        'Creating new user base, mapping IP addresses.'
    )
    user_base_file = get_user_base_file_path(
        args.userbase, 'user_base.txt'
    )

    # seed the creation of user base
    random.seed(args.seed)

    # create usernames and write to file
    sim.utils.make_user_base(user_base_file)
```

```

# create 1 or more IP addresses per user, save mapping
valid_users = sim.utils.get_valid_users(user_base_file)
sim.utils.save_user_ips(
    sim.utils.assign_ip_addresses(valid_users),
    user_ip_mapping_file
)

```

Afterward, we parse the start date from the command-line arguments, and determine the end date by adding the duration from the command-line arguments to the start date:

```

try:
    start = \
        dt.datetime(*map(int, args.start_date.split('-')))
except TypeError:
    logger.error('Start date must be in "YYYY-MM-DD" form')
    raise
except ValueError:
    logger.warning(
        f'Could not interpret {args.start_date}, '
        'using January 1, 2020 at 12AM as start instead'
    )
    start = dt.datetime(2020, 1, 1)
end = start + dt.timedelta(days=args.days)

```

Tip

Check out the `try...except` block in the previous code snippet. We have a single `try` clause and multiple `except` clauses. We can specify how to handle specific errors occurring during code execution (called **exceptions**) by stating which exception type belongs to a given `except` clause. In this case, we have the `logger` object print a more helpful message for the user, and then re-raise the same exception (because we don't intend to handle it) by simply writing `raise`. This ends the program—the user can then try again with valid input. Try triggering this exception to see how much more useful this is. One thing to keep in mind, though, is that order matters—be sure to handle specific exceptions before having a general `except` clause; otherwise, the code specific to each exception type will never trigger. Also, note that using `except` without providing a specific exception will catch everything, even exceptions not meant to be caught.

Finally, we run the actual simulation and write our results to the files specified (or the default paths). We set the probability of attack in a given hour to 10% (`attack_prob`), the probability the hacker will attempt to guess all usernames at 20% (`try_all_users_prob`), and have the hackers use the same IP address for all of their attempts (`vary_ips`):

```
try:
    logger.info(f'Simulating {args.days} days...')
    simulator = sim.LoginAttemptSimulator(
        user_ip_mapping_file, start, end, seed=args.seed
    )
    simulator.simulate(
        attack_prob=0.1, try_all_users_prob=0.2,
        vary_ips=False
    )

    # save logs
    logger.info('Saving logs')
    simulator.save_hack_log(
        get_log_file_path(args.hacklog, 'attacks.csv')
    )
    simulator.save_log(
        get_log_file_path(args.log, 'log.csv')
    )
    logger.info('All done!')

except:
    logger.error('Oops! Something went wrong... ')
    raise
```

Tip

Notice that we used the `logger` object to print helpful messages to the screen throughout the script; this will help the users of this script know how far along in the process it is. These messages come in different levels of severity (we are using `INFO`, `WARNING`, and `ERROR` here), allowing them to be placed for debugging (the `DEBUG` level), and left there once the code goes into production, since the minimum level for printing can be raised to `INFO`, so that no `DEBUG` messages are printed. This is leaps and bounds above simple `print()` statements, since we don't have to worry about removing them as we move to production or adding back these messages as development continues.

Let's now take a look at how we can run this script. We know that `simulate.py` can be run on the command line, but how can we see what arguments we need to pass? Simple—we add the help flag (`-h` or `--help`) to the call:

```
(book_env) $ python3 simulate.py -h
usage: simulate.py [-h] [-m] [-s SEED] [-u USERBASE] [-i IP]
                   [-l LOG] [-hl HACKLOG]
                   days start_date

positional arguments:
  days                  number of days to simulate from start
  start_date            datetime to start in the form
                        'YYYY-MM-DD' or 'YYYY-MM-DD-HH'

optional arguments:
  -h, --help             show this help message and exit
  -m, --make              make user base
  -s SEED, --seed SEED   set a seed for reproducibility
  -u USERBASE, --userbase USERBASE
                        file to write the user base to
  -i IP, --ip IP         file to write the user-IP address
                        map to
  -l LOG, --log LOG      file to write the attempt log to
  -hl HACKLOG, --hacklog HACKLOG
                        file to write the hack log to
```

Important note

Note that we didn't specify the `help` argument when we added the other arguments with `argparse`; it was automatically created by `argparse`.

Once we know which arguments we can pass and have decided which of these we want to provide, we can run the simulation. Let's simulate 30 days, starting from 12 AM on November 1, 2018, while having the script create the user base and IP address mappings needed:

```
(book_env) $ python3 simulate.py -ms 0 30 '2018-11-01'
[WARNING] [ simulate.py ] Creating new user base and mapping IP
addresses to them.
[INFO]  [ simulate.py ] Simulating 30.0 days...
[INFO]  [ simulate.py ] Saving logs
[INFO]  [ simulate.py ] All done!
```

Tip

Since we set a seed (`-s 0`), the output of this simulation is reproducible. Simply remove the seed or change it to get a different result.

Python modules can also be run as scripts. As opposed to importing a module, when we run one as a script, any code underneath `if __name__ == '__main__'` will also be run, meaning we don't always need to write a separate script. Most of the modules we have built only defined functions and classes, so running them as scripts wouldn't do anything; however, the way we created our virtual environment with `venv` back in *Chapter 1, Introduction to Data Analysis*, was an example of this. The previous code block is therefore equivalent to the following command:

```
# leave off the .py
(book_env) $ python3 -m simulate -ms 0 30 "2018-11-01"
```

Now that we have our simulated data, let's begin our analysis.

Exploratory data analysis

In this scenario, we have the benefit of access to labeled data (`logs/attacks.csv`) and will use it to investigate how to distinguish between valid users and attackers. However, this is a luxury that we often don't have, especially once we leave the research phase and enter the application phase. In *Chapter 11, Machine Learning Anomaly Detection*, we will revisit this scenario, but begin without the labeled data for more of a challenge. As usual, we start with our imports and reading in the data:

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

>>> log = pd.read_csv(
...     'logs/log.csv', index_col='datetime', parse_dates=True
... )
```

The login attempts dataframe (`log`) contains the date and time of each attempt in the `datetime` column, the IP address it came from (`source_ip`), the username that was used (`username`), whether the attempt was successful (`success`), and the reason for failure if it wasn't (`failure_reason`):

	source_ip	username	success	failure_reason
datetime				
2018-11-01 00:36:52.617978	142.89.86.32	vkim	True	NaN
2018-11-01 01:00:23.166623	5.118.187.36	kkim	True	NaN
2018-11-01 01:31:50.779608	142.89.86.32	vkim	False	error_wrong_password
2018-11-01 01:31:51.779608	142.89.86.32	vkim	True	NaN
2018-11-01 01:32:44.016230	15.176.178.91	kkim	True	NaN

Figure 8.3 – Sample of the login attempt data

When approaching this data, we need to think about what normal activity and hacker activity would look like. Any big differences between the groups could potentially be leveraged to identify the hackers. We would expect valid users to have high success rates, with the most common reason for failure being an incorrect password. We would expect users to log in from a few different IP addresses (phone, home computer, work computer, and any other device they may have), and it is possible that people share devices. Without knowing the nature of this web application, we can't say anything about whether it is normal to log in many times throughout the day. We also don't know what time zone this data is in, so we can't make any inferences about the login times. Potentially, we could look at which countries these IP addresses are from, but there are ways of masking IP addresses, so we won't go down that path. This leaves us with a few viable options, given our available data:

- Investigate any spikes in attempts and failures (both overall and per IP address).
- Examine cases where the failure reason was an incorrect username.
- Look at the failure rate per IP address.
- Find IP addresses trying to log in with many distinct usernames.

One other thing to note is that we would want to flag anomalous behavior sooner rather than later. Waiting a month to flag something is less valuable (the value drops quickly over time), so we need to find a way to flag much sooner; say, using an hourly frequency. Since we are in the research phase, we have some labeled data to work with:

```
>>> attacks = pd.read_csv(
...     'logs/attacks.csv',
...     converters={
...         'start': np.datetime64,
...         'end': np.datetime64
...     }
... ) # make start and end columns datetimes but not the index
```

This data is the record of attacks on the web application (`attacks`). It contains the date and time of the start of the attack (`start`), the date and time of the end of the attack (`end`), and the IP address associated with the attack (`source_ip`):

	start	end	source_ip
0	2018-11-02 05:06:17.152636	2018-11-02 05:10:30.152636	212.79.15.228
1	2018-11-02 11:42:38.771415	2018-11-02 11:45:58.771415	44.207.171.119
2	2018-11-03 17:49:39.023954	2018-11-03 17:52:27.023954	15.223.158.165
3	2018-11-03 19:45:05.820292	2018-11-03 19:49:11.820292	68.102.121.161
4	2018-11-04 02:51:07.163402	2018-11-04 02:52:09.163402	103.93.254.233

Figure 8.4 – Sample of the labeled data

Using the `shape` property, we can see that we had 72 attacks and 12,836 login attempts from valid and nefarious users, and with `nunique()`, we see that 22% of the IP addresses were associated with attacks:

```
>>> attacks.shape, log.shape
((72, 3), (12836, 4))
>>> attacks.source_ip.nunique() / log.source_ip.nunique()
0.22018348623853212
```

Important note

Normally, it wouldn't be this trivial to know when the attacks occurred—they can go a long time without detection, and, even then, it's not so simple to isolate the attacker's actions from those of normal users.

Our data is pretty clean (we designed it just for this purpose, after all), so let's see whether we can find anything interesting by performing some **exploratory data analysis (EDA)**. First, let's look to see how many attempts are coming through on an hourly basis:

```
>>> log.assign(attempts=1).attempts.resample('1H').sum() \
...     .plot(figsize=(15, 5), title='hourly attempts') \
...     .set(xlabel='datetime', ylabel='attempts')
```

Several hours had very large peaks, which could possibly be when attacks occurred. Using this plot, we could report on hours that had a high level of login attempt activity, but nothing beyond that:

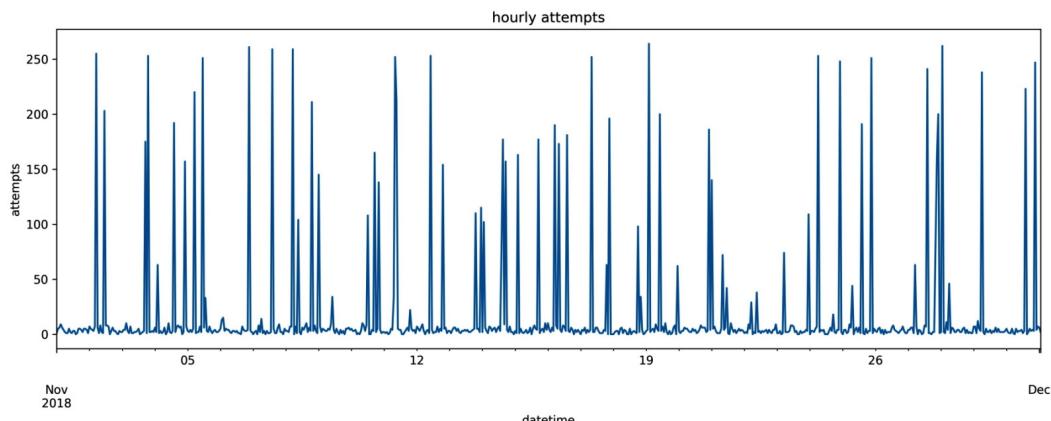


Figure 8.5 – Hourly login attempts

Another interesting avenue of exploration would be to see how many attempts came from each IP address. We can achieve this by running the following command:

```
>>> log.source_ip.value_counts().describe()
count    327.000000
mean      39.253823
std       69.279330
min       1.000000
25%      5.000000
50%     10.000000
75%     22.500000
max     257.000000
Name: source_ip, dtype: float64
```

This data definitely appears to have some outliers, which pull the number of attempts per IP address up quite high. Let's create some plots to better assess this:

```
>>> fig, axes = plt.subplots(1, 2, figsize=(15, 5))
>>> log.source_ip.value_counts() \
...     .plot(kind='box', ax=axes[0]).set_ylabel('attempts')
>>> log.source_ip.value_counts() \
...     .plot(kind='hist', bins=50, ax=axes[1]) \
...     .set_xlabel('attempts')
>>> fig.suptitle('Attempts per IP Address')
```

The distribution of attempts per IP address is the sum of the distributions for both valid users and attackers. The histogram indicates that this distribution is bimodal, but we are unable to determine whether all of those IP addresses with high attempts are actually hackers by just looking at the plot:

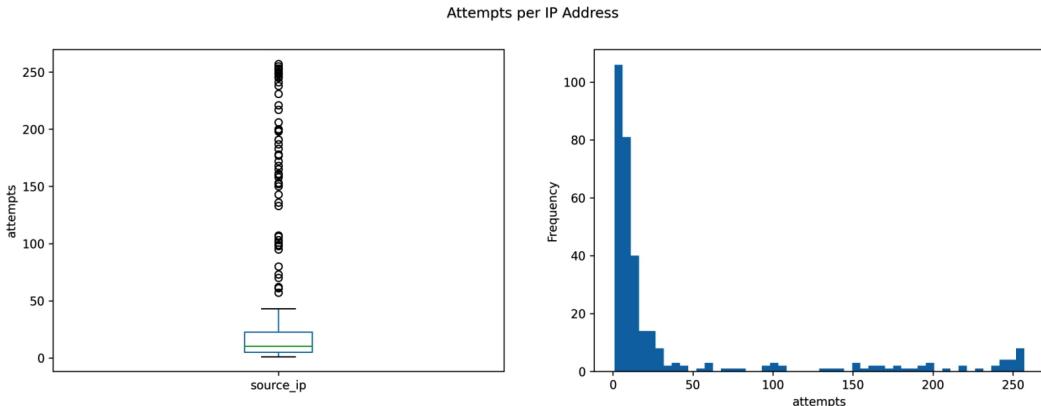


Figure 8.6 – Distribution of login attempts per IP address

Since we have access to the details of each attack, we can check whether the right part of the histogram is the distribution for the hackers. Their IP addresses make up 88.9% of the top IP addresses ranked by number of attempts:

```
>>> num_hackers = attacks.source_ip.nunique()
>>> log.source_ip.value_counts().index[:num_hackers] \
...     .isin(attacks.source_ip).sum() / num_hackers
0.8888888888888888
```

We could simply stop here and flag any IP address that shows up in a list of IP addresses with the most attempts per month, but we most likely want a more robust solution, since the hackers could simply change their IP address each time and avoid detection. Ideally, we would also be able to detect the attacks without waiting for a full month's worth of data. Looking at the hourly attempts made by each IP address unfortunately doesn't give us much information, though:

```
>>> log.assign(attempts=1).groupby('source_ip').attempts\
...     .resample('1H').sum().unstack().mean() \
...     .plot(
...         figsize=(15, 5),
...         title='average hourly attempts per IP address'
...     ).set_ylabel('average hourly attempts per IP address')
```

Remember from *Chapter 1, Introduction to Data Analysis*, that the mean is not robust to outliers. If the attackers make many attempts, they will bring the average hourly attempts per IP address higher. We can see several large peaks in this line plot, but notice that many of them only go up to two or three. Can we really expect only one user to access the web application from a given IP address? This is probably not a realistic assumption:

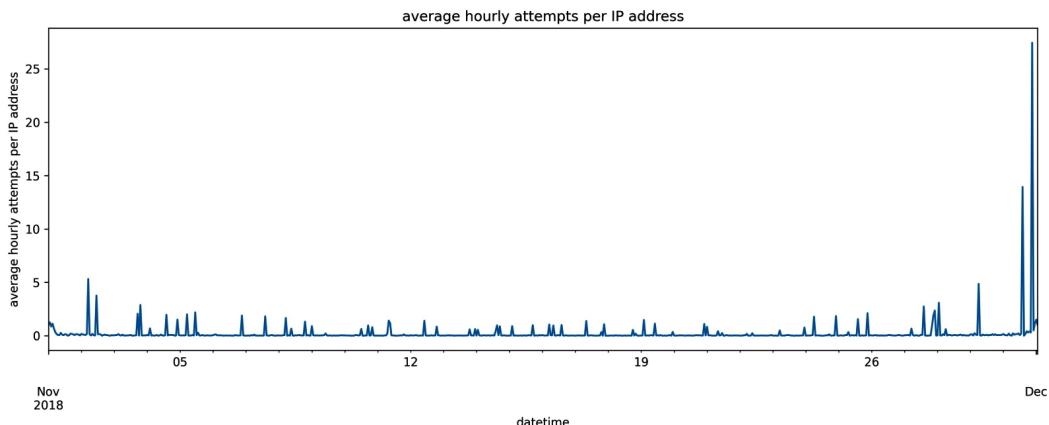


Figure 8.7 – Average hourly login attempts per IP address

So, if we can't rely on the IP address (after all, the hacker could be smart enough to spread the attack over many different addresses), what else can we try? Perhaps the hackers have more trouble logging in successfully:

```
>>> log[log.source_ip.isin(attacks.source_ip)] \
...     .success.value_counts(normalize=True)
```

```
False    0.831801
True    0.168199
Name: success, dtype: float64
```

The hackers are only successful 17% of the time, but how often are the valid users successful? This information is important for determining a baseline of what normal behavior looks like for the website. As we would expect, valid users have much higher success rates:

```
>>> log[~log.source_ip.isin(attacks.source_ip)] \
...     .success.value_counts(normalize=True)
True    0.873957
False   0.126043
Name: success, dtype: float64
```

Since the logs come with the reason that a login attempt failed, we can use a crosstab to see why hackers and valid users fail to log in successfully. Any differences here may help us separate the two groups:

```
>>> pd.crosstab(
...     index=pd.Series(
...         log.source_ip.isin(attacks.source_ip),
...         name='is_hacker'
...     ), columns=log.failure_reason
... )
```

Valid users sometimes enter their passwords or usernames incorrectly, but the hacker has way more issues getting both the username and password correct:

	failure_reason	error_account_locked	error_wrong_password	error_wrong_username
is_hacker				
False	1	299	2	
True	0	3316	5368	

Figure 8.8 – Reason for failed login attempts

Valid users don't make many mistakes with their credentials, so if the hackers make many attempts with many users, we can flag it. To confirm, we can look at average hourly attempts per user:

```
>>> log.assign(attempts=1).groupby('username').attempts \
...     .resample('1H').sum().unstack().mean()\
```

```

...     .plot(figsize=(15, 5),
...             title='average hourly attempts per user') \
...     .set_ylabel('average hourly attempts per user')

```

For the most part, less than one attempt per hour is made per username. There's also no guarantee that spikes in this metric are indications of an attack. Perhaps the website is having a flash sale; in that case, we would likely see a spike in this metric caused by valid users:

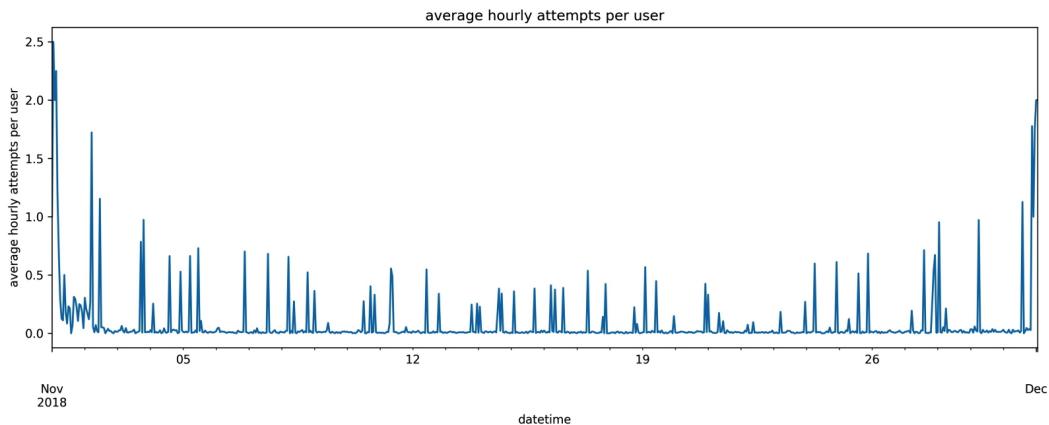


Figure 8.9 – Average hourly login attempts per username

Based on our findings, error rates seem to be the most fruitful metric for detecting attacks, so we will look into IP addresses that have high error rates. To do so, we can create a pivot table to calculate some helpful metrics:

```

>>> pivot = log.pivot_table(
...     values='success', index=log.source_ip,
...     columns=log.failure_reason.fillna('success'),
...     aggfunc='count', fill_value=0
... )
>>> pivot.insert(0, 'attempts', pivot.sum(axis=1))
>>> pivot = pivot.sort_values('attempts', ascending=False) \
...     .assign(
...         success_rate=lambda x: x.success / x.attempts,
...         error_rate=lambda x: 1 - x.success_rate
... )
>>> pivot.head()

```

Tip

The `insert()` method allows us to insert the newly created `attempts` column at a specific position in the current dataframe in place. We created the `attempts` column as the sum of errors and successes (we fill in the NaN values in the `failure_reason` column with `success` to count it here) by summing with `axis=1`.

This yields the following pivot table sorted by attempts (from most to fewest):

failure_reason	attempts	error_account_locked	error_wrong_password	error_wrong_username	success	success_rate	error_rate
source_ip							
85.1.221.89	257	0	92		128	37	0.143969 0.856031
109.67.154.113	255	0	78		144	33	0.129412 0.870588
212.79.15.228	253	0	89		127	37	0.146245 0.853755
181.217.195.170	253	0	70		138	45	0.177866 0.822134
211.56.212.113	253	0	88		120	45	0.177866 0.822134

Figure 8.10 – Metrics per IP address

We know that certain IP addresses are making many attempts, so it's worth looking into how many usernames are attempting to log in per IP address; we would expect valid users to only log in from a few IP addresses and not to share their IP address with many others. This can be determined with a group by and an aggregation:

```
>>> log.groupby('source_ip').agg(dict(username='nunique'))\
...     .username.value_counts().describe()
count      53.000000
mean       6.169811
std        34.562505
min       1.000000
25%       1.000000
50%       1.000000
75%       2.000000
max      253.000000
Name: username, dtype: float64
```

This definitely appears to be a good strategy for isolating nefarious users. The majority of the IP addresses are used by two or fewer users, but the maximum stands at 253. While this criterion could help us identify some of the attackers, it won't help if the hackers are clever enough to vary their IP addresses throughout their attack.

Before we move on to anomaly detection methods, let's see whether we can visually identify the hackers. Let's create a scatter plot for the successes and attempts for each IP address:

```
>>> pivot.plot(  
...     kind='scatter', x='attempts', y='success', alpha=0.25,  
...     title='successes vs. attempts by IP address'  
... )
```

There appear to be a few distinct clusters. In the bottom-left corner of the plot, we see points forming a line with a one-to-one relationship of successes to attempts. The upper-right portion of the plot contains a less dense cluster with a high number of attempts and moderate successes. Since we used the `alpha` parameter to control transparency, we can see that the trail of points that seem to connect the two clusters is not densely populated. Even without the axis scales, we would predict the bottom-left cluster to be regular users and the top-right to be hackers (since we imagine there are more regular users than hackers, and regular users have higher success rates). The points in the middle are more difficult to judge, however:

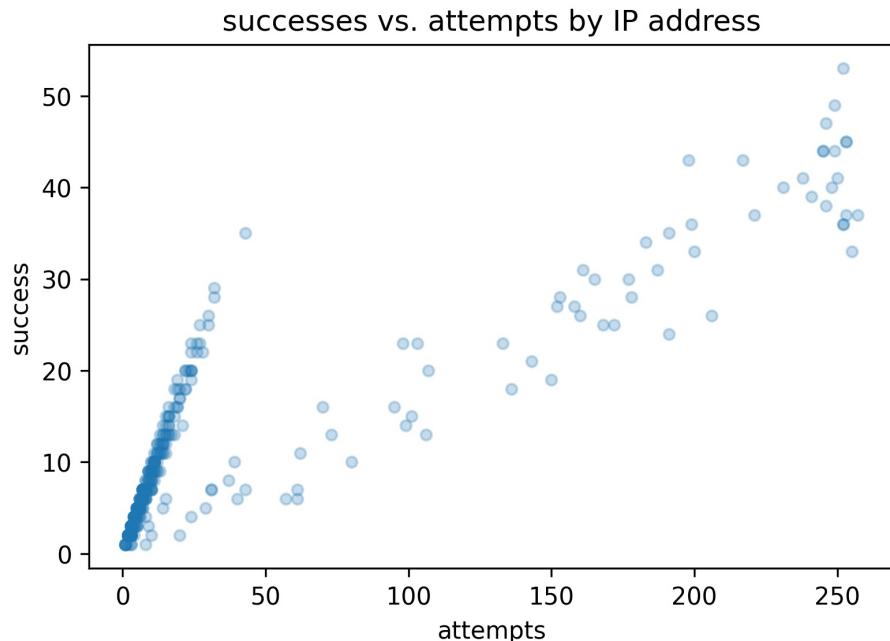


Figure 8.11 – Scatter plot of successes versus attempts by IP address

Without making any assumptions, we can draw a boundary line grouping the middle points with their nearest cluster:

```
>>> ax = pivot.plot(  
...     kind='scatter', x='attempts', y='success', alpha=0.25,  
...     title='successes vs. attempts by IP address'  
... )  
>>> plt.axvline(  
...     125, label='sample boundary',  
...     color='red', linestyle='--'  
... )  
>>> plt.legend(loc='lower right')
```

Of course, when lacking labeled data, it is difficult to evaluate the effectiveness of this decision boundary:

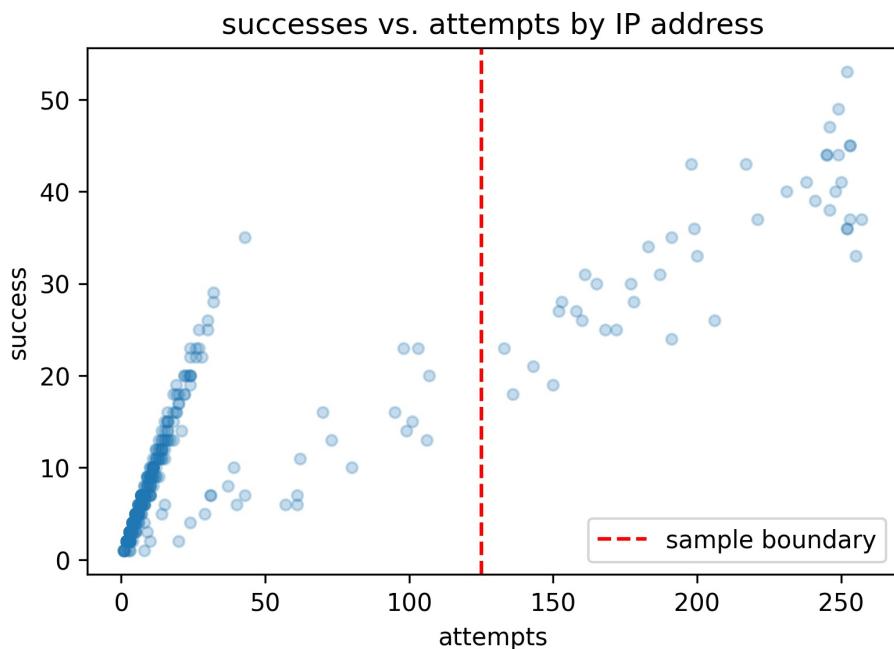


Figure 8.12 – Visualizing a decision boundary

Luckily for us, we have data on which IP addresses the hackers used because we have been given labeled data to conduct our research, so we can use `seaborn` to actually see the separation:

```
>>> fig, axes = plt.subplots(1, 2, figsize=(15, 5))
>>> for ax in axes:
...     sns.scatterplot(
...         y=pivot.success, x=pivot.attempts,
...         hue=pivot.assign(
...             is_hacker=\'
...                 lambda x: x.index.isin(attacks.source_ip)
...             ).is_hacker,
...         ax=ax, alpha=0.5
...     )
...     for spine in ['top', 'right']: # make less boxy
...         ax.spines[spine].set_visible(False)
>>> axes[1].set_xscale('log')
>>> plt.suptitle('successes vs. attempts by IP address')
```

Our intuition about there being two distinct clusters was dead-on. The middle area, however, was much trickier to determine. The blue (darker) points on the left do appear to be following a line upward, while the orange (lighter) points on the left are following a line to the orange cluster. By plotting the log of the attempts instead, we get a little more separation between our orange middle points and the blue points:

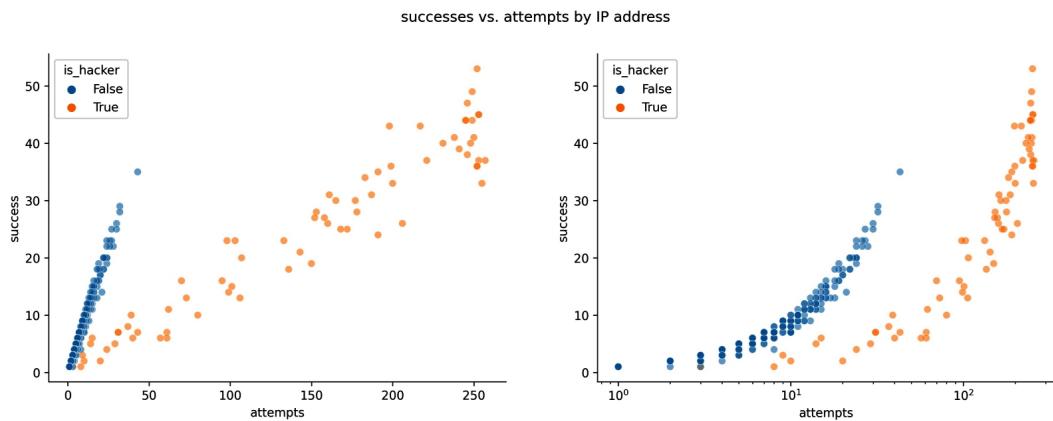


Figure 8.13 – Using labeled data to check our intuition

Remember, we can also use a box plot to check for possible outliers, which will be shown as points. Let's see what successes and attempts look like per IP address:

```
>>> pivot[['attempts', 'success']].plot(
...     kind='box', subplots=True, figsize=(10, 3),
...     title='stats per IP address'
... )
```

The points marked as outliers coincide with the points in the upper-right corner of the scatter plots we made:

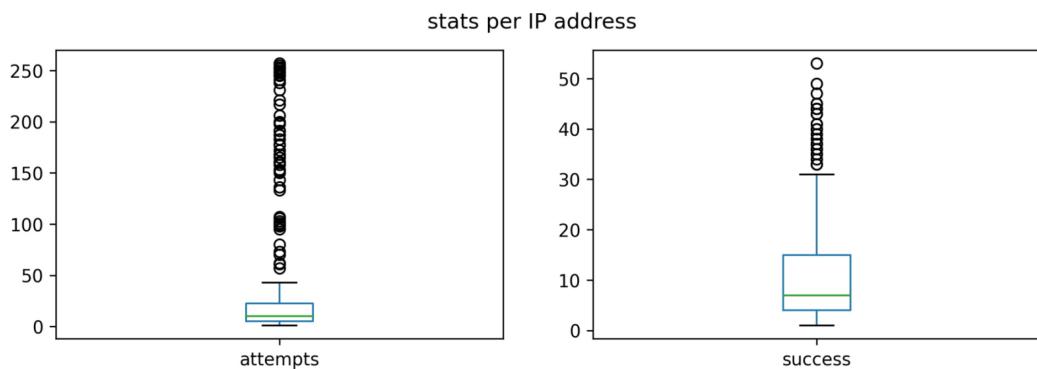


Figure 8.14 – Checking for outliers

Now that we have a good understanding of our data, we are ready to learn how to implement a few simple anomaly detection strategies.

Implementing rule-based anomaly detection

It's time to catch those hackers. After the EDA in the previous section, we have an idea of how we might go about this. In practice, this is much more difficult to do, as it involves many more dimensions, but we have simplified it here. **We want to find the IP addresses with excessive amounts of attempts accompanied by low success rates, and those attempting to log in with more unique usernames than we would deem normal (anomalies).** To do this, we will employ threshold-based rules as our first foray into anomaly detection; then, in *Chapter 11, Machine Learning Anomaly Detection*, we will explore a few machine learning techniques as we revisit this scenario.

Since we are interested in flagging IP addresses that are suspicious, we are going to arrange the data so that we have hourly aggregated data per IP address (if there was activity for that hour):

```
>>> hourly_ip_logs = log.assign(
...     failures=lambda x: np.invert(x.success)
... ).groupby('source_ip').resample('1H').agg({
...     'username': 'nunique', 'success': 'sum',
...     'failures': 'sum'
... }).assign(
...     attempts=lambda x: x.success + x.failures,
...     success_rate=lambda x: x.success / x.attempts,
...     failure_rate=lambda x: 1 - x.success_rate
... ).dropna().reset_index()
```

Tip

The `np.invert()` function is an easy way to flip Boolean values. It turns `True` to `False` and `False` to `True` along a NumPy array-like structure.

The aggregated data looks like this:

	source_ip	datetime	username	success	failures	attempts	success_rate	failure_rate
0	1.138.149.116	2018-11-01 04:00:00		1	5	1	0.833333	0.166667
1	1.138.149.116	2018-11-05 18:00:00		1	1	0	1.000000	0.000000
2	1.138.149.116	2018-11-05 19:00:00		1	1	0	1.000000	0.000000
3	1.138.149.116	2018-11-06 03:00:00		1	2	0	1.000000	0.000000
4	1.138.149.116	2018-11-06 04:00:00		1	2	0	1.000000	0.000000

Figure 8.15 – Hourly aggregated data per IP address

The simplest form of rule-based anomaly detection involves calculating a threshold value and checking to see whether the data is beyond the threshold. This could mean values falling below some lower bound threshold, or values exceeding some upper bound threshold. Since we are looking at login attempts, we are interested in values that are greater than normal. Therefore, we will be calculating the threshold for our upper bounds and comparing that to our data.

Percent difference

Provided that we have an idea of what normal login attempt activity (minus the hackers) looks like on the site, we can flag values that deviate from this by a certain percentage. In order to calculate this baseline, we could take a few IP addresses at random with replacement for each hour, and average the number of login attempts they made. We are bootstrapping since we don't have much data (about 50 unique IP addresses to pick from for each of the 24 hours).

To do this, we could write a function that takes in the aggregated dataframe we just made, along with the name of a statistic to calculate per column of the data to use as the starting point for the threshold:

```
>>> def get_baselines(hourly_ip_logs, func, *args, **kwargs):
...     """
...     Calculate hourly bootstrapped statistic per column.
...
...     Parameters:
...         - hourly_ip_logs: Data to sample from.
...         - func: Statistic to calculate.
...         - args: Additional positional arguments for `func`\
...         - kwargs: Additional keyword arguments for `func`\
...
...     Returns:
...         `DataFrame` of hourly bootstrapped statistics
...     """
...     if isinstance(func, str):
...         func = getattr(pd.DataFrame, func)
...
...     return hourly_ip_logs.assign(
...         hour=lambda x: x.datetime.dt.hour
...     ).groupby('hour').apply(
...         lambda x: x\
...             .sample(10, random_state=0, replace=True)\\
...             .pipe(func, *args, **kwargs, numeric_only=True)
...     )
```

Important note

In the previous code snippet, `random_state` is used with `sample()` for reproducibility; however, in practice, we will probably not want to always pick the same rows.

Notice that we can get equally sized samples for all groups (hours, here) if we use `sample()` inside `apply()` after grouping by the column we want to sample with. This means that we are selecting 10 rows with replacement per hour for each column. We have to sample by hour here because, if we do simple random sampling, there is a good chance we won't have a statistic for every hour. Let's use `get_baselines()` to calculate the column baselines using the mean:

```
>>> averages = get_baselines(hourly_ip_logs, 'mean')
>>> averages.shape
(24, 7)
```

Tip

If, instead, we wanted to perform stratified random sampling, we could replace 10 in the `get_baselines()` function with `x.shape[0] * pct`, where `pct` is the percentage we want to sample from each group.

Each column has the mean per hour for the 10 IP addresses chosen randomly to estimate normal behavior. This technique, however, doesn't guarantee that we won't mix any of the hacker activity into our baseline calculations. For example, let's take a look at the six hours with the highest baseline values for failure rate:

```
>>> averages.nlargest(6, 'failure_rate')
```

We might find it difficult to flag any activity at hours **19**, **23**, or **14** with this baseline because the failure rate and unique usernames tried are both high:

	username	success	failures	attempts	success_rate	failure_rate	hour
hour							
19	14.9	5.5	21.4	26.9	0.736876	0.263124	19.0
23	12.4	3.9	18.7	22.6	0.791195	0.208805	23.0
3	1.0	1.1	0.4	1.5	0.800000	0.200000	3.0
11	1.1	2.0	0.6	2.6	0.816667	0.183333	11.0
14	24.7	8.4	35.5	43.9	0.833401	0.166599	14.0
16	1.0	1.5	0.4	1.9	0.841667	0.158333	16.0

Figure 8.16 – Hourly baselines using the mean

To combat this issue, we could trim our summary statistics by making the top $x\%$ ineligible for use in our baseline calculation. Let's remove values greater than the 95th percentile of data from each hour. First, we will write a function to trim rows from a given hour that have data above a given quantile:

```
>>> def trim(x, quantile):
...     """
...     Remove rows with entries for the username, attempts,
...     or failure_rate columns above a given quantile.
...     """
...     mask = (
...         (x.username <= x.username.quantile(quantile)) &
...         (x.attempts <= x.attempts.quantile(quantile)) &
...         (x.failure_rate
...          <= x.failure_rate.quantile(quantile))
...     )
...     return x[mask]
```

Next, we will group the IP address data by hour and apply our trimming function. Since we will be using our bootstrapping function, we need to clean up some of the extra columns that will result from this operation, so we drop the hour column, reset the index, and then remove the grouping column and the old index:

```
>>> trimmed_hourly_logs = hourly_ip_logs\
...     .assign(hour=lambda x: x.datetime.dt.hour)\ \
...     .groupby('hour').apply(lambda x: trim(x, 0.95))\ \
...     .drop(columns='hour').reset_index().iloc[:,2:]
```

Now, we can use the `get_baselines()` function to grab our baseline using the average with the trimmed data:

```
>>> averages = get_baselines(trimmed_hourly_logs, 'mean')
>>> averages.iloc[[19, 23, 3, 11, 14, 16]]
```

The trimmed baseline is now quite different from *Figure 8.16* at hours **19**, **23**, and **14**:

	username	success	failures	attempts	success_rate	failure_rate	hour
hour							
19	1.0	1.4	0.4	1.8	0.871429	0.128571	19.0
23	1.0	2.0	0.1	2.1	0.966667	0.033333	23.0
3	1.0	2.0	0.3	2.3	0.925000	0.075000	3.0
11	1.1	1.9	0.2	2.1	0.933333	0.066667	11.0
14	1.0	1.4	0.2	1.6	0.950000	0.050000	14.0
16	1.0	1.4	0.2	1.6	0.925000	0.075000	16.0

Figure 8.17 – Trimmed hourly baselines using the mean

Now that we have our baseline, let's write a function that will do the heavy lifting of calculating the threshold from our baseline and the percentage difference per column, returning the IP addresses that have been flagged as hackers:

```
>>> def pct_change_threshold(hourly_ip_logs, baselines,
...                           pcts=None):
...     """
...     Return flagged IP addresses based on thresholds.
...
...     Parameters:
...         - hourly_ip_logs: Aggregated data per IP address.
...         - baselines: Hourly baselines per column in data.
...         - pcts: Dictionary of custom percentages per column
...                 for calculating upper bound thresholds
...                 (baseline * pct). If not provided, pct will be 1
...
...     Returns: `Series` containing the IP addresses flagged.
...     """
...     pcts = {} if not pcts else pcts
...
...     return hourly_ip_logs.assign(
...         hour=lambda x: x.datetime.dt.hour
...     ).join(
...         baselines, on='hour', rsuffix='_baseline'
...     ).assign(
...         too_many_users=lambda x: x.username_baseline \
...             * pcts.get('username', 1) <= x.username,
```

```

...
    too_many_attempts=lambda x: x.attempts_baseline \
        * pcts.get('attempts', 1) <= x.attempts,
...
    high_failure_rate=lambda x: \
        x.failure_rate_baseline \
        * pcts.get('failure_rate', 1) <= x.failure_rate
...
).query(
    'too_many_users and too_many_attempts '
    'and high_failure_rate'
...
).source_ip.drop_duplicates()

```

The `pct_change_threshold()` function uses a series of chained operations to give us the flagged IP addresses:

1. First, it joins the baselines to the hourly IP address logs on the `hour` column. Since all the baseline columns have the same names as the hourly IP address logs, and we don't want to join on them, we suffix their names with '`_baseline`'.
2. After that, all the data we need to check whether the thresholds were exceeded is in the same dataframe. We use `assign()` to make three new Boolean columns, indicating whether each of our conditions (too many users, too many attempts, and high failure rate) has been violated.
3. Then, we chain a call to the `query()` method, which lets us easily select rows where all of these Boolean columns are `True` (notice we don't need to explicitly say `<column> == True`).
4. Lastly, we make sure to return just the IP addresses and to drop any duplicates in case the same IP address was flagged for multiple hours.

In order to use this function, we need to pick a percentage difference from each of our baselines. By default, that will be 100% of the baseline, which, since it is the average, will flag way too many IP addresses. Instead, let's get the IP addresses this flags with values 25% higher than the baseline for each criterion:

```

>>> pct_from_mean_ips = pct_change_threshold(
...     hourly_ip_logs, averages,
...     {key: 1.25 for key in [
...         'username', 'attempts', 'failure_rate'
...     ]}
... )

```

Tip

The percentages we use are in a dictionary, with the key being the column they are for and the value being the percentage itself. If the caller of the function doesn't provide these, we have default values of 100%, since we are using `get()` to select from the dictionary.

These rules flagged 73 IP addresses:

```
>>> pct_from_mean_ips.nunique()
73
```

Important note

In practice, we probably wouldn't run this rule on the entries used to calculate the baselines because they influence the definition of the baseline with their behavior.

Tukey fence

As we discussed in *Chapter 1, Introduction to Data Analysis*, the mean is not robust to outliers. If we feel there are many outliers influencing our baselines, we could go back to the percent difference and try out the median or look into using a **Tukey fence**.

Remember from previous chapters that the Tukey fence gets its bounds from the first and third quartiles and the **interquartile range (IQR)**. Since we only care about exceeding the upper bound, this solves the issue with the mean, provided that outliers make up less than 25% of our data. We can use the following to calculate the upper bound:

$$\text{Upper Bound} = Q_3 + k \times IQR$$

Our `get_baselines()` function will still help us, but we need to do some additional processing. We will write a function that will calculate the upper bound of the Tukey fence and let us test out various values for the multiplier (`k`). Notice that we also have the option to use percentages with the Tukey fence here:

```
>>> def tukey_fence_test(trimmed_data, logs, k, pct=None):
...     """
...     See which IP addresses get flagged with a Tukey fence
...     with multiplier k and optional percent differences.
...
...     Parameters:
...         - trimmed_data: Data for calculating the baselines
...         - logs: The data to test
```

```

...
    - k: The multiplier for the IQR
...
    - pct: Dictionary of percentages per column for use
          with `pct_change_threshold()`
...
    Returns:
...
    `pandas.Series` of flagged IP addresses
"""
...
q3 = get_baselines(trimmed_data, 'quantile', .75) \
    .drop(columns=['hour'])
...
q1 = get_baselines(trimmed_data, 'quantile', .25) \
    .drop(columns=['hour'])
...
iqr = q3 - q1
upper_bound = (q3 + k * iqr).reset_index()
...
return pct_change_threshold(logs, upper_bound, pct)

```

Let's use the `tukey_fence_test()` function to grab the IP addresses that exceed the upper bound of the Tukey fence using an IQR multiplier of 3:

```

>>> tukey_fence_ips = tukey_fence_test(
...     trimmed_hourly_logs, hourly_ip_logs, k=3
... )

```

With this method, we flag 83 IP addresses:

```

>>> tukey_fence_ips.nunique()
83

```

Important note

We used a multiplier of 3 here. However, depending on the application, we may see 1.5 used in order to be less restrictive. In reality, we can use any number; finding the best one may require some trial and error.

Z-score

Remember, from *Chapter 1, Introduction to Data Analysis*, that we can also calculate Z-scores and flag IP addresses a given number of standard deviations from the mean. The `pct_change_threshold()` function we wrote earlier won't help us as is, since we aren't just comparing with the baseline. Instead, we need to subtract the baseline for the mean from all the values and divide by the baseline for the standard deviation, so we must rework our approach.

Let's write a new function, `z_score_test()`, to perform our Z-score tests using any number of standard deviations above the mean as a cutoff. First, we will use the `get_baselines()` function to calculate the baseline standard deviations by hour with the trimmed data. Then, we join the standard deviations and means together, adding the suffixes. This allows us to adapt the logic of `pct_change_threshold()` for this task:

```
>>> def z_score_test(trimmed_data, logs, cutoff):
...     """
...     See which IP addresses get flagged with a Z-score
...     greater than or equal to a cutoff value.
...
...     Parameters:
...         - trimmed_data: Data for calculating the baselines
...         - logs: The data to test
...         - cutoff: Flag row when z_score >= cutoff
...
...     Returns:
...         `pandas.Series` of flagged IP addresses
...     """
...     std_dev = get_baselines(trimmed_data, 'std') \
...             .drop(columns=['hour'])
...     averages = get_baselines(trimmed_data, 'mean') \
...             .drop(columns=['hour'])
...
...     return logs.assign(hour=lambda x: x.datetime.dt.hour) \
...             .join(std_dev.join(
...                 averages, lsuffix='_std', rsuffix='_mean'
...             ), on='hour') \
...             .assign(
...                 too_many_users=lambda x: (
...                     x.username - x.username_mean
...                 )/x.username_std >= cutoff,
```

```
...         too_many_attempts=lambda x: (
...             x.attempts - x.attempts_mean
...         )/x.attempts_std >= cutoff,
...         high_failure_rate=lambda x: (
...             x.failure_rate - x.failure_rate_mean
...         )/x.failure_rate_std >= cutoff
...     ).query(
...         'too_many_users and too_many_attempts '
...         'and high_failure_rate'
...     ).source_ip.drop_duplicates()
```

Let's call our function with a cutoff of three or more standard deviations from the mean:

```
>>> z_score_ips = \
...     z_score_test(trimmed_hourly_logs, hourly_ip_logs, 3)
```

With this method, we flag 62 IP addresses:

```
>>> z_score_ips.nunique()
62
```

Important note

In practice, the cutoff value for the Z-score is also a parameter we will want to tune.

Evaluating performance

So, we now have a series of IP addresses for each set of rules, but we would like to know how well each method did (assuming we can actually check). In this case, we have the attacker IP addresses for our research, so we can see how many each method got right—this is not so trivial in practice; instead, we could mark things that we have discovered to be malicious in the past and look out for similar behavior in the future.

This is a classification problem with two classes; we want to classify each IP address as either a valid user or a nefarious one. This leaves us with four possible outcomes that we can visualize using a **confusion matrix**:

		Confusion Matrix	
		True	False
Predicted	True	TP (True Positive)	FP (False Positive)
	False	FN (False Negative)	TN (True Negative)
		True	False
		Actual	

Figure 8.18 – The confusion matrix

In this application, these outcomes mean the following:

- **True Positive (TP)**: Our method flagged it as malicious, and it was.
- **True Negative (TN)**: Our method didn't flag it, and it wasn't malicious.
- **False Positive (FP)**: Our method flagged it, but it wasn't malicious.
- **False Negative (FN)**: Our method didn't flag it, but it was malicious.

True positives and true negatives mean our method did well, but false positives and false negatives are possible areas for improvement (bear in mind that this will never be perfect). Let's now write a function that will help determine where each method stands:

```
>>> def evaluate(altered_ips, attack_ips, log_ips):
...     """
...     Calculate true positives (TP), false positives (FP),
...     true negatives (TN), and false negatives (FN) for
...     IP addresses flagged as suspicious.
...
...     Parameters:
...         - alerted_ips: `Series` of flagged IP addresses
```

```

...
    - attack_ips: `Series` of attacker IP addresses
...
    - log_ips: `Series` of all IP addresses seen
...
...
    Returns:
    Tuple of the form (TP, FP, TN, FN)
"""
...
tp = alerted_ips.isin(attack_ips).sum()
tn = np.invert(np.isin(
    log_ips[~log_ips.isin(alerted_ips)].unique(),
    attack_ips
)).sum()
fp = np.invert(alerted_ips.isin(attack_ips)).sum()
fn = np.invert(attack_ips.isin(alerted_ips)).sum()
...
return tp, fp, tn, fn

```

Before we begin calculating metrics, let's make a partial function so we don't have to keep passing in the series of attacker IP addresses (`attacks.source_ip`) and IP addresses in the logs (`pivot.index`). Remember, a partial function allows us to fix the values for certain arguments and call the function later:

```

>>> from functools import partial
>>> scores = partial(
...     evaluate,
...     attack_ips=attacks.source_ip,
...     log_ips=pivot.index
... )

```

Now, let's use this to calculate some metrics to measure our performance. One common metric is the **false positive rate (FPR)**, which tells us the **false alarm rate**. It is calculated by taking the ratio of false positives to everything that was actually negative:

$$FPR = \frac{FP}{FP + TN}$$

The **false discovery rate (FDR)**, which tells us the percentage of positives that are incorrect, is another way of looking at false alarms:

$$FDR = \frac{FP}{FP + TP}$$

Let's see what the FPR and FDR are for our percent difference from the mean approach:

```
>>> tp, fp, tn, fn = scores(pct_from_mean_ips)
>>> fp / (fp + tn), fp / (fp + tp)
(0.00392156862745098, 0.0136986301369863)
```

Another metric of interest is the **false negative rate (FNR)**, which tells us what we fail to detect (the **miss rate**). It is calculated by taking the ratio of false negatives to everything that was actually positive:

$$FNR = \frac{FN}{FN + TP}$$

An alternative way of looking at false negatives is the **false omission rate (FOR)**, which tells us the percentage of cases we incorrectly mark as negatives:

$$FOR = \frac{FN}{FN + TN}$$

Our percent difference from the mean method has no false negatives, so both FNR and FOR are zero:

```
>>> fn / (fn + tp), fn / (fn + tn)
(0.0, 0.0)
```

There is typically a trade-off here—do we want to catch as many hackers as possible, and risk flagging valid users (by focusing on FNR/FOR), or do we want to keep from inconveniencing our valid users and risk missing hacker activity (by minimizing FPR/FDR)? These questions are tough to answer and will depend on the domain, as the cost of false positives is not necessarily equal to (or even close in scale to) the cost of false negatives.

Tip

We will discuss additional metrics that can be used to evaluate our performance in *Chapter 9, Getting Started with Machine Learning in Python*.

Let's now write a function to handle all these calculations for us:

```
>>> def classification_stats(tp, fp, tn, fn):
...     """Calculate metrics"""
...     return {
...         'FPR': fp / (fp + tn), 'FDR': fp / (fp + tp),
...         'FNR': fn / (fn + tp), 'FOR': fn / (fn + tn)
...     }
```

We can now use the results from the `evaluate()` function to calculate our metrics. For the percentage difference from the mean, we get the following output:

```
>>> classification_stats(tp, fp, tn, fn)
{'FPR': 0.00392156862745098, 'FDR': 0.0136986301369863,
 'FNR': 0.0, 'FOR': 0.0}
```

It looks like our trio of criteria did quite well. If we were concerned with the hacker IP addresses being chosen when we calculated the baselines, but didn't want to trim, we could have run this with the median instead of the mean:

```
>>> medians = get_baselines(hourly_ip_logs, 'median')
>>> pct_from_median_ips = pct_change_threshold(
...     hourly_ip_logs, medians,
...     {key: 1.25 for key in
...      ['username', 'attempts', 'failure_rate']}
... )
```

Using the median, we achieve similar performance to the mean. In this case, however, we didn't need to trim the data beforehand. This is because the median is robust to outliers, meaning that picking a single hacker IP address in a given hour doesn't affect that hour's baseline as it would the mean:

```
>>> tp, fp, tn, fn = scores(pct_from_median_ips)
>>> classification_stats(tp, fp, tn, fn)
{'FPR': 0.00784313725490196, 'FDR': 0.02702702702702703,
 'FNR': 0.0, 'FOR': 0.0}
```

To compare each of the methods discussed, we can use dictionary comprehensions to populate a `DataFrame` object with the performance metrics:

```
>>> pd.DataFrame({
...     method: classification_stats(*scores(ips))
...     for method, ips in {
...         'means': pct_from_mean_ips,
...         'medians': pct_from_median_ips,
...         'Tukey fence': tukey_fence_ips,
...         'Z-scores': z_score_ips
...     }.items()
... })
```

Tip

The `scores()` function returns a tuple of (`tp`, `fp`, `tn`, `fn`), but the `classification_stats()` function expects four arguments. However, since `scores()` returns them in the same order that `classification_stats()` expects them, we can use `*` to unpack the tuple and send the values as four positional arguments.

The mean is affected by outliers, but once we trimmed the data, it became a viable method. We didn't need to trim the data to work with the median; the usefulness of the median hinges on the data containing fewer than 50% outliers. The Tukey fence takes this a step further by using the third quartile and assuming that fewer than 25% of the data points are outliers. The Z-score method is also affected by outliers because it uses the mean; however, with the trimmed data, we were able to achieve good performance with a modest cutoff of three:

	means	medians	Tukey fence	Z-scores
FPR	0.003922	0.007843	0.078431	0.000000
FDR	0.013699	0.027027	0.240964	0.000000
FNR	0.000000	0.000000	0.125000	0.138889
FOR	0.000000	0.000000	0.036885	0.037736

Figure 8.19 – Comparing performance

Ultimately, which method we use in practice will depend on how costly it is to have a false positive versus a false negative—is it worse to raise the alarm when nothing is wrong, or to be silent when something is? In this case, we would err on the side of minimizing false negatives since we don't want to miss anything.

Important note

Another common use case for anomaly detection is in quality or process control in industrial settings, such as monitoring factory equipment performance and output. Process control uses threshold-based and pattern-based rules to determine whether systems are out of control. These can be used for things such as determining when the distribution of the underlying data has changed, which could be a precursor for later problems.

Western Electric rules and **Nelson rules** are common ones. References for both can be found in the *Further reading* section at the end of this chapter.

Summary

In our second application chapter, we learned how to simulate events in Python and got additional exposure to writing packages. We also saw how to write Python scripts that can be run from the command line, which we used to run our simulation of the login attempt data. Then, we performed some EDA on the simulated data to see whether we could figure out what would make hacker activity easy to spot.

This led us to zero in on the number of distinct usernames attempting to authenticate per IP address per hour, as well as the number of attempts and failure rates. Using these metrics, we were able to create a scatter plot, which appeared to show two distinct groups of points, along with some other points connecting the two groups; naturally, these represented the groups of valid users and the nefarious ones, with some of the hackers not being as obvious as others.

Finally, we set about creating rules that would flag the hacker IP addresses for their suspicious activity. First, we used `pandas` to reshape our data into hourly aggregates per IP address. Then, we wrote functions to trim values greater than the 95th percentile and calculate baselines for a given statistic per hour, which we used to create our rules based on percentage difference from the mean and median, exceeding the upper bound of a Tukey fence, and using Z-scores. We saw that building good rules depended on carefully tuning our parameters: the percentage for the differences from the mean and median, the multiplier for the Tukey fence, and the threshold for the Z-score. To determine which of the rules was performing the best, we used the miss rate, false omission rate, false discovery rate, and the false alarm rate.

In the next two chapters, we will introduce machine learning in Python using `scikit-learn`, and in *Chapter 11, Machine Learning Anomaly Detection*, we will revisit this scenario for anomaly detection using machine learning.

Exercises

Complete the following exercises to practice the concepts covered in this chapter:

1. Run the simulation for December 2018 into new log files without making the user base again. Be sure to run `python3 simulate.py -h` to review the command-line arguments. Set the seed to 27. This data will be used for the remaining exercises.
2. Find the number of unique usernames, attempts, successes, and failures, as well as the success/failure rates per IP address, using the data simulated from exercise 1.
3. Create two subplots with failures versus attempts on the left, and failure rate versus distinct usernames on the right. Draw decision boundaries for the resulting plots. Be sure to color each data point by whether or not it is a hacker IP address.
4. Build a rule-based criteria using the percentage difference from the median that flags an IP address if the failures and attempts are both five times their respective medians, or if the distinct usernames count is five times its median. Be sure to use a one-hour window. Remember to use the `get_baselines()` function to calculate the metrics needed for the baselines.
5. Calculate metrics to evaluate how well these rules performed using the `evaluate()` and `classification_stats()` functions from this chapter.

Further reading

Check out the following resources for more information on the topics covered in this chapter:

- *A Gentle Introduction to the Bootstrap Method*: <https://machinelearningmastery.com/a-gentle-introduction-to-the-bootstrap-method/>
- *An Introduction to the Bootstrap Method*: <https://towardsdatascience.com/an-introduction-to-the-bootstrap-method-58bcb51b4d60>
- *Adding Salt to Hashing: A Better Way to Store Passwords*: <https://auth0.com/blog/adding-salt-to-hashing-a-better-way-to-store-passwords/>
- *Brute-Force Attack*: https://en.wikipedia.org/wiki/Brute-force_attack

- *Classification Accuracy Is Not Enough: More Performance Measures You Can Use*: <https://machinelearningmastery.com/classification-accuracy-is-not-enough-more-performance-measures-you-can-use/>
- *Dictionary Attack*: https://en.wikipedia.org/wiki/Dictionary_attack
- *Nelson Rules*: https://en.wikipedia.org/wiki/Nelson_rules
- *Offline Password Cracking: The Attack and the Best Defense*: <https://www.alpinesecurity.com/blog/offline-password-cracking-the-attack-and-the-best-defense-against-it>
- *Poisson Point Process*: https://en.wikipedia.org/wiki/Poisson_point_process
- *Precision and Recall*: https://en.wikipedia.org/wiki/Precision_and_recall
- *Probability Distributions in Python*: <https://www.datacamp.com/community/tutorials/probability-distributions-python>
- *Rainbow Tables: Your Password's Worst Nightmare*: <https://www.lifewire.com/rainbow-tables-your-passwords-worst-nightmare-2487288>
- *RFC 1597 (Address Allocation for Private Internets)*: <http://www.faqs.org/rfcs/rfc1597.html>
- *Sampling Techniques*: <https://towardsdatascience.com/sampling-techniques-a4e34111d808>
- *Trimmed Estimator*: https://en.wikipedia.org/wiki/Trimmed_estimator
- *Western Electric rules*: https://en.wikipedia.org/wiki/Western_Electric_rules

Section 4: Introduction to Machine Learning with Scikit-Learn

Up to this point in the book, we have focused on data analysis tasks using `pandas`, but there is so much more data science we can do with Python. These next three chapters will serve as an introduction to machine learning in Python with `scikit-learn`—that's not to say that we will be abandoning everything we have worked on so far, though. As we have seen, `pandas` is an essential tool for quickly exploring, cleaning, visualizing, and analyzing data—all of which still need to be done before attempting any machine learning. We won't go into any theory; instead, we will show how machine learning tasks, such as clustering, classification, and regression, can be easily implemented in Python.

This section comprises the following chapters:

- *Chapter 9, Getting Started with Machine Learning in Python*
- *Chapter 10, Making Better Predictions – Optimizing Models*
- *Chapter 11, Machine Learning Anomaly Detection*

9

Getting Started with Machine Learning in Python

This chapter will expose us to the vernacular of machine learning and the common tasks that machine learning can be used to solve. Afterward, we will learn how we can prepare our data for use in machine learning models. We have discussed data cleaning already, but only for human consumption—machine learning models require different **preprocessing** (cleaning) techniques. There are quite a few nuances here, so we will take our time with this topic and discuss how we can use `scikit-learn` to build preprocessing pipelines that streamline this procedure, since our models will only be as good as the data they are trained on.

Next, we will walk through how we can use `scikit-learn` to build a model and evaluate its performance. Scikit-learn has a very user-friendly API, so once we know how to build one model, we can build any number of them. We won't be going into any of the mathematics behind the models; there are entire books on this, and the goal of this chapter is to serve as an introduction to the topic. By the end of this chapter, we will be able to identify what type of problem we are looking to solve and some algorithms that can help us, as well as how to implement them.

The following topics will be covered in this chapter:

- Overview of the machine learning landscape
- Performing exploratory data analysis using skills learned in previous chapters
- Preprocessing data for use in a machine learning model
- Clustering to help understand unlabeled data
- Learning when regression is appropriate and how to implement it with scikit-learn
- Understanding classification tasks and learning how to use logistic regression

Chapter materials

In this chapter, we will be working with three datasets. The first two come from data on wine quality that was donated to the UCI Machine Learning Data Repository (<http://archive.ics.uci.edu/ml/index.php>) by P. Cortez, A. Cerdeira, F. Almeida, T. Matos, and J. Reis, which contains information on the chemical properties of various wine samples, along with a rating of the quality from a blind tasting by a panel of wine experts. These files can be found in the `data/` folder inside this chapter's folder in the GitHub repository (https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_09) as `winequality-red.csv` and `winequality-white.csv` for red and white wine, respectively.

Our third dataset was collected using the Open Exoplanet Catalogue database, which can be found at https://github.com/OpenExoplanetCatalogue/open_exoplanet_catalogue/. This database provides data in **eXtensible Markup Language (XML)** format, which is similar to HTML. The `planet_data_collection.ipynb` notebook on GitHub contains the code that was used to parse this information into the CSV files we will use in this chapter; while we won't be going over this explicitly, I encourage you to take a look at it. The data files can be found in the `data/` folder, as well. We will use `planets.csv` for this chapter; however, the parsed data for the other hierarchies is provided for exercises and further exploration. These are `binaries.csv`, `stars.csv`, and `systems.csv`, which contain data on binaries (stars or binaries forming a group of two), data on a single star, and data on planetary systems, respectively.

We will be using the `red_wine.ipynb` notebook to predict red wine quality, the `wine.ipynb` notebook to classify wines as red or white based on their chemical properties, and the `planets_ml.ipynb` notebook to build a regression model to predict the year length of planets and perform clustering to find similar planet groups. We will use the `preprocessing.ipynb` notebook for the section on preprocessing.

Back in *Chapter 1, Introduction to Data Analysis*, when we set up our environment, we installed a package from GitHub called `ml_utils`. This package contains utility functions and classes that we will use for our three chapters on machine learning. Unlike the last two chapters, we won't be discussing how to make this package; however, those interested can look through the code at https://github.com/stefmolin/ml-utils/tree/2nd_edition and follow the instructions from *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*, to install it in editable mode.

The following are the reference links for the data sources:

- *Open Exoplanet Catalogue database*, available at https://github.com/OpenExoplanetCatalogue/open_exoplanet_catalogue/#data-structure.
- *P. Cortez, A. Cerdeira, F. Almeida, T. Matos and J. Reis. Modeling wine preferences by data mining from physicochemical properties. In Decision Support Systems, Elsevier, 47(4):547-553, 2009. Available online at http://archive.ics.uci.edu/ml/datasets/Wine+Quality.*
- *Dua, D. and Karra Taniskidou, E. (2017). UCI Machine Learning Repository [http://archive.ics.uci.edu/ml/index.php]. Irvine, CA: University of California, School of Information and Computer Science.*

Overview of the machine learning landscape

Machine learning is a subset of **artificial intelligence (AI)** whereby an algorithm can learn to predict values from input data without explicitly being taught rules. These algorithms rely on statistics to make inferences as they learn; they then use what they learn to make predictions.

Applying for a loan, using a search engine, sending a robot vacuum to clean a specific room with a voice command—machine learning can be found everywhere we look. This is because it can be used for many purposes, for example, voice recognition by AI assistants such as Alexa, Siri, or Google Assistant, mapping floor plans by exploring surroundings, determining who will default on a loan, figuring out which search results are relevant, and even painting (<https://www.boredpanda.com/computer-deep-learning-algorithm-painting-masters/>).

Machine learning models can be made to adapt to changes in the input over time and are a huge help in making decisions without the need for a human each time. Think about applying for a loan or a credit line increase on a credit card; the bank or credit card company will rely on a machine learning algorithm to look up things from the applicant's credit score and history with them to determine whether the applicant should be approved. Most likely, they will only approve the applicant at that moment if the model predicts a strong chance he or she can be trusted with the loan or new credit limit. In the case where the model can't be so sure, they can send it over to a human to make the final decision. This reduces the amount of applications employees have to sift through to just the borderline cases, while also providing faster answers for those non-borderline cases (the process can be nearly instantaneous).

One important thing to call out here is that models that are used for tasks such as loan approvals, by law, have to be interpretable. There needs to be a way to explain to the applicant why they were rejected—sometimes, reasons beyond technology can influence and limit what approaches or data we use.

Types of machine learning

Machine learning is typically divided into three categories: unsupervised learning, supervised learning, and reinforcement learning. We use **unsupervised learning** when we don't have labeled data telling us what our model should say for each data point. In many cases, gathering labeled data is costly or just not feasible, so unsupervised learning will be used. Note that it is more difficult to optimize the performance of these models because we don't know how well they are performing. If we do have access to the labels, we can use **supervised learning**; this makes it much easier for us to evaluate our models and look to improve them since we can calculate metrics on their performance compared to the true labels.

Tip

Since unsupervised learning looks to find meaning in the data without a correct answer, it can be used to learn more about the data as a part of the analysis or before moving on to supervised learning.

Reinforcement learning is concerned with reacting to feedback from the environment; this is used for things such as robots and AI in games. It is well beyond the scope of this book, but there are resources in the *Further reading* section for more information.

Note that not all machine learning approaches fit neatly into the aforementioned categories. One example is **deep learning**, which aims to learn data representations using methods such as **neural networks**. Deep learning methods are often seen as black boxes, which has prevented their use in certain domains where interpretable models are required; however, they are used for tasks such as speech recognition and image classification. Deep learning is also beyond the scope of this book, but it is good to be aware that it is also machine learning.

Important note

Interpretable machine learning is an active area of research. Check out the resources in the *Further reading* section for more information.

Common tasks

The most common machine learning tasks are clustering, classification, and regression. In **clustering**, we look to assign data into groups, with the goal being that the groups are well-defined, meaning that members of the group are close together and groups are separated from other groups. Clustering can be used in an unsupervised manner in an attempt to gain a better understanding of the data, or in a supervised manner to try to predict which cluster data belongs to (essentially classification). Note that clustering can be used for prediction in an unsupervised manner; however, we will need to decipher what each cluster means. Labels that are obtained from clustering can even be used as the input for a supervised learner to model how observations are mapped to each group; this is called **semi-supervised learning**.

Classification, as we discussed in the previous chapter, looks to assign a class label to the data, such as *benign* or *malicious*. This may sound like assigning it to a cluster, however, we aren't worried about how similar the values that are assigned to *benign* are, just marking them as *benign*. Since we are assigning to a class or category, this class of models is used to predict a discrete label. **Regression**, on the other hand, is for predicting numeric values, such as housing prices or book sales; it models the strength and magnitude of the relationships between variables. Both can be performed as unsupervised or supervised learning; however, supervised models are more likely to perform better.

Machine learning in Python

Now that we know what machine learning is, we need to know how we can build our own models. Python offers many packages for building machine learning models; some libraries we should be aware of include the following:

- **scikit-learn**: Easy to use (and learn), it features a consistent API for machine learning in Python (<https://scikit-learn.org/stable/index.html>)
- **statsmodels**: A statistical modeling library that also provides statistical tests (<https://www.statsmodels.org/stable/index.html>)
- **tensorflow**: A machine learning library developed by Google that features faster calculations (<https://www.tensorflow.org/>)
- **keras**: A high-level API for running deep learning from libraries such as TensorFlow (<https://keras.io/>)
- **pytorch**: A deep learning library developed by Facebook (<https://pytorch.org>)

Tip

Most of these libraries use NumPy and SciPy, a library built on top of NumPy for statistics, mathematics, and engineering purposes. SciPy can be used to handle linear algebra, interpolation, integration, and clustering algorithms, among other things. More information on SciPy can be found at <https://docs.scipy.org/doc/scipy/reference/tutorial/general.html>.

In this book, we will be using **scikit-learn** for its user-friendly API. In **scikit-learn**, our base class is an **estimator** (not to be confused with a model when used in statistical terms), which is capable of learning from the data via its `fit()` method. We use **transformers** to prepare our data with their `transform()` method—transforming the data into something **predictors** (classes for supervised or unsupervised learning) can use with their `predict()` method. The **model** classes are capable of calculating how well they perform using a `score()` method. Knowing just these four methods, we can easily build any machine learning model offered by **scikit-learn**. More information on this design pattern can be found at <https://scikit-learn.org/stable/developers/develop.html>.

Exploratory data analysis

As we have learned throughout this book, our first step should be to engage in some **exploratory data analysis (EDA)** to get familiar with our data. In the interest of brevity, this section will include a subset of the EDA that's available in each of the notebooks—be sure to check out the respective notebooks for the full version.

Tip

While we will use `pandas` code to perform our EDA, be sure to check out the `pandas-profiling` package (<https://github.com/pandas-profiling/pandas-profiling>), which can be used to quickly perform some initial EDA on the data via an interactive HTML report.

Let's start with our imports, which will be the same across the notebooks we will use in this chapter:

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

We will start our EDA with the wine quality data before moving on to the planets.

Red wine quality data

Let's read in our red wine data and do some EDA using techniques we have learned throughout this book:

```
>>> red_wine = pd.read_csv('data/winequality-red.csv')
```

We have data on 11 different chemical properties of red wine, along with a column indicating the quality score from the wine experts that participated in the blind taste testing. We can try to predict the quality score by looking at the chemical properties:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	5
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	5
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	6
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5

Figure 9.1 – Red wine dataset

Let's see what the distribution of the quality column looks like:

```
>>> def plot_quality_scores(df, kind):
...     ax = df.quality.value_counts().sort_index().plot.barh(
...         title=f'{kind.title()} Wine Quality Scores',
...         figsize=(12, 3)
...     )
...     ax.axes.invert_yaxis()
...     for bar in ax.patches:
...         ax.text(
...             bar.get_width(),
...             bar.get_y() + bar.get_height()/2,
...             f'{bar.get_width()/df.shape[0]:.1%}',
...             verticalalignment='center'
...         )
...     plt.xlabel('count of wines')
...     plt.ylabel('quality score')
...
...     for spine in ['top', 'right']:
...         ax.spines[spine].set_visible(False)
...
...     return ax
>>> plot_quality_scores(red_wine, 'red')
```

The information on the dataset says that quality varies from 0 (terrible) to 10 (excellent); however, we only have values in the middle of that range. An interesting task for this dataset could be to see if we can predict high-quality red wines (a quality score of 7 or higher):

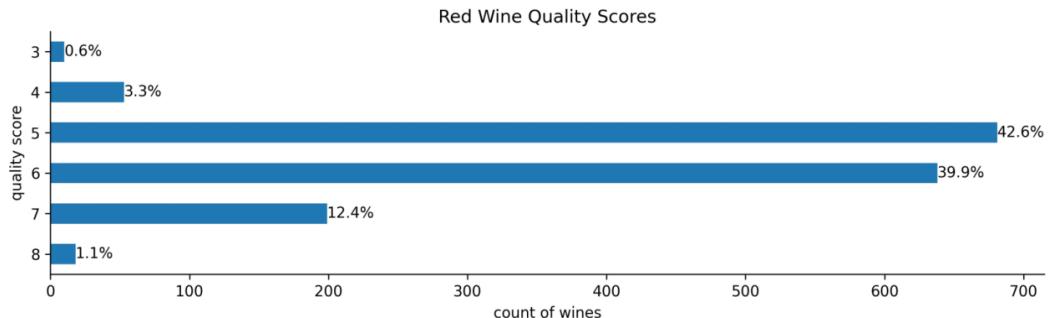


Figure 9.2 – Distribution of red wine quality scores

All of our data is numeric, so we don't have to worry about handling text values; we also don't have any missing values:

```
>>> red_wine.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1599 entries, 0 to 1598
Data columns (total 12 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   fixed acidity    1599 non-null   float64
 1   volatile acidity 1599 non-null   float64
 2   citric acid      1599 non-null   float64
 3   residual sugar   1599 non-null   float64
 4   chlorides         1599 non-null   float64
 5   free sulfur dioxide 1599 non-null   float64
 6   total sulfur dioxide 1599 non-null   float64
 7   density           1599 non-null   float64
 8   pH                1599 non-null   float64
 9   sulphates         1599 non-null   float64
 10  alcohol           1599 non-null   float64
 11  quality            1599 non-null   int64  
dtypes: float64(11), int64(1)
memory usage: 150.0 KB
```

We can use `describe()` to get an idea of what scale each of the columns is on:

```
>>> red_wine.describe()
```

The result indicates that we will definitely have to do some scaling if our model uses distance metrics for anything because our columns aren't all on the same range:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
count	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000
mean	8.319637	0.527821	0.270976	2.538806	0.087467	15.874922	46.467792	0.996747	3.311113	0.658149	10.422983	5.636023
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.895324	0.001887	0.154386	0.169507	1.065668	0.807569
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	0.990070	2.740000	0.330000	8.400000	3.000000
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	0.995600	3.210000	0.550000	9.500000	5.000000
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	0.996750	3.310000	0.620000	10.200000	6.000000
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	0.997835	3.400000	0.730000	11.100000	6.000000
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000	1.003690	4.010000	2.000000	14.900000	8.000000

Figure 9.3 – Summary statistics for the red wine dataset

Lastly, let's use `pd.cut()` to bin our high-quality red wines (roughly 14% of the data) for later:

```
>>> red_wine['high_quality'] = pd.cut(
...     red_wine.quality, bins=[0, 6, 10], labels=[0, 1]
... )
>>> red_wine.high_quality.value_counts(normalize=True)
0    0.86429
1    0.13571
Name: high_quality, dtype: float64
```

Important note

We are stopping our EDA here for brevity; however, we should make sure to fully explore our data and consult domain experts before attempting any modeling. One thing to pay particular attention to is correlations between variables and what we are trying to predict (high-quality red wine, in this case). Variables with strong correlations may be good features to include in a model. However, note that correlation does not imply causation. We already learned a few ways to use visualizations to look for correlations: the scatter matrix we discussed in *Chapter 5, Visualizing Data with Pandas and Matplotlib*, and the heatmap and pair plot from *Chapter 6, Plotting with Seaborn and Customization Techniques*. A pair plot is included in the `red_wine.ipynb` notebook.

White and red wine chemical properties data

Now, let's look at the red and white wine data together. Since the data comes in separate files, we need to read in both and concatenate them into a single dataframe. The white wine file is actually semi-colon (;) separated, so we must provide the `sep` argument to `pd.read_csv()`:

```
>>> red_wine = pd.read_csv('data/winequality-red.csv')
>>> white_wine = \
...     pd.read_csv('data/winequality-white.csv', sep=';')
```

We can also look at the quality scores of the white wines, just as we did with the red ones, and we will find that the white wines tend to be rated higher overall. This might bring us to question whether the judges preferred white wine over red wine, thus creating a bias in their ratings. As it is, the rating system that was used seems to be pretty subjective:

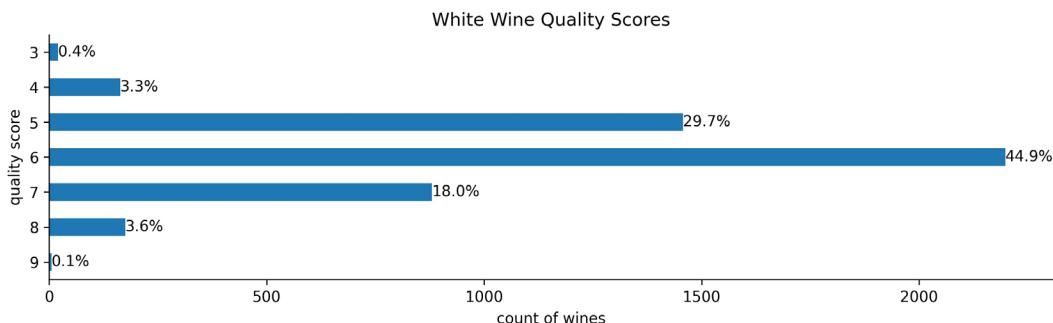


Figure 9.4 – Distribution of white wine quality scores

Both of these dataframes have the same columns, so we can combine them without further work. Here, we use `pd.concat()` to stack the white wine data on top of the red wine data after adding a column to identify which wine type each observation belongs to:

```
>>> wine = pd.concat([
...     white_wine.assign(kind='white'),
...     red_wine.assign(kind='red')
... ])
>>> wine.sample(5, random_state=10)
```

As we did with the red wine dataset, we can run `info()` to check whether we need to perform type conversion or whether we are missing any data; thankfully, we have no need here either. Our combined wine dataset looks like this:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	pH	sulphates	alcohol	quality	kind
848	6.4	0.64	0.21	1.8	0.081	14.0	31.0	0.99689	3.59	0.66	9.8	5 red
2529	6.6	0.42	0.13	12.8	0.044	26.0	158.0	0.99772	3.24	0.47	9.0	5 white
131	5.6	0.50	0.09	2.3	0.049	17.0	99.0	0.99370	3.63	0.63	13.0	5 red
244	15.0	0.21	0.44	2.2	0.075	10.0	24.0	1.00005	3.07	0.84	9.2	7 red
1551	6.6	0.19	0.99	1.2	0.122	45.0	129.0	0.99360	3.09	0.31	8.7	6 white

Figure 9.5 – Combined wine dataset

Using `value_counts()`, we can see that we have many more white wines than red wines in the data:

```
>>> wine.kind.value_counts()
white      4898
red       1599
Name: kind, dtype: int64
```

Lastly, let's examine box plots for each chemical property broken out by wine type using `seaborn`. This can help us identify **features** (model inputs) that will be helpful when building our model to distinguish between red and white wine:

```
>>> import math
>>> chemical_properties = [col for col in wine.columns
...                         if col not in ['quality', 'kind']]
>>> melted = \
...     wine.drop(columns='quality').melt(id_vars=['kind'])
>>> fig, axes = plt.subplots(
...     math.ceil(len(chemical_properties) / 4), 4,
...     figsize=(15, 10)
... )
>>> axes = axes.flatten()
>>> for prop, ax in zip(chemical_properties, axes):
...     sns.boxplot(
...         data=melted[melted.variable.isin([prop])],
...         x='variable', y='value', hue='kind', ax=ax
...     ).set_xlabel('')
>>> for ax in axes[len(chemical_properties):]:
...     ax.remove() # remove the extra subplots
```

```
>>> plt.suptitle(
...     'Comparing Chemical Properties of Red and White Wines'
... )
>>> plt.tight_layout()
```

Given the following result, we might look to use fixed acidity, volatile acidity, total sulfur dioxide, and sulphates when building a model since they seem to be distributed differently for red and white wines:

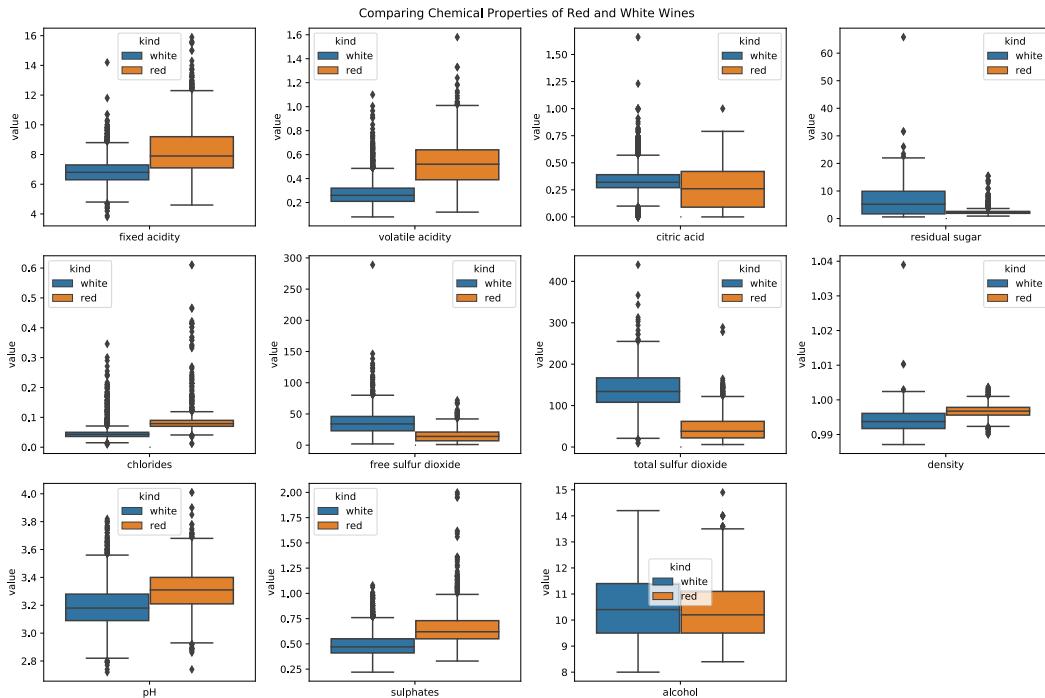


Figure 9.6 – Comparing red and white wine on a chemical level

Tip

Comparing the distributions of variables across classes can help inform feature selection for our model. If we see that the distribution for a variable is very different between classes, that variable may be very useful to include in our model. It is essential that we perform an in-depth exploration of our data before moving on to modeling. Be sure to use the visualizations we covered in *Chapter 5, Visualizing Data with Pandas and Matplotlib*, and *Chapter 6, Plotting with Seaborn and Customization Techniques*, as they will prove invaluable for this process.

We will come back to this visualization in *Chapter 10, Making Better Predictions – Optimizing Models*, when we examine incorrect predictions made by our model. Now, let's take a look at the other dataset we will be working with.

Planets and exoplanets data

An **exoplanet** is simply a planet that orbits a star outside of our solar system, so from here on out we will refer to both collectively as **planets**. Let's read in our planets data now:

```
>>> planets = pd.read_csv('data/planets.csv')
```

Some interesting tasks we can do with this data would be to find clusters of similar planets based on their orbits and try to predict the orbit period (how long a year is on a planet), in Earth days:

	mass	description	periastrontime	semimajoraxis	discoveryyear	list	eccentricity	period	discoverymethod	lastupdate	periastron	name
0	19.400	11 Com ...	2452899.60	1.290	2008.0	Confirmed planets	0.231	326.03	RV	15/09/20	94.800	11 Com b
1	11.200	11 Ursa...	2452861.04	1.540	2009.0	Confirmed planets	0.080	516.22	RV	15/09/20	117.630	11 UMi b
2	4.800	14 Andr...	2452861.40	0.830	2008.0	Confirmed planets	0.000	185.84	RV	15/09/20	0.000	14 And b
3	4.975	The sta...	NaN	2.864	2002.0	Confirmed planets	0.359	1766.00	RV	15/09/21	22.230	14 Her b
4	7.679	14 Her ...	NaN	9.037	2006.0	Controversial	0.184	9886.00	RV	15/09/21	189.076	14 Her c

Figure 9.7 – Planets dataset

We can build a correlation matrix heatmap to help find the best features to use:

```
>>> fig = plt.figure(figsize=(7, 7))
>>> sns.heatmap(
...     planets.drop(columns='discoveryyear').corr(),
...     center=0, vmin=-1, vmax=1, square=True, annot=True,
...     cbar_kws={'shrink': 0.8}
... )
```

The heatmap shows us that the semi-major axis of a planet's orbit is highly positively correlated to the length of its period, which makes sense since the semi-major axis (along with eccentricity) helps define the path that a planet travels around its star:

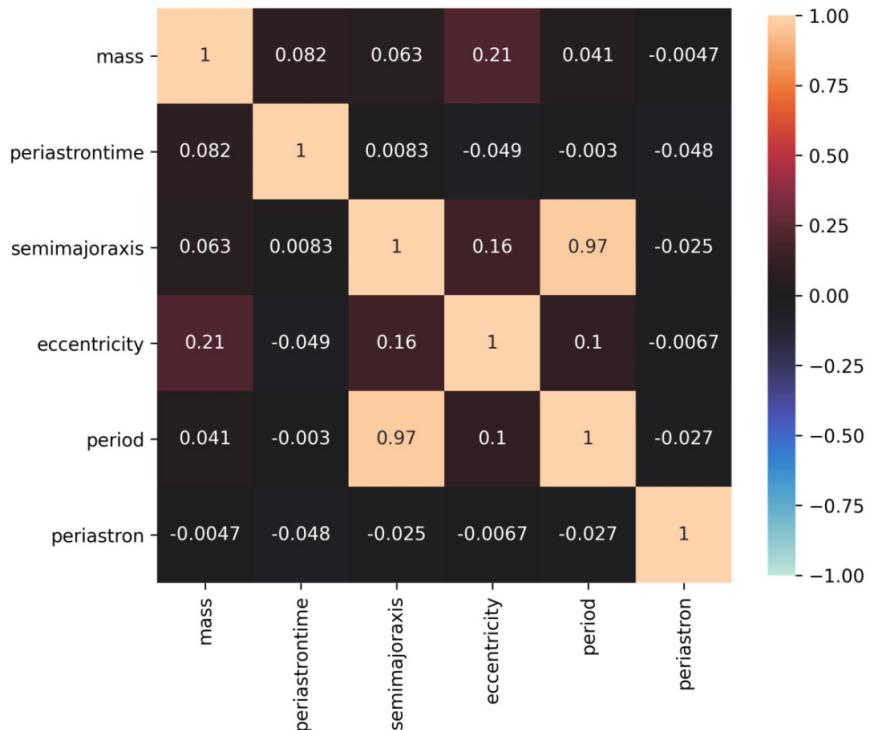


Figure 9.8 – Correlations between features in the planets dataset

To predict `period`, we probably want to look at `semimajoraxis`, `mass`, and `eccentricity`. The orbit eccentricity quantifies how much the orbit differs from a perfect circle:

Eccentricity	Orbit Shape
0	Circular
(0, 1)	Elliptical
1	Parabolic
> 1	Hyperbolic

Figure 9.9 – Understanding eccentricity

Let's see what shapes the orbits we have are:

```
>>> planets.eccentricity.min(), planets.eccentricity.max()
(0.0, 0.956) # circular and elliptical eccentricities
>>> planets.eccentricity.hist()
>>> plt.xlabel('eccentricity')
>>> plt.ylabel('frequency')
>>> plt.title('Orbit Eccentricities')
```

It looks like nearly everything is an ellipse, which we would expect since these are planets:

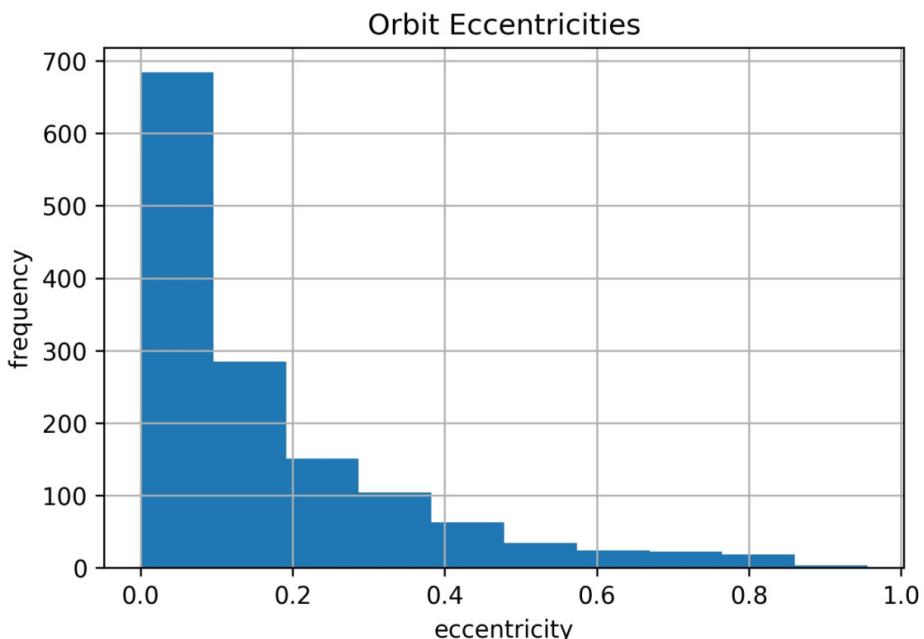


Figure 9.10 – Distribution of orbit eccentricities

An ellipse, being an elongated circle, has two axes: *major* and *minor* for the longest and shortest ones, respectively. The semi-major axis is half the major axis. When compared to a circle, the axes are analogous to the diameter, crossing the entire shape, and the semi-axes are akin to the radius, being half the diameter. The following is how this would look in the case where the planet orbited a star that was exactly in the center of its elliptical orbit (due to gravity from other objects, in reality, the star can be anywhere inside the orbit path):

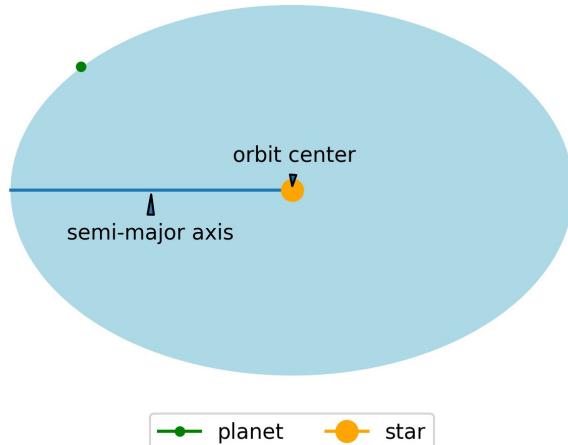


Figure 9.11 – Understanding the semi-major axis

Now that we understand what these columns mean, let's do some more EDA. This data isn't as clean as our wine data was—it's certainly much easier to measure everything when we can reach out and touch it. We only have `eccentricity`, `semimajoraxis`, or `mass` data for a fraction of the planets, despite knowing most of the `period` values:

```
>>> planets[[
...     'period', 'eccentricity', 'semimajoraxis', 'mass'
... ]].info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4094 entries, 0 to 4093
Data columns (total 4 columns):
 #   Column           Non-Null Count  Dtype  
---  --  
 0   period          3930 non-null    float64 
 1   eccentricity    1388 non-null    float64 
 2   semimajoraxis   1704 non-null    float64 
 3   mass            1659 non-null    float64 
dtypes: float64(4)
memory usage: 128.1 KB
```

If we were to drop data where any of these columns was null, we would be left with about 30% of it:

```
>>> planets[[
...     'period', 'eccentricity', 'semimajoraxis', 'mass'
... ]].dropna().shape
(1222, 4)
```

If we are simply looking for a way to predict the length of the year (when we have these values available) to learn more about their relationship, we wouldn't necessarily worry about throwing out the missing data. Imputing it here could be far worse for our model. At least everything is properly encoded as a decimal (`float64`); however, let's check whether we need to do some scaling (beneficial if our model is sensitive to differences in magnitude):

```
>>> planets[['period', 'eccentricity', 'semimajoraxis', 'mass']].describe()
```

This shows us that, depending on our model, we will definitely have to do some scaling because the values in the `period` column are much larger than the others:

	period	eccentricity	semimajoraxis	mass
count	3930.000000	1388.000000	1704.000000	1659.000000
mean	524.084969	0.159016	5.837964	2.702061
std	7087.428665	0.185041	110.668743	8.526177
min	0.090706	0.000000	0.004420	0.000008
25%	4.552475	0.013000	0.051575	0.085000
50%	12.364638	0.100000	0.140900	0.830000
75%	46.793136	0.230000	1.190000	2.440000
max	320000.000000	0.956000	3500.000000	263.000000

Figure 9.12 – Summary statistics for the planets dataset

We could also look at some scatter plots. Note that there is a `list` column for the group the planet belongs to, such as `Solar System` or `Controversial`. We might want to see if the period (and distance from the star) influences this:

```
>>> sns.scatterplot(
...     x=planets.semimajoraxis, y=planets.period,
...     hue=planets.list, alpha=0.5
... )
>>> plt.title('period vs. semimajoraxis')
>>> plt.legend(title='')
```

The controversial planets appear to be spread throughout and have larger semi-major axes and periods. Perhaps they are controversial because they are very far from their star:

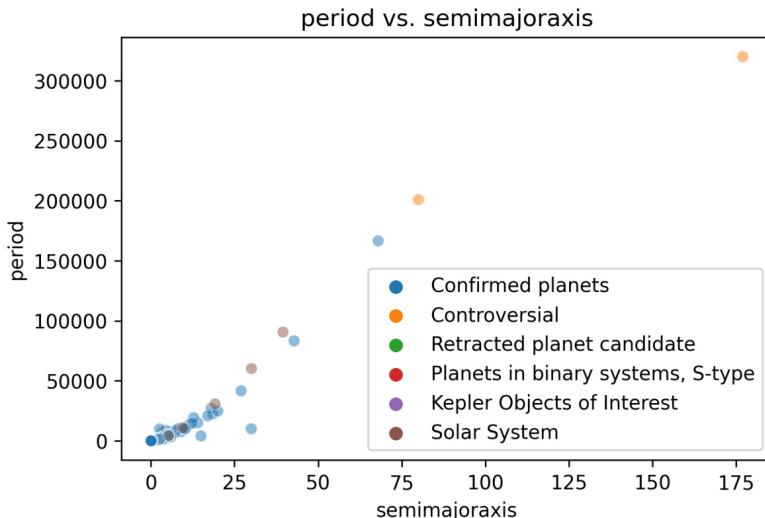


Figure 9.13 – Planet period versus semi-major axis

Unfortunately, we can see that the scale of `period` is making this pretty difficult to read, so we could try a log transformation on the `y`-axis to get more separation in the denser section on the lower-left. Let's just point out the planets in our solar system this time:

```
>>> fig, ax = plt.subplots(1, 1, figsize=(10, 10))
>>> in_solar_system = (planets.list == 'Solar System') \
...     .rename('in solar system?')
>>> sns.scatterplot(
...     x=planets.semimajoraxis, y=planets.period,
...     hue=in_solar_system, ax=ax
... )
>>> ax.set_yscale('log')
>>> solar_system = planets[planets.list == 'Solar System']
>>> for planet in solar_system.name:
...     data = solar_system.query(f'name == "{planet}"')
...     ax.annotate(
...         planet,
...         (data.semimajoraxis, data.period),
...         (7 + data.semimajoraxis, data.period),
...         arrowprops=dict(arrowstyle='->')
...     )
>>> ax.set_title('log(orbital period) vs. semi-major axis')
```

There were certainly a lot of planets hiding in that lower-left corner of the plot. We can see many planets with years shorter than Mercury's 88 Earth-day year now:

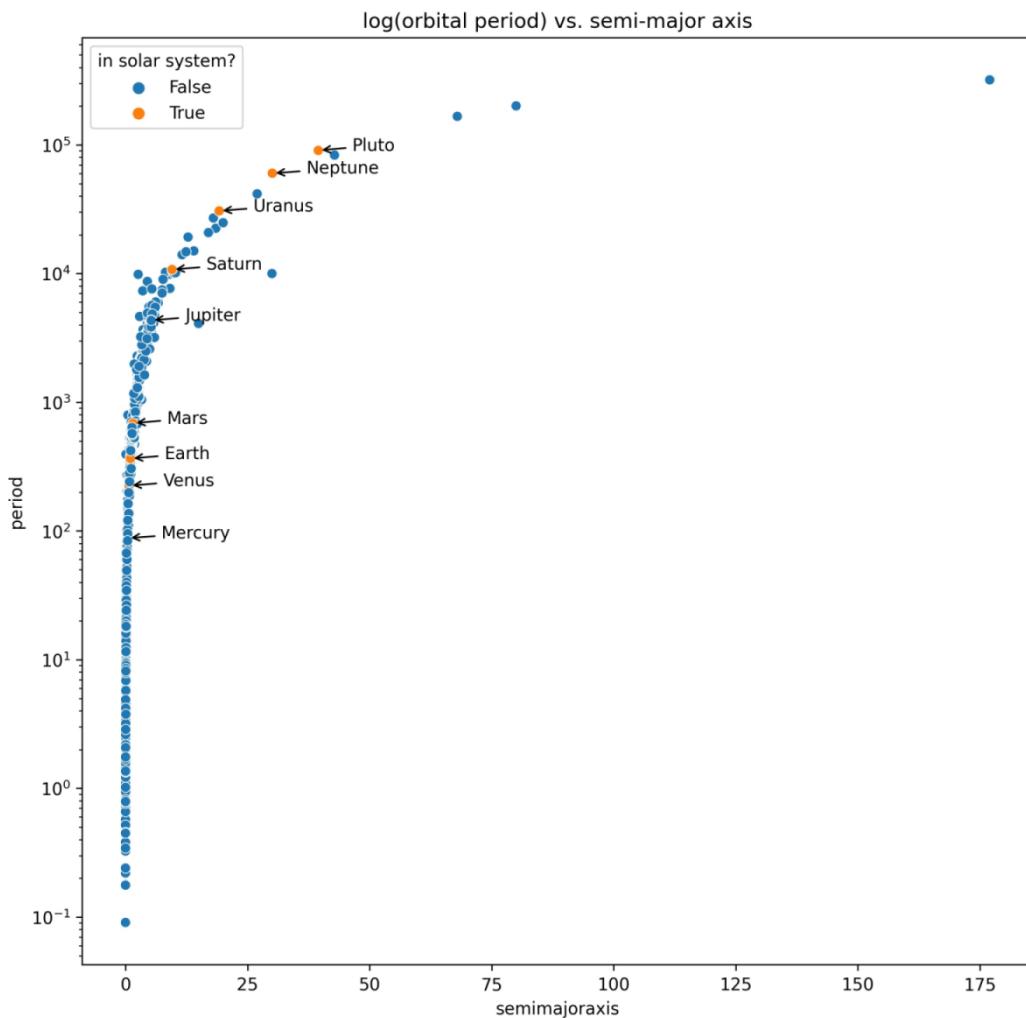


Figure 9.14 – Our solar system compared to exoplanets

Now that we have a feel for the data we will be working with, let's learn how to prepare it for use in a machine learning model.

Preprocessing data

In this section, we will be working in the `preprocessing.ipynb` notebook before we return to the notebooks we used for EDA. We will begin with our imports and read in the data:

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

>>> planets = pd.read_csv('data/planets.csv')
>>> red_wine = pd.read_csv('data/winequality-red.csv')
>>> wine = pd.concat([
...     pd.read_csv(
...         'data/winequality-white.csv', sep=';',
...         ).assign(kind='white'),
...     red_wine.assign(kind='red')
... ])
```

Machine learning models follow the garbage in, garbage out principle. We have to make sure that we **train** our models (have them learn) on the best possible version of the data. What this means will depend on the model we choose. For instance, models that use a distance metric to calculate how similar observations are will easily be confused if our features are on wildly different scales. Unless we are working with a **natural language processing (NLP)** problem to try and understand the meaning of words, our model will have no use for—or worse, be unable to interpret—textual values. Missing or invalid data will also cause problems; we will have to decide whether to drop them or impute them. All of the adjustments we make to our data before giving it to our model to learn from are collectively called **preprocessing**.

Training and testing sets

So far, machine learning sounds pretty great, though—we can build a model that will learn how to perform a task for us. Therefore, we should give it all the data we have so that it learns well, right? Unfortunately, it's not that simple. If we give the model all of our data, we risk **overfitting** it, meaning that it won't be able to generalize well to new data points because it was fit to the sample rather than the population. On the other hand, if we don't give it enough data, it will **underfit** and be unable to capture the underlying information in the data.

Tip

When a model fits the randomness in the data, it is said to fit the **noise** in the data.

Another thing to consider is that if we use all of our data to train the model, how can we evaluate its performance? If we test it on the data we used for training, we will be overestimating how good it is because our model will always perform better on the training data. For these reasons, it's important to split our data into a **training set** and **testing set**. To do so, we could shuffle our dataframe and select the top $x\%$ of the rows for training and leave the rest for testing:

```
shuffled = \
    planets.reindex(np.random.permutation(planets.index))
train_end_index = int(np.ceil(shuffled.shape[0] * .75))
training = shuffled.iloc[:train_end_index,]
testing = shuffled.iloc[train_end_index:,]
```

This would work, but it's a lot to write every time. Thankfully, `scikit-learn` provides us with the `train_test_split()` function in the `model_selection` module, which is a more robust, easier-to-use solution. It requires us to separate our input data (X) from our output data (y) beforehand. Here, we will pick 75% of the data to be used for the training set ($X_{\text{train}}, y_{\text{train}}$) and 25% for the testing set ($X_{\text{test}}, y_{\text{test}}$). We will set a seed (`random_state=0`) so that the split is reproducible:

```
>>> from sklearn.model_selection import train_test_split

>>> X = planets[['eccentricity', 'semimajoraxis', 'mass']]
>>> y = planets.period

>>> X_train, X_test, y_train, y_test = train_test_split(
...     X, y, test_size=0.25, random_state=0
... )
```

While there are no specific criteria for what constitutes a good size for the test set, a rule of thumb is usually between 10% and 30% of the data. However, if we don't have much data, we will shift toward a 10% testing set to make sure that we have enough data to learn from. Conversely, if we have a lot of data, we may move toward 30% testing, since, not only do we not want to overfit, but we want to give our model a good amount of data to prove its worth. Note that there is a big caveat with this rule of thumb: there are diminishing returns on the amount of training data we use. If we have a ton of data, we will most likely use much less than 70% of it for training because our computational costs may rise significantly for possibly minuscule improvements and an increased risk of overfitting.

Important note

When building models that require tuning, we split the data into training, validation, and testing sets. We will introduce validation sets in *Chapter 10, Making Better Predictions – Optimizing Models*.

Let's take a look at the dimensions of our training and testing sets now. Since we are using three features (`eccentricity`, `semimajoraxis`, and `mass`), `x_train` and `x_test` have three columns. The `y_train` and `y_test` sets will be a single column each. The number of observations in the `x` and `y` data for training will be equal, as will be the case for the testing set:

```
>>> X.shape, y.shape # original data
((4094, 3), (4094,))
>>> X_train.shape, y_train.shape # training data
((3070, 3), (3070,))
>>> X_test.shape, y_test.shape # testing data
((1024, 3), (1024,))
```

`X_train` and `X_test` are returned to us as dataframes since that is the format we passed them in as. If we are working with data in NumPy directly, we will get NumPy arrays or `ndarrays` back instead. We are going to work with this data for other examples in the *Preprocessing data* section, so let's take a look at the first five rows of the `X_train` dataframe. Don't worry about the `NaN` values for now; we will discuss different ways of handling them in the *Imputing* section:

```
>>> X_train.head()
   eccentricity  semimajoraxis    mass
1390        NaN            NaN    NaN
2837        NaN            NaN    NaN
3619        NaN           0.0701    NaN
1867        NaN            NaN    NaN
1869        NaN            NaN    NaN
```

Both `y_train` and `y_test` are series since that is what we passed into the `train_test_split()` function. If we had passed in a NumPy array, that is what we would have gotten back instead. The rows in `y_train` and `y_test` must line up with the rows in `X_train` and `X_test`, respectively. Let's confirm this by looking at the first five rows of `y_train`:

```
>>> y_train.head()
```

```
1390      1.434742
2837      51.079263
3619      7.171000
1867      51.111024
1869      62.869161
Name: period, dtype: float64
```

Indeed, everything matches up, as expected. Note that for our wine models, we need to use stratified sampling, which can also be done with `train_test_split()` by passing the values to `stratify` on in the `stratify` argument. We will see this in the *Classification* section. For now, let's move on to the rest of our preprocessing.

Scaling and centering data

We've seen that our dataframes had columns with very different scales; if we want to use any model that calculates a distance metric (such as k-means, which we will discuss in this chapter, or **k-nearest neighbors (k-NN)**, which we will discuss briefly in *Chapter 10, Making Better Predictions – Optimizing Models*), we will need to scale these. As we discussed back in *Chapter 1, Introduction to Data Analysis*, we have quite a few options for doing so. Scikit-learn provides options in the `preprocessing` module for standardizing (scaling by calculating Z-scores) and min-max scaling (to normalize data to be in the range [0, 1]), among others.

Important note

We should check the requirements of the model we are building to see if the data needs to be scaled.

For standard scaling, we use the `StandardScaler` class. The `fit_transform()` method combines `fit()`, which figures out the mean and standard deviation needed to center and scale, and `transform()`, which applies the transformation to the data. Note that, when instantiating a `StandardScaler` object, we can choose to not subtract the mean or not divide by the standard deviation by passing `False` to `with_mean` or `with_std`, respectively. Both are `True` by default:

```
>>> from sklearn.preprocessing import StandardScaler

>>> standardized = StandardScaler().fit_transform(X_train)

# examine some of the non-NaN values
>>> standardized[~np.isnan(standardized)][::30]
```

```
array([-5.43618156e-02,  1.43278593e+00,  1.95196592e+00,
       4.51498477e-03, -1.96265630e-01,  7.79591646e-02,
       ...,
      -2.25664815e-02,  9.91013258e-01, -7.48808523e-01,
     -4.99260165e-02, -8.59044215e-01, -5.49264158e-02])
```

After this transformation, the data is in **scientific notation**. The information after the character e tells us where the decimal point got moved to. For a + sign, we move the decimal point to the right by the number of places indicated; we move to the left for a - sign. Therefore, $1.00\text{e}+00$ is equivalent to 1, $2.89\text{e}-02$ is equivalent to 0.0289, and $2.89\text{e}+02$ is equivalent to 289. The transformed planets data is mostly between -3 and 3 because everything is now a Z-score.

Other scalers can be used with the same syntax. Let's use the `MinMaxScaler` class to transform the planets data into the range [0, 1]:

```
>>> from sklearn.preprocessing import MinMaxScaler

>>> normalized = MinMaxScaler().fit_transform(X_train)

# examine some of the non-NaN values
>>> normalized[~np.isnan(normalized)][:30]
array([2.28055906e-05, 1.24474091e-01, 5.33472803e-01,
       1.71374569e-03, 1.83543340e-02, 1.77824268e-01,
       ...,
      9.35966714e-04, 9.56961137e-02, 2.09205021e-02,
     1.50201619e-04, 0.00000000e+00, 6.59028789e-06])
```

Tip

Another option is the `RobustScaler` class, which uses the median and IQR for robust to outliers scaling. There is an example of this in the notebook. More preprocessing classes can be found at <https://scikit-learn.org/stable/modules/classes.html#module-sklearn.preprocessing>.

Encoding data

All of the scalers discussed so far address the preprocessing of our numeric data, but how can we deal with categorical data? We need to encode the categories into integer values. There are a few options here, depending on what the categories represent. If our category is binary (such as 0/1, True/False, or yes/no), then we will **encode** these as a single column for both options, where 0 is one option and 1 is the other. We can easily do this with the `np.where()` function. Let's encode the wine data's `kind` field as 1 for red and 0 for white:

```
>>> np.where(wine.kind == 'red', 1, 0)
array([0, 0, 0, ..., 1, 1, 1])
```

This is effectively a column that tells us whether or not the wine is red. Remember, we concatenated the red wines to the bottom of the white wines when we created our wine dataframe, so `np.where()` will return zeros for the top rows and ones for the bottom rows, just like we saw in the previous result.

Tip

We can also use the `LabelBinarizer` class from `scikit-learn` to encode the `kind` field. Note that if our data is actually continuous, but we want to treat it as a binary categorical value, we could use the `Binarizer` class and provide a threshold or `pd.cut()`/`pd.qcut()`. There are examples of these in the notebook.

If our categories are ordered, we may want to use **ordinal encoding** on those columns; this will preserve the ordering of the categories. For instance, if we wanted to classify the red wines as low, medium, or high quality, we could encode this as 0, 1, and 2, respectively. The advantages of this are that we can use regression techniques to predict the quality, or we can use this as a feature in the model to predict something else; this model would be able to use the fact that high is better than medium, which is better than low quality. We can achieve this with the `LabelEncoder` class. Note that the labels will be created according to alphabetical order, so the first category alphabetically will be 0:

```
>>> from sklearn.preprocessing import LabelEncoder

>>> pd.Series(LabelEncoder().fit_transform(pd.cut(
...     red_wine.quality,
...     bins=[-1, 3, 6, 10],
...     labels=['0-3 (low)', '4-6 (med)', '7-10 (high)']
... ))).value_counts()
```

```
1    1372
2     217
0      10
dtype: int64
```

Important note

Scikit-learn provides the `OrdinalEncoder` class, but our data is not in the correct format—it expects 2D data (such as a `DataFrame` or `ndarray` object), instead of the 1D `Series` object we are working with here. We still need to ensure that the categories are in the proper order beforehand.

However, note that the ordinal encoding may create a potential data issue. In our example, if high-quality wines are now 2 and medium-quality wines are 1, the model may interpret that `2 * med = high`. This is implicitly creating an association between the levels of quality that we may not agree with.

Alternatively, a safer approach would be to perform **one-hot encoding** to create two new columns—`is_low` and `is_med`, which take only 0 or 1. Using those two, we automatically know whether the wine quality was high (when `is_low = is_med = 0`). These are called **dummy variables** or **indicator variables**; they numerically represent group membership for use in machine learning. If the indicator or dummy has a value of 1, that row is a member of that group; in our example of wine quality categories, if `is_low` is 1, then that row is a member of the low-quality group. This can be achieved with the `pd.get_dummies()` function and the `drop_first` argument, which will remove the redundant column.

Let's use one-hot encoding to encode the `list` column in the `planets` data, since the categories have no inherent order. Before we do any transformations, let's take a look at the lists we have in the data:

```
>>> planets.list.value_counts()
Confirmed planets                  3972
Controversial                      97
Retracted planet candidate          11
Solar System                        9
Kepler Objects of Interest          4
Planets in binary systems, S-type   1
Name: list, dtype: int64
```

We can use the `pd.get_dummies()` function to create dummy variables if we want to include the planet list in our models:

```
>>> pd.get_dummies(planets.list).head()
```

This turns our single series into the following dataframe, where the dummy variables were created in the order they appeared in the data:

	Confirmed planets	Controversial	Kepler Objects of Interest	Planets in binary systems, S-type	Retracted planet candidate	Solar System
0	1	0	0	0	0	0
1	1	0	0	0	0	0
2	1	0	0	0	0	0
3	1	0	0	0	0	0
4	0	1	0	0	0	0

Figure 9.15 – One-hot encoding

As we discussed previously, one of these columns is redundant because the values in the remaining ones can be used to determine the value for the redundant one. Some models may be significantly affected by the high correlation between these columns (referred to as **multicollinearity**), so we should remove one redundant column by passing in the `drop_first` argument:

```
>>> pd.get_dummies(planets.list, drop_first=True).head()
```

Note that the first column from the previous result has been removed, but we can still determine that all but the last row were in the `Confirmed Planets` list:

	Controversial	Kepler Objects of Interest	Planets in binary systems, S-type	Retracted planet candidate	Solar System
0	0	0	0	0	0
1	0	0	0	0	0
2	0	0	0	0	0
3	0	0	0	0	0
4	1	0	0	0	0

Figure 9.16 – Dropping redundant columns after one-hot encoding

Note that we can obtain a similar result by using the `LabelBinarizer` class and its `fit_transform()` method on our planets list. This won't drop a redundant feature, so we once again have the first feature belonging to the confirmed planets list, which can be seen in bold in the following result:

```
>>> from sklearn.preprocessing import LabelBinarizer

>>> LabelBinarizer().fit_transform(planets.list)
array([[1, 0, 0, 0, 0, 0],
       [1, 0, 0, 0, 0, 0],
       [1, 0, 0, 0, 0, 0],
       ...,
       [1, 0, 0, 0, 0, 0],
       [1, 0, 0, 0, 0, 0],
       [1, 0, 0, 0, 0, 0]])
```

Important note

Scikit-learn provides the `OneHotEncoder` class, but our data is not in the correct format—it expects the data to come in a 2D array, and our series is just 1D. We will see an example of how to use this in the *Additional transformers* section.

Imputing

We already know that we have some missing values in our planet data, so let's discuss a few of the options scikit-learn offers for handling them, which can be found in the `impute` module: imputing with a value (using constants or summary statistics), imputing based on similar observations, and indicating what is missing.

Back in the *Exploratory data analysis* section, we ran `dropna()` on the planets data we planned to model with. Let's say we don't want to get rid of it, and we want to try imputing it instead. The last few rows of our data have some missing values for `semimajoraxis`:

```
>>> planets[['semimajoraxis', 'mass', 'eccentricity']].tail()
   semimajoraxis    mass  eccentricity
4089        0.08150  1.9000        0.000
4090        0.04421  0.7090        0.038
4091          NaN    0.3334        0.310
4092          NaN    0.4000        0.270
4093          NaN    0.4200        0.160
```

We can use the `SimpleImputer` class to impute with a value, which will be the mean by default:

```
>>> from sklearn.impute import SimpleImputer

>>> SimpleImputer().fit_transform(
...     planets[['semimajoraxis', 'mass', 'eccentricity']]
... )
array([[ 1.29      ,  19.4      ,   0.231      ],
       [ 1.54      ,  11.2      ,   0.08       ],
       [ 0.83      ,   4.8      ,   0.         ],
       ...,
       [ 5.83796389,  0.3334    ,   0.31       ],
       [ 5.83796389,   0.4      ,   0.27       ],
       [ 5.83796389,   0.42     ,   0.16       ]])
```

The mean hardly seems like a good strategy here since the planets we know about may share something in common, and surely things like what system a planet is a part of and its orbit can be good indicators of some of the missing data points. We have the option to provide the `strategy` parameter with a method other than the mean; currently, it can be `median`, `most_frequent`, or `constant` (specify the value with `fill_value`). None of these is really appropriate for us; however, scikit-learn also provides the `KNNImputer` class for imputing missing values based on similar observations. By default, it uses the five nearest neighbors and runs k-NN, which we will discuss in *Chapter 10, Making Better Predictions – Optimizing Models*, using the features that aren't missing:

```
>>> from sklearn.impute import KNNImputer

>>> KNNImputer().fit_transform(
...     planets[['semimajoraxis', 'mass', 'eccentricity']]
... )
array([[ 1.29      ,  19.4      ,   0.231      ],
       [ 1.54      ,  11.2      ,   0.08       ],
       [ 0.83      ,   4.8      ,   0.         ],
       ...,
       [ 0.404726 ,  0.3334    ,   0.31       ],
       [ 0.85486 ,   0.4      ,   0.27       ],
       [ 0.15324 ,   0.42     ,   0.16       ]])
```

Notice that each of the bottom three rows has a unique value imputed for the semi-major axis now. This is because the mass and eccentricity were used to find similar planets from which to impute the semi-major axis. While this is certainly better than using the `SimpleImputer` class for the planets data, imputing can be dangerous.

Rather than imputing the data, in some cases, we may be more interested in noting where we have missing data and using that as a feature in our model. This can be achieved with the `MissingIndicator` class:

```
>>> from sklearn.impute import MissingIndicator

>>> MissingIndicator().fit_transform(
...     planets[['semimajoraxis', 'mass', 'eccentricity']])
... )
array([[False, False, False],
       [False, False, False],
       [False, False, False],
       ...,
       [True, False, False],
       [True, False, False],
       [True, False, False]])
```

As we turn our attention to the final set of preprocessors that we will discuss, notice that all of them have a `fit_transform()` method, along with `fit()` and `transform()` methods. This API design decision makes it very easy to figure out how to use new classes and is one of the reasons why `scikit-learn` is so easy to learn and use—it's very consistent.

Additional transformers

What if, rather than scaling our data or encoding it, we want to run a mathematical operation, such as taking the square root or the logarithm? The `preprocessing` module also has some classes for this. While there are a few that perform a specific transformation, such as the `QuantileTransformer` class, we will focus our attention on the `FunctionTransformer` class, which lets us provide an arbitrary function to use:

```
>>> from sklearn.preprocessing import FunctionTransformer

>>> FunctionTransformer(
...     np.abs, validate=True
... ).fit_transform(X_train.dropna())
```

```
array([[0.51      , 4.94      , 1.45      ],
       [0.17      , 0.64      , 0.85      ],
       [0.08      , 0.03727  , 1.192     ],
       ...,
       [0.295     , 4.46      , 1.8       ],
       [0.34      , 0.0652   , 0.0087   ],
       [0.3      , 1.26      , 0.5       ]])
```

Here, we took the absolute value of every number. Take note of the `validate=True` argument; the `FunctionTransformer` class knows that scikit-learn models won't accept NaN values, infinite values, or missing ones, so it will throw an error if we get those back. For this reason, we run `dropna()` here as well.

Notice that for scaling, encoding, imputing, and transforming data, everything we passed was transformed. If we have features of different data types, we can use the `ColumnTransformer` class to map transformations to a column (or group of columns) in a single call:

```
>>> from sklearn.compose import ColumnTransformer
>>> from sklearn.impute import KNNImputer
>>> from sklearn.preprocessing import (
...     MinMaxScaler, StandardScaler
... )

>>> ColumnTransformer([
...     ('impute', KNNImputer(), [0]),
...     ('standard_scale', StandardScaler(), [1]),
...     ('min_max', MinMaxScaler(), [2])
... ]).fit_transform(X_train)[10:15]
array([[ 0.17      , -0.04747176,  0.0107594 ],
       [ 0.08      , -0.05475873,  0.01508851],
       [ 0.15585591,         nan,  0.13924042],
       [ 0.15585591,         nan,         nan],
       [ 0.          , -0.05475111,  0.00478471]])
```

There is also the `make_column_transformer()` function, which will name the transformers for us. Let's make a `ColumnTransformer` object that will treat categorical data and numerical data differently:

```
>>> from sklearn.compose import make_column_transformer
>>> from sklearn.preprocessing import (
...     OneHotEncoder, StandardScaler
... )

>>> categorical = [
...     col for col in planets.columns
...     if col in [
...         'list', 'name', 'description',
...         'discoverymethod', 'lastupdate'
...     ]
... ]
>>> numeric = [
...     col for col in planets.columns
...     if col not in categorical
... ]
>>> make_column_transformer(
...     (StandardScaler(), numeric),
...     (OneHotEncoder(sparse=False), categorical)
... ).fit_transform(planets.dropna())
array([[ 3.09267587, -0.2351423 , -0.40487424, ...,
        0.          ,  0.          ],
       [ 1.432445   , -0.24215395, -0.28360905, ...,
        0.          ,  0.          ],
       [ 0.13665505, -0.24208849, -0.62800218, ...,
        0.          ,  0.          ],
       ...,
       [-0.83289954, -0.76197788, -0.84918988, ...,
        1.          ,  0.          ],
       [ 0.25813535,  0.38683239, -0.92873984, ...,
        0.          ,  0.          ],
       [-0.26827931, -0.21657671, -0.70076129, ...,
        0.          ,  1.          ]])
```

Tip

We are passing `sparse=False` upon instantiating our `OneHotEncoder` object so that we can see our result. In practice, we don't need to do this since `scikit-learn` models know how to handle NumPy sparse matrices.

Building data pipelines

It sure seems like there are a lot of steps involved in preprocessing our data, and they need to be applied in the correct order for both training and testing data—quite tedious. Thankfully, `scikit-learn` offers the ability to create pipelines to streamline the preprocessing and ensure that the training and testing sets are treated the same. This prevents issues, such as calculating the mean using all the data in order to standardize it and then splitting it into training and testing sets, which will create a model that looks like it will perform better than it actually will.

Important note

When information from outside the training set (such as using the full dataset to calculate the mean for standardization) is used to train the model, it is referred to as **data leakage**.

We are learning about pipelines before we build our first models because they ensure that the models are built properly. Pipelines can contain all the preprocessing steps and the model itself. Making a pipeline is as simple as defining the steps and naming them:

```
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import StandardScaler
>>> from sklearn.linear_model import LinearRegression

>>> Pipeline([
...     ('scale', StandardScaler()), ('lr', LinearRegression())
... ])
Pipeline(steps=[('scale', StandardScaler()),
                ('lr', LinearRegression())])
```

We aren't limited to using pipelines with models—they can also be used inside other `scikit-learn` objects, for example, `ColumnTransformer` objects. This makes it possible for us to first use k-NN imputing on the semi-major axis data (the column at index 0) and then standardize the result. We can then include this as part of a pipeline, which gives us tremendous flexibility in how we build our models:

```
>>> from sklearn.compose import ColumnTransformer
>>> from sklearn.impute import KNNImputer
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import (
...     MinMaxScaler, StandardScaler
... )

>>> ColumnTransformer([
...     ('impute', Pipeline([
...         ('impute', KNNImputer()),
...         ('scale', StandardScaler())
...     ]), [0]),
...     ('standard_scale', StandardScaler(), [1]),
...     ('min_max', MinMaxScaler(), [2])
... ]).fit_transform(X_train)[10:15]
array([[ 0.13531604, -0.04747176,  0.0107594 ],
       [-0.7257111 , -0.05475873,  0.01508851],
       [ 0.          , nan,      0.13924042],
       [ 0.          , nan,      nan],
       [-1.49106856, -0.05475111,  0.00478471]])
```

Just like with the `ColumnTransformer` class, we have a function that can make pipelines for us without having to name the steps. Let's make another pipeline, but this time we will use the `make_pipeline()` function:

```
>>> from sklearn.pipeline import make_pipeline
>>> make_pipeline(StandardScaler(), LinearRegression())
Pipeline(steps=[('standardscaler', StandardScaler()),
                ('linearregression', LinearRegression())])
```

Note that the steps have been automatically named the lowercase version of the class name. As we will see in the next chapter, naming the steps will make it easier to optimize model parameters by name. The consistency of the `scikit-learn` API will also allow us to use this pipeline to fit our model and make predictions using the same object, which we will see in the next section.

Clustering

We use clustering to divide our data points into groups of similar points. The points in each group are more like their fellow group members than those of other groups. Clustering is commonly used for tasks such as recommendation systems (think of how Netflix recommends what to watch based on what other people who've watched similar things are watching) and market segmentation.

For example, say we work at an online retailer and want to segment our website users for more targeted marketing efforts; we can gather data on time spent on the site, page visits, products viewed, products purchased, and much more. Then, we can have an unsupervised clustering algorithm find groups of users with similar behavior; if we make three groups, we can come up with labels for each group according to its behavior:

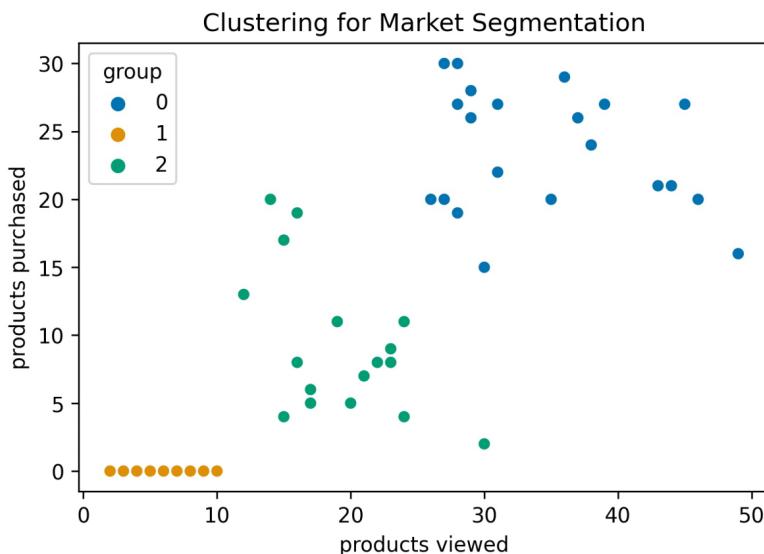


Figure 9.17 – Clustering website users into three groups

Since we can use clustering for unsupervised learning, we will need to interpret the groups that are created and then try to derive a meaningful name for each group. If our clustering algorithm identified the three clusters in the preceding scatter plot, we may be able to make the following behavioral observations:

- **Frequent customers (group 0):** Purchase a lot and look at many products.
- **Occasional customers (group 1):** Have made some purchases, but less than the most frequent customers.
- **Browsers (group 2):** Visit the website, but haven't bought anything.

Once these groups have been identified, the marketing team can focus on marketing to each of these groups differently; it's clear that the frequent customers will do more for the bottom line, but if they are already buying a lot, perhaps the marketing budget is better utilized trying to increase the purchases of the occasional customers or converting browsers into occasional customers.

Important note

Deciding on the number of groups to create can clearly influence how the groups are later interpreted, meaning that this is not a trivial decision. We should at least visualize our data and obtain some domain knowledge on it before attempting to guess the number of groups to split it into.

Alternatively, clustering can be used in a supervised fashion if we know the group labels for some of the data for training purposes. Say we collected data on login activity, like in *Chapter 8, Rule-Based Anomaly Detection*, but we had some examples of what attacker activity looks like; we could gather those data points for all activity and then use a clustering algorithm to assign to the valid users group or to the attacker group. Since we have the labels, we can tweak our input variables and/or the clustering algorithm we use to best align these groups to their true group.

k-means

The clustering algorithms offered by `scikit-learn` can be found in the `cluster` module's documentation at <https://scikit-learn.org/stable/modules/classes.html#module-sklearn.cluster>. We will take a look at **k-means**, which iteratively assigns points to the nearest group using the distance from the **centroid** of the group (center point), making k groups. Since this model uses distance calculations, it is imperative that we understand the effect scale will have on our results beforehand; we can then decide which columns, if any, to scale.

Important note

There are many ways to measure the distance between points in space. Often, Euclidean distance, or straight-line distance, is the default; however, another common one is Manhattan distance, which can be thought of as city-block distance.

When we plotted out the period versus the semi-major axis for all the planets using a log scale for the period, we saw a nice separation of the planets along an arc. We are going to use k-means to find groups of planets with similar orbits along that arc.

Grouping planets by orbit characteristics

As we discussed in the *Preprocessing data* section, we can build a pipeline to scale and then model our data. Here, our model will be a `KMeans` object that makes eight clusters (for the number of planets in our solar system—sorry, Pluto). Since the k-means algorithm randomly picks its starting centroids, it's possible to get different cluster results unless we specify the seed. Therefore, we also provide `random_state=0` for reproducibility:

```
>>> from sklearn.cluster import KMeans
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import StandardScaler

>>> kmeans_pipeline = Pipeline([
...     ('scale', StandardScaler()),
...     ('kmeans', KMeans(8, random_state=0))
... ])
```

Once we have our pipeline, we fit it on all the data since we aren't trying to predict anything (in this case)—we just want to find similar planets:

```
>>> kmeans_data = planets[['semimajoraxis', 'period']].dropna()
>>> kmeans_pipeline.fit(kmeans_data)
Pipeline(steps=[('scale', StandardScaler()),
                ('kmeans', KMeans(random_state=0))])
```

Once the model is fit to our data, we can use the `predict()` method to get the cluster labels for each point (on the same data that we used previously). Let's take a look at the clusters that k-means identified:

```
>>> fig, ax = plt.subplots(1, 1, figsize=(7, 7))
>>> sns.scatterplot(
...     x=kmeans_data.semimajoraxis,
...     y=kmeans_data.period,
...     hue=kmeans_pipeline.predict(kmeans_data),
...     ax=ax, palette='Accent'
... )
>>> ax.set_yscale('log')
>>> solar_system = planets[planets.list == 'Solar System']
```

```

>>> for planet in solar_system.name:
...     data = solar_system.query(f'name == "{planet}"')
...     ax.annotate(
...         planet,
...         (data.semimajoraxis, data.period),
...         (7 + data.semimajoraxis, data.period),
...         arrowprops=dict(arrowstyle='->')
...     )
>>> ax.get_legend().remove()
>>> ax.set_title('KMeans Clusters')

```

Mercury and Venus landed in the same cluster, as did Earth and Mars. Jupiter, Saturn, and Uranus each belong to separate clusters, while Neptune and Pluto share a cluster:

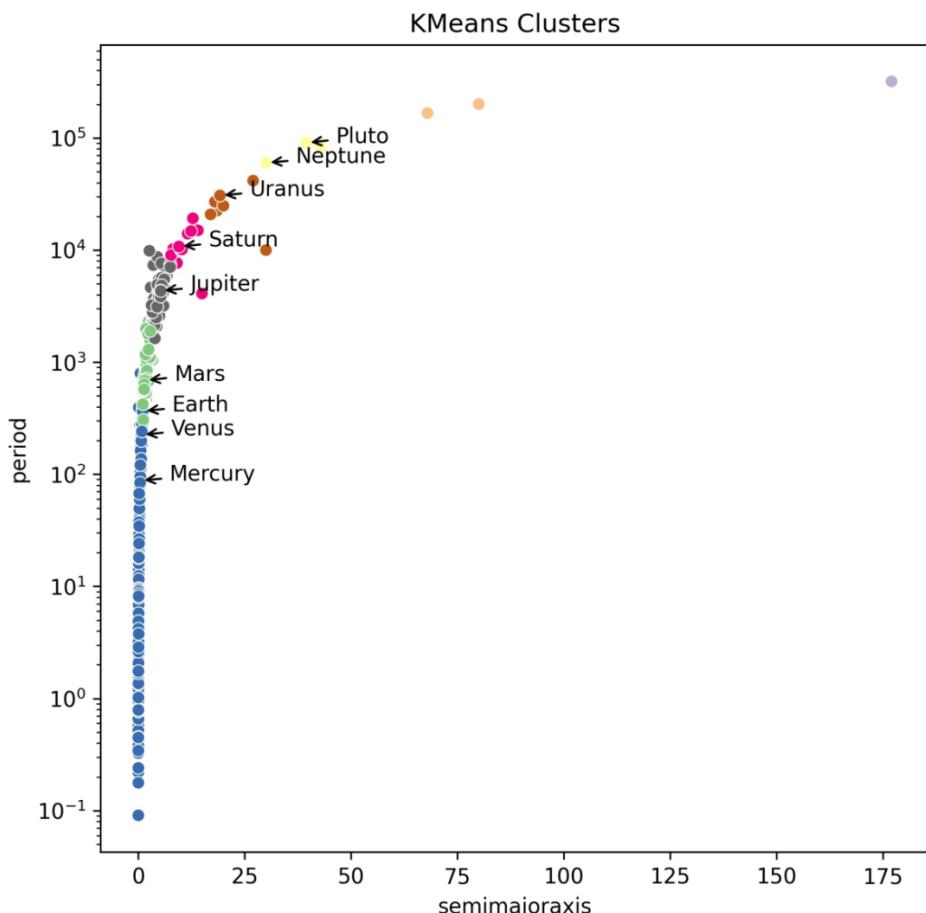


Figure 9.18 – Eight clusters of planets identified by k-means

We picked eight clusters arbitrarily here, since this is the number of planets in our solar system. Ideally, we would have some domain knowledge about the true groupings or need to pick a specific number. For example, say we want to fit wedding guests at five tables so that they all get along, then our k is 5; if we can run three marketing campaigns on user groups, we have a k of 3. If we have no intuition as to the number of groups there will be in the data, a rule of thumb is to try the square root of our observations, but this can yield an unmanageable amount of clusters. Therefore, if it doesn't take too long to create many k-means models on our data, we can use the elbow point method.

The elbow point method for determining k

The **elbow point method** involves creating multiple models with many values of k and plotting each model's **inertia** (**within-cluster sum of squares**) versus the number of clusters. We want to minimize the sum of squared distances from points to their cluster's center while not creating too many clusters.

The `ml_utils.elbow_point` module contains our `elbow_point()` function, which has been reproduced here:

```
import matplotlib.pyplot as plt

def elbow_point(data, pipeline, kmeans_step_name='kmeans',
                k_range=range(1, 11), ax=None):
    """
    Plot the elbow point to find an appropriate k for
    k-means clustering.

    Parameters:
        - data: The features to use
        - pipeline: The scikit-learn pipeline with `KMeans`
        - kmeans_step_name: Name of `KMeans` step in pipeline
        - k_range: The values of `k` to try
        - ax: Matplotlib `Axes` to plot on.

    Returns:
        A matplotlib `Axes` object
    """
    scores = []
    for k in k_range:
        pipeline.named_steps[kmeans_step_name].n_clusters = k
        pipeline.fit(data)
```

```
# score is -1*inertia so we multiply by -1 for inertia
scores.append(pipeline.score(data) * -1)

if not ax:
    fig, ax = plt.subplots()

ax.plot(k_range, scores, 'bo-')
ax.set_xlabel('k')
ax.set_ylabel('inertias')
ax.set_title('Elbow Point Plot')

return ax
```

Let's use the elbow point method to find an appropriate value for k :

```
>>> from ml_utils.elbow_point import elbow_point

>>> ax = elbow_point(
...     kmeans_data,
...     Pipeline([
...         ('scale', StandardScaler()),
...         ('kmeans', KMeans(random_state=0))
...     ])
... )
>>> ax.annotate(
...     'possible appropriate values for k', xy=(2, 900),
...     xytext=(2.5, 1500), arrowprops=dict(arrowstyle='->')
... )
>>> ax.annotate(
...     '', xy=(3, 3480), xytext=(4.4, 1450),
...     arrowprops=dict(arrowstyle='->')
... )
```

The point at which we see diminishing returns is an appropriate k , which may be around two or three here:

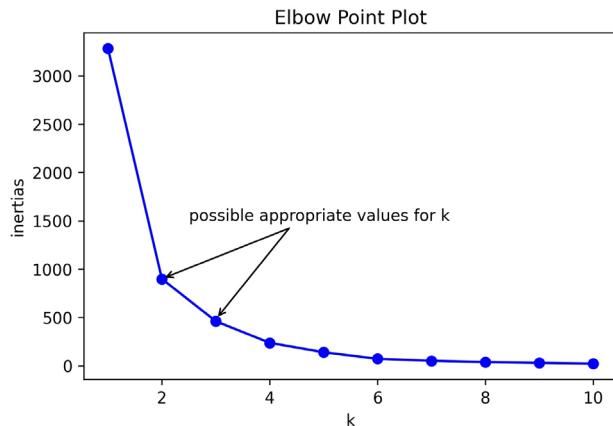


Figure 9.19 – Interpreting an elbow point plot

If we create just two clusters, we divide the planets into a group with most of the planets (orange) and a second group with only a few in the upper-right (blue), which are likely to be outliers:

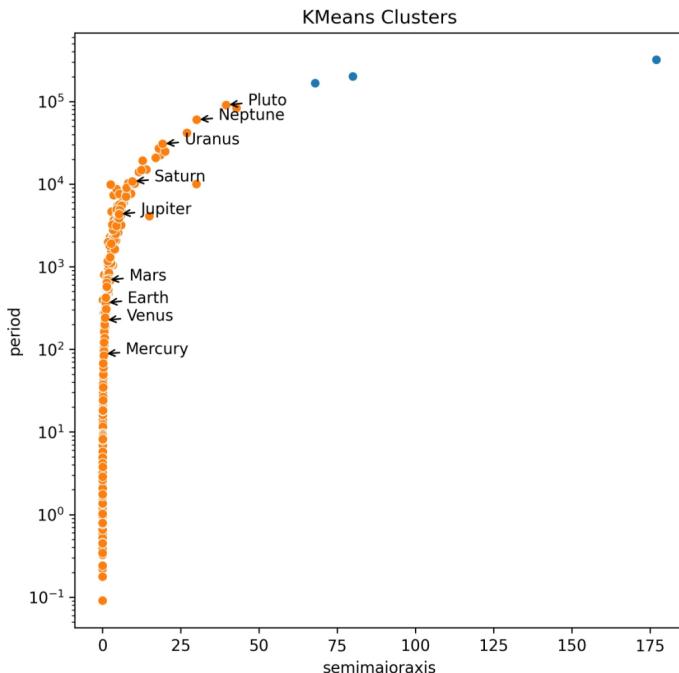


Figure 9.20 – Two clusters of planets identified by k-means

Note that while this may have been an appropriate amount of clusters, it doesn't tell us as much as the previous attempt. If we wanted to know about planets that are similar to each of the planets in our solar system, we would want to use a larger k .

Interpreting centroids and visualizing the cluster space

Since we standardized our data before clustering, we can look at the **centroids**, or cluster centers, to see the Z-score that the members are closest to. A centroid's location will be the average of each of the dimensions of the points in the cluster. We can grab this with the `cluster_centers_` attribute of the model. The centroid of the blue cluster is located at (18.9, 20.9), which is in the (semi-major axis, period) format; remember, these are Z-scores, so these are quite far from the rest of the data. The orange cluster, on the other hand, is centered at (-0.035, -0.038).

Let's build a visualization that shows us the location of the centroids with the scaled input data and the cluster distance space (where points are represented as the distance to their cluster's centroid). First, we will set up our layout for a smaller plot inside of a larger one:

```
>>> fig = plt.figure(figsize=(8, 6))
>>> outside = fig.add_axes([0.1, 0.1, 0.9, 0.9])
>>> inside = fig.add_axes([0.6, 0.2, 0.35, 0.35])
```

Next, we grab the scaled version of the input data and the distances between those data points and the centroid of the cluster they belong to. We can use the `transform()` and `fit_transform()` (`fit()` followed by `transform()`) methods to convert the input data into cluster distance space. We get NumPy ndarrays back, where each value in the outer array represents the coordinates of a point:

```
>>> scaled = kmeans_pipeline_2.named_steps['scale']\
...     .fit_transform(kmeans_data)
>>> cluster_distances = kmeans_pipeline_2\
...     .fit_transform(kmeans_data)
```

Since we know that each array in the outer array will have the semi-major axis as the first entry and the period as the second, we use `[:, 0]` to select all the semi-major axis values and `[:, 1]` to select all the period values. These will be the x and y for our scatter plot. Note that we actually don't need to call `predict()` to get the cluster labels for the data because we want the labels for the data we trained the model on; this means that we can use the `labels_` attribute of the `KMeans` object:

```
>>> for ax, data, title, axes_labels in zip(
...     [outside, inside], [scaled, cluster_distances],
...     ['Visualizing Clusters', 'Cluster Distance Space'],
...     ['standardized', 'distance to centroid']
... ) :
...     sns.scatterplot(
...         x=data[:,0], y=data[:,1], ax=ax, alpha=0.75, s=100,
...         hue=kmeans_pipeline_2.named_steps['kmeans'].labels_
...     )
...
...     ax.get_legend().remove()
...     ax.set_title(title)
...     ax.set_xlabel(f'semimajoraxis ({axes_labels})')
...     ax.set_ylabel(f'period ({axes_labels})')
...     ax.set_ylim(-1, None)
```

Lastly, we annotate the location of the centroids on the outer plot, which shows the scaled data:

```
>>> cluster_centers = kmeans_pipeline_2\
...     .named_steps['kmeans'].cluster_centers_
>>> for color, centroid in zip(
...     ['blue', 'orange'], cluster_centers
... ) :
...     outside.plot(*centroid, color=color, marker='x')
...     outside.annotate(
...         f'{color} center', xy=centroid,
...         xytext=centroid + [0, 5],
...         arrowprops=dict(arrowstyle='->')
...     )
```

In the resulting plot, we can easily see that the three blue points are quite different from the rest and that they are the only members of the second cluster:

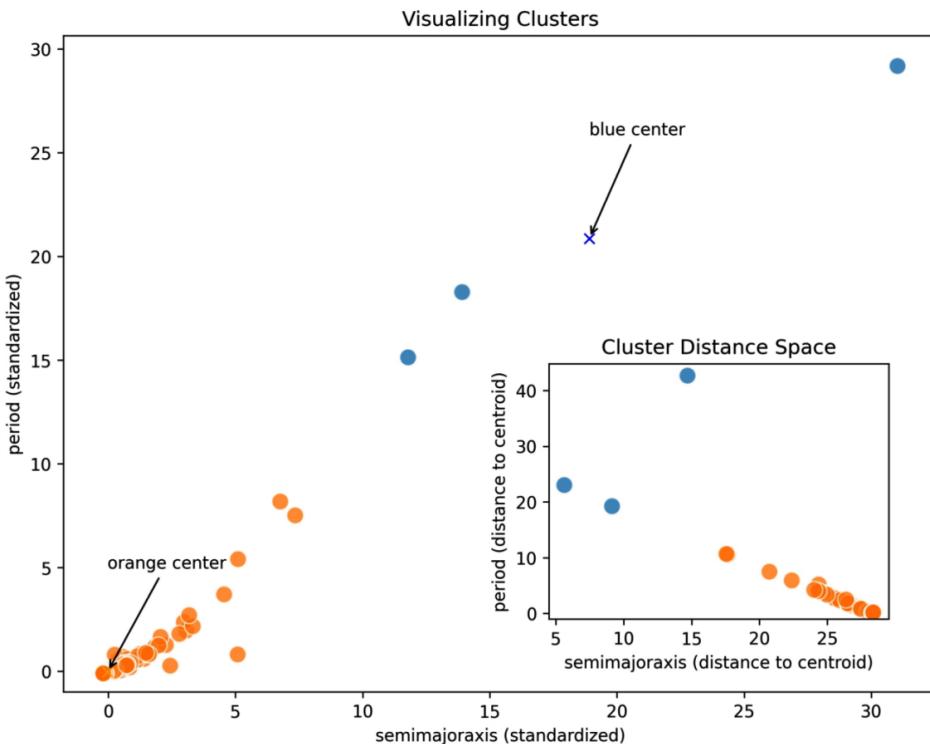


Figure 9.21 – Visualizing the planets in the cluster distance space

So far, we have been using `transform()` or combination methods, such as `fit_predict()` or `fit_transform()`, but not all models will support these methods. We will see a slightly different workflow in the *Regression* and *Classification* sections. In general, most `scikit-learn` objects will support the following, based on what they are used for:

Method	Action	Used when...
<code>fit()</code>	Train the model or preprocessor	Modeling, preprocessing
<code>transform()</code>	Transform the data into the new space	Clustering, preprocessing
<code>fit_transform()</code>	Run <code>fit()</code> , followed by <code>transform()</code>	Clustering, preprocessing
<code>score()</code>	Evaluate the model using the default scoring method	Modeling
<code>predict()</code>	Use model to predict output values for given inputs	Modeling
<code>fit_predict()</code>	Run <code>fit()</code> , followed by <code>predict()</code>	Modeling
<code>predict_proba()</code>	Like <code>predict()</code> , but returns the probability of belonging to each class	Classification

Figure 9.22 – General reference for the scikit-learn model API

Now that we have built a few models, we are ready for the next step: quantifying their performance. The `metrics` module in `scikit-learn` contains various metrics for evaluating model performance across clustering, regression, and classification tasks; the API lists the functions at <https://scikit-learn.org/stable/modules/classes.html#module-sklearn.metrics>. Let's discuss how to evaluate an unsupervised clustering model next.

Evaluating clustering results

The most important criterion for evaluating our clustering results is that they are useful for what we set out to do; we used the elbow point method to pick an appropriate value for k , but that wasn't as useful to us as the original model with eight clusters. That being said, when looking to quantify the performance, we need to pick metrics that match the type of learning we performed.

When we know the true clusters for our data, we can check that our clustering model places the points together in a cluster as they are in the true cluster. The cluster label given by our model can be different than the true one—all that matters is that the points in the same true cluster are also together in the predicted clusters. One such metric is the **Fowlkes-Mallows Index**, which we will see in the end-of-chapter exercises.

With the planets data, we performed unsupervised clustering because we don't have labels for each data point, and therefore, we can't measure how well we did against those. This means that we have to use metrics that evaluate aspects of the clusters themselves, such as how far apart they are and how close the points in a cluster are together. We can compare multiple metrics to get a more well-rounded evaluation of the performance.

One such method is called the **silhouette coefficient**, which helps quantify cluster separation. It is calculated by subtracting the mean of the distances between every two points in a cluster (a) from the mean of distances between points in a given cluster and the closest different cluster (b) and dividing by the maximum of the two:

$$\frac{b - a}{\max(a, b)}$$

This metric returns values in the range [-1, 1], where -1 is the worst (clusters are wrongly assigned) and 1 is the best; values near 0 indicate overlapping clusters. The higher this number is, the better defined (more separated) the clusters are:

```
>>> from sklearn.metrics import silhouette_score
>>> silhouette_score(
...     kmeans_data, kmeans_pipeline.predict(kmeans_data)
... )
0.7579771626036678
```

Another score we could use to evaluate our clustering result is the ratio of **within-cluster distances** (distances between points in a cluster) to the **between-cluster distances** (distances between points in different clusters), called the **Davies-Bouldin score**. Values closer to zero indicate better partitions between clusters:

```
>>> from sklearn.metrics import davies_bouldin_score
>>> davies_bouldin_score(
...     kmeans_data, kmeans_pipeline.predict(kmeans_data)
... )
0.4632311032231894
```

One last metric for unsupervised clustering that we will discuss here is the **Calinski and Harabasz score**, or **Variance Ratio Criterion**, which is the ratio of dispersion within a cluster to dispersion between clusters. Higher values indicate better defined (more separated) clusters:

```
>>> from sklearn.metrics import calinski_harabasz_score
>>> calinski_harabasz_score(
...     kmeans_data, kmeans_pipeline.predict(kmeans_data)
... )
21207.276781867335
```

For a complete list of clustering evaluation metrics offered by `scikit-learn` (including supervised clustering) and when to use them, check out the *Clustering performance evaluation* section of their guide at <https://scikit-learn.org/stable/modules/clustering.html#clustering-evaluation>.

Regression

With the planets dataset, we want to predict the length of the year, which is a numeric value, so we will turn to regression. As mentioned at the beginning of this chapter, regression is a technique for modeling the strength and magnitude of the relationship between independent variables (our X data)—often called **regressors**—and the dependent variable (our y data) that we want to predict.

Linear regression

Scikit-learn provides many algorithms that can handle regression tasks, ranging from decision trees to linear regression, spread across modules according to the various algorithm classes. However, typically, the best starting point is a linear regression, which can be found in the `linear_model` module. In **simple linear regression**, we fit our data to a line of the following form:

$$y = \beta_0 + \beta_1 x + \varepsilon$$

Here, epsilon (ε) is the error term and betas (β) are coefficients.

Important note

The coefficients we get from our model are those that minimize the **cost function**, or error between the observed values (y) and those predicted with the model (\hat{y} , pronounced *y-hat*). Our model gives us estimates of these coefficients, and we write them as $\hat{\beta}_i$ (pronounced *beta-hat*).

However, if we want to model additional relationships, we need to use **multiple linear regression**, which contains multiple regressors:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_n x_n + \varepsilon$$

Linear regression in `scikit-learn` uses **ordinary least squares (OLS)**, which yields the coefficients that minimize the sum of squared errors (measured as the distance between y and \hat{y}). The coefficients can be found using the closed-form solution, or estimated with optimization methods, such as **gradient descent**, which uses the negative gradient (direction of steepest ascent calculated with partial derivatives) to determine which coefficients to try next (see the link in the *Further reading* section for more information). We will use gradient descent in *Chapter 11, Machine Learning Anomaly Detection*.

Important note

Linear regression makes some assumptions about the data, which we must keep in mind when choosing to use this technique. It assumes that the residuals are normally distributed and homoskedastic and that there is no multicollinearity (high correlations between the regressors).

Now that we have a little background on how linear regression works, let's build a model to predict the orbit period of a planet.

Predicting the length of a year on a planet

Before we can build our model, we must isolate the columns that are used to predict (`semimajoraxis`, `mass`, and `eccentricity`) from the column that will be predicted (`period`):

```
>>> data = planets[
...      ['semimajoraxis', 'period', 'mass', 'eccentricity']
... ].dropna()
>>> X = data[['semimajoraxis', 'mass', 'eccentricity']]
>>> y = data.period
```

This is a supervised task. We want to be able to predict the length of a year on a planet using its semi-major axis, mass, and eccentricity of orbit, and we have the period lengths for most of the planets in the data. Let's create a 75/25 split of training to testing data so that we can assess how well this model predicts year length:

```
>>> from sklearn.model_selection import train_test_split
>>> X_train, X_test, y_train, y_test = train_test_split(
...      X, y, test_size=0.25, random_state=0
... )
```

Once we have separated the data into the training and testing sets, we can create and fit the model:

```
>>> from sklearn.linear_model import LinearRegression
>>> lm = LinearRegression().fit(X_train, y_train)
```

This fitted model can be used to examine the estimated coefficients and also to predict the value of the dependent variable for a given set of independent variables. We will cover both of these use cases in the next two sections.

Interpreting the linear regression equation

The equation derived from a linear regression model gives coefficients to quantify the relationships between the variables. Care must be exercised when attempting to interpret these coefficients if we are dealing with more than a single regressor. In the case of multicollinearity, we can't interpret them because we are unable to hold all other regressors constant to examine the effect of a single one.

Thankfully, the regressors we are using for the planets data aren't correlated, as we saw from the correlation matrix heatmap we made in the *Exploratory data analysis* section (*Figure 9.8*). So, let's get the intercept and coefficients from the fitted linear model object:

```
# get intercept
>>> lm.intercept_
-622.9909910671811

# get coefficients
>>> [(col, coef) for col, coef in
... zip(X_train.columns, lm.coef_)]
[('semimajoraxis', 1880.4365990440929),
 ('mass', -90.18675916509196),
 ('eccentricity', -3201.078059333091)]
```

This yields the following equation for our linear regression model of planet year length:

$$\text{period} = -623 + 1880 \times \text{semimajoraxis} - 90.2 \times \text{mass} - 3201 \times \text{eccentricity}$$

In order to interpret this more completely, we need to understand the units everything is in:

- `period` (length of year): Earth days
- `semimajoraxis`: **Astronomical units (AUs)**
- `mass`: Jupiter masses (planet mass divided by Jupiter's mass)
- `eccentricity`: N/A

Tip

An astronomical unit is the average distance between the Earth and the Sun, which is equivalent to 149,597,870,700 meters.

The intercept in this particular model doesn't have any meaning: if the planet had a semi-major axis of zero, no mass, and a perfect circle eccentricity, its year would be -623 Earth days long. A planet must have a non-negative, non-zero period, semi-major axis, and mass, so this clearly makes no sense. We can, however, interpret the other coefficients. The equation says that, holding mass and eccentricity constant, adding one additional AU to the semi-major axis distance increases the year length by 1,880 Earth days. Holding the semi-major axis and eccentricity constant, each additional Jupiter mass decreases the year length by 90.2 Earth days.

Going from a perfectly circular orbit (`eccentricity=0`) to a nearly parabolic escape orbit (`eccentricity=1`) will decrease the year length by 3,201 Earth days; note that these are approximate for this term because, with a parabolic escape orbit, the planet will never return, and consequently, this equation wouldn't make sense. In fact, if we tried to use this equation for eccentricities greater than or equal to 1, we would be extrapolating because we have no such values in the training data. This is a clear example of when extrapolation doesn't work. The equation tells us that the larger the eccentricity, the shorter the year, but once we get to eccentricities of one and beyond, the planets never come back (they have reached escape orbits), so the year is infinite.

All of the eccentricity values in the training data are in the range [0, 1), so we are interpolating (predicting period values using data in the ranges we trained on). This means that as long as the eccentricity of the planet we want to predict is also in the range [0, 1), we can use this model to make the prediction.

Making predictions

Now that we have an idea of the effect each of our regressors has, let's use our model to make predictions of year length for the planets in the test set:

```
>>> preds = lm.predict(X_test)
```

Let's visualize how well we did by plotting the actual and predicted values:

```
>>> fig, axes = plt.subplots(1, 1, figsize=(5, 3))
>>> axes.plot(
...     X_test.semimajoraxis, y_test, 'ob',
...     label='actuals', alpha=0.5
... )
>>> axes.plot(
...     X_test.semimajoraxis, preds, 'or',
...     label='predictions', alpha=0.5
... )
```

```
>>> axes.set(xlabel='semimajoraxis', ylabel='period')
>>> axes.legend()
>>> axes.set_title('Linear Regression Results')
```

The predicted values seem pretty close to the actual values and follow a similar pattern:

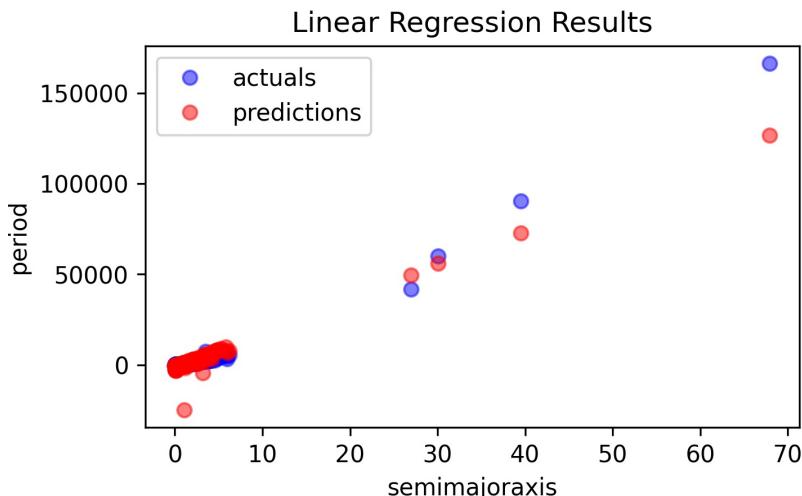


Figure 9.23 – Predictions versus actual values

Tip

Try running this regression with just the `semimajoraxis` regressor. Some reshaping of the data will be necessary, but this will show how much better this performs as we add in `eccentricity` and `mass`. In practice, we often have to build many versions of our model to find one we are happy with.

We can check their correlation to see how well our model tracks the true relationship:

```
>>> np.corrcoef(y_test, preds)[0][1]
0.9692104355988059
```

Our predictions are very strongly positively correlated with the actual values (0.97 correlation coefficient). Note that the correlation coefficient will tell us whether our model moves with the actual data; however, it will not tell us whether we are off magnitude-wise. For that, we will use the metrics discussed in the following section.

Evaluating regression results

When looking to evaluate a regression model, we are interested in how much of the variance in the data our model is able to capture, as well as how accurate the predictions are. We can use a combination of metrics and visuals to assess the model for each of these aspects.

Analyzing residuals

Whenever we work with linear regression, we should visualize our **residuals**, or the discrepancies between the actual values and the model's predictions; as we learned in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*, they should be centered around zero and homoskedastic (similar variance throughout). We can use a kernel density estimate to assess whether the residuals are centered around zero and a scatter plot to see if they are homoskedastic.

Let's look at the utility function in `ml_utils.regression`, which will create these subplots for checking the residuals:

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

def plot_residuals(y_test, preds):
    """
    Plot residuals to evaluate regression.

    Parameters:
    - y_test: The true values for y
    - preds: The predicted values for y

    Returns:
    Subplots of residual scatter plot and residual KDE
    """
    residuals = y_test - preds

    fig, axes = plt.subplots(1, 2, figsize=(15, 3))

    axes[0].scatter(np.arange(residuals.shape[0]), residuals)
    axes[0].set(xlabel='Observation', ylabel='Residual')
```

```
residuals.plot(kind='kde', ax=axes[1])
axes[1].set_xlabel('Residual')

plt.suptitle('Residuals')
return axes
```

Now, let's look at the residuals for this linear regression:

```
>>> from ml_utils.regression import plot_residuals
>>> plot_residuals(y_test, preds)
```

It looks like our predictions don't have a pattern (left subplot), which is good; however, they aren't quite centered around zero and the distribution has negative skew (right subplot). These negative residuals occur when the predicted year was longer than the actual year:

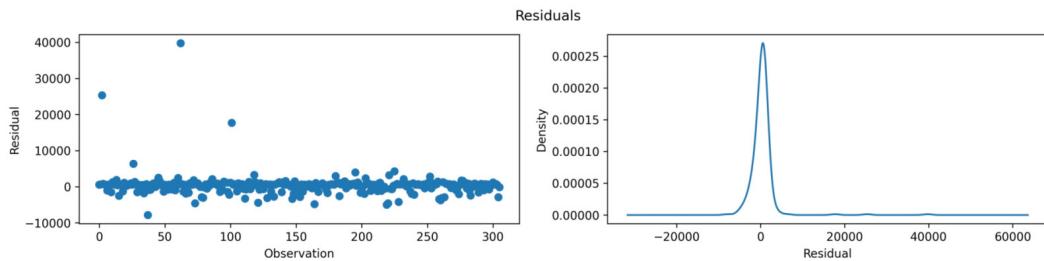


Figure 9.24 – Examining the residuals

Tip

If we find patterns in the residuals, our data isn't linear and the chances are that visualizing the residuals could help us plan our next move. This may mean employing strategies such as polynomial regression or log transformations of the data.

Metrics

In addition to examining the residuals, we should calculate metrics to evaluate our regression model. Perhaps the most common is **R²** (pronounced *R-squared*), or the **coefficient of determination**, which quantifies the proportion of variance in the dependent variable that we can predict from our independent variables. It is calculated by subtracting the ratio of the sum of squared residuals to the total sum of squares from 1:

$$R^2 = 1 - \frac{SS_{residual}}{SS_{total}} = 1 - \frac{\sum_i (y_i - \hat{y}_i)^2}{\sum_i (y_i - \bar{y})^2}$$

Tip

Sigma (Σ) represents the sum. The average of the y values is denoted as \bar{y} (pronounced *y-bar*). The predictions are denoted with \hat{y} (pronounced *y-hat*).

This value will be in the range [0, 1], where higher values are better. Objects of the `LinearRegression` class in `scikit-learn` use R^2 as their scoring method. Therefore, we can simply use the `score()` method to calculate it for us:

```
>>> lm.score(x_test, y_test)
0.9209013475842684
```

We can also get R^2 from the `metrics` module:

```
>>> from sklearn.metrics import r2_score
>>> r2_score(y_test, preds)
0.9209013475842684
```

This model has a very good R^2 ; however, keep in mind that there are many factors that affect the period, such as the stars and other planets, which exert a gravitational force on the planet in question. Despite this abstraction, our simplification does pretty well because the orbital period of a planet is determined in large part by the distance that must be traveled, which we account for by using the semi-major axis data.

There is a problem with R^2 , though; we can keep adding regressors, which would make our model more and more complex while at the same time increasing R^2 . We need a metric that penalizes model complexity. For that, we have **adjusted R²**, which will only increase if the added regressor improves the model more than what would be expected by chance:

$$\text{Adjusted } R^2 = 1 - (1 - R^2) \times \frac{n_{obs} - 1}{n_{obs} - n_{regressors} - 1}$$

Unfortunately, `scikit-learn` doesn't offer this metric; however, it is very easy to implement ourselves. The `ml_utils.regression` module contains a function for calculating the adjusted R² for us. Let's take a look at it:

```
from sklearn.metrics import r2_score

def adjusted_r2(model, X, y):
    """
    Calculate the adjusted R^2.

    Parameters:
    - model: Estimator object with a `predict()` method
    - X: The values to use for prediction.
    - y: The true values for scoring.

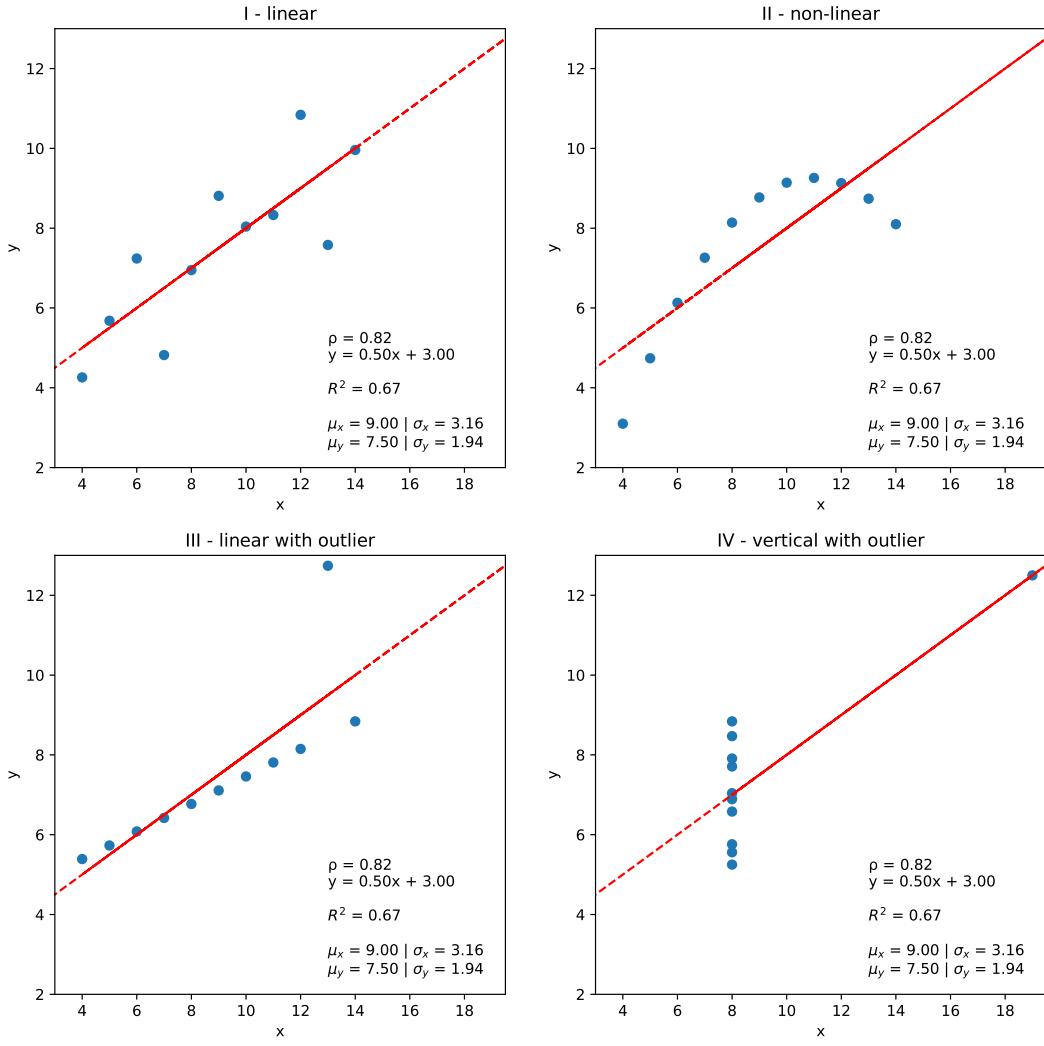
    Returns:
    The adjusted R^2 score.
    """
    r2 = r2_score(y, model.predict(X))
    n_obs, n_regressors = X.shape
    adj_r2 = \
        1 - (1 - r2) * (n_obs - 1) / (n_obs - n_regressors - 1)
    return adj_r2
```

Adjusted R² will always be lower than R². By using the `adjusted_r2()` function, we can see that our adjusted R² is slightly lower than the R² value:

```
>>> from ml_utils.regression import adjusted_r2
>>> adjusted_r2(lm, X_test, y_test)
0.9201155993814631
```

Unfortunately, R² (and adjusted R²) values don't tell us anything about our prediction error or even whether we specified our model correctly. Think back to when we discussed Anscombe's quartet in *Chapter 1, Introduction to Data Analysis*. These four different datasets have the same summary statistics. They also have the same R² when fit with a linear regression line (0.67), despite some of them not indicating a linear relationship:

Anscombe's Quartet

Figure 9.25 – R^2 can be misleading

Another metric offered by `scikit-learn` is the **explained variance score**, which tells us the percentage of the variance that is explained by our model. We want this as close to 1 as possible:

$$\text{explained variance} = 1 - \frac{\text{var(residuals)}}{\text{var(actuals)}} = 1 - \frac{\text{var}(y - \hat{y})}{\text{var}(y)}$$

We can see that our model explains 92% of the variance:

```
>>> from sklearn.metrics import explained_variance_score  
>>> explained_variance_score(y_test, preds)  
0.9220144218429371
```

We aren't limited to looking at variance when evaluating our regression models; we can also look at the magnitude of the errors themselves. The remaining metrics we will discuss in this section all yield errors in the same unit of measurement we are using for prediction (Earth days here), so we can understand the meaning of the size of the error.

Mean absolute error (MAE) tells us the average error our model made in either direction. Values range from 0 to ∞ (infinity), with smaller values being better:

$$MAE = \frac{\sum_i |y_i - \hat{y}_i|}{n}$$

By using the `scikit-learn` function, we can see that our MAE was 1,369 Earth days:

```
>>> from sklearn.metrics import mean_absolute_error  
>>> mean_absolute_error(y_test, preds)  
1369.441817073533
```

Root mean squared error (RMSE) allows for further penalization of poor predictions:

$$RMSE = \sqrt{\frac{\sum_i (y_i - \hat{y}_i)^2}{n}}$$

Scikit-learn provides a function for the **mean squared error (MSE)**, which is the portion of the preceding equation inside the square root; therefore, we simply have to take the square root of the result. We would use this metric when large errors are undesirable:

```
>>> from sklearn.metrics import mean_squared_error  
>>> np.sqrt(mean_squared_error(y_test, preds))  
3248.499961928374
```

An alternative to all these mean-based measures is the **median absolute error**, which is the median of the residuals. This can be used in cases where we have a few outliers in our residuals, and we want a more accurate description of the bulk of the errors. Note that this is smaller than the MAE for our data:

```
>>> from sklearn.metrics import median_absolute_error  
>>> median_absolute_error(y_test, preds)  
759.8613358335442
```

There is also a `mean_squared_log_error()` function, which can only be used for non-negative values. Some of the predictions are negative, which prevents us from using this. Negative predictions happen when the semi-major axis is very small (less than 1) since that is the only portion of the regression equation with a positive coefficient. If the semi-major axis isn't large enough to balance out the rest of our equation, the prediction will be negative and, thus, automatically incorrect. For a complete list of regression metrics offered by `scikit-learn`, check out <https://scikit-learn.org/stable/modules/classes.html#regression-metrics>.

Classification

The goal of classification is to determine how to label data using a set of discrete labels. This probably sounds similar to supervised clustering; however, in this case, we don't care how close members of the groups are spatially. Instead, we concern ourselves with classifying them with the correct class label. Remember, in *Chapter 8, Rule-Based Anomaly Detection*, when we classified the IP addresses as valid user or attacker? We didn't care how well-defined clusters of IP addresses were—we just wanted to find the attackers.

Just as with regression, `scikit-learn` provides many algorithms for classification tasks. These are spread across modules, but will usually say *Classifier* at the end for classification tasks, as opposed to *Regressor* for regression tasks. Some common methods are logistic regression, **support vector machines (SVMs)**, k-NN, decision trees, and random forests; here, we will discuss logistic regression.

Logistic regression

Logistic regression is a way to use linear regression to solve classification tasks. However, it uses the logistic sigmoid function to return probabilities in the range [0, 1] that can be mapped to class labels:

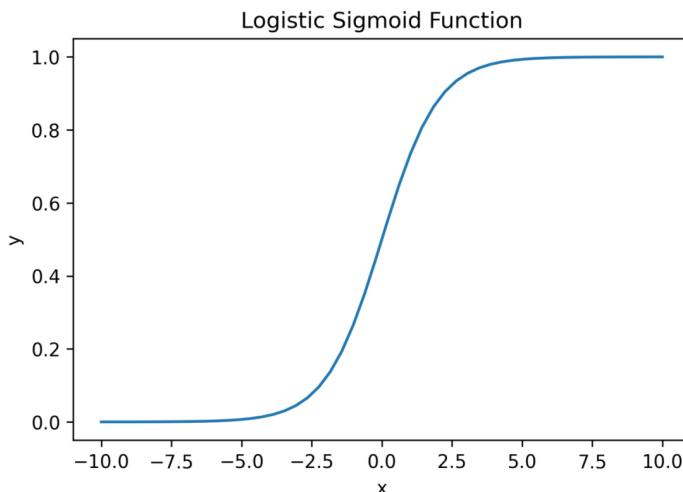


Figure 9.26 – The logistic sigmoid function

Let's use logistic regression to classify red wines as high or low quality and to classify wines as red or white based on their chemical properties. We can treat logistic regression as we did the linear regression in the previous section, using the `linear_model` module in `scikit-learn`. Just like the linear regression problem, we will be using a supervised method, so we have to split our data into testing and training sets.

Tip

While the examples discussed in this section are both binary classification problems (two classes), `scikit-learn` provides support for multiclass problems as well. The process of building multiclass models will be nearly identical to the binary case but may require passing an additional parameter to let the model know that there are more than two classes. You will have a chance to build a multiclass classification model in the exercises at the end of this chapter.

Predicting red wine quality

We made the `high_quality` column back at the beginning of this chapter, but remember that there was a large imbalance in the number of red wines that were high quality. So, when we split our data, we will stratify by that column for a stratified random sample to make sure that both the training and testing sets preserve the ratio of high-quality to low-quality wines in the data (roughly 14% are high quality):

```
>>> from sklearn.model_selection import train_test_split

>>> red_y = red_wine.pop('high_quality')
>>> red_X = red_wine.drop(columns='quality')

>>> r_X_train, r_X_test, \
... r_y_train, r_y_test = train_test_split(
...     red_X, red_y, test_size=0.1, random_state=0,
...     stratify=red_y
... )
```

Let's make a pipeline that will first standardize all of our data and then build a logistic regression. We will provide the seed (`random_state=0`) for reproducibility and `class_weight='balanced'` to have `scikit-learn` compute the weights of the classes, since we have an imbalance:

```
>>> from sklearn.preprocessing import StandardScaler
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.linear_model import LogisticRegression

>>> red_quality_lr = Pipeline([
...     ('scale', StandardScaler()),
...     ('lr', LogisticRegression(
...         class_weight='balanced', random_state=0
...     ))
... ])
```

The class weights determine how much the model will be penalized for wrong predictions for each class. By selecting balanced weights, wrong predictions on smaller classes will carry more weight, where the weight will be inversely proportional to the frequency of the class in the data. These weights are used for regularization, which we will discuss more in *Chapter 10, Making Better Predictions – Optimizing Models*.

Once we have our pipeline, we can fit it to the data with the `fit()` method:

```
>>> red_quality_lr.fit(r_X_train, r_y_train)
Pipeline(steps=[('scale', StandardScaler()),
                 ('lr', LogisticRegression(
                     class_weight='balanced',
                     random_state=0))])
```

Lastly, we can use our model fit on the training data to predict the red wine quality for the test data:

```
>>> quality_preds = red_quality_lr.predict(r_X_test)
```

Tip

Scikit-learn makes it easy to switch between models because we can count on them to have the same methods, such as `score()`, `fit()`, and `predict()`. In some cases, we also can use `predict_proba()` for probabilities or `decision_function()` to evaluate a point with the equation derived by the model instead of `predict()`.

Before we move on to evaluating the performance of this model, let's build another classification model using the full wine dataset.

Determining wine type by chemical properties

We want to know whether it is possible to tell red and white wine apart based solely on their chemical properties. To test this, we will build a second logistic regression model, which will predict whether a wine is red or white. First, let's split our data into testing and training sets:

```
>>> from sklearn.model_selection import train_test_split

>>> wine_y = np.where(wine.kind == 'red', 1, 0)
>>> wine_X = wine.drop(columns=['quality', 'kind'])

>>> w_X_train, w_X_test, \
...     w_y_train, w_y_test = train_test_split(
...         wine_X, wine_y, test_size=0.25,
...         random_state=0, stratify=wine_y
...     )
```

We will once again use logistic regression in a pipeline:

```
>>> from sklearn.linear_model import LogisticRegression
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import StandardScaler

>>> white_or_red = Pipeline([
...     ('scale', StandardScaler()),
...     ('lr', LogisticRegression(random_state=0))
... ]).fit(w_X_train, w_y_train)
```

Finally, we will save our predictions of which kind of wine each observation in the test set was:

```
>>> kind_preds = white_or_red.predict(w_X_test)
```

Now that we have predictions for both of our logistic regression models using their respective testing sets, we are ready to evaluate their performance.

Evaluating classification results

We evaluate the performance of classification models by looking at how well each class in the data was predicted by the model. The **positive class** is the class of interest to us; all other classes are considered **negative classes**. In our red wine classification, the positive class is high quality, while the negative class is low quality. Despite our problem only being a binary classification problem, the metrics that are discussed in this section extend to multiclass classification problems.

Confusion matrix

As we discussed in *Chapter 8, Rule-Based Anomaly Detection*, a classification problem can be evaluated by comparing the predicted labels to the actual labels using a **confusion matrix**:

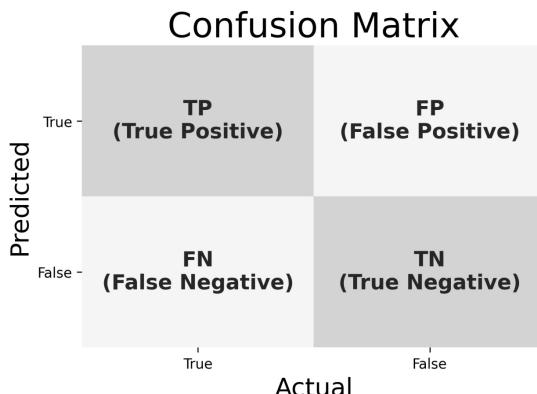


Figure 9.27 – Evaluating classification results with a confusion matrix

Each prediction can be one of four outcomes, based on how it matches up to the actual value:

- **True Positive (TP)**: Correctly predicted to be the positive class
- **False Positive (FP)**: Incorrectly predicted to be the positive class
- **True Negative (TN)**: Correctly predicted to not be the positive class
- **False Negative (FN)**: Incorrectly predicted to not be the positive class

Important note

False positives are also referred to as **type I errors**, while false negatives are **type II errors**. Given a certain classifier, an effort to reduce one will cause an increase in the other.

Scikit-learn provides the `confusion_matrix()` function, which we can pair with the `heatmap()` function from `seaborn` to visualize our confusion matrix. In the `ml_utils.classification` module, the `confusion_matrix_visual()` function handles this for us:

```
import matplotlib.pyplot as plt
import numpy as np
import seaborn as sns
from sklearn.metrics import confusion_matrix
```

```
def confusion_matrix_visual(y_true, y_pred, class_labels,
                            normalize=False, flip=False,
                            ax=None, title=None, **kwargs):
    """
    Create a confusion matrix heatmap

    Parameters:
    - y_true: The true values for y
    - preds: The predicted values for y
    - class_labels: What to label the classes.
    - normalize: Whether to plot the values as percentages.
    - flip: Whether to flip the confusion matrix. This is
        helpful to get TP in the top left corner and TN in
        the bottom right when dealing with binary
        classification with labels True and False.
    - ax: The matplotlib `Axes` object to plot on.
    - title: The title for the confusion matrix
    - kwargs: Additional keyword arguments to pass down.

    Returns: A matplotlib `Axes` object.
    """
    mat = confusion_matrix(y_true, y_pred)
    if normalize:
        fmt, mat = '.2%', mat / mat.sum()
    else:
        fmt = 'd'
    if flip:
        class_labels = class_labels[::-1]
        mat = np.flip(mat)

    axes = sns.heatmap(
        mat.T, square=True, annot=True, fmt=fmt,
        cbar=True, cmap=plt.cm.Blues, ax=ax, **kwargs
    )
    axes.set(xlabel='Actual', ylabel='Model Prediction')
    tick_marks = np.arange(len(class_labels)) + 0.5
    axes.set_xticks(tick_marks)
    axes.set_xticklabels(class_labels)
    axes.set_yticks(tick_marks)
    axes.set_yticklabels(class_labels, rotation=0)
    axes.set_title(title or 'Confusion Matrix')
    return axes
```

Let's call our confusion matrix visualization function to see how we did for each of our classification models. First, we will look at how well the model identified high-quality red wines:

```
>>> from ml_utils.classification import confusion_matrix_visual
>>> confusion_matrix_visual(
...     r_y_test, quality_preds, ['low', 'high']
... )
```

Using the confusion matrix, we can see that the model had trouble finding the high-quality red wines consistently (bottom row):

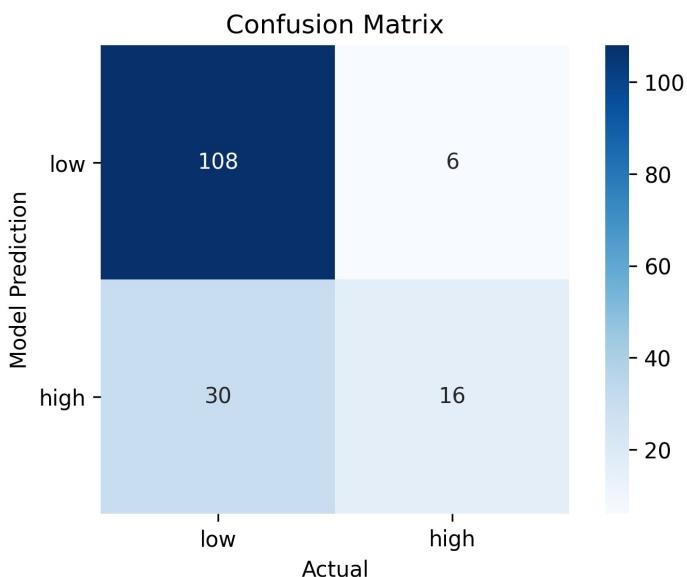


Figure 9.28 – Results for the red wine quality model

Now, let's look at how well the `white_or_red` model predicted the wine type:

```
>>> from ml_utils.classification import confusion_matrix_visual
>>> confusion_matrix_visual(
...     w_y_test, kind_preds, ['white', 'red']
... )
```

It looks like this model had a much easier time, with very few incorrect predictions:

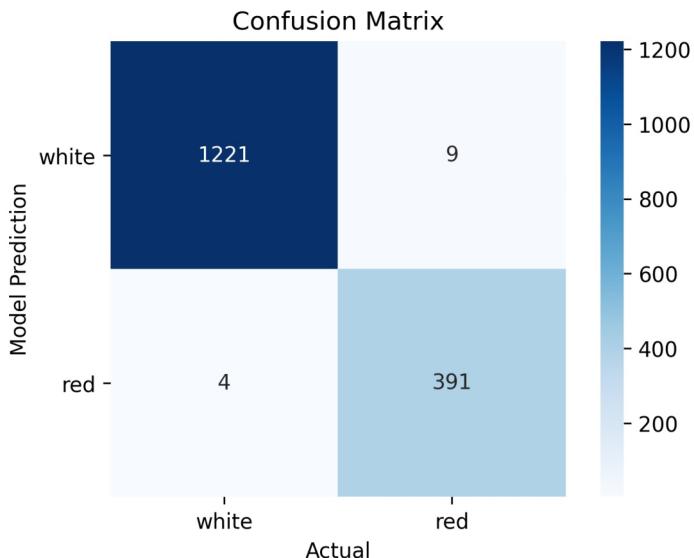


Figure 9.29 – Results for the white or red wine model

Now that we understand the composition of the confusion matrix, we can use it to calculate additional performance metrics.

Classification metrics

Using the values in the confusion matrix, we can calculate metrics to help evaluate the performance of a classifier. The best metrics will depend on the goal for which we are building the model and whether our classes are balanced. The formulas in this section are derived from the data we get from the confusion matrix, where TP is the number of true positives, TN is the number of true negatives, and so on.

Accuracy and error rate

When our classes are roughly equal in size, we can use **accuracy**, which will give us the percentage of correctly classified values:

$$\text{accuracy} = \frac{TP + TN}{TP + FP + TN + FN}$$

The `accuracy_score()` function in `sklearn.metrics` will calculate the accuracy as per the formula; however, the `score()` method of our model will also give us the accuracy (this isn't always the case, as we will see with grid search in *Chapter 10, Making Better Predictions – Optimizing Models*):

```
>>> red_quality_lr.score(r_X_test, r_y_test)
0.775
```

Since accuracy is the percentage we correctly classified (our **success rate**), it follows that our **error rate** (the percentage we got wrong) can be calculated as follows:

$$\text{error rate} = 1 - \text{accuracy} = \frac{FP + FN}{TP + FP + TN + FN}$$

Our accuracy score tells us that we got 77.5% of the red wines correctly classified according to their quality. Conversely, the `zero_one_loss()` function gives us the percentage of values that were misclassified, which is 22.5% for the red wine quality model:

```
>>> from sklearn.metrics import zero_one_loss
>>> zero_one_loss(r_y_test, quality_preds)
0.2249999999999998
```

Note that while both of these are easy to compute and understand, they require a threshold. By default, this is 50%, but we can use any probability we wish as a cutoff when predicting the class using the `predict_proba()` method in `scikit-learn`. In addition, accuracy and error rate can be misleading in cases of class imbalance.

Precision and recall

When we have a **class imbalance**, accuracy can become an unreliable metric for measuring our performance. For instance, if we had a 99/1 split between two classes, A and B, where the rare event, B, is our positive class, we could build a model that was 99% accurate by just saying everything belonged to class A. This problem stems from the fact that true negatives will be very large, and being in the numerator (in addition to the denominator), they will make the results look better than they are. Clearly, we shouldn't bother building a model if it doesn't do anything to identify class B; thus, we need different metrics that will discourage this behavior. For this, we use precision and recall instead of accuracy. **Precision** is the ratio of true positives to everything flagged positive:

$$\text{precision} = \frac{TP}{TP + FP}$$

Recall gives us the **true positive rate (TPR)**, which is the ratio of true positives to everything that was actually positive:

$$\text{recall} = \frac{TP}{TP + FN}$$

In the case of the 99/1 split between classes A and B, the model that classifies everything as A would have a recall of 0% for the positive class, B (precision would be undefined—0/0). Precision and recall provide a better way of evaluating model performance in the face of a class imbalance. They will correctly tell us that the model has little value for our use case.

Scikit-learn provides the `classification_report()` function, which will calculate precision and recall for us. In addition to calculating these metrics per class label, it also calculates the **macro** average (unweighted average between classes) and the **weighted** average (average between classes weighted by the number of observations in each class). The **support** column indicates the count of observations that belong to each class using the labeled data.

The classification report indicates that our model does well at finding the low-quality red wines, but not so great with the high-quality red wines:

```
>>> from sklearn.metrics import classification_report
>>> print(classification_report(r_y_test, quality_preds))
      precision    recall  f1-score   support
0           0.95    0.78    0.86     138
1           0.35    0.73    0.47      22

accuracy                           0.78     160
macro avg       0.65    0.75    0.66     160
weighted avg    0.86    0.78    0.80     160
```

Given that the quality scores are very subjective and not necessarily related to the chemical properties, it is no surprise that this simple model doesn't perform too well. On the other hand, chemical properties are different between red and white wines, so this information is more useful for the `white_or_red` model. As we can imagine, based on the confusion matrix for the `white_or_red` model, the metrics are good:

```
>>> from sklearn.metrics import classification_report
>>> print(classification_report(w_y_test, kind_preds))
      precision    recall  f1-score   support
0           0.99    1.00      0.99     1225
1           0.99    0.98      0.98      400

accuracy                           0.99      1625
macro avg       0.99    0.99      0.99      1625
weighted avg    0.99    0.99      0.99      1625
```

Just like accuracy, both precision and recall are easy to compute and understand, but require thresholds. In addition, precision and recall each only consider half of the confusion matrix:

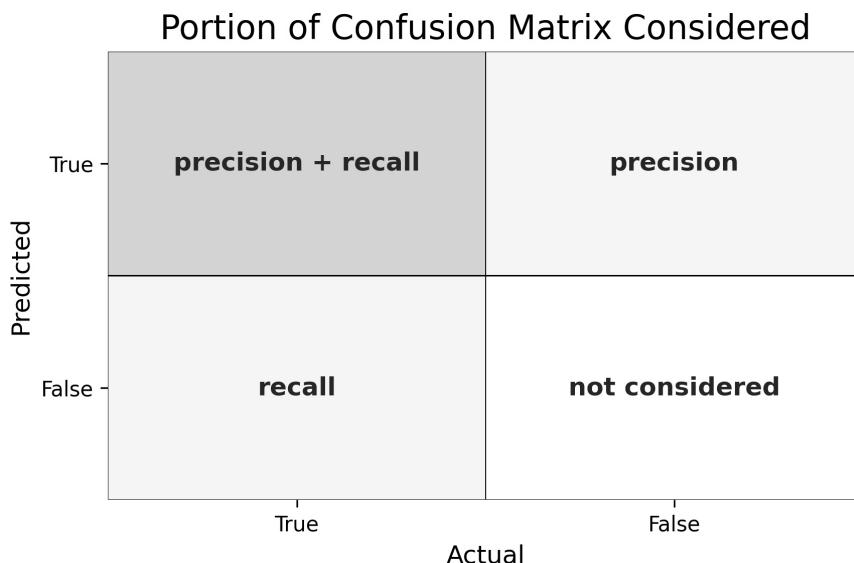


Figure 9.30 – Confusion matrix coverage for precision and recall

There is typically a trade-off between maximizing recall and maximizing precision, and we have to decide which is more important to us. This preference can be quantified using the F score.

F score

The classification report also includes the **F_1 score**, which helps us balance precision and recall using the **harmonic mean** of the two:

$$F_1 = 2 \times \frac{\text{precision} \times \text{recall}}{\text{precision} + \text{recall}} = \frac{2 \times TP}{2 \times TP + FP + FN}$$

Important note

The harmonic mean is the reciprocal of the arithmetic mean, and is used with rates to get a more accurate average (compared to the arithmetic mean of the rates). Both precision and recall are proportions in the range [0, 1], which we can treat as rates.

The **F_β score**, pronounced *F-beta*, is the more general formulation for the F score. By varying β , we can put more weight on precision (β between 0 and 1) or on recall (β greater than 1), where β is how many more times recall is valued over precision:

$$F_\beta = (1 + \beta^2) \times \frac{\text{precision} \times \text{recall}}{\beta^2 \times \text{precision} + \text{recall}}$$

Some commonly used values for β are as follows:

- **$F_{0.5}$ score:** Precision twice as important as recall
- **F_1 score:** Harmonic mean (equal importance)
- **F_2 score:** Recall twice as important as precision

The F score is also easy to compute and relies on thresholds. However, it doesn't consider true negatives and is hard to optimize due to the trade-offs between precision and recall. Note that when working with large class imbalances, we are typically more concerned with predicting the positive class correctly, meaning that we may be less interested in true negatives, so using a metric that ignores them isn't necessarily an issue.

Tip

Functions for precision, recall, F_1 score, and F_β score can be found in the `sklearn.metrics` module.

Sensitivity and specificity

Along the lines of the precision and recall trade-off, we have another pair of metrics that can be used to illustrate the delicate balance we strive to achieve with classification problems: sensitivity and specificity.

Sensitivity is the true positive rate, or recall, which we saw previously. **Specificity**, however, is the **true negative rate**, or the proportion of true negatives to everything that should have been classified as negative:

$$\text{specificity} = \frac{TN}{TN + FP}$$

Note that, together, specificity and sensitivity consider the full confusion matrix:

		Portion of Confusion Matrix Considered	
		True	False
Predicted	True	sensitivity	specificity
	False	sensitivity	specificity
	Actual		

Figure 9.31 – Confusion matrix coverage for sensitivity and specificity

We would like to maximize both sensitivity and specificity; however, we could easily maximize specificity by decreasing the number of times we classify something as the positive class, which would decrease sensitivity. Scikit-learn doesn't offer specificity as a metric—preferring precision and recall—however, we can easily make our own by writing a function or using the `make_scorer()` function from `scikit-learn`. We are discussing them here because they form the basis of the sensitivity-specificity plot, or ROC curve, which is the topic of the following section.

ROC curve

In addition to using metrics to evaluate classification problems, we can turn to visualizations. By plotting the true positive rate (*sensitivity*) versus the false positive rate ($1 - specificity$), we get the **Receiver Operating Characteristic (ROC) curve**. This curve allows us to visualize the trade-off between the true positive rate and the false positive rate. We can identify a false positive rate that we are willing to accept and use that to find the threshold to use as a cutoff when predicting the class with probabilities using the `predict_proba()` method in `scikit-learn`. Say that we find the threshold to be 60%—we would require `predict_proba()` to return a value greater than or equal to 0.6 to predict the positive class (`predict()` uses 0.5 as the cutoff).

The `roc_curve()` function from `scikit-learn` calculates the false and true positive rates at thresholds from 0 to 100% using the probabilities of an observation belonging to a given class, as determined by the model. We can then plot this, with the goal being to maximize the **area under the curve (AUC)**, which is in the range [0, 1]; values below 0.5 are worse than guessing and good scores are above 0.8. Note that when referring to the area under a ROC curve, the AUC may also be written as **AUROC**. The AUROC summarizes the model's performance across thresholds.

The following are examples of good ROC curves. The dashed line would be random guessing (no predictive value) and is used as a baseline; anything below that is considered worse than guessing. We want to be toward the top-left corner:

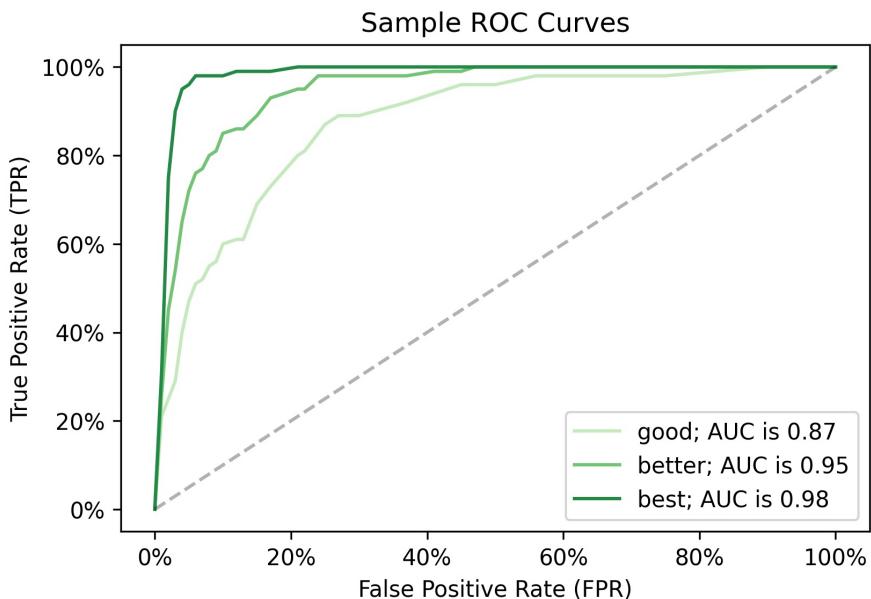


Figure 9.32 – Comparing ROC curves

The `ml_utils.classification` module contains a function for plotting our ROC curve. Let's take a look at it:

```
import matplotlib.pyplot as plt
from sklearn.metrics import auc, roc_curve

def plot_roc(y_test, preds, ax=None):
    """
    Plot ROC curve to evaluate classification.

    Parameters:
    - y_test: The true values for y
    - preds: The predicted values for y as probabilities
    - ax: The `Axes` object to plot on

    Returns:
    A matplotlib `Axes` object.
    """
    if not ax:
        fig, ax = plt.subplots(1, 1)

    fpr, tpr, thresholds = roc_curve(y_test, preds)

    ax.plot(
        [0, 1], [0, 1], color='navy', lw=2,
        linestyle='--', label='baseline'
    )
    ax.plot(fpr, tpr, color='red', lw=2, label='model')

    ax.legend(loc='lower right')
    ax.set_title('ROC curve')
    ax.set_xlabel('False Positive Rate (FPR)')
    ax.set_ylabel('True Positive Rate (TPR)')

    ax.annotate(
        f'AUC: {auc(fpr, tpr):.2}', xy=(0.5, 0),
        horizontalalignment='center'
    )

    return ax
```

As we can imagine, our `white_or_red` model will have a very good ROC curve. Let's see what that looks like by calling the `plot_roc()` function. Since we need to pass the probabilities of each entry belonging to the positive class, we need to use the `predict_proba()` method instead of `predict()`. This gives us the probabilities that each observation belongs to each class.

Here, for every row in `w_X_test`, we have a NumPy array of $[P(\text{white}), P(\text{red})]$. Therefore, we use slicing to select the probabilities that the wine is red for the ROC curve (`[:,1]`):

```
>>> from ml_utils.classification import plot_roc
>>> plot_roc(
...     w_y_test, white_or_red.predict_proba(w_X_test)[:,1]
... )
```

Just as we expected, the ROC curve for the `white_or_red` model is very good, with an AUC of nearly 1:

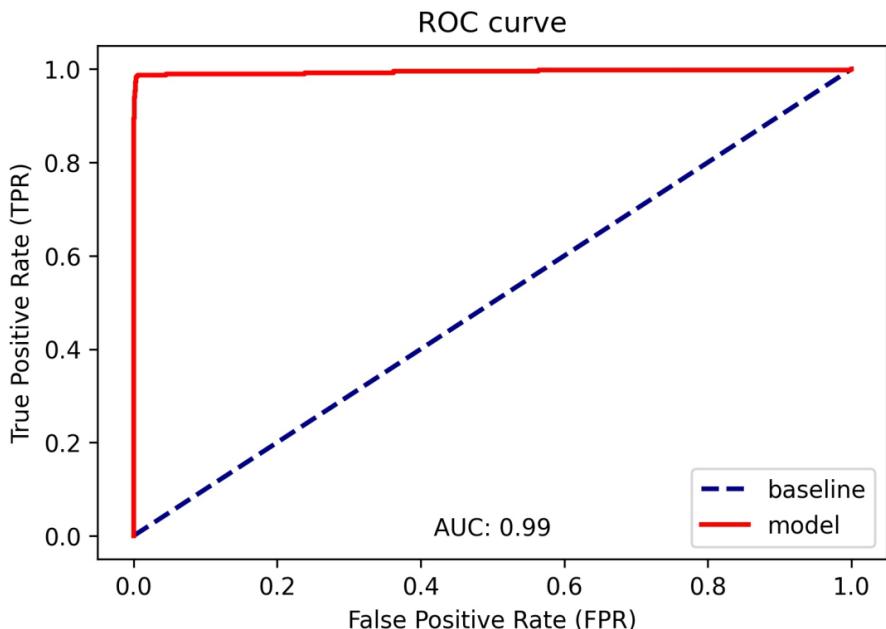


Figure 9.33 – ROC curve for the white or red wine model

Given the other metrics we have looked at, we don't expect the red wine quality prediction model to have a great ROC curve. Let's call our function to see what the ROC curve for the red wine quality model looks like:

```
>>> from ml_utils.classification import plot_roc
>>> plot_roc(
...     r_y_test, red_quality_lr.predict_proba(r_X_test)[:,1]
... )
```

This ROC curve isn't as good as the previous one, as expected:

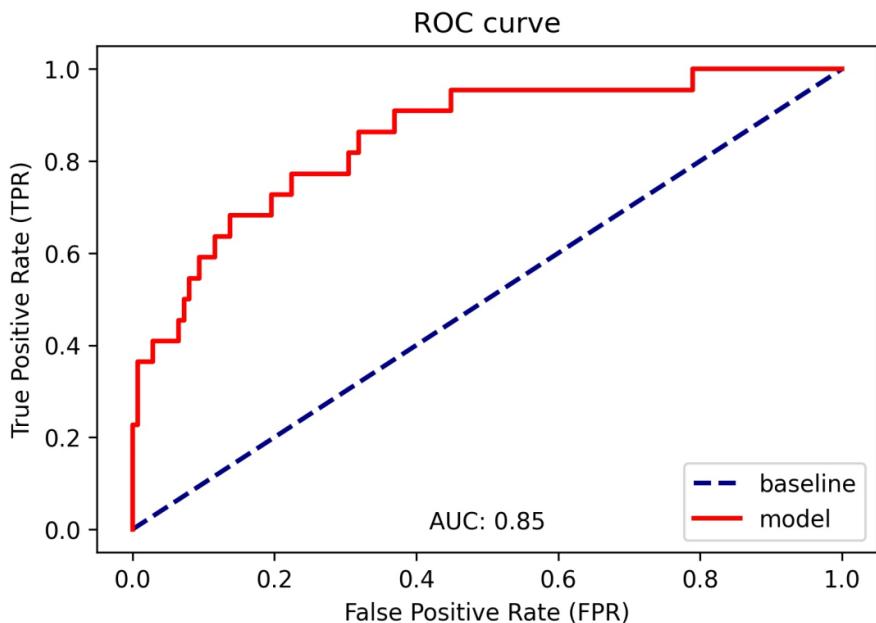


Figure 9.34 – ROC curve for the red wine quality model

Our AUROC is 0.85; however, note that the AUROC provides optimistic estimates under class imbalance (since it considers true negatives). For this reason, we should also look at the precision-recall curve.

Precision-recall curve

When faced with a class imbalance, we use **precision-recall curves** instead of ROC curves. This curve shows precision versus recall at various probability thresholds. The baseline is a horizontal line at the percentage of the data that belongs to the positive class. We want our curve above this line, with an **area under the precision-recall curve (AUPR)** greater than that percentage (the higher the better).

The `ml_utils.classification` module contains the `plot_pr_curve()` function for drawing precision-recall curves and providing the AUPR:

```
import matplotlib.pyplot as plt
from sklearn.metrics import (
    auc, average_precision_score, precision_recall_curve
)

def plot_pr_curve(y_test, preds, positive_class=1, ax=None):
    """
    Plot precision-recall curve to evaluate classification.

    Parameters:
        - y_test: The true values for y
        - preds: The predicted values for y as probabilities
        - positive_class: Label for positive class in the data
        - ax: The matplotlib `Axes` object to plot on

    Returns: A matplotlib `Axes` object.
    """
    precision, recall, thresholds = \
        precision_recall_curve(y_test, preds)

    if not ax:
        fig, ax = plt.subplots()

    ax.axhline(
        sum(y_test == positive_class) / len(y_test),
        color='navy', lw=2, linestyle='--', label='baseline'
    )
    ax.plot(
        recall, precision, color='red', lw=2, label='model'
    )
    ax.legend()
    ax.set_title(
        'Precision-recall curve\n'
        f'"""\nAP: {average_precision_score(\n            y_test, preds, pos_label=positive_class\n        ):.2}\n"""\nAUC: {auc(recall, precision):.2}\n'
    )
    ax.set(xlabel='Recall', ylabel='Precision')
```

```

    ax.set_xlim(-0.05, 1.05)
    ax.set_ylim(-0.05, 1.05)

    return ax

```

Since the implementation of the AUC calculation in scikit-learn uses interpolation, it may give an optimistic result, so our function also calculates **average precision (AP)**, which summarizes the precision-recall curve as the weighted mean of the precision scores (P_n) achieved at various thresholds. The weights are derived from the change in recall (R_n) between one threshold and the next. Values are between 0 and 1, with higher values being better:

$$AP = \sum_n (R_n - R_{n-1}) \times P_n$$

Let's take a look at the precision-recall curve for the red wine quality model:

```

>>> from ml_utils.classification import plot_pr_curve
>>> plot_pr_curve(
...     r_y_test, red_quality_lr.predict_proba(r_X_test)[:,1]
... )

```

This still shows that our model is better than the baseline of random guessing; however, the performance reading we get here seems more in line with the lackluster performance we saw in the classification report. We can also see that the model loses lots of precision when going from a recall of 0.2 to 0.4. Here, the trade-off between precision and recall is evident, and we will likely choose to optimize one:

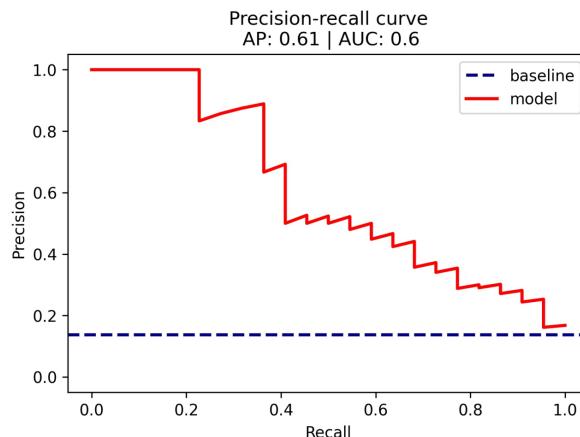


Figure 9.35 – Precision-recall curve for the red wine quality model

Since we have a class imbalance between the high-quality and low-quality red wines (less than 14% are high quality), we must make a choice as to whether we optimize precision or recall. Our choice would depend on who we work for in the wine industry. If we are renowned for producing high-quality wine, and we are choosing which wines to provide to critics for reviews, we want to make sure we pick the best ones and would rather miss out on good ones (false negatives) than tarnish our name with low-quality ones that the model classifies as high quality (false positives). However, if we are trying to make the best profit from selling the wines, we wouldn't want to sell such a high-quality wine for the same price as a low-quality wine (false negative), so we would rather overprice some low-quality wines (false positives).

Note that we could easily have classified everything as low quality to never disappoint or as high quality to maximize our profit selling them; however, this isn't too practical. It's clear that we need to strike an acceptable balance between false positives and false negatives. To do so, we need to quantify this trade-off between the two extremes in terms of what matters to us more. Then, we can use the precision-recall curve to find a threshold that meets our precision and recall targets. In *Chapter 11, Machine Learning Anomaly Detection*, we will work through an example of this.

Let's now take a look at the precision-recall curve for our white or red wine classifier:

```
>>> from ml_utils.classification import plot_pr_curve
>>> plot_pr_curve(
...     w_y_test, white_or_red.predict_proba(w_X_test)[:,1]
... )
```

Note that this curve is in the upper right-hand corner. With this model, we can achieve high precision and high recall:

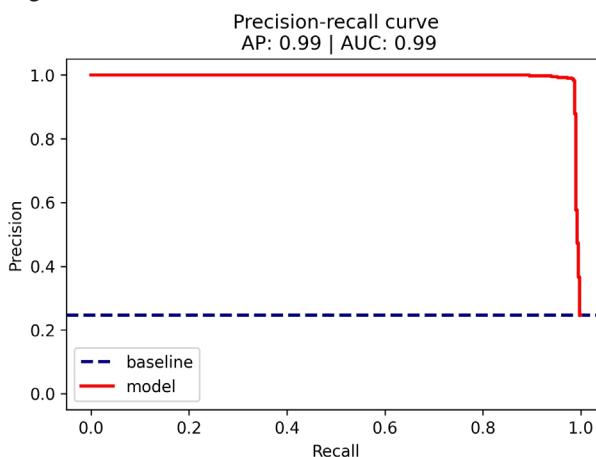


Figure 9.36 – Precision-recall curve for the white or red wine model

As we saw with the red wine quality model, AUPR works very well with class imbalance. However, it can't be compared across datasets, is expensive to compute, and is hard to optimize. Note that this was just a subset of the metrics we can use to evaluate classification problems. All the classification metrics offered by `scikit-learn` can be found at <https://scikit-learn.org/stable/modules/classes.html#classification-metrics>.

Summary

This chapter served as an introduction to machine learning in Python. We discussed the terminology that's commonly used to describe learning types and tasks. Then, we practiced EDA using the skills we learned throughout this book to get a feel for the wine and planet datasets. This gave us some ideas about what kinds of models we would want to build. A thorough exploration of the data is essential before attempting to build a model.

Next, we learned how to prepare our data for use in machine learning models and the importance of splitting the data into training and testing sets before modeling. In order to prepare our data efficiently, we used pipelines in `scikit-learn` to package up everything from our preprocessing through our model.

We used unsupervised k-means to cluster the planets using their semi-major axis and period; we also discussed how to use the elbow point method to find a good value for k . Then, we moved on to supervised learning and made a linear regression model to predict the period of a planet using its semi-major axis, eccentricity of orbit, and mass. We learned how to interpret the model coefficients and how to evaluate the model's predictions. Finally, we turned to classification to identify high-quality red wines (which had a class imbalance) and distinguish between red and white wine by their chemical properties. Using precision, recall, F_1 score, confusion matrices, ROC curves, and precision-recall curves, we discussed how to evaluate classification models.

It's important to remember that machine learning models make assumptions about the underlying data, and while this wasn't a chapter on the mathematics of machine learning, we should make sure that we understand that there are consequences for violating these assumptions. In practice, when looking to build models, it's crucial that we have a solid understanding of statistics and domain-level expertise. We saw that there is a multitude of metrics for evaluating our models. Each metric has its strengths and weaknesses, and, depending on the problem, some are better than others; we must take care to choose the appropriate metrics for the task at hand.

In the next chapter, we will learn how to tune our models to improve their performance, so make sure to complete the exercises to practice this chapter's material before moving on.

Exercises

Practice building and evaluating machine learning models in `scikit-learn` with the following exercises:

1. Build a clustering model to distinguish between red and white wine by their chemical properties:
 - a) Combine the red and white wine datasets (`data/winequality-red.csv` and `data/winequality-white.csv`, respectively) and add a column for the kind of wine (red or white).
 - b) Perform some initial EDA.
 - c) Build and fit a pipeline that scales the data and then uses k-means clustering to make two clusters. Be sure not to use the `quality` column.
 - d) Use the Fowlkes-Mallows Index (the `fowlkes_mallows_score()` function is in `sklearn.metrics`) to evaluate how well k-means is able to make the distinction between red and white wine.
 - e) Find the center of each cluster.
2. Predict star temperature:
 - a) Using the `data/stars.csv` file, perform some initial EDA and then build a linear regression model of all the numeric columns to predict the temperature of the star.
 - b) Train the model on 75% of the initial data.
 - c) Calculate the R^2 and RMSE of the model.
 - d) Find the coefficients for each regressor and the intercept of the linear regression equation.
 - e) Visualize the residuals using the `plot_residuals()` function from the `ml_utils.regression` module.

3. Classify planets that have shorter years than Earth:
 - a) Using the `data/planets.csv` file, build a logistic regression model with the `eccentricity`, `semimajoraxis`, and `mass` columns as regressors. You will need to make a new column to use for the y (year shorter than Earth).
 - b) Find the accuracy score.
 - c) Use the `classification_report()` function from `scikit-learn` to see the precision, recall, and F_1 score for each class.
 - d) With the `plot_roc()` function from the `ml_utils.classification` module, plot the ROC curve.
 - e) Create a confusion matrix using the `confusion_matrix_visual()` function from the `ml_utils.classification` module.
4. Multiclass classification of white wine quality:
 - a) Using the `data/winequality-white.csv` file, perform some initial EDA on the white wine data. Be sure to look at how many wines had a given quality score.
 - b) Build a pipeline to standardize the data and fit a multiclass logistic regression model. Pass `multi_class='multinomial'` and `max_iter=1000` to the `LogisticRegression` constructor.
 - c) Look at the classification report for your model.
 - d) Create a confusion matrix using the `confusion_matrix_visual()` function from the `ml_utils.classification` module. This will work as is for multiclass classification problems.
 - e) Extend the `plot_roc()` function to work for multiple class labels. To do so, you will need to create a ROC curve for each class label (which are quality scores here), where a true positive is correctly predicting that quality score and a false positive is predicting any other quality score. Note that `ml_utils` has a function for this, but try to build your own implementation.
 - f) Extend the `plot_pr_curve()` function to work for multiple class labels by following a similar method to part e). However, give each class its own subplot. Note that `ml_utils` has a function for this, but try to build your own implementation.

5. We have seen how easy the `scikit-learn` API is to navigate, making it a cinch to change which algorithm we are using for our model. Rebuild the red wine quality model that we created in this chapter using an SVM instead of logistic regression. We haven't discussed this model, but you should still be able to use it in `scikit-learn`. Check out the link in the *Further reading* section to learn more about the algorithm. Some guidance for this exercise is as follows:
 - a) You will need to use the `SVC` (support vector classifier) class from `scikit-learn`, which can be found at <https://scikit-learn.org/stable/modules/generated/sklearn.svm.SVC.html>.
 - b) Use `C=5` as an argument to the `SVC` constructor.
 - c) Pass `probability=True` to the `SVC` constructor to be able to use the `predict_proba()` method.
 - d) Build a pipeline first using the `StandardScaler` class and then the `SVC` class.
 - e) Be sure to look at the classification report, precision-recall curve, and confusion matrix for the model.

Further reading

Check out the following resources for more information on the topics that were covered in this chapter:

- *A Beginner's Guide to Deep Reinforcement Learning*: <https://pathmind.com/wiki/deep-reinforcement-learning>
- *An Introduction to Gradient Descent and Linear Regression*: <https://spin.atomicobject.com/2014/06/24/gradient-descent-linear-regression/>
- *Assumptions of Multiple Linear Regression*: <https://www.statisticssolutions.com/assumptions-of-multiple-linear-regression/>
- *Clustering*: <https://scikit-learn.org/stable/modules/clustering.html>
- *Generalized Linear Models*: https://scikit-learn.org/stable/modules/linear_model.html
- *Guide to Interpretable Machine Learning – Techniques to dispel the black box myth of deep learning*: <https://towardsdatascience.com/guide-to-interpretable-machine-learning-d40e8a64b6cf>

- *In Depth: k-Means*: <https://jakevdp.github.io/PythonDataScienceHandbook/05.11-k-means.html>
- *Interpretable Machine Learning – A Guide for Making Black Box Models Explainable*: <https://christophm.github.io/interpretable-ml-book/>
- *Interpretable Machine Learning – Extracting human understandable insights from any Machine Learning model*: <https://towardsdatascience.com/interpretable-machine-learning-1dec0f2f3e6b>
- *MAE and RMSE – Which Metric is Better?*: <https://medium.com/human-in-a-machine-world/mae-and-rmse-which-metric-is-better-e60ac3bde13d>
- *Model evaluation: quantifying the quality of predictions*: https://scikit-learn.org/stable/modules/model_evaluation.html
- *Preprocessing data*: <https://scikit-learn.org/stable/modules/preprocessing.html>
- *Scikit-learn Glossary of Common Terms and API Elements*: <https://scikit-learn.org/stable/glossary.html#glossary>
- *Scikit-learn User Guide*: https://scikit-learn.org/stable/user_guide.html
- *Seeing Theory Chapter 6: Regression Analysis*: <https://seeing-theory.brown.edu/index.html#secondPage/chapter6>
- *Simple Beginner's Guide to Reinforcement Learning & its implementation*: <https://www.analyticsvidhya.com/blog/2017/01/introduction-to-reinforcement-learning-implementation/>
- *Support Vector Machine – Introduction to Machine Learning Algorithms*: <https://towardsdatascience.com/support-vector-machine-introduction-to-machine-learning-algorithms-934a444fca47>
- *The 5 Clustering Algorithms Data Scientists Need to Know*: <https://towardsdatascience.com/the-5-clustering-algorithms-data-scientists-need-to-know-a36d136ef68>

10

Making Better Predictions – Optimizing Models

In the previous chapter, we learned how to build and evaluate our machine learning models. However, we didn't touch upon what we can do if we want to improve their performance. Of course, we could try out a different model and see if it performs better—unless there are requirements that we use a specific method for legal reasons or in order to be able to explain how it works. We want to make sure we use the best version of the model that we can, and for that, we need to discuss how to tune our models.

This chapter will introduce techniques for the optimization of machine learning model performance using `scikit-learn`, as a continuation of the content in *Chapter 9, Getting Started with Machine Learning in Python*. Nonetheless, it should be noted that there is no panacea. It is entirely possible to try everything we can think of and still have a model with little predictive value; such is the nature of modeling.

Don't be discouraged though—if the model doesn't work, consider whether the data collected suffices to answer the question, and whether the algorithm chosen is appropriate for the task at hand. Often, subject matter expertise will prove crucial when building machine learning models, because it helps us determine which data points will be relevant, as well as to take advantage of known interactions between the variables collected.

In particular, the following topics will be covered:

- Hyperparameter tuning with grid search
- Feature engineering
- Building ensemble models combining many estimators
- Inspecting classification prediction confidence
- Addressing class imbalance
- Penalizing high regression coefficients with regularization

Chapter materials

In this chapter, we will be working with three datasets. The first two come from data on wine quality donated to the UCI Machine Learning Data Repository (<http://archive.ics.uci.edu/ml/index.php>) by P. Cortez, A. Cerdeira, F. Almeida, T. Matos, and J. Reis, and contain information on the chemical properties of various wine samples along with a rating of the quality from a blind tasting session by a panel of wine experts. These files can be found in the `data/` folder inside this chapter's folder in the GitHub repository (https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_10) as `winequality-red.csv` and `winequality-white.csv` for red and white wine, respectively.

Our third dataset was collected using the Open Exoplanet Catalogue database, at https://github.com/OpenExoplanetCatalogue/open_exoplanet_catalogue/, which provides data in XML format. The parsed planet data can be found in the `data/planets.csv` file. For the exercises, we will also be working with the star temperature data from *Chapter 9, Getting Started with Machine Learning in Python*, which can be found in the `data/stars.csv` file.

For reference, the following data sources were used:

- *Open Exoplanet Catalogue database*, available at https://github.com/OpenExoplanetCatalogue/open_exoplanet_catalogue/#data-structure.
- *P. Cortez, A. Cerdeira, F. Almeida, T. Matos and J. Reis. Modeling wine preferences by data mining from physicochemical properties. In Decision Support Systems, Elsevier, 47(4):547-553, 2009.* Available online at <http://archive.ics.uci.edu/ml/datasets/Wine+Quality>.
- *Dua, D. and Karra Taniskidou, E. (2017). UCI Machine Learning Repository* (<http://archive.ics.uci.edu/ml/index.php>). Irvine, CA: University of California, School of Information and Computer Science.

We will be using the `red_wine.ipynb` notebook to predict red wine quality, `wine.ipynb` to distinguish between red and white wine based on their chemical properties, and the `planets_ml.ipynb` notebook to build a regression model to predict the year length of planets in Earth days.

Before we get started, let's handle our imports and read in our data:

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

>>> planets = pd.read_csv('data/planets.csv')
>>> red_wine = pd.read_csv('data/winequality-red.csv')
>>> white_wine = \
...     pd.read_csv('data/winequality-white.csv', sep=';')
>>> wine = pd.concat([
...     white_wine.assign(kind='white'),
...     red_wine.assign(kind='red')
... ])
>>> red_wine['high_quality'] = pd.cut(
...     red_wine.quality, bins=[0, 6, 10], labels=[0, 1]
... )
```

Let's also create our training and testing sets for the red wine quality, wine type by chemical properties, and planets models:

```
>>> from sklearn.model_selection import train_test_split

>>> red_y = red_wine.pop('high_quality')
>>> red_X = red_wine.drop(columns='quality')
>>> r_X_train, r_X_test, \
... r_y_train, r_y_test = train_test_split(
...     red_X, red_y, test_size=0.1, random_state=0,
...     stratify=red_y
... )

>>> wine_y = np.where(wine.kind == 'red', 1, 0)
>>> wine_X = wine.drop(columns=['quality', 'kind'])
>>> w_X_train, w_X_test, \
... w_y_train, w_y_test = train_test_split(
...     wine_X, wine_y, test_size=0.25,
...     random_state=0, stratify=wine_y
... )

>>> data = planets[
...     ['semimajoraxis', 'period', 'mass', 'eccentricity']
... ].dropna()
>>> planets_X = data[
...     ['semimajoraxis', 'mass', 'eccentricity']
... ]
>>> planets_y = data.period
>>> pl_X_train, pl_X_test, \
... pl_y_train, pl_y_test = train_test_split(
...     planets_X, planets_y, test_size=0.25, random_state=0
... )
```

Important note

Remember that we will be working in dedicated notebooks for each of the datasets, so while the setup code is all in the same code block to make it easier to follow in the book, make sure to work in the notebook corresponding to the data in question.

Hyperparameter tuning with grid search

No doubt you have noticed that we can provide various parameters to the model classes when we instantiate them. These model parameters are not derived from the data itself and are referred to as **hyperparameters**. Some examples of these are regularization terms, which we will discuss later in this chapter, and weights. Through the process of **model tuning**, we seek to optimize our model's performance by tuning these hyperparameters.

How can we know we are picking the best values to optimize our model's performance? One way is to use a technique called **grid search** to tune these hyperparameters. Grid search allows us to define a search space and test all combinations of hyperparameters in that space, keeping the ones that result in the best model. The scoring criterion we define will determine the best model.

Remember the elbow point method we discussed in *Chapter 9, Getting Started with Machine Learning in Python*, for finding a good value for k in k-means clustering? We can employ a similar visual method to find the best value for our hyperparameters. This will involve splitting our training data into **training** and **validation sets**. We need to save the test set for the final evaluation of the model, so we use the validation set to test each of our models when searching for the best values of the hyperparameters. To reiterate, the validation set and the test set are not the same—they must be disjoint datasets. This split can be done with `train_test_split()`. Here, we will use the red wine quality dataset:

```
>>> from sklearn.model_selection import train_test_split

>>> r_X_train_new, r_X_validate,\ 
... r_y_train_new, r_y_validate = train_test_split(
...     r_X_train, r_y_train, test_size=0.3,
...     random_state=0, stratify=r_y_train
... )
```

Then, we can build the model multiple times for all the values of the hyperparameters we want to test, and score them based on the metric that matters most to us. Let's try to find a good value for C, the inverse of the regularization strength, which determines the weight of the penalty term for logistic regression and is discussed more in-depth in the *Regularization* section toward the end of this chapter; we tune this hyperparameter to reduce overfitting:

```
>>> from sklearn.linear_model import LogisticRegression
>>> from sklearn.metrics import f1_score
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import MinMaxScaler
```

```
# we will try 10 values from 10^-1 to 10^1 for C
>>> inv_regularization_strengths = \
...     np.logspace(-1, 1, num=10)
>>> scores = []

>>> for inv_reg_strength in inv_regularization_strengths:
...     pipeline = Pipeline([
...         ('scale', MinMaxScaler()),
...         ('lr', LogisticRegression(
...             class_weight='balanced', random_state=0,
...             C=inv_reg_strength
...         ))
...     ]).fit(r_X_train_new, r_y_train_new)
...     scores.append(f1_score(
...         pipeline.predict(r_X_validate), r_y_validate
...     ))
```

Tip

Here, we are using `np.logspace()` to get our range of values to try for C. To use this function, we supply starting and stopping exponents to use with a base number (10, by default). So `np.logspace(-1, 1, num=10)` gives us 10 evenly spaced numbers between 10^{-1} and 10^1 .

This is then plotted as follows:

```
>>> plt.plot(inv_regularization_strengths, scores, 'o-')
>>> plt.xscale('log')
>>> plt.xlabel('inverse of regularization strength (C)')
>>> plt.ylabel(r'$F_1$ score')
>>> plt.title(
...     r'$F_1$ score vs. '
...     'Inverse of Regularization Strength'
... )
```

Using the resulting plot, we can pick the value that maximizes our performance:

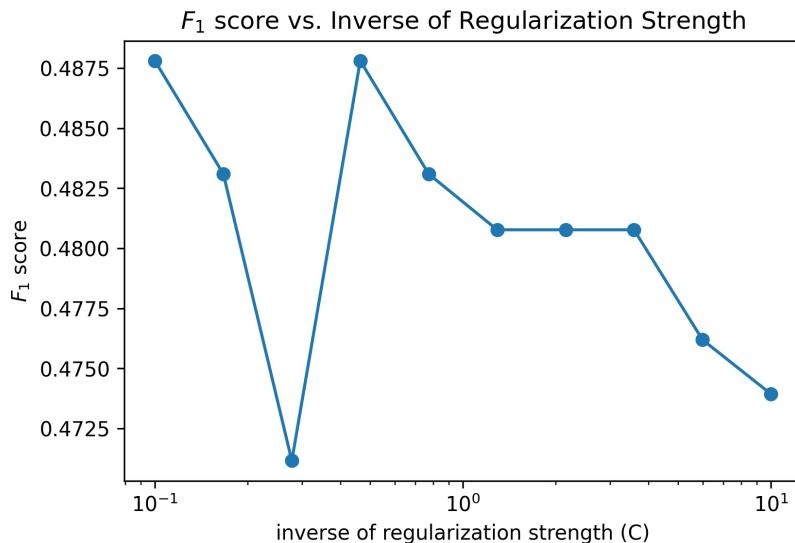


Figure 10.1 – Searching for the best hyperparameters

Scikit-learn provides the `GridSearchCV` class in the `model_selection` module for carrying out this exhaustive search much more easily. Classes that end with **CV** utilize **cross-validation**, meaning they divide up the training data into subsets, some of which will be the validation set for scoring the model (without needing the testing data until after the model is fit).

One common method of cross-validation is **k-fold cross-validation**, which splits the training data into k subsets and will train the model k times, each time leaving one subset out to use as the validation set. The score for the model will be the average across the k validation sets. Our initial attempt was 1-fold cross-validation. When $k=3$, this process looks like the following diagram:

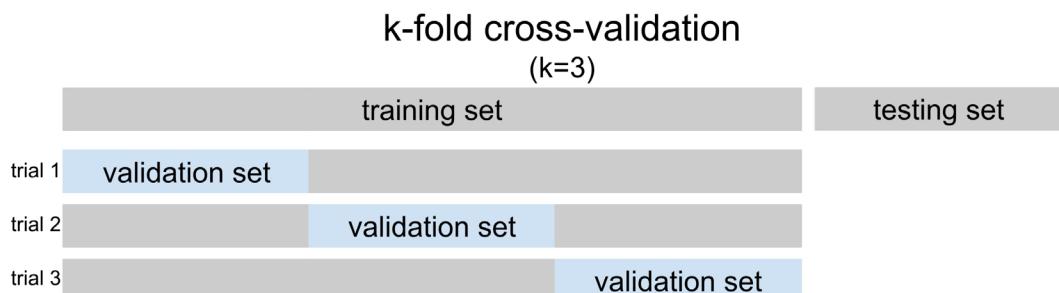


Figure 10.2 – Understanding k-fold cross-validation

Tip

When working with classification problems, `scikit-learn` will implement stratified k-fold cross-validation. This ensures that the percentage of samples belonging to each class will be preserved across folds. Without stratification, it's possible some validation sets will see a disproportionately low (or high) amount of a given class, which can distort the results.

`GridSearchCV` uses cross-validation to find the best hyperparameters in the search space, without the need to use the testing data. Remember, test data should not influence the training process in any way—neither when training the model nor when tuning hyperparameters—otherwise, the model will have issues generalizing. This happens because we would be picking the hyperparameters that give the best performance on the test set, thus leaving no way to test on unseen data, and overestimating our performance.

In order to use `GridSearchCV`, we need to provide a model (or pipeline) and a search space, which will be a dictionary mapping the hyperparameter to tune (by name) to a list of values to try. Optionally, we can provide a scoring metric to use, as well as the number of folds to use with cross-validation. We can tune any step in the pipeline by prefixing the hyperparameter name with the name of that step, followed by two underscores. For instance, if we have a logistic regression step called `lr` and want to tune `C`, we use `lr__C` as the key in the search space dictionary. Note that if our model has any preprocessing steps, it's imperative that we use a pipeline.

Let's use `GridSearchCV` for the red wine quality logistic regression, searching for whether or not to fit our model with an intercept and the best value for the inverse of the regularization strength (`C`). We will use the F_1 score macro average as the scoring metric. Note that, due to the consistency of the API, `GridSearchCV` can be used to score, fit, and predict with the same methods as the underlying models. By default, the grid search will run in series, but `GridSearchCV` is capable of performing multiple searches in parallel, greatly speeding up this process:

```
>>> from sklearn.linear_model import LogisticRegression
>>> from sklearn.model_selection import GridSearchCV
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import MinMaxScaler

>>> pipeline = Pipeline([
...     ('scale', MinMaxScaler()),
...     ('lr', LogisticRegression(class_weight='balanced',
...                               random_state=0))
... ])
```

```
>>> search_space = {
...     'lr_C': np.logspace(-1, 1, num=10),
...     'lr_fit_intercept': [True, False]
... }

>>> lr_grid = GridSearchCV(
...     pipeline, search_space, scoring='f1_macro', cv=5
... ).fit(r_X_train, r_y_train)
```

Once the grid search completes, we can isolate the best hyperparameters from the search space with the `best_params_` attribute. Notice that this result is different from our 1-fold cross-validation attempt because each of the folds has been averaged together to find the best hyperparameters overall, not just for a single fold:

```
# best values of `C` and `fit_intercept` in search space
>>> lr_grid.best_params_
{'lr_C': 3.593813663804626, 'lr_fit_intercept': True}
```

Tip

We can also retrieve the best version of the pipeline from the grid search with the `best_estimator_` attribute. If we want to see the score the best estimator (model) had, we can grab it from the `best_score_` attribute; note that this will be the score we specified with the `scoring` argument.

Our F_1 score macro average is now higher than what we achieved in *Chapter 9, Getting Started with Machine Learning in Python*:

```
>>> from sklearn.metrics import classification_report
>>> print(classification_report(
...     r_y_test, lr_grid.predict(r_X_test)
... ))
          precision    recall  f1-score   support
          0       0.94      0.80      0.87      138
          1       0.36      0.68      0.47       22

      accuracy                           0.79      160
  macro avg       0.65      0.74      0.67      160
weighted avg       0.86      0.79      0.81      160
```

Note that the `cv` argument doesn't have to be an integer—we can provide one of the splitter classes mentioned at <https://scikit-learn.org/stable/modules/classes.html#splitter-classes> if we want to use a method other than the default of k-fold for regression or stratified k-fold for classification. For example, when working with time series, we can use `TimeSeriesSplit` as the cross-validation object to work with successive samples and avoid shuffling. Scikit-learn shows how the cross-validation classes compare at https://scikit-learn.org/stable/auto_examples/model_selection/plot_cv_indices.html.

Let's test out `RepeatedStratifiedKFold` on the red wine quality model instead of the default `StratifiedKFold`, which will repeat the stratified k-fold cross-validation 10 times by default. All we have to do is change what we passed in as `cv` in the first `GridSearchCV` example to be a `RepeatedStratifiedKFold` object. Note that—despite using the same pipeline, search space, and scoring metric—we have different values for `best_params_` because our cross-validation process has changed:

```
>>> from sklearn.model_selection import RepeatedStratifiedKFold

>>> lr_grid = GridSearchCV(
...     pipeline, search_space, scoring='f1_macro',
...     cv=RepeatedStratifiedKFold(random_state=0)
... ).fit(r_X_train, r_y_train)

>>> print('Best parameters (CV score=% .2f):\n      %s' % (
...     lr_grid.best_score_, lr_grid.best_params_
... )) # f1 macro score
Best parameters (CV score=0.69):
{'lr__C': 5.994842503189409, 'lr__fit_intercept': True}
```

In addition to cross-validation, `GridSearchCV` allows us to specify the metric we want to optimize with the `scoring` parameter. This can be a string for the name of the score (as in the previous code blocks), provided that it is in the list at https://scikit-learn.org/stable/modules/model_evaluation.html#common-cases-predefined-values; otherwise, we can either pass the function itself or make our own using the `make_scorer()` function from `sklearn.metrics`. We can even provide a dictionary of scorers (in the form of `{name: function}`) for grid search, provided that we specify which one we want to use for optimization by passing its name to the `refit` parameter. Therefore, we can use grid search to find the hyperparameters that help us maximize our performance on the metrics we discussed in the previous chapter.

Important note

The time it takes to train our model should also be something we evaluate and look to optimize. If it takes us double the training time to get one more correct classification, it's probably not worth it. If we have a `GridSearchCV` object called `grid`, we can see the average fit time by running `grid.cv_results_['mean_fit_time']`.

We can use `GridSearchCV` to search for the best parameters for any step in our pipeline. For example, let's use grid search with a pipeline of preprocessing and linear regression on the planets data (similar to when we modeled planet year length in *Chapter 9, Getting Started with Machine Learning in Python*) while minimizing **mean absolute error (MAE)** instead of the default R^2 :

```
>>> from sklearn.linear_model import LinearRegression
>>> from sklearn.metrics import \
...     make_scorer, mean_squared_error
>>> from sklearn.model_selection import GridSearchCV
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import StandardScaler

>>> model_pipeline = Pipeline([
...     ('scale', StandardScaler()),
...     ('lr', LinearRegression())
... ])
>>> search_space = {
...     'scale_with_mean': [True, False],
...     'scale_with_std': [True, False],
...     'lr_fit_intercept': [True, False],
...     'lr_normalize': [True, False]
... }
>>> grid = GridSearchCV(
...     model_pipeline, search_space, cv=5,
...     scoring={
...         'r_squared': 'r2',
...         'mse': 'neg_mean_squared_error',
...         'mae': 'neg_mean_absolute_error',
...         'rmse': make_scorer(
...             lambda x, y: \
...                 -np.sqrt(mean_squared_error(x, y))
...         ),
...         }, refit='mae'
... ).fit(pl_X_train, pl_y_train)
```

Note that we are using the negative of all the metrics except R². This is because GridSearchCV will attempt to maximize the score, and we want to minimize our errors. Let's check the best parameters for the scaling and linear regression in this grid:

```
>>> print('Best parameters (CV score=% .2f):\n%s' % (
...     grid.best_score_, grid.best_params_
... )) # MAE score * -1
Best parameters (CV score=-1215.99):
{'lr__fit_intercept': False, 'lr__normalize': True,
 'scale__with_mean': False, 'scale__with_std': True}
```

The tuned model's MAE is more than 120 Earth days smaller than the MAE we got in *Chapter 9, Getting Started with Machine Learning in Python*:

```
>>> from sklearn.metrics import mean_absolute_error
>>> mean_absolute_error(pl_y_test, grid.predict(pl_X_test))
1248.3690943844194
```

It's important to note that while a model may be fast to train, we shouldn't create a large, granular search space; in practice, it's better to start with a few different spread-out values, and then examine the results to see which areas warrant a more in-depth search. For instance, say we are looking to tune the C hyperparameter. On our first pass, we may look at the result of np.logspace(-1, 1). If we see that the best value for C is at either end of the spectrum, we can then look at values above/below the value. If the best value is in the range, we may look at a few values around it. This process can be performed iteratively until we don't see additional improvement. Alternatively, we could use RandomizedSearchCV, which will try 10 random combinations in the search space (by default) and find the best estimator (model). We can change this number with the n_iter argument.

Important note

Since the process of tuning hyperparameters requires us to train our model multiple times, we must consider the time complexity of our models. Models that take a long time to train will be very costly to use with cross-validation. This will likely cause us to shrink our search space.

Feature engineering

When trying to improve performance, we may also consider ways to provide the best **features** (model inputs) to our model through the process of **feature engineering**. The *Preprocessing data* section in *Chapter 9, Getting Started with Machine Learning in Python*, introduced us to **feature transformation** when we scaled, encoded, and imputed our data. Unfortunately, feature transformation may mute some elements of our data that we want to use in our model, such as the unscaled value of the mean of a specific feature. For this situation, we can create a new feature with this value; this and other new features are added during **feature construction** (sometimes called **feature creation**).

Feature selection is the process of determining which features to train the model on. This can be done manually or through another process, such as machine learning. When looking to choose features for our model, we want features that have an impact on our dependent variable without unnecessarily increasing the complexity of our problem. Models built with many features increase in complexity, but also, unfortunately, have a higher tendency to fit noise, because our data is sparse in such a high-dimensional space. This is referred to as the **curse of dimensionality**. When a model has learned the noise in the training data, it will have a hard time generalizing to unseen data; this is called **overfitting**. By restricting the number of features the model uses, feature selection can help address overfitting.

Feature extraction is another way we can address the curse of dimensionality. During feature extraction, we reduce the dimensionality of our data by constructing combinations of features through a transformation. These new features can be used in place of the originals, thereby reducing the dimensionality of the problem. This process, called **dimensionality reduction**, also includes techniques where we find a certain number of components (less than the original) that explain most of the variance in the data. Feature extraction is often used in image recognition problems, since the dimensionality of the task is the total number of pixels in the image. For instance, square ads on websites are 350x350 pixels (this is one of the most common sizes), so an image recognition task using images that size has 122,500 dimensions.

Tip

Thorough EDA and domain knowledge are a must for feature engineering.

Feature engineering is the subject of entire books; however, as it is a more advanced topic, we will go over just a few techniques in this section. There is a good book on the subject in the *Further reading* section, which also touches upon using machine learning for feature learning.

Interaction terms and polynomial features

We discussed the use of dummy variables back in the *Preprocessing data* section of *Chapter 9, Getting Started with Machine Learning in Python*; however, we merely considered the effect of that variable on its own. In our model that tries to predict red wine quality using chemical properties, we are considering each property separately. However, it is important to consider whether the interaction between these properties has an effect. Perhaps when the levels of citric acid and fixed acidity are both high or both low, the wine quality is different than if one is high and one is low. In order to capture the effect of this, we need to add an **interaction term**, which will be the product of the features.

We may also be interested in increasing the effect of a feature in the model through feature construction; we can achieve this by adding **polynomial features** made from this feature. This involves adding higher degrees of the original feature, so we could have *citric acid*, *citric acid*², *citric acid*³, and so on in the model.

Tip

We can generalize linear models by using interaction terms and polynomial features because they allow us to model the linear relationship of non-linear terms. Since linear models tend to underperform in the presence of multiple or non-linear decision boundaries (the surface or hypersurface that separates the classes), this can improve performance.

Scikit-learn provides the `PolynomialFeatures` class in the `preprocessing` module for easily creating interaction terms and polynomial features. This comes in handy when building models with categorical and continuous features. By specifying just the degree, we can get every combination of the features less than or equal to the degree. High degrees will increase model complexity greatly and may lead to overfitting.

If we use `degree=2`, we can turn *citric acid* and *fixed acidity* into the following, where *1* is the bias term that can be used in a model as an intercept term:

$$1 + \text{citric acid} + \text{fixed acidity} + \text{citric acid}^2 + \text{citric acid} \times \text{fixed acidity} + \text{fixed acidity}^2$$

By calling the `fit_transform()` method on the `PolynomialFeatures` object, we can generate these features:

```
>>> from sklearn.preprocessing import PolynomialFeatures

>>> PolynomialFeatures(degree=2).fit_transform(
...     r_X_train[['citric acid', 'fixed acidity']]
... )
```

```
array([[1.000e+00, 5.500e-01, 9.900e+00, 3.025e-01,
       5.445e+00, 9.801e+01],
      [1.000e+00, 4.600e-01, 7.400e+00, 2.116e-01,
       3.404e+00, 5.476e+01],
      [1.000e+00, 4.100e-01, 8.900e+00, 1.681e-01,
       3.649e+00, 7.921e+01],
      ...,
      [1.000e+00, 1.200e-01, 7.000e+00, 1.440e-02,
       8.400e-01, 4.900e+01],
      [1.000e+00, 3.100e-01, 7.600e+00, 9.610e-02,
       2.356e+00, 5.776e+01],
      [1.000e+00, 2.600e-01, 7.700e+00, 6.760e-02,
       2.002e+00, 5.929e+01]])
```

Let's dissect the first row of our array in the previous code block (highlighted in bold) to understand how we got each of these values:

term	<i>bias</i>	<i>citric acid</i>	<i>fixed acidity</i>	<i>citric acid</i> ²	<i>citric acid</i> × <i>fixed acidity</i>	<i>fixed acidity</i> ²
value	1.000e+00	5.500e-01	9.900e+00	3.025e-01	5.445e+00	9.801e+01

Figure 10.3 – Examining the interaction terms and polynomial features created

If we are only interested in the interaction variables (*citric acid* × *fixed acidity*, here), we can specify `interaction_only=True`. In this case, we also don't want the bias term, so we specify `include_bias=False` as well. This will give us the original variables along with their interaction term(s):

```
>>> PolynomialFeatures(
...     degree=2, include_bias=False, interaction_only=True
... ).fit_transform(
...     r_X_train[['citric acid', 'fixed acidity']]
... )
array([[0.55 , 9.9   , 5.445],
       [0.46 , 7.4   , 3.404],
       [0.41 , 8.9   , 3.649],
       ...,
       [0.12 , 7.    , 0.84 ],
       [0.31 , 7.6   , 2.356],
       [0.26 , 7.7   , 2.002]])
```

We can add these polynomial features to our pipeline:

```
>>> from sklearn.linear_model import LogisticRegression
>>> from sklearn.model_selection import GridSearchCV
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import (
...     MinMaxScaler, PolynomialFeatures
... )

>>> pipeline = Pipeline([
...     ('poly', PolynomialFeatures(degree=2)),
...     ('scale', MinMaxScaler()),
...     ('lr', LogisticRegression(
...         class_weight='balanced', random_state=0
...     ))
... ]).fit(r_X_train, r_y_train)
```

Note that this model is slightly better than before we added these additional terms, which was the model used in *Chapter 9, Getting Started with Machine Learning in Python*:

```
>>> from sklearn.metrics import classification_report

>>> preds = pipeline.predict(r_X_test)
>>> print(classification_report(r_y_test, preds))
      precision    recall  f1-score   support
          0       0.95      0.79      0.86      138
          1       0.36      0.73      0.48       22

  accuracy                           0.78      160
  macro avg       0.65      0.76      0.67      160
weighted avg       0.87      0.78      0.81      160
```

Adding polynomial features and interaction terms increases the dimensionality of our data, which may not be desirable. Sometimes, rather than looking to create more features, we look for ways to consolidate them and reduce the dimensionality of our data.

Dimensionality reduction

Dimensionality reduction shrinks the number of features we train our model on. This is done to reduce the computational complexity of training the model without sacrificing much performance. We could just choose to train on a subset of the features (feature selection); however, if we think there is value in those features, albeit small, we may look for ways to extract the information we need from them.

One common strategy for feature selection is to discard features with low variance. These features aren't very informative since they are mostly the same value throughout the data. Scikit-learn provides the `VarianceThreshold` class for carrying out feature selection according to a minimum variance threshold. By default, it will discard any features that have zero variance; however, we can provide our own threshold. Let's perform feature selection on our model that predicts whether a wine is red or white based on its chemical composition. Since we have no features with zero variance, we will choose to keep features whose variance is greater than 0.01:

```
>>> from sklearn.feature_selection import VarianceThreshold
>>> from sklearn.linear_model import LogisticRegression
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import StandardScaler

>>> white_or_red_min_var = Pipeline([
...     ('feature_selection',
...      VarianceThreshold(threshold=0.01)),
...     ('scale', StandardScaler()),
...     ('lr', LogisticRegression(random_state=0))
... ]).fit(w_X_train, w_y_train)
```

This removed two features with low variance. We can get their names with the Boolean mask returned by the `VarianceThreshold` object's `get_support()` method, which indicates the features that were kept:

```
>>> w_X_train.columns[
...     ~white_or_red_min_var.named_steps[
...         'feature_selection'
...     ].get_support()
... ]
Index(['chlorides', 'density'], dtype='object')
```

Using only 9 of the 11 features, our performance hasn't been affected much:

```
>>> from sklearn.metrics import classification_report
>>> print(classification_report(
...     w_y_test, white_or_red_min_var.predict(w_X_test)
... ))
          precision    recall  f1-score   support
...
        0       0.98      0.99      0.99      1225
        1       0.98      0.95      0.96      400

   accuracy                           0.98      1625
  macro avg       0.98      0.97      0.97      1625
weighted avg       0.98      0.98      0.98      1625
```

Tip

Check out the other feature selection options in the `feature_selection` module at https://scikit-learn.org/stable/modules/classes.html#module-sklearn.feature_selection.

If we believe there is value in all the features, we may decide to use feature extraction rather than discarding them entirely. **Principal component analysis (PCA)** performs feature extraction by projecting high-dimensional data into lower dimensions, thereby reducing the dimensionality. In return, we get the n components that maximize explained variance. This will be sensitive to the scale of the data, so we need to do some preprocessing beforehand.

Let's take a look at the `pca_scatter()` function in the `ml_utils.pca` module, which will help us visualize our data when reduced to two dimensions:

```
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import MinMaxScaler

def pca_scatter(X, labels, cbar_label, cmap='brg'):
    """
    Create a 2D scatter plot from 2 PCA components of X

    Parameters:
    - X: The X data for PCA
    - labels: The y values
```

```

        - cbar_label: The label for the colorbar
        - cmap: Name of the colormap to use.

    Returns:
        Matplotlib `Axes` object
    """
pca = Pipeline([
    ('scale', MinMaxScaler()),
    ('pca', PCA(2, random_state=0))
]).fit(X)
data, classes = pca.transform(X), np.unique(labels)

ax = plt.scatter(
    data[:, 0], data[:, 1],
    c=labels, edgecolor='none', alpha=0.5,
    cmap=plt.cm.get_cmap(cmap, classes.shape[0])
)

plt.xlabel('component 1')
plt.ylabel('component 2')

cbar = plt.colorbar()
cbar.set_label(cbar_label)
cbar.set_ticks(classes)

plt.legend([
    'explained variance\n',
    'comp. 1: {:.3}\ncomp. 2: {:.3}'.format(
        *pca.named_steps['pca'].explained_variance_ratio_
    )
])
return ax

```

Let's visualize the wine data with two PCA components to see if there is a way to separate red from white:

```

>>> from ml_utils.pca import pca_scatter

>>> pca_scatter(wine_X, wine_y, 'wine is red?')
>>> plt.title('Wine Kind PCA (2 components)')

```

Most of the red wines are in the bright green mass of points at the top, and the white wines are in the blue point mass at the bottom. Visually, we can see how to separate them, but there is still some overlap:

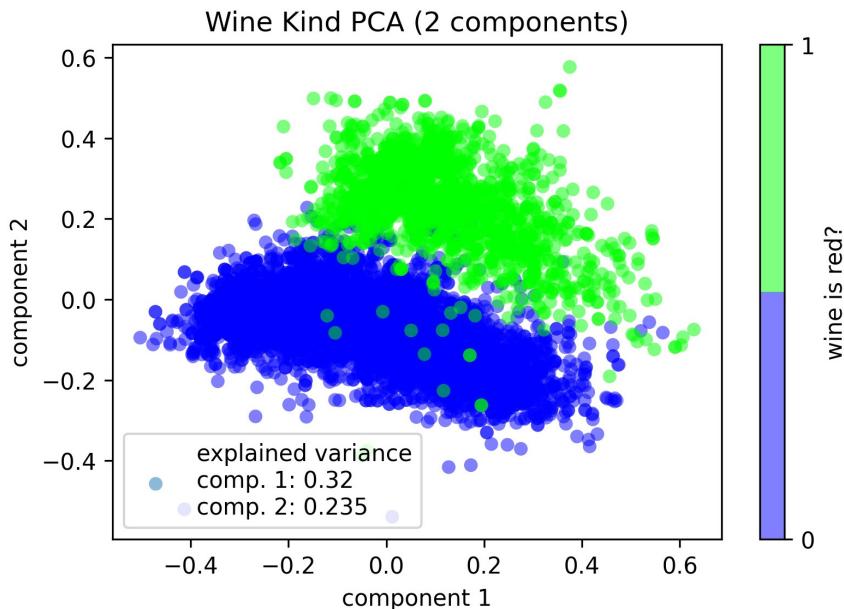


Figure 10.4 – Using two PCA components to separate wines by type

Tip

PCA components will be linearly uncorrelated, since they were obtained through an orthogonal transformation (perpendicularity extended to higher dimensions). Linear regression assumes the regressors (input data) are not correlated, so this can help address multicollinearity.

Note the explained variances of each component from the previous plot's legend—the components explain over 50% of the variance in the wine data. Let's see if using three dimensions improves the separation. The `pca_scatter_3d()` function in the `ml_utils.pca` module uses `mpl_toolkits`, which comes with `matplotlib` for 3D visualizations:

```
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D
from sklearn.decomposition import PCA
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import MinMaxScaler
```

```
def pca_scatter_3d(X, labels, cbar_label, cmap='brg',
                    elev=10, azim=15):
    """
    Create a 3D scatter plot from 3 PCA components of X

    Parameters:
        - X: The X data for PCA
        - labels: The y values
        - cbar_label: The label for the colorbar
        - cmap: Name of the colormap to use.
        - elev: The degrees of elevation to view the plot from.
        - azim: The azimuth angle on the xy plane (rotation
              around the z-axis).

    Returns:
        Matplotlib `Axes` object
    """
    pca = Pipeline([
        ('scale', MinMaxScaler()),
        ('pca', PCA(3, random_state=0))
    ]).fit(X)
    data, classes = pca.transform(X), np.unique(labels)

    fig = plt.figure()
    ax = fig.add_subplot(111, projection='3d')

    p = ax.scatter3D(
        data[:, 0], data[:, 1], data[:, 2],
        alpha=0.5, c=labels,
        cmap=plt.cm.get_cmap(cmap, classes.shape[0])
    )

    ax.view_init(elev=elev, azim=azim)

    ax.set_xlabel('component 1')
    ax.set_ylabel('component 2')
    ax.set_zlabel('component 3')

    cbar = fig.colorbar(p, pad=0.1)
    cbar.set_ticks(classes)
    cbar.set_label(cbar_label)
```

```

    plt.legend([
        'explained variance\ncomp. 1: {:.3}\n',
        'comp. 2: {:.3}\ncomp. 3: {:.3}'.format(
            *pca.named_steps['pca'].explained_variance_ratio_
        )
    ])

    return ax

```

Let's use our 3D visualization function on the wine data again to see if white and red are easier to separate with three PCA components:

```

>>> from ml_utils.pca import pca_scatter_3d

>>> pca_scatter_3d(
...     wine_X, wine_y, 'wine is red?', elev=20, azim=-10
... )
>>> plt.suptitle('Wine Type PCA (3 components)')

```

It seems like we could slice off the green (right) point mass from this angle, although we still have a few points in the wrong section:

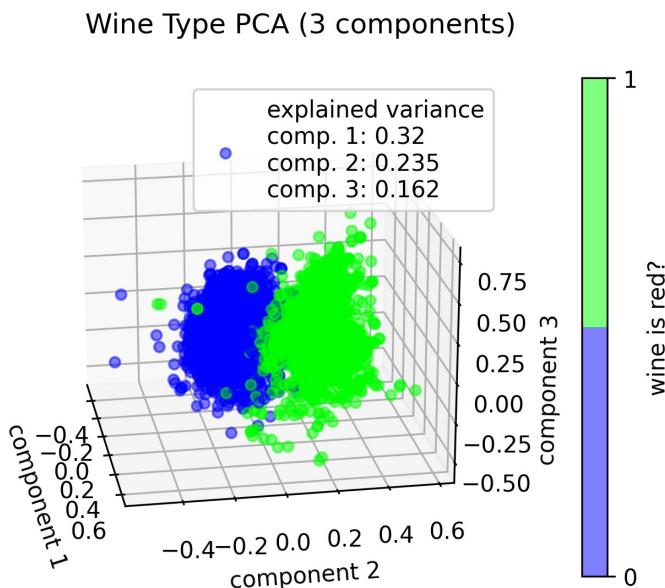


Figure 10.5 – Using three PCA components to separate wines by type

Important note

PCA performs linear dimensionality reduction. Check out t-SNE and Isomap to perform manifold learning for non-linear dimensionality reduction.

We can use the `pca_explained_variance_plot()` function from the `ml_utils.pca` module to visualize the cumulative explained variance as a function of the number of PCA components:

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

def pca_explained_variance_plot(pca_model, ax=None):
    """
    Plot the cumulative explained variance of PCA components.

    Parameters:
        - pca_model: The PCA model that has been fit already
        - ax: Matplotlib `Axes` object to plot on.

    Returns:
        A matplotlib `Axes` object
    """
    if not ax:
        fig, ax = plt.subplots()

    ax.plot(
        np.append(
            0, pca_model.explained_variance_ratio_.cumsum()
        ), 'o-'
    )

    ax.set_title(
        'Total Explained Variance Ratio for PCA Components'
    )
    ax.set_xlabel('PCA components used')
    ax.set_ylabel('cumulative explained variance ratio')

    return ax
```

We can pass the PCA part of our pipeline to this function in order to see the cumulative explained variance:

```
>>> from sklearn.decomposition import PCA
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import MinMaxScaler
>>> from ml_utils.pca import pca_explained_variance_plot

>>> pipeline = Pipeline([
...     ('normalize', MinMaxScaler()),
...     ('pca', PCA(8, random_state=0))
... ]).fit(w_X_train, w_y_train)

>>> pca_explained_variance_plot(pipeline.named_steps['pca'])
```

The first four PCA components explain about 80% of the variance:

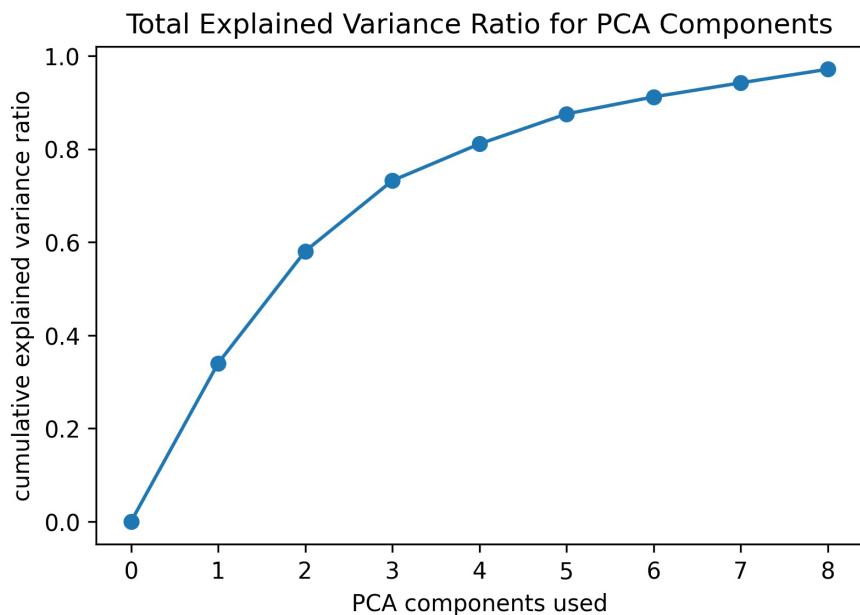


Figure 10.6 – Explained variance for PCA components used

We can also use the elbow point method to find a good value for the number of PCA components to use, just as we did with k-means in *Chapter 9, Getting Started with Machine Learning in Python*. For this, we need to make a **scree plot**, which shows the explained variance for each component. The `ml_utils.pca` module has the `pca_scree_plot()` function for creating this visualization:

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

def pca_scree_plot(pca_model, ax=None):
    """
    Plot explained variance of each consecutive PCA component.

    Parameters:
    - pca_model: The PCA model that has been fit already
    - ax: Matplotlib `Axes` object to plot on.

    Returns: A matplotlib `Axes` object
    """
    if not ax:
        fig, ax = plt.subplots()

    values = pca_model.explained_variance_
    ax.plot(np.arange(1, values.size + 1), values, 'o-')
    ax.set_title('Scree Plot for PCA Components')
    ax.set_xlabel('component')
    ax.set_ylabel('explained variance')
    return ax
```

We can pass the PCA part of our pipeline to this function in order to see the variance explained by each PCA component:

```
>>> from sklearn.decomposition import PCA
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import MinMaxScaler
>>> from ml_utils.pca import pca_scree_plot

>>> pipeline = Pipeline([
...     ('normalize', MinMaxScaler()),
...     ('pca', PCA(8, random_state=0))
... ]).fit(w_X_train, w_y_train)
>>> pca_scree_plot(pipeline.named_steps['pca'])
```

The scree plot tells us we should try four PCA components because there are diminishing returns after that component:

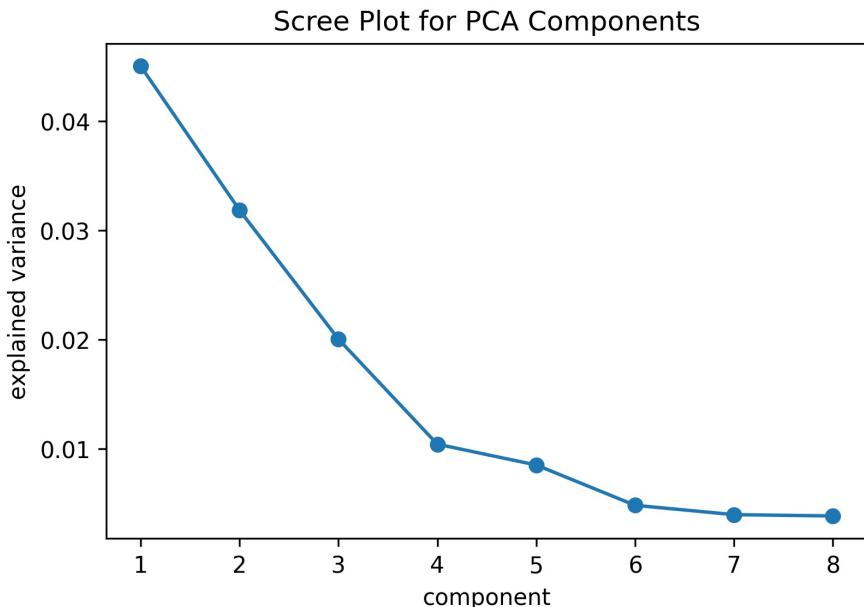


Figure 10.7 – Diminishing returns for each additional PCA component after the fourth

We can build a model on top of these four PCA features in a process called **meta-learning**, where the last model in the pipeline is trained on the output from a different model, not the original data itself:

```
>>> from sklearn.decomposition import PCA
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import MinMaxScaler
>>> from sklearn.linear_model import LogisticRegression

>>> pipeline = Pipeline([
...     ('normalize', MinMaxScaler()),
...     ('pca', PCA(4, random_state=0)),
...     ('lr', LogisticRegression(
...         class_weight='balanced', random_state=0
...     ))
... ]).fit(w_X_train, w_y_train)
```

Our new model performs nearly as well as the original logistic regression that used 11 features, with just 4 features made with PCA:

```
>>> from sklearn.metrics import classification_report

>>> preds = pipeline.predict(w_X_test)
>>> print(classification_report(w_y_test, preds))
      precision    recall  f1-score   support

          0       0.99     0.99     0.99     1225
          1       0.96     0.96     0.96     400

   accuracy                           0.98    1625
  macro avg       0.98     0.98     0.98    1625
weighted avg       0.98     0.98     0.98    1625
```

After performing dimensionality reduction, we no longer have all of the features we started with—reducing the number of features was the point after all. However, it is possible that we will want to perform different feature engineering techniques on subsets of our features; in order to do so, we need to understand feature unions.

Feature unions

We may want to build a model on features from a variety of sources, such as PCA, in addition to selecting a subset of the features. For these purposes, scikit-learn provides the `FeatureUnion` class in the `pipeline` module. This also allows us to perform multiple feature engineering techniques at once, such as feature extraction followed by feature transformation, when we combine this with a pipeline.

Creating a `FeatureUnion` object is just like creating a pipeline, but rather than passing the steps in order, we pass the transformations we want to make. These will be stacked side by side in the result. Let's use a feature union of interaction terms and select the features with a variance above 0.01 to predict red wine quality:

```
>>> from sklearn.feature_selection import VarianceThreshold
>>> from sklearn.pipeline import FeatureUnion, Pipeline
>>> from sklearn.preprocessing import (
...     MinMaxScaler, PolynomialFeatures
... )
>>> from sklearn.linear_model import LogisticRegression
```

```
>>> combined_features = FeatureUnion([
...     ('variance', VarianceThreshold(threshold=0.01)),
...     ('poly', PolynomialFeatures(
...         degree=2, include_bias=False, interaction_only=True
...     ))
... ])
```



```
>>> pipeline = Pipeline([
...     ('normalize', MinMaxScaler()),
...     ('feature_union', combined_features),
...     ('lr', LogisticRegression(
...         class_weight='balanced', random_state=0
...     ))
... ]).fit(r_X_train, r_y_train)
```

To illustrate the transformation that took place, let's examine the first row from the training set for the red wine quality data after the `FeatureUnion` object transforms it. Since we saw that our variance threshold results in nine features, we know they are the first nine entries in the resulting NumPy array, and the rest are the interaction terms:

```
>>> pipeline.named_steps['feature_union'] \
...     .transform(r_X_train)[0]
array([9.900000e+00, 3.500000e-01, 5.500000e-01, 5.000000e+00,
       1.400000e+01, 9.971000e-01, 3.260000e+00, 1.060000e+01,
       9.900000e+00, 3.500000e-01, 5.500000e-01, 2.100000e+00,
       6.200000e-02, 5.000000e+00, 1.400000e+01, 9.971000e-01,
       ..., 3.455600e+01, 8.374000e+00])
```

We can also look at the classification report to see that we got a marginal improvement in F_1 score:

```
>>> from sklearn.metrics import classification_report

>>> preds = pipeline.predict(r_X_test)
>>> print(classification_report(r_y_test, preds))
          precision    recall  f1-score   support

             0       0.94      0.80      0.87      138
             1       0.36      0.68      0.47       22

      accuracy                           0.79      160
   macro avg       0.65      0.74      0.67      160
weighted avg       0.86      0.79      0.81      160
```

In this example, we selected our features such that they had variance greater than 0.01, making the assumption that if the feature doesn't take on many different values then it may not be that helpful. Rather than making this assumption, we can use a machine learning model to help determine which features are important.

Feature importances

Decision trees recursively split the data, making decisions on which features to use for each split. They are **greedy learners**, meaning they look for the largest split they can make each time; this isn't necessarily the optimal split when looking at the output of the tree. We can use a decision tree to gauge **feature importances**, which determine how the tree splits the data at the decision nodes. These feature importances can help inform feature selection. Note that feature importances will sum to one, and higher values are better. Let's use a decision tree to see how red and white wine can be separated on a chemical level:

```
>>> from sklearn.tree import DecisionTreeClassifier

>>> dt = DecisionTreeClassifier(random_state=0).fit(
...     w_X_train, w_y_train
... )

>>> pd.DataFrame([(col, coef) for col, coef in zip(
...     w_X_train.columns, dt.feature_importances_
... )], columns=['feature', 'importance']
... ).set_index('feature').sort_values(
...     'importance', ascending=False
... ).T
```

This shows us that the most important chemical properties in distinguishing between red and white wine are total sulfur dioxide and chlorides:

feature	total sulfur dioxide	chlorides	density	volatile acidity	sulphates	pH	residual sugar	alcohol	fixed acidity	citric acid	free sulfur dioxide
importance	0.687236	0.210241	0.050201	0.016196	0.012143	0.01143	0.005513	0.005074	0.001811	0.000113	0.000042

Figure 10.8 – Importance of each chemical property in predicting wine type

Tip

Using the top features, as indicated by the feature importances, we can try to build a simpler model (by using fewer features). If possible, we want to simplify our models without sacrificing much performance. See the `wine.ipynb` notebook for an example.

If we train another decision tree with a max depth of two, we can visualize the top of the tree (it is too large to visualize if we don't limit the depth):

```
>>> from sklearn.tree import export_graphviz
>>> import graphviz

>>> graphviz.Source(export_graphviz(
...     DecisionTreeClassifier(
...         max_depth=2, random_state=0
...         ).fit(w_X_train, w_y_train),
...     feature_names=w_X_train.columns
... ))
```

Important note

Graphviz software will need to be installed (if it isn't already) in order to visualize the tree. It can be downloaded at <https://graphviz.gitlab.io/download/>, with the installation guide at <https://graphviz.readthedocs.io/en/stable/manual.html#installation>. Note that the kernel will need to be restarted after installing. Otherwise, pass `out_file='tree.dot'` to the `export_graphviz()` function and then generate a PNG file by running `dot -T png tree.dot -o tree.png` from the command line. As an alternative, scikit-learn provides the `plot_tree()` function, which uses `matplotlib`; consult the notebook for an example.

This results in the following tree, which first splits on total sulfur dioxide (which has the highest feature importance), followed by chlorides on the second level. The information at each node tells us the criterion for the split (the top line), the value of the cost function (**gini**), the number of samples at that node (**samples**), and the number of samples in each class at that node (**values**):

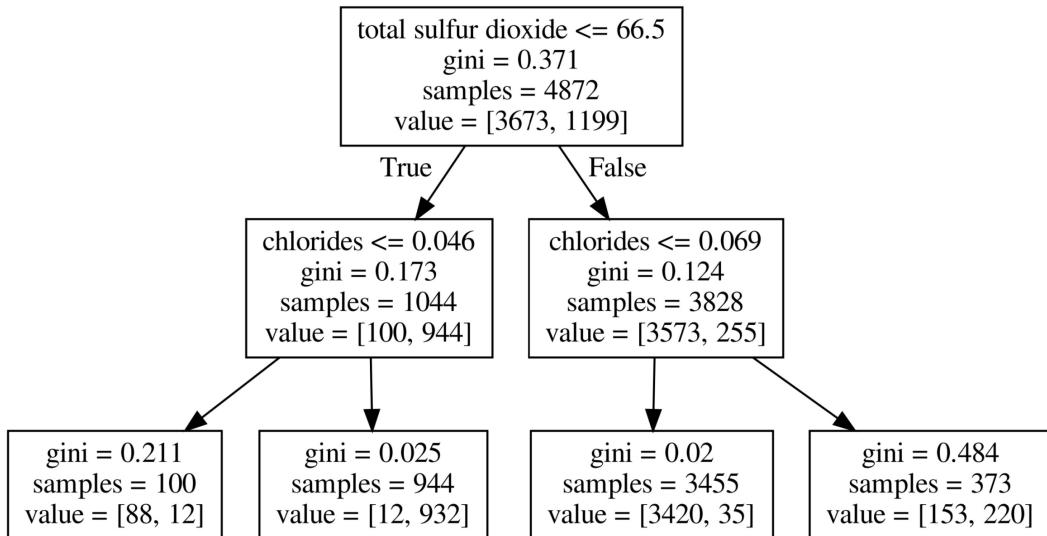


Figure 10.9 – Decision tree for predicting wine type based on chemical properties

We can also apply decision trees to regression problems. Let's find the feature importances for the planets data using the `DecisionTreeRegressor` class:

```

>>> from sklearn.tree import DecisionTreeRegressor

>>> dt = DecisionTreeRegressor(random_state=0).fit(
...     pl_X_train, pl_y_train
... )
>>> [(col, coef) for col, coef in zip(
...     pl_X_train.columns, dt.feature_importances_
... )]
[('semimajoraxis', 0.9969449557611615),
 ('mass', 0.0015380986260574154),
 ('eccentricity', 0.0015169456127809738)]
  
```

Basically, the semi-major axis is the main determinant in the period length, which we already knew, but if we visualize a tree, we can see why. The first four splits are all based on the semi-major axis:

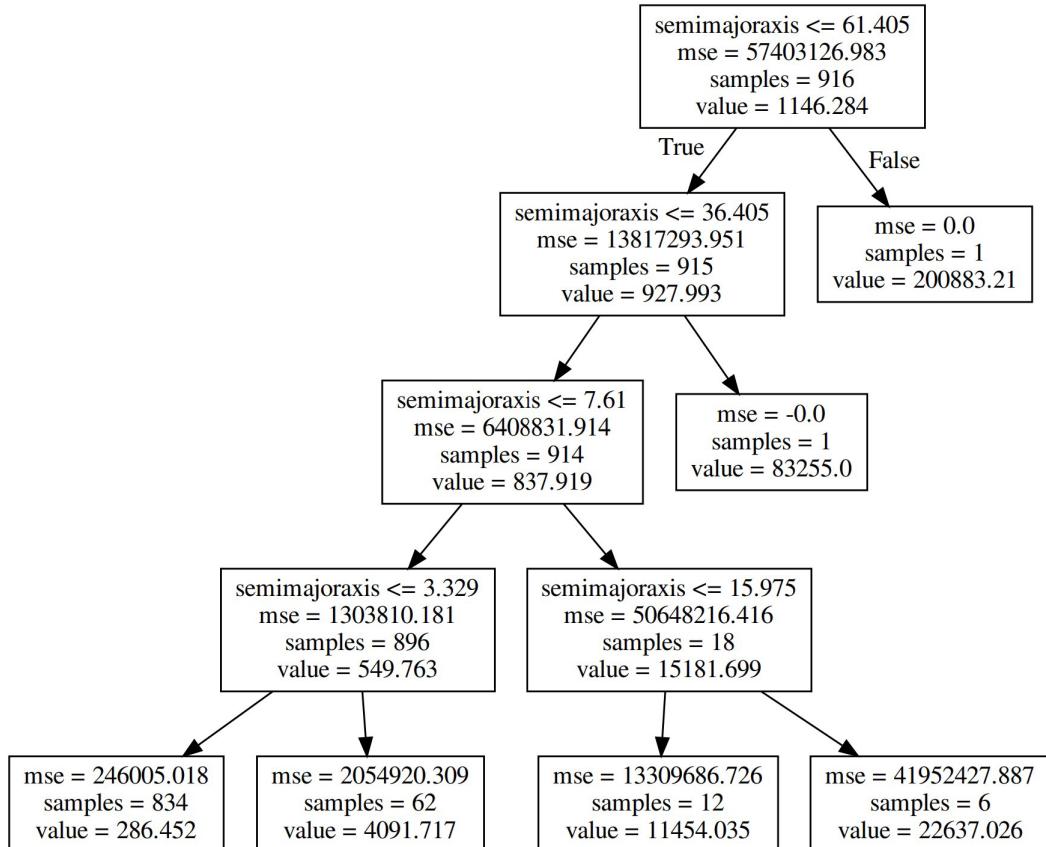


Figure 10.10 – Decision tree for predicting planet period

Decision trees can be **pruned** after being grown to maximum depth, or provided with a max depth before training, to limit growth and thus avoid overfitting. The `scikit-learn` documentation provides tips to address overfitting and other potential issues when using decision trees at <https://scikit-learn.org/stable/modules/tree.html#tips-on-practical-use>. Keep this in mind as we discuss ensemble methods.

Ensemble methods

Ensemble methods combine many models (often weak ones) to create a stronger one that will either minimize the average error between observed and predicted values (the **bias**) or improve how well it generalizes to unseen data (minimize the **variance**). We have to strike a balance between complex models that may increase variance, as they tend to overfit, and simple models that may have high bias, as these tend to underfit. This is called the **bias-variance trade-off**, which is illustrated in the following subplots:

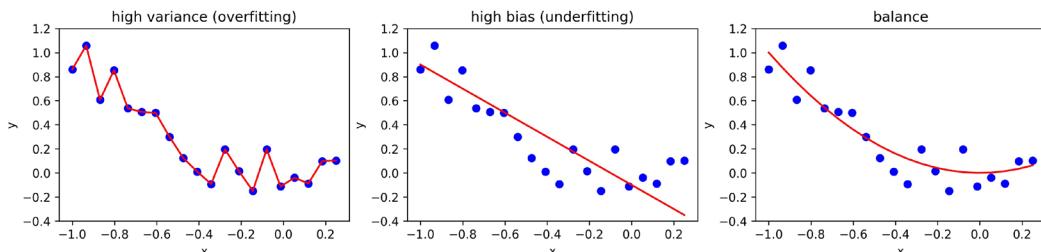


Figure 10.11 – The bias-variance trade-off

Ensemble methods can be broken down into three categories: **boosting**, **bagging**, and **stacking**. **Boosting** trains many weak learners, which learn from each other's mistakes to reduce bias, making a stronger learner. **Bagging**, on the other hand, uses **bootstrap aggregation** to train many models on bootstrap samples of the data and aggregate the results together (using voting for classification, and the average for regression) to reduce variance. We can also combine many different model types together with voting. **Stacking** is an ensemble technique where we combine many different model types using the outputs of some as the inputs to others; this is done to improve predictions. We saw an example of stacking when we combined PCA and logistic regression in the *Dimensionality reduction* section earlier in this chapter.

Random forest

Decision trees have a tendency to overfit, especially if we don't set limits on how far they can grow (with the `max_depth` and `min_samples_leaf` parameters). We can address this overfitting issue with a **random forest**, which is a bagging algorithm where we train many decision trees in parallel using bootstrap samples of our data and aggregate the output. In addition, we have the option of scoring each tree on the data in the training set that it didn't receive in its bootstrap sample, called **out-of-bag samples**, with the `oob_score` parameter.

Important note

The `min_samples_leaf` parameter requires a minimum number of samples to be on the final nodes in the tree (or leaves); this prevents the trees from being fit until they only have a single observation at each leaf.

Each of the trees also gets a subset of the features (random feature selection), which defaults to the square root of the number of features (the `max_features` parameter). This can help address the curse of dimensionality. As a consequence, however, the random forest can't be as easily interpreted as the decision trees that make it up. We can, however, extract feature importances from the random forest, just as we did with the decision tree.

Let's use the `RandomForestClassifier` class from the `ensemble` module to build a random forest (with `n_estimators` trees in it) for the classification of high-quality red wines:

```
>>> from sklearn.ensemble import RandomForestClassifier
>>> from sklearn.model_selection import GridSearchCV

>>> rf = RandomForestClassifier(
...     n_estimators=100, random_state=0
... )

>>> search_space = {
...     'max_depth': [4, 8], # keep trees small
...     'min_samples_leaf': [4, 6]
... }

>>> rf_grid = GridSearchCV(
...     rf, search_space, cv=5, scoring='precision'
... ).fit(r_X_train, r_y_train)

>>> rf_grid.score(r_X_test, r_y_test)
0.6
```

Note that our precision with the random forest is already much better than the 0.35 we got in *Chapter 9, Getting Started with Machine Learning in Python*. The random forest is robust to outliers and able to model non-linear decision boundaries to separate the classes, which may explain part of this dramatic improvement.

Gradient boosting

Boosting looks to improve upon the mistakes of previous models. One way of doing this is to move in the direction of the steepest reduction in the loss function for the model. Since the **gradient** (the multi-variable generalization of the derivative) is the direction of steepest ascent, this can be done by calculating the negative gradient, which yields the direction of steepest descent, meaning the best improvement in the loss function from the current result. This technique is called **gradient descent**.

Important note

Although gradient descent sounds great, there are some potential issues with it. It's possible to end up in a local minimum (a minimum in a certain region of the cost function); the algorithm will stop, thinking that we have the optimal solution, when in fact we don't, because we would like the global minimum (the minimum over the whole region).

Scikit-learn's `ensemble` module provides the `GradientBoostingClassifier` and `GradientBoostingRegressor` classes for gradient boosting using decision trees. These trees will boost their performance through gradient descent. Note that gradient boosted trees are more sensitive to noisy training data than the random forest. In addition, we must consider the additional time required to build all the trees in series, unlike the parallel training we can benefit from with the random forest.

Let's use grid search and gradient boosting to train another model for classifying the red wine quality data. In addition to searching for the best values for the `max_depth` and `min_samples_leaf` parameters, we will search for a good value for the `learning_rate` parameter, which determines the contribution each tree will make in the final estimator:

```
>>> from sklearn.ensemble import GradientBoostingClassifier
>>> from sklearn.model_selection import GridSearchCV

>>> gb = GradientBoostingClassifier(
...     n_estimators=100, random_state=0
... )

>>> search_space = {
...     'max_depth': [4, 8], # keep trees small
...     'min_samples_leaf': [4, 6],
...     'learning_rate': [0.1, 0.5, 1]
... }
```

```
>>> gb_grid = GridSearchCV(  
...     gb, search_space, cv=5, scoring='f1_macro'  
... ).fit(r_X_train, r_y_train)
```

The F_1 macro score we achieve with gradient boosting is better than the 0.66 we got with logistic regression in *Chapter 9, Getting Started with Machine Learning in Python*:

```
>>> gb_grid.score(r_X_test, r_y_test)  
0.7226024272287617
```

Both bagging and boosting have given us better performance than the logistic regression model; however, we may find that the models don't always agree and that we could improve performance even more by having the models vote before making the final prediction.

Voting

When trying out different models for classification, it may be interesting to measure their agreement using Cohen's kappa score. We can use the `cohen_kappa_score()` function in the `sklearn.metrics` module to do so. The score ranges from complete disagreement (-1) to complete agreement (1). Our boosting and bagging predictions have a high level of agreement:

```
>>> from sklearn.metrics import cohen_kappa_score  
  
>>> cohen_kappa_score(  
...     rf_grid.predict(r_X_test), gb_grid.predict(r_X_test)  
... )  
0.7185929648241206
```

Sometimes, we can't find a single model that works well for all of our data, so we may want to find a way to combine the opinions of various models to make the final decision. Scikit-learn provides the `VotingClassifier` class for aggregating model opinions on classification tasks. We have the option of specifying the voting type, where `hard` results in majority rules and `soft` will predict the class with the highest sum of probabilities across the models.

As an example, let's create a classifier for each voting type using the three estimators (models) from this chapter—logistic regression, random forest, and gradient boosting. Since we will run `fit()`, we pass in the best estimator from each of our grid searches (`best_estimator_`). This avoids running each grid search again unnecessarily, which will also train our model faster:

```
>>> from sklearn.ensemble import VotingClassifier

>>> majority_rules = VotingClassifier(
...     [ ('lr', lr_grid.best_estimator_),
...      ('rf', rf_grid.best_estimator_),
...      ('gb', gb_grid.best_estimator_) ],
...     voting='hard'
... ).fit(r_X_train, r_y_train)

>>> max_probabilities = VotingClassifier(
...     [ ('lr', lr_grid.best_estimator_),
...      ('rf', rf_grid.best_estimator_),
...      ('gb', gb_grid.best_estimator_) ],
...     voting='soft'
... ).fit(r_X_train, r_y_train)
```

Our `majority_rules` classifier requires two of the three models to agree (at a minimum), while the `max_probabilities` classifier has each model vote with its predicted probabilities. We can measure how well they perform on the test data with the `classification_report()` function, which tells us that `majority_rules` is a little better than `max_probabilities` in terms of precision. Both are better than the other models we have tried:

```
>>> from sklearn.metrics import classification_report

>>> print(classification_report(
...     r_y_test, majority_rules.predict(r_X_test)
... ))
          precision    recall  f1-score   support

          0       0.92      0.95      0.93      138
          1       0.59      0.45      0.51       22

  accuracy                           0.88      160
  macro avg       0.75      0.70      0.72      160
weighted avg       0.87      0.88      0.87      160
```

```
>>> print(classification_report(  
...     r_y_test, max_probabilities.predict(r_X_test)  
... ))  
              precision    recall   f1-score   support  
  
          0      0.92      0.93      0.92      138  
          1      0.52      0.50      0.51       22  
  
  accuracy                           0.87      160  
  macro avg      0.72      0.71      0.72      160  
weighted avg      0.87      0.87      0.87      160
```

Another important option with the `VotingClassifier` class is the `weights` parameter, which lets us place more or less emphasis on certain estimators when voting. For example, if we pass `weights=[1, 2, 2]` to `majority_rules`, we are giving extra weight to the predictions made by the random forest and gradient boosting estimators. In order to determine which models (if any) should be given extra weight, we can look at individual performance and prediction confidence.

Inspecting classification prediction confidence

As we saw with ensemble methods, when we know the strengths and weaknesses of our model, we can employ strategies to attempt to improve performance. We may have two models to classify something, but they most likely won't agree on everything. However, say that we know that one does better on edge cases, while the other is better on the more common ones. In that case, we would likely want to investigate a voting classifier to improve our performance. How can we know how the models perform in different situations, though?

By looking at the probabilities the model predicts of an observation belonging to a given class, we can gain insight into how confident our model is when it is correct and when it errs. We can use our pandas data wrangling skills to make quick work of this. Let's see how confident our original `white_or_red` model from *Chapter 9, Getting Started with Machine Learning in Python*, was in its predictions:

```
>>> prediction_probabilities = pd.DataFrame(  
...     white_or_red.predict_proba(w_X_test),  
...     columns=['prob_white', 'prob_red'])  
... ).assign(  
...     is_red=w_y_test == 1,  
...     pred_white=lambda x: x.prob_white >= 0.5,  
...     pred_red=lambda x: np.invert(x.pred_white),  
...     correct=lambda x: (np.invert(x.is_red) & x.pred_white)  
...                     | (x.is_red & x.pred_red)  
... )
```

Tip

We can tweak the probability threshold for our model's predictions by using the `predict_proba()` method, instead of `predict()`. This will give us the probabilities that the observation belongs to each class. We can then compare that to our custom threshold. For example, we could use 75%: `white_or_red.predict_proba(w_X_test)[:,1] >= .75`.

One way to identify this threshold is to determine the false positive rate we are comfortable with, and then use the data from the `roc_curve()` function in the `sklearn.metrics` module to find the threshold that results in that false positive rate. Another way is to find a satisfactory spot along the precision-recall curve, and then get the threshold from the `precision_recall_curve()` function. We will work through an example in *Chapter 11, Machine Learning Anomaly Detection*.

Let's use `seaborn` to make a plot showing the distribution of the prediction probabilities when the model was correct versus when it was incorrect. The `displot()` function makes it easy to plot the **kernel density estimate (KDE)** superimposed on a histogram. Here, we will also add a **rug plot**, which shows where each of our predictions ended up:

```
>>> g = sns.displot(
...     data=prediction_probabilities, x='prob_red',
...     rug=True, kde=True, bins=20, col='correct',
...     facet_kws={'sharey': True}
... )
>>> g.set_axis_labels('probability wine is red', None)
>>> plt.suptitle('Prediction Confidence', y=1.05)
```

The KDE for correct predictions is bimodal, with modes near 0 and near 1, meaning the model is very confident when it is correct, which, since it is correct most of the time, means it is very confident in general. The peak of the correct predictions KDE at 0 is much higher than the one at 1 because we have many more white wines than red wines in the data. Note that the KDE shows probabilities of less than zero and greater than one as possible. For this reason, we add the histogram to confirm that the shape we are seeing is meaningful. The histogram for correct predictions doesn't have much in the middle of the distribution, so we include the rug plot to better see which probabilities were predicted. The incorrect predictions don't have many data points, but it appears to be all over the place, because when the model got it wrong, it got fooled pretty badly:

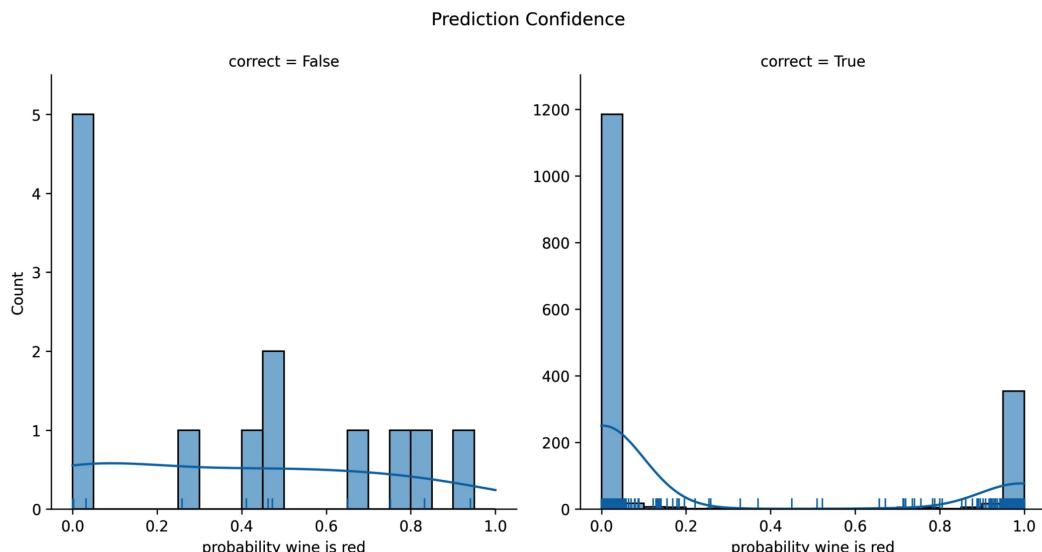


Figure 10.12 – Prediction confidence when the model was correct versus incorrect

This outcome tells us we may want to look into the chemical properties of the wines that were incorrectly classified. It's possible they were outliers and that is why they fooled the model. We can modify the box plots by wine type from the *Exploratory data analysis* section in *Chapter 9, Getting Started with Machine Learning in Python*, to see if anything stands out (*Figure 9.6*).

First, we isolate the chemical properties for the incorrectly classified wines:

```
>>> incorrect = w_X_test.assign(is_red=w_y_test).iloc[
...     prediction_probabilities.query('not correct').index
... ]
```

Then, we add some calls to `scatter()` on the `Axes` object to mark these wines on the box plots from before:

```
>>> import math

>>> chemical_properties = [col for col in wine.columns
...                         if col not in ['quality', 'kind']]
>>> melted = \
...     wine.drop(columns='quality').melt(id_vars=['kind'])

>>> fig, axes = plt.subplots(
...     math.ceil(len(chemical_properties) / 4), 4,
...     figsize=(15, 10)
... )
>>> axes = axes.flatten()

>>> for prop, ax in zip(chemical_properties, axes):
...     sns.boxplot(
...         data=melted[melted.variable.isin([prop])],
...         x='variable', y='value', hue='kind', ax=ax,
...         palette={'white': 'lightyellow', 'red': 'orchid'},
...         saturation=0.5, fliersize=2
...     ).set_xlabel('')
...     for _, wrong in incorrect.iterrows():
...         # _ is convention for collecting info we won't use
...         x_coord = -0.2 if not wrong['is_red'] else 0.2
...         ax.scatter(
...             x_coord, wrong[prop], marker='x',
...             color='red', s=50
...         )
```

```

>>> for ax in axes[len(chemical_properties)::]:
...     ax.remove()

>>> plt.suptitle(
...     'Comparing Chemical Properties of Red and White Wines',
...     '\n(classification errors are red x\'s)'
... )
>>> plt.tight_layout() # clean up layout

```

This results in each of the incorrectly classified wines being marked with a red X. In each subplot, the points on the left box plot are white wines and those on the right box plot are red wines. It appears that some of them may have been outliers for a few characteristics—such as red wines with high residual sugar or sulfur dioxide, and white wines with high volatile acidity:

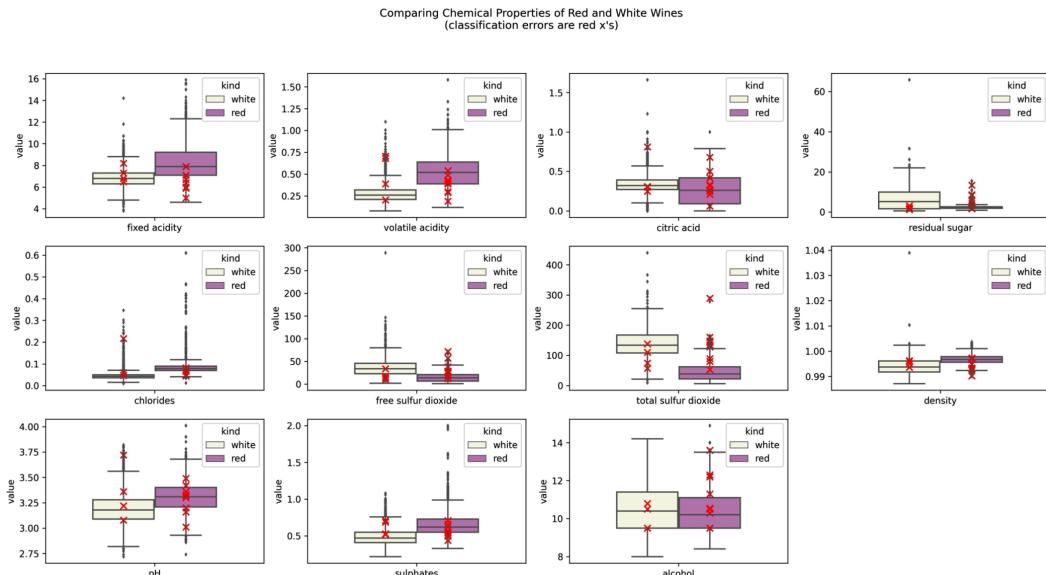


Figure 10.13 – Checking whether incorrect predictions were outliers

Despite having many more white wines than red wines in the data, our model is able to distinguish between them pretty well. This isn't always the case. Sometimes, in order to improve our performance, we need to address the class imbalance.

Addressing class imbalance

When faced with a class imbalance in our data, we may want to try to balance the training data before we build a model around it. In order to do this, we can use one of the following imbalanced sampling techniques:

- Over-sample the minority class.
- Under-sample the majority class.

In the case of **over-sampling**, we pick a larger proportion from the minority class in order to get closer to the amount of the majority class; this may involve a technique such as bootstrapping or generating new data similar to the values in the existing data (using machine learning algorithms such as nearest neighbors). **Under-sampling**, on the other hand, will take less data overall by reducing the amount taken from the majority class. The decision to use over-sampling or under-sampling will depend on the amount of data we started with, and in some cases, computational costs. In practice, we wouldn't try either of these without first trying to build the model with the class imbalance. It's important not to try to optimize things prematurely; not to mention that by building the model first, we have a baseline to compare our imbalanced sampling attempts against.

Important note

Huge performance issues can arise if the minority class that we have in the data isn't truly representative of the full spectrum present in the population. For this reason, our method of collecting the data in the first place should be both known to us and carefully evaluated before proceeding to modeling. If we aren't careful, we could easily build a model that can't generalize to new data, regardless of how we handle the class imbalance.

Before we explore any imbalanced sampling techniques, let's create a baseline model using **k-nearest neighbors (k-NN)** classification, which will classify observations according to the class of the k-nearest observations in the n-dimensional space of the data (our red wine quality data is 11-dimensional). For comparison purposes, we will use the same number of neighbors for all the models in this section; however, it is certainly possible that the sampling techniques will result in a different value performing better. We will use five neighbors:

```
>>> from sklearn.neighbors import KNeighborsClassifier  
>>> knn = KNeighborsClassifier(n_neighbors=5).fit(  
...     r_X_train, r_y_train  
... )  
>>> knn_preds = knn.predict(r_X_test)
```

Our k-NN model is fast to train because it is a **lazy learner**—calculations are made at classification time. It is important to keep in mind the time our models take to train and make predictions, as this can dictate which models we can use in practice. A model that performs marginally better but takes twice as long to train or predict may not be worth it. As the dimensionality of our data increases, the k-NN model will become less and less feasible. We can use the `%%timeit` magic to get an estimate of how long it takes on average to train. Note that this will train the model multiple times, so it might not be the best strategy to time a computationally intense model:

```
>>> %%timeit
>>> from sklearn.neighbors import KNeighborsClassifier
>>> knn = KNeighborsClassifier(n_neighbors=5).fit(
...     r_X_train, r_y_train
... )
3.24 ms ± 599 µs per loop
(mean ± std. dev. of 7 runs, 100 loops each)
```

Let's compare this result with training a **support vector machine (SVM)**, which projects the data into a higher dimension to find the **hyperplane** that separates the classes. A hyperplane is the n-dimensional equivalent of a plane, just like a plane is the two-dimensional equivalent of a line. SVMs are typically robust to outliers and can model non-linear decision boundaries; however, SVMs get slow very quickly, so it will be a good comparison:

```
>>> %%timeit
>>> from sklearn.svm import SVC
>>> svc = SVC(gamma='auto').fit(r_X_train, r_y_train)
153 ms ± 6.7 ms per loop
(mean ± std. dev. of 7 runs, 1 loop each)
```

Now that we have our baseline model and an idea of how it works, let's see how the baseline k-NN model performs:

```
>>> from sklearn.metrics import classification_report
>>> print(classification_report(r_y_test, knn_preds))
          precision    recall  f1-score   support
          0       0.91      0.93      0.92      138
          1       0.50      0.41      0.45       22

      accuracy                           0.86      160
  macro avg       0.70      0.67      0.69      160
weighted avg       0.85      0.86      0.86      160
```

With this performance benchmark, we are ready to try out imbalanced sampling. We will be using the `imblearn` package, which is provided by the `scikit-learn` community. It provides implementations for over- and under-sampling using various strategies, and it is just as easy to use as `scikit-learn`, since they both follow the same API conventions. For reference, the documentation can be found at <https://imbalanced-learn.readthedocs.io/en/stable/api.html>.

Under-sampling

As we hinted at earlier, under-sampling will reduce the amount of data available to train our model on. This means we should only attempt this if we have enough data that we can accept eliminating some of it. Let's see what happens with the red wine quality data, since we don't have much data to begin with.

We will use the `RandomUnderSampler` class from `imblearn` to randomly under-sample the low-quality red wines in the training set:

```
>>> from imblearn.under_sampling import RandomUnderSampler

>>> X_train_undersampled, y_train_undersampled = \
...     RandomUnderSampler(random_state=0) \
...     .fit_resample(r_X_train, r_y_train)
```

We went from almost 14% of the training data being high-quality red wine to 50% of it; however, notice that this came at the price of 1,049 training samples (more than half of our training data):

```
# before
>>> r_y_train.value_counts()
0    1244
1     195
Name: high_quality, dtype: int64

# after
>>> pd.Series(y_train_undersampled).value_counts().sort_index()
0     195
1     195
dtype: int64
```

Fitting our model with the under-sampled data is no different from before:

```
>>> from sklearn.neighbors import KNeighborsClassifier  
  
>>> knn_undersampled = KNeighborsClassifier(n_neighbors=5) \  
...     .fit(X_train_undersampled, y_train_undersampled)  
>>> knn_undersampled_preds = knn_undersampled.predict(r_X_test)
```

Using the classification report, we see that under-sampling is definitely not an improvement—we hardly had any data for this model:

```
>>> from sklearn.metrics import classification_report  
  
>>> print(  
...     classification_report(r_y_test, knn_undersampled_preds)  
... )  
          precision    recall   f1-score    support  
  
          0      0.93      0.65      0.77      138  
          1      0.24      0.68      0.35       22  
  
accuracy                           0.66      160  
macro avg      0.58      0.67      0.56      160  
weighted avg     0.83      0.66      0.71      160
```

In situations where we have limited data to start with, under-sampling is simply not feasible. Here, we lost over half of the already small amount of data we had. Models need a good amount of data to learn from, so let's try over-sampling the minority class now.

Over-sampling

It's clear that with smaller datasets, it won't be beneficial to under-sample. Instead, we can try over-sampling the minority class (the high-quality red wines, in this case). Rather than doing random over-sampling with the `RandomOverSampler` class, we are going to use the **Synthetic Minority Over-sampling Technique (SMOTE)** to create *new* (synthetic) red wines similar to the high-quality ones using the k-NN algorithm. By doing this, we are making a big assumption that the data we have collected about the chemical properties of the red wine does influence the quality rating of the wine.

Important note

The SMOTE implementation in imblearn comes from this paper:

N. V. Chawla, K. W. Bowyer, L. O.Hall, W. P. Kegelmeyer, SMOTE: synthetic minority over-sampling technique, Journal of Artificial Intelligence Research, 321-357, 2002, available at <https://arxiv.org/pdf/1106.1813.pdf>.

Let's use SMOTE with the five nearest neighbors to over-sample the high-quality red wines in our training data:

```
>>> from imblearn.over_sampling import SMOTE

>>> X_train_oversampled, y_train_oversampled = SMOTE(
...     k_neighbors=5, random_state=0
... ).fit_resample(r_X_train, r_y_train)
```

Since we over-sampled, we will have more data than we did before, gaining an extra 1,049 high-quality red wine samples:

```
# before
>>> r_y_train.value_counts()
0    1244
1    195
Name: high_quality, dtype: int64

# after
>>> pd.Series(y_train_oversampled).value_counts().sort_index()
0    1244
1    1244
dtype: int64
```

Once again, we will fit a k-NN model, using the over-sampled data this time:

```
>>> from sklearn.neighbors import KNeighborsClassifier

>>> knn_oversampled = KNeighborsClassifier(n_neighbors=5) \
...     .fit(X_train_oversampled, y_train_oversampled)

>>> knn_oversampled_preds = knn_oversampled.predict(r_X_test)
```

Over-sampling performed much better than under-sampling, but unless we were looking to maximize recall, we are better off sticking with our original strategy for k-NN:

```
>>> from sklearn.metrics import classification_report

>>> print(
...     classification_report(r_y_test, knn_oversampled_preds)
... )
          precision    recall  f1-score   support
0         0.96      0.78      0.86      138
1         0.37      0.82      0.51       22

   accuracy                           0.78      160
  macro avg       0.67      0.80      0.68      160
weighted avg       0.88      0.78      0.81      160
```

Note that since SMOTE is creating synthetic data, we must carefully consider the side effects this may have on our model. If we can't make the assumption that all the values of a given class are representative of the full spectrum of the population and that this won't change over time, we cannot expect SMOTE to work well.

Regularization

When working with regressions, we may look to add a penalty term to our regression equation to reduce overfitting by punishing certain decisions for coefficients made by the model; this is called **regularization**. We are looking for the coefficients that will minimize this penalty term. The idea is to shrink the coefficients toward zero for features that don't contribute much to reducing the error of the model. Some common techniques are ridge regression, LASSO (short for *Least Absolute Shrinkage and Selection Operator*) regression, and elastic net regression, which combines the LASSO and ridge penalty terms. Note that since these techniques rely on the magnitude of the coefficients, the data should be scaled beforehand.

Ridge regression, also called **L2 regularization**, punishes high coefficients ($\hat{\beta}$) by adding the sum of the squares of the coefficients to the cost function (which regression looks to minimize when fitting), as per the following penalty term:

$$\text{L2 penalty} = \lambda \sum_j \hat{\beta}_j^2$$

This penalty term is also weighted by λ (lambda), which indicates how large the penalty will be. When this is zero, we have ordinary least squares regression, as before.

Important note

Remember the C parameter from the LogisticRegression class? By default, the LogisticRegression class will use the L2 penalty term, where C is $1/\lambda$. However, it also supports L1, but only with certain solvers.

LASSO regression, also called **L1 regularization**, drives coefficients to zero by adding the sum of the absolute values of the coefficients to the cost function. This is more robust than L2 regularization because it is less sensitive to extreme values:

$$\text{L1 penalty} = \lambda \sum_j |\hat{\beta}_j|$$

Since LASSO drives coefficients of certain features in the regression to zero (where they won't contribute to the model), it is said to perform feature selection.

Important note

Both the L1 and L2 penalties are also referred to as **L1 and L2 norms** (a mathematical transformation on a vector to be in the range $[0, \infty)$) and written as $\|\beta\|_1$ and $\|\beta\|_2^2$, respectively.

Elastic net regression combines both LASSO and ridge penalty terms into the following penalty term, where we can tune both the strength of the penalty (λ) and the percentage of the penalty that is L1 (and consequently, the percentage that is L2) with α (alpha):

$$\text{elastic net penalty} = \lambda \left(\frac{1-\alpha}{2} \sum_j \hat{\beta}_j^2 + \alpha \sum_j |\hat{\beta}_j| \right)$$

Scikit-learn implements ridge, LASSO, and elastic net regressions with the Ridge, Lasso, and ElasticNet classes, respectively, which can be used in the same way as the LinearRegression class. There is also a CV version of each of these (RidgeCV, LassoCV, and ElasticNetCV), which features built-in cross-validation. Using all the defaults for these models, we find that LASSO performs the best at predicting the length of the year in Earth days with the planet data:

```
>>> from sklearn.linear_model import Ridge, Lasso, ElasticNet
>>> ridge, lasso, elastic = Ridge(), Lasso(), ElasticNet()
```

```
>>> for model in [ridge, lasso, elastic]:  
...     model.fit(pl_X_train, pl_y_train)  
...     print(  
...         f'{model.__class__.__name__}: ' # get model name  
...         f'{model.score(pl_X_test, pl_y_test):.4}'  
...     )  
Ridge: 0.9206  
Lasso: 0.9208  
ElasticNet: 0.9047
```

Note that these `scikit-learn` classes have an `alpha` parameter, which lines up with λ in the previous equations (not α). For `ElasticNet`, α in the equations lines up with the `l1_ratio` parameter, which defaults to 50% LASSO. In practice, both of these hyperparameters are determined with cross-validation.

Summary

In this chapter, we reviewed various techniques we can employ to improve model performance. We learned how to use grid search to find the best hyperparameters in a search space, and how to tune our model using the scoring metric of our choosing with `GridSearchCV`. This means we don't have to accept the default in the `score()` method of our model and can customize it to our needs.

In our discussion of feature engineering, we learned how to reduce the dimensionality of our data using techniques such as PCA and feature selection. We saw how to use the `PolynomialFeatures` class to add interaction terms to models with categorical and numerical features. Then, we learned how to use the `FeatureUnion` class to augment our training data with transformed features. In addition, we saw how decision trees can help us understand which features in the data contribute most to the classification or regression task at hand, using feature importances. This helped us see the importance of sulfur dioxide and chlorides in distinguishing between red and white wine on a chemical level, as well as the importance of a planet's semi-major axis in determining its period.

Afterward, we took a look at the random forest, gradient boosting, and voting classifiers to discuss ensemble methods and how they seek to address the bias-variance trade-off through bagging, boosting, and voting strategies. We also saw how to measure agreement between classifiers with Cohen's kappa score. This led us to examine our `white_or_red` wine classifier's confidence in its correct and incorrect predictions. Once we know the ins and outs of our model's performance, we can try to improve upon it through the appropriate ensemble method to capitalize on its strengths and mitigate its weaknesses.

After that, we learned how to use the `imblearn` package to implement over- and under-sampling strategies when faced with a class imbalance. We tried to use this to improve our ability to predict red wine quality scores. In this example, we got some exposure to the k-NN algorithm and the issues with modeling small datasets. Finally, we learned how we can use regularization to penalize high coefficients and reduce overfitting with regression, using ridge (L2 norm), LASSO (L1 norm), and elastic net penalties; remember, LASSO is often used as a method of feature selection since it drives coefficients to zero.

In the next chapter, we will revisit the simulated login attempt data and use machine learning to detect anomalies. We will also see how we can apply both unsupervised and supervised learning in practice.

Exercises

Complete the following exercises to practice the skills covered in this chapter. Be sure to consult the *Machine learning workflow* section in the *Appendix* as a refresher on the process of building models:

1. Predict star temperature with elastic net linear regression as follows:
 - a) Using the `data/stars.csv` file, build a pipeline to normalize the data with a `MinMaxScaler` object and then run elastic net linear regression using all the numeric columns to predict the temperature of the star.
 - b) Run grid search on the pipeline to find the best values for `alpha`, `l1_ratio`, and `fit_intercept` for the elastic net in the search space of your choice.
 - c) Train the model on 75% of the initial data.
 - d) Calculate the R^2 of your model.
 - e) Find the coefficients for each regressor and the intercept.
 - f) Visualize the residuals using the `plot_residuals()` function from the `ml_utils.regression` module.

2. Perform multiclass classification of white wine quality using a support vector machine and feature union as follows:
 - a) Using the `data/winequality-white.csv` file, build a pipeline to standardize data, then create a feature union between interaction terms and a feature selection method of your choice from the `sklearn.feature_selection` module, followed by an SVM (use the `SVC` class).
 - b) Run grid search on your pipeline with 85% of the data to find the best values for the `include_bias` parameter (`PolynomialFeatures`) and the `C` parameter (`SVC`) in the search space of your choosing with `scoring='f1_macro'`.
 - c) Look at the classification report for your model.
 - d) Create a confusion matrix using the `confusion_matrix_visual()` function from the `ml_utils.classification` module.
 - e) Plot a precision-recall curve for multiclass data using the `plot_multiclass_pr_curve()` function from the `ml_utils.classification` module.
3. Perform multiclass classification of white wine quality using k-NN and over-sampling as follows:
 - a) Using the `data/winequality-white.csv` file, create a test and training set with 85% of the data in the training set. Stratify on `quality`.
 - b) With `imblearn`, use the `RandomOverSampler` class to over-sample the minority quality scores.
 - c) Build a pipeline to standardize data and run k-NN.
 - d) Run grid search on your pipeline with the over-sampled data on the search space of your choosing to find the best value for k-NN's `n_neighbors` parameter with `scoring='f1_macro'`.
 - e) Look at the classification report for your model.
 - f) Create a confusion matrix using the `confusion_matrix_visual()` function from the `ml_utils.classification` module.
 - g) Plot a precision-recall curve for multiclass data using the `plot_multiclass_pr_curve()` function from the `ml_utils.classification` module.

4. Can wine type (red or white) help determine the quality score?
 - a) Using the `data/winequality-white.csv` and `data/winequality-red.csv` files, create a dataframe with the concatenated data and a column indicating which wine type the data belongs to (red or white).
 - b) Create a test and training set with 75% of the data in the training set. Stratify on `quality`.
 - c) Build a pipeline using a `ColumnTransformer` object to standardize the numeric data while one-hot encoding the wine type column (something like `is_red` and `is_white`, each with binary values), and then train a random forest.
 - d) Run grid search on your pipeline with the search space of your choosing to find the best value for the random forest's `max_depth` parameter with `scoring='f1_macro'`.
 - e) Take a look at the feature importances from the random forest.
 - f) Look at the classification report for your model.
 - g) Plot a ROC curve for multiclass data using the `plot_multiclass_roc()` function from the `ml_utils.classification` module.
 - h) Create a confusion matrix using the `confusion_matrix_visual()` function from the `ml_utils.classification` module.
5. Make a multiclass classifier to predict wine quality with majority rules voting by performing the following steps:
 - a) Using the `data/winequality-white.csv` and `data/winequality-red.csv` files, create a dataframe with concatenated data and a column indicating which wine type the data belongs to (red or white).
 - b) Create a test and training set with 75% of the data in the training set. Stratify on `quality`.
 - c) Build a pipeline for each of the following models: random forest, gradient boosting, k-NN, logistic regression, and Naive Bayes (`GaussianNB`). The pipeline should use a `ColumnTransformer` object to standardize the numeric data while one-hot encoding the wine type column (something like `is_red` and `is_white`, each with binary values), and then build the model. Note that we will discuss Naive Bayes in *Chapter 11, Machine Learning Anomaly Detection*.

- d) Run grid search on each pipeline except Naive Bayes (just run `fit()` on it) with `scoring='f1_macro'` on the search space of your choosing to find the best values for the following:
- i) **Random forest:** `max_depth`
 - ii) **Gradient boosting:** `max_depth`
 - iii) **k-NN:** `n_neighbors`
 - iv) **Logistic regression:** `C`
- e) Find the level of agreement between each pair of two models using the `cohen_kappa_score()` function from the `metrics` module in `scikit-learn`. Note that you can get all the combinations of the two easily using the `combinations()` function from the `itertools` module in the Python standard library.
- f) Build a voting classifier with the five models built using majority rules (`voting='hard'`) and weighting the Naive Bayes model half as much as the others.
- g) Look at the classification report for your model.
- h) Create a confusion matrix using the `confusion_matrix_visual()` function from the `ml_utils.classification` module.

Further reading

Check out the following resources for more information on the topics covered in this chapter:

- *A Gentle Introduction to the Gradient Boosting Algorithm for Machine Learning:* <https://machinelearningmastery.com/gentle-introduction-gradient-boosting-algorithm-machine-learning/>
- *A Kaggle's Guide to Model Stacking in Practice:* <https://github.com/datasciblog/a-kagglers-guide-to-model-stacking-in-practice/>
- *Choosing the right estimator:* https://scikit-learn.org/stable/tutorial/machine_learning_map/index.html
- *Cross-validation: evaluating estimator performance:* https://scikit-learn.org/stable/modules/cross_validation.html

- *Decision Trees in Machine Learning*: <https://towardsdatascience.com/decision-trees-in-machine-learning-641b9c4e8052>
- *Ensemble Learning to Improve Machine Learning Results*: <https://blog.statsbot.co/ensemble-learning-d1dcfd548e936>
- *Ensemble Methods*: <https://scikit-learn.org/stable/modules/ensemble.html>
- *Feature Engineering Made Easy by Divya Susarla and Sinan Ozdemir*: <https://www.packtpub.com/big-data-and-business-intelligence/feature-engineering-made-easy>
- *Feature Selection*: https://scikit-learn.org/stable/modules/feature_selection.html#feature-selection
- *Gradient Boosting vs Random Forest*: <https://medium.com/@aravanshad/gradient-boosting-versus-random-forest-cfa3fa8f0d80>
- *Hyperparameter Optimization in Machine Learning*: <https://www.datacamp.com/community/tutorials/parameter-optimization-machine-learning-models>
- *L1 Norms versus L2 Norms*: <https://www.kaggle.com/residentmario/l1-norms-versus-l2-norms>
- *Modern Machine Learning Algorithms: Strengths and Weaknesses*: <https://elitedatascience.com/machine-learning-algorithms>
- *Principal component analysis*: https://en.wikipedia.org/wiki/Principal_component_analysis
- *Regularization in Machine Learning*: <https://towardsdatascience.com/regularization-in-machine-learning-76441ddcf99a>
- *The Elements of Statistical Learning by Jerome H. Friedman, Robert Tibshirani, and Trevor Hastie*: <https://web.stanford.edu/~hastie/ElemStatLearn/>

11

Machine Learning Anomaly Detection

For our final application chapter, we will be revisiting **anomaly detection** on login attempts. Let's imagine we work for a company that launched its web application at the beginning of 2018. This web application has been collecting log events for all login attempts since it launched. We know the IP address that the attempt was made from, the result of the attempt, when it was made, and which username was entered. What we don't know is whether the attempt was made by one of our valid users or a nefarious party.

Our company has been expanding and, since data breaches seem to be in the news every day, has created an information security department to monitor the traffic. The CEO saw our rule-based approach to identifying hackers from *Chapter 8, Rule-Based Anomaly Detection*, and was intrigued by our initiative, but wants us to move beyond using rules and thresholds for such a vital task. We have been tasked with developing a machine learning model for anomaly detection of the login attempts on the web application.

Since this will require a good amount of data, we have been given access to all the logs from January 1, 2018 through December 31, 2018. In addition, the newly formed **security operations center (SOC)** will be auditing all this traffic now and will indicate which time frames contain nefarious users based on their investigations. Since the SOC members are subject matter experts, this data will be exceptionally valuable to us. We will be able to use the labeled data they provide to build a supervised learning model for future use; however, it will take them some time to sift through all the traffic, so we should get started with some unsupervised learning until they have that ready for us.

In this chapter, we will cover the following topics:

- Exploring the simulated login attempts data
- Utilizing unsupervised methods of anomaly detection
- Implementing supervised anomaly detection
- Incorporating a feedback loop with online learning

Chapter materials

The materials for this chapter can be found at https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/ch_11. In this chapter, we will be revisiting attempted login data; however, the `simulate.py` script has been updated to allow additional command-line arguments. We won't be running the simulation this time, but be sure to take a look at the script and check out the process that was followed to generate the data files and create the database for this chapter in the `0-simulating_the_data.ipynb` notebook. The `user_data/` directory contains the files used for this simulation, but we won't be using them directly in this chapter.

The simulated log data we will be using for this chapter can be found in the `logs/` directory. The `logs_2018.csv` and `hackers_2018.csv` files are logs of login attempts and a record of hacker activity from all 2018 simulations, respectively. Files with the `hackers` prefix are treated as the labeled data we will receive from the SOC, so we will pretend we don't have them initially. The files with 2019 instead of 2018 in the name are the data from simulating the first quarter of 2019, rather than the full year. In addition, the CSV files have been written to the `logs.db` SQLite database. The `logs` table contains the data from `logs_2018.csv` and `logs_2019.csv`; the `attacks` table contains the data from `hackers_2018.csv` and `hackers_2019.csv`.

The parameters of the simulation vary per month, and in most months, the hackers are varying their IP addresses for each username they attempt to log in with. This will make our method from *Chapter 8, Rule-Based Anomaly Detection*, useless because we were looking for IP addresses with many attempts and high failure rates. If the hackers now vary their IP addresses, we won't have many attempts associated with them. Therefore, we won't be able to flag them with that strategy, so we will have to find another way around this:

	Jan 2018	Feb 2018	Mar 2018	Apr 2018	May 2018	Jun 2018	Jul 2018	Aug 2018	Sep 2018	Oct 2018	Nov 2018	Dec 2018	Jan 2019	Feb 2019	Mar 2019
Probability of attack in a given hour	1.00%	0.50%	0.10%	1.00%	0.01%	0.05%	1.00%	0.50%	0.50%	0.20%	0.70%	1.00%	0.80%	0.20%	1.00%
Probability of trying entire user base	50%	25%	10%	65%	5%	5%	15%	10%	10%	12%	17%	88%	8%	18%	18%
Vary IP addresses?	Yes	No	No	Yes	Yes	Yes	Yes	Yes							

Figure 11.1 – Simulation parameters

Important note

The `merge_logs.py` file contains the Python code to merge the logs from each of the individual simulations, and `run_simulations.sh` contains a Bash script for running the entire process. These are provided for completeness, but we don't need to use them (or worry about Bash).

Our workflow for this chapter has been split across several notebooks, which are all preceded by a number indicating their order. Before we have the labeled data, we will conduct some EDA in the `1-EDA_unlabeled_data.ipynb` notebook, and then move on to the `2-unsupervised_anomaly_detection.ipynb` notebook to try out some unsupervised anomaly detection methods. Once we have the labeled data, we will perform some additional EDA in the `3-EDA_labeled_data.ipynb` notebook, and then move on to the `4-supervised_anomaly_detection.ipynb` notebook for supervised methods. Finally, we will use the `5-online_learning.ipynb` notebook for our discussion of online learning. As usual, the text will indicate when it is time to switch between notebooks.

Exploring the simulated login attempts data

We don't have labeled data yet, but we can still examine the data to see whether there is something that stands out. This data is different from the data in *Chapter 8, Rule-Based Anomaly Detection*. The hackers are smarter in this simulation—they don't always try as many users or stick with the same IP address every time. Let's see whether we can come up with some features that will help with anomaly detection by performing some EDA in the `1-EDA_unlabeled_data.ipynb` notebook.

As usual, we begin with our imports. These will be the same for all notebooks, so it will be reproduced in this section only:

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

Next, we read in the 2018 logs from the `logs` table in the SQLite database:

```
>>> import sqlite3

>>> with sqlite3.connect('logs/logs.db') as conn:
...     logs_2018 = pd.read_sql(
...         """
...         SELECT *
...         FROM logs
...         WHERE
...             datetime BETWEEN "2018-01-01" AND "2019-01-01";
...         """,
...         conn,
...         parse_dates=['datetime'],
...         index_col='datetime'
...     )
```

Tip

If the SQLAlchemy package (<https://www.sqlalchemy.org/>) is installed in the environment we are working with (as is the case for us), we have the option of providing the database **uniform resource identifier (URI)** for the connection when calling `pd.read_sql()`, eliminating the need for the `with` statement. In our case, this would be `sqlite:///logs/logs.db`, where `sqlite` is the dialect and `logs/logs.db` is the path to the file. Note that there are three / characters in a row.

Our data looks like this:

	source_ip	username	success	failure_reason
datetime				
2018-01-01 00:05:32.988414	223.178.55.3	djones	1	None
2018-01-01 00:08:00.343636	223.178.55.3	djones	0	error_wrong_password
2018-01-01 00:08:01.343636	223.178.55.3	djones	1	None
2018-01-01 01:06:59.640823	208.101.11.88	wbrown	1	None
2018-01-01 02:40:47.769630	11.76.99.35	tkim	1	None

Figure 11.2 – Login attempt logs for 2018

Our data types will be the same as in *Chapter 8, Rule-Based Anomaly Detection*, with the exception of the success column. SQLite doesn't support Boolean values, so this column was converted to the binary representation of its original form (stored as an integer) upon writing the data to the database:

```
>>> logs_2018.dtypes
source_ip          object
username          object
success           int64
failure_reason    object
dtype: object
```

Important note

We are using a SQLite database here because the Python standard library provides the means to make the connection already (`sqlite3`). If we want to use another type of database, such as MySQL or PostgreSQL, we will need to install SQLAlchemy (and possibly additional packages, depending on the database dialect). More information can be found at https://pandas.pydata.org/pandas-docs/stable/user_guide/io.html#sql-queries. Check the *Further reading* section at the end of this chapter for a SQLAlchemy tutorial.

Using the `info()` method, we see that `failure_reason` is the only column with nulls. It is null when the attempt is successful. When looking to build a model, we should also pay attention to the memory usage of our data. Some models will require increasing the dimensionality of our data, which can quickly get too large to hold in memory:

```
>>> logs_2018.info()
<class 'pandas.core.frame.DataFrame'>
DatetimeIndex: 38700 entries,
2018-01-01 00:05:32.988414 to 2018-12-31 23:29:42.482166
Data columns (total 4 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   source_ip        38700 non-null   object  
 1   username         38700 non-null   object  
 2   success          38700 non-null   int64  
 3   failure_reason   11368 non-null   object  
dtypes: int64(1), object(3)
memory usage: 1.5+ MB
```

Running the `describe()` method tells us that the most common reason for failure is providing the wrong password. We can also see that the number of unique usernames tried (1,797) is well over the number of users in our user base (133), indicating some suspicious activity. The most frequent IP address made 314 attempts, but since that isn't even one per day (remember we are looking at the full year of 2018), we can't make any assumptions:

```
>>> logs_2018.describe(include='all')
      source_ip    username       success      failure_reason
count      38700      38700  38700.000000            11368
unique     4956       1797        NaN                  3
top      168.123.156.81  wlopez        NaN  error_wrong_password
freq      314        387        NaN                  6646
mean      NaN         NaN      0.706253                  NaN
std       NaN         NaN      0.455483                  NaN
min       NaN         NaN      0.000000                  NaN
25%      NaN         NaN      0.000000                  NaN
50%      NaN         NaN      1.000000                  NaN
75%      NaN         NaN      1.000000                  NaN
max       NaN         NaN      1.000000                  NaN
```

We can look at the unique usernames with attempted logins per IP address, as in *Chapter 8, Rule-Based Anomaly Detection*, which shows us that most of the IP addresses have a few usernames, but there is at least one with many:

```
>>> logs_2018.groupby('source_ip')\n...     .agg(dict(username='nunique'))\n...     .username.describe()\ncount      4956.000000\nmean        1.146287\nstd         1.916782\nmin        1.000000\n25%        1.000000\n50%        1.000000\n75%        1.000000\nmax       129.000000\nName: username, dtype: float64
```

Let's calculate the metrics per IP address:

```
>>> pivot = logs_2018.pivot_table(\n...     values='success', index='source_ip',\n...     columns=logs_2018.failure_reason.fillna('success'),\n...     aggfunc='count', fill_value=0\n... )\n>>> pivot.insert(0, 'attempts', pivot.sum(axis=1))\n>>> pivot = pivot\\n     .sort_values('attempts', ascending=False)\\n     .assign(\n...         success_rate=lambda x: x.success / x.attempts,\n...         error_rate=lambda x: 1 - x.success_rate\n...     )\n>>> pivot.head()
```

The top five IP addresses with the most attempts appear to be valid users since they have relatively high success rates:

failure_reason	attempts	error_account_locked	error_wrong_password	error_wrong_username	success	success_rate	error_rate
source_ip							
168.123.156.81	314	0	37	0	277	0.882166	0.117834
24.112.17.125	309	0	37	0	272	0.880259	0.119741
16.118.156.50	289	0	41	1	247	0.854671	0.145329
25.246.225.197	267	0	43	0	224	0.838951	0.161049
30.67.241.95	265	0	37	0	228	0.860377	0.139623

Figure 11.3 – Metrics per IP address

Let's use this dataframe to plot successes versus attempts per IP address to see whether there is a pattern we can exploit to separate valid activity from malicious activity:

```
>>> pivot.plot(
...     kind='scatter', x='attempts', y='success',
...     title='successes vs. attempts by IP address',
...     alpha=0.25
... )
```

There appear to be a few points at the bottom that don't belong, but notice the scales on the axes don't perfectly line up. The majority of the points are along a line that is slightly less than a 1:1 relationship of attempts to successes. Recall that this chapter's simulation is more realistic than the one we used in *Chapter 8, Rule-Based Anomaly Detection*; as such, if we compare *Figure 8.11* to this plot, we can observe that it is much more difficult to separate valid from malicious activity here:

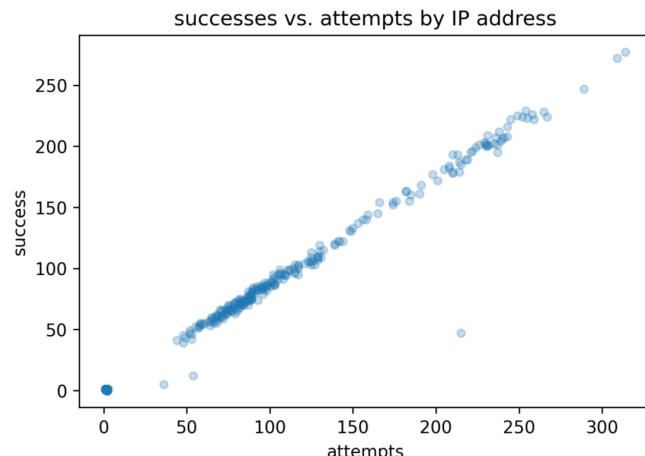


Figure 11.4 – Scatter plot of successes versus attempts per IP address

Remember, this is a binary classification problem where we want to find a way to distinguish between valid user and attacker login activity. We want to build a model that will learn some decision boundary that separates valid users from attackers. Since valid users have a higher probability of entering their password correctly, the relationship between attempts and successes will be closer to 1:1 compared to the attackers. Therefore, we may imagine the separation boundary looking something like this:

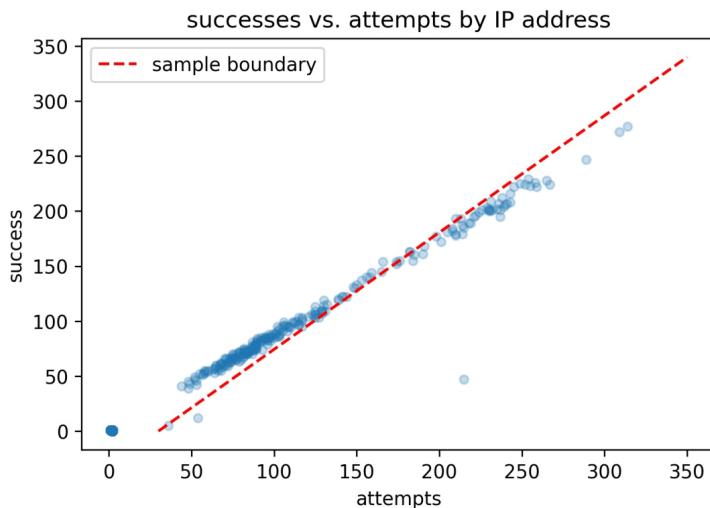


Figure 11.5 – A possible decision boundary

Now, the question is, which of those two groups is the attackers? Well, if more of the IP addresses are the attackers (since they use different IP addresses for each username they attempt), then the valid users would be considered outliers, and the attackers would be considered "inliers" with a box plot. Let's create one to see if that is what is happening:

```
>>> pivot[['attempts', 'success']].plot(
...     kind='box', subplots=True, figsize=(10, 3),
...     title='stats per IP address'
... )
```

Indeed, this appears to be what is happening. Our valid users have more successes than the attackers because they only use 1-3 different IP addresses:

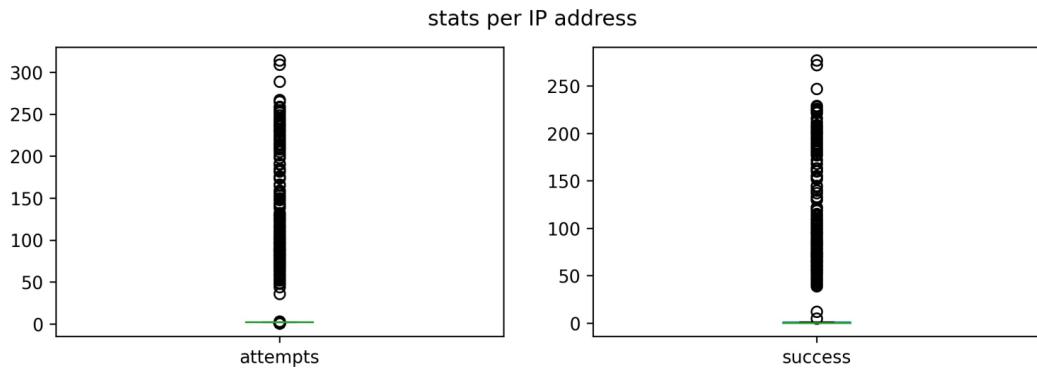


Figure 11.6 – Looking for outliers using metrics per IP address

Clearly, looking at the data like this isn't helping too much, so let's see whether a smaller granularity can help us. Let's visualize the distributions of attempts, the number of usernames, and the number of failures per IP address on a minute-by-minute resolution for January 2018:

```
>>> from matplotlib.ticker import MultipleLocator

>>> ax = logs_2018.loc['2018-01'].assign(
...     failures=lambda x: 1 - x.success
... ).groupby('source_ip').resample('1min').agg({
...     'username': 'nunique',
...     'success': 'sum',
...     'failures': 'sum'
... }).assign(
...     attempts=lambda x: x.success + x.failures
... ).dropna().query('attempts > 0').reset_index().plot(
...     y=['attempts', 'username', 'failures'], kind='hist',
...     subplots=True, layout=(1, 3), figsize=(20, 3),
...     title='January 2018 distributions of minutely stats'
...         'by IP address'
... )
>>> for axes in ax.flatten():
...     axes.xaxis.set_major_locator(MultipleLocator(1))
```

It looks like most of the IP addresses have just a single username associated with them; however, some IP addresses also have multiple failures for their attempts:

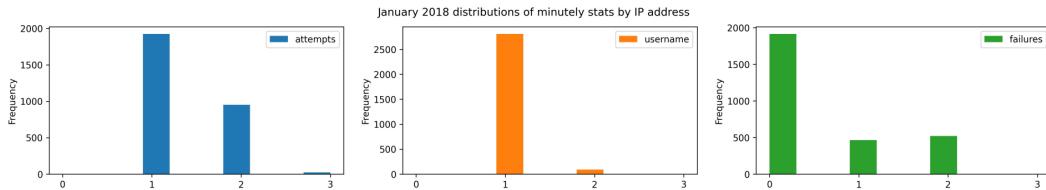


Figure 11.7 – Distribution of metrics per minute per IP address

Perhaps a combination of unique usernames and failures will give us something that doesn't rely on the IP address being constant. Let's visualize the number of usernames with failures per minute over 2018:

```
>>> logs_2018.loc['2018'].assign(
...     failures=lambda x: 1 - x.success
... ).query('failures > 0').resample('1min').agg(
...     {'username': 'nunique', 'failures': 'sum'}
... ).dropna().rename(
...     columns={'username': 'usernames_with_failures'}
... ).usernames_with_failures.plot(
...     title='usernames with failures per minute in 2018',
...     figsize=(15, 3)
... ).set_ylabel('usernames with failures')
```

This looks promising; we should definitely be looking into spikes in usernames with failures. It could be an issue with our website, or something malicious:

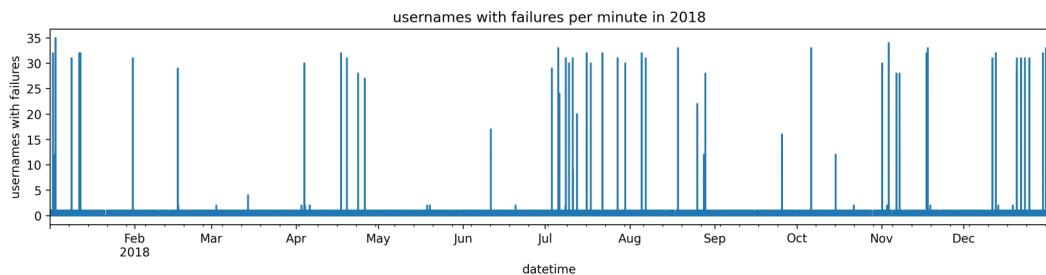


Figure 11.8 – Usernames with failures over time

After a thorough exploration of the data we will be working with, we have an idea of what features we could use when building machine learning models. Since we don't yet have the labeled data, let's try out some unsupervised models next.

Utilizing unsupervised methods of anomaly detection

If the hackers are conspicuous and distinct from our valid users, unsupervised methods may prove pretty effective. This is a good place to start before we have labeled data, or if the labeled data is difficult to gather or not guaranteed to be representative of the full spectrum we are looking to flag. Note that, in most cases, we won't have labeled data, so it is crucial that we are familiar with some unsupervised methods.

In our initial EDA, we identified the number of usernames with a failed login attempt in a given minute as a feature for anomaly detection. We will now test out some unsupervised anomaly detection algorithms, using this feature as the jumping-off point. Scikit-learn provides a few such algorithms. In this section, we will look at isolation forest and local outlier factor; a third method, using a one-class **support vector machine (SVM)**, is in the *Exercises* section.

Before we can try out these methods, we need to prepare our training data. Since the SOC will be sending over the labeled data for January 2018 first, we will use just the January 2018 minute-by-minute data for our unsupervised models. Our features will be the day of the week (one-hot encoded), the hour of the day (one-hot encoded), and the number of usernames with failures. See the *Encoding data* section in *Chapter 9, Getting Started with Machine Learning in Python*, for a refresher on one-hot encoding, if needed.

Let's turn to the `2-unsupervised_anomaly_detection.ipynb` notebook and write a utility function to grab this data easily:

```
>>> def get_X(log, day):
...     """
...     Get data we can use for the X
...
...     Parameters:
...         - log: The logs dataframe
...         - day: A day or single value we can use as a
...                datetime index slice
...
...     Returns:
...         A `pandas.DataFrame` object
...     """
```

```

...
    return pd.get_dummies(
...
        log.loc[day].assign(
            failures=lambda x: 1 - x.success
        ).query('failures > 0').resample('1min').agg(
            {'username': 'nunique', 'failures': 'sum'}
        ).dropna().rename(
            columns={'username': 'usernames_with_failures'}
        ).assign(
            day_of_week=lambda x: x.index.dayofweek,
            hour=lambda x: x.index.hour
        ).drop(columns=['failures']),
...
        columns=['day_of_week', 'hour']
...
)

```

Now, we can grab January and store it in X:

```

>>> X = get_X(logs_2018, '2018-01')
>>> X.columns
Index(['usernames_with_failures', 'day_of_week_0',
       'day_of_week_1', 'day_of_week_2', 'day_of_week_3',
       'day_of_week_4', 'day_of_week_5', 'day_of_week_6',
       'hour_0', 'hour_1', ..., 'hour_22', 'hour_23'],
      dtype='object')

```

Isolation forest

The **isolation forest** algorithm uses splitting techniques to isolate outliers from the rest of the data; therefore, it can be used for anomaly detection. Under the hood, it is a random forest where the splits are made on randomly chosen features. A random value of that feature between its maximum and its minimum is selected to split on. Note that this range is from the range of the feature at that node in the tree, not the starting data.

A single tree in the forest will look something like the following:

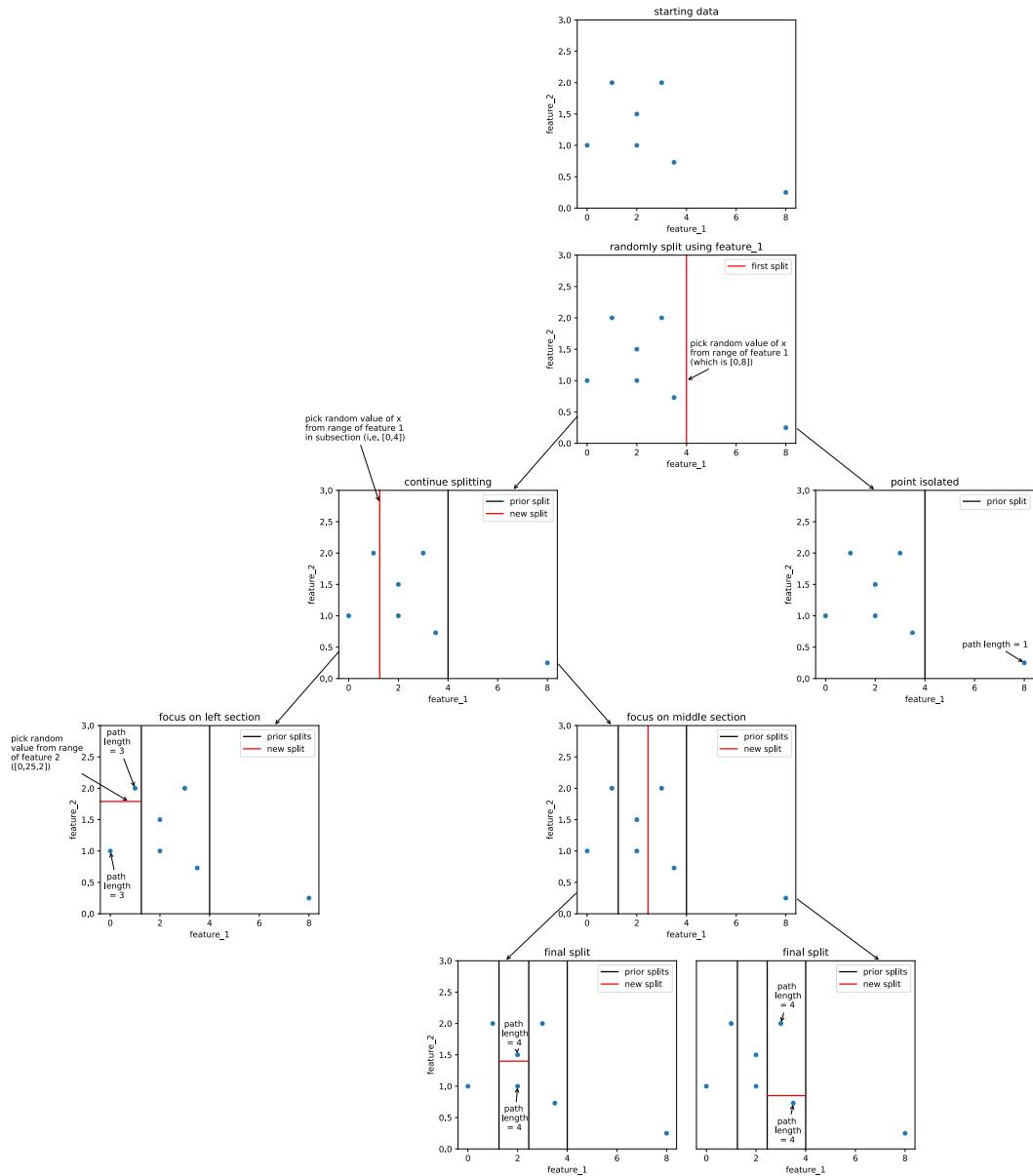


Figure 11.9 – Example of a single tree in an isolation forest

The average length of the path that must be traveled from the top of each tree in the forest to the leaf containing a given point is used to score a point as an outlier or inlier. The outliers have much shorter paths, since they will be one of the few on a given side of a split and have less in common with other points. Conversely, points with many dimensions in common will take more splits to separate.

Important note

More information on this algorithm can be found at https://scikit-learn.org/stable/modules/outlier_detection.html#isolation-forest.

Let's implement an isolation forest with a pipeline that first standardizes our data:

```
>>> from sklearn.ensemble import IsolationForest
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import StandardScaler

>>> iso_forest_pipeline = Pipeline([
...     ('scale', StandardScaler()),
...     ('iforest', IsolationForest(
...         random_state=0, contamination=0.05
...     ))
... ]).fit(X)
```

We had to specify how much of the data was expected to be outliers (`contamination`), which we estimated to be 5%; this will be difficult to choose since we don't have labeled data. There is an `auto` option that will determine a value for us but, in this case, it gives us no outliers, so it's clear that that value isn't the one we want. In practice, we could perform a statistical analysis on the data to determine an initial value or consult domain experts.

The `predict()` method can be used to check whether each data point is an outlier. Anomaly detection algorithms implemented in `scikit-learn` typically return 1 or -1 if the point is an inlier or outlier, respectively:

```
>>> isolation_forest_preds = iso_forest_pipeline.predict(X)
>>> pd.Series(np.where(
...     isolation_forest_preds == -1, 'outlier', 'inlier'
... )).value_counts()
inlier      42556
outlier      2001
dtype: int64
```

Since we don't have the labeled data yet, we will come back to evaluate this later; for now, let's take a look at the second unsupervised algorithm that we will discuss in this chapter.

Local outlier factor

While inliers are typically located in denser regions of the dataset (32-dimensional here), outliers tend to be located in sparser, more isolated regions with few neighboring points. The **local outlier factor (LOF)** algorithm looks for these sparsely populated regions to identify outliers. It scores all points based on the ratio of the density around each point to that of its nearest neighbors. Points that are considered normal will have similar densities to their neighbors; those with few others nearby will be considered abnormal.

Important note

More information on this algorithm can be found at https://scikit-learn.org/stable/modules/outlier_detection.html#local-outlier-factor.

Let's build another pipeline, but swap out the isolation forest for LOF. Note that we have to guess the best value for the `n_neighbors` parameter, because `GridSearchCV` has nothing to score models on if we don't have labeled data. We are using the default value for this parameter, which is 20:

```
>>> from sklearn.neighbors import LocalOutlierFactor
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import StandardScaler

>>> lof_pipeline = Pipeline([
...     ('scale', StandardScaler()),
...     ('lof', LocalOutlierFactor())
... ]).fit(X)
```

Now, let's see how many outliers we have this time. LOF doesn't have a `predict()` method, so we have to check the `negative_outlier_factor_` attribute of the LOF object to see the scores of each of the data points we fit it with:

```
>>> lof_preds = lof_pipeline.named_steps['lof'] \
...     .negative_outlier_factor_
>>> lof_preds
array([-1.33898756e+10, -1.00000000e+00, -1.00000000e+00, ...,
       -1.00000000e+00, -1.00000000e+00, -1.11582297e+10])
```

There is another difference between LOF and isolation forests: the values for the `negative_outlier_factor_` attribute aren't strictly -1 or 1. In fact, they can be any number—take a look at the first and last values in the previous result, and you'll see that they are way less than -1. This means we can't use the method we used with the isolation forest to count the inliers and outliers. Instead, we need to compare the `negative_outlier_factor_` attribute to the `offset_` attribute of the LOF model, which tells us the cutoff value as determined by the LOF model during training (using the `contamination` parameter):

```
>>> pd.Series(np.where(
...     lof_preds < lof_pipeline.named_steps['lof'].offset_,
...     'outlier', 'inlier'
... )).value_counts()
inlier    44248
outlier      309
dtype: int64
```

Now that we have two unsupervised models, we need to compare them to see which one would be more beneficial to our stakeholders.

Comparing models

LOF indicates fewer outliers than the isolation forest, but perhaps they don't even agree with each other. As we learned in *Chapter 10, Making Better Predictions – Optimizing Models*, we can use the `cohen_kappa_score()` function from `sklearn.metrics` to check their level of agreement:

```
>>> from sklearn.metrics import cohen_kappa_score

>>> is_lof_outlier = np.where(
...     lof_preds < lof_pipeline.named_steps['lof'].offset_,
...     'outlier', 'inlier'
... )
>>> is_iso_outlier = np.where(
...     isolation_forest_preds == -1, 'outlier', 'inlier'
... )

>>> cohen_kappa_score(is_lof_outlier, is_iso_outlier)
0.25862517997335677
```

They have a low level of agreement, indicating that it's not so obvious which data points are anomalies. Without labeled data, however, it really is impossible for us to tell which one is better. We would have to work with the consumers of the results to determine which model gives them the most useful data. Thankfully, the SOC has just sent over the January 2018 labeled data, so we can determine which of our models is better and let them start using it until we get a supervised model ready.

First, we will read in the labeled data they wrote to the database in the `attacks` table and add some columns indicating the minute the attack started, the duration, and when it ended:

```
>>> with sqlite3.connect('logs/logs.db') as conn:
...     hackers_jan_2018 = pd.read_sql(
...         """
...         SELECT *
...         FROM attacks
...         WHERE start BETWEEN "2018-01-01" AND "2018-02-01";
...         """ , conn, parse_dates=['start', 'end'])
...     ).assign(
...         duration=lambda x: x.end - x.start,
...         start_floor=lambda x: x.start.dt.floor('min'),
...         end_ceil=lambda x: x.end.dt.ceil('min')
...     )
>>> hackers_jan_2018.shape
(7, 6)
```

Note that the SOC only has a single IP address for the ones involved in each attack, so it's a good thing we aren't relying on that anymore. Instead, the SOC wants us to tell them at which minute there was suspicious activity so that they can investigate further. Also note that while the attacks are quick in duration, our minute-by-minute data means we will trigger many alerts per attack:

	start	end	source_ip	duration	start_floor	end_ceil
0	2018-01-02 02:31:43.326264	2018-01-02 02:35:16.326264	102.139.159.128	0 days 00:03:33	2018-01-02 02:31:00	2018-01-02 02:36:00
1	2018-01-02 20:14:02.279476	2018-01-02 20:14:28.279476	119.218.239.234	0 days 00:00:26	2018-01-02 20:14:00	2018-01-02 20:15:00
2	2018-01-03 01:25:48.667114	2018-01-03 01:29:13.667114	151.93.164.203	0 days 00:03:25	2018-01-03 01:25:00	2018-01-03 01:30:00
3	2018-01-08 21:41:43.985324	2018-01-08 21:45:56.985324	226.98.192.152	0 days 00:04:13	2018-01-08 21:41:00	2018-01-08 21:46:00
4	2018-01-11 17:38:30.974748	2018-01-11 17:42:33.974748	23.81.78.129	0 days 00:04:03	2018-01-11 17:38:00	2018-01-11 17:43:00
5	2018-01-12 03:32:20.284167	2018-01-12 03:36:29.284167	74.90.28.4	0 days 00:04:09	2018-01-12 03:32:00	2018-01-12 03:37:00
6	2018-01-31 07:39:17.514901	2018-01-31 07:43:29.514901	236.174.156.247	0 days 00:04:12	2018-01-31 07:39:00	2018-01-31 07:44:00

Figure 11.10 – Labeled data for evaluating our models

Using the `start_floor` and `end_ceil` columns, we can create a range of datetimes and can check whether the data we marked as outliers falls within that range. For this, we will use the following function:

```
>>> def get_y(datetimes, hackers, resolution='1min'):
...     """
...     Get data we can use for the y (whether or not a
...     hacker attempted a log in during that time).
...
...     Parameters:
...         - datetimes: The datetimes to check for hackers
...         - hackers: The dataframe indicating when the
...                 attacks started and stopped
...         - resolution: The granularity of the datetime.
...                 Default is 1 minute.
...
...     Returns: `pandas.Series` of Booleans.
...
...     """
...     date_ranges = hackers.apply(
...         lambda x: pd.date_range(
...             x.start_floor, x.end_ceil, freq=resolution
...         ),
...         axis=1
...     )
...     dates = pd.Series(dtype='object')
...     for date_range in date_ranges:
...         dates = pd.concat([dates, date_range.to_series()])
...     return datetimes.isin(dates)
```

Now, let's find the datetimes in our X data that had hacker activity:

```
>>> is_hacker = \
...     get_y(X.reset_index().datetime, hackers_jan_2018)
```

We now have everything we need to make a classification report and a confusion matrix. Since we will be passing in the `is_hacker` series a lot, we will make some partials to reduce our typing a bit:

```
>>> from functools import partial
>>> from sklearn.metrics import classification_report
>>> from ml_utils.classification import confusion_matrix_visual

>>> report = partial(classification_report, is_hacker)
```

```
>>> conf_matrix = partial(
...     confusion_matrix_visual, is_hacker,
...     class_labels=[False, True]
... )
```

Let's start with the classification reports, which indicate that the isolation forest is much better in terms of recall:

```
>>> iso_forest_predicts_hacker = isolation_forest_preds == -1
>>> print(report(iso_forest_predicts_hacker)) # iso. forest
      precision    recall   f1-score   support
False        1.00     0.96     0.98    44519
True        0.02     0.82     0.03      38

accuracy                           0.96    44557
macro avg        0.51     0.89     0.50    44557
weighted avg     1.00     0.96     0.98    44557

>>> lof_predicts_hacker = \
...     lof_preds < lof_pipeline.named_steps['lof'].offset_
>>> print(report(lof_predicts_hacker)) # LOF
      precision    recall   f1-score   support
False        1.00     0.99     1.00    44519
True        0.03     0.26     0.06      38

accuracy                           0.99    44557
macro avg        0.52     0.63     0.53    44557
weighted avg     1.00     0.99     1.00    44557
```

To better understand the results in the classification report, let's create confusion matrices for our unsupervised methods and place them side-by-side for comparison:

```
>>> fig, axes = plt.subplots(1, 2, figsize=(15, 5))

>>> conf_matrix(
...     iso_forest_predicts_hacker,
...     ax=axes[0], title='Isolation Forest'
... )
```

```
>>> conf_matrix(
...     lof_predicts_hacker,
...     ax=axes[1], title='Local Outlier Factor'
... )
```

The isolation forest has more true positives and a greater number of false positives compared to LOF, but it has fewer false negatives:

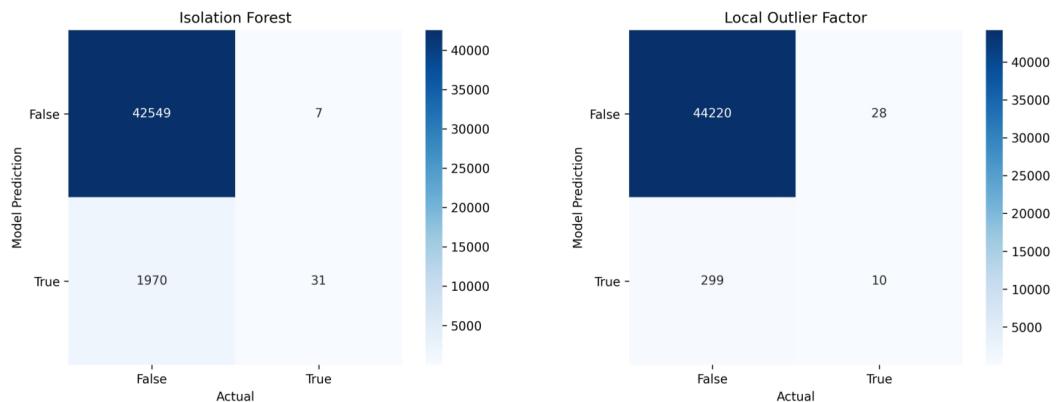


Figure 11.11 – Confusion matrices for our unsupervised models

The SOC has informed us that false negatives are much more costly than false positives. However, they would like us to keep false positives in check to avoid bogging down the team with an excessive number of false alarms. This tells us that recall (the **true positive rate (TPR)**) is more valuable than precision as a performance metric. The SOC wants us to target a *recall of at least 70%*.

Since we have a very large class imbalance, the **false positive rate (FPR)** won't be too informative for us. Remember, the FPR is the ratio of false positives to the sum of false positives and true negatives (everything belonging to the negative class). Due to the nature of the attacks being rare, we will have a very large number of true negatives and, therefore, our FPR will remain very low. Consequently, the secondary metric determined by the SOC is to attain a *precision of 85% or greater*.

The isolation forest model exceeds our target recall, but the precision is too low. Since we were able to obtain some labeled data, we can now use supervised learning to find the minutes with suspicious activity (note that this won't always be the case). Let's see whether we can use this extra information to find the minutes of interest more precisely.

Implementing supervised anomaly detection

The SOC has finished up labeling the 2018 data, so we should revisit our EDA to make sure our plan of looking at the number of usernames with failures on a minute resolution does separate the data. This EDA is in the `3-EDA_labeled_data.ipynb` notebook. After some data wrangling, we are able to create the following scatter plot, which shows that this strategy does indeed appear to separate the suspicious activity:

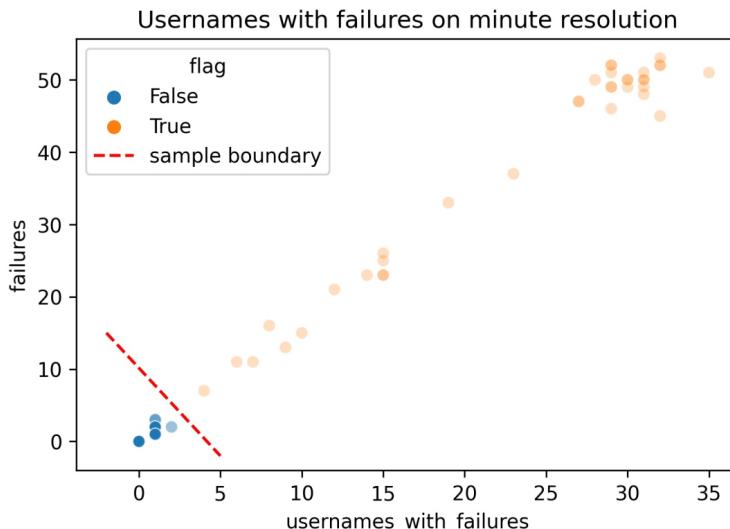


Figure 11.12 – Confirming that our features can help form a decision boundary

In the `4-supervised_anomaly_detection.ipynb` notebook, we will create some supervised models. This time we need to read in all the labeled data for 2018. Note that the code for reading in the logs is omitted since it is the same as in the previous section:

```
>>> with sqlite3.connect('logs/logs.db') as conn:
...     hackers_2018 = pd.read_sql(
...         """
...             SELECT *
...             FROM attacks
...             WHERE start BETWEEN "2018-01-01" AND "2019-01-01";
...             """, conn, parse_dates=['start', 'end'])
...     .assign(
...         duration=lambda x: x.end - x.start,
...         start_floor=lambda x: x.start.dt.floor('min'),
...         end_ceil=lambda x: x.end.dt.ceil('min'))
...     )
```

Before we build our models, however, let's create a new function that will create both X and y at the same time. The `get_X_y()` function will use the `get_X()` and `get_y()` functions we made earlier, returning both X and y:

```
>>> def get_X_y(log, day, hackers):
...     """
...     Get the X, y data to build a model with.
...
...     Parameters:
...         - log: The logs dataframe
...         - day: A day or single value we can use as a
...                datetime index slice
...         - hackers: The dataframe indicating when the
...                 attacks started and stopped
...
...     Returns:
...         X, y tuple where X is a `pandas.DataFrame` object
...         and y is a `pandas.Series` object
...
...     """
...     X = get_X(log, day)
...     y = get_y(X.reset_index().datetime, hackers)
...     return X, y
```

Now, let's make a training set with January 2018 data and a testing set with February 2018 data, using our new function:

```
>>> X_train, y_train = \
...     get_X_y(logs_2018, '2018-01', hackers_2018)
>>> X_test, y_test = \
...     get_X_y(logs_2018, '2018-02', hackers_2018)
```

Important note

While we have a very large class imbalance, we don't jump right to balancing the training sets. It's crucial to try out the model without premature optimization. If we build our model and see that it is being affected by the class imbalance, then we can try those techniques. Remember to be very cautious with over-/under-sampling techniques, as some make assumptions of the data that aren't always applicable or realistic. Think about SMOTE—would we really expect all future attackers to be similar to the ones we have in the data?

Let's use this data to build some supervised anomaly detection models. Remember that the SOC has given us the performance requirements in terms of recall (at least 70%) and precision (85% or greater), so we will use those metrics to evaluate our models.

Baselining

Our first step will be to build some baseline models, so we know that our machine learning algorithms are performing better than some simpler models and have predictive value. We will build two such models:

- A dummy classifier that will predict labels based on the stratification in the data.
- A Naive Bayes model that will predict the labels leveraging Bayes' theorem.

Dummy classifier

A dummy classifier will give us a model that is equivalent to the baseline we have been drawing on our ROC curves. The results will be poor on purpose. We will never use this classifier to actually make predictions; rather, we can use it to see whether the models we are building are better than random guessing strategies. In the `dummy` module, `scikit-learn` provides the `DummyClassifier` class precisely for this purpose.

Using the `strategy` parameter, we can specify how the dummy classifier will make its predictions. Some interesting options are as follows:

- `uniform`: The classifier will guess each time whether or not the observation belongs to a hacking attempt.
- `most_frequent`: The classifier will always predict the most frequent label, which, in our case, will result in never marking anything as nefarious. This will achieve high accuracy, but be useless since the minority class is the class of interest.
- `stratified`: The classifier will use the class distribution from the training data and maintain that ratio with its guesses.

Let's build a dummy classifier with the `stratified` strategy:

```
>>> from sklearn.dummy import DummyClassifier

>>> dummy_model = DummyClassifier(
...     strategy='stratified', random_state=0
... ).fit(X_train, y_train)
>>> dummy_preds = dummy_model.predict(X_test)
```

Now that we have our first baseline model, let's measure its performance for comparisons. We will be using both the ROC curve and the precision-recall curve to show how the class imbalance can make the ROC curve optimistic of performance. To reduce typing, we will once again make some partials:

```
>>> from functools import partial
>>> from sklearn.metrics import classification_report
>>> from ml_utils.classification import (
...     confusion_matrix_visual, plot_pr_curve, plot_roc
... )

>>> report = partial(classification_report, y_test)
>>> roc = partial(plot_roc, y_test)
>>> pr_curve = partial(plot_pr_curve, y_test)
>>> conf_matrix = partial(
...     confusion_matrix_visual, y_test,
...     class_labels=[False, True]
... )
```

Recall from our initial discussion of ROC curves in *Chapter 9, Getting Started with Machine Learning in Python*, that the diagonal line was random guessing of a dummy model. If our performance isn't better than this line, our model has no predictive value. The dummy model we just created is equivalent to this line. Let's visualize the baseline ROC curve, precision-recall curve, and confusion matrix using subplots:

```
>>> fig, axes = plt.subplots(1, 3, figsize=(20, 5))
>>> roc(dummy_model.predict_proba(X_test)[:,1], ax=axes[0])
>>> conf_matrix(dummy_preds, ax=axes[1])
>>> pr_curve(
...     dummy_model.predict_proba(X_test)[:,1], ax=axes[2]
... )
>>> plt.suptitle('Dummy Classifier with Stratified Strategy')
```

The dummy classifier wasn't able to flag any of the attackers. The ROC curve (TPR versus FPR) indicates that the dummy model has no predictive value, with an **area under the curve (AUC)** of 0.5. Note that the area under the precision-recall curve is nearly zero:

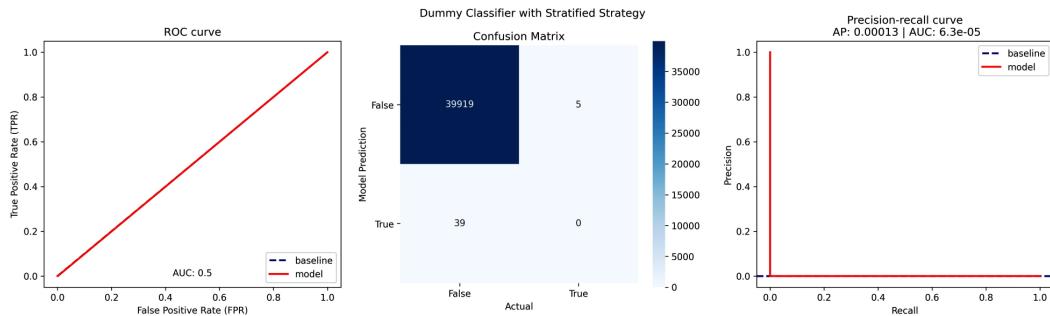


Figure 11.13 – Baseling with a dummy classifier

Since we have a very large class imbalance, the stratified random guessing strategy should perform horrendously on the minority class and very well on the majority class. We can observe this by examining the classification report:

```
>>> print(report(dummy_preds))
              precision    recall    f1-score   support
False          1.00     1.00     1.00      39958
True          0.00     0.00     0.00       5
accuracy           -         -         -      39963
macro avg       0.50     0.50     0.50      39963
weighted avg    1.00     1.00     1.00      39963
```

Naive Bayes

Our last baseline model will be a Naive Bayes classifier. Before we discuss this model, we need to review a few concepts of probability. The first is conditional probability. When dealing with two events, A and B , the probability of event A happening *given* that event B happened is the **conditional probability** and is written as $P(A|B)$. When events A and B are independent, meaning B happening doesn't tell us anything about A happening and vice versa, $P(A|B)$ is $P(A)$.

The conditional probability is defined as the **joint probability** of both A and B occurring (which is the intersection of these events), written as $P(A \cap B)$, divided by the probability of B occurring (provided this is not zero):

$$P(A|B) = \frac{P(A \cap B)}{P(B)}, \text{ if } P(B) \neq 0$$

This equation can be rearranged as follows:

$$P(A \cap B) = P(A|B) \times P(B)$$

The joint probability of $A \cap B$ is equivalent to $B \cap A$; therefore, we get the following equation:

$$P(A \cap B) = P(B \cap A) = P(B|A) \times P(A)$$

It then follows that we can change the first equation to use conditional probabilities instead of the joint probability. This gives us **Bayes' theorem**:

$$P(A|B) = \frac{P(B|A) \times P(A)}{P(B)}$$

When working with the previous equation, $P(A)$ is referred to as the **prior probability**, or initial degree of belief that event A will happen. After accounting for event B occurring, this initial belief gets updated; this is represented as $P(A|B)$ and is called the **posterior probability**. The **likelihood** of event B given event A is $P(B|A)$. The support that event B occurring gives to our belief of observing event A is the following:

$$\frac{P(B|A)}{P(B)}$$

Let's take a look at an example—say we are building a spam filter, and we find that 10% of emails are spam. This 10% is our prior, or $P(\text{spam})$. We want to know the probability an email we just received is spam given that it contains the word *free*—we want to find $P(\text{spam}|\text{free})$. In order to find this, we need the probability that the word *free* is in an email given that it is spam, or $P(\text{free}|\text{spam})$, and the probability of the word *free* being in an email, or $P(\text{free})$.

Suppose we learned that 12% of emails contained the word *free* and 20% of the emails that were determined to be spam contained the word *free*. Plugging all this into the equation from before, we see that once we know an email contains the word *free*, our belief that it is spam increases from 10% to 16.7%, which is our posterior probability:

$$P(\text{spam}|\text{free}) = \frac{P(\text{free}|\text{spam}) \times P(\text{spam})}{P(\text{free})} = \frac{0.20 \times 0.10}{0.12} \approx 16.7\%$$

Bayes' theorem can be leveraged in a type of classifier called **Naive Bayes**. Depending on the assumptions we make of the data, we get a different member of the Naive Bayes family of classifiers. These models are very fast to train because they make a simplifying assumption of conditional independence of each pair of the x features, given the y variable (meaning $P(x_i|y, x_1, \dots, x_n)$ is equivalent to $P(x_i|y)$). They are called *naive* because this assumption is often incorrect; however, these classifiers have traditionally worked well in building spam filters.

Let's say we also find multiple dollar signs in the email and the word *prescription*, and we want to know the probability of it being spam. While some of these features may depend on each other, the Naive Bayes model will treat them as conditionally independent. This means our equation for the posterior probability is now the following:

$$P(\text{spam}|\text{free}, \text{$$$}, \text{prescription}) = \frac{P(\text{free}|\text{spam}) \times P(\text{$$$}|\text{spam}) \times P(\text{prescription}|\text{spam}) \times P(\text{spam})}{P(\text{free}) \times P(\text{$$$}) \times P(\text{prescription})}$$

Suppose we find out that 5% of spam emails contain multiple dollar signs, 55% of spam emails contain the word *prescription*, 25% of emails contain multiple dollar signs, and the word *prescription* is found in 2% of emails overall. This means that our belief of the email being spam, given that it has the words *free* and *prescription* and multiple dollar signs, increases from 10% to 91.7%:

$$P(\text{spam}|\text{free}, \text{$$$}, \text{prescription}) = \frac{0.20 \times 0.05 \times 0.55 \times 0.10}{0.12 \times 0.25 \times 0.02} \approx 91.7\%$$

Now that we understand the basics of the algorithm, let's build a Naive Bayes classifier. Note that `scikit-learn` provides various Naive Bayes classifiers that differ by the assumed distributions of the likelihoods of the features, which we defined as $P(x_i|y, x_1, \dots, x_n)$. We will use the version that assumes they are normally distributed, `GaussianNB`:

```
>>> from sklearn.naive_bayes import GaussianNB
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import StandardScaler
```

```
>>> nb_pipeline = Pipeline([
...     ('scale', StandardScaler()),
...     ('nb', GaussianNB())
... ]).fit(X_train, y_train)
>>> nb_preds = nb_pipeline.predict(X_test)
```

We can retrieve the class priors from the model, which, in this case, tells us that the prior for a minute containing normal activity is 99.91% versus 0.09% for abnormal activity:

```
>>> nb_pipeline.named_steps['nb'].class_prior_
array([9.99147160e-01, 8.52840182e-04])
```

Naive Bayes makes a nice baseline model because we don't have to tune any hyperparameters, and it is quick to train. Let's see how it performs on the test data (February 2018):

```
>>> fig, axes = plt.subplots(1, 3, figsize=(20, 5))
>>> roc(nb_pipeline.predict_proba(X_test)[:,1], ax=axes[0])
>>> conf_matrix(nb_preds, ax=axes[1])
>>> pr_curve(
...     nb_pipeline.predict_proba(X_test)[:,1], ax=axes[2]
... )
>>> plt.suptitle('Naive Bayes Classifier')
```

The Naive Bayes classifier finds all five attackers and is above the baseline (the dashed line) in both the ROC curve and precision-recall curve, meaning this model has some predictive value:

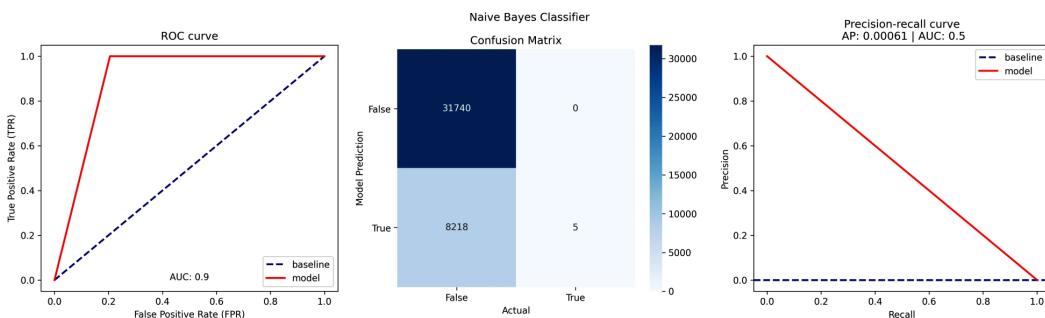


Figure 11.14 – Performance of the Naive Bayes classifier

Unfortunately, we are triggering an enormous quantity of false positives (8,218). For the month of February, roughly 1 out of every 1,644 attack classifications was indeed an attack. This has the effect of desensitizing the users of these classifications. They may choose to always ignore our classifications because they are too noisy and, consequently, miss a real issue. This trade-off can be captured in the metrics of the classification report:

```
>>> print(report(nb_preds))
```

	precision	recall	f1-score	support
False	1.00	0.79	0.89	39958
True	0.00	1.00	0.00	5
accuracy			0.79	39963
macro avg	0.50	0.90	0.44	39963
weighted avg	1.00	0.79	0.89	39963

While the Naive Bayes classifier outperforms the dummy classifier, it does not meet the requirements of our stakeholders. Precision rounds to zero for the target class because we have lots of false positives. Recall is higher than precision because the model is better with false negatives than false positives (since it isn't very discerning). This leaves the F_1 score at zero. Now, let's try to beat these baseline models.

Logistic regression

Since logistic regression is another simple model, let's try it out next. We used logistic regression in *Chapter 9, Getting Started with Machine Learning in Python*, for classification problems, so we already know how it works. As we learned in *Chapter 10, Making Better Predictions – Optimizing Models*, we will use a grid search to find a good value for the regularization hyperparameter in our desired search space, using `recall_macro` for scoring. Remember there is a large cost associated with false negatives, so we are focusing on recall. The `_macro` suffix indicates that we want to average the recall between the positive and negative classes, instead of looking at it overall (due to the class imbalance).

Tip

If we know exactly how much more valuable recall is to us over precision, we can replace this with a custom scorer made using the `make_scorer()` function in `sklearn.metrics`. The notebook we are working in has an example.

When using grid search, warnings from `scikit-learn` may be printed at each iteration. Therefore, to avoid having to scroll through all that, we will use the `%%capture` magic command to capture everything that would have been printed, keeping our notebook clean:

```
>>> %%capture
>>> from sklearn.linear_model import LogisticRegression
>>> from sklearn.model_selection import GridSearchCV
>>> from sklearn.pipeline import Pipeline
>>> from sklearn.preprocessing import StandardScaler

>>> lr_pipeline = Pipeline([
...     ('scale', StandardScaler()),
...     ('lr', LogisticRegression(random_state=0))
... ])

>>> search_space = {'lr__C': [0.1, 0.5, 1, 2]}

>>> lr_grid = GridSearchCV(
...     lr_pipeline, search_space, scoring='recall_macro', cv=5
... ).fit(X_train, y_train)

>>> lr_preds = lr_grid.predict(X_test)
```

Tip

With `%%capture`, all errors and output will be captured by default. We have the option of writing `--no-stderr` to hide errors only and `--no-stdout` to hide output only. These go after `%%capture`; for example, `%%capture --no-stderr`.

If we want to hide specific errors, we can use the `warnings` module, instead. For example, after importing `filterwarnings` from the `warnings` module, we can run the following to ignore warnings of future deprecations:

```
filterwarnings('ignore',
               category=DeprecationWarning)
```

Now that we have our logistic regression model trained, let's check on the performance:

```
>>> fig, axes = plt.subplots(1, 3, figsize=(20, 5))
>>> roc(lr_grid.predict_proba(X_test)[:,1], ax=axes[0])
>>> conf_matrix(lr_preds, ax=axes[1])
>>> pr_curve(lr_grid.predict_proba(X_test)[:,1], ax=axes[2])
>>> plt.suptitle('Logistic Regression Classifier')
```

This model has no false positives and is much better than the baselines. The ROC curve is significantly closer to the top-left corner, as is the precision-recall curve to the top-right corner. Notice that the ROC curve is a bit more optimistic about the performance:

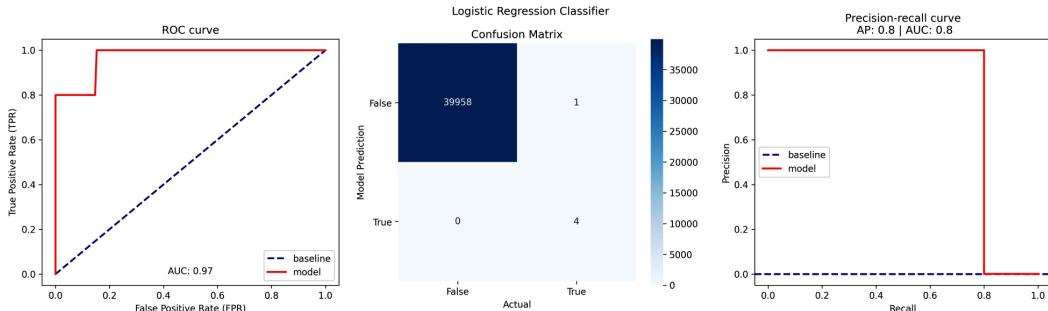


Figure 11.15 – Performance using logistic regression

This model meets the requirements of the SOC. Our recall is at least 70% and our precision is at least 85%:

```
>>> print(report(lr_preds))
      precision    recall  f1-score   support

  False        1.00     1.00     1.00     39958
  True        1.00     0.80     0.89      5

accuracy                           1.00     39963
macro avg        1.00     0.90     0.94     39963
weighted avg     1.00     1.00     1.00     39963
```

The SOC has given us data for January and February 2019, and they want us to update our model. Unfortunately, our model has already been trained, so we have the choice of rebuilding from scratch or ignoring this new data. Ideally, we would build a model with a feedback loop to incorporate this (and future) new data. In the next section, we will discuss how to do this.

Incorporating a feedback loop with online learning

There are some big issues with the models we have built so far. Unlike the data we worked with in *Chapter 9, Getting Started with Machine Learning in Python*, and *Chapter 10, Making Better Predictions – Optimizing Models*, we wouldn't expect the attacker behavior to be static over time. There is also a limit to how much data we can hold in memory, which limits how much data we can train our model on. Therefore, we will now build an online learning model to flag anomalies in usernames with failures per minute.

An **online learning** model is constantly getting updated (in near real time via streaming, or in batches). This allows us to learn from new data as it comes and then get rid of it (to keep space in memory).

In addition, the model can evolve over time and adapt to changes in the underlying distribution of the data. We will also be providing our model with feedback as it learns so that we are able to make sure it stays robust to changes in the hacker behavior over time. This is called **active learning**. Not all models in `scikit-learn` support this kind of behavior; so, we are limited to the models that offer a `partial_fit()` method (models without this need to be trained from scratch with new data).

Tip

Scikit-learn refers to models implementing the `partial_fit()` method as **incremental learners**. More information, including which models support this, can be found at https://scikit-learn.org/stable/computing/scaling_strategies.html#incremental-learning.

Our data is currently being rolled up to the minute and then passed to the model, so this will be batch learning, not streaming; however, note that if we were to put this into production, we could update our model each minute, if desired.

Creating the PartialFitPipeline subclass

We saw in *Chapter 9, Getting Started with Machine Learning in Python*, that the `Pipeline` class made streamlining our machine learning processes a cinch, but unfortunately, we can't use it with the `partial_fit()` method. To get around this, we can create our own `PartialFitPipeline` class, which is a subclass of the `Pipeline` class but supports calling `partial_fit()`. The `PartialFitPipeline` class is located in the `ml_utils.partial_fit_pipeline` module.

We simply inherit from `sklearn.pipeline.Pipeline` and define a single new method—`partial_fit()`—which will call `fit_transform()` on all the steps except the last one, and `partial_fit()` on the last step:

```
from sklearn.pipeline import Pipeline

class PartialFitPipeline(Pipeline):
    """
    Subclass of sklearn.pipeline.Pipeline that supports the
    `partial_fit()` method.
    """

    def partial_fit(self, X, y):
        """
        Run `partial_fit()` for online learning estimators
        when used in a pipeline.
        """
        # for all but last step
        for _, step in self.steps[:-1]: # (name, object) tuples
            X = step.fit_transform(X)

        # grab object from tuple position 1 for partial_fit()
        self.steps[-1][1].partial_fit(X, y)

    return self
```

Now that we have the `PartialFitPipeline` class, the last piece that remains is to select a model capable of online learning.

Stochastic gradient descent classifier

Our logistic regression model performed well—it met the requirements for recall and precision. However, the `LogisticRegression` class does not support online learning because the method it uses to calculate the coefficients is a closed-form solution. We have the option of using an optimization algorithm, such as gradient descent, to determine the coefficients instead; this will be capable of online learning.

Rather than use a different incremental learner, we can train a new logistic regression model with the `SGDClassifier` class. It uses **stochastic gradient descent (SGD)** to optimize the loss function of our choice. For this example, we will be using log loss, which gives us a logistic regression where the coefficients are found using SGD.

Whereas standard gradient descent optimization looks at all the samples or batches to estimate the gradient, SGD reduces the computational cost by selecting samples at random (stochastically). How much the model learns from each sample is determined by the **learning rate**, with earlier updates having more of an effect than later ones. A single iteration of SGD is carried out as follows:

1. Shuffle the training data.
2. For each sample in the training data, estimate the gradient and update the model with decreasing strength as determined by the learning rate.
3. Repeat *step 2* until all samples have been used.

In machine learning, we use **epochs** to refer to the number of times the full training set is used. The process of SGD we just outlined is for a single epoch. When we train for multiple epochs, we repeat the preceding steps for the desired number of epochs, continuing each time from where we left off.

Now that we understand how SGD works, we are ready to build our model. Here's an overview of the process we will follow before presenting it to the SOC:



Figure 11.16 – Process for preparing our online learning model

Let's now turn to the `5-online_learning.ipynb` notebook to build our online learning model.

Building our initial model

First, we will use the `get_X_y()` function to get our `X` and `y` training data using the full year of 2018:

```
>>> X_2018, y_2018 = get_X_y(logs_2018, '2018', hackers_2018)
```

Since we will be updating this model in batches, our test set will always be the data we are using for our current predictions. After we do so, it will become the training set and be used to update the model. Let's build our initial model trained on the 2018 labeled data. Note that the `PartialFitPipeline` object is created in the same way we create a `Pipeline` object:

```
>>> from sklearn.linear_model import SGDClassifier
>>> from sklearn.preprocessing import StandardScaler
>>> from ml_utils.partial_fit_pipeline import \
...     PartialFitPipeline

>>> model = PartialFitPipeline([
...     ('scale', StandardScaler()),
...     ('sgd', SGDClassifier(
...         random_state=10, max_iter=1000,
...         tol=1e-3, loss='log', average=1000,
...         learning_rate='adaptive', eta0=0.01
...     ))
... ]).fit(X_2018, y_2018)
```

Our pipeline will first standardize the data, and then pass it to the model. We start building our model using the `fit()` method so that we have a good starting point for our updates with `partial_fit()` later. The `max_iter` parameter defines the number of epochs for the training. The `tol` parameter (tolerance) specifies when to stop iterating, which occurs when the loss from the current iteration is greater than the previous loss minus the tolerance (or we have reached `max_iter` iterations). We specified `loss='log'` to use logistic regression; however, there are many other options for the loss functions, including the default value of '`'hinge'` for a linear SVM.

Here, we also passed in a value for the `average` parameter, telling the `SGDClassifier` object to store the coefficients as averages of the results once 1,000 samples have been seen; note that this parameter is optional and, by default, this won't be calculated. Examining these coefficients can be achieved as follows:

```
>>> [(col, coef) for col, coef in
...     zip(X_2018.columns, model.named_steps['sgd'].coef_[0])]
[('usernames_with_failures', 0.9415581997027198),
 ('day_of_week_0', 0.05040751530926895),
 ...,
 ('hour_23', -0.02176726532333003)]
```

Lastly, we passed in `eta0=0.01` for our starting learning rate and specified to only adjust the learning rate when we have failed to improve our loss by the tolerance defined for a given number of consecutive epochs (`learning_rate='adaptive'`). This number of epochs is defined by the `n_iter_no_change` parameter, which will be 5 (the default), since we aren't setting it explicitly.

Evaluating the model

Since we now have labeled data for January and February 2019, we can evaluate how the model performs each month. First, we read in the 2019 data from the database:

```
>>> with sqlite3.connect('logs/logs.db') as conn:  
...     logs_2019 = pd.read_sql(  
...         """  
...         SELECT *  
...         FROM logs  
...         WHERE  
...             datetime BETWEEN "2019-01-01" AND "2020-01-01";  
...         """,  
...         conn, parse_dates=['datetime'],  
...         index_col='datetime'  
...     )  
...     hackers_2019 = pd.read_sql(  
...         """  
...         SELECT *  
...         FROM attacks  
...         WHERE start BETWEEN "2019-01-01" AND "2020-01-01";  
...         """,  
...         conn, parse_dates=['start', 'end'])  
...     ).assign(  
...         start_floor=lambda x: x.start.dt.floor('min'),  
...         end_ceil=lambda x: x.end.dt.ceil('min')  
...     )
```

Next, we isolate the January 2019 data:

```
>>> X_jan, y_jan = get_X_y(logs_2019, '2019-01', hackers_2019)
```

The classification report indicates that this model performs pretty well, but our recall for the positive class is lower than our target:

```
>>> from sklearn.metrics import classification_report
>>> print(classification_report(y_jan, model.predict(X_jan)))
          precision    recall  f1-score   support
False        1.00     1.00     1.00     44559
 True        1.00    0.64    0.78      44
accuracy                           1.00     44603
macro avg        1.00    0.82    0.89    44603
weighted avg     1.00     1.00     1.00     44603
```

Remember, our stakeholders have specified we must achieve a recall (TPR) of at least 70% and a precision of at least 85%. Let's write a function that will show us the ROC curve, confusion matrix, and precision-recall curve and indicate the region we need to be in as well as where we currently are:

```
>>> from ml_utils.classification import (
...     confusion_matrix_visual, plot_pr_curve, plot_roc
... )

>>> def plot_performance(model, X, y, threshold=None,
...                       title=None, show_target=True):
...     """
...     Plot ROC, confusion matrix, and precision-recall curve.
...
...     Parameters:
...         - model: The model object to use for prediction.
...         - X: The features to pass in for prediction.
...         - y: The actuals to evaluate the prediction.
...         - threshold: Value to use as when predicting
...                     probabilities.
...         - title: A title for the subplots.
...         - show_target: Whether to show the target regions.
...
...     Returns:
...         Matplotlib `Axes` object.
...     """
...     fig, axes = plt.subplots(1, 3, figsize=(20, 5))
```

```
...     # plot each visualization
...     plot_roc(y, model.predict_proba(X)[:,1], ax=axes[0])
...     confusion_matrix_visual(
...         Y,
...         model.predict_proba(X)[:,1] >= (threshold or 0.5),
...         class_labels=[False, True], ax=axes[1]
...     )
...     plot_pr_curve(
...         y, model.predict_proba(X)[:,1], ax=axes[2]
...     )
...
...     # show the target regions if desired
...     if show_target:
...         axes[0] \
...             .axvspan(0, 0.1, color='lightgreen', alpha=0.5)
...         axes[0] \
...             .axhspan(0.7, 1, color='lightgreen', alpha=0.5)
...         axes[0].annotate(
...             'region with acceptable\nFPR and TPR',
...             xy=(0.1, 0.7), xytext=(0.17, 0.65),
...             arrowprops=dict(arrowstyle='->')
...         )
...
...         axes[2] \
...             .axvspan(0.7, 1, color='lightgreen', alpha=0.5)
...         axes[2].axhspan(
...             0.85, 1, color='lightgreen', alpha=0.5
...         )
...         axes[2].annotate(
...             'region with acceptable\nprecision and recall',
...             xy=(0.7, 0.85), xytext=(0.3, 0.6),
...             arrowprops=dict(arrowstyle='->')
...         )
...
...     # mark the current performance
...     tn, fn, fp, tp = \
...         [int(x.get_text()) for x in axes[1].texts]
...     precision, recall = tp / (tp + fp), tp / (tp + fn)
...     fpr = fp / (fp + tn)
...
...     prefix = 'current performance' if not threshold \
...             else f'chosen threshold: {threshold:.2%}'
```

```

...
        axes[0].annotate(
...
            f'{prefix}\n- FPR={fpr:.2%}',
            f'\n- TPR={recall:.2%}',
            xy=(fpr, recall), xytext=(0.05, 0.45),
            arrowprops=dict(arrowstyle='->')
        )
        axes[2].annotate(
...
            f'{prefix}\n- precision={precision:.2%}',
            f'\n- recall={recall:.2%}',
            xy=(recall, precision), xytext=(0.2, 0.85),
            arrowprops=dict(arrowstyle='->')
        )
...
...
    if title: # show the title if specified
        plt.suptitle(title)
...
...
    return axes

```

Now, let's call the function to see how we are doing:

```

>>> axes = plot_performance(
...     model, X_jan, y_jan,
...     title='Stochastic Gradient Descent Classifier '
...         '(Tested on January 2019 Data)'
... )

```

Notice we are not currently meeting the specifications of our stakeholders; our performance is not in the target region:

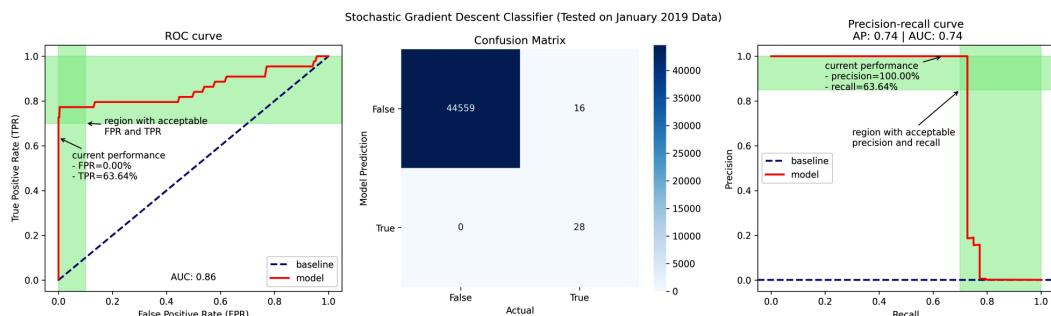


Figure 11.17 – Model performance with a default threshold

Our resulting recall (TPR) is 63.64%, which doesn't meet the goal of 70% or better. By default, when we use the `predict()` method, our probability threshold is 50%. If we are targeting a specific precision/recall or TPR/FPR region, we may have to change the threshold and use `predict_proba()` to get the desired performance.

The `ml_utils.classification` module contains the `find_threshold_roc()` and `find_threshold_pr()` functions, which will help us pick a threshold along the ROC curve or precision-recall curve, respectively. Since we are targeting a specific precision/recall region, we will use the latter. This function uses the `precision_recall_curve()` function from `scikit-learn` also, but instead of plotting the resulting precision and recall data, we use it to select the thresholds that meet our criteria:

```
from sklearn.metrics import precision_recall_curve

def find_threshold_pr(y_test, y_preds, *, min_precision,
                      min_recall):
    """
    Find the threshold to use with `predict_proba()` for
    classification based on the minimum acceptable precision
    and the minimum acceptable recall.

    Parameters:
        - y_test: The actual labels.
        - y_preds: The predicted labels.
        - min_precision: The minimum acceptable precision.
        - min_recall: The minimum acceptable recall.

    Returns: The thresholds that meet the criteria.
    """
    precision, recall, thresholds = \
        precision_recall_curve(y_test, y_preds)

    # precision and recall have one extra value at the end
    # for plotting -- needs to be removed to make a mask
    return thresholds[
        (precision[:-1] >= min_precision) &
        (recall[:-1] >= min_recall)
    ]
```

Important note

The notebook also shows an example of finding a threshold for a TPR/FPR goal. Our current target precision/recall happens to give the same threshold as targeting a TPR (recall) of at least 70% and an FPR of at most 10%.

Let's use this function to find a threshold that meets our stakeholders' specifications. We take the max of the probabilities that fall in the desired region to pick the least sensitive of the candidate thresholds:

```
>>> from ml_utils.classification import find_threshold_pr
>>> threshold = find_threshold_pr(
...     y_jan, model.predict_proba(X_jan)[:,1],
...     min_precision=0.85, min_recall=0.7
... ).max()
>>> threshold
0.0051533333839830974
```

This result tells us that we can reach the desired precision and recall if we flag results that have a 0.52% chance of being in the positive class. No doubt this seems like a very low probability, or that the model isn't sure of itself, but we can think about it this way: if the model thinks there is even a slight chance that the login activity is suspicious, we want to know. Let's see how our performance looks using this threshold:

```
>>> axes = plot_performance(
...     model, X_jan, y_jan, threshold=threshold,
...     title='Stochastic Gradient Descent Classifier '
...         '(Tested on January 2019 Data)'
... )
```

This threshold gives us a recall of 70.45%, satisfying our stakeholders. Our precision is in the acceptable range as well:

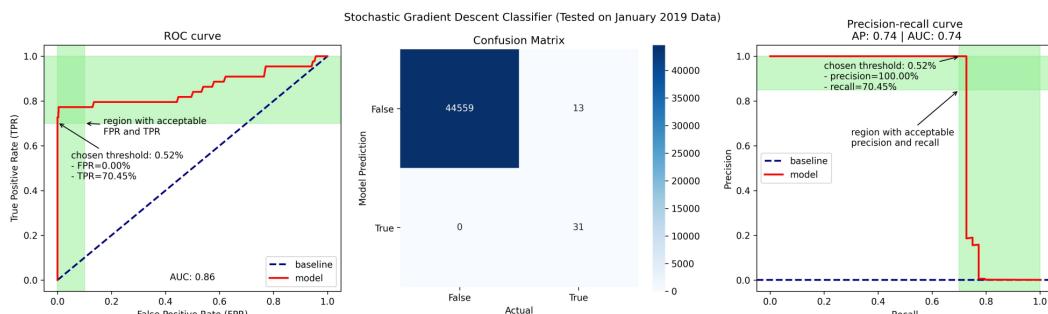


Figure 11.18 – Model performance using a custom threshold

Using the custom threshold, we have correctly identified another three cases, reducing our false negatives, which are very costly for the SOC. Here, this improvement didn't come at the cost of additional false positives, but remember, there is often a trade-off between reducing false negatives (**type II error**) and reducing false positives (**type I error**). In some cases, we have a very low tolerance for type I errors (the FPR must be very small), whereas in others, we are more concerned with finding all the positive cases (the TPR must be high). In information security, we have a low tolerance for false negatives because they are very costly; therefore, we will move forward with the custom threshold.

Important note

Sometimes, the requirements of a model's performance aren't feasible. It's important to maintain an open line of communication with stakeholders to explain the issues and discuss relaxing criteria when necessary.

Updating the model

Continuous updating will help the model adapt to changes in hacker behavior over time. Now that we have evaluated our January predictions, we can use them to update the model. To do so, we use the `partial_fit()` method and the labeled data for January, which will run a single epoch on the January data:

```
>>> model.partial_fit(X_jan, y_jan)
```

Our model has now been updated, so we can test its performance on the February data now. Let's grab the February data first:

```
>>> X_feb, y_feb = get_X_y(logs_2019, '2019-02', hackers_2019)
```

February had fewer attacks, but we caught a higher percentage of them (80%):

```
>>> print(classification_report(
...     y_feb, model.predict_proba(X_feb)[:,1] >= threshold
... ))
      precision    recall   f1-score   support
False        1.00     1.00     1.00     40248
 True        1.00     0.80     0.89      10
accuracy                           1.00     40258
macro avg        1.00     0.90     0.94     40258
weighted avg     1.00     1.00     1.00     40258
```

Let's look at the performance plots for February to see how they changed:

```
>>> axes = plot_performance(
...     model, X_feb, y_feb, threshold=threshold,
...     title='Stochastic Gradient Descent Classifier '
...         '(Tested on February 2019 Data)'
... )
```

Notice the area under the precision-recall curve has increased and more of the curve is in the target region:

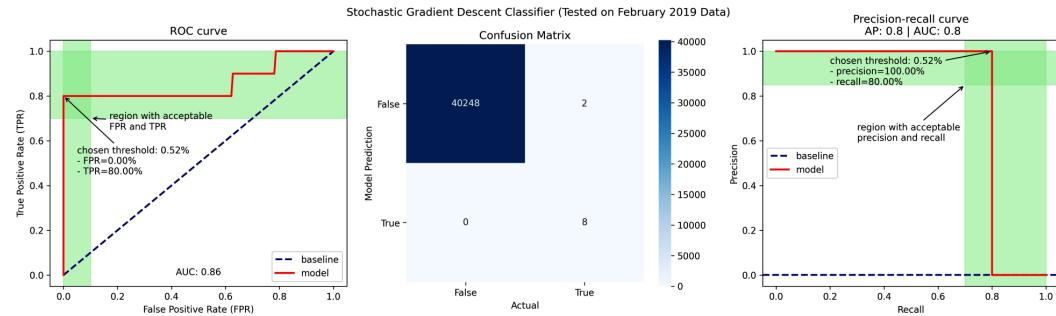


Figure 11.19 – Model performance after one update

Presenting our results

The SOC has finished up the March data. They want us to implement into our model the feedback they gave on our February predictions, and then make predictions for the March data for them to review. They will be evaluating our performance on each minute in March, using the classification report, ROC curve, confusion matrix, and precision-recall curve. It's time to put our model to the test.

First, we need to update our model for the February data:

```
>>> model.partial_fit(X_feb, y_feb)
```

Next, we grab the March data and make our predictions, using a threshold of 0.52%:

```
>>> X_march, y_march = \
...     get_X_y(logs_2019, '2019-03', hackers_2019)
>>> march_2019_preds = \
...     model.predict_proba(X_march)[:,1] >= threshold
```

Our classification report looks good. We have a recall of 76%, a precision of 88%, and a solid F_1 score:

```
>>> from sklearn.metrics import classification_report
>>> print(classification_report(y_march, march_2019_preds))
              precision    recall  f1-score   support
False          1.00     1.00     1.00    44154
 True          0.88     0.76     0.81      29
accuracy                           1.00    44183
macro avg       0.94     0.88     0.91    44183
weighted avg    1.00     1.00     1.00    44183
```

Now, let's see how the plots look:

```
>>> axes = plot_performance(
...     model, X_march, y_march, threshold=threshold,
...     title='Stochastic Gradient Descent Classifier '
...             '(Tested on March 2019 Data)'
... )
```

Our AUC for the ROC curve is slightly higher now, while it dropped for the precision-recall curve:

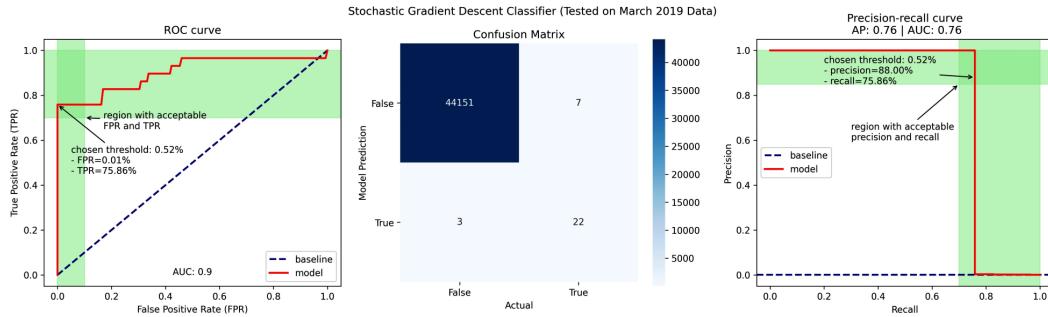


Figure 11.20 – Model performance after two updates

Further improvements

The SOC is pleased with our results and now wants us to provide predictions each minute. They have also promised to provide feedback within an hour. We won't implement this request here, but we will briefly discuss how we could go about this.

We have been using batch processing to update the model each month; however, in order to provide our stakeholders with what they want, we will need to shorten our feedback loop by performing the following actions:

- Running `predict_proba()` on our model every single minute and having the predictions sent to our stakeholders. This will require setting up a process to pass the logs one minute at a time to a preprocessing function, and then to the model itself.
- Delivering the results to our stakeholders via an agreed-upon medium.
- Updating the model with `partial_fit()` every hour using the feedback we receive from the stakeholders (once we have determined how to have them share this information with us).

After the aforementioned actions are implemented, all that remains is for us to put the model into production and determine the update and prediction frequencies everyone will be accountable for meeting.

Summary

In practice, detecting attackers isn't easy. Real-life hackers are much savvier than the ones in this simulation. Attacks are also much less frequent, creating a huge class imbalance. Building machine learning models that will catch everything just isn't possible. That is why it is so vital that we work with those who have domain knowledge; they can help us squeeze some extra performance out of our models by really understanding the data and its peculiarities. No matter how experienced we become with machine learning, we should never turn down help from someone who often works with the data in question.

Our initial attempts at anomaly detection were unsupervised while we waited for the labeled data from our subject matter experts. We tried LOF and isolation forest using `scikit-learn`. Once we received the labeled data and performance requirements from our stakeholders, we determined that the isolation forest model was better for our data.

However, we didn't stop there. Since we had just been given the labeled data, we tried our hand at supervised methods. We learned how to build baseline models using dummy classifiers and Naive Bayes. Then, we revisited logistic regression to see whether it could help us. Our logistic regression model performed well; however, since it used a closed-form solution to find the coefficients, we were unable to incorporate a feedback loop without retraining the model from scratch.

This limitation led us to build an online learning model, which is constantly updated. First, we had to make a subclass to allow pipelines to use the `partial_fit()` method. Then, we tried SGD classification with log loss. We were able to train on an entire year of data at once, and then update our model when we received new labeled data. This allows the model to adjust to changes in the distributions of the features over time.

In the next chapter, we will recap what we have learned throughout the book and introduce additional resources for finding data, as well as working with it in Python.

Exercises

Complete the following exercises for some practice with the machine learning workflow and exposure to some additional anomaly detection strategies:

1. A one-class SVM is another model that can be used for unsupervised outlier detection. Build a one-class SVM with the default parameters, using a pipeline with a `StandardScaler` object followed by a `OneClassSVM` object. Train the model on the January 2018 data, just as we did for the isolation forest. Make predictions on that same data. Count the number of inliers and outliers this model identifies.
2. Using the 2018 minutely data, build a k-means model with two clusters after standardizing the data with a `StandardScaler` object. With the labeled data in the `attacks` table in the SQLite database (`logs/logs.db`), see whether this model gets a good Fowlkes-Mallows score (use the `fowlkes_mallows_score()` function in `sklearn.metrics`).
3. Evaluate the performance of a random forest classifier for supervised anomaly detection. Set `n_estimators` to 100 and use the remaining defaults, including the prediction threshold. Train on January 2018 and test on February 2018.
4. The `partial_fit()` method isn't available with the `GridSearchCV` class. Instead, we can use its `fit()` method with a model that has a `partial_fit()` method (or a `PartialFitPipeline` object) to find the best hyperparameters in our search space. Then, we can grab the best model from the grid search (`best_estimator_`) and use `partial_fit()` on it. Try this with the `PassiveAggressiveClassifier` class from the `sklearn.linear_model` module and a `PartialFitPipeline` object. This online learning classifier is passive when it makes a correct prediction, but aggressive in correcting itself when it makes an incorrect prediction. Don't worry about selecting a custom threshold. Be sure to follow these steps:
 - a) Run a grid search using the January 2018 data for the initial training.
 - b) Grab the tuned model with the `best_estimator_` attribute.
 - c) Evaluate the best estimator with the February 2018 data.
 - d) Make updates with the February 2018 data.
 - e) Evaluate the final model on March through June 2018 data.

Further reading

Check out the following resources for more information on the topics covered in this chapter:

- *Deploying scikit-learn Models at Scale*: <https://towardsdatascience.com/deploying-scikit-learn-models-at-scale-f632f86477b8>
- *Local Outlier Factor for Anomaly Detection*: <https://towardsdatascience.com/local-outlier-factor-for-anomaly-detection-cc0c770d2ebe>
- *Model Persistence (from the scikit-learn user guide)*: https://scikit-learn.org/stable/modules/model_persistence.html
- *Novelty and Outlier Detection (from the scikit-learn user guide)*: https://scikit-learn.org/stable/modules/outlier_detection.html
- *Naive Bayes (from the scikit-learn user guide)*: https://scikit-learn.org/stable/modules/naive_bayes.html
- *Outlier Detection with Isolation Forest*: <https://towardsdatascience.com/outlier-detection-with-isolation-forest-3d190448d45e>
- *Passive Aggressive Algorithm (video explanation)*: <https://www.youtube.com/watch?v=uxGDwyPWNkU>
- *Python Context Managers and the "with" Statement*: <https://blog.ramosly.com/python-context-managers-and-the-with-statement-8f53d4d9f87>
- *Seeing Theory - Chapter 5, Bayesian Inference*: <https://seeing-theory.brown.edu/index.html#secondPage/chapter5>
- *SQLAlchemy — Python Tutorial*: <https://towardsdatascience.com/sqlalchemy-python-tutorial-79a577141a91>
- *Stochastic Gradient Descent (from the scikit-learn user guide)*: <https://scikit-learn.org/stable/modules/sgd.html>
- *Strategies to scale computationally: bigger data (from the scikit-learn user guide)*: https://scikit-learn.org/stable/computing/scaling_strategies.html
- *Unfair Coin Bayesian Simulation*: <https://github.com/xofbd/unfair-coin-bayes>

Section 5: Additional Resources

In this concluding section, we will recap everything we have covered in this book and provide you with some additional books, web resources, and documentation that you can use to dive further into various data science topics and practice your skills.

This section comprises the following chapter:

- *Chapter 12, The Road Ahead*

12

The Road Ahead

Throughout this book, we have covered a lot of material, and you are now capable of performing data analysis and machine learning tasks entirely in Python. We began our journey by learning about some introductory statistics and how to set up our environment for data science in Python. Then, we learned about the basics of using `pandas` and how to bring data into Python. With this knowledge, we were able to work with APIs, read from files, and query databases to grab data for our analyses.

After we collected our data, we learned how to perform data wrangling in order to clean up our data and get it into a usable format. Next, we learned how to work with time series and combine data from different sources as well as aggregate it. Once we had a good handle on data wrangling, we moved on to visualizations and used `pandas`, `matplotlib`, and `seaborn` to create a variety of plot types, and we also learned how to customize them.

Armed with this knowledge, we were able to tackle some real-world analyses by looking at the financial data for bitcoin and the FAANG stocks and trying to detect hackers attempting to authenticate to a web application. In addition, we learned how to build our own Python packages, write our own classes, and simulate data.

Finally, we got an introduction to machine learning using `scikit-learn`. We discussed how to build model pipelines, taking us from preprocessing the data through to model fitting. Afterward, we discussed how we can evaluate the performance of our models and how we can try to improve their performance. Our discussion of machine learning culminated in using machine learning models to detect hackers attempting to gain access to a web application through a brute-force attack.

Now that you have gained all this knowledge, it is important to nurture it so that you retain it. This means that you must practice every chance you get. This chapter provides the following resources for continuing your data science journey:

- Resources for finding data on a variety of topics
- Websites and services to practice working with data
- Coding challenges and educational content to improve your Python skills

Data resources

As with any skill, to get better we need to practice, which for us means we need to find data to practice on. There is no best dataset to practice with; rather, each person should find data that they are interested in exploring. While this section is by no means comprehensive, it contains resources for data from various topics in the hopes that everyone will find something they want to use.

Tip

Unsure of what kind of data to look for? What are some of the things you have wondered about related to a topic that you find interesting? Has data been collected on this topic, and can you access it? Let your curiosity guide you.

Python packages

Both `seaborn` and `scikit-learn` provide built-in sample datasets that you can experiment with in order to get more practice with the material we've covered in the book and to try out new techniques. These datasets are often very clean and thus easy to work with. Once you're comfortable with the techniques, you can move on to finding data using the other resources that are mentioned in the following sections, which will be more representative of real-world data.

Seaborn

Seaborn provides the `load_dataset()` function, which reads the data from a CSV file in a small GitHub repository for `seaborn` data. These datasets are the ones that are used in the `seaborn` documentation, so it is important to keep in mind that they may change. The data can be obtained from the repository directly at <https://github.com/mwaskom/seaborn-data>.

Scikit-learn

Scikit-learn includes a `datasets` module, which can be used to generate random datasets to test algorithms or to import certain datasets that are popular in the machine learning community. Be sure to check out the documentation for more information:

- **Generating random datasets for machine learning tasks:** <https://scikit-learn.org/stable/modules/classes.html#samples-generator>
- **Loading supported datasets:** <https://scikit-learn.org/stable/modules/classes.html#loaders>

There is also the `fetch_openml()` function in the `sklearn.datasets` module, which will fetch datasets by name from OpenML (<https://www.openml.org/>), which contains many free datasets for machine learning.

Searching for data

The following are a few places you can use to search for data on a variety of topics:

- **DataHub:** <https://datahub.io/search>
- **Google Dataset Search:** <https://datasetsearch.research.google.com/>
- **Open Data on Amazon Web Services:** <https://registry.opendata.aws/>
- **OpenML:** <https://www.openml.org>
- **SNAP library of datasets collected by Stanford University:** <https://snap.stanford.edu/data/index.html>
- **UCI Machine Learning Repository:** <http://archive.ics.uci.edu/ml/index.php>

APIs

We saw how great working with APIs can be for gathering data; the following are some APIs for gathering data that may be of interest to you:

- **Facebook API:** <https://developers.facebook.com/docs/graph-api>
- **NOAA Climate Data API:** <https://www.ncdc.noaa.gov/cdo-web/webservices/v2>
- **NYTimes API:** <https://developer.nytimes.com/>
- **OpenWeatherMap API:** <https://openweathermap.org/api>

- **Twitter API:** <https://developer.twitter.com/en/docs>
- **USGS Earthquake API:** <https://earthquake.usgs.gov/fdsnws/event/1/>

Websites

This section contains selected data resources across various topics that can be accessed through a website. Obtaining the data for an analysis may be as simple as downloading a CSV file or it may require parsing HTML with pandas. If you must resort to scraping the page (make sure you have tried the ways we discussed in this book first), be sure that you aren't violating the terms of use of the website.

Finance

We worked with finance data several times throughout this book. If you are interested in further financial analysis, in addition to the `pandas_datareader` package we discussed in *Chapter 7, Financial Analysis – Bitcoin and the Stock Market*, consult the following resources:

- **Google Finance:** <https://google.com/finance>
- **NASDAQ historical stock prices:** <https://www.nasdaq.com/market-activity/quotes/historical>
- **Quandl:** <https://www.quandl.com>
- **Yahoo! Finance:** <https://finance.yahoo.com>

Government data

Government data is often open to the public. The following resources contain data provided by some governments:

- **European Union open data:** <http://data.europa.eu/euodp/en/data>
- **NASA:** <https://nasa.github.io/data-nasa-gov-frontpage/>
- **NYC data:** <https://opendata.cityofnewyork.us/data/>
- **UK government data:** <https://data.gov.uk/>
- **UN data:** <http://data.un.org/>
- **US census data:** <https://census.gov/data.html>
- **US government data:** <https://www.data.gov/>

Health and economy

Economic, medical, and social data from around the world is available at the following websites:

- **Gapminder:** <https://www.gapminder.org/data/>
- **Health Data:** <https://healthdata.gov/search/type/dataset>
- **World Health Organization:** <https://www.who.int/data/gho>

The following are additional resources for data on the COVID-19 pandemic:

- **Coronavirus (COVID-19) data in the United States (NYTimes):** <https://github.com/nytimes/covid-19-data>
- **COVID-19 data repository by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University:** <https://github.com/CSSEGISandData/COVID-19>
- **COVID-19 pandemic (ECDC):** <https://www.ecdc.europa.eu/en/covid-19-pandemic>
- **Open COVID-19 datasets:** <https://researchdata.wisc.edu/open-covid-19-datasets/>

Social networks

For those interested in text-based data or graph data, check out the following resources on social networks:

- **List of Twitter data resources:** <https://github.com/shaypal5/awesome-twitter-data>
- **Social network data:** <https://snap.stanford.edu/data/ego-Facebook.html>

Sports

For the sports lover, check out the following websites, which provide databases and web pages for statistics on all your favorite players:

- **Baseball database (practice working with a DB):** <http://www.seanlahman.com/baseball-archive/statistics/>
- **Baseball player statistics:** <https://www.baseball-reference.com/players/>

- **Basketball player statistics:** <https://www.basketball-reference.com/players/>
- **Football (American) player statistics:** <https://www.pro-football-reference.com/players/>
- **Football (soccer) statistics:** <https://www.whoscored.com/Statistics>
- **Hockey player statistics:** <https://www.hockey-reference.com/players/>

Miscellaneous

The following resources vary in topic, but be sure to check these out if nothing has piqued your interest so far:

- **Amazon reviews data:** <https://snap.stanford.edu/data/web-Amazon.html>
- **Data extracted from Wikipedia:** <https://wiki.dbpedia.org/develop/datasets>
- **Google Trends:** <https://trends.google.com/trends/>
- **Movies from MovieLens:** <https://grouplens.org/datasets/movielens/>
- **Yahoo Webscope (reference library of datasets):** <https://webscope.sandbox.yahoo.com/>

Practicing working with data

Throughout this book, we have worked with various datasets from different sources with step-by-step instructions. It doesn't have to stop here, though. This section is dedicated to some resources that can be used to continue with guided instruction and, eventually, work toward building a model for a predefined problem.

Kaggle (<https://www.kaggle.com/>) offers content for learning data science, datasets for exploration that are shared by members of the community, and competitions that have been posted by companies—perhaps the Netflix recommendation contest sounds familiar (<https://www.kaggle.com/netflix-inc/netflix-prize-data>)? These contests are a great way for you to practice your machine learning skills and become more visible in the community (especially to potential employers).

Important note

Kaggle isn't the only place you can participate in data science competitions. Some additional ones are listed at <https://towardsdatascience.com/top-competitive-data-science-platforms-other-than-kaggle-2995e9dad93c>.

DataCamp (<https://www.datacamp.com/>), while not entirely free, provides various data science courses in Python. They include instructional videos and fill-in-the-blank coding practice problems so that you can build up your understanding of the topics.

Python practice

We have seen throughout this book that working with data in Python isn't just pandas, matplotlib, and numpy; there are many ways our workflow can benefit from us being strong Python programmers in general. With strong Python skills, we can build web applications with Flask, make requests of an API, efficiently iterate over combinations or permutations, and find ways to speed up our code. While this book didn't focus on honing these skills directly, here are some free resources for practicing with Python and thinking like a programmer:

- **HackerRank:** <https://www.hackerrank.com>
- **Codewars:** <https://www.codewars.com>
- **LeetCode:** <https://www.leetcode.com>
- **CodinGame:** <https://www.codingame.com>

While not free, **Python Morsels** (<https://www.pythonomorsels.com/>) provides weekly Python exercises that will help you learn to write more Pythonic code and get more familiar with the Python standard library. Exercises vary in difficulty but can be set to a higher or lower difficulty as needed.

Another great resource is **Pramp** (<https://www.pramp.com>), which lets you practice for a programming interview with a randomly assigned peer. Your peer will interview you with a random question and evaluate how you approach the interview, your code, and how well you explain yourself. After 30 minutes, it's your turn to interview your peer.

Khan Academy (<https://www.khanacademy.org/>) can be a great resource for learning more about a subject. If you want a primer on computer science algorithms or some of the mathematics behind machine learning algorithms (such as linear algebra and calculus), then this is a great place to start.

Lastly, **LinkedIn Learning** (<https://www.linkedin.com/learning/>) has many video courses on a wide range of topics, including Python, data science, and machine learning. New users get a free month-long trial. Consider taking the *Learning the Python 3 Standard Library* course (<https://www.linkedin.com/learning/learning-the-python-3-standard-library>) to level up your Python skills; as we saw throughout this book, a solid command of the standard library helps us write more concise and efficient code.

Summary

This chapter provided you with many places where you can find datasets across myriad topics. In addition, you also learned about various websites where you can take courses and work through tutorials, practice machine learning, and improve your Python skills. It's important to keep your skills sharp and stay curious, so, for whatever interests you, look for data and perform your own analyses. These are things you can put on your GitHub account as your data portfolio.



Thank you for reading this book! I hope you got just as much out of it as these two data-analyzing pandas.

Exercises

The exercises in this chapter are open-ended—no solutions are provided. They are meant to give you some ideas so that you can get started on your own:

1. Practice machine learning classification by participating in the Titanic challenge on Kaggle at <https://www.kaggle.com/c/titanic>.
2. Practice machine learning regression techniques by participating in the housing prices challenge on Kaggle at <https://www.kaggle.com/c/house-prices-advanced-regression-techniques>.
3. Perform an analysis on something that interests you. Some interesting ideas include the following:
 - a) *Predicting likes on Instagram*: <https://towardsdatascience.com/predict-the-number-of-likes-on-instagram-a7ec5c020203>
 - b) *Analyzing delays of NJ transit trains*: <https://medium.com/@pranavbadami/how-data-can-help-fix-nj-transit-c0d15c0660fe>
 - c) *Using visualizations to solve data science problems*: <https://towardsdatascience.com/solving-a-data-science-challenge-the-visual-way-355cfabcb1c5>
4. Complete five challenges across any one of the sites in the *Python practice* section of this chapter. For example, you can try the following challenges:
 - a) *Finding two numbers that add to a specific sum exactly*: <https://leetcode.com/problems/two-sum/>
 - b) *Validating credit card numbers*: <https://www.hackerrank.com/challenges/validating-credit-card-number/problem>

Further reading

You can consult the following blogs and articles to stay up to date with Python and data science:

- *Armin Ronacher's blog (author of Flask)*: <http://lucumr.pocoo.org/>
- *Data Science Central*: <http://www.datasciencecentral.com/>
- *Data Science Topic on Medium*: <https://medium.com/topic/data-science>
- *Kaggle blog*: <https://medium.com/kaggle-blog>
- *KD Nuggets*: <http://www.kdnuggets.com/websites/blogs.html>
- *Machine Learning topic on Medium*: <https://medium.com/topic/machine-learning>
- *Planet Python*: <https://planetpython.org/>
- *Programming topic on Medium*: <https://medium.com/topic/programming>
- *Python tips*: <http://book.pythontips.com/en/latest/index.html>
- *Python 3 Module of the Week*: <https://pymotw.com/3/>
- *Towards Data Science*: <https://towardsdatascience.com/>
- *Trey Hunner's blog (creator of Python Morsels)*: <https://treyhunner.com/blog/archives/>

The following resources contain information for learning how to build custom scikit-learn classes:

- *Building scikit-learn transformers*: <https://dreisbach.us/articles/building-scikit-learn-compatible-transformers/>
- *Creating your own estimator in scikit-learn*: <http://danielhnyk.cz/creating-your-own-estimator-scikit-learn/>
- *Scikit-learn BaseEstimator*: <https://scikit-learn.org/stable/modules/generated/sklearn.base.BaseEstimator.html>
- *Scikit-learn rolling your own estimator*: <https://scikit-learn.org/stable/developers/develop.html#developing-scikit-learn-estimators>
- *Scikit-learn TransformerMixin*: <https://scikit-learn.org/stable/modules/generated/sklearn.base.TransformerMixin.html#sklearn.base.TransformerMixin>

Cheat sheets for coding with Python's data science stack can be found here:

- *Jupyter Notebook Cheat Sheet*: https://s3.amazonaws.com/assets.datacamp.com/blog_assets/Jupyter_Notebook_Cheat_Sheet.pdf
- *Jupyter Notebook Keyboard Shortcuts*: https://www.cheatography.com/weidadeyue/cheat-sheets/jupyter-notebook/pdf_bw/
- *Matplotlib Cheat Sheet*: https://s3.amazonaws.com/assets.datacamp.com/blog_assets/Python_Matplotlib_Cheat_Sheet.pdf
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- *Pandas Cheat Sheet*: http://pandas.pydata.org/Pandas_Cheat_Sheet.pdf
- *Scikit-Learn Cheat Sheet*: https://s3.amazonaws.com/assets.datacamp.com/blog_assets/Scikit_Learn_Cheat_Sheet_Python.pdf

Cheat sheets for machine learning algorithms, mathematics, probability, and statistics can be found here:

- *Calculus Cheat Sheet*: <https://ml-cheatsheet.readthedocs.io/en/latest/calculus.html>
- *Linear Algebra in 4 Pages*: https://minireference.com/static/tutorials/linear_algebra_in_4_pages.pdf
- *Probability and Statistics Cheat Sheet*: http://web.mit.edu/~covooss/Public/usabo/stats_handout.pdf
- *15 Statistical Hypothesis Tests in Python (Cheat Sheet)*: <https://machinelearningmastery.com/statistical-hypothesis-tests-in-python-cheat-sheet/>

For additional resources on machine learning algorithms, linear algebra, calculus, probability, and statistics, you can refer to the following:

- *An Interactive Guide to the Fourier Transform*: <https://betterexplained.com/articles/an-interactive-guide-to-the-fourier-transform/>
- *Introduction to Probability* by Joseph Blitzstein and Jessica Hwang: <https://www.amazon.com/Introduction-Probability-Chapman-Statistical-Science/dp/1138369918>
- *An Introduction to Statistical Learning* by Gareth James, Daniela Witten, Trevor Hastie, and Robert Tibshirani: <https://www.statlearning.com/>
- *Fourier Transforms (scipy.fft)*: <https://docs.scipy.org/doc/scipy/reference/tutorial/fft.html>
- *Find likeliest periodicity for time series with numpy's Fourier Transform? (StackOverflow question)*: <https://stackoverflow.com/questions/44803225/find-likeliest-periodicity-for-time-series-with-numpys-fourier-transform>
- *Numerical Computing is Fun (GitHub)*: <https://github.com/eka-foundation/numerical-computing-is-fun>
- *Probabilistic Programming and Bayesian Methods for Hackers (GitHub)*: <https://github.com/CamDavidsonPilon/Probabilistic-Programming-and-Bayesian-Methods-for-Hackers>
- *Seeing Theory (A visual introduction to probability and statistics)*: <https://seeing-theory.brown.edu/index.html>
- *Think Stats: Exploratory Data Analysis in Python*: <http://greenteapress.com/thinkstats2/html/index.html>

Miscellaneous reading on Python and programming in general can be found here:

- *Defining Custom Magics (IPython)*: <https://ipython.readthedocs.io/en/stable/config/custommagics.html>
- *Flask Tutorial (Build Web Applications in Python)*: <https://flask.palletsprojects.com/en/1.1.x/tutorial/>
- *IPython Tutorial*: <https://ipython.readthedocs.io/en/stable/interactive/>
- *Programming Best Practices*: <https://thefullstack.xyz/dry-yagni-kiss-tdd-soc-bdfu>

Relevant MOOCs and videos can be found here:

- *Advanced Optimization (Harvard)*: <https://online-learning.harvard.edu/course/advanced-optimization>
- *Linear Algebra – Foundations to Frontiers (edX)*: <https://www.edx.org/course/linear-algebra-foundations-to-frontiers>
- *Machine Learning (Coursera with Andrew Ng)*: <https://www.coursera.org/learn/machine-learning>
- *Mathematics for Machine Learning (Coursera)*: <https://www.coursera.org/specializations/mathematics-machine-learning>
- *Statistics 110 (Harvard) on YouTube*: <https://www.youtube.com/playlist?list=PL2SOU6wwxB0uwwH80KTQ6ht66KWxbzTlO>
- *Statistical Learning (Stanford)*: <https://online.stanford.edu/courses/sohs-ystatslearning-statistical-learning>

The following books are helpful for getting experience with many different facets of the Python language:

- *Automate the Boring Stuff with Python by Al Sweigart*: <https://automatetheboringstuff.com/>
- *Learn Python 3 the Hard Way by Zed A. Shaw*: <https://learnpythonthehardway.org/python3/preface.html>

Python machine learning books and training resources can be found here:

- *Hands-on Machine Learning with Scikit-Learn and TensorFlow Jupyter Notebooks*: <https://github.com/ageron/handson-ml>
- *Introduction to Machine Learning with Python: A Guide for Data Scientists by Andreas C. Müller and Sarah Guido*: <https://www.amazon.com/Introduction-Machine-Learning-Python-Scientists/dp/1449369413>
- *ML training repositories from scikit-learn core developer Andreas Müller (training given at conferences)*: <https://github.com/amueller?tab=repositories&q=ml-training&type=&language=&sort=>
- *Python Machine Learning – Third Edition by Sebastian Raschka and Vahid Mirjalili*: <https://www.packtpub.com/product/python-machine-learning-third-edition/9781789955750>

The following resources introduce the concepts of bias and fairness in machine learning models as well as tools for mitigating bias:

- *AI Fairness 360 (IBM)*: <https://developer.ibm.com/technologies/artificial-intelligence/projects/ai-fairness-360/>
- *Weapons of Math Destruction by Cathy O'Neil*: <https://www.amazon.com/Weapons-Math-Destruction-Increases-Inequality/dp/0553418815>
- *What-If Tool (Google)*: <https://pair-code.github.io/what-if-tool/>

Resources for getting started with interactive and animated visualizations can be found here:

- *Getting Started with Holoviews*: <https://coderzcolumn.com/tutorials/data-science/getting-started-with-holoviews-basic-plotting>
- *How to Create Animated Graphs in Python*: <https://towardsdatascience.com/how-to-create-animated-graphs-in-python-bb619cc2dec1>
- *Interactive Data Visualization in Python with Bokeh*: <https://realpython.com/python-data-visualization-bokeh/>
- *PyViz Tutorial*: <https://pyviz.org/tutorials/index.html>

Solutions

Solutions for each chapter's exercises can be found at <https://github.com/stefmolin/Hands-On-Data-Analysis-with-Pandas-2nd-edition/tree/master/solutions> in their respective folders.

Appendix

Data analysis workflow

The following diagram depicts a generalized data analysis workflow from data collection and processing through drawing conclusions and deciding next steps:

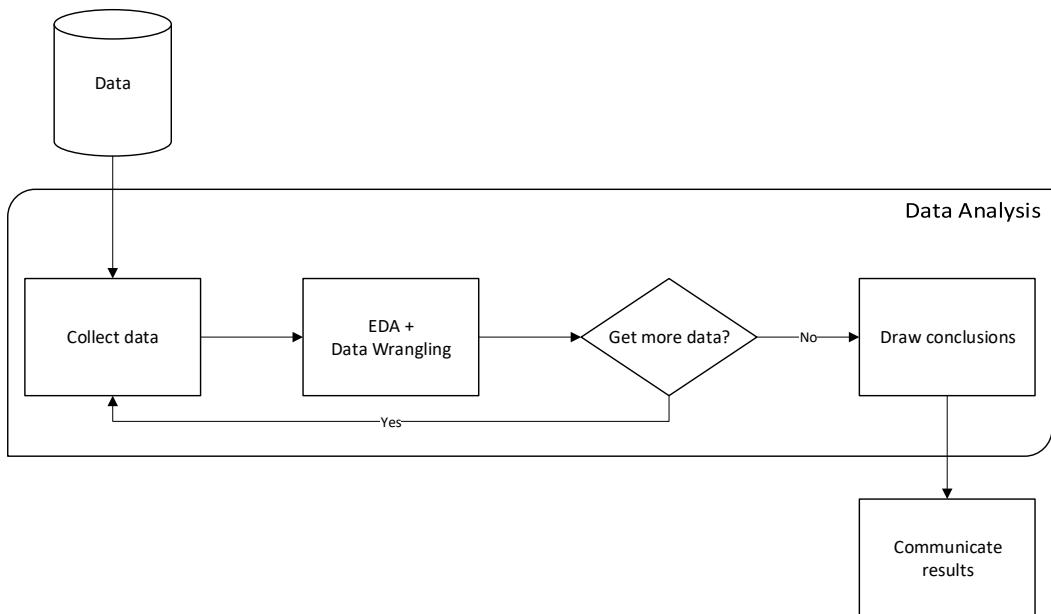


Figure 1 – Generalized data analysis workflow

Choosing the appropriate visualization

When creating a data visualization, it is paramount that we select an appropriate plot type; the following diagram can be used to help select the proper visualization:

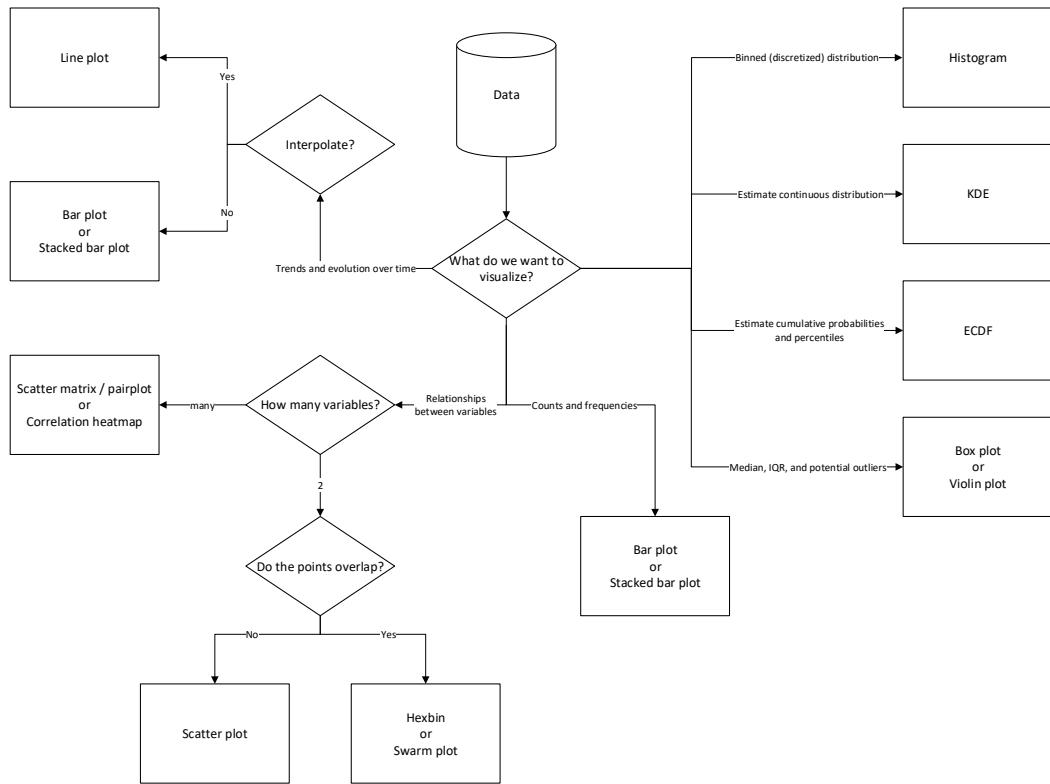


Figure 2 – Flow chart for choosing an appropriate visualization

Machine learning workflow

The following diagram summarizes the workflow for building machine learning models from data collection and data analysis through training and evaluating the model:

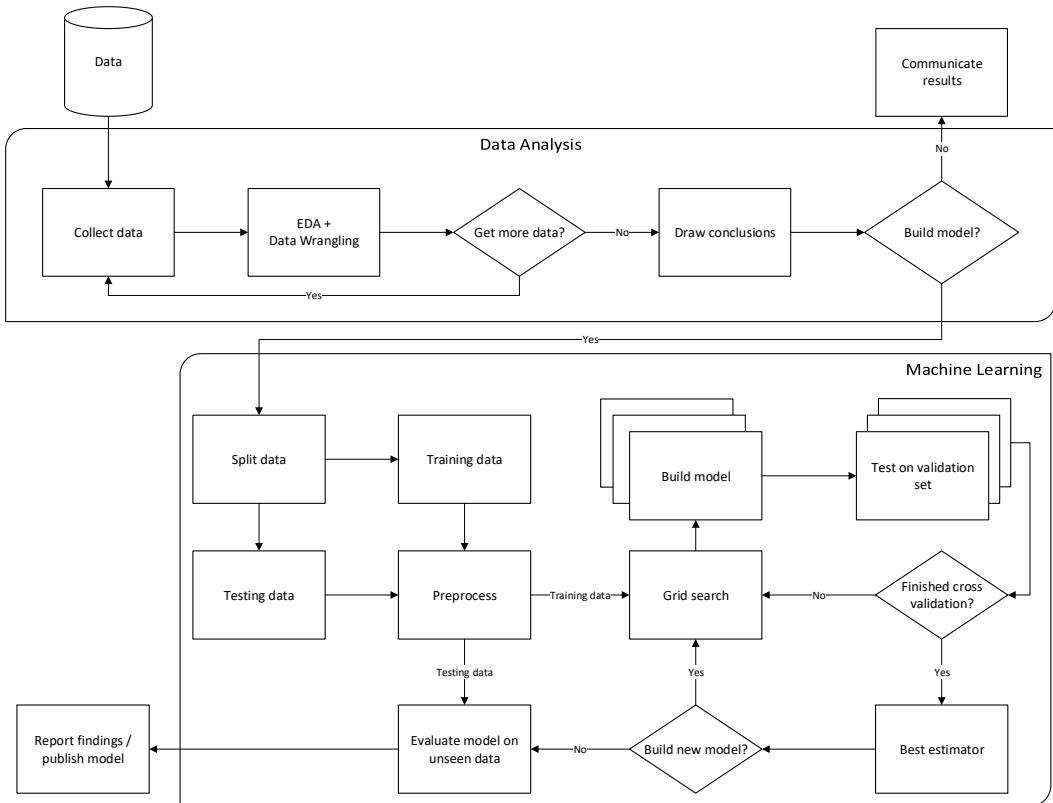


Figure 3 – Overview of the process of building a machine learning model



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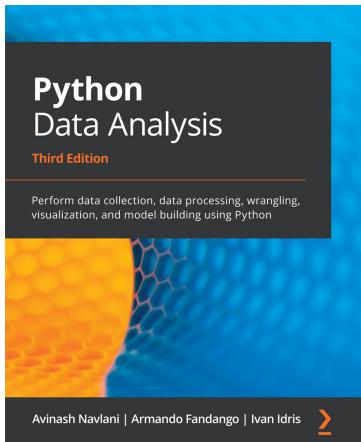
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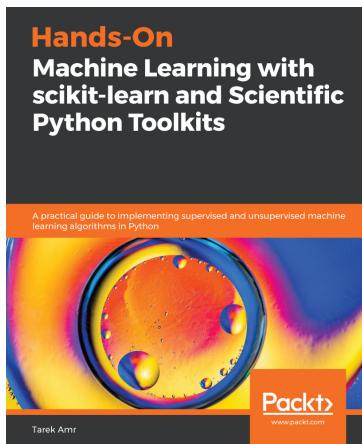


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