1

Jupyter Fundamentals

Lesson objectives

In this lesson, you will do the following:

- Learn what a Jupyter Notebook is and why it's useful for data analysis
- See basic Jupyter Notebook usage and features
- Be introduced to Python data science libraries
- Perform exploratory data analysis

Logistics

Start with a friendly and brief introduction of yourself. List your educational qualifications and your experience in teaching and working with the technology, both as a user and teacher. Give a brief summary of how this class will be conducted: slide presentation coupled with lecture and activities. Mention any attendance or other relevant policies now.

Discussion

Ask the students what the difference is between data analysis and data analytics.

Answer

Data analytics is a subtype of data analysis which requires tools for data analysis.

Introduction

LESSON TIME
3H 30M

Jupyter Notebooks are one of the most important tools for data scientists using Python. This is because they're an ideal environment for developing reproducible data analysis pipelines. Data can be loaded, transformed, and modeled all inside a single Notebook, where it's quick and easy to test out code and explore ideas along the way. Furthermore, all of this can be documented "inline" using formatted text, so you can make notes for yourself or even produce a structured report.

Other comparable platforms - for example, RStudio or Spyder - present the user with multiple windows, which promote arduous tasks such as copy and pasting code around and rerunning code that has already been executed. These tools also tend to involve **Read Eval Prompt Loops** (**REPLs**) where code is run in a terminal session that has saved memory. This type of development environment is bad for reproducibility and not ideal for development either. Jupyter Notebooks solve all these issues by giving the user a single window where code snippets are executed and outputs are displayed inline. This lets users develop code efficiently and allows them to look back at previous work for reference, or even to make alterations.

We'll start the lesson by explaining exactly what Jupyter Notebooks are and continue to discuss why they are so popular among data scientists. Then, we'll open a Notebook together and go through some exercises to learn how the platform is used. Finally, we'll dive into our first analysis and perform an exploratory analysis in *Topic A: Basic functionality and features*.

Discussion

Have any students used Jupyter Notebooks before? What did you use them for?

Answers

- Testing code snippets during development of a Python script
- Experimenting with a new external Python library
- Making bar plots from a CSV file instead of using Excel
- Merging tables on shared data series
- Breaking down and exploring a JSON data structure

Topic A: Basic Functionality and Features

00M

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In this section, we first demonstrate the usefulness of Jupyter Notebooks with examples and through discussion. Then, in order to cover the fundamentals of Jupyter Notebooks for beginners, we'll see the basic usage in terms of launching and interacting with the platform. For those who have used Jupyter Notebooks before, this will be mostly review; however, you will certainly see new things in this topic as well.

Subtopic A: What is a Jupyter Notebook and Why is it Useful?

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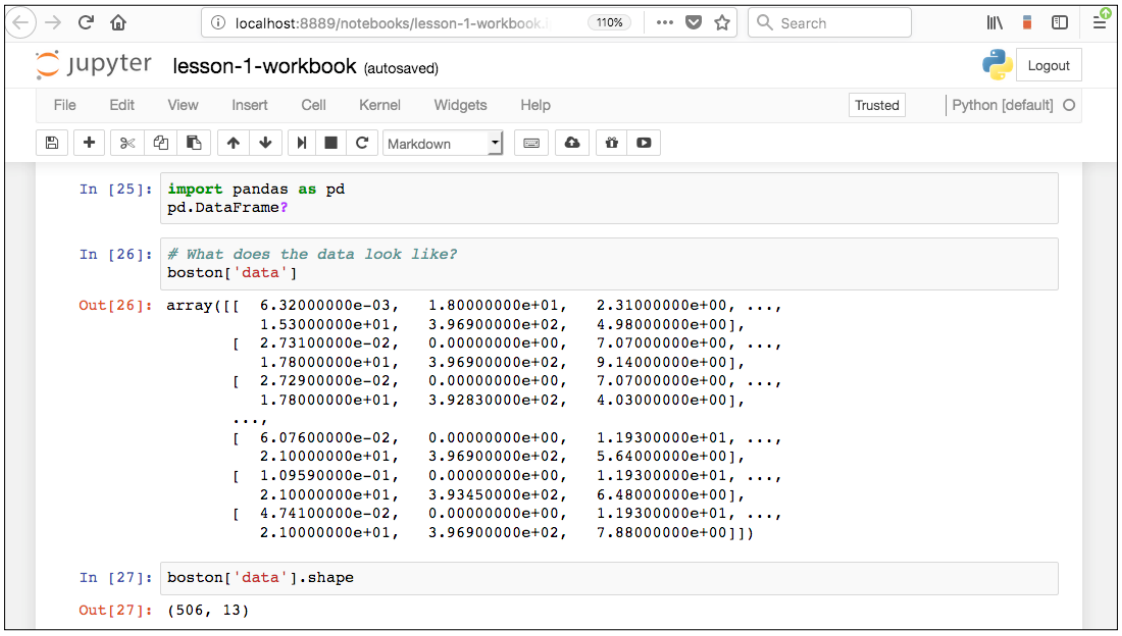
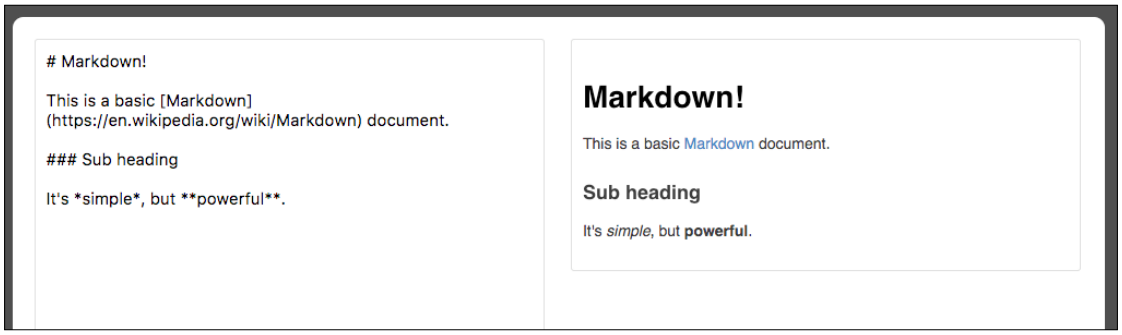
Jupyter Notebooks are locally run web applications which contain live code, equations, figures, interactive apps, and Markdown text. The standard language is Python, and that's what we'll be using for this course; however, note that a variety of alternatives are supported. This includes the other dominant data science language, R:



Those familiar with R will know about R Markdown. Markdown documents allow for Markdown-formatted text to be combined with executable code. Markdown is a simple language used for styling text on the web. For example, most GitHub repositories have a `README.md` Markdown file. This format is useful for basic text formatting. It's comparable to HTML but allows for much less customization. Commonly used symbols in Markdown include hashes (`#`) to make text into a heading, square and round brackets to insert hyperlinks, and stars to create italicized or bold text:



Having seen the basics of Markdown, let's come back to R Markdown, where Markdown text can be written alongside executable code. Jupyter Notebooks offer equivalent functionality for Python, although, as we'll see, they function quite differently than R Markdown documents. For example, R Markdown assumes you are writing Markdown unless otherwise specified, whereas Jupyter Notebooks assume you are inputting code. This makes it more appealing to use Jupyter Notebooks for rapid development and testing.

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From a data science perspective, there are two primary types for a Jupyter Notebook depending on how they are used: lab-style and deliverable.

Lab-style Notebooks are meant to serve as the programming analog of research journals. These should contain all the work you've done to load, process, analyze, and model the data. The idea here is to document everything you've done for future reference, so it's usually not advisable to delete or alter previous lab-style Notebooks. It's also a good idea to accumulate multiple date-stamped versions of the Notebook as you progress through the analysis, in case you want to look back at previous states.

Deliverable Notebooks are intended to be presentable and should contain only select parts of the lab-style Notebooks. For example, this could be an interesting discovery to share with your colleagues, an in-depth report of your analysis for a manager, or a summary of the key findings for stakeholders.

In either case, an important concept is reproducibility. If you've been diligent in documenting your software versions, anyone receiving the reports will be able to rerun the Notebook and compute the same results as you did. In the scientific community, where reproducibility is becoming increasingly difficult, this is a breath of fresh air.

Note

Open a terminal window and navigate to the root directory where the lesson files are contained. Start up a Jupyter Notebook with the commands given in the following exercise. Students should be following along on their own computers.

If you wish, you can instruct students to upgrade their version of Jupyter using the following:

```
conda update jupyter
```

This will only work if the student has installed Anaconda. Prepared students should already have the correct version installed. If you have a large class of students then consider not having them update, as things can go wrong.

Subtopic B: Navigating the Platform

Now we are going to open up a Jupyter Notebook and start to learn the interface. Here we will assume you have no prior knowledge of the platform and go over the basic usage.

Topic objectives

In this topic, you will:

- Be able to open, interact with, and shut down a Jupyter Notebook
- Use basic components of the interface to edit and navigate a Notebook instance

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Exercise

Introducing Jupyter Notebooks

1. Navigate to the companion material directory in the terminal.

Note

On Unix machines such as Mac or Linux, command-line navigation can be done using `ls` to display directory contents and `cd` to change directories.

On Windows machines, instead use `dir` to display directory contents and use `cd` to change directories. If, for example, you want to change the drive from `C:` to `D:`, you should execute `d:` to change drives.

2. Start a new local Notebook server here by typing the following into the terminal:

```
jupyter notebook
```

A new window or tab of your default browser will open the Notebook Dashboard to the working directory. Here you will see a list of folders and files contained therein.

3. Click on a folder to navigate to that particular path and open a file by clicking on it. Although its main use is editing IPYNB Notebook files, Jupyter functions as a standard text editor as well.
4. Reopen the terminal window used to launch the app.
   We can see the `NotebookApp` being run on a local server. In particular, you should see a line like this:

```
[I 20:03:01.045 NotebookApp] The Jupyter
Notebook is running at: http://localhost:8888/
?token=e915bb06866f19ce462d959a9193a94c7c088e81765f9d8a
```

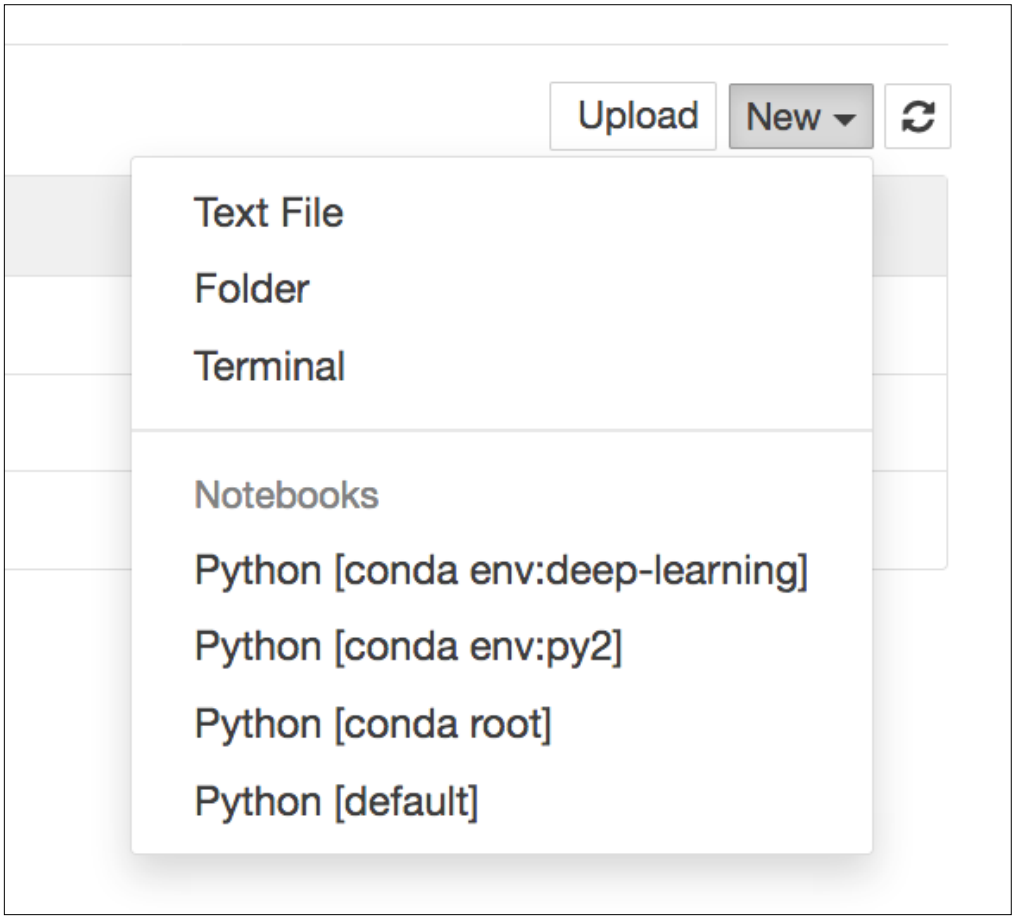
   Going to that HTTP address will load the app in your browser window, as was done automatically when starting the app. Closing the window does not stop the app; this should be done from the terminal by typing *Ctrl* + *C*.
5. Close the app by typing *Ctrl* + *C* in the terminal. You may also have to confirm by entering `y`. Close the web browser window as well.
6. When loading the `NotebookApp`, there are various options available to you. In the terminal, see the list of available options by running the following:

```
jupyter notebook --help
```

7. One such option is to specify a specific port.
   Open a `NotebookApp` at local port `9000` by running the following:

```
jupyter notebook --port 9000
```

8. The primary way to create a new Jupyter Notebook is from the Jupyter Dashboard. Click **New** in the upper-right corner and select a kernel from the drop-down menu (that is, select something in the **Notebooks** section):



Kernels provide programming language support for the Notebook. If you have installed Python with Anaconda, that version should be the default kernel. Conda virtual environments will also be available here.

Note

Virtual environments are a great tool for managing multiple projects on the same machine. Each virtual environment may contain a different version of Python and external libraries. Python has built-in virtual environments; however, the Conda virtual environment integrates better with Jupyter Notebooks and boasts other nice features. The documentation is available at `https://conda.io/docs/user-guide/tasks/manage-environments.html`.

Discussion

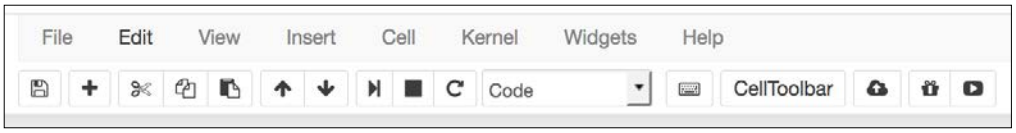
Ask the students whether they have used Markdown before. What for?

Answer

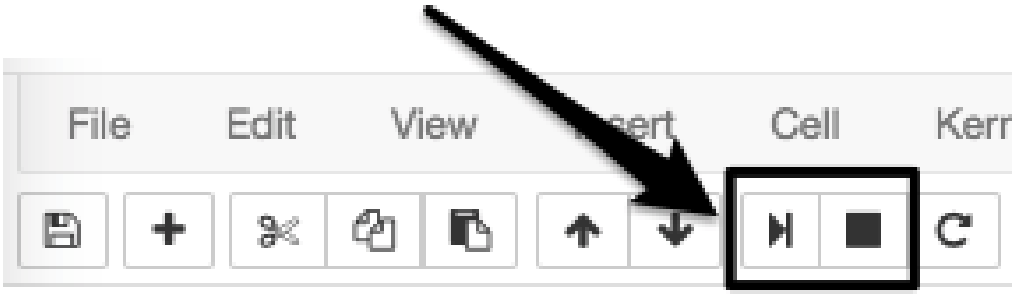
Markdown is a simple language for adding formatting to plain text. Some common formatting symbols are the hash for headings (#, ##, ###), stars or underscores for bold/italicized text, and dashes for bullet points. A common use case is for `README.md` files, for instance on GitHub.

9. With the newly created blank Notebook, click in the top cell and type `print('hello world')`, or any other code snippet that writes to the screen. Execute it by clicking in the cell and pressing *Shift* + *Enter*, or by selecting **Run Cell** in the **Cell** menu.
   Any `stdout` or `stderr` output from the code will be displayed beneath as the cell runs. Furthermore, the string representation of the object written in the final line will be displayed as well. This is very handy, especially for displaying tables, but sometimes we don't want the final object to be displayed. In such cases, a semicolon (`;`) can be added to the end of the line to suppress the display.

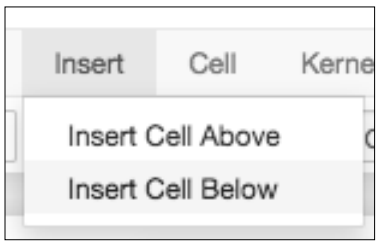
   New cells expect and run code input by default; however, they can be changed to render Markdown instead.
10. Click into an empty cell and change it to accept Markdown-formatted text. This can be done from the drop-down menu icon in the toolbar or by selecting **Markdown** from the **Cell** menu. Write some text in here (any text will do), making sure to utilize Markdown formatting symbols such as `#`.
11. Focus on the toolbar at the top of the Notebook:



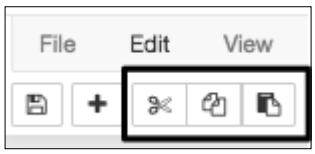
There is a Play icon in the toolbar, which can be used to run cells. As we'll see later, however, it's handier to use the keyboard shortcut *Shift* + *Enter* to run cells. Right next to this is a Stop icon, which can be used to stop cells from running. This is useful, for example, if a cell is taking too long to run:

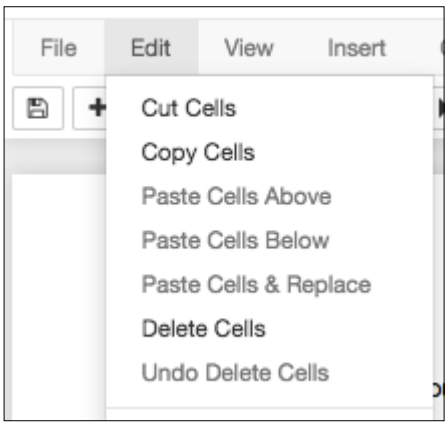


New cells can be manually added from the **Insert** menu:

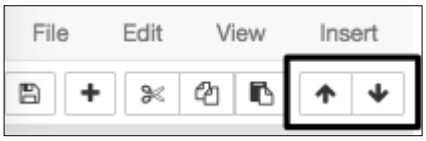


Cells can be copied, pasted, and deleted using icons or by selecting options from the **Edit** menu:

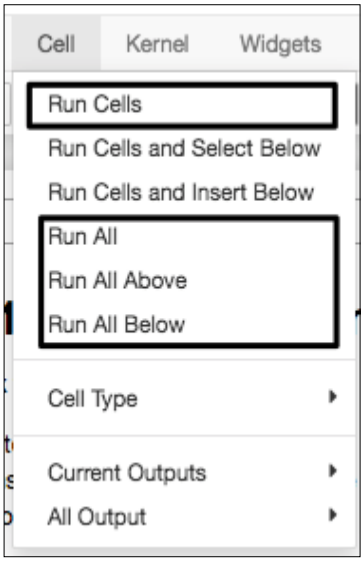




Cells can also be moved up and down this way:



There are useful options under the **Cell** menu to run a group of cells or the entire Notebook:



12. Experiment with the toolbar options to move cells up and down, insert new cells, and delete cells.
    An important thing to understand about these Notebooks is the shared memory between cells. It's quite simple: every cell existing on the sheet has access to the global set of variables. So, for example, a function defined in one cell could be called from any other, and the same applies to variables. As one would expect, anything within the scope of a function will not be a global variable and can only be accessed from within that specific function.
13. Open the **Kernel** menu to see the selections. The **Kernel** menu is useful for stopping script executions and restarting the Notebook if the kernel dies. Kernels can also be swapped here at any time, but it is unadvisable to use multiple kernels for a single Notebook due to reproducibility concerns.
14. Open the **File** menu to see the selections. The **File** menu contains options for downloading the Notebook in various formats. In particular, it's recommended to save an HTML version of your Notebook, where the content is rendered statically and can be opened and viewed "as you would expect" in web browsers.
    The Notebook name will be displayed in the upper-left corner. New Notebooks will automatically be named **Untitled**.
15. Change the name of your IPYNB Notebook file by clicking on the current name in the upper-left corner and typing the new name. Then save the file.
16. Close the current tab in your web browser (exiting the Notebook) and go to the **Jupyter Dashboard** tab, which should still be open. (If it's not open then reload it by copy and pasting the HTTP link from the terminal.)
    Since we didn't shut down the Notebook, we just saved and exited, it will have a green book symbol next to its name in the **Files** section of the Jupyter Dashboard and will be listed as **Running** on the right side next to the last modified date. Notebooks can be shut down from here.
17. Quit the Notebook you have been working on by selecting it (checkbox to the left of the name) and clicking the orange **Shutdown** button:

Note

If you plan to spend a lot of time working with Jupyter Notebooks, it's worthwhile to learn the keyboard shortcuts. This will speed up your workflow considerably. Particularly useful commands to learn are the shortcuts for manually adding new cells and converting cells from code to Markdown formatting. Click on **Keyboard Shortcuts** from the **Help** menu to see how.

Subtopic C: Jupyter Features

Jupyter has many appealing features that make for efficient Python programming. These include an assortment of things, from methods for viewing docstrings to executing Bash commands. Let's explore some of these features together in this section.

Topic objectives

In this topic, you will:

- Improve your ability to use Jupyter Notebooks efficiently, by learning useful keyboard shortcuts and important features
- Be able to install and use Jupyter special functions, in order to get the most out of the platform

Note

The official IPython documentation can be found here: `http://ipython.readthedocs.io/en/stable/`. It has details on the features we will discuss here and others.

Note

Read through the basic keyboard shortcuts with the students and allow some time to test them.

Exercise

Explore some of Jupyter's most useful features

1. From the Jupyter Dashboard, navigate to the `lesson-1` directory and open the `lesson-1-workbook.ipynb` file by selecting it. The standard file extension for Jupyter Notebooks is `.ipynb`, which was introduced back when they were called IPython Notebooks.
2. Scroll down to `Subtopic C: Jupyter Features` in the Jupyter Notebook. We start by reviewing the basic keyboard shortcuts. These are especially helpful to avoid having to use the mouse so often, which will greatly speed up workflow.

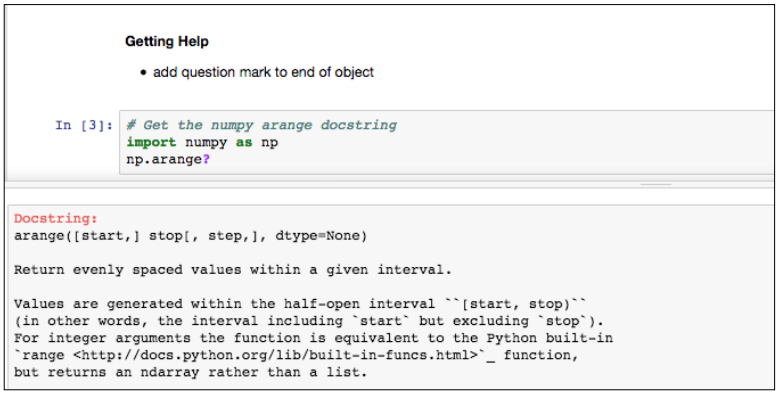
   Here are the most useful keyboard shortcuts. Learning to use these will greatly improve your experience with Jupyter Notebooks as well as your efficiency:

   » *Shift* + *Enter* is used to run a cell
   » The *Esc* key is used to leave a cell
   » The *M* key is used to change a cell to Markdown (after pressing *Esc*)
   » The *Y* key is used to change a cell to code (after pressing *Esc*)
   » Arrow keys move cells (after pressing *Esc*)
   » The *Enter* key is used to enter a cell

   Moving on from shortcuts, the help option is useful for beginners and experienced coders alike. It can help provide guidance at each uncertain step.

   Users can get help by adding a question mark to the end of any object and running the cell. Jupyter finds the docstring for that object and returns it in a pop-out window at the bottom of the app.

3. Run the **Getting Help** section cells and check out how Jupyter displays the docstrings at the bottom of the Notebook. Add a cell in this section and get help on the object of your choice:

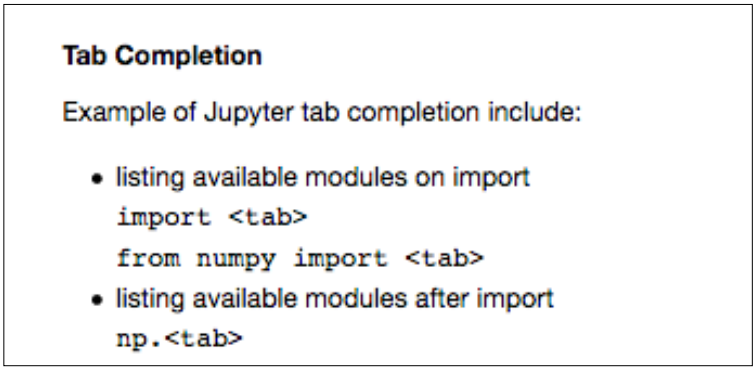


Tab completion can be used to do the following:

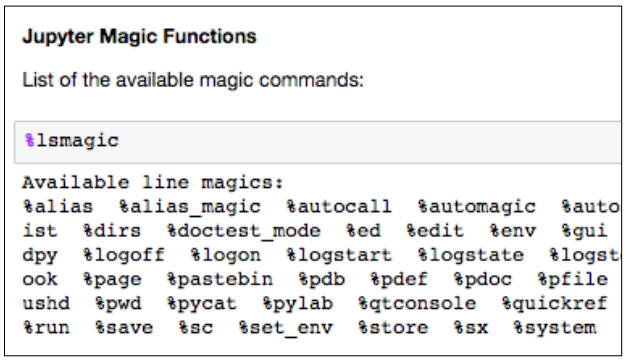
» List available modules when importing external libraries
» List available modules of imported external libraries
» Function and variable completion

This can be especially useful when you need to know the available input arguments for a module, when exploring a new library, to discover new modules, or simply to speed up workflow. They will save time writing out variable names or functions and reduce bugs from typos. The tab completion works so well that you may have difficulty coding Python in other editors after today!

4. Click into an empty code cell in the **Tab Completion** section and try using tab completion in the ways suggested immediately above. For example, the first suggestion can be done by typing `import` (including the space after) and then pressing the *Tab* key:



5. Last but not least of the basic Jupyter Notebook features are **magic** commands. These consist of one or two percent signs followed by the command. Magics starting with `%%` will apply to the entire cell, and magics starting with `%` will only apply to that line. This will make sense when seen in an example.
Scroll to the **Jupyter Magic Functions** section and run the cells containing `%lsmagic` and `%maplotlib inline`:



Note

There's an opportunity here to point out how list comprehensions are quicker than loops in Python. This can be seen by comparing the wall time for the first and second cell, where the same calculation is done significantly faster with the list comprehension.

`%lsmagic` lists the available options. We will discuss and show examples of some of the most useful ones. The most common magic command you will probably see is `%matplotlib inline`, which allows matplotlib figures to be displayed in the Notebook without having to explicitly use `plt.show()`.

The timing functions are very handy and come in two varieties: a standard timer (`%time` or `%%time`) and a timer that measures the average runtime of many iterations (`%timeit` and `%%timeit`).

6. Run the cells in the **Timers** section. Note the difference between using one and two percent signs.
   Even using a Python kernel (as you are currently doing), other languages can be invoked using magic commands. The built-in options include JavaScript, R, Pearl, Ruby, and Bash. Bash is particularly useful, as you can use Unix commands to find out where you are currently (`pwd`), what's in the directory (`ls`), make new folders (`mkdir`), and write file contents (`cat` / `head` / `tail`).

7. Run the first cell in the **Using bash in the notebook** section. This cell writes some text to a file in the working directory, prints the directory contents, prints an empty line, and then writes back the contents of the newly created file before removing it:

Using bash in the notebook

```
In [9]: %%bash

        echo "using bash from inside Jupyter!" > test-file.txt
        ls
        echo ""
        cat test-file.txt
        rm test-file.txt
```

```
Lesson 1
Lesson 1.docx
Lesson 1.pptx
lesson-1-workbook.html
lesson-1-workbook.ipynb
test-file.txt
~$sson 1.docx

using bash from inside Jupyter!
```

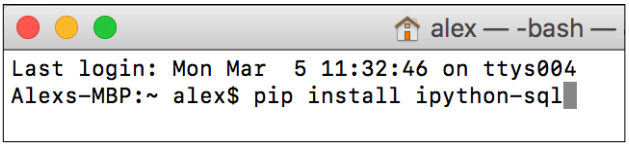
8. Run the following cells containing only `ls` and `pwd`. Note how we did not have to explicitly use the Bash magic command for these to work.
   There are plenty of external magic commands that can be installed. A popular one is `ipython-sql`, which allows for SQL code to be executed in cells.

Note

If this does not work for the students, that is OK as it's not used again in this course.

9. If not already done, install `ipython-sql` now. Open a new terminal window and execute the following code:

```
pip install ipython-sql
```



10. Run the `%load_ext sql` cell to load the external command into the Notebook:

```
# Source: https://github.com/catherinedevlin/ipython-sql
# do pip install ipython-sql in the terminal
%load_ext sql
```

This allows for connections to remote databases such that queries can be executed (and thereby documented) right inside the Notebook.

11. Run the cell containing the SQL sample query:

```
%%sql sqlite://

SELECT *
FROM (
    SELECT 'Hello' as msg_1
) A JOIN (
    SELECT 'World!' as msg_2
) B;
```

```
Done.
```

msg_1	msg_2
Hello	World!

Here we first connect to the local sqlite source; however, this line could instead point to a specific database on a local or remote server. Then we execute a simple `SELECT` to show how the cell has been converted to run SQL code instead of Python.

12. Moving on to other useful magic functions, we'll briefly discuss one that helps with documentation. The command is `%version_information`, but it does not come as standard with Jupyter. Like the SQL one we just saw, it can be installed from the command line with `pip`.
    If not already done, install the version documentation tool now from the terminal using `pip`. Open up a new window and run the following code:

```
pip install version_information
```

    Once installed, it can then be imported into any Notebook using `%load_ext version_information`. Finally, once loaded, it can be used to display the versions of each piece of software in the Notebook.

13. Run the cell that loads and calls the `version_information` command:

```
%load_ext version_information
%version_information requests, numpy, pandas, matplotlib, seaborn, sklearn
```

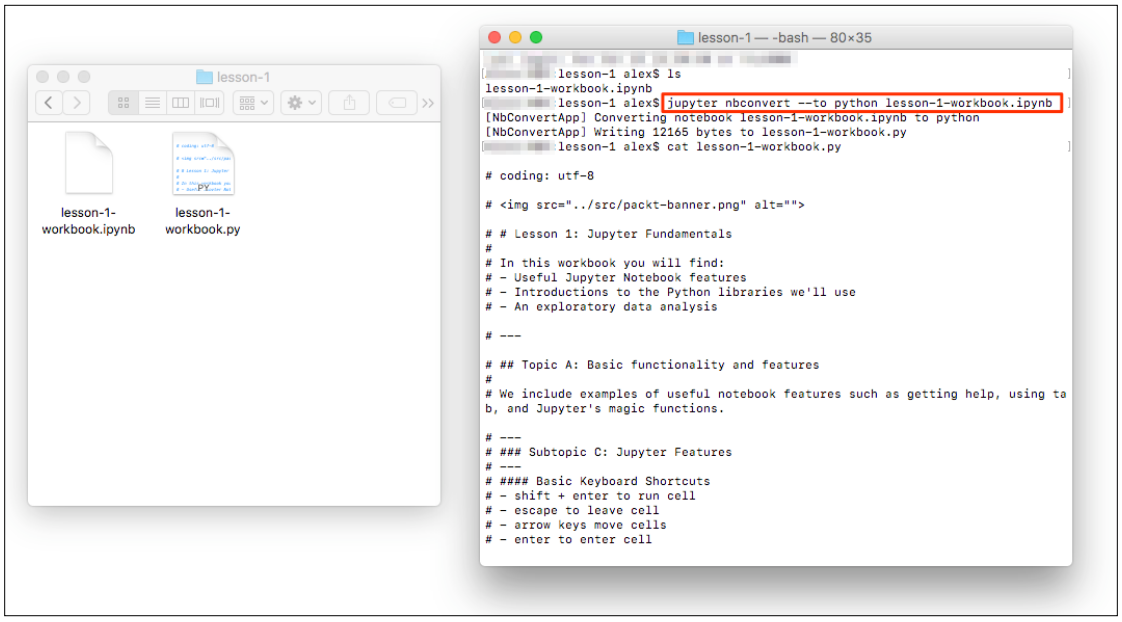
Software	Version
Python	3.5.4 64bit [GCC 4.2.1 Compatible Clang 4.0.1 (tags/RELEASE_401/final)]
IPython	6.1.0
OS	Darwin 16.5.0 x86_64 i386 64bit
requests	2.18.4
numpy	1.13.1
pandas	0.20.3
matplotlib	2.0.2
seaborn	0.8.0
sklearn	0.19.0
Wed Oct 11 19:46:08 2017 PDT	

Converting a Jupyter Notebook to a Python Script

You can convert a Jupyter Notebook to a Python script. This is equivalent to copy and pasting the contents of each code cell into a single `.py` file. The Markdown sections are also included as comments.

The conversion can be done from the `NotebookApp` or in the command line as follows:

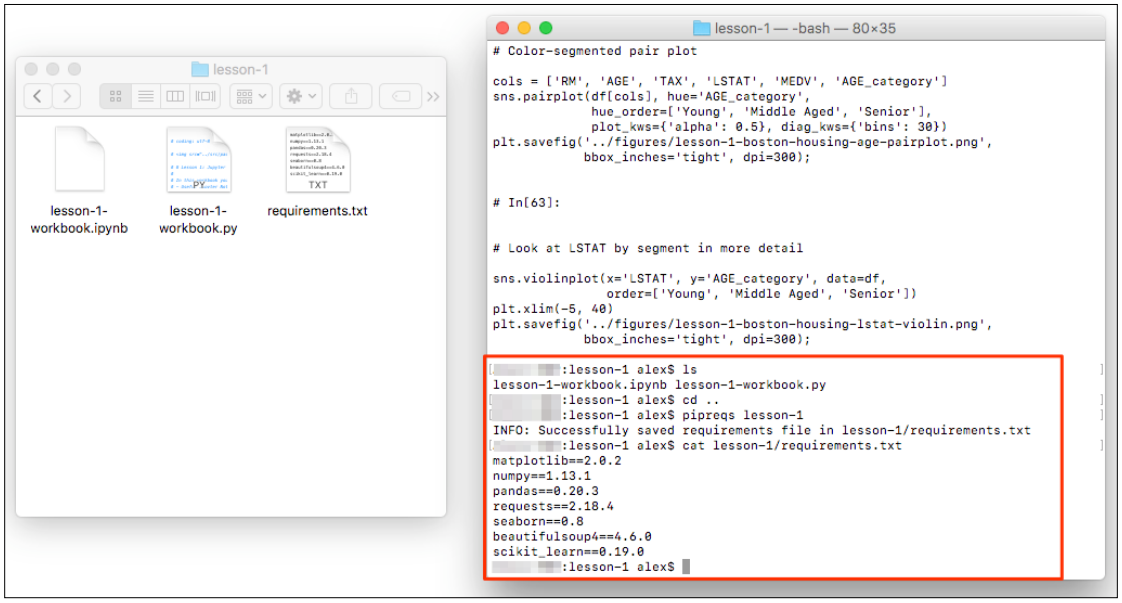
```
jupyter nbconvert --to=python lesson-1-notebook.ipynb
```



This is useful, for example, when you want to determine the library requirements for a Notebook using a tool such as `pipreqs`. This tool determines the libraries used in a project and exports them into a `requirements.txt` file (and it can be installed by running `pip install pipreqs`).

The command is called from outside the folder containing your `.py` files. For example, if the `.py` files are inside a folder called `lesson-1`, you could do the following:

```
pipreqs lesson-1/
```



The resulting `requirements.txt` file for `lesson-1-workbook.ipynb` looks like this:

```
cat lesson-1/requirements.txt
matplotlib==2.0.2
numpy==1.13.1
pandas==0.20.3
requests==2.18.4
seaborn==0.8
beautifulsoup4==4.6.0
scikit_learn==0.19.0
```

Discussion

Ask the students what libraries come to mind when they think about Python and data science. Probe for details on the libraries they mention: where they saw it in use, and when and why they used it themselves. If students aren't answering, see if you can jog their memory by mentioning one or more libraries we use in this course (listed below).

Answer

- **matplotlib**: For creating scatter plots, bar plots, histograms, and so on.
- **pandas**: For opening CSC files or otherwise handling tables
- **scikit-learn** or **statsmodels**: For building predictive models
- **Keras**, **TensorFlow**, or **Theano**: For building neural networks

Subtopic D: Python Libraries

Topic objectives

In this topic, you will:

» Be able to recognize the external libraries we use in this course and understand generally what they are each used for.

Having now seen all the basics of Jupyter Notebooks, and even some more advanced features, we'll shift our attention to the Python libraries we'll be using in this course. Libraries, in general, extend the default set of Python functions. Examples of commonly used standard libraries are `datetime`, `time`, and `os`. These are called standard libraries because they come standard with every installation of Python.

For data science with Python, the most important libraries are external, which means they do not come standard with Python.

The external data science libraries we'll be using in this course are NumPy, Pandas, Seaborn, matplotlib, scikit-learn, Requests, and Bokeh. Let's briefly introduce each.

Caution

It's a good idea to import libraries using industry standards, for example, `import numpy as np`; this way, your code is more readable. Try to avoid doing things such as `from numpy import *`, as you may unwittingly overwrite functions. Furthermore, it's often nice to have modules linked to the library via a dot (`.`) for code readability.

» **NumPy** offers multi-dimensional data structures (arrays) on which operations can be performed far quicker than standard Python data structures (for example, lists). This is done in part by performing operations in the background using C. NumPy also offers various mathematical and data manipulation functions.
» **Pandas** is Python's answer to the R DataFrame. It stores data in 2D tabular structures where columns represent different variables and rows correspond to samples. Pandas provides many handy tools for data wrangling such as filling in NaN entries and computing statistical descriptions of the data. Working with Pandas DataFrames will be a big focus of this course.

- **Matplotlib** is a plotting tool inspired by the MATLAB platform. Those familiar with R can think of it as Python's version of ggplot. It's the most popular Python library for plotting figures and allows for a high level of customization.
- **Seaborn** works as an extension to matplotlib, where various plotting tools useful for data science are included. Generally speaking, this allows for analysis to be done much faster than if you were to create the same things *manually* with libraries such as matplotlib and Scikit-learn.
- **Scikit-learn** is the most commonly used machine learning library. It offers top-of-the-line algorithms and a very elegant API where models are instantiated and then *fit* with data. It also provides data processing modules and other tools useful for predictive analytics.
- **Requests** is the go-to library for making HTTP requests. It makes it straightforward to get HTML from web pages and interface with APIs. For parsing the HTML, many choose BeautifulSoup4, which we will also cover in this course.
- **Bokeh** is an interactive visualization library. It functions similar to matplotlib, but allows us to add hover, zoom, click, and other interactive tools to our plots. It also allows us to render and play with the plots inside our Jupyter Notebook.

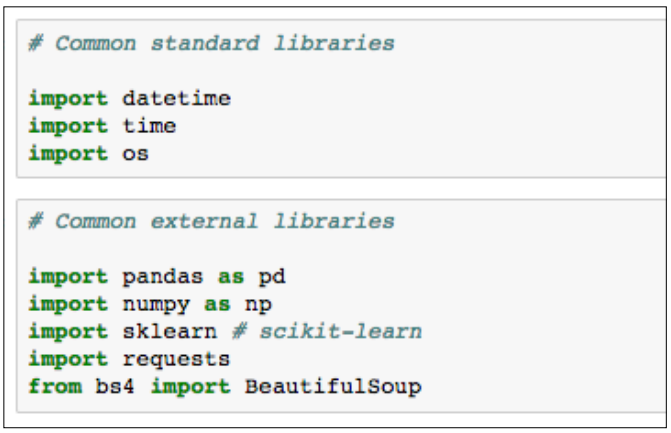
Having introduced these libraries, let's go back to our Notebook and load them, by running the `import` statements. This will lead us into our first analysis, where we finally start working with a dataset.

Exercise

Import the external libraries and set up the plotting environment

14. Open up the `lesson 1` Jupyter Notebook and scroll to the `Subtopic D: Python Libraries` section.
    Just like for regular Python scripts, libraries can be imported into the Notebook at any time. It's best practice to put the majority of the packages you use at the top of the file. Sometimes it makes sense to load things midway through the Notebook and that is completely OK.

15. Run the cells to import the external libraries and set the plotting options:



```
# Common standard libraries

import datetime
import time
import os
```

```
# Common external libraries

import pandas as pd
import numpy as np
import sklearn # scikit-learn
import requests
from bs4 import BeautifulSoup
```

For a nice Notebook setup, it's often useful to set various options along with the imports at the top. For example, the following can be run to change the figure appearance to something more aesthetically pleasing than the matplotlib and Seaborn defaults:

```
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns

# See here for more options: https://matplotlib.org/users/
customizing.html
%config InlineBackend.figure_format='retina'
sns.set() # Revert to matplotlib defaults
plt.rcParams['figure.figsize'] = (9, 6)
plt.rcParams['axes.labelpad'] = 10
sns.set_style("darkgrid")
```

So far in this course, we've gone over the basics of using Jupyter Notebooks for data science. We started by exploring the platform and finding our way around the interface. Then we discussed the most useful features, which include tab completion and magic functions. Finally, we introduced the Python libraries we'll be using in this course.

The next section will be very interactive as we perform our first analysis together using the Jupyter Notebook.

Discussion

Ask the students whether they have ever used MS Excel for data analysis. If they answer yes, ask them what analysis they have done on Excel.

Topic B: Our First Analysis - the Boston Housing Dataset

1H 10M

12

Topic objectives

In this topic, you will:

- Know some important questions to ask when first looking at a dataset, such as what the *shape* of the data is, what the datatypes are, and how many missing values there are.
- Be able to load tabular data into a Jupyter Notebook as a DataFrame, so that it can be analyzed using Pandas.
- Learn the basic methods to summarize and transform DataFrames. This includes selecting subsets, adding and removing columns, and calculating summary statistics such as the size, mean, standard deviation, and number of missing values.
- Learn how to create lines of best fit using scikit-learn, so that you are able to apply simple predictive analytics in the Notebook.

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So far, this lesson has focused on the features and basic usage of Jupyter. Now we'll put this into practice and do some data exploration and analysis.

The dataset we'll look at in this section is the so-called *Boston housing dataset*. It contains US census data concerning houses in various areas around the city of Boston. Each sample corresponds to a unique area and has about a dozen measures. We should think of samples as rows and measures as columns. The data was first published in 1978 and is quite small, containing only about 500 samples.

Now that we know something about the context of the dataset, let's decide on a rough plan for the exploration and analysis. If applicable, this plan would accommodate the relevant question(s) under study. In this case, the goal is not to answer a question but instead to show Jupyter in action and illustrate some basic data analysis methods.


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Our general approach to this analysis will be to do the following:

» Load and scrub the data
» Quantitatively understand the features
» Look for patterns and generate questions
» Answer the questions to the problems

Subtopic A: Loading the Data into Jupyter Using a Pandas DataFrame


15

Oftentimes data is stored in tables, which means it can be saved as a **comma-separated variable** (**CSV**) file. This format, and many others, can be read into Python as a DataFrame object, using the Pandas library. Other common formats include **tab-separated variable** (**TSV**), SQL tables, and JSON data structures. Indeed, Pandas has support for all of these. In this example, however, we are not going to load the data this way because the dataset is available directly through scikit-learn.

Note

An important part of loading data for analysis is ensuring that it's clean. For example, we would generally need to deal with missing data and ensure that all columns have the correct datatypes. The dataset we use in this section has already been cleaned, so we will not need to worry about this now. However, we'll see messier data in the second lesson and explore techniques for dealing with it.

Exercise

Load the Boston housing dataset

1. In the `lesson 1` Jupyter Notebook, scroll to `Subtopic A` of `Topic B: Our first Analysis: the Boston Housing Dataset`.
   The Boston housing dataset can be accessed from the `sklearn.datasets` module using the `load_boston` method.

2. Run the first two cells in this section to load the Boston dataset and see the `datastructures` type:

```
from sklearn import datasets
boston = datasets.load_boston()
```

```
type(boston)
```

```
sklearn.utils.Bunch
```

The output of the second cell tells us that it's a scikit-learn `Bunch` object. Let's get some more information about that to understand what we are dealing with.

3. Run the next cell to import the base object from scikit-learn `utils` and print the docstring in our Notebook:

```
In [4]: from sklearn.utils import Bunch
        Bunch?
```

```
Init signature: Bunch(**kwargs)
Docstring:
Container object for datasets

Dictionary-like object that exposes its keys as attributes.

>>> b = Bunch(a=1, b=2)
>>> b['b']
2
```

Reading the resulting docstring suggests that it's basically a dictionary, and can essentially be treated as such.

4. Print the field names (that is, the keys to the dictionary) by running the next cell.
We find these fields to be self-explanatory: `['DESCR', 'target', 'data', 'feature_names']`.

5. Run the next cell to print the dataset description contained in `boston['DESCR']`.

Note

Allow the students some time to briefly read through the feature descriptions and/or describe them yourself. For the purposes of this tutorial, the most important fields to understand are **RM**, **AGE**, **LSTAT**, and **MEDV**.

Ask the students to note down the important variables that we will use in the dataset, such as **RM**, **AGE**, **LSTAT**, and **MEDV**.

Note that in this call, we explicitly want to print the field value so that the Notebook renders the content in a more readable format than the string representation (that is, if we just type `boston['DESCR']` without wrapping it in a `print` statement). We then see the dataset information as we've previously summarized:

```
Boston House Prices dataset
===========================

Notes
------
Data Set Characteristics:

    :Number of Instances: 506
    :Number of Attributes: 13 numeric/categorical
predictive
    :Median Value (attribute 14) is usually the target
    :Attribute Information (in order):
        - CRIM     per capita crime rate by town
…
…
        - MEDV     Median value of owner-occupied homes in
$1000's

    :Missing Attribute Values: None
```

Of particular importance here are the feature descriptions (under `Attribute Information`). We will use this as reference during our analysis.

Note

For the complete code, refer to the `Lesson 1.txt` file.

Now we are going to create a Pandas DataFrame that contains the data. This is beneficial for a few reasons: all of our data will be contained in one object, there are useful and computationally efficient DataFrame methods we can use, and other libraries such as Seaborn have tools that integrate nicely with DataFrames.

In this case, we will create our DataFrame with the standard constructor method.

6. Run the cell where Pandas is imported and the docstring is retrieved for `pd.DataFrame`:

```
In [5]: import pandas as pd
        pd.DataFrame?
```

```
Init signature: pd.DataFrame(data=None, index=None, columns=None, dtype=None, copy=False)
Docstring:
Two-dimensional size-mutable, potentially heterogeneous tabular data
structure with labeled axes (rows and columns). Arithmetic operations
align on both row and column labels. Can be thought of as a dict-like
container for Series objects. The primary pandas data structure

Parameters
----------
data : numpy ndarray (structured or homogeneous), dict, or DataFrame
    Dict can contain Series, arrays, constants, or list-like objects
index : Index or array-like
    Index to use for resulting frame. Will default to np.arange(n) if
    no indexing information part of input data and no index provided
columns : Index or array-like
    Column labels to use for resulting frame. Will default to
    np.arange(n) if no column labels are provided
```

The docstring reveals the DataFrame input parameters. We want to feed in `boston['data']` for the data and use `boston['feature_names']` for the headers.

7. Run the next few cells to print the data, its shape, and the feature names:

```
# What does the data look like?
boston['data']
```

```
array([[  6.32000000e-03,   1.80000000e+01,   2.31000000e+00, ...,
          1.53000000e+01,   3.96900000e+02,   4.98000000e+00],
       [  2.73100000e-02,   0.00000000e+00,   7.07000000e+00, ...,
          1.78000000e+01,   3.96900000e+02,   9.14000000e+00],
       [  2.72900000e-02,   0.00000000e+00,   7.07000000e+00, ...,
          1.78000000e+01,   3.92830000e+02,   4.03000000e+00],
       ...,
       [  6.07600000e-02,   0.00000000e+00,   1.19300000e+01, ...,
          2.10000000e+01,   3.96900000e+02,   5.64000000e+00],
       [  1.09590000e-01,   0.00000000e+00,   1.19300000e+01, ...,
          2.10000000e+01,   3.93450000e+02,   6.48000000e+00],
       [  4.74100000e-02,   0.00000000e+00,   1.19300000e+01, ...,
          2.10000000e+01,   3.96900000e+02,   7.88000000e+00]])
```

```
boston['data'].shape
```

```
(506, 13)
```

```
boston['feature_names']
```

```
array(['CRIM', 'ZN', 'INDUS', 'CHAS', 'NOX', 'RM', 'AGE', 'DIS', 'RAD',
       'TAX', 'PTRATIO', 'B', 'LSTAT'],
      dtype='<U7')
```

Looking at the output, we see that our data is in a 2D NumPy array. Running the command `boston['data'].shape` returns the length (number of samples) and the number of features as the first and second outputs, respectively.

8. Load the data into a Pandas DataFrame `df` by running the following:

```
df = pd.DataFrame(data=boston['data'],
columns=boston['feature_names'])
```

In machine learning, the variable that is being modeled is called the target variable; it's what you are trying to predict given the features. For this dataset, the suggested target is **MEDV**, the median house value in 1000s of dollars.

9. Run the next cell to see the shape of the target:

```
# Still need to add the target variable
boston['target'].shape
```

```
(506,)
```

We see that it has the same length as the features, which is what we expect. It can therefore be added as a new column to the DataFrame.

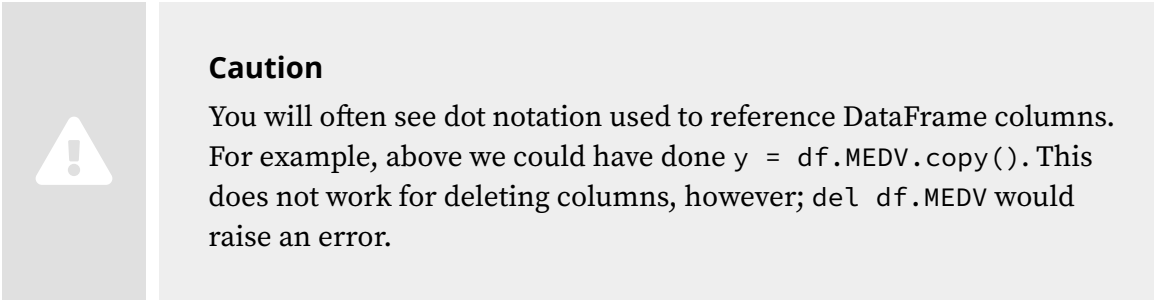
10. Add the target variable to `df` by running the cell with the following:

```
df['MEDV'] = boston['target']
```

11. To distinguish the target from our features, it can be helpful to store it at the front of our DataFrame.
Move the target variable to the front of `df` by running the cell with the following:

```
y = df['MEDV'].copy()
del df['MEDV']
df = pd.concat((y, df), axis=1)
```

Here we introduce a dummy variable `y` to hold a copy of the target column before removing it from the DataFrame. We then use the Pandas concatenation function to combine it with the remaining DataFrame along the 1st axis (as opposed to the 0th axis, which combines rows).



Caution

You will often see dot notation used to reference DataFrame columns. For example, above we could have done `y = df.MEDV.copy()`. This does not work for deleting columns, however; `del df.MEDV` would raise an error.

12. Now that the data has been loaded in its entirety, let's take a look at the DataFrame. We can do `df.head()` or `df.tail()` to see a glimpse of the data and `len(df)` to make sure the number of samples is what we expect. Run the next few cells to see the head, tail and length of `df`:

```
df.head()
```

	MEDV	CRIM	ZN	INDUS	CHAS	NOX	RM	AGE	DIS	RAD	TAX	PTRATIO	B
0	24.0	0.00632	18.0	2.31	0.0	0.538	6.575	65.2	4.0900	1.0	296.0	15.3	396.90
1	21.6	0.02731	0.0	7.07	0.0	0.469	6.421	78.9	4.9671	2.0	242.0	17.8	396.90
2	34.7	0.02729	0.0	7.07	0.0	0.469	7.185	61.1	4.9671	2.0	242.0	17.8	392.83
3	33.4	0.03237	0.0	2.18	0.0	0.458	6.998	45.8	6.0622	3.0	222.0	18.7	394.63
4	36.2	0.06905	0.0	2.18	0.0	0.458	7.147	54.2	6.0622	3.0	222.0	18.7	396.90

```
df.tail()
```

	MEDV	CRIM	ZN	INDUS	CHAS	NOX	RM	AGE	DIS	RAD	TAX	PTRATIO	B
501	22.4	0.06263	0.0	11.93	0.0	0.573	6.593	69.1	2.4786	1.0	273.0	21.0	391.99
502	20.6	0.04527	0.0	11.93	0.0	0.573	6.120	76.7	2.2875	1.0	273.0	21.0	396.90
503	23.9	0.06076	0.0	11.93	0.0	0.573	6.976	91.0	2.1675	1.0	273.0	21.0	396.90
504	22.0	0.10959	0.0	11.93	0.0	0.573	6.794	89.3	2.3889	1.0	273.0	21.0	393.45
505	11.9	0.04741	0.0	11.93	0.0	0.573	6.030	80.8	2.5050	1.0	273.0	21.0	396.90

```
len(df)
```

```
506
```

Each row is labeled with an index value, as seen in bold on the left side of the table. By default, these are a set of integers starting at 0 and incrementing by one for each row.

13. Printing `df.dtypes` will show the datatype contained within each column. Run the next cell to see the datatypes of each column.

    For this dataset, we see that every field is a float and therefore most likely a continuous variable, including the target. This means that predicting the target variable is a regression problem.

14. The next thing we need to do is clean the data by dealing with any missing data, which Pandas automatically sets as `NaN` values. These can be identified by running `df.isnull()`, which returns a Boolean DataFrame of the same shape as `df`. To get the number of NaNs per column, we can do `df.isnull().sum()`.
    Run the next cell to calculate the number of `NaN` values in each column:

```
# Identify and NaNs
df.isnull().sum()
```

```
MEDV       0
CRIM       0
ZN         0
INDUS      0
CHAS       0
NOX        0
RM         0
AGE        0
DIS        0
RAD        0
TAX        0
PTRATIO    0
B          0
LSTAT      0
dtype: int64
```

    For this dataset, we see there are no NaNs, which means we have no immediate work to do in cleaning the data and can move on.

15. To simplify the analysis, the final thing we'll do before exploration is remove some of the columns. We won't bother looking at these, and instead focus on the remainder in more detail.

Discussion

Ask to students to identify anything interesting they see in this table.

Answer

Possible answers include the following:

- MEDV has min of 5k and max of 50k, suggesting this field may have been censored (limited).
- CRIM and CHAS have high std compared to the mean. Looking at min, 25%, 50%, 75%, and max cutoffs indicates high skew to the right.

Remove some columns by running the cell that contains the following code:

```
for col in ['ZN', 'NOX', 'RAD', 'PTRATIO', 'B']:
    del df[col]
```

Subtopic B: Data Exploration

Since this is an entirely new dataset that we've never seen before, the first goal here is to understand the data. We've already seen the textual description of the data, which is important for qualitative understanding. We'll now compute a quantitative description.

Exercise

Explore the Boston housing dataset

1. Navigate to `Subtopic B: Data exploration` in the Jupyter Notebook and run the cell containing `df.describe()`:


```
df.describe().T
```

	count	mean	std	min	25%	50%	75%	max
MEDV	506.0	22.532806	9.197104	5.00000	17.025000	21.20000	25.000000	50.0000
CRIM	506.0	3.593761	8.596783	0.00632	0.082045	0.25651	3.647423	88.9762
INDUS	506.0	11.136779	6.860353	0.46000	5.190000	9.69000	18.100000	27.7400
CHAS	506.0	0.069170	0.253994	0.00000	0.000000	0.00000	0.000000	1.0000
RM	506.0	6.284634	0.702617	3.56100	5.885500	6.20850	6.623500	8.7800
AGE	506.0	68.574901	28.148861	2.90000	45.025000	77.50000	94.075000	100.0000
DIS	506.0	3.795043	2.105710	1.12960	2.100175	3.20745	5.188425	12.1265
TAX	506.0	408.237154	168.537116	187.00000	279.000000	330.00000	666.000000	711.0000
LSTAT	506.0	12.653063	7.141062	1.73000	6.950000	11.36000	16.955000	37.9700

This computes various properties including the mean, standard deviation, minimum, and maximum for each column. This table gives a high-level idea of how everything is distributed. Note that we have taken the transform of the result by adding a `.T` to the output; this swaps the rows and columns.

Going forward with the analysis, we will specify a set of columns to focus on.

2. Run the cell where these "focus columns" are defined:

```
cols = ['RM', 'AGE', 'TAX', 'LSTAT', 'MEDV']
```

3. This subset of columns can be selected from `df` using square brackets. Display this subset of the DataFrame by running `df[cols].head()`:

```
df[cols].head()
```

	RM	AGE	TAX	LSTAT	MEDV
0	6.575	65.2	296.0	4.98	24.0
1	6.421	78.9	242.0	9.14	21.6
2	7.185	61.1	242.0	4.03	34.7
3	6.998	45.8	222.0	2.94	33.4
4	7.147	54.2	222.0	5.33	36.2

As a reminder, let's recall what each of these columns is. From the dataset documentation, we have the following:

```
        - RM       average number of rooms per dwelling
        - AGE      proportion of owner-occupied units built
prior to 1940
        - TAX      full-value property-tax rate per $10,000
        - LSTAT    % lower status of the population
        - MEDV     Median value of owner-occupied homes in
$1000's
```

To look for patterns in this data, we can start by calculating the pairwise correlations using `pd.DataFrame.corr`.

4. Calculate the pairwise correlations for our selected columns by running the cell containing the following code:

```
df[cols].corr()
```

	RM	AGE	TAX	LSTAT	MEDV
RM	1.000000	-0.240265	-0.292048	-0.613808	0.695360
AGE	-0.240265	1.000000	0.506456	0.602339	-0.376955
TAX	-0.292048	0.506456	1.000000	0.543993	-0.468536
LSTAT	-0.613808	0.602339	0.543993	1.000000	-0.737663
MEDV	0.695360	-0.376955	-0.468536	-0.737663	1.000000

This resulting table shows the correlation score between each set of values. Large positive scores indicate a strong positive (that is, in the same direction) correlation. As expected, we see maximum values of 1 on the diagonal.

Note

By default, Pandas calculates the standard correlation coefficient for each pair, which is also called the Pearson coefficient. This is defined as the covariance between two variables, divided by the product of their standard deviations:

$$\rho_{X,Y} = \frac{cov(X,Y)}{\sigma_X \sigma_Y}$$

The covariance, in turn, is defined as follows:

$$cov(X,Y) = \frac{1}{n}\sum_{i=0}^{n}(x_i - \bar{X})(y_i - \bar{Y})$$

~~Here, is the number of samples, and are the individual samples being summed over, and and are the means of each set.~~

Discussion

Ask the students to interpret this. Remind them that values can be anywhere from -1 to 1, with large positive values representing strong positive correlation and large negative values representing strong negative correlation. Uncorrelated features will have zero covariances. They should think about how these correlations relate to the underlying phenomena causing the measured values in the dataset.

- For example, mean number of rooms per house (**RM**) is negatively correlated with the % of the population that is lower class (**LSTAT**). In other words, in areas where there are fewer lower class inhabitants, the houses tend to have more rooms.
- Age (**AGE**) is positively correlated with % of population that is lower class. This means that in lower class areas, inhabitants tend to occupy houses that were built prior to 1940.
- The features that show the strongest correlation with the median house value (**MDEV**) are the number of rooms (**RM**) and the percentage of the population that is lower class (**LSTAT**).

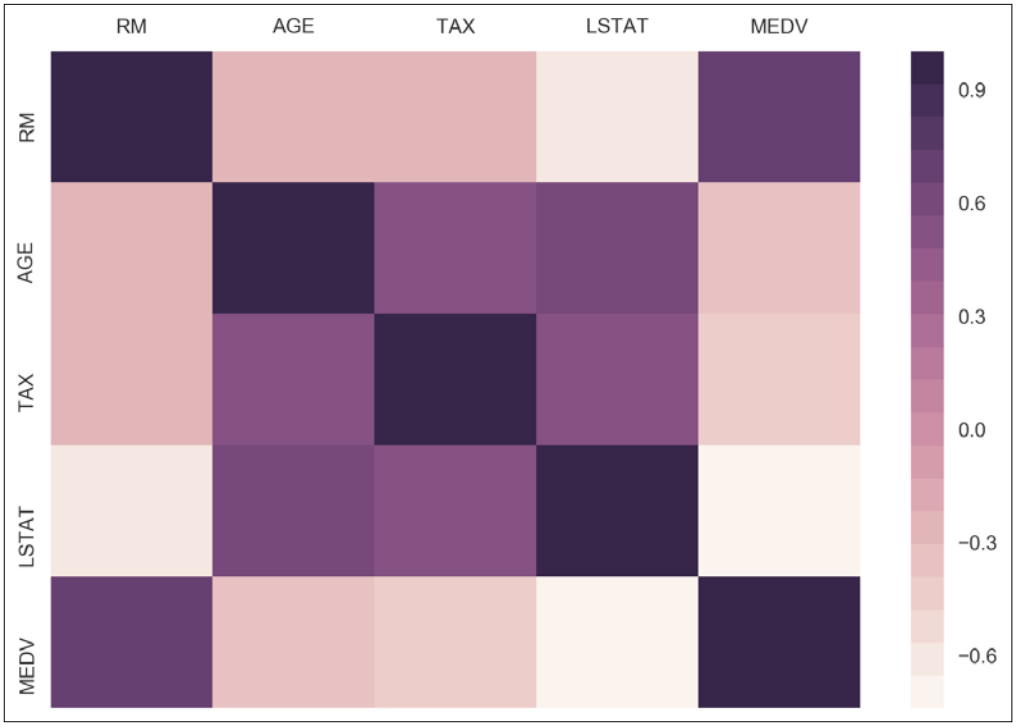
Instead of straining our eyes to look at the table above, it's nicer to visualize it with a heatmap. This can be done easily with Seaborn.

5. Run the next cell to initialize the plotting environment, as discussed earlier in the lesson. Then, to create the heatmap, run the cell containing the following code:

```
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline

ax = sns.heatmap(df[cols].corr(),
                 cmap=sns.cubehelix_palette(20, light=0.95,
dark=0.15))
ax.xaxis.tick_top() # move labels to the top

plt.savefig('../figures/lesson-1-boston-housing-corr.png',
            bbox_inches='tight', dpi=300)
```

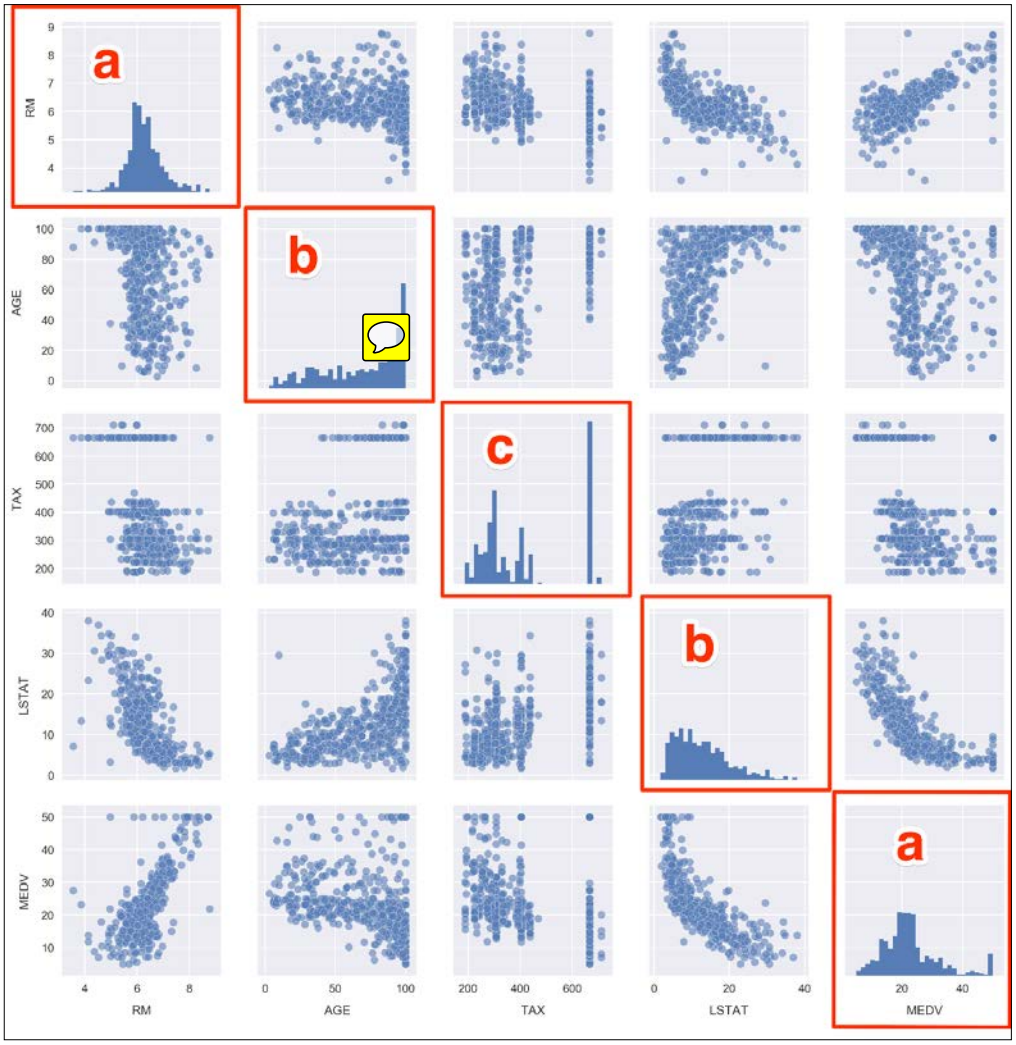


We call `sns.heatmap` and pass the pairwise correlation matrix as input. We use a custom color palette here to override the Seaborn default. The function returns a `matplotlib.axes` object which is referenced by the variable `ax`. The final figure is then saved as a high resolution PNG to the `figures` folder.

6. For the final step in our dataset exploration exercise, we'll visualize our data using Seaborn's `pairplot` function.

   Visualize the DataFrame using Seaborn's `pairplot` function. Run the cell containing the following code:

```
sns.pairplot(df[cols],
             plot_kws={'alpha': 0.6},
             diag_kws={'bins': 30})
```



Having previously used a heatmap to visualize a simple overview of the correlations, this plot allows us to see the relationships in far more detail.

Discussion

Ask the students about their previous experience with predictive analytics. Have they used machine learning algorithms before? In particular, ask them to speak about the difference between supervised and unsupervised learning.

Answer

Supervised learning consists of training models on labeled data. For example, using linear regression to determine a line of best fit or a decision tree for classification.

Unsupervised learning is necessary when there is no access to labeled data, and consists of training models based only on patterns in the feature set, for example, using clustering algorithms to label similar groups of data.

Note

Inform the students that unsupervised learning techniques are outside the scope of this course.

Looking at the histograms on the diagonal, we see the following:

» **RM** and **MEDV** have the closest shape to normal distributions.
» **AGE** is skewed to the left and **LSTAT** is skewed to the right (this may seem counterintuitive but skew is defined in terms of where the mean is positioned with relation to the max).
» ~~For~~ **TAX**, we find a large amount of the distribution is around 700. This is also evident from the scatter plots.

Taking a closer look at the **MEDV** histogram in the bottom right, we actually see something similar to **TAX** where there is a large upper-limit bin around $50,000. Recall when we did `df.describe()`, the min and max of **MDEV** was 5k and 50k, respectively. This suggests that median house values in the dataset were capped at 50k.

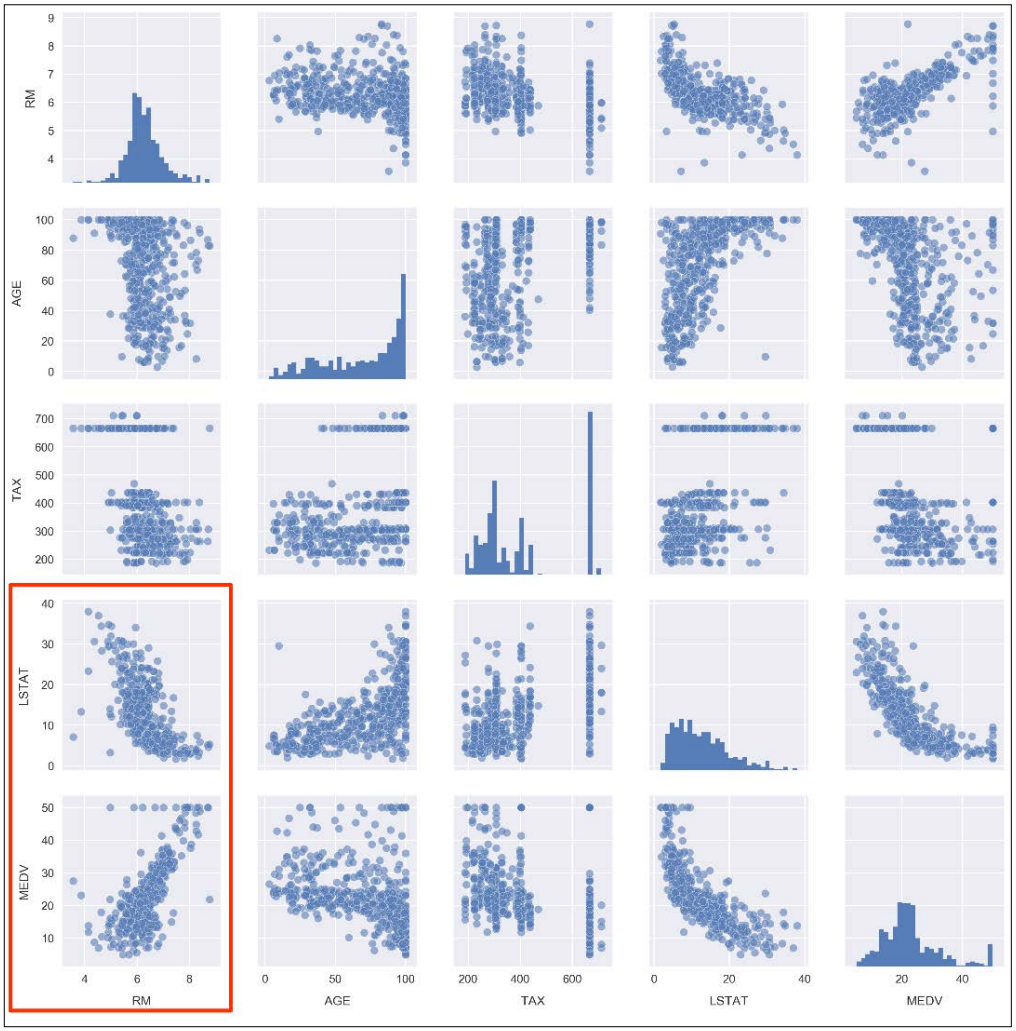
Subtopic C: Introduction to Predictive Analytics with Jupyter Notebooks


Continuing our analysis of the Boston housing dataset, we can see that it presents us with a regression problem where we predict a continuous target variable given a set of features. In particular, we'll be predicting the median house value (**MEDV**). We'll train models that take only one feature as input to make this prediction. This way, the models will be conceptually simple to understand and we can focus more on the technical details of the scikit-learn API. Then, in the next lesson, you'll be more comfortable dealing with the relatively complicated models.

Exercise

Linear models with Seaborn and scikit-learn

1. Scroll to `Subtopic C: Introduction to predictive analytics` in the Jupyter Notebook and look just above at the pairplot we created in the previous section. In particular, look at the scatter plots in the bottom-left corner:

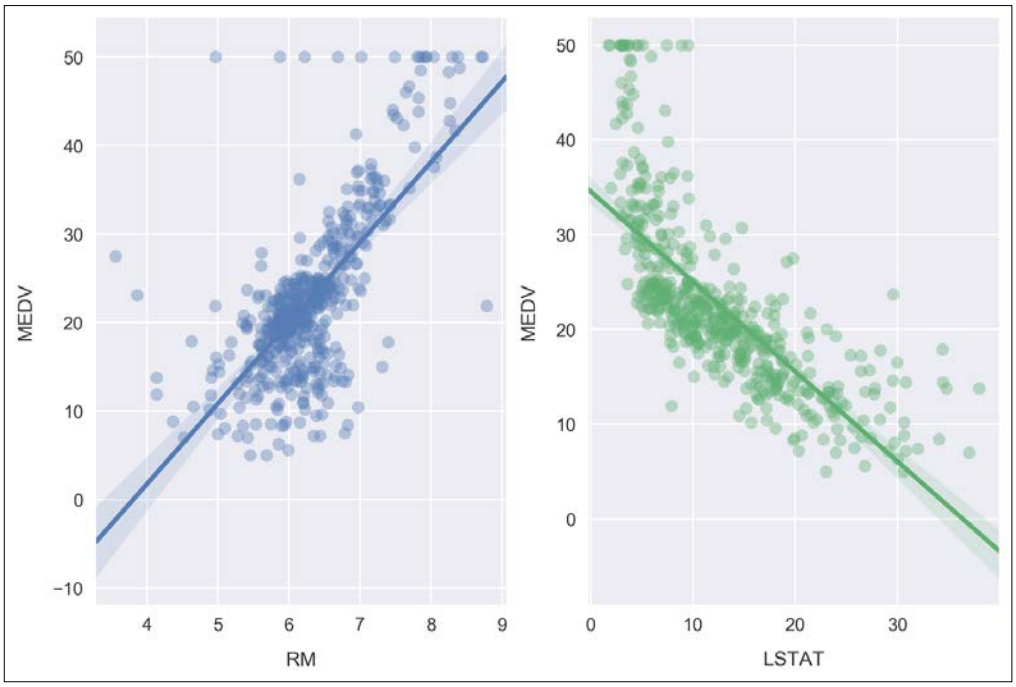


Note how the number of rooms per house (**RM**) and the % of the population that is lower class (**LSTAT**) are highly correlated with the median house value (**MDEV**). Let's pose the following question: how well can we predict **MDEV** given these variables?

To help answer this, let's first visualize the relationships using Seaborn. We will draw the scatter plots along with the line of best fit linear models.

2. Draw scatter plots along with the linear models by running the cell that contains the following:

```
fig, ax = plt.subplots(1, 2)
sns.regplot('RM', 'MEDV', df, ax=ax[0],
            scatter_kws={'alpha': 0.4}))
sns.regplot('LSTAT', 'MEDV', df, ax=ax[1],
            scatter_kws={'alpha': 0.4}))
```



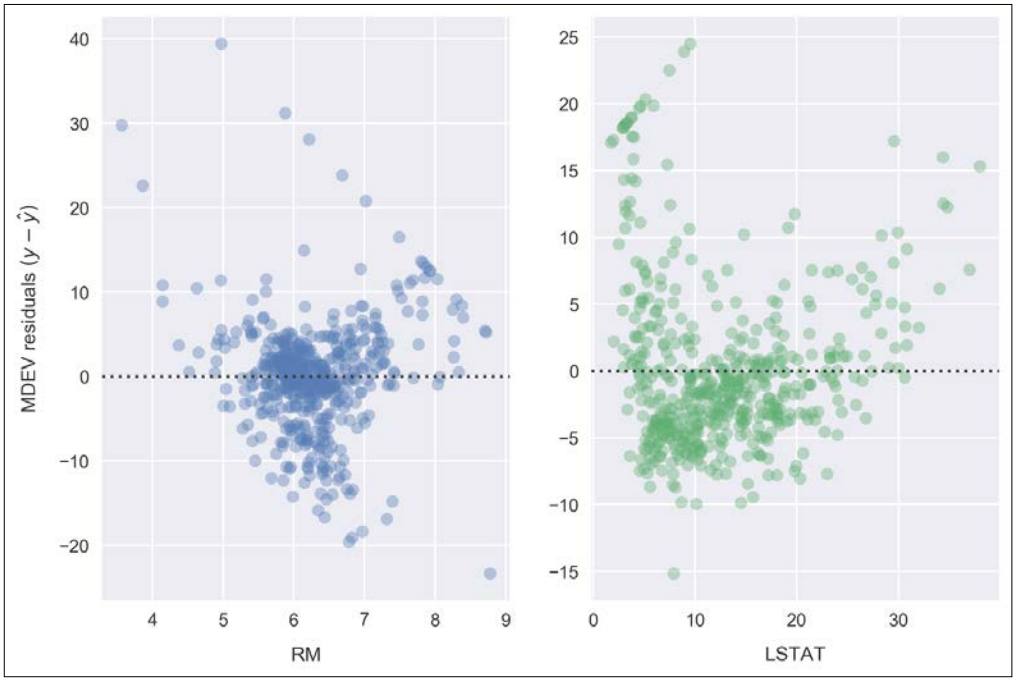
The line of best fit is calculated by minimizing the ordinary least squares error function, something Seaborn does automatically when we call the `regplot` function. Also note the shaded areas around the lines, which represent 95% confidence intervals.

Note

These 95% confidence intervals are calculated by taking the standard deviation of data in bins perpendicular to the line of best fit, effectively determining the confidence intervals at each point along the line of best fit. In practice, this involves Seaborn bootstrapping the data, a process where new data is created through random sampling with replacement. The number of bootstrapped samples is automatically determined based on the size of the dataset, but can be manually set as well by passing the `n_boot` argument.

3. Seaborn can also be used to plot the residuals for these relationships. Plot the residuals by running the cell containing the following:

```
fig, ax = plt.subplots(1, 2)
ax[0] = sns.residplot('RM', 'MEDV', df, ax=ax[0],
                      scatter_kws={'alpha': 0.4})
ax[0].set_ylabel('MDEV residuals $(y-\hat{y})$')
ax[1] = sns.residplot('LSTAT', 'MEDV', df, ax=ax[1],
                      scatter_kws={'alpha': 0.4})
ax[1].set_ylabel('')
```



Each point on these residual plots is the difference between that sample (y) and the linear model ~~prediction~~ (ŷ). Residuals greater than zero are data points that would be underestimated by the model. Likewise, residuals less than zero are data points that would be overestimated by the model.

Patterns in these plots can indicate suboptimal modeling. In each case above, we see diagonally arranged scatter points in the positive region. These are caused by the $50,000 cap on **MEDV**. The **RM** data is clustered nicely around 0, which indicates good fit. On the other hand, **LSTAT** appears to be clustered lower than 0.

4. Moving on from visualizations, the fits can be quantified by calculating the mean squared error. We'll do this now using scikit-learn. Define a function that calculates the line of best fit and mean squared error, by running the cell that contains the following:

```
from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_squared_error

…
…
    error = mean_squared_error(y, y_pred)
    print('mse = {:.2f}'.format(error))
    print()
```

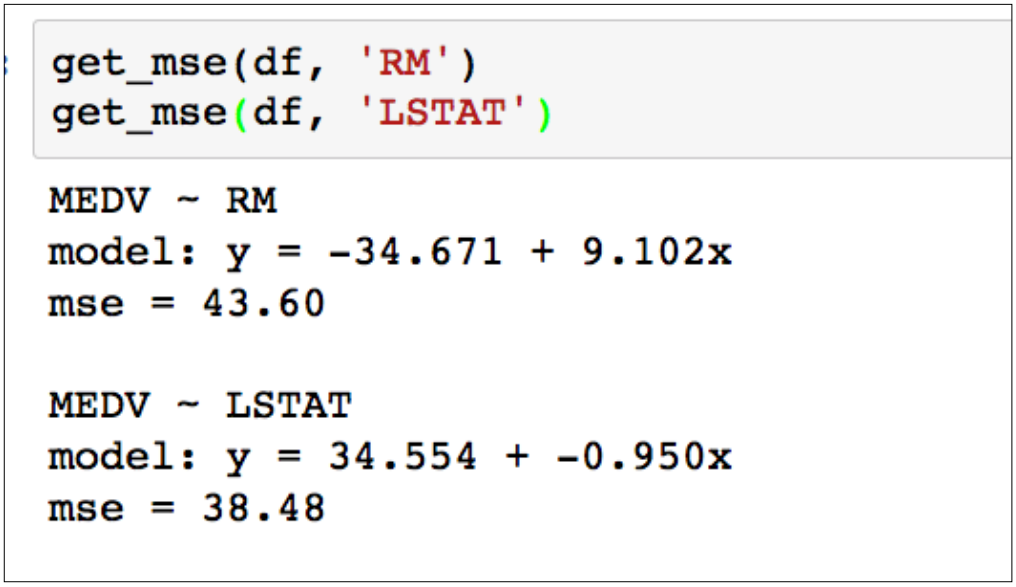

Note

For the complete code, refer to the `Lesson 1.txt` file.

In the `get_mse` function, we first assign the variables `y` and `x` to the target **MDEV** and the dependent feature, respectively. These are cast as a NumPy arrays by calling the `values` attribute. The dependent feature's array is reshaped to the format expected by scikit-learn; this is only necessary when modeling a one-dimensional feature space. The model is then instantiated and fitted on the data. For linear regression, the fitting consists of computing the model parameters using the ordinary least squares method (minimizing the sum of squared errors for each sample). Finally, after determining the parameters, we predict the target variable and use the results to calculate the **MSE**.

5. Call the `get_mse` function for both **RM** and **LSTAT**, by running the cell containing the following:

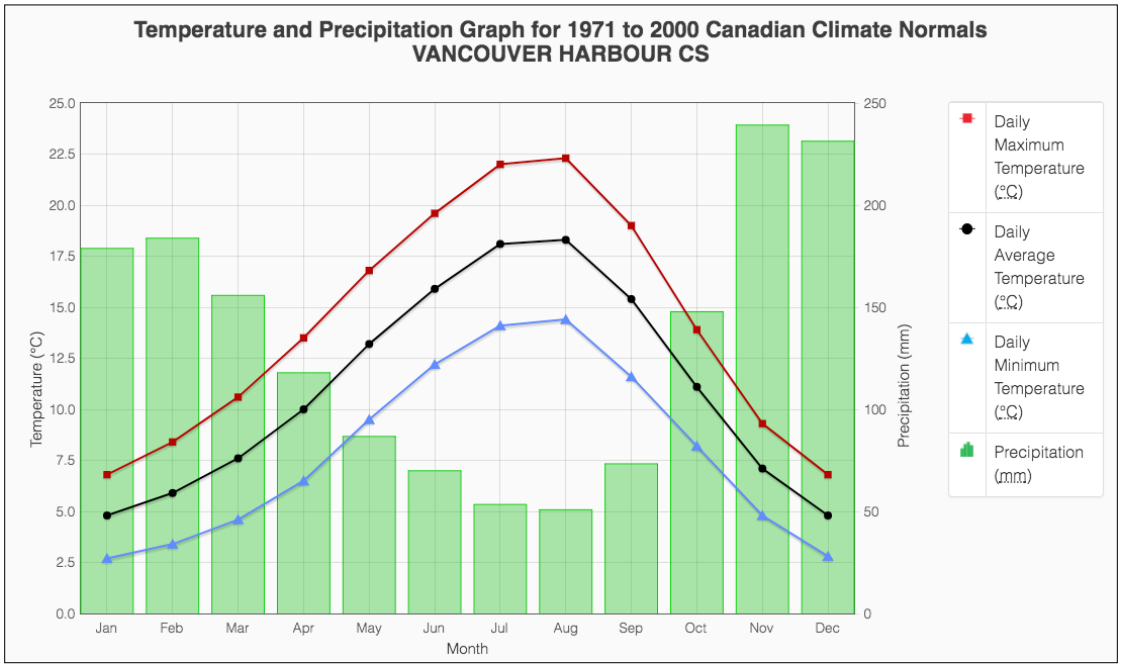
```
get_mse(df, 'RM')
get_mse(df, 'LSTAT')
```



Comparing the **MSE**, it turns out the error is slightly lower for **LSTAT**. Looking back to the scatter plots, however, it appears that we might have even better success using a polynomial model for **LSTAT**. In the next activity, we will test this by computing a third-order polynomial model with scikit-learn.

20

Forgetting about our Boston housing dataset for a minute, consider another real-world situation where you might employ polynomial regression. The following example is modeling weather data. In the following plot, we see temperatures (lines) and precipitations (bars) for Vancouver, BC, Canada:

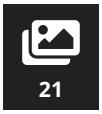


Any of these fields are likely to be fit quite well by a fourth-order polynomial. This would be a very valuable model to have, for example, if you were interested in predicting the temperature or precipitation for a continuous range of dates.

Note

You can find the data source for this here: `http://climate.weather.gc.ca/climate_normals/results_e.html?stnID=888`.

Activity B: Building a Third-Order Polynomial Model



Scenario

Shifting our attention back to the Boston housing dataset, we would like to build a third-order polynomial model to compare against the linear one. Recall the actual problem we are trying to solve: predicting the median house value, given the lower class population percentage. This model could benefit a prospective Boston house purchaser who cares about how much of their community would be lower class.

Aim

Use scikit-learn to fit a polynomial regression model to predict the median house value (**MEDV**), given the **LSTAT** values. We are hoping to build a model that a lower mean-squared error (**MSE**).

Steps for completion

1. Scroll to the empty cells at the bottom of `Subtopic C` in your Jupyter Notebook. These will be found beneath the linear-model **MSE** calculation cell under the `Activity` heading.

Note

You should fill these empty cells in with code as we complete the activity. You may need to insert new cells as these become filled up; please do so as needed!

2. Given that our data is contained in the DataFrame `df`, we will first pull out our dependent feature and target variable using the following:

```
y = df['MEDV'].values
x = df['LSTAT'].values.reshape(-1,1)
```

This is identical to what we did earlier for the linear model.

3. Check out what x looks like by printing the first few samples with `print(x[:3])`:

```
print('x =')
print(x[:3], '...etc')
```

```
x =
[[ 4.98]
 [ 9.14]
 [ 4.03]] ...etc
```

Notice how each element in the array is itself an array with length 1. This is what `reshape(-1,1)` does, and it is the form expected by scikit-learn.

4. Next we are going to transform x into "polynomial features". The rationale for this may not be immediately obvious but will be explained shortly.
Import the appropriate transformation tool from scikit-learn and instantiate the third-degree polynomial feature transformer:

```
from sklearn.preprocessing import PolynomialFeatures
poly = PolynomialFeatures(degree=3)
```

5. At this point, we simply have an instance of our feature transformer. Now let's use it to transform the **LSTAT** feature (as stored in the variable x) by running the `fit_transform` method.
Build the polynomial feature set by running the following code:

```
x_poly = poly.fit_transform(x)
```

6. Check out what `x_poly` looks like by printing the first few samples with `print(x_poly[:3])`.

```
print('x_poly =')
print(x_poly[:3], '...etc')
```

```
x_poly =
[[   1.         4.98      24.8004   123.505992]
 [   1.         9.14      83.5396   763.551944]
 [   1.         4.03      16.2409    65.450827]] ...etc
```

Unlike x, the arrays in each row now have length 4, where the values have been calculated as x^0, x^1, x^2 and x^3.

We are now going to use this data to fit a linear model. Labeling the features as *a*, *b*, *c* and *d* and we will calculate the coefficients a^0, a^1, a^2, and a^4 and of the linear model:

$$y=a_0a+a_1b+a_2c+a_3d$$

We can plug in the definitions of , , and to get the following polynomial model, where the coefficients are the same as above:

$$y=a_0+a_1x+a_2x^2+a_3x^3$$

7. We'll import the `LinearRegression` class and build our linear classification model the same way as before, when we calculated the MSE. Run the following:

```
from sklearn.linear_model import LinearRegression
clf = LinearRegression()
clf.fit(x_poly, y)
```

8. Extract the coefficients and print the polynomial model using the following code:

```
a_0 = clf.intercept_ + clf.coef_[0] # intercept
a_1, a_2, a_3 = clf.coef_[1:]       # other coefficients

msg = 'model: y = {:.3f} + {:.3f}x + {:.3f}x^2 + {:.3f}
x^3'\
        .format(a_0, a_1, a_2, a_3)
print(msg)
```

```
msg = 'model: y = {:.3f} + {:.3f}x + {:.3f}x^2 + {:.3f}x^3'\
        .format(x_0, x_1, x_2, x_3)
print(msg)
```

```
model: y = 48.650 + -3.866x + 0.149x^2 + -0.002x^3
```

To get the actual model intercept, we have to add the `intercept_` and `coef_[0]` attributes. The higher-order coefficients are then given by the remaining values of `coef_`.

9. Determine the predicted values for each sample and calculate the residuals by running the following code:

```
y_pred = clf.predict(x_poly)
resid_MEDV = y - y_pred
```

10. Print some of the residual values by running `print(resid_MEDV[:10])`:

```
print('residuals =')
print(resid_MEDV[:10], '...etc')

residuals =
[ -8.84025736  -2.61360313  -0.65577837  -5.11949581   4.23191217
  -3.56387056   3.16728909  12.00336372   4.03348935   2.87915437] ...etc
```

We'll plot these soon to compare with the linear model residuals, but first we will calculate the MSE.

1. Run the following code to print the MSE for the third-order polynomial model:

```
from sklearn.metrics import mean_squared_error
error = mean_squared_error(y, y_pred)
print('mse = {:.2f}'.format(error))
```

```
error = mean_squared_error(y, y_pred)
print('mse = {:.2f}'.format(error))

mse = 28.88
```

As can be seen, the **MSE** is significantly less for the polynomial model compared to the linear model (which was 38.5). This error metric can be converted to an average error in dollars by taking the square root. Doing this for the polynomial model, we find the average error for the median house value is only $5,300.

Now we'll visualize the model by plotting the polynomial line of best fit along with the data.

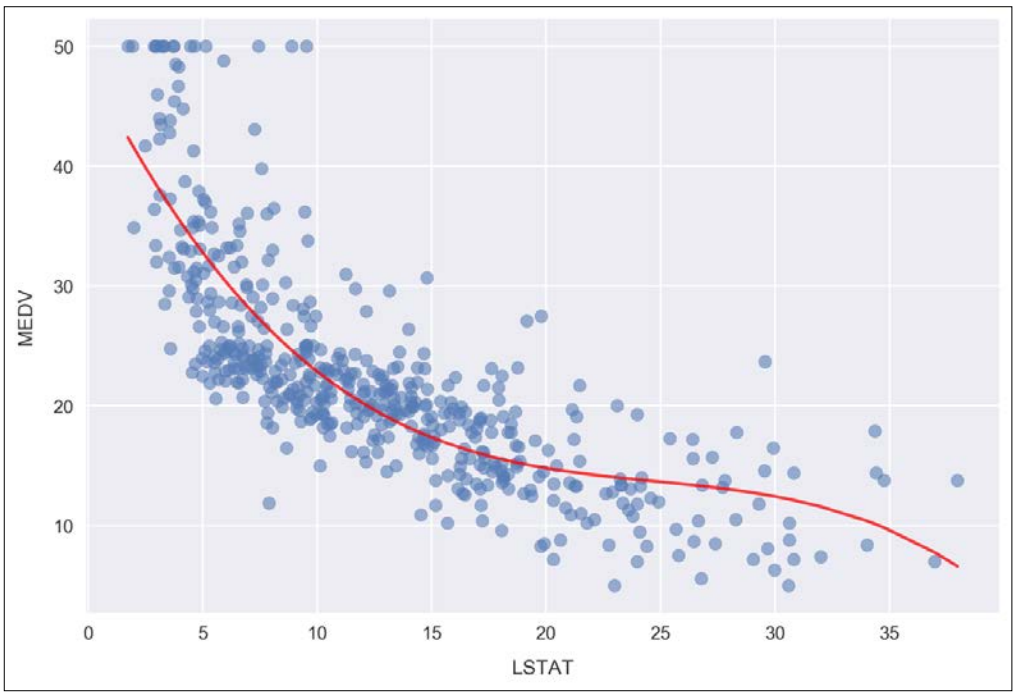
2. Plot the polynomial model along with the samples by running the following:

```
fig, ax = plt.subplots()

# Plot the samples
ax.scatter(x.flatten(), y, alpha=0.6)

# Plot the polynomial model
x_ = np.linspace(2, 38, 50).reshape(-1, 1)
x_poly = poly.fit_transform(x_)
y_ = clf.predict(x_poly)
ax.plot(x_, y_, color='red', alpha=0.8)

ax.set_xlabel('LSTAT'); ax.set_ylabel('MEDV');
```

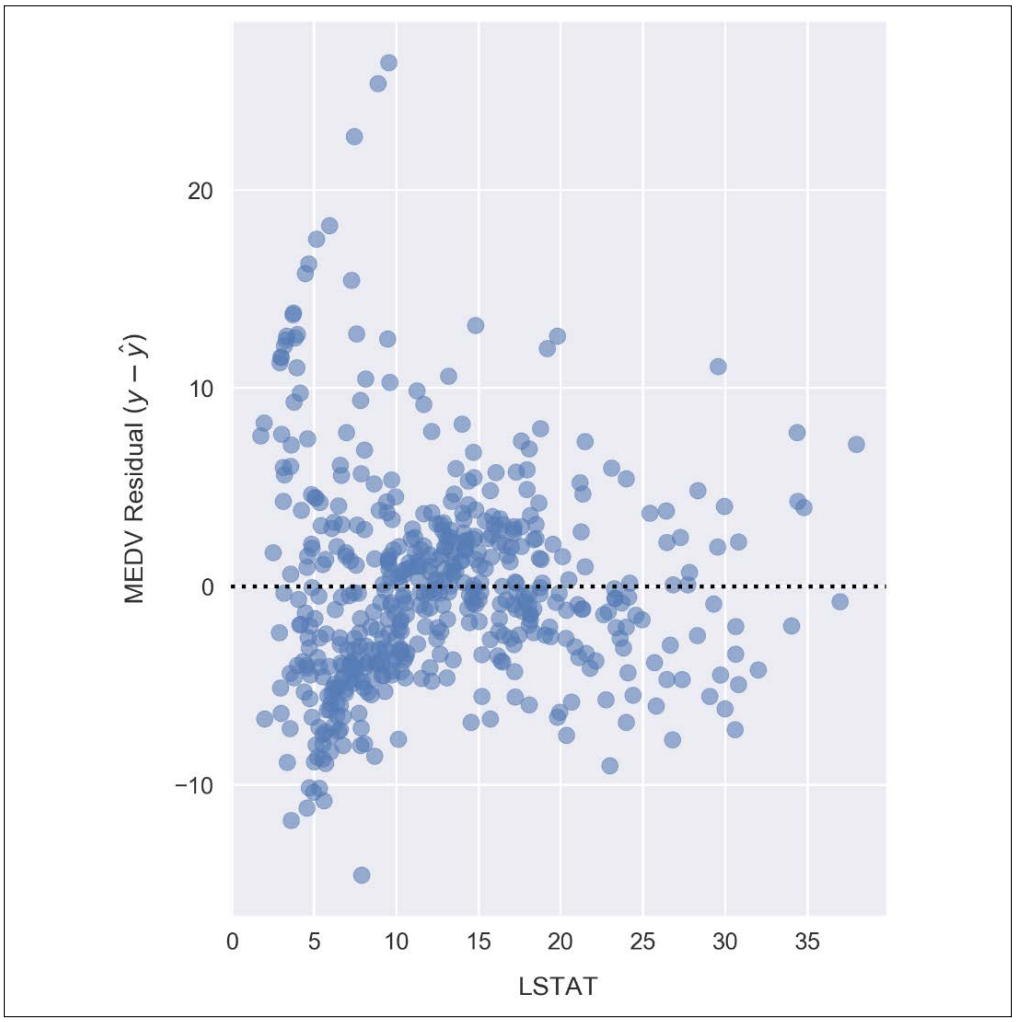


Here we are plotting the red curve by calculating the polynomial model predictions on an array of `x` values. The array of `x` values was created using `np.linspace`, resulting in 50 values arranged evenly between 2 and 38.

Now we'll plot the corresponding residuals. Whereas we used Seaborn for this earlier, we'll have to do it manually to show results for a scikit-learn model. Since we already calculated the residuals earlier, as reference by the `resid_MEDV` variable, we simply need to plot this list of values on a scatter chart.

3. Plot the residuals by running the following:

```
fig, ax = plt.subplots(figsize=(5, 7))
ax.scatter(x, resid_MEDV, alpha=0.6)
ax.set_xlabel('LSTAT')
ax.set_ylabel('MEDV Residual $(y-\hat{y})$')
plt.axhline(0, color='black', ls='dotted');
```



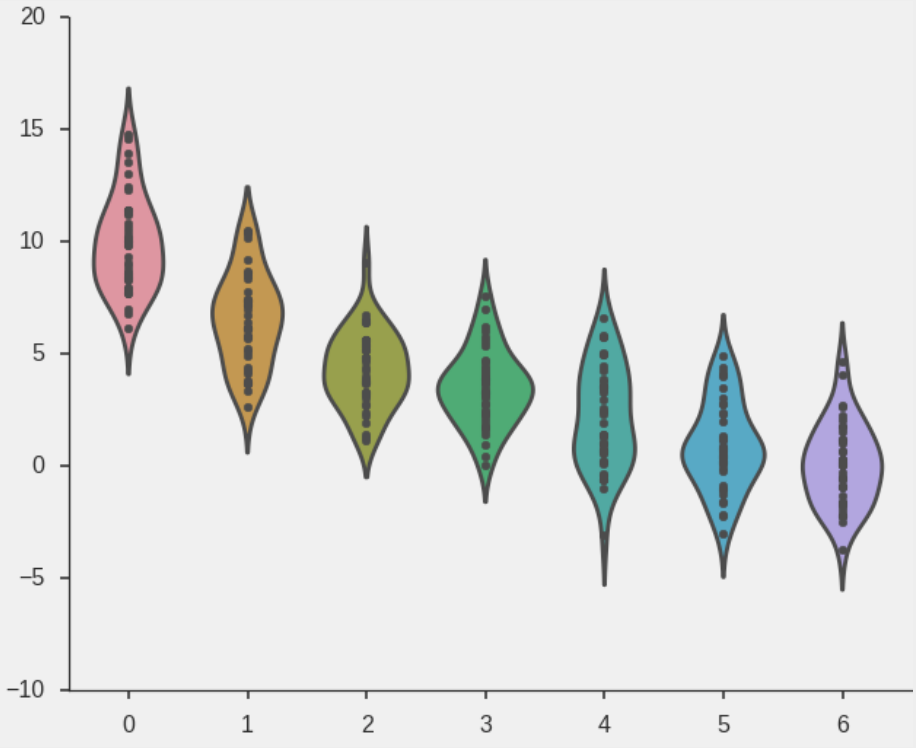
Compared to the linear model LSTAT residual plot, the polynomial model residuals appear to be more closely clustered around $y - \hat{y} = 0$. Note that y is the sample **MEDV** and ŷ is the predicted value. There are still clear patterns, such as the cluster near $x = 7$ and $y = -7$ that indicates suboptimal modeling.

Having successfully modeled the data using a polynomial model, let's finish up this lesson by looking at categorical features. In particular, we are going to build a set of categorical features and use them to explore the dataset in more detail.

Illustrate

Use this illustration point to show the students an example of using segmentation in data analysis.

As a specific example, imagine you are evaluating the return on investment from an ad campaign. The data you have access to contain measures of some calculated **return on investment** (**ROI**) metric. These values were calculated and recorded daily and you are analyzing data from the last year. You have been tasked with finding data-driven insights on ways to improve the ad campaign. Looking at the ROI daily timeseries, you see a weekly oscillation in the data. Segmenting by day of the week, you find the following ROI distributions (where 0 represents the first day of the week and 6 represents the last).



This shows clearly that the ad campaign achieves the largest ROI near the beginning of the week, tapering off later. The recommendation, therefore, may be to reduce ad spending in the latter half of the week. To continue searching for insights, you could also imagine repeating the same process for ROI grouped by month.

Subtopic D: Using Categorical Features for Segmentation Analysis

22

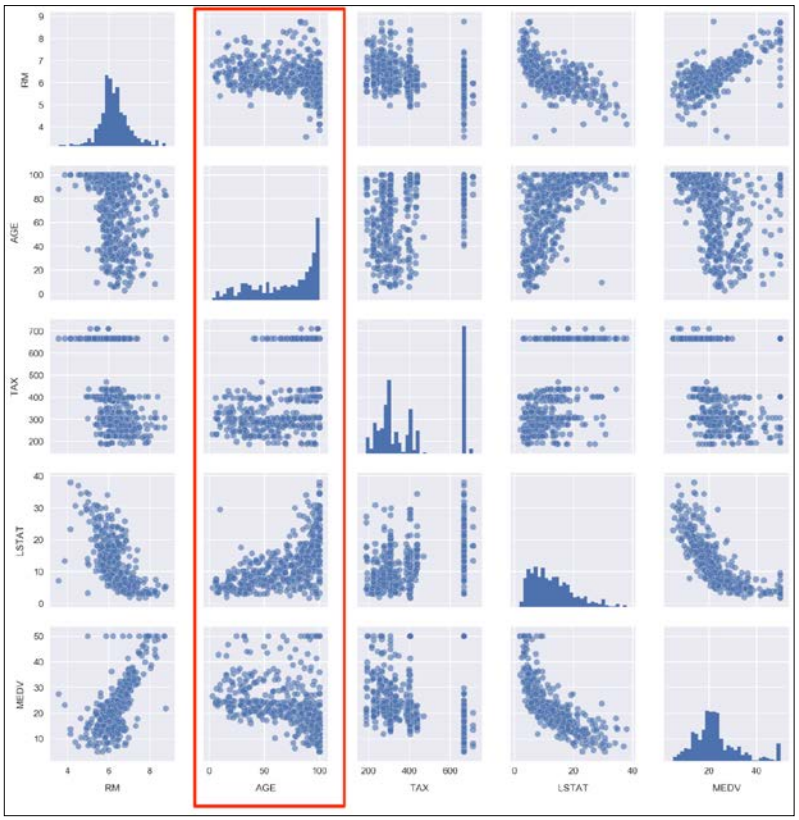
Often, we find datasets where there are a mix of continuous and categorical fields. In such cases, we can learn about our data and find patterns by segmenting the continuous variables with the categorical fields.

Since we don't have any categorical fields in the Boston housing dataset we are working with, we'll create one by effectively discretizing a continuous field. In our case, this will involve binning the data into "low", "medium", and "high" categories. It's important to note that we are not simply creating a categorical data field to illustrate the data analysis concepts in this section. As will be seen, doing this can reveal insights from the data that would otherwise be difficult to notice or altogether unavailable.

Exercise

Create categorical fields from continuous variables and make segmented visualizations

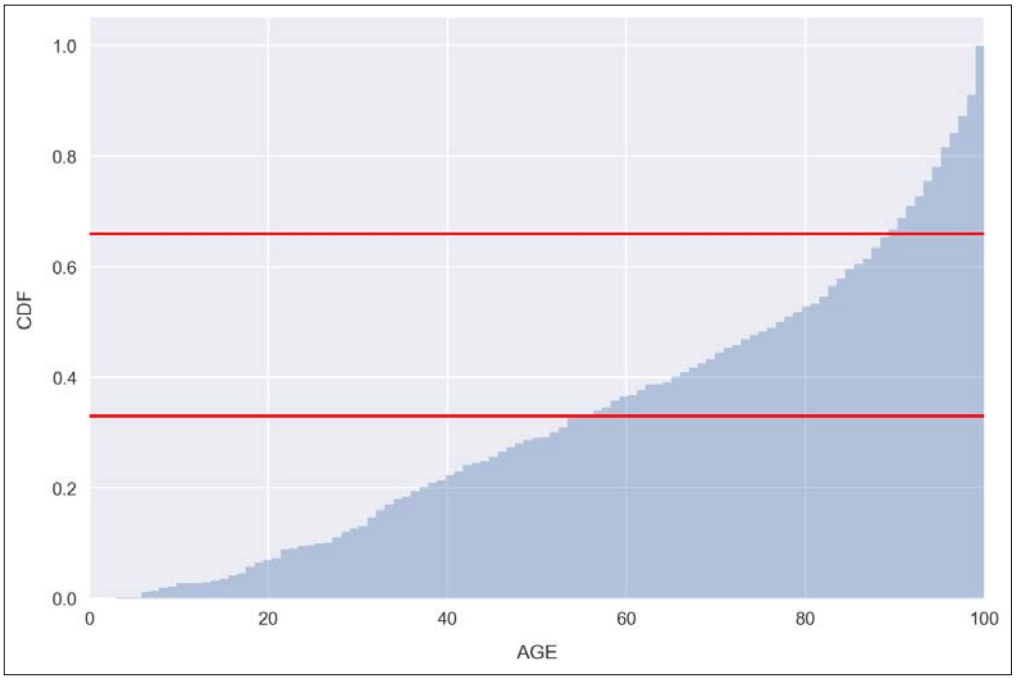
1. Scroll up to the pairplot in the Jupyter Notebook where we compared **MEDV**, **LSTAT**, **TAX**, **AGE**, and **RM**:



Take a look at the panels containing AGE. As a reminder, this feature is defined as the *proportion of owner-occupied units built prior to 1940*. We are going to convert this feature to a categorical variable. Once it's been converted, we'll be able to replot this figure with each panel segmented by color according to the age category.

2. Scroll down to `Subtopic D: Building and exploring categorical features` and click into the first cell. Type and execute the following to plot the AGE cumulative distribution:

```
sns.distplot(df.AGE.values, bins=100,
             hist_kws={'cumulative': True},
             kde_kws={'lw': 0})
plt.xlabel('AGE')
plt.ylabel('CDF')
plt.axhline(0.33, color='red')
plt.axhline(0.66, color='red')
plt.xlim(0, df.AGE.max());
```



Note that we set `kde_kws={'lw': 0}` in order to bypass plotting the kernel density estimate in the above figure.

Looking at the plot, there are very few samples with low AGE, whereas there are far more with a very large AGE. This is indicated by the steepness of the distribution on the far right-hand side.

The red lines indicate 1/3 and 2/3 points in the distribution. Looking at the places where our distribution intercepts these horizontal lines, we can see that only about 33% of the samples have AGE less than 55 and 33% of the samples have AGE greater than 90! In other words, a third of the housing communities have less than 55% of houses build prior to 1940. These would be considered relatively new communities. On the other end of the spectrum, another third of the housing communities have over 90% of homes built prior to 1940. These would be considered very old.

We'll use the places where the red horizontal lines intercept the distribution as a guide to split the feature into categories: **Relatively New**, **Relatively Old**, and **Very Old**.

3. Setting the segmentation points as 50 and 85, create a new categorical feature by running the following code:

```
def get_age_category(x):
    if x < 50:
        return 'Relatively New'
    elif 50 <= x < 85:
        return 'Relatively Old'
    else:
        return

'Very Old'

df['AGE_category'] = df.AGE.apply(get_age_category)
```

Here we are using the very handy Pandas method `apply`, which applies a function to a given column or set of columns. The function being applied, in this case `get_age_category`, should take one argument representing a row of data and return one value for the new column. In this case, the row of data being passed is just a single value, the AGE of the sample.

Caution

The `apply` method is great because it can solve a variety of problems and allows for easily readable code. Often though, vectorized methods such as `pd.Series.str` can accomplish the same thing much faster. Therefore, it's advised to avoid using it if possible, especially when working with large datasets. We'll see some examples of vectorized methods in the upcoming lessons.

4. Check on how may samples we've grouped into each age category by typing `df.groupby('AGE_category').size()` into a new cell and running it:

```
# Check the segmented counts
df.groupby('AGE_category').size()
```

```
AGE_category
Relatively New    147
Relatively Old    149
Very Old          210
dtype: int64
```

Looking at the result, it can be seen that two class sizes are fairly equal, and the Very Old group is about 40% larger. We are interested in keeping the classes comparable in size, so that each is well represented and it's straightforward to make inferences from the analysis.

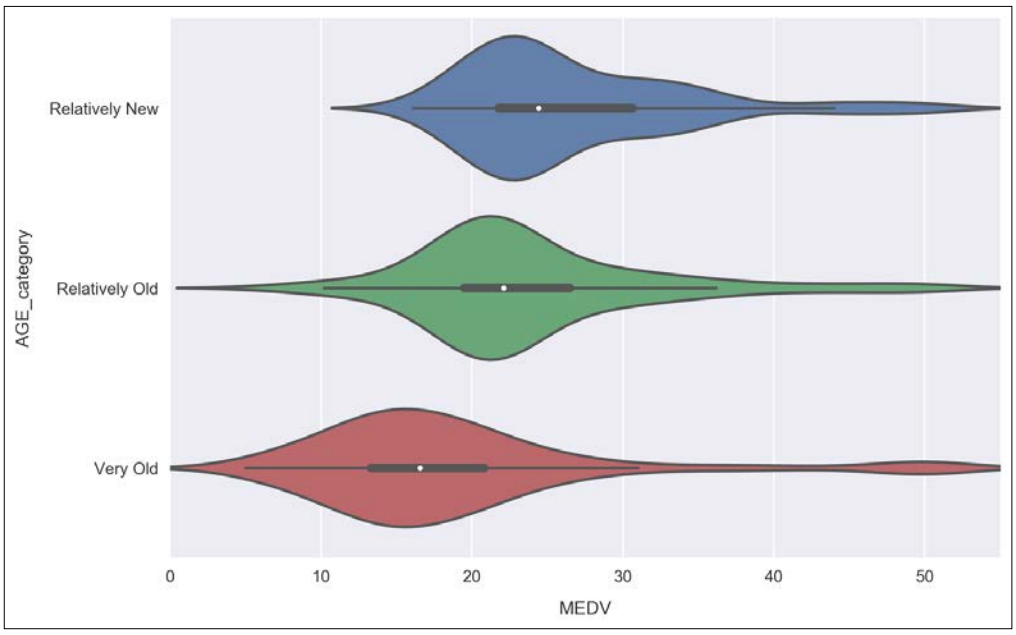
Note

It may not always be possible to assign samples into classes evenly, and in real-world situations, it's very common to find highly imbalanced classes. In such cases, it's important to keep in mind that it will be difficult to make statistically significant claims with respect to the under-represented class. Predictive analytics with imbalanced classes can be particularly difficult. The following blog post offers an excellent summary on methods for handling imbalanced classes when doing machine learning: `https://svds.com/learning-imbalanced-classes/`.

Let's see how the target variable is distributed when segmented by our new feature `AGE_category`.

5. Make a violin plot by running the following code:

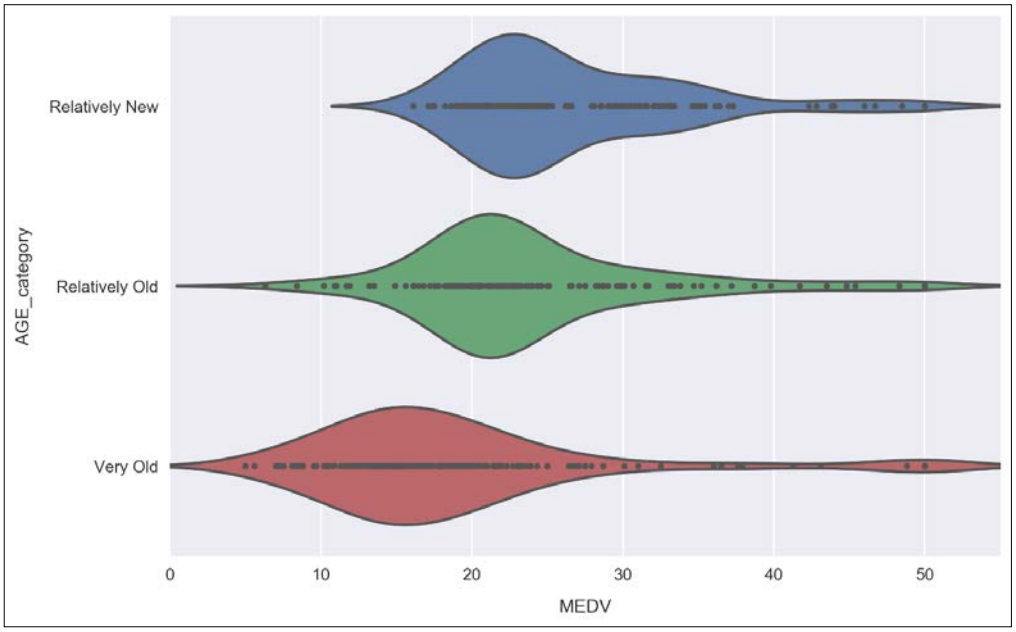
```
sns.violinplot(x='MEDV', y='AGE_category', data=df,
               order=['Relatively New', 'Relatively Old',
'Very Old']
```



The violin plot shows a kernel density estimate of the median house value distribution for each age category. We see that they all resemble a normal distribution. The Very Old group contains the lowest median house value samples and has a relatively large width, whereas the other groups are more tightly centered around ~~the~~ average. The young group is skewed to the high end, which is evident from the enlarged right half and position of the white dot in the thick black line within the body of the distribution.

This white dot represents the mean and the thick black line spans roughly 50% of the population (it fills to the first quantile on either side of the white dot). The thin black line represents boxplot whiskers and spans 95% of the population. This inner visualization can be modified to show the individual data points instead, by passing `inner='point'` to `sns.violinplot()`. Let's do that now.

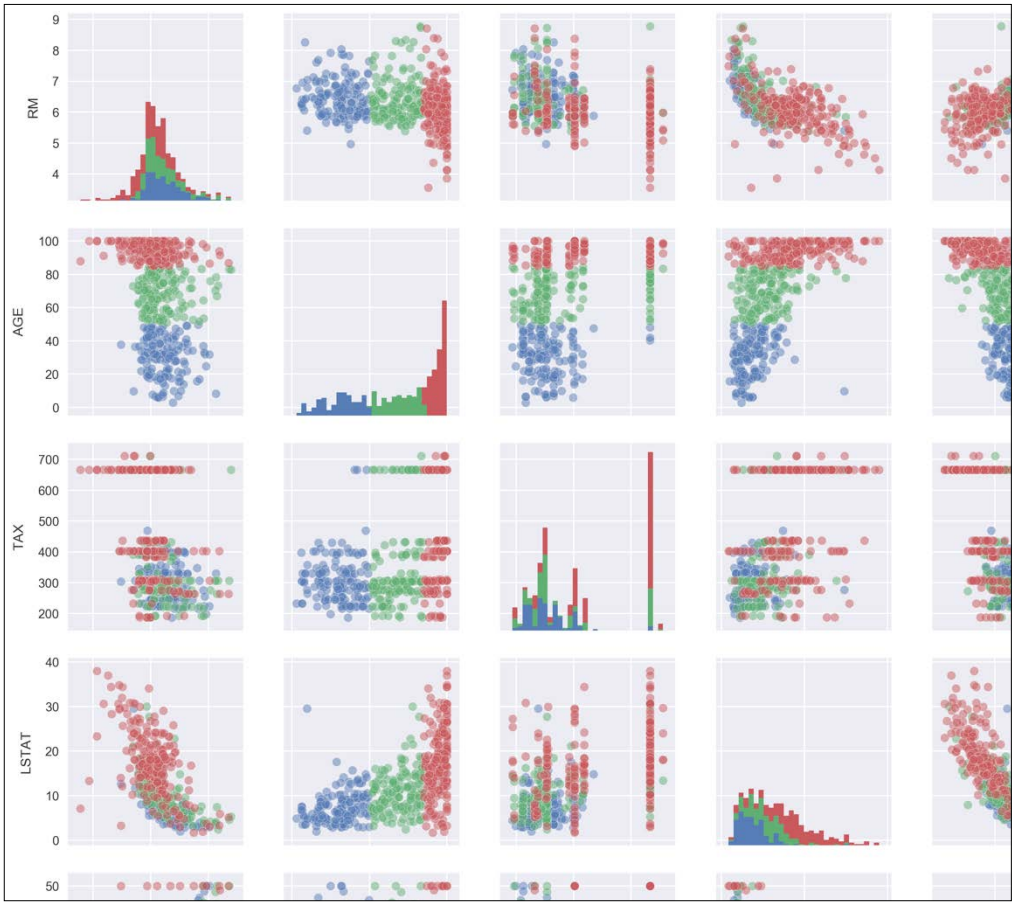
6. Redo the violin plot adding the `inner='point'` argument to the `sns.violinplot` call:



It's good to make plots like this for test purposes, to see how the underlying data connects to the visual. We can see, for example, how there are no median house values lower than roughly $16,000 for the Relatively New segment, and therefore the distribution tail actually contains no data. Due to the small size of our dataset (only about 500 rows), we can see this is the case for each segment.

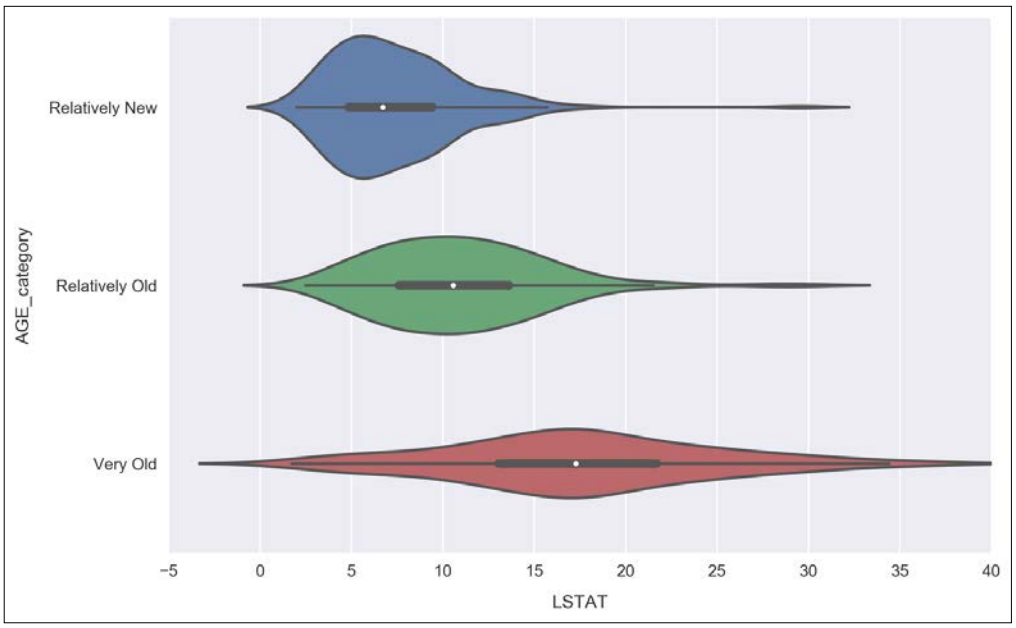
7. Re-do the pairplot from earlier, but now include color labels for each **AGE** category. This is done by simply passing the `hue` argument, as seen below:

```
cols = ['RM', 'AGE', 'TAX', 'LSTAT', 'MEDV', 'AGE_
category']
sns.pairplot(df[cols], hue='AGE_category',
             hue_order=['Relatively New', 'Relatively Old',
'Very Old'],
             plot_kws={'alpha': 0.5}, diag_kws={'bins':
30}
```



Looking at the histograms, the underlying distributions of each segment appear similar for **RM** and **TAX**. The **LSTAT** distributions, on the other hand, look more distinct. We can focus on them in more detail by again using a violin plot.

8. Make a violin plot comparing the **LSTAT** distributions for each `AGE_category` segment:



Unlike the **MEDV** violin plot, where each distribution had roughly the same width, here we see the width increasing along with **AGE**. Communities with primarily old houses (the Very Old segment) contain anywhere from very few to many lower class residents, whereas Relatively New communities are much more likely to be predominantly higher class, with over 95% of samples having less lower class percentages than the Very Old communities. This makes sense, because Relatively New neighborhoods would be more expensive.

Answers

1. True
2. a
3. b
4. c
5. False
6. d
7. d
8. True
9. a
10. b
11. a
12. d
13. c
14. b
15. True

Summary

In this lesson, you have seen the fundamentals of data analysis in Jupyter.

We began with usage instructions and features of Jupyter such as magic functions and tab completion. Then, transitioning to data-science-specific material, we introduced the most important libraries for data science with Python.

In the latter half of the lesson, we ran an exploratory analysis in a live Jupyter Notebook. Here we used visual assists such as scatter plots, histograms, and violin plots to deepen our understanding of the data. We also performed simple predictive modeling, a topic which will be the focus of the following lesson in this course.

Practice Questions

1. A Jupyter Notebook is usually run on a locally hosted web server, for example, `http://localhost:8888`.
   a. True
   b. False

2. A Jupyter Notebook has shared memory between all cells. For example, if `a = 5` is run in a cell, then any other cell will know the value for `a` is `5`.
   a. Yes
   b. No, only cells below previously run cells share their memory
   c. No, cells never share memory

3. A Jupyter Notebook kernel does what function?
   a. Manages external packages
   b. Provides programming language support (Python)
   c. Renders the Notebook GUI

4. Jupyter has special functions such as `%time` and `%matplotlib inline`. What are these called?
   a. Jupyter commands
   b. IPython modules
   c. Magic functions

5. Don't bother keeping the rough work you've done in a Jupyter Notebook. Only the final version matters.
   a. True
   b. False

6. When running a cell, which of the following will be displayed under the cell?
   a. `stdout` code output (for example, result of a `print` statement)
   b. `stderr` code output (for example, an error message)
   c. The string representation of the object in the final line
   d. All of the above

7. Tab completion can do which of the following?
   a. List available modules of imported external libraries
   b. Function and variable completion
   c. Get help by displaying the docstring
   d. Both a and b

8. The most important Python libraries for data science are external (that is, not in the standard library that is usually distributed with Python).
   a. True
   b. False

9. What is the Pandas library useful for?
   a. Working with tabular data
   b. Working with 3D matrices
   c. Working with dictionaries
   d. Working with long strings

10. How is the Seaborn library different from matplotlib?
    a. Seaborn is lower level, offering more options for customizing plot details but requiring more code
    b. Seaborn is higher level, allowing for more complicated plots with less code

11. Of the following list, what is the most important thing to do to ensure your Jupyter Notebook is reproducible?
    a. Print your PC, Python, and external library software versions in the Notebook
    b. Export the Notebook as HTML
    c. Save and timestamp your rough work
    d. Use Python 3

12. What code returns the column `val_1` from the Pandas DataFrame `df`?
    a. `df.val_1`
    b. `df.loc['val_1']`
    c. `df['val_1']`
    d. Both a and c
    e. All of the above

13. What is the name of the Pandas DataFrame method that calculates a table of metrics for the dataset, including the mean and standard deviation?
    a. `summary`
    b. `dtypes`
    c. `describe`
    d. `corr`

14. Patterns in the residual plot indicate which of the following?
    a. The model has a good fit
    b. The model has room for improvement
    c. There are outliers in the dataset

15. After instantiating a scikit-learn model as referenced by the variable `clf`, the model parameters are calculated by running `clf.fit(x, y)`, where `x` references the feature(s) and `y` references the target.
    a. True
    b. False