
Minimalist Data Wrangling with Python

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Marek Gagolewski

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This is a draft of *Minimalist Data Wrangling with Python* by Marek Gagolewski¹. It's distributed in the hope that it'll be useful. Any bug/typos reports/fixes² are appreciated. Although available online, this is a whole course, and should be read from the beginning to the end. In particular, refer to the *Preface* for general introductory remarks. Enjoy.

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¹ <https://www.gagolewski.com>

² https://github.com/gagolews/datawranglingpy/blob/master/CODE_OF_CONDUCT.md

³ <https://www.gagolewski.com>

⁴ <https://creativecommons.org/licenses/by-nc-nd/4.0/>

⁵ <https://datawranglingpy.gagolewski.com/datawranglingpy.pdf>

⁶ <https://datawranglingpy.gagolewski.com/>

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Preface

0.1 The Art of Data Wrangling

The broadly-conceived *data science*²⁹ aims at making sense of and generating predictions from data that have been collected in large quantities from various sources, e.g., physical sensors, files, databases, or (pseudo)random number generators. It can take different forms, e.g., vectors, matrices and other tensors, graphs, audio/video streams, text, etc. With the advent of the internet era, data have become ubiquitous.

Exercise 0.1 *Think about how much information you consume and generate when you interact with social media or news feeds every day.*

Data-driven decision making, modelling, and prediction has already proven itself very useful in numerous different domains:

- healthcare,
- food production,
- pharmaceuticals,
- transportation,
- financial services (banking, insurance, investment funds),
- real estate,
- retail.

Okay, to be frank, the above list was generated by duckduckgoing the “biggest industries” query. That was a very easy task; data science (and its very different flavours, including statistics, operational research, machine learning, artificial intelligence, and so forth) is everywhere. Basically, wherever we have data and there is a need to improve some processes or discover new aspects about a problem domain, there is a place for data-driven solutions.

²⁹ Traditionally known under the name *statistics*.

Of course, it's not all about business revenue (luckily). We can do a lot of great work for greater good; with the increased availability of open data, everyone can be a reporter, an engaged citizen that seeks truth, a volunteer for a non-for profit NGO, etc. Also, there are researchers (remember that the main role of most universities is still to spread the advancement of knowledge and not to make money!) that need these methods to make new discoveries, e.g., in psychology, economics, sociology, agriculture, engineering, biotechnology, pharmacy, medicine, genetics, you name it.

Important: Data rarely come in a *tidy* and *tamed* form. Performing accurate exploration and modelling heavily relies on *data wrangling*, which is the very broad process of appropriately preparing raw data for further analysis.

And thus, in this course, we are going to explore methods for:

- performing exploratory data analysis, including aggregating and visualising numerical and categorical data,
- working with different types of data (e.g., numerical, categorical, text, time series),
- cleaning data gathered from structured and unstructured sources, e.g., by identifying outliers, normalising strings, extracting numbers from text, imputing missing data,
- transforming, selecting, and extracting features, dimensionality reduction,
- identifying naturally occurring data clusters, comparing data between groups,
- data approximation/modelling using the simplest probability distributions and the most easy to understand statistical/machine learning algorithms.

0.2 Aims, Scope, and Design Philosophy

Most of the time during the course of this course, we will be writing code in [Python⁷](#). The [2021 StackOverflow Developer Survey⁸](#) lists it as the 2nd most popular programming language used nowadays (slightly behind JavaScript).

Over the last years, Python has proven a very robust choice for learning and applying

⁷ <https://www.python.org/>

⁸ <https://insights.stackoverflow.com/survey/2021#technology-most-popular-technologies>

data wrangling techniques. This is possible thanks to the famous⁹ high quality packages written by the devoted community of open source programmers, including but not limited to `numpy`¹⁰, `scipy`¹¹, `pandas`¹², `matplotlib`¹³, `seaborn`¹⁴, and `sklearn`¹⁵.

Important: Note that we will introduce the Python language from scratch and that we do not require any prior programming experience. Nevertheless, learning how to code is hard work; if you want to succeed, you will have to spend a decent amount of time getting your hands dirty by writing programs which solve the suggested problem sets, studying technical manuals, and so forth. One does not become a qualified and respected engineer by simply *reading* online tutorials or books.

Python and third-party packages written therein are amongst many software tools which can help gain new knowledge from data. Other open source choices include, e.g., `R`¹⁶ and `Julia`¹⁷. There are also some commercial solutions available on the market, but we believe that ultimately all software should be free¹⁸, therefore we are not going to talk about them at all.

Note: We put great emphasis on developing *transferable skills* so that all that we learn here can be then applied quite easily in other environments. In other words, this is a course on data wrangling (*with* Python), and not a course *on* Python (with examples in data wrangling). This is not a book of recipes. We are aiming for understanding and becoming independent learners.

The skills we are going to develop in this course are *fundamental* for the success in the numerous jobs available in our industry all over the world. And data engineers, data scientists, machine learning specialists, statisticians, and business analysts are amongst the most well-paid specialists¹⁹. Money does not bring joy, but luckily it is a very interesting domain anyway. All what we shall learn here can be used for improving different processes, in research, helping NGOs, debunking false news or wishful thinking, main-

⁹ <https://insights.stackoverflow.com/survey/2021#other-frameworks-and-libraries>

¹⁰ <https://numpy.org/>

¹¹ <https://scipy.org/>

¹² <https://pandas.pydata.org/>

¹³ <https://matplotlib.org/>

¹⁴ <https://seaborn.pydata.org/>

¹⁵ <https://scikit-learn.org/>

¹⁶ <https://www.r-project.org/>

¹⁷ <https://julialang.org/>

¹⁸ <https://www.gnu.org/philosophy/free-sw.en.html>

¹⁹ <https://insights.stackoverflow.com/survey/2021#other-frameworks-and-libraries>

taining quality of various industries, and doing any other good deeds for the advancement of humanity.

We are going to study many methods and algorithms that stood the test of time and that continue to inspire the researchers and practitioners. After all, many *complex* algorithms are merely variations on or clever combinations of the most basic ones. You might not see it now, but this will become evident as we progress.

Most importantly, however, we will get to know their limitations, which they are many. Being sceptical and cautious is one of the traits of a good scientist.

Note that we will definitely not be avoiding mathematical notation so as to maintain a healthy level of generality. Mathematics is both a universal tool and a language for describing the methods for processing various data structures and analysing the properties thereof. The people fluent in mathematics are those who have invented or derived most of the methods discussed herein, we must thus be too.

0.3 ✖ Structure

Note: This part is under construction. Please come back later.

The material has been divided into 5 parts.

0.4 The Rules

Our goal here, in the long run, is for you to become a skilled expert who is independent, ethical, and capable of critical thinking; one who hopefully will make a small contribution to make this world a slightly better place.

To guide you through it, and not to get lost, we have a few rules for you.

1. *Follow the rules.*
2. *Technical textbooks are not belletristic.* Sometimes a single page will be very meaning-intense. Do not try to consume too much at the same time. Go for a walk, reflect on what you have learned, build connections between different concepts. In case of any

doubt, go back to one of the previous sections. Learning is an iterative process, not a linear one.

3. *Solve all the suggested exercises.* Also, try to implement most of the methods you learn about from scratch instead of looking for copy-paste solutions on the internet. How else are you going to master the material and learn the necessary programming skills?
4. *Code is an integral part of the text.* Each piece of good code is worth 1234 words (on average). Do not skip it. On the contrary, you should play and experiment with it. Run every major line of code and inspect the results generated. What is the type (class) of object returned. If it is an array or a data frame, what is its shape? And so forth. What would happen if we replaced X by Y? Do not fret, your computer will not blow up.
5. *Harden up³⁰.* Your journey towards expertise will take years, there are no shortcuts, but it will be quite enjoyable every now and then, so don't give up. Still, sitting all day in front of your computer is unhealthy – exercise and socialise between 28 and 31 times per month, because you're not, nor will ever be, a robot!
6. *Learn maths.* Our field has a very long history and stands on the shoulders of many giants; the methods we use these days are merely minor variations on the classical, fundamental results that date back to Newton, Leibniz, Gauss, and Laplace. Therefore, in the long run, you will need some working knowledge in mathematics in order to be able to understand them (linear algebra, calculus, probability and statistics). Remember that software products/APIs seem to change frequently, but they are just a facade, a flashy wrapping around the methods we have been using for a very long time.
7. *Use only methods that you can explain.* Even though they may be easily accessible, you should refrain from working with algorithms/methods/models whose definitions (pseudocode, mathematical formulae, objective function they are trying to optimise) and properties you do not know, understand, or cannot rephrase in your own words.
8. *Compromises are inevitable³¹.* There will never be a single best metric, algorithm, way to solve all the problems. Even though some solutions might be better than others with regards to certain criteria, this will only be true under certain assumptions (*if* they fit a theoretical model). Beware that sometimes focusing too much on one criterion leads to undesirable consequences with respect to other ones. Therefore,

³⁰ Cyclists know.

³¹ Some people would refer to this rule as *There is no free lunch*, but in our – overall friendly – world, many things are actually free (see Rule #9), therefore this name is strongly misleading.

fraining from improving things might sometimes be better than pushing too hard. Always apply common sense.

9. *Be scientific and ethical.* Make your reports reproducible, your toolkit well-organised, and all the assumptions you make explicit. Develop a dose of scepticism and impartiality towards everything, from marketing slogans, through your ideological biases and other hotly debated topics. Most data analysis exercises end up with conclusions like: “it’s too early to tell”, “data don’t show it’s either way”, “there is a difference, but it is hardly significant”, “yeah, but our sample is not representative for the whole population” – and there is nothing wrong with this. Remember that it is highly unethical to use statistics to tell lies; this includes presenting only one side of the very complex reality and totally ignoring all the other ones (compare Rule#8). Using statistics for doing bad things (tracking users to find their vulnerabilities, developing products and services which are addictive) is a huge no-no!
 10. *The best things in life are free.* This includes the open source software we use in our journey. Spread the good news about it and – if you can – contribute something (even as small as reporting typos in their documentation or helping others in different forums when they are stuck with something) so that you are not only a taker. After all, it is our common responsibility.
-

0.5 About the Author

Marek Gagolewski²⁰ is currently a Senior Lecturer in Applied AI at Deakin University in Melbourne, VIC, Australia and an Associate Professor in Data Science (on long-term leave) at the Faculty of Mathematics and Information Science, Warsaw University of Technology, Poland and Systems Research Institute of the Polish Academy of Sciences.

His research interests include machine learning, data aggregation and clustering, computational statistics, mathematical modelling (science of science, sport, economics, etc.), and free (libre) data analysis software (`stringi`²¹, `genieclust`²², among `others`²³).

²⁰ <https://www.gagolewski.com>

²¹ <https://stringi.gagolewski.com>

²² <https://genieclust.gagolewski.com>

²³ <https://github.com/gagolews>

0.6 Acknowledgements

Minimalist Data Wrangling with Python bases on my experience as an author of a quite successful textbook *Przetwarzanie i analiza danych w języku Python* (Data Processing and Analysis in Python), [[GBC16]] that I have written (in Polish, 2016, published by PWN) with my former (successful) PhD students Maciej Bartoszuk and Anna Cena – thanks! The current book is a completely different work; however, its predecessor served as a great testbed for many ideas conveyed here.

The ideas have also been battle-tested at Warsaw University of Technology, Data Science Retreat (Berlin), and Deakin University (Geelong/Melbourne) – I thank all my students for the feedback given over the last 10 or so years.

Thank-you to all the authors and contributors of the Python packages that we use throughout this course: `numpy` [[H+20]], `scipy` [[V+20]], `matplotlib` [[Hun07]], `seaborn` [[Was21]], `pandas` [[McK17]], and `sklearn` [[PVG+11]]. Their version numbers are given in Section 1.4.

This book has been prepared in a Markdown superset called `MyST`²⁴, `Sphinx`²⁵, and TeX (XeLaTeX). Python code chunks have been processed with the R (sic!) package `knitr` [[Xie15]]. A little help of Makefiles, custom shell scripts, and Sphinx plugins (`sphinxcontrib-bibtex`²⁶, `sphinxcontrib-proof`²⁷) dotted the j's and crossed the f's. The `Ubuntu Mono`²⁸ font is used for the display of code.

²⁴ <https://myst-parser.readthedocs.io/en/latest/index.html>

²⁵ <https://www.sphinx-doc.org/>

²⁶ <https://pypi.org/project/sphinxcontrib-bibtex/>

²⁷ <https://pypi.org/project/sphinxcontrib-proof/>

²⁸ <http://font.ubuntu.com/>

Part I

Introducing Python

Getting Started with Python

1.1 Installing Python

Python³² was designed and implemented by a Dutch programmer Guido van Rossum in the late 1980s. It is a very popular³³ object-oriented programming language that is quite suitable for rapid prototyping. Its name is a tribute to the funniest British comedy troupe ever, therefore we will surely be having a jolly good laugh along our journey.

We will be using the reference implementation of the Python language (called `CPython`³⁴), version 3.8 (not: 2.x!).

A convenient way to start with Python is by installing a data science-oriented distribution called Anaconda, which features the language interpreter, the `conda` package manager, as well as a number of pre-installed packages (including `numpy`, `scipy`, `pandas`, `matplotlib`, `seaborn`, `jupyter`, etc.).

Exercise 1.1 Download³⁵ and install the latest version of Anaconda Individual Edition. If you run into any troubles, consult the official product documentation³⁶.

Note: The users of Unix-like operating systems (GNU/Linux, FreeBSD, etc.), just like yours truly, should prefer downloading Python via their native package manager (e.g., `sudo apt install python3` in Debian and Ubuntu). Then, installing³⁷ additional Python packages can either be installed by the said manager or directly from the Python Package Index (`PyPI`³⁸) via the `pip` tool.

GNU/Linux is the language of choice of machine learning engineers and data scientists

³² <https://www.python.org/>

³³ <https://insights.stackoverflow.com/survey/2021#technology-most-popular-technologies>

³⁴ <https://www.python.org>

³⁵ <https://www.anaconda.com/products/individual>

³⁶ <https://docs.anaconda.com/anaconda/install/>

³⁷ <https://packaging.python.org/en/latest/tutorials/installing-packages/>

³⁸ <https://pypi.org/>

both on the desktop and in the cloud. Switching to a free system at some point cannot be recommended highly enough.

1.2 Working with Jupyter Notebooks

JupyterLab³⁹ is a web-based development environment supporting numerous⁴⁰ programming languages, including of course Python; see Figure 1.1.

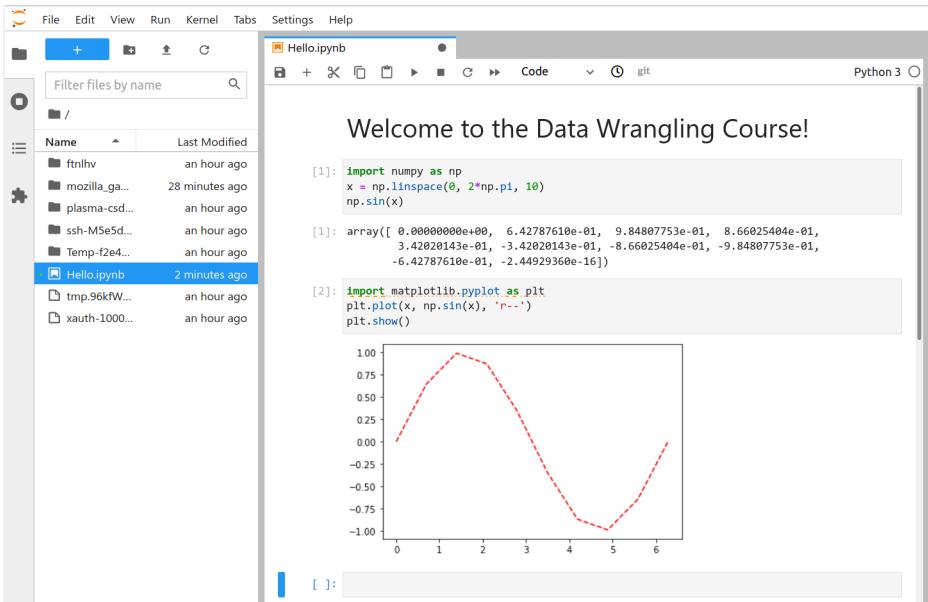


Figure 1.1: JupyterLab at a glance

In JupyterLab, we can work with:

- Jupyter notebooks⁴¹ – .ipynb documents combining code, text, plots, and other rich outputs; importantly, code chunks can be created, modified, and run interactively;

³⁹ <https://jupyterlab.readthedocs.io/en/stable/>

⁴⁰ <https://github.com/jupyter/jupyter/wiki/Jupyter-kernels>

⁴¹ <https://jupyterlab.readthedocs.io/en/stable/user/notebook.html>

the results together with discussion in textual form can be embedded inside the documents, which makes it a good reporting tool for our data science needs;

- code consoles – terminals for running code chunks interactively (read-eval-print loop);
- source files for many different languages – with syntax highlighting and the ability to send code to the associated consoles;

and many more.

Exercise 1.2 Head to the official [documentation⁴²](#) of the JupyterLab project and watch the introductory video linked in the Overview section.

Note: (***) JupyterLab is the definitely not the most convenient environment for doing real data science in Python (writing standalone scripts is the preferred option), but we have chosen it here because of its educative advantages (interactive, easy to start with, etc.).

If you are a more advanced student, you can consider, for example, [jupytext⁴³](#) as a means to create .ipynb files directly from Markdown files.

1.2.1 Launching JupyterLab

How we launch JupyterLab will vary from system to system and everyone needs to determine what is the best way to do it by themselves.

1. Users of the Anaconda distribution should be able to start JupyterLab via the [Anaconda Navigator⁴⁴](#), which can be accessed through the Start menu/application launcher. Read more in the [official manual⁴⁵](#).
2. Alternatively, open the Anaconda Prompt (Windows) or start the ordinary system terminal (`bash`, `zsh`, etc.) and type:

```
cd your/favourite/directory # change directory  
jupyter lab # or jupyter-lab, depending on the system
```

This should launch the JupyterLab server and open the corresponding web app in your default web browser.

⁴² <https://jupyterlab.readthedocs.io/en/stable/index.html>

⁴³ <https://jupytext.readthedocs.io/en/latest/>

⁴⁴ <https://docs.anaconda.com/anaconda/navigator/getting-started/#navigator-starting-navigator>

⁴⁵ <https://docs.anaconda.com/anaconda/user-guide/getting-started/#run-python-in-a-jupyter-notebook>

Note: Some commercial cloud-hosted instances or forks of the open source JupyterLab project are available on the market, but we endorse none of them (even though some of them are provided gratis, there are always strings attached). It is best to run our applications locally, where we are free⁴⁶ to be in full control over the software environment.

1.2.2 First Notebook

1. From JupyterLab, create a new notebook running a Python 3 kernel (for example, by selecting File → New → Notebook in the web app menu).
2. Select File → Rename Notebook and change the filename to `HelloWorld.ipynb`.

Important: The file is stored relative to the current working directory of the running JupyterLab server instance. Make sure you are able to locate `HelloWorld.ipynb` on your disk using your favourite file explorer (by the way, `.ipynb` is just a JSON file which can also be edited using an ordinary text editor).

3. Input the following in the code cell:

```
print("G'day!")
```

4. Press **Ctrl+Enter** (or **Cmd+Return** on macOS) to execute the code cell and display the result; see also Figure 1.2.

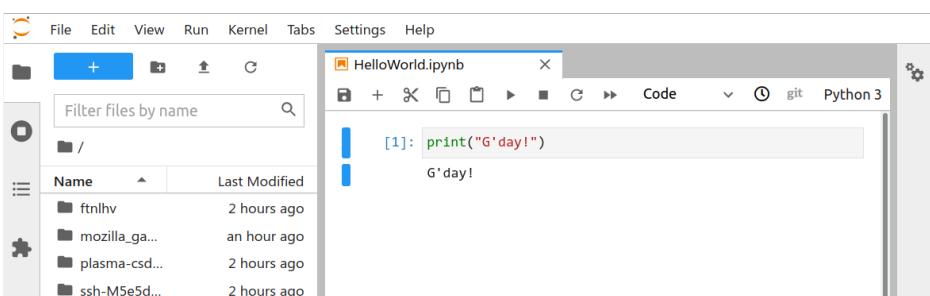


Figure 1.2: “Hello World” in a Jupyter Notebook

⁴⁶ https://www.youtube.com/watch?v=Ag1AKl_2GM

1.2.3 More Cells

1. By pressing **Enter**, we can enter the *Edit mode*. Modify the cell's contents so that it now reads:

```
# My first code cell (this is a comment)
print("G'day!") # prints a message (this is a comment too)
print(2+5) # prints a number
```

2. Press **Ctrl+Enter** to execute the code and replace the results with the new ones.
3. Change `print(2+5)` to `PRINT(2+5)`. Also, enter a command to print some other message that is to your liking. Note that character strings in Python must be enclosed in either double quotes or apostrophes.
4. Press **Shift+Enter**. This will not only execute the code cell, but also create a new one below and enter the edit mode.
5. In the new cell, enter and then execute the following:

```
import matplotlib.pyplot as plt # basic plotting library
plt.bar(
    ["Python", "JavaScript", "HTML", "CSS"], # a list of strings
    [80, 30, 10, 15] # a list of integers (the corresponding bar heights)
)
plt.title("What makes you happy?")
plt.show()
```

6. Add 3 more code cells, displaying some text or creating other bar plots.

Note: In the *Edit mode*, JupyterLab behaves like an ordinary text editor. Keyboard shortcuts probably known from elsewhere are available, for example:

- **Shift+LeftArrow**, **DownArrow**, **UpArrow**, or **RightArrow** – select text,
- **Ctrl+c** – copy,
- **Ctrl+x** – cut,
- **Ctrl+v** – paste,
- **Ctrl+z** – undo,
- **Ctrl+]** – indent,
- **Ctrl+[** – dedent,

- `Ctrl+/-` toggle comment.
-

1.2.4 Edit vs Command Mode

1. By pressing `ESC`, we can enter the *Command mode*.

Important: We will be using `ESC` and `Enter` to switch between the *Command* and *Edit* modes, respectively.

2. In the *Command mode*, we can use the arrow `DownArrow` and `UpArrow` keys to move between the code cells.
3. In the *Command mode* pressing `d,d` (`d` followed by another `d`) deletes the currently selected cell.
4. Press `z` to undo the last operation.
5. Press `a` and `b` to insert a new blank cell above and below the current one, respectively.
6. Note that cells can be moved by a simple drag and drop with your mouse.

1.2.5 Markdown Cells

So far we have been playing with *Code* cells.

We can turn the current cell to become a *Markdown* cell by pressing `m` in the *Command mode*. Note that by pressing `y` we can turn it back to a *Code* cell.

Markdown is a lightweight, human-readable markup language widely used for formatting text documents.

1. Enter the following into a new *Markdown* cell:

```
# Section  
## Subsection  
  
This ~~~was~~~ *is* **really** nice.  
  
* one  
* two  
1. aaa
```

(continues on next page)

(continued from previous page)

```
2. bbbb
* three

```python
some code to display (but not execute)
2+2
```

```

! [Python] (<https://www.python.org/static/img/python-logo.png>)

2. Press **Ctrl+Enter** to display the formatted text.
3. Note that the Markdown call can be modified by entering the *Edit mode* as usual (Enter key).

Exercise 1.3 Read the [official introduction⁴⁷](#) to the Markdown syntax.

Exercise 1.4 Follow [this⁴⁸](#) interactive Markdown tutorial.

Exercise 1.5 Apply what you have learned by making the current Jupyter notebook more readable. Add a header at the beginning of the report featuring your name and email address. Before and after each code cell, explain (in your own words) what we are about to do and how to interpret the obtained results.

1.3 Best Note Taking App

Studying, and this is what we are here for, is not effective without making notes of the concepts that we come across in the course of this course – many of them will be new to us. We need to memorise some new material (e.g., definitions of the data processing methods that we introduce), build connections between different topics, derive or check a simple mathematical formula or facts ourselves.

The best and most versatile note takins solution is an ordinary piece of A4 paper and a pen or a pencil. Loose sheets of paper, 5 mm grid ruled for graphs and diagrams work nicely. The can be held together by means of a cheap landscape clipfolder (the one with a clip on the long side). An advantage of this solution is that pages can be browsed like

⁴⁷ <https://daringfireball.net/projects/markdown/syntax>

⁴⁸ <https://commonmark.org/help/tutorial/>

in an ordinary notebook. Also, new pages can be added anywhere, and their ordering altered arbitrarily.

1.4 Initialising Each Session and Getting Example Data (!)

From now on, we assume that at the beginning of each session, the following commands have been issued:

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

np.random.seed(123) # initialise the pseudorandom number generator
pd.set_option("display.notebook_repr_html", False) # disable "rich" output

plt.style.use("seaborn") # plot style

sns.set_palette([ # the "R4" palette
    "#000000", "#DF536B", "#61D04F", "#2297E6",
    "#28E2E5", "#CD0BBC", "#F5C710", "#999999"
])

plt.rcParams.update({
    "font.size": 11,
    "font.family": "sans-serif",
    "font.sans-serif": ["Alegreya Sans", "Alegreya"],
    "figure.autolayout": True,
    "figure.dpi": 300,
    "figure.figsize": (6, 3.5), # default is [8.0, 5.5],
})
```

This imports the most frequently used packages (together with their common aliases, we'll get to that later) and sets up some further options that we particularly like. For the discussion on reproducible pseudorandom number generation, see [Section 6.4.2](#).

The software we use receives feature upgrades, API changes, and bug fixes on a regular

basis, therefore it is good to know which version of the Python environment was used to evaluate all the code included therein:

```
import sys
print(sys.version)
## 3.9.7 (default, Sep 10 2021, 14:59:43)
## [GCC 11.2.0]
```

The versions of the packages that we use in this course are given below. On a side note, they can be fetched by querying, for example, `np.__version__`, etc.

| Package | Version |
|-------------------------|---------|
| <code>numpy</code> | 1.22.4 |
| <code>scipy</code> | 1.8.1 |
| <code>pandas</code> | 1.4.2 |
| <code>matplotlib</code> | 3.5.2 |
| <code>seaborn</code> | 0.11.2 |
| <code>sklearn</code> | 0.24.1 |

Important: All datasets that we use as examples are available for download at https://github.com/gagolews/teaching_data.

Exercise 1.6 Make sure you are comfortable with accessing raw data files from the above repository. Choose any file, e.g., `nhanes_adult_female_height_2020.txt` in the `marek` folder, and then click Raw. It is the URL that you have been redirected to, not the previous one, that includes information from within your Python session.

Also note that each dataset starts with a number of comment lines explaining its structure, the meaning of the variables, etc.

1.5 Further Reading

Markdown is one of many markup languages. Other learn-worthy ones include HTML (for the Web) and LaTeX (especially for beautiful typesetting of maths, print-ready articles and books, e.g., PDF; see [[O+21]] for a good introduction).

Jupyter Notebooks can be converted to different formats using the `jupyter-nbconvert`⁴⁹ command line tool.

More generally, `pandoc`⁵⁰ is a generic converter between different formats, e.g., it can be used to convert between the highly universal (although primitive) Markdown and the said LaTeX and HTML. Also, it can be used for preparing presentations.

1.6 Exercises

Exercise 1.7 *What is the difference between the Edit and the Command mode in Jupyter?*

Exercise 1.8 *What is Markdown?*

Exercise 1.9 *How to format a table in Markdown?*

⁴⁹ <https://pypi.org/project/nbconvert/>

⁵⁰ <https://pandoc.org/>

2

Scalar Types and Control Structures in Python

In this part we quickly introduce the basics of the Python language itself. Being a general purpose tool, various packages supporting data wrangling operations are provided as third-party extensions (of course, all of them are free and open source). Based on the discussed concepts, we will be able to use `numpy`, `scipy`, `pandas`, `sklearn`, `matplotlib`, `seaborn`, and other packages with some healthy degree of confidence.

2.1 Scalar Types

The five ubiquitous scalar (i.e., *single* or *atomic* value) types are:

- `bool` – logical,
- `int`, `float`, `complex` – numeric,
- `str` – character.

2.1.1 Logical Values

There are only two possible logical (Boolean) values: `True` and `False`.

We can type:

```
True  
## True
```

and instantiate one of them. This might seem boring, unless when trying to play with the above code by themselves, the kind reader fell into the following pitfall:

Important: Python is case-sensitive. Writing “`TRUE`” or “`true`” instead of “`True`” results in an error.

2.1.2 Numeric Values

The three numeric scalar types are:

- `int` — integers, e.g., `1`, `-42`, `1_000_000`;
- `float` — floating-point (real) numbers, e.g., `-1.0`, `3.14159`, `1.23e-4`;
- `complex` (*) — complex numbers, e.g., `1+2j` (these are rather infrequently used in our applications).

In practice, `int` and `float` often work together seamlessly and we usually do not have to think about their being distinctive types.

Exercise 2.1 `1.23e-4` and `9.8e5` are examples of numbers entered using the so-called scientific notation, where “`e`” stands for “times 10 to the power of”. Moreover, `1_000_000` is a decorated (more human-readable) version of `1000000`. Use the `print` function to check their values.

Arithmetic Operators

Here is the list of available arithmetic operators:

```
1 + 2      # addition
## 3
1 - 7      # subtraction
## -6
4 * 0.5    # multiplication
## 2.0
7 / 3      # float division (the result is always of type float)
## 2.3333333333333335
7 // 3     # integer division
## 2
7 % 3      # division remainder
## 1
2 ** 4     # exponentiation
## 16
```

The precedence of these operators is quite predictable⁵¹, e.g., exponentiation has higher priority than multiplication and division which in turn binds more strongly than addition and subtraction. Hence:

```
1 + 2 * 3 ** 4  # the same as 1+(2*(3**4))
## 163
```

⁵¹ <https://docs.python.org/3/reference/expressions.html#operator-precedence>

is different than, e.g., $((1+2)*3)**4$.

Creating Named Variables

Named variables can be introduced using the *assignment operator*, `=`. They can store arbitrary Python objects and be referred to at any time.

```
x = 7 # read: let `x` from now on be equal to 7
print(x)
## 7
```

New variables can be created based on other ones:

```
y = x*x-10 # creates `y`
print(y)
## 39
```

Also, existing variables can be re-bound to any other value whenever we please:

```
x = x/3 # let new `x` be equal to the old `x` (7) divided by 3
print(x)
## 2.333333333333335
```

Keep in mind that computers' floating-point arithmetic is precise only up to a few significant digits, hence the results we generate will often be approximate.

Exercise 2.2 Create two named variables *height* and *width*. Based on them, determine your *BMI*⁵².

Note: (*) Augmented assignments are also available. For example:

```
x *= 3 # the same as: x = x*3
print(x)
## 7.0
```

They often modify the objects they act upon in-place, compare [Section 3.5](#).

⁵² https://en.wikipedia.org/wiki/Body_mass_index

2.1.3 Character Strings

Character strings (objects of type `str`), which can consist of arbitrary text, are created using either double quotes or apostrophes:

```
print("spam, spam, #, bacon, and spam")
print("рус Cześć ☺ ☀ ¿Qué tal? Привет ☀")
## spam, spam, #, bacon, and spam
## russ Cześć ☺ ☀ ¿Qué tal? Привет ☀
print('G\'day, howya goin\''," he asked.\n"Fine, thanks," I responded.')
## "G'day, howya goin'," he asked.
## "Fine, thanks," I responded.
```

Above, “`\'`” (a way to include an apostrophe in an apostrophe-delimited string) and “`\n`” (newline character) are examples of *escape sequences*⁵³.

Multiline strings are also possible:

```
"""
spam\\spam
This is Python, therefore references
to Monty Python's Flying Circuseses are a must
sorry not sorry
tasty\t"spam"
lovely\t'spam'
"""

## '|nspam|spam|nThis is Python, therefore references|nto Monty Python|'s
# Flying Circuseses are a must|nsorry not sorry|ntasty|t"spam"|nlovely|t|
# 'spam| '|n'
```

Exercise 2.3 Call the `print` function on the above object to reveal the special meaning of the included escape sequences.

Important: There are many string operations available – related for example to formatting, pattern searching, extracting chunks; they are very important in the art of data wrangling as oftentimes information comes to us in textual form. We shall be covering this topic in great detail in [Chapter 14](#).

⁵³ https://docs.python.org/3/reference/lexical_analysis.html#string-and-bytes-literals

F-Strings (Formatted String Literals)

Also, the so-called *f-strings* (formatted string literals) can be used to prepare nice output messages:

```
x = 2
f"x is {x}"
## 'x is 2'
```

Note the `f` prefix. The `{x}` part was replaced with the value stored in the `x` variable.

There are many options available and it's best – as usual – to study the [documentation](#)⁵⁴ in search for interesting features. Here, let us just mention that we will frequently be referring to placeholders like `{variable:width}` and `{variable:width.precision}`, which specify the field width and the number of fractional digits of a number. This can result in a series of values nicely aligned one below another.

```
pi = 3.14159265358979323846
e = 2.71828182845904523536
print(f"""
pi = {pi:10.8f}
e = {e:10.8f}
""")
##
## pi = 3.14159265
## e = 2.71828183
```

`10.8f` means that a value is to be formatted as a `float`, be of at least width 10, and use 8 fractional digits.

2.2 Calling Built-in Functions

There are quite a few built-in functions ready for use. For instance:

```
e = 2.718281828459045
round(e, 2)
## 2.72
```

Rounds `e` to 2 decimal digits.

⁵⁴ https://docs.python.org/3/reference/lexical_analysis.html#f-strings

Exercise 2.4 Call `help("round")` or `?round` (this is IPython/Jupyter-specific) to access the function's manual. Note that the second argument, called `ndigits`, which we have set to 2, has a default value of `None`. Check what happens when we omit it during the call.

2.2.1 Positional and Keyword Arguments

As `round` has two parameters, `number` and `ndigits`, the following (and no other) calls are equivalent:

```
round(e, 2) # two arguments matched positionally
round(e, ndigits=2) # positional and keyword argument
round(number=e, ndigits=2) # 2 keyword arguments
round(ndigits=2, number=e) # order does not matter for keyword arguments
## 2.72
## 2.72
## 2.72
## 2.72
```

That no other form is allowed is left as an exercise, i.e., positionally matched arguments must be listed before the keyword ones.

2.2.2 Modules and Packages

Other functions are available in numerous Python modules and packages (which are collections of modules).

For example, `math` features many mathematical functions:

```
import math # the math module must be imported prior its first use
print(math.log(2.718281828459045)) # the natural logarithm (base e)
## 1.0
print(math.floor(-7.33)) # the floor function
## -8
print(math.sin(math.pi)) # sin(pi) equals 0 (with some numeric error)
## 1.2246467991473532e-16
```

See the [official documentation](#)⁵⁵ for the comprehensive list of objects defined therein. On a side note, all floating-point computations in any programming language are subject to round-off errors and other inaccuracies, hence the result of $\sin \pi$ not being exactly 0, but some value very close thereto. We will elaborate on this topic in [Section 5.5.4](#).

⁵⁵ <https://docs.python.org/3/library/math.html>

2.2.3 Slots and Methods

Python is an object-oriented programming language. Each object is an instance of some class whose name we can reveal by calling the **type** function:

```
x = 1+2j
type(x)
## <class 'complex'>
```

Important: Classes define the following kinds of *attributes*:

- *slots* – associated data,
 - *methods* – associated functions.
-

Exercise 2.5 Call **help("complex")** to reveal that the *complex* class features, amongst others, the **conjugate** method and the **real** and **imag** slots.

Here is how we can access the two slots:

```
print(x.real) # access the `real` slot of object `x` of class `complex`
## 1.0
print(x.imag)
## 2.0
```

And here is an example of a method call:

```
x.conjugate() # equivalently: complex.conjugate(x)
## (1-2j)
```

Importantly, the user manual on this function can be accessed by typing **help("complex.conjugate")** (*class name – dot – method name*).

2.3 Controlling Program Flow

2.3.1 Relational and Logical Operators

Further, we have a number of operators which return a single logical value:

```
1 == 1.0 # is equal to?
## True
2 != 3 # is not equal to?
## True
"spam" < "eggs" # is less than? (compare using the lexicographic order)
## False
```

Some more examples:

```
math.sin(math.pi) == 0.0 # well, numeric error...
## False
abs(math.sin(math.pi)) <= 1e-9 # is close to 0?
## True
```

Logical results might be combined using **and** (conjunction; for testing if both operands are true) and **or** (alternative; for determining whether at least one operand is true). Furthermore, **not** (negation) is available too.

```
3 <= math.pi and math.pi <= 4
## True
not (1 > 2 and 2 < 3) and not 100 <= 3
## True
```

Note that **not** `100 <= 3` is equivalent to `100 > 3`. Also, via the de Morgan's laws, **not** `(1 > 2 and 2 < 3)` is true if and only if `1 <= 2 or 2 >= 3` holds.

Exercise 2.6 Assuming that p, q, r are logical and a, b, c, d are float-type variables, simplify the following expressions:

- **not not** p ,
- **not** p **and not** q ,
- **not** (**not** p **or** **not** q **or** **not** r),
- **not** $a == b$,
- **not** ($b > a$ **and** $b < c$),
- **not** ($a \geq b$ **and** $b \geq c$ **and** $a \geq c$),
- $(a > b$ **and** $a < c)$ **or** $(a < c$ **and** $a > d)$.

2.3.2 The if Statement

The `if` statement allows us to execute a chunk of code conditionally – whether the provided expression is true or not.

```
import numpy as np      # imports the `numpy` package and sets an alias
x = np.random.rand()   # pseudorandom value in [0.0, 1.0)
print(x)
if x < 0.5: print("spam!")
## 0.6964691855978616
```

Note the colon after the tested condition.

Further, a number of `elif` (*else-if*) parts can be added followed by an optional `else` part, which is executed if all the conditions tested are not true.

```
if x < 0.25:  print("spam!")
elif x < 0.5:  print("ham!")    # i.e., x in [0.25, 0.5)
elif x < 0.75: print("bacon!") # i.e., x in [0.5, 0.75)
else:          print("eggs!")  # i.e., x >= 0.75
## bacon!
```

If more than one statement is to be executed conditionally, an indented code block can be introduced.

```
if x >= 0.25 and x <= 0.75:
    print("spam!")
    print("I love it!")

else:
    print("ham!")
    print("I'd rather eat spam!")
print("more spam!") # executed regardless of the condition tested
## spam!
## I love it!
## more spam!
```

Important: We recommend using four spaces. The indentation must be neat and consistent. The reader is encouraged to try to execute the following code chunk and note what kind of error is generated:

```
if x < 0.5:  
    print("spam!")  
    print("ham!")    # :(
```

Exercise 2.7 For a given BMI (see one of the above exercises), print out the corresponding category as defined by the WHO (underweight if below 18.5, normal range up to 25.0, etc.). Note that the BMI is a very simple measure and both the medical and statistical community point out its inherent limitations, read the Wikipedia article thereon for more details (and note there was a lot of data wrangling involved in its preparation – tables, charts, calculations; something that we will be able to do quite soon — give good reference data, of course).

Exercise 2.8 (*) Check if it is easy to find on the internet (at reliable sources) some raw data sets related to the body mass studies, e.g., measuring subjects' height, weight, body fat and muscle percentage, etc.

2.3.3 The while Loop

The `while` loop executes a given statement or a series of statements as long as a given condition is true.

For example, here is a simple simulator determining how long we have to wait until drawing the first number not greater than 0.01 whilst generating numbers in the unit interval:

```
count = 0  
while np.random.rand() > 0.01:  
    count = count + 1  
print(count)  
## 117
```

Exercise 2.9 Using the `while` loop, determine the arithmetic mean of 10 random numbers (i.e., the sum of the numbers divided by 10).

2.4 Defining Own Functions

We can also define our own functions as a means for code reuse.

For instance, here is one that determines the minimum (with respect to the `<` relation) of three given objects:

```
def min3(a, b, c):
    """
    A function to determine the minimum of three
    given inputs.

    (this is the so-called docstring –
     call help("min3") later)
    """
    if a < b:
        if a < c:
            return a
        else:
            return c
    else:
        if b < c:
            return b
        else:
            return c
```

Example calls:

```
print(min3(10, 20, 30),
      min3(10, 30, 20),
      min3(20, 10, 30),
      min3(20, 30, 10),
      min3(30, 10, 20),
      min3(30, 20, 10))
## 10 10 10 10 10 10
```

Note that the function *returns* a value. Hence, the result can be fetched and used in further computations.

```
x = min3(np.random.rand(), 0.5, np.random.rand()) # minimum of 3 numbers
x = round(x, 3) # do something with the result
print(x)
## 0.5
```

Exercise 2.10 Write a function named **bmi** which computes and returns a person's BMI, given

their weight (in kg) and height (in cm). As it is a good development practice to document your functions, do not forget about including the appropriate docstring.

We can also introduce new variables inside a function's body. This can aid the function in doing the right thing, i.e., what it has been designed to do.

```
def min3(a, b, c):
    """
    A function to determine the minimum of three
    given inputs (alternative version).
    """
    m = a # a local (temporary auxiliary) variable
    if b < m:
        m = b
    if c < m: # be careful! no `else` or `elif` here – it's a separate `if`
        m = c
    return m
```

Example call:

```
m = 7
n = 10
o = 3
min3(m, n, o)
## 3
```

All *local variables* cease to exist after the function is called. Also note that `m` inside the function is a variable independent of `m` in the global (calling) scope.

```
print(m) # this is still the global `m` from before the call
## 7
```

Exercise 2.11 Write a function `max3` which determines the maximum of 3 given values.

Exercise 2.12 Write a function `med3` which defines the median of 3 given values (the one value that is in-between the other ones).

Exercise 2.13 (*) Write a function `min4` to compute the minimum of 4 values.

Note: *Lambda expressions* give us an easy way to define functions using a single line of code. Their syntax is: `lambda argument_name: return_value`.

```
square = lambda x: x**2 # i.e., def square(x): return x**2
square(4)
## 16
```

Function objects generated through lambda expressions do not have to be assigned a name – they can be anonymous. It is useful when we are calling other functions that take other functions as their arguments. With lambdas, the latter can be generated on the fly.

```
def print_x_and_fx(x, f):
    print(f"x = {x} and f(x) = {f(x)}")

print_x_and_fx(4, lambda x: x**2)
## x = 4 and f(x) = 16
print_x_and_fx(math.pi/4, lambda x: round(math.cos(x), 5))
## x = 0.7853981633974483 and f(x) = 0.70711
```

2.5 Exercises

Exercise 2.14 What does `import xxxxxx as x` mean?

Exercise 2.15 What is the difference between `if` and `while`?

Exercise 2.16 Name the scalar types we have introduced here.

Exercise 2.17 What is a docstring and how to create and access it?

Exercise 2.18 What are keyword arguments?

3

Sequential and Other Types in Python

3.1 Sequential Types

Sequential objects store data items that can be accessed by index (position). The three main types of sequential objects are: lists, tuples, and ranges.

Actually, strings (which we often treat as scalars) can also be classified as such. Therefore, the four main types of sequential objects are:

- lists,
- tuples,
- ranges, and
- strings.

3.1.1 Lists

Lists consist of arbitrary Python objects and are created using square brackets:

```
x = [True, "two", 3, [4j, 5, "six"]]
x
## [True, 'two', 3, [4j, 5, 'six']]
```

Above is an example list featuring objects of type: `bool`, `str`, `int`, and `list` (yes, it is possible to have a list inside another list), in this order.

Note: We will often be using lists when creating vectors in `numpy` or data frame columns in `pandas`. Further, lists of lists of equal lengths can be used to create matrices.

Each list is *mutable* and hence its state may be changed arbitrarily. For instance, we can append a new object at its end:

```
x.append("spam")
print(x)
## [True, 'two', 3, [4j, 5, 'six'], 'spam']
```

3.1.2 Tuples

Next, *tuples* are like lists, but they are *immutable* (read-only) – once created, their state cannot be changed.

```
("one", [], (3j, 4, "five", "six"))
## ('one', [], (3j, 4, 'five', 'six'))
```

This gave us a triple (3-tuple) featuring a string, an empty list, and a 4-tuple.

Furthermore, note that we can drop the round brackets and still get a tuple:

```
1, 2, 3 # the same as `'(1, 2, 3)`
## (1, 2, 3)
```

Also:

```
1, # i.e., `'(1,)`
## (1,)
```

Note that the above is not the same as simply 1 or (1), representing an object of type `int`.

Note: Having a separate data type representing an immutable sequence actually makes sense in certain contexts. For example, a data frame's *shape* is its inherent property that should not be tinkered with. If a tabular dataset has 10 rows and 5 columns, we should not allow the user to set the former to 15 (without making further assumptions, providing extra data, etc.).

When creating collections of items, usually we prefer lists as they are more flexible a data type, but in [Section 3.4.2](#) we note that many functions return tuples, therefore we should be able to handle them with confidence.

3.1.3 Ranges

Moreover, *ranges* are of the form `range(from, to)` or `range(from, to, by)` and represent arithmetic progressions of integers.

For the sake of illustration, we convert them to lists below:

```
list(range(0, 5)) # i.e., range(0, 5, 1) - from 0 to 5 (exclusive) by 1
## [0, 1, 2, 3, 4]
list(range(10, 0, -1)) # from 10 to 0 (exclusive) by -1
## [10, 9, 8, 7, 6, 5, 4, 3, 2, 1]
```

Note that the rightmost boundary (`to`) is exclusive and that `by` defaults to 1.

3.1.4 Strings (Again)

Recall that we have already discussed character strings in Section 2.1.3.

```
"example\nstring"
## 'example\nstring'
```

Strings are often treated as scalars (atomic entities, as in: a sting as a whole). However, as we will soon find out, the individual characters are also accessible by index.

Furthermore, in Chapter 14 we will discuss numerous operations on text.

3.2 Working with Sequences

3.2.1 Extracting Elements

The index operator, ``[...]``, can be applied on any sequential object to extract an element at a position specified by a single integer.

```
x = ["one", "two", "three", "four", "five"]
x[0] # the first element
## 'one'
x[len(x)-1] # the last element
## 'five'
```

Therefore, the valid indices are $0, 1, \dots, n-2, n-1$, where n is the length of the sequence.

Important: Think of an index as the distance from the start of a sequence. For example, `x[3]` means “3 items away from the beginning”, hence, the 4th element.

Negative indices count from the end:

```
x[-1] # the last element
## 'five'
x[-2] # the second to last
## 'four'
x[-len(x)] # the first element; `len(x)` gives the number of elements in `x`
## 'one'
```

The index operator can be applied on any sequential object:

```
"string"[3]
## 'i'
```

Note that indexing a string returns a string – that is why we have classified strings as scalars too.

More examples:

```
range(0, 10)[-1] # the last item in an arithmetic progression
## 9
(1,)[:0] # extract from a 1-tuple
## 1
```

3.2.2 Slicing

We can also use slices of the form `from:to` or `from:to:by` to select a subsequence of a given sequence. Slices are similar to ranges, but `:` can only be used within square brackets.

```
x = ["one", "two", "three", "four", "five"]
x[1:4] # from 2nd to 5th (exclusive)
## ['two', 'three', 'four']
x[-1:0:-2] # from last to first (exclusive) by every 2nd backwards
## ['five', 'three']
```

Actually, `from` and `to` are optional – when omitted, they default to one of the sequence boundaries.

```
x[3:] # from 3rd to end
## ['four', 'five']
x[::-2] # every 2nd from the start
## ['one', 'three', 'five']
x[::-1] # elements in the reversed order
## ['five', 'four', 'three', 'two', 'one']
```

And, of course, they can be applied on other sequential objects as well:

```
"spam, bacon, spam, and eggs"[13:17]
## 'spam'
```

Important: It is crucial to know the difference between element extraction and subsetting a sequence (creating a subsequence).

For example:

```
x[0] # extraction (indexing with a single integer)
## 'one'
```

gives the object *at* that index.

```
x[0:1] # subsetting (indexing with a slice)
## ['one']
```

gives the object of the same type as `x` (here, a list) featuring the items at that indices (in this case, only the first object, but a slice can potentially select more than one element).

`pandas` data frames and `numpy` arrays will behave similarly, but there will be many more indexing options (as discussed in [Section 5.4](#), [Section 8.2](#), and [Section 10.5](#)).

3.2.3 Modifying Elements

Lists are *mutable* – their state may be changed. The index operator can be used to replace the elements at given indices.

```
x = ["one", "two", "three", "four", "five"]
x[0] = "spam" # replace the first element
```

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```
x[-3:] = ["bacon", "eggs"] # replace last three with given two
print(x)
## ['spam', 'two', 'bacon', 'eggs']
```

Exercise 3.1 There are quite a few methods which we can use to modify list elements: **append**, **insert**, **remove**, **pop**, etc. Invoke **help("list")** to access their descriptions and call them on a few example lists.

3.2.4 Searching Elements

The **in** operator and its negation, **not in**, determine whether an element exists in a given sequence:

```
7 in range(0, 10)
## True
[2, 3] in [1, [2, 3], [4, 5, 6]]
## True
```

For strings, **in** tests whether a string features a specific *substring*, so we don't have to restrict ourselves to single characters:

```
"spam" in "lovely spams"
## True
```

Exercise 3.2 Check out the **count** and **index** methods in the *list* and other classes.

3.2.5 Arithmetic Operators

Some arithmetic operators have been *overloaded* for certain sequential types, but they of course carry different meanings than those for integers and floats.

In particular, `+` can be used to join (concatenate) strings, lists, and tuples:

```
"spam" + " " + "bacon"
## 'spam bacon'
[1, 2, 3] + [4]
## [1, 2, 3, 4]
```

and `*` duplicates (recycles) a given sequence:

```
"spam" * 3
## 'spamspamspam'
(1, 2) * 4
## (1, 2, 1, 2, 1, 2, 1, 2)
```

3.3 Dictionaries (*)

Dictionaries (objects of type `dict`) are sets of `key: value` pairs, where the `values` (any Python object) can be accessed by `key` (usually a string).

```
x = {
    "a": [1, 2, 3],
    "b": 7,
    "z": "spam!"
}
print(x)
## {'a': [1, 2, 3], 'b': 7, 'z': 'spam! '}
```

We can also create a dictionary with string keys using the `dict` function which expects a number of keyword arguments:

```
dict(a=[1, 2, 3], b=7, z="spam!")
## {'a': [1, 2, 3], 'b': 7, 'z': 'spam! '}
```

The index operator can be used to extract specific elements:

```
x["a"]
## [1, 2, 3]
```

Note that `x[0]` is not valid – it is not an object of sequential type; a key of `0` does not exist in a given dictionary.

The `in` operator can be used to check whether a given key exists:

```
"a" in x, 0 not in x, "z" in x, "w" in x # a tuple of 4 check results
## (True, True, True, False)
```

We can also add new elements to a dictionary:

```
x["f"] = "more spam!"
print(x)
## {'a': [1, 2, 3], 'b': 7, 'z': 'spam!', 'f': 'more spam!'}
```

Example 3.3 (*) In practice, we often import JSON files (which is popular data exchange format on the internet) exactly in the form of Python dictionaries. Let's demo it quickly:

```
import requests
x = requests.get("https://api.github.com/users/gagolews/starred").json()
```

Now *x* is a sequence of dictionaries giving the information on the repositories starred by yours truly on GitHub. As an exercise, the reader is encouraged to inspect its structure.

3.4 Iterable Types

All the objects we have discussed here are *iterable*. In other words, we can iterate through each element contained therein.

In particular, the `list` and `tuple` functions take any iterable object and convert it to a sequence of the corresponding type, for instance:

```
list("spam")
## ['s', 'p', 'a', 'm']
tuple(range(0, 10, 2))
## (0, 2, 4, 6, 8)
list({ "a": 1, "b": ["spam", "bacon", "spam"] })
## ['a', 'b']
```

Exercise 3.4 Take a look at the documentation of the `extend` method in the `list` class. The manual page suggests that this operation takes any iterable object. Feed it with a list, tuple, range, and a string and see what happens.

The notion of iterable objects is important, as they appear in many contexts. There are quite a few other iterable types which are for example non-sequential (we cannot access their elements at random using the index operator).

Exercise 3.5 (*) Check out the `enumerate`, `zip`, and `reversed` functions and what kind of iterable objects do they return.

3.4.1 The `for` loop

The `for` loop iterates over every element in an iterable object, allowing us to perform a specific action. For example:

```
x = [1, "two", ["three", 3j, 3], False] # some iterable object
for el in x: # for every element in `x`, let's call it `el`
    print(el) # do something on `el`
## 1
## two
## ['three', 3j, 3]
## False
```

Another example:

```
for i in range(len(x)):
    print(i, ":", x[i])
## 0 : 1
## 1 : two
## 2 : ['three', 3j, 3]
## 3 : False
```

One more example – computing the elementwise multiply of two vectors of equal lengths:

```
x = [1, 2, 3, 4, 5] # for testing
y = [1, 10, 100, 1000, 10000] # just a test
z = [] # result list - start with an empty one
for i in range(len(x)):
    z.append(x[i] * y[i])
print(z)
## [1, 20, 300, 4000, 50000]
```

Yet another example: here is a function which determines the minimum of a given iterable object (compare the built-in `min` function, see `help("min")`).

```
import math
def mymin(x):
    """
    The smallest element in an iterable object x.
    We assume that x consists of numbers only.
    """

```

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```
curmin = math.inf # infinity is greater than any other number
for e in x:
    if e < curmin:
        curmin = e # a better candidate for the minimum
return curmin
```

Exercise 3.6 Write your own basic versions (using the `for` loop) of the built-in `max`, `sum`, `any`, and `all` functions.

Exercise 3.7 (*) The `glob` function in the `glob` module can be used to list all files in a given directory whose names match a specific wildcard, e.g., `glob.glob("~/Music/*.mp3")` (note that “`~`” points to the current user’s home directory). Moreover, `getsize` from the `os.path` module returns the size of a given file, in bytes. Write a function that determines the total size of all the files in a given directory.

3.4.2 Tuple Assignment

We can create many variables in one line of code by using the syntax `tuple_of_identifiers = iterable_object`, which unpacks the iterable:

```
a, b, c = [1, "two", [3, 3j, "three"]]
print(a)
print(b)
print(c)
## 1
## two
## [3, 3j, 'three']
```

This is useful, for example, when the swapping of two elements is needed:

```
a, b = 1, 2 # the same as (a, b) = (1, 2)
a, b = b, a # swap a and b
print(a)
print(b)
## 2
## 1
```

Another use case is where we fetch outputs of functions that return many objects at once. For instance, in Chapter 11 we will learn about `numpy.unique` which (depending on arguments passed) can return a tuple of arrays:

```
import numpy as np
result = np.unique([1, 2, 1, 2, 1, 1, 3, 2, 1], return_counts=True)
result
## (array([1, 2, 3]), array([5, 3, 1]))
```

That this is indeed a tuple of length two (which we suspect anyway – note the round brackets and two objects separated by a comma) can be verified as follows:

```
type(result), len(result)
## (<class 'tuple'>, 2)
```

Hence, we could have written instead:

```
values, counts = np.unique([1, 2, 1, 2, 1, 1, 3, 2, 1], return_counts=True)
```

This gives two separate variables, each storing a different array. And now:

```
values
## array([1, 2, 3])
counts
## array([5, 3, 1])
```

Also note that if only the second item was of our interest, we could have written:

```
counts = np.unique([1, 2, 1, 2, 1, 1, 3, 2, 1], return_counts=True)[1]
```

because a tuple is a sequential object.

Example 3.8 (*) For example, knowing that the `dict.items` method generates an iterable object that can be used to traverse through all the (key, value) pairs:

```
x = { "a": 1, "b": ["spam", "bacon", "spam"] }
print(list(x.items())) # just a demo
## [('a', 1), ('b', ['spam', 'bacon', 'spam'])]
```

we can utilise tuple assignments in contexts such as:

```
for k, v in x.items(): # or: for (k, v) in x.items()...
    print(k, v, sep=":")
## a: 1
## b: ['spam', 'bacon', 'spam']
```

Note: (***) Also note that, if there are too many values to unpack, we can use the notation like `*name`. This will serve as a placeholder that gathers all the remaining values and wraps them up in a list:

```
a, b, *c, d = range(10)
print(a, b, c, d, sep="\n")
## 0
## 1
## [2, 3, 4, 5, 6, 7, 8]
## 9
```

This placeholder may appear only once on the lefthand side of the assignment operator.

3.4.3 Argument Unpacking (*)

Sometimes we will need to call a function with many parameters or call a series of functions with similar arguments (e.g., when plotting a number of objects using the same plotting style like colour, shape, font). In such scenarios, it may be convenient to pre-prepare the data to be passed as their inputs.

Consider the following function that takes 4 arguments and simply prints them out:

```
def test(a, b, c, d):
    "It's just a test - simply prints the arguments passed"
    print("a =", a, "b =", b, "c =", c, "d =", d)
```

Arguments to be match positionally can be wrapped inside any iterable object and then unpacked using the asterisk operator:

```
args = [1, 2, 3, 4] # merely an example
test(*args) # just like test(1, 2, 3, 4)
## a = 1 b = 2 c = 3 d = 4
```

Furthermore, keyword arguments can be wrapped inside a dictionary and unpacked with a double asterisk:

```
kwargs = dict(a=1, c=3, d=4, b=2)
test(**kwargs)
## a = 1 b = 2 c = 3 d = 4
```

The unpackings can be intertwined, hence the following calls are equivalent:

```
test(1, *range(2, 4), 4)
test(1, **dict(d=4, c=3, b=2))
test(*range(1, 3), **dict(d=4, c=3))
## a = 1 b = 2 c = 3 d = 4
## a = 1 b = 2 c = 3 d = 4
## a = 1 b = 2 c = 3 d = 4
```

3.4.4 Variadic arguments: *args and **kwargs (*)

We can also construct a function that takes any number of positional or keyword arguments by including `*args` or `**kwargs` (those are customary names) on their parameter list:

```
def test(a, b, *args, **kwargs):
    "simply prints the arguments passed"
    print("a =", a, "b =", b, "args =", args, "kwargs =", kwargs)
```

For example:

```
test(1, 2, 3, 4, 5, spam=6, eggs=7)
## a = 1 b = 2 args = (3, 4, 5) kwargs = {'spam': 6, 'eggs': 7}
```

We see that `*args` gathers all remaining positionally matched arguments (except `a` and `b` which were set explicitly) into a tuple. On the other hand `**kwargs` is a dictionary.

Exercise 3.9 From time to time, we will be coming across `*args` and `**kwargs` in various contexts. Study what `matplotlib.pyplot.plot` uses them for:

```
help(plt.plot)
```

3.5 Object References and Copying (*)

3.5.1 Copying References

It is important to always keep in mind that when writing:

```
x = [1, 2, 3]
y = x
```

the assignment operator does not create a copy of `x`; both `x` and `y` refer to the same object in computer's memory.

Important: If `x` is mutable, any change made to it will of course affect `y` (as, again, they are two different means to access the same object).

Hence:

```
x.append(4)
print(y)
## [1, 2, 3, 4]
```

gives the same result as a call to `print(x)`.

3.5.2 Pass by Assignment

Arguments are passed to functions by assignment too. In other words, they behave as if ``=`` was used – what we get is another reference to the existing object.

```
def myadd(z, i):
    z.append(i)
```

And now:

```
myadd(x, 5)
myadd(y, 6)
print(x)
## [1, 2, 3, 4, 5, 6]
```

3.5.3 Object Copies

If we find the above behaviour undesirable, we can always make a copy of an object. It is customary for the mutable objects to be equipped with a relevant method:

```
x = [1, 2, 3]
y = x.copy()
x.append(4)
print(y)
## [1, 2, 3]
```

This did not change the object referred to as `y`, because it is now a different entity.

3.5.4 Modify In-Place or Return a Modified Copy?

We now know that we *can* have functions or methods that change the state of a given object. Hence, for all the functions we apply, it is important to read their documentation to determine if they modify their inputs in-place or return a completely new object. Although surely some patterns can be identified (such as: a method is likely to modify an object in-place whereas a similar standalone function would be returning a copy) – ultimately the functions' developers are free to come up with some exceptions to them if they deem it more sensible or convenient.

Consider the following examples. The `sorted` function returns a sorted version of the input iterable:

```
x = [5, 3, 2, 4, 1]
print(sorted(x)) # returns a sorted copy of x (does not change x)
print(x) # unchanged
## [1, 2, 3, 4, 5]
## [5, 3, 2, 4, 1]
```

The `list.sorted` method modifies the list it is applied on in-place:

```
x = [5, 3, 2, 4, 1]
x.sort() # modifies x in-place
print(x)
## [1, 2, 3, 4, 5]
```

To add to joy, `random.shuffle` is a function (not a method) that changes the state of the argument:

```
x = [5, 3, 2, 4, 1]
import random
random.shuffle(x) # modifies x in-place
print(x)
## [3, 4, 2, 1, 5]
```

Moreover, later we will learn about `Series` objects in `pandas`, which represent data frame columns. They have the `sort_values` method which by default returns a sorted copy of the object it acts upon:

```
import pandas as pd
x = pd.Series([5, 3, 2, 4, 1])
print(list(x.sort_values())) # inplace=False
print(list(x)) # unchanged
```

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```
## [1, 2, 3, 4, 5]
## [5, 3, 2, 4, 1]
```

However, this behaviour might be changed:

```
x = pd.Series([5, 3, 2, 4, 1])
x.sort_values(inplace=True)
print(list(x)) # changed
## [1, 2, 3, 4, 5]
```

Important: We should always carefully study the official documentation (not some random page on the internet displaying us ads) of every function we call.

3.6 Further Reading

Our overview of the Python language is by no means comprehensive, however it touches upon the most important topics from the perspective of data wrangling.

We will mention a few additional language elements in the course of this course (list comprehensions, file handling, string formatting, regular expressions, etc.).

However, we have deliberately decided *not* to introduce some language constructs which we can easily do without (e.g., `else` clauses on `for` and `while` loops, the `match` statement) or are perhaps too technical for an introductory course (`yield`, `iter` and `next`, sets, name binding scopes, deep copying of objects, defining own classes, function factories and closures).

Also, we skipped the constructs that do not work well with the third-party packages we are soon going to be using (e.g., notation like `x < y < z` is not valid if the three involved variables are `numpy` vectors).

The said simplifications have been brought in so that the reader is not overwhelmed – we strongly advocate for minimalism in software development. Python is the basis of one of a few programming environments for exercising data science and, in the long run, it is best to focus on developing the most *transferable* skills.

We encourage at some point to skim through at least the following chapters of the official Python 3 tutorial⁵⁶:

- 3. An Informal Introduction to Python⁵⁷,
 - 4. More Control Flow Tools⁵⁸,
 - 5. Data Structures⁵⁹.
-

3.7 Exercises

Exercise 3.10 Name the sequential objects we have introduced.

Exercise 3.11 Is every iterable object sequential?

Exercise 3.12 Is `dict` an instance of a sequential type?

Exercise 3.13 What is the meaning of `+` and `*` operations on strings and lists?

Exercise 3.14 Given a list `x` featuring numeric scalars, how to create a new list of the same length giving the squares of all the elements in the former?

Exercise 3.15 (*) How to make an object copy and when we should do so?

Exercise 3.16 What is the difference between `x[0]` and `x[:0]`, where `x` is a sequential object?

⁵⁶ <https://docs.python.org/3/tutorial/index.html>

⁵⁷ <https://docs.python.org/3/tutorial/introduction.html>

⁵⁸ <https://docs.python.org/3/tutorial/controlflow.html>

⁵⁹ <https://docs.python.org/3/tutorial/datastructures.html>

Part II

Unidimensional Data

4

Unidimensional Numeric Data and Their Distribution

Let's assume that we have dozens of data points at hand, representing some measurements, such as sensor readings for some industrial processes, body measures for patients in a clinic, salaries of employees, sizes of cities, etc.

For instance, consider the heights of adult females (≥ 18 years old, in cm) in the longitudinal study called National Health and Nutrition Examination Survey ([NHANES⁶⁰](#)) conducted by the US Centres for Disease Control and Prevention.

```
heights = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_adult_female_height_2020.txt")
```

Let's preview a few first observations:

```
heights[:6] # first six
## array([160.2, 152.7, 161.2, 157.4, 154.6, 144.7])
```

This is an example of *quantitative* (numeric) data in form of a series of numbers on which it makes sense to apply various mathematical operations such as subtraction, division, taking logarithms, comparing which one is greater than the other, and so forth.

Most importantly, here, all the observations are *independent* of each other; the ordering of values does not matter.

Our data sample consists 4221 points on the real line (a “bag” of points), see [Figure 4.1](#), but merely looking at the numbers themselves tells us nothing. There are too many of them.

In this chapter we introduce basic ways to create vectors in the **numpy** package, which are an efficient data structure for storing and operating on numeric data just like the ones above. Then, we discuss some basic tools for inspecting their the distribution.

⁶⁰ <https://www.cdc.gov/nchs/nhanes/search/datapage.aspx>

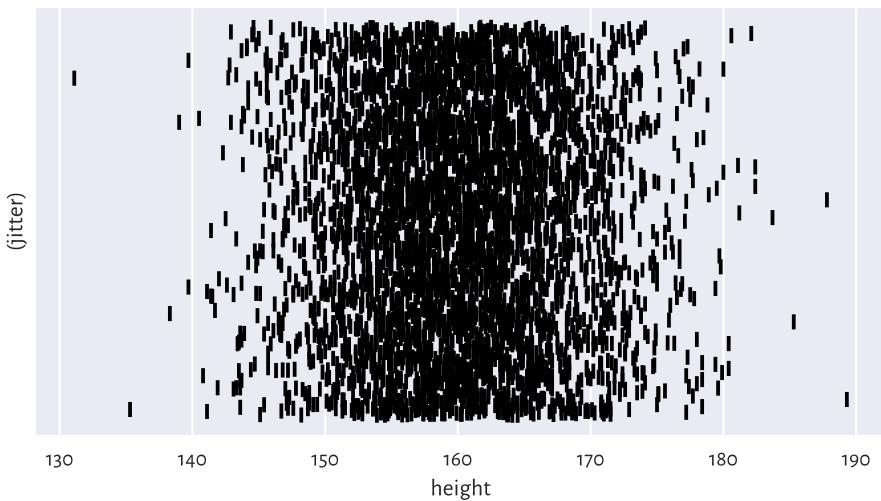


Figure 4.1: The heights dataset is comprised of independent points on the real like; we have added some jitter on the y-axis for dramatic effects only

4.1 Creating Vectors in `numpy`

`numpy`⁶¹ [[H+20]] is an open source add-on for numerical computing written by Travis Oliphant and other developers in 2005 (although the project has a much longer history⁶² and stands on the shoulders of many giants (e.g., concepts from the APL and Fortran languages). It adds support for multi-dimensional arrays and numerous operations on them, similar to those available in R, S, MATLAB, GNU Octave, Scilab, Julia, Perl (via **Perl Data Language**), and some numerical analysis libraries such as LAPACK, GNU GSL, etc.

Many other packages are built on top of `numpy` (including `scipy` [[V+20]], `pandas` [[McK17]], and `sklearn` [[PVG+11]]), hence our studying it in very detail is utterly important. In particular, whatever we learn about vectors here will be transferable to the case of the processing of data frame columns.

Recall that Python lists, e.g., [1, 2, 3], represent simple sequences of objects of any

⁶¹ <https://numpy.org/doc/stable/reference/index.html>

⁶² https://scipy.github.io/old-wiki/pages/History_of_SciPy

kind. Their use cases are very broad, which is both an advantage and something quite the opposite.

Vectors in **numpy** are 1-dimensional arrays which are like lists, but on steroids, which make them strong at scientific computing.

A vector of length n will often be used to represent a point in an n dimensional space (for example, GPS coordinates of a place on Earth assume $n=2$) or n readings of some 1-dimensional quantity (e.g., recorded heights of n people).

Note: (*) **numpy** vectors are powerful because of the underlying assumption that each object they store is of the same type. Although it is possible to save references to arbitrary objects therein, in majority of the cases we will be dealing with vectors of logical values, integers, and floating-point numbers.

Those are directly representable as simple arrays in the C programming language, in which **numpy** is written. Hence, operations on vectors will be very fast provided that we are using the functions working on them *as a whole*. Hence, the readers having some background in other lower-level languages, will need to change their habits of processing individual elements in a sequence, e.g., by means of a **for** loop.

It is customary to import the **numpy** package under the `np` alias:

```
import numpy as np
```

Hence, we can now refer to objects defined therein as `np.spam`, `np.bacon`, or `np.spam`.

4.1.1 Enumerating Elements

One way to create a vector is by calling the **numpy.array** function:

```
x = np.array([10, 20, 30, 40, 50, 60])
x
## array([10, 20, 30, 40, 50, 60])
```

Note that the vector elements were specified by means of an ordinary list. Ranges and tuples can also be used as content providers, which the kind reader is encouraged to check themselves.

The length of the vector can either be read using the previously mentioned `len` function:

```
len(x)
## 6
```

or by reading the array's `shape` slot:

```
x.shape
## (6,)
```

Note that a vector is a 1-dimensional array, hence its shape is stored as a tuple of length 1 (the number of dimensions is stored as `x.ndim`). We can get its length by accessing `x.shape[0]`.

On a side note, matrices (2-dimensional arrays), which we shall study later, will be of shape like (`number_of_rows`, `number_of_columns`).

All vector elements are generally of the same type. Above we have a sequence of integers:

```
x.dtype # data type
## dtype('int64')
```

However, logical, float, complex, but also string vectors are possible too:

```
np.array([True, False, False, True])
## array([ True, False, False,  True])
x.astype(float) # or np.array(x, dtype=float)
## array([10., 20., 30., 40., 50., 60.])
np.array(["spam", "spam", "bacon", "spam"])
## array(['spam', 'spam', 'bacon', 'spam'], dtype='<U5')
```

In the last example we have an array of strings in Unicode (i.e., capable of storing any character in any alphabet, emojis, mathematical symbols, etc.), each of no more than 5 code points in length. It is important to know this, because, as we will point out in [Chapter 14](#), replacing any element with new content will result in the too long strings' truncation. This can be remedied by calling `x.astype("<U10")`, for example.

4.1.2 Arithmetic Progressions

`numpy`'s `arange` is similar to the built-in `range`, but outputs a vector:

```
np.arange(0, 10, 2)
## array([0, 2, 4, 6, 8])
```

`linspace` (*linear space*) creates a sequence of equidistant points in a given interval:

```
np.linspace(0, 1, 5)
## array([0. , 0.25, 0.5 , 0.75, 1. ])
```

Exercise 4.1 Call `help(np.linspace)` and study the meaning of the `endpoint` argument. Also, find the same documentation page at the `numpy` project's website⁶³. Another way is to use your favourite search engine such as DuckDuckGo and query “`linspace site: numpy.org`”. Always remember to gather information from first hand sources! If you are serious about data science in Python, you will become a frequent visitor at this page (and similar ones). In particular, every so often it's a good idea to check out for significant updates at <https://numpy.org/news/>.

4.1.3 Repeating Values

`numpy.repeat` repeats each value a number of times:

```
np.repeat(5, 6)
## array([5, 5, 5, 5, 5, 5])
np.repeat([1, 2], 3)
## array([1, 1, 1, 2, 2, 2])
np.repeat([1, 2], [3, 5])
## array([1, 1, 1, 2, 2, 2, 2, 2])
```

Here, each element from the 1st argument was repeated the corresponding number of times, as defined by the 2nd argument.

`numpy.tile`, on the other hand, repeats a whole sequence with *recycling*:

```
np.tile([1, 2], 3)
## array([1, 2, 1, 2, 1, 2])
```

See also `numpy.zeros` and `numpy.ones` for some specialised versions of the above.

4.1.4 Generating Pseudorandom Variates

The `numpy.random` module defines many functions to generate pseudorandom numbers. We will be discussing the reason for our using the *pseudo* prefix together with various

⁶³ <https://numpy.org/doc/stable/reference/index.html>

probability distributions in a further part, so let's now just quickly take note of a way to sample from the uniform distribution on the unit interval:

```
np.random.rand(5)
## array([0.49340194, 0.41614605, 0.69780667, 0.45278338, 0.84061215])
```

and picking values from a given set:

```
np.random.choice(np.arange(1, 10), 3, replace=False)
## array([1, 5, 8])
```

This gave 3 values from the set $\{1, 2, \dots, 9\}$, without replacement (so that all the numbers are unique).

4.1.5 Loading Data from Files

We will usually be reading whole heterogeneous tabular data sets using `pandas.read_csv` being the topic we shall cover in [Chapter 10](#).

It is worth knowing, though, that arrays with elements of the same type can be read efficiently from text (e.g., CSV) files using `numpy.loadtxt`, for example:

```
heights = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_adult_female_height_2020.txt")
```

Exercise 4.2 Use `numpy.loadtxt` to read this dataset⁶⁴ from GitHub (click Raw to get access to its contents).

4.1.6 `numpy.r_(*)`

`numpy.r_` is perhaps the most flexible means for creating vectors involving quite a few of the aforementioned scenarios, however it has a quirky syntax.

For example:

```
np.r_[1, 2, 3, np.nan, 5, np.inf]
## array([ 1.,  2.,  3., nan,  5., inf])
```

Note that `nan` stands for a *not-a-number* and is used as a placeholder for missing values (discussed later) or *wrong* results, such as the square root of -1 in the domain of reals. `inf`, on the other hand, means *infinity*, ∞ .

⁶⁴ https://github.com/gagolews/teaching_data/blob/master/marek/population_largest_cities_unnamed.txt

We see that square brackets are used instead of the round ones. This is actually smart, because we've mentioned that slices (`:`) can only be used inside them. And so they can:

```
np.r_[0:10:2] # like np.arange(0, 10, 2)
## array([0, 2, 4, 6, 8])
```

What's more, **numpy** authors added the following syntactic sugar:

```
np.r_[0:1:5j] # like np.linspace(0, 1, 5)
## array([0., 0.25, 0.5, 0.75, 1.])
```

Finally, note that we can combine many chunks into one:

```
np.r_[1, 2, [3]*2, 0:3, 0:3:3j]
## array([1., 2., 3., 3., 0., 1., 2., 0., 1.5, 3.])
```

4.2 Mathematical Notation

Mathematically, we will be denoting number sequences with

$$\mathbf{x} = (x_1, x_2, \dots, x_n),$$

where x_i is the i -th element therein and n is the size of the sample. The bold font (hopefully visible) is to emphasise that \mathbf{x} is not an atomic entity (x), but rather a collection thereof.

For brevity, instead of saying “let \mathbf{x} be a real-valued sequence⁷³ of length n ”, we shall write “let $\mathbf{x} \in \mathbb{R}^n$ ”. Here, the “ \in ” symbol stand for “is in” or “is a member of” and \mathbb{R} denotes the set of real numbers (the very one that features, 0, -358745.2394 , 42 and π , amongst uncountably many others) and \mathbb{R}^n is the set of real-valued sequences of length n (i.e., n such numbers considered at a time). For instance, \mathbb{R}^2 includes pairs such as $(1, 2)$, $(\pi/3, \sqrt{2}/2)$, and $(1/3, 10^3)$.

Note: Mathematical notation is pleasantly *abstract* (general) in the sense that \mathbf{x} can be anything, e.g., data on the incomes of households, sizes of the largest cities in a given

⁷³ If $\mathbf{x} \in \mathbb{R}^n$, then we often say that \mathbf{x} is a sequence of n numbers, a (numeric) n -tuple, a n -dimensional real vector, a point in a n -dimensional real space, or an element of a real n -space, etc. In many contexts, these are more or less synonyms of each other.

country, or heights of participants in a study. At a first glance, such a representation of objects from the so-called real world might seem overly simplistic, especially if we'd wish to store information on very complex entities. However, it turns out that in most cases expressing them as *vectors* (i.e., establishing a set of numeric attributes that best describe them in a task at hand) is not only natural but also perfectly sufficient for achieving whatever we aim at.

Exercise 4.3 Consider the following problems:

- How would you represent a patient in a clinic (for the purpose of conducting research in cardiology)?
- How would you represent a car in an insurance company's database (for the purpose of determining how much a driver should pay annually for the mandatory policy)?
- How would you represent a student in an university (for the purpose of granting them scholarships)?

In each case, list a few numeric features that best describe the reality of concern. Note that descriptive labels can always be encoded as numbers, e.g., female = 1, male = 2.

Using the programming syntax, n corresponds to `len(x)` or equivalently `x.shape[0]` and x_i is `x[i-1]` (because the first element is at index 0).

Furthermore, by $x_{(i)}$ (note the bracket) we will denote the i -th smallest value in x (some textbooks denote it with $x_{i:n}$, but we will not). In particular, $x_{(1)}$ is the minimum and $x_{(n)}$ is the maximum.

```
x = np.array([5, 4, 2, 1, 3]) # just an example
x_sorted = np.sort(x)
x_sorted[0], x_sorted[-1] # the minimum and the maximum
## (1, 5)
```

We shall sometimes be referring to $x_{(i)}$ as the i -th *order statistic*.

Also, for to avoid the clutter of notation, in certain formulas we will be assuming that $x_{(0)}$ is the same as $x_{(1)}$ and $x_{(n+1)}$ is equivalent to $x_{(n)}$.

4.3 Histograms

Histograms are one of the most intuitive tools for depicting the empirical distribution of a data sample. We'll be drawing them using the statistical data visualisation package

called `seaborn`⁶⁵ [[Was21]] (written by Michael Waskom), which was built on top of the classic plotting library `matplotlib`⁶⁶ [[Hun07]] (originally developed by John D. Hunter). Let's import both packages and set their traditional aliases:

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

Note: We will frequently be calling a single function from `seaborn` and then performing a series of additional calls to `matplotlib` to tweak the display details. It is important to remember that the former uses the latter to achieve its goals, not the other way around.

4.3.1 heights – A Bell-Shaped Distribution

Let's draw a histogram for the `heights` dataset, see Figure 4.2.

```
sns.histplot(heights, bins=11, color="lightgray")
plt.show()
```

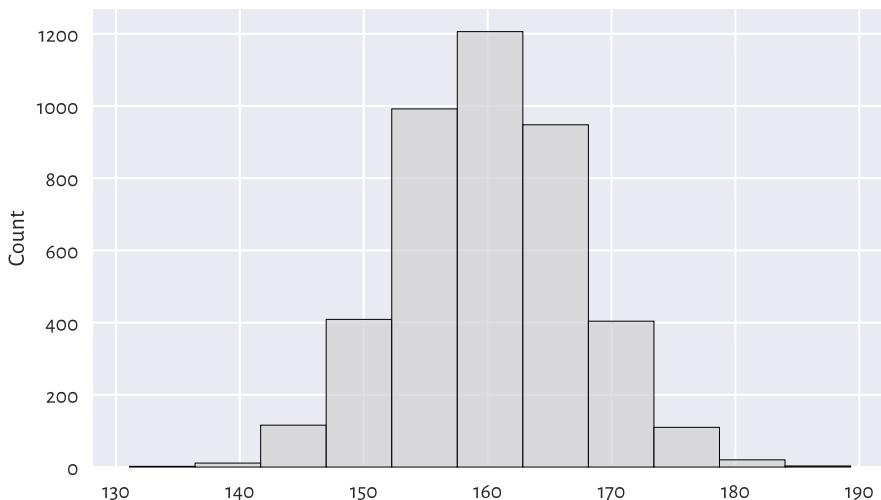


Figure 4.2: Histogram for the `heights` dataset

⁶⁵ <https://seaborn.pydata.org>

⁶⁶ <https://matplotlib.org/>

The data were split into 11 bins and plotted in such a way that bar heights are proportional to the number of observations falling into each interval.

The bins are non-overlapping, adjacent to each other, and of equal lengths and we can read their coordinates by looking at the bottom side of each rectangular bar.

This distribution is bell-shaped – nicely symmetrical around about 160 cm. It resembles a *normal* distribution (which we cover in [Chapter 6](#)) – the most typical (*normal*) observations are somewhere in the middle, and the probability mass decreases quickly. We will learn that, for instance, observations outside the (more or less) [139, 181] interval (mean ± 3 standard deviations – the 3σ rule) are very rare (less than 1% probability).

Note: For some of us, a normal distribution is a prototypical one – we think of many phenomena to be distributed in this way. And that is indeed the case, e.g., in psychology (IQ or personality tests), physiology (the above heights), or when measuring stuff with not-so-precise devices (distribution of errors).

(*) In fact, we have a proposition saying that the sum or average of many observations, assuming that they are independent and follow the same (any!) distribution with finite variance, is approximately normally distributed. This is called the Central Limit Theorem and it is a very strong mathematical result.

We might be tempted to think now that everything is normally distributed, but this is very much untrue.

4.3.2 income – A Right-Skewed Distribution

Let us therefore consider another dataset. In [Figure 4.3](#) we depict the distribution of a simulated sample of disposable income (financial year ending 2020) of 1000 randomly chosen UK households, in £ (of course, the UK Office for National Statistics does not provide us with details on each tax payer, for privacy and other reasons, hence we needed to recreate it based on data from this report⁶⁷):

```
income = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/uk_income_simulated_2020.txt")
sns.histplot(income, stat="percent", bins=20, color="lightgray")
plt.show()
```

⁶⁷ <https://www.ons.gov.uk/peoplepopulationandcommunity/personalandhouseholdfinances/incomeandwealth/bulletins/householddisposableincomeandinequality/financialyear2020>

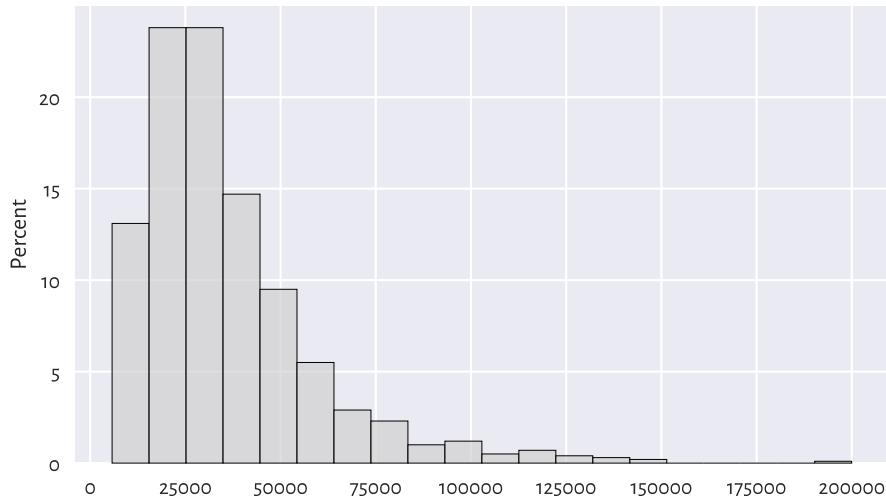


Figure 4.3: Histogram for the `income` dataset

We have normalised (`stat="percent"`) the bar heights so that they all sum to 1 (or, equivalently, 100%), which resulted in a *probability* histogram.

Now we see that the probability density quickly increases, reaches peak at around £15,500–£35,000 and then slowly goes down. It has a *long tail* on the right (and hence it is *right- or positive-skewed*), which means that high salaries are quite likely.

Thus, it's quite a non-normal distribution. Most people are rather poor, they do not earn the average salary. We will get back to that later.

Also take note of the higher bars, as compared to their neighbours, at ca. £100,000 and £120,000. Some of us might be tempted to try to invent a *story* about why there can be some difference in the relative probability mass, but we will refrain from it. Our data sample is quite small and it is likely that they are merely due to some natural variability. Of course, there might be some reasons behind it (theoretically), but we cannot read this by merely looking at a single histogram – a careful further inspection is necessary, but maybe not today.

Example 4.4 In the documentation of `seaborn.histplot` (and `matplotlib.pyplot.hist` which the former extends), we read that the `bins` argument is passed to `numpy.histogram_bin_edges`, which determines the intervals into which our data is split. Similarly, `numpy.histogram` uses the same function and additionally returns the corresponding counts (how many observations fall into each bin) instead of plotting them:

```
counts, bins = np.histogram(income, 20)
counts
bins
## array([131, 238, 238, 147, 95, 55, 29, 23, 10, 12, 5, 7, 4,
##        3, 2, 0, 0, 0, 1])
## array([
  5750. , 15460.95, 25171.9 , 34882.85, 44593.8 , 54304.75,
  64015.7 , 73726.65, 83437.6 , 93148.55, 102859.5 , 112570.45,
  122281.4 , 131992.35, 141703.3 , 151414.25, 161125.2 , 170836.15,
  180547.1 , 190258.05, 199969. ])
])
```

Thus, there are 238 observations both in the [15460.95, 25171.9) and [25171.9, 34882.85) intervals. We will discuss the topic of manual data binning in greater detail in Chapter 11.

Exercise 4.5 There is also the corresponding `nhanes_adult_female_weight_2020`⁶⁸ dataset in our data repository, giving weights (in kgs) of the participants. Draw a histogram. Does its shape resemble the `income` or `heights` distribution more?

4.3.3 marathon (up to 3 hours) – A Left-Skewed Distribution

Next, let's consider the 37th PZU Warsaw Marathon (2015) results.

```
marathon = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
                      "teaching_data/master/marek/37_pzu_warsaw_marathon_mins.txt")
```

Here are the top 5 gun times (in minutes):

```
marathon[:5] # preview first 5 (data are already sorted increasingly)
## array([129.32, 130.75, 130.97, 134.17, 134.68])
```

Plotting the histogram for the participants who finished the 42.2 km run in less than three hours reveals (see Figure 4.4) that the data are highly left-skewed.

```
sns.histplot(marathon[marathon < 180], color="lightgray")
plt.show()
```

This is of course to be expected – there are only few elite runners in the game. Yours truly wishes his personal best becomes < 180 minutes someday. We shall see. Running is fun, so is walking; why not taking a break for an hour and going outside?

Exercise 4.6 Plot the histogram of the untruncated (complete) version of this dataset.

⁶⁸ https://github.com/gagolews/teaching_data/blob/master/marek/nhanes_adult_female_weight_2020.txt

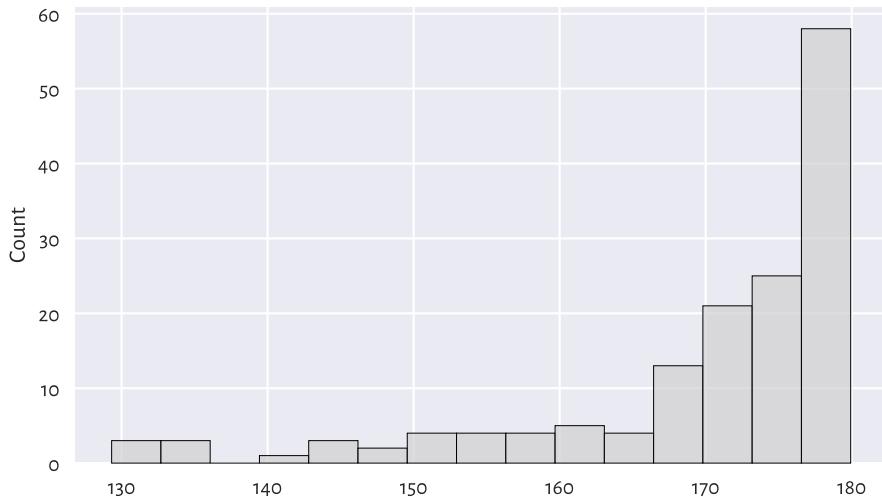


Figure 4.4: Histogram for a subset of the `marathon` dataset

4.3.4 How Many Bins?

Unless some stronger assumptions about the data distribution are made, choosing the right number of bins is more art than science:

- too many will result in a rugged histogram,
- too few might result in our missing of important details.

Figure 4.5 illustrates this.

```
plt.subplot(121) # 1 row, 2 columns, 1st plot
sns.histplot(income, bins=5, color="lightgray")
plt.subplot(122) # 1 row, 2 columns, 2nd plot
sns.histplot(income, bins=200, color="lightgray")
plt.ylabel(None)
plt.show()
```

For example, in the histogram with 5 bins, we miss the information that the ca. £16,000 income is more popular than the ca. £12,000 one.

The other histogram seems too fine-grained already.

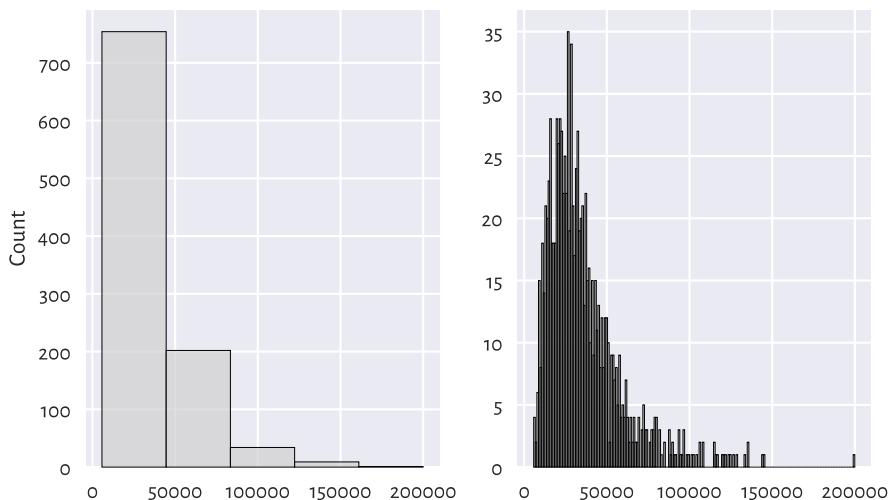


Figure 4.5: Too few and too many histogram bins (the `income` dataset)

Important: As usual, the “truth” is probably somewhere in-between. When preparing a histogram for publication (e.g., in a report or on a webpage), we might be tempted to think “I need to choose one and only one bin count”. In fact, we do not have to – even though some people will insist on it, remember that it is we who are responsible for the data be presented in an as unambiguous fashion as possible. Thus, actually, providing 2 or 3 histograms is often a much better idea.

Further, note that someone might want to trick us by choosing the number of bins that depict the reality in a good light, when the truth is quite the opposite. For instance, the histogram on the left above hides the poorest households inside the first bar – the first income bracket is very wide. If we cannot request access to the original data, best thing we can do is to simply ignore such a data visualisation instance as non-informative and tell others not to trust it. A real scientist is a sceptic, first and foremost.

Exercise 4.7 *Studying the manual of the `seaborn.histplot` function, we see that we can provide the function with custom bin breaks. Plot a histogram which has breaks at 0, 10,000, 20,000, etc.*

Note: (*) There are quite a few heuristics to determine the number of bins automagically, see `numpy.histogram_bin_edges` for a few formulae. Check out how different values of

the `bins` argument (e.g., "sturges", "fd") affect the histogram shapes on both `income` and `heights` datasets. Each has its own limitations, but some might be a good starting point for further fine-tuning.

4.3.5 Manual Binning (*)

`numpy.histogram` can be used to apply the binning of a numeric vector manually and then count the number of items falling into each bin. This can for instance be useful for data reporting – a table of ranges and corresponding counts is more informative and takes less space. Also, it can increase privacy (making subjects less identifiable) or hide some uncomfortable facts ("there are 10 people in our company earning more than £200,000 p.a." – this can be as much as £10,000,000, but shush).

We will discuss this topic in more detail in [Section 11.1.5](#).

Exercise 4.8 (*) Use `numpy.histogram` on the `marathon` data.

4.3.6 `peds` – A Bimodal Distribution (Already Binned)

Sometimes data we get access to have already been binned by somebody else. For instance, here are the December 2019 hourly averages `pedestrian counts`⁶⁹ near the Southern Cross Station in Melbourne:

```
peds = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/southern_cross_station_peds_2019_dec.txt")
peds
## array([ 31.22580645,  18.38709677,  11.77419355,   8.48387097,
##        8.58064516,  58.70967742, 332.93548387, 1121.96774194,
##       2061.87096774, 1253.41935484, 531.64516129,  502.35483871,
##       899.06451613,  775.          , 614.87096774,  825.06451613,
##      1542.74193548, 1870.48387097, 884.38709677, 345.83870968,
##      203.48387097, 150.4516129 , 135.67741935,  94.03225806])
```

We cannot thus use `seaborn.histplot` to depict them. Instead, we can rely on a more low-level function, `matplotlib.pyplot.bar`, see [Figure 4.6](#).

```
plt.bar(np.arange(0, 24), width=1, height=peds,
        color="lightgray", edgecolor="black", alpha=0.8)
plt.show()
```

⁶⁹ <http://www.pedestrian.melbourne.vic.gov.au/>

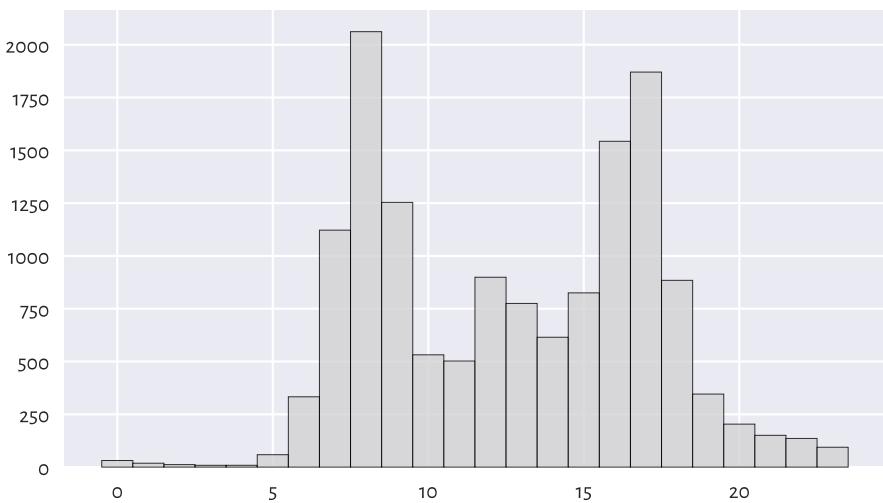


Figure 4.6: Histogram for the `peds` dataset

This is an example of a bimodal (or even trimodal) distribution: there is a morning peak and an evening peak (and some analysts probably would distinguish a lunch-time one too).

4.3.7 `matura` – A Bell-Shaped Distribution (Almost)

Figure 4.7 depicts a histogram for another interesting dataset which has already been pre-summarised.

```
matura = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/matura_2019_polish.txt")
plt.bar(np.arange(0, 71), width=1, height=matura,
        color="lightgray", edgecolor="black", alpha=0.8)
plt.show()
```

This gives the distribution⁷⁰ of the 2019 Matura⁷¹ exam scores in Poland (in %) – Polish literature at basic level.

⁷⁰ https://cke.gov.pl/images/_EGZAMIN_MATURALNY_OD_2015/Informacje_o_wynikach/2019/sprawozdanie/Sprawozdanie%202019%20-%20%C4%99zyk%20polski.pdf

⁷¹ <https://en.wikipedia.org/wiki/Matura>

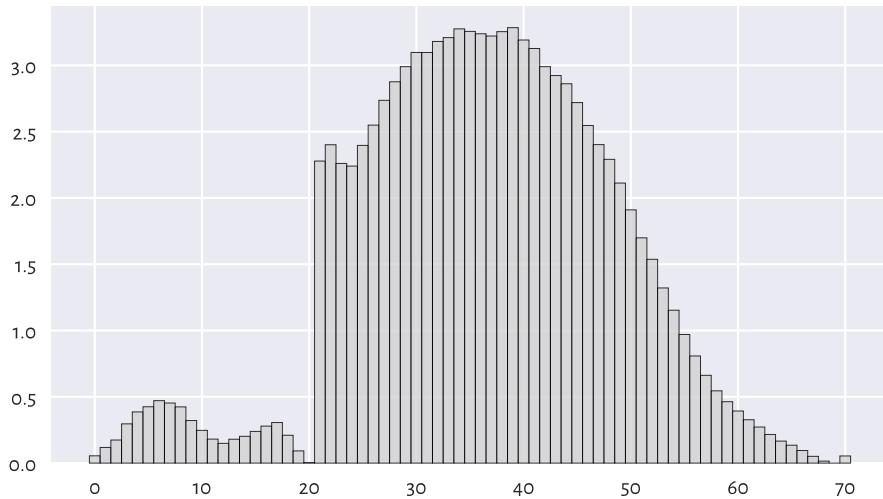


Figure 4.7: Histogram for `matura` dataset

It seems that the distribution should be bell-shaped, but someone tinkered with it. However, knowing that:

- the examiners are good people – we teachers love our students,
- 20 points were required to pass,
- 50 points were for an essay – and beauty is in the eye of beholder,

this actually starts to make sense. Without graphically depicting this dataset, we wouldn't know that such (albeit lucky for some students) *anomalies* occurred.

4.3.8 Cumulative Counts and the Empirical Cumulative Distribution Function (‘`)

Let's get back to the `heights` dataset. The histogram above told us that, e.g., ca. 30% of women are approximately 160 ± 5 cm tall.

However, sometimes we might be more interested in *cumulative* counts, see Figure 4.8.

```
sns.histplot(heights, stat="percent", cumulative=True, color="lightgray")
plt.show()
```

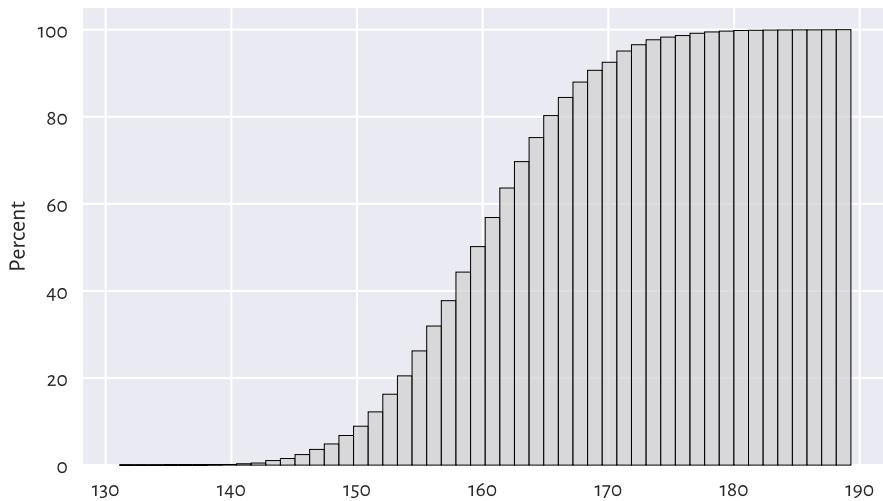


Figure 4.8: Cumulative histogram for the `heights` dataset

This has a different interpretation: we can read that, e.g., 60% of all women are *no more than* ca. 162 cm tall (or that 40% are taller).

Very similar is the plot of the *empirical cumulative distribution function* (ECDF), which for a sample $\mathbf{x} = (x_1, \dots, x_n)$ we denote as \hat{F}_n .

At any given point $t \in \mathbb{R}$, $\hat{F}_n(t)$ is a step function⁷⁴ that gives the *proportion of observations in our sample that are not greater than t*:

$$\hat{F}_n(t) = \frac{|i : x_i \leq t|}{n}$$

(read $|i : x_i \leq t|$ as the number of i s such that the corresponding x_i is greater than or equal to t)

Given ordered inputs, $x_{(1)} \leq x_{(2)} \leq \dots \leq x_{(n)}$, we have:

$$\hat{F}_n(t) = \begin{cases} 0 & \text{for } t < x_{(1)}, \\ k/n & \text{for } x_{(k)} \leq t < x_{(k+1)}, \\ 1 & \text{for } t \geq x_{(n)}. \end{cases}$$

⁷⁴ We cannot see the steps in Figure 4.9, because the points are too plentiful.

Note that drawing the ECDF does not involve binning – we only need to arrange the observations in an ascending order. Then, assuming that all observations are unique (there are no ties), the arithmetic progression $1/n, 2/n, \dots n/n$ is plotted against them, see Figure 4.9.

```
n = len(heights)
heights_sorted = np.sort(heights)
plt.plot(heights_sorted, np.arange(1, n+1)/n, drawstyle="steps-post")
plt.xlabel("$t$")
plt.ylabel("$\hat{F}_n(t)$, i.e., Prob(height $\leq t$)")
plt.show()
```

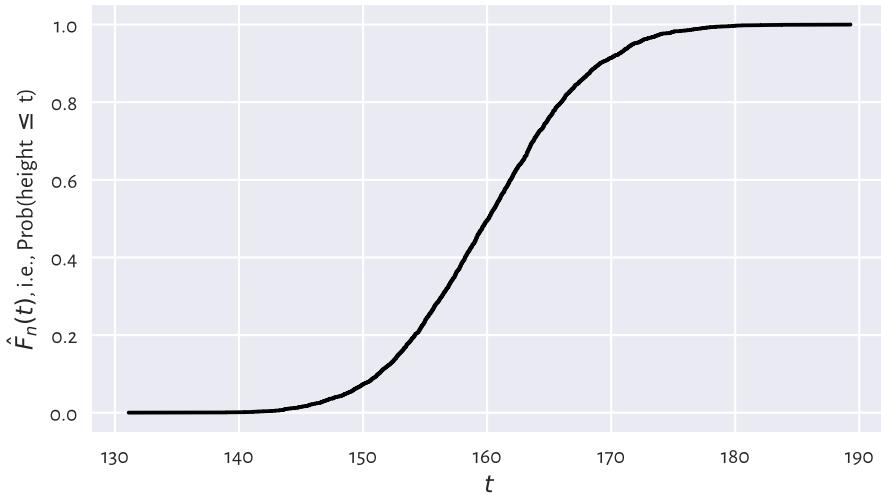


Figure 4.9: Empirical cumulative distribution function for the `heights` dataset

Exercise 4.9 Check out `seaborn.ecdfplot` for a built-in method implementing the drawing of an ECDF.

Note: (*) Quantiles that we introduce in Section 5.1.1 can be considered a generalised inverse of the ECDF.

4.3.9 Log-scale and Heavy-Tailed Distributions

Consider the dataset⁷² on the populations of cities in the 2000 US Census:

```
cities = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/other/us_cities_2000.txt")
```

Let's restrict ourselves only to the cities whose population is no less than 10,000. Even though they constitute ca. 14% of all the US settlements, about 84% of all the citizens live there.

```
large_cities = cities[cities >= 10000]
```

Here are the populations of the 5 largest cities:

```
large_cities[-5:] # preview last 5 - data are sorted increasingly
## array([1517550., 1953633., 2896047., 3694742., 8008654.])
```

The histogram is depicted in Figure 4.10.

```
sns.histplot(large_cities, bins=20, color="lightgray")
plt.show()
```

is basically unreadable because the distribution is not just right-skewed; it's extremely *heavy-tailed*: most cities are small, and those that are large – such as New York – are *really* unique. Had we plotted the whole dataset (`cities` instead of `large_cities`), the results' intelligibility would be even worse.

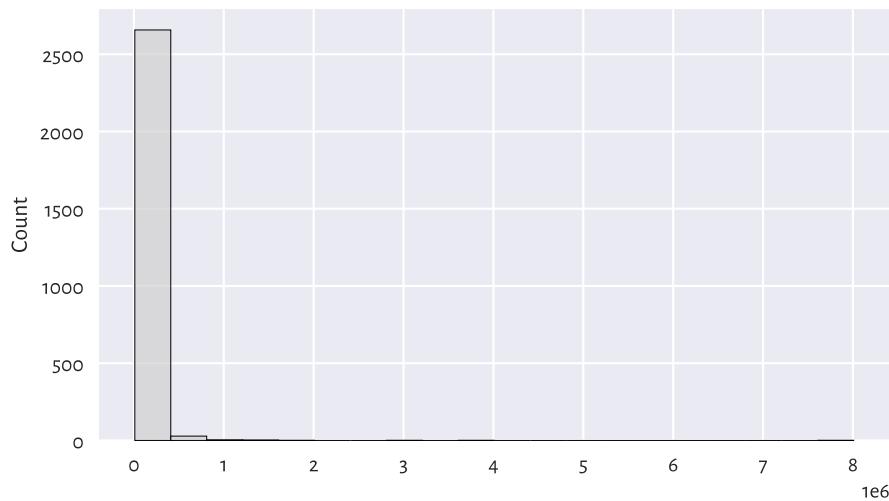
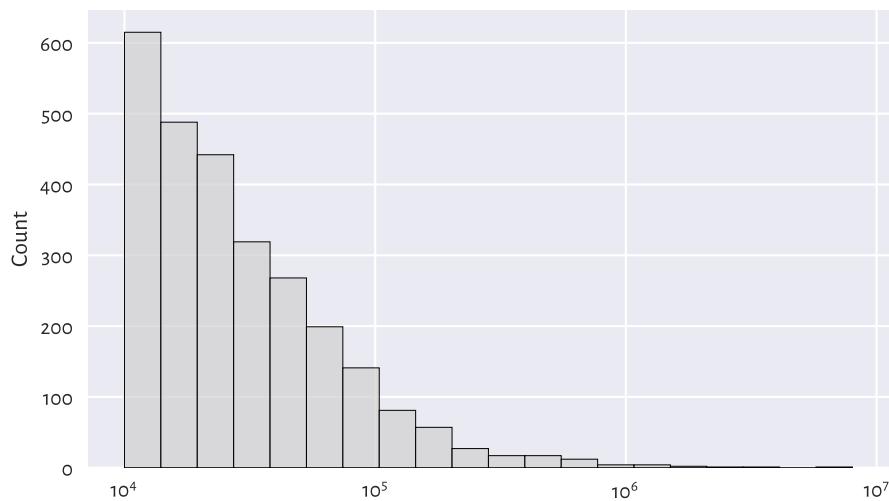
This is why we should rather draw such a distribution on the *logarithmic* scale, see Figure 4.11.

```
sns.histplot(large_cities, bins=20, log_scale=True, color="lightgray")
plt.show()
```

The log-scale on the x axis does not increase linearly – based on steps of equal sizes 0, 1,000,000, 2,000,000, ..., and so forth. Now the increases are geometrical: 10,000, 100,000, 1,000,000.

This is a right-skewed distribution even on the logarithmic scale. Many real-world datasets have a similar behaviour, for instance, the frequencies of occurrences of words in books. In Section 11.1.5 we will discuss the Pareto distribution family which yields similar histograms.

⁷² <https://arxiv.org/abs/0706.1062v2>

Figure 4.10: Histogram for the `large_cities` datasetFigure 4.11: Histogram for the `large_cities` dataset (logarithmic scale)

Exercise 4.10 Draw the histogram of `income` on the logarithmic scale. Does it resemble a bell-shaped distribution?

Exercise 4.11 (*) Use `numpy.geomspace` and `numpy.histogram` to apply logarithmic binning of the `large_cities` dataset manually, i.e., to create bins of equal lengths on the log-scale.

4.4 Exercises

Exercise 4.12 What are some benefits of using a `numpy` vector over an ordinary Python list? What are the drawbacks?

Exercise 4.13 What is the difference between `numpy.arange` and `numpy.linspace`?

Exercise 4.14 (*) What happens when we convert a logical vector to a numeric one? (We will discuss that later but you might want to check it yourself now.)

Exercise 4.15 (*) What happens when we convert a numeric vector to a logical one?

Exercise 4.16 What is a bell-shaped distribution?

Exercise 4.17 What is a right-skewed distribution?

Exercise 4.18 What is a heavy-tailed distribution?

Exercise 4.19 What is a multi-modal distribution?

Exercise 4.20 (*) When does logarithmic binning make sense?

5

Processing Unidimensional Data

It is extremely rare for our datasets to bring interesting and valid insights out of the box. The ones we are using for illustrational purposes in the first part of our series have already been curated. After all, this is an introductory course, and we need to build up the necessary skills and not overwhelm the kind reader with too much information at the same time. We learn simple things first, learn them well, so that then we can move to more complex matters with a healthy level of confidence.

In real life, various *data cleansing* and *feature engineering* techniques will need to be performed on data. Generally, most of them can be reduced to simple operations on vectors:

- summarising data (for example, computing the median or sum),
- transforming values (applying mathematical operations on each element, such as subtracting a scalar or taking the natural logarithm),
- filtering (selecting or removing observations that meet specific criteria, e.g., those that are larger than the arithmetic mean ± 5 standard deviations).

We cover them below.

Important: The same operations we are going to be applying on individual data frame columns in [Chapter 10](#).

5.1 Aggregating Numeric Data

Histograms are based on binned data and hence provide us with snapshots of how much probability mass is allocated in different parts of the data domain.

For instance, here is a textual summary of the UK income data that we have studied in the previous part (compare also [Figure 4.3](#)):

```

income = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/uk_income_simulated_2020.txt")
b = [0, 10000, 20000, 30000, 40000, 50000, 60000, 80000, np.inf] # bounds
c = np.histogram(income, bins=b)[0] # counts
for i in range(len(c)):
    print(f"[{b[i]:5}-{b[i+1]:5}]: {c[i]:4}")
##      0-10000:   29
## 10000-20000:  207
## 20000-30000:  263
## 30000-40000:  196
## 40000-50000:  117
## 50000-60000:  74
## 60000-80000:  64
## 80000- inf:   50

```

Instead of dealing with a large dataset, we have obtained only a few counts. Below we will also be using the `heights` dataset as an illustration (recall Figure 4.2), so let's load it now.

```

heights = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_adult_female_height_2020.txt")

```

Generally, the process of binning and its textual or visual depictions are useful in determining whether the distribution is unimodal or multimodal, left or right skewed or maybe symmetric around some point, what range of values contains most of the observations, how small or large are extreme values, etc.

Still, too much information may sometimes be overwhelming. Also, revealing it might not be a good idea for privacy or confidentially reasons (although we strongly advocate for all information of concern to the general public be openly available!).

Thus, oftentimes we will be interested in even more synthetic descriptions – data aggregates which reduce the whole dataset into a *single* number reflecting one of its many characteristics and thus providing a kind of bird's eye view on some aspect of it. We refer to such a process as data *aggregation* [[Gagi15a], [GMMP09]].

In this part we discuss a few noteworthy *measures* of:

- *location*; e.g., central tendency measures such as mean and median;
- *dispersion*; e.g., standard deviation and interquartile range;

- distribution *shape*; e.g., skewness.

We also introduce *box and whisker plots*.

5.1.1 Measures of Location

Arithmetic Mean and Median

Two main measures of *central tendency* are:

- *the arithmetic mean* (sometimes for simplicity called the mean or average), defined as the sum of all observations divided by the sample size:

$$\bar{x} = \frac{(x_1 + x_2 + \dots + x_n)}{n} = \frac{1}{n} \sum_{i=1}^n x_i,$$

- *the median*, being the middle value in a sorted version of the sample if its length is odd or the arithmetic mean of the two middle values otherwise:

$$m = \begin{cases} x_{(n+1)/2} & \text{if } n \text{ is odd,} \\ \frac{x_{(n/2)} + x_{(n/2+1)}}{2} & \text{if } n \text{ is even.} \end{cases}$$

They can be computed using the `numpy.mean` and `numpy.median` functions.

```
np.mean(heights), np.median(heights)
## (160.13679222932953, 160.1)
np.mean(income), np.median(income)
## (35779.994, 30042.0)
```

We note what follows:

- for symmetric distributions, the arithmetic mean and the median are expected to be more or less equal,
- for skewed distributions, the arithmetic mean will be biased towards the heavier tail.

Exercise 5.1 Compute the arithmetic mean and median for the `37_pzu_warsaw_marathon_mins` dataset mentioned in [Chapter 4](#).

Exercise 5.2 (*) Write a function that computes the median without the use of `numpy.median` (based on its mathematical definition and `numpy.sort`).

Note: (*) On a technical note, the arithmetic mean can also be computed using the `mean`

`method` in the `numpy.ndarray` class – it will sometimes be the case that we have many different ways to perform the same operation. Or, we can “implement” it manually using the `sum` function. Thus, the following expressions are equivalent:

```
np.mean(heights), heights.mean(), \
    np.sum(heights)/len(heights), heights.sum()/heights.shape[0]
## (160.13679222932953, 160.13679222932953, 160.13679222932953, 160.
    ↵13679222932953)
```

On the other hand, there exists the `numpy.median` function but, unfortunately, the `median` method for vectors is not available.

Sensitive to Outliers vs Robust

The arithmetic mean is strongly influenced by very large or very small observations (which in some context we refer to as *outliers*). For instance, assume that we are adding one billionaire to the `income` dataset:

```
income2 = np.append(income, [1_000_000_000])
np.mean(income2)
## 1034745.2487512487
```

We feel we are all richer now, right? In fact, the arithmetic mean reflects the income each of us would get if the all the wealth was gathered in a single Santa Claus (or Robin Hood) sack and then distributed equally amongst all of us. But we do not live in a utopia, so let us move on.

On the other hand, the median is the value such that 50% of the observations are less than or equal to it and 50% of the remaining ones are no less than it.

Hence, it completely ignores most of the data points – on both the left and the right side of the distribution:

```
np.median(income2)
## 30076.0
```

Because of this, we cannot say that one measure is better than the other. Certainly for symmetrical distributions with no outliers (e.g., `heights`), the mean will be better as it uses *all* data (and its efficiency can be proven for certain statistical models). For skewed distributions (e.g., `income`), the median has a nice interpretation: what is the “middle” value? Let us still remember that these are data summaries – they only allow us to look

at a single data aspect, and there can be many different, valid perspectives. The reality is complex.

We will explore the concept of robust aggregation measures in more detail in [Section 15.4.2](#).

Sample Quantiles

Quantiles generalise the notion of the sample median and the inverse of the empirical cumulative distribution function ([Section 4.3.8](#)), giving the value that is not exceeded by the elements in a given sample with a predefined probability.

Before proceeding with a formal definition, which is quite technical, let's note that for larger sample sizes, we have the following rule of thumb.

Important: For any p between 0 and 1, the p -quantile, denoted with q_p , is a value dividing the sample in such a way that approximately $100p\%$ of observations are not greater than q_p , and the remaining ca. $100(1-p)\%$ are not less than q_p .

Quantiles appear under many different names, but they all refer to the same concept. In particular, we can speak about $100p$ -th *percentiles*, e.g., the 0.5-quantile is the same as the 50th percentile.

Furthermore:

- 0-quantile (q_0) – the minimum (also: `numpy.min`),
- 0.25-quantile ($q_{0.25}$) – the 1st quartile (denoted Q_1),
- 0.5-quantile ($q_{0.5}$) – the 2nd quartile a.k.a. median (denoted m or Q_2),
- 0.75-quantile ($q_{0.75}$) – the 3rd quartile (denoted Q_3),
- 1.0-quantile (q_1) – the maximum (also: `numpy.max`).

Here are the above five aggregates for the two datasets:

```
np.quantile(income, [0, 0.25, 0.5, 0.75, 1])
## array([ 5750. , 20669.75, 30042. , 44123.75, 199969. ])
np.quantile(heights, [0, 0.25, 0.5, 0.75, 1])
## array([131.1, 155.3, 160.1, 164.8, 189.3])
```

Exercise 5.3 What is the income bracket for 95% of the “most typical” taxpayers? In other words, determine the 2.5- and 97.5-percentiles.

Exercise 5.4 Compute the midrange of *income* and *heights*, being the arithmetic mean of the minimum and the maximum. Note that this measure is extremely sensitive to outliers.

Note: (*) As we do not like the *approximately* part in the “asymptotic definition” above, in this course we shall assume that for any $p \in [0, 1]$, the p -quantile is given by

$$q_p = x_{(\lfloor k \rfloor)} + (k - \lfloor k \rfloor)(x_{(\lfloor k \rfloor + 1)} - x_{(\lfloor k \rfloor)}),$$

where $k = (n - 1)p + 1$ and $\lfloor k \rfloor$ is the floor function, i.e., the greatest integer less than or equal to k (e.g., $\lfloor 2.0 \rfloor = \lfloor 2.1 \rfloor = \lfloor 2.999 \rfloor = 2$ and $\lfloor 3.0 \rfloor = 3$).

q_p is thus a function that linearly interpolates between the points featuring the consecutive order statistics, $((k - 1)/(n - 1), x_{(k)})$ for $k = 1, \dots, n$. For instance, for $n = 5$, we are linearly interpolating between the points $(0, x_{(1)}), (0.25, x_{(2)}), (0.5, x_{(3)}), (0.75, x_{(4)}), (1, x_{(5)})$, whereas for $n = 6$, we do the same for $(0, x_{(1)}), (0.2, x_{(2)}), (0.4, x_{(3)}), (0.6, x_{(4)}), (0.8, x_{(5)}), (1, x_{(6)})$, see Figure 5.1 for an illustration.

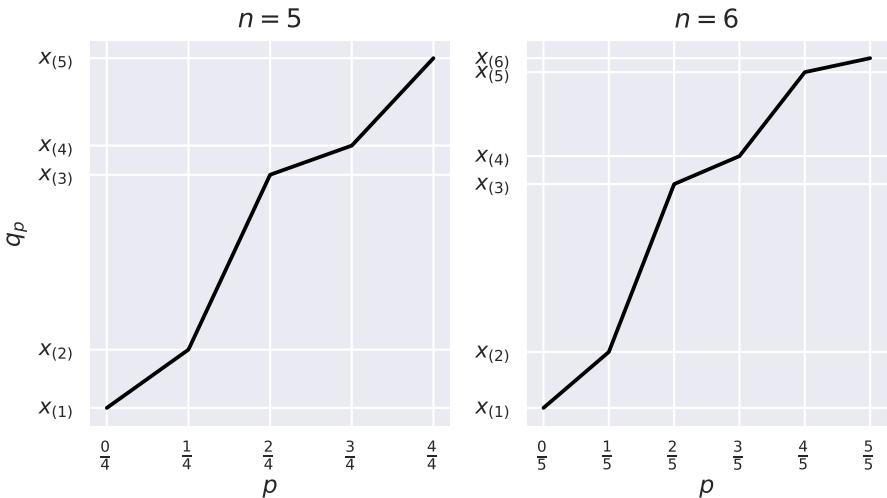


Figure 5.1: q_p as a function of p for two example vectors of length 5 (left subfigure) and 6 (right)

Note that for $p=0.5$ we get the median regardless of whether n is even or not.

Note: (***) There are many definitions of quantiles across statistical software, see the `method` argument to `numpy.quantile`. They have been nicely summarised in [[HF96]] as well as in the corresponding Wikipedia⁷⁵ article. They are all approximately equivalent for large sample sizes (i.e., asymptotically), but the best practice is to be explicit about which variant we are using in the computations when reporting data analysis results. And thus, in our case, we say that we are relying on the type-7 quantiles as described in [[HF96]], see also [[Gum39]].

Actually, simply mentioning that our computations are done with `numpy` version 1.xx implicitly implies that the default method parameters are used everywhere, unless otherwise stated.

5.1.2 Measures of Dispersion

Measures of central tendency quantify the location of the most *typical* value (whatever that means, and we already know it's complicated). That of dispersion (spread), on the other hand, will tell us how much *variability* is in our data.

After all, when we say that the height of a group of people is 160 cm (on average) \pm 14 cm (here, 2 standard deviations), the latter piece of information is a valuable addition (and is much different to the imaginary \pm 4 cm case).

Some degree of variability might be good in certain contexts and bad in other ones. A bolt factory should keep the variance of the fasteners' diameters as low as possible – after all, this is how we define quality products (assuming that on average they all meet the required specification). On the other hand, too much diversity in human behaviour, where everyone feels that they are special, is not really sustainable (but lack thereof would be extremely boring), and so forth.

Standard Deviation (and Variance)

The standard deviation (** in the so-called uncorrected for bias version), is the average distance to the arithmetic mean:

$$s = \sqrt{\frac{(x_1 - \bar{x})^2 + (x_2 - \bar{x})^2 + \dots + (x_n - \bar{x})^2}{n}} = \sqrt{\frac{1}{n} \sum_{i=1}^n (x_i - \bar{x})^2},$$

Computing the above with `numpy`:

⁷⁵ <https://en.wikipedia.org/wiki/Quantile>

```
np.std(income), np.std(heights)
## (22888.77122437908, 7.062021850008261)
```

The standard deviation measures the average degree of spread around the arithmetic mean. Thus, it makes most sense for data distributions that are symmetric around the mean. This measure is useful overall for making comparisons across different samples. However, without further assumptions, it's quite difficult to express the meaning of a particular value of s (e.g., the statement that the standard deviation of income is £22,900 is hard to interpret).

Note: (*) For bell-shaped data (like `heights`, more precisely, for normally-distributed samples, see the next chapter), we sometimes report $\bar{x} \pm 2s$, as the theoretical expectancy is that ca. 95% of data points fall into the $[\bar{x} - 2s, \bar{x} + 2s]$ interval (the so-called 2-sigma rule).

Note: (*) Passing `ddof=1` (*delta degrees of freedom*) to `numpy.std` will apply division by $n-1$ instead of n in the denominator. This estimator has slightly better statistical properties (which we normally explore in a course in mathematical statistics, which this one is not); interestingly, the `std` methods in the `pandas` package has `ddof=1` by default, therefore we might be interested in setting `ddof=0` therein.

Further, the *variance* is the square of the standard deviation, s^2 . Note that if data are expressed in centimetres, then the variance is in centimetres *squared*, which is not very intuitive. The standard deviation does not have this drawback. Mathematicians find the square root annoying though (for many reasons); that is we will come across s^2 every now and then below too.

Interquartile Range

The interquartile range (IQR) is another popular measure of dispersion. It is defined as the difference between the 3rd and the 1st quartile:

$$\text{IQR} = q_{0.75} - q_{0.25} = Q_3 - Q_1.$$

Computing the above is almost effortless:

```
np.quantile(income, 0.75) - np.quantile(income, 0.25)
## 23454.0
```

(continues on next page)

(continued from previous page)

```
np.quantile(heights, 0.75) - np.quantile(heights, 0.25)
## 9.5
```

The IQR has an appealing interpretation, because we may say that this is the range comprised of the 50% *most typical* values. It is a quite robust measure, as it ignores the 25% smallest and 25% largest observations. Standard deviation, on the other hand, is extremely sensitive to outliers.

Furthermore, by *range* (or *support*) we will mean a measure based on extremal quantiles: it is the difference between the maximal and minimal observation.

5.1.3 Measures of Shape (*)

Note that from a histogram we can easily deduce if a dataset is symmetric or skewed. It turns out that we can also give a numerical summary of such a feature. Namely, the *skewness* is given by:

$$g = \frac{\frac{1}{n} \sum_{i=1}^n (x_i - \bar{x})^3}{\left(\sqrt{\frac{1}{n} \sum_{i=1}^n (x_i - \bar{x})^2} \right)^3}.$$

For symmetric distributions, skewness is approximately zero. Positive and negative skewness indicates a heavier right and left tail, respectively.

For example:

```
scipy.stats.skew(heights)
## 0.0811184528074054
```

is thus an instance of almost-symmetric distribution.

```
scipy.stats.skew(income)
## 1.9768735693998942
```

Income is right-skewed, and now we have this expressed as a single number.

5.1.4 Box (and Whisker) Plots

The box and whisker plot (or the box plot for short) depicts some of the most noteworthy features of a data sample and is based only on the aggregates

```
plt.subplot(211) # 2 rows, 1 column, 1st subplot
sns.boxplot(data=income, orient="h", color="lightgray")
plt.yticks([0], ["income"])
plt.subplot(212) # 2 rows, 1 column, 2nd subplot
sns.boxplot(data=heights, orient="h", color="lightgray")
plt.yticks([0], ["heights"])
plt.show()
```

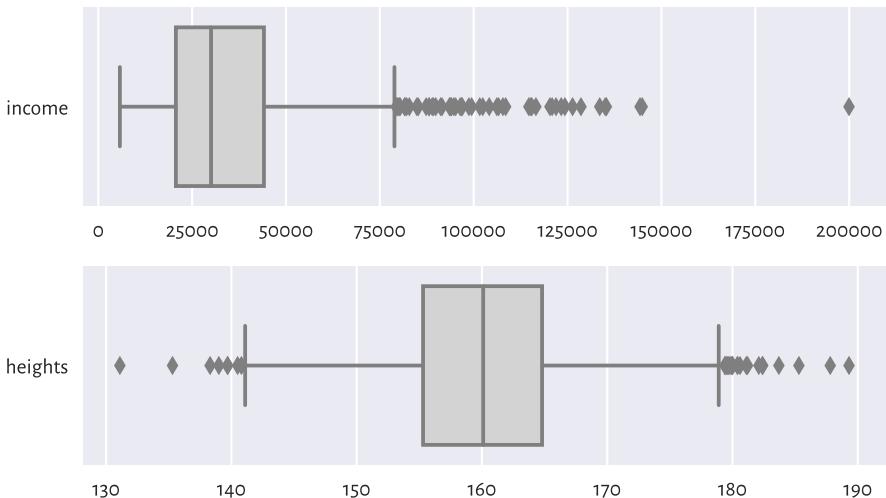


Figure 5.2: Example box-and-whisker plots

Each box plot (compare Figure 5.2) consists of:

- the box, which spans between the 1st and the 3rd quartile:
 - the median is clearly marked by a vertical bar inside the box;
 - note that the width of the box corresponds to the IQR;
- the whiskers, which span⁸⁰ between:
 - the smallest observation (the minimum) or $Q_1 - 1.5\text{IQR}$ (the left side of the box minus 3/2 of its width), whichever is larger, and

⁸⁰ The 1.5IQR rule seems to be the most popular in the statistical literature, but by no means it's a standard; some plotting software may use different whisker ranges.

- the largest observation (the maximum) or $Q_3 + 1.5\text{IQR}$ (the right side of the box plus $3/2$ of its width), whichever is smaller.

Additionally, all observations that are less than $Q_1 - 1.5\text{IQR}$ (if any) or greater than $Q_3 + 1.5\text{IQR}$ (if any) are separately marked.

Note: We are used to referring to the marked points as *outliers*, however, it doesn't automatically mean there is anything *anomalous* about them. They are *atypical* in the sense that they are considerably farther away from the box. However, they might also indicate some problems in data quality (e.g., when one made a typo entering the data). Actually, box plots are calibrated (via the nicely round magic constant 1.5) in such a way that we expect there to be no or only few outliers if the data are normally distributed. For skewed distributions, there will naturally be many outliers on either side.

Important: Most of the statistical packages *do not* include the arithmetic mean when drawing a box plot. If they do, it is marked with a special symbol.

Important: Box plots will be particularly useful for comparing data samples with each other (e.g., body measures of men and women separately); both in terms of the relative shift (location) as well as spread and skewness, see [Figure 12.1](#).

Exercise 5.5 Call `matplotlib.pyplot.plot(numpy.mean(..data..), 0, "wX")` after `seaborn.boxplot` to mark the arithmetic mean with a white cross.

Note: We may also sometimes be interested in a *violin plot* ([Figure 5.3](#)), which combines the box plot (although with no outliers marked) and the so-called kernel density estimator (which is a smoothed version of a histogram, see [Section 15.4.3](#)).

```
sns.violinplot(data=income, orient="h", color="lightgray")
plt.yticks([0], ["income"])
plt.show()
## ([<matplotlib.axis.YTick object at 0x7fa67faadc10>], [Text(0, 0, 'income
˓→')])
```

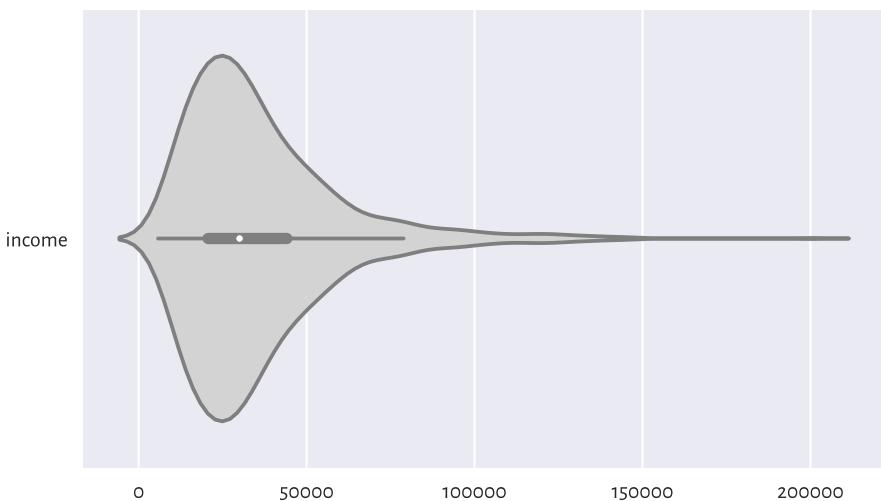


Figure 5.3: An example violin plot

5.1.5 Further Methods (*)

We have said that the arithmetic mean is very sensitive to extreme observations. In [Section 15.4.2](#), we will consider the *trimmed* and *winsorised* means which are more *robust* in presence of outliers – they remove or replace a few smallest and largest observations in a sample.

Similarly, the *mean absolute deviation from the mean* or from the median or even the *median absolute deviation from the median* can be used as more robust versions of dispersion measures.

The arithmetic mean is not the only mean of interest. The two other very famous means are the *harmonic* and *geometric* ones. The former can be used for computing the average speed from speed measurements at sections of identical lengths and the latter is more meaningful for averaging growth rates and speedups.

The *coefficient of variation*, being the standard deviation dived by the arithmetic mean, is an example of a *relative* (or normalised) spread measure. It can be useful for comparing data on different scales, as it is unit-less (think how standard deviation changes when you convert between metres and kilometres).

The *Gini index* widely used in economics, can serve as a measure of dispersion (or shape – depending how we look at it), but assumes that all data points are nonnegative.

$$G = \frac{\sum_{i=1}^n \sum_{j=1}^n |x_i - x_j|}{2(n-1)n\bar{x}} = \frac{\sum_{i=1}^n (n-2i+1)x_{(n-i+1)}}{(n-1) \sum_{i=1}^n x_i}.$$

It is normalised so that it takes values in the unit interval. An index of 0 reflects the situation where all values in a sample are the same (0 variance; perfect equality). If there is a single entity in possession of all the “wealth”, and the remaining ones are 0, then the index is equal to 1.

Exercise 5.6 (*) It may be shown that the sample variance is equal to

$$s^2 = \frac{\sum_{i=1}^n \sum_{j=1}^n |x_i - x_j|}{n^2}.$$

Based on this, show the relationship between the Gini index and the coefficient of variation.

Entropy can be used as a measure of spread for data which sum to 1, e.g., probabilities.

Kurtosis (or excess kurtosis) is another measure of shape, describing whether a distribution is heavy- or thin-tailed.

For some more generic treatment of aggregation functions see, e.g., [[GMMPO9]] and [[Gag15b]].

5.2 Vectorised Mathematical Functions

Numpy, just like any other comprehensive numerical computing package, library, or environment (e.g., R and Julia), defines many basic mathematical functions:

- absolute value: `numpy.abs`,
- square and square root: `numpy.square` and `numpy.sqrt`,
- (natural) exponential function: `numpy.exp`,
- logarithms: `numpy.log` (the natural logarithm, i.e., base e), `numpy.log10` (base 10), etc.,
- trigonometric functions: `numpy.cos`, `numpy.sin`, `numpy.tan`, etc., and their inverses: `numpy.arccos`, etc.
- rounding and truncating: `numpy.round`, `numpy.floor`, `numpy.ceil`, `numpy.trunc`.

Each of these functions is *vectorised*: if we apply, say, f , on a vector like $\mathbf{x} = (x_1, \dots, x_n)$, we obtain a sequence of the same size with all elements appropriately transformed:

$$f(\mathbf{x}) = (f(x_1), f(x_2), \dots, f(x_n)).$$

We will frequently be using such operations for adjusting the data, e.g., as in [Figure 6.5](#) where we note that the *logarithm* of the UK incomes has a bell-shaped distribution.

For example, the absolute value of a single x is given by

$$|x| = \begin{cases} x & \text{if } x \geq 0, \\ -x & \text{otherwise.} \end{cases}$$

and its vectorised version yields

```
np.abs([-2, -1, 0, 1, 2, 3])
## array([2, 1, 0, 1, 2, 3])
```

Note that the input list has automatically been converted to a **numpy** vector.

Important: Thanks to the vectorised functions, our code is not only more readable, but also it runs faster – as otherwise we would have to employ a **while** or **for** loop to traverse through each element in a given sequence.

Note: Here are some noteworthy properties of the exponential function and its inverse, the natural logarithm, that we should know. By convention, the Euler's number $e = \exp(1) \approx 2.718$, $\exp(x) = e^x$, and $\log x = \log_e x$.

- $e^{\log x} = x$
- $\log e^x = x$
- $\log(xy) = \log x + \log y$, $\log(x/y) = \log x - \log y$
- $e^{x+y} = e^x e^y$
- $\log 1 = 0$, $\log e = 1$

Note that both functions are strictly increasing. For $x \geq 1$, the logarithm grows very slowly whereas the exponential function increases very rapidly, see [Figure 5.4](#).

Further, logarithms are only defined for $x > 0$. In the limit as $x \rightarrow 0$, we have that $\log x \rightarrow -\infty$.

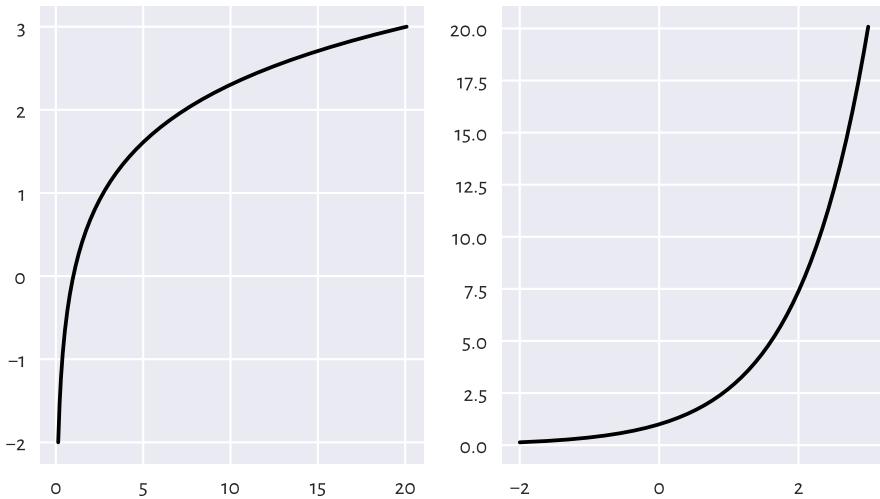


Figure 5.4: The natural logarithm (left) and the exponential function (right)

Note: Logarithms of different bases and non-natural exponential function are also possible. In particular, when drawing plots, we have already used base-10 logarithmic scales on the axes. It holds $\log_{10} x = \frac{\log x}{\log 10}$ and its inverse is 10^x .

For example:

```
np.log10([-1, 0.01, 0.1, 1, 2, 5, 10, 100, 1000, 10000])
## array([-nan, -2., -1., 0., 0.30103, 0.69897,
##        1., 2., 3., 4.])
## <string>:1: RuntimeWarning: invalid value encountered in log10
```

Note the warning and the not-a-number (NaN) generated.

Exercise 5.7 Check that when using the log-scale on the OX axis (`plt.xscale("log")`), the plot of the logarithm (of any base) is a straight line. Similarly, the log-scale on the OY axis (`plt.yscale("log")`) makes the exponential function linear.

Note: Trigonometric functions in `numpy` accept angles in radians; if x is the degree in angles, then to compute its cosine we will be thus writing $\cos(x\pi/180)$ instead; see Figure 5.5.

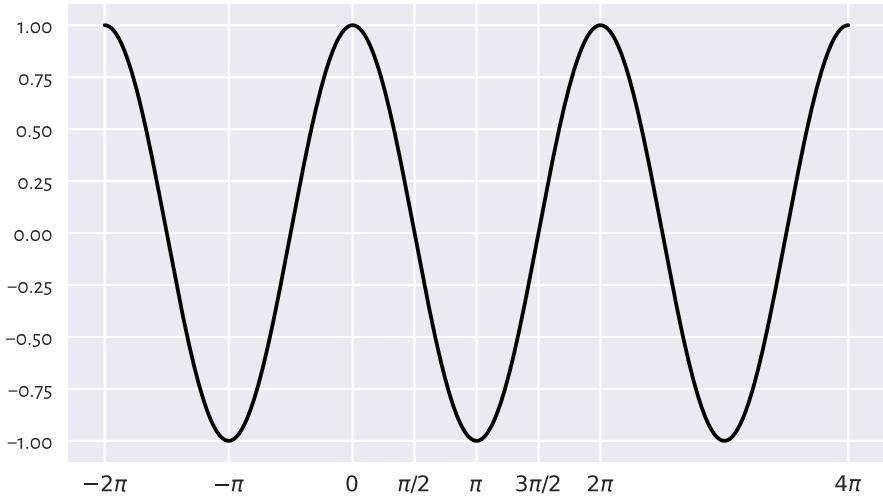


Figure 5.5: The cosine

Some identities worth memorising:

- $\sin x = \cos(\pi/2 - x)$,
- $\cos(-x) = \cos x$,
- $\cos^2 x + \sin^2 x = 1$, where $\cos^2 x = (\cos x)^2$,
- $\cos(x + y) = \cos x \cos y - \sin x \sin y$,
- $\cos(x - y) = \cos x \cos y + \sin x \sin y$.

we will refer to them later.

Important: The classical handbook of mathematical functions and the (in)equalities related to them is [[AS72]], see [[O+22]] for its updated version.

5.3 Arithmetic Operators

We can apply the standard binary (two-argument) arithmetic operators `+`, `-`, `*`, `/` , `**` , `%` , `/` on vectors too. Below we discuss the possible cases of the operands' lengths.

5.3.1 Vector-Scalar Case

Often we will be referring to the binary operators in contexts where one operand is a vector and the other one is a single value, for example:

```
np.array([-2, -1, 0, 1, 2, 3])**2
## array([4, 1, 0, 1, 4, 9])
(np.array([-2, -1, 0, 1, 2, 3])+2)/5
## array([0., 0.2, 0.4, 0.6, 0.8, 1.])
```

In such a case, each element in the vector is being operated upon (e.g., squared, divided by 5) and we get a vector of the same length in return. Hence, in this case the operators behave just like the vectorised mathematical functions discussed above.

Mathematically, it is common to assume that scalar multiplication and, less commonly, addition is performed in this way.

$$cx + t = (cx_1 + t, cx_2 + t, \dots, cx_n + t).$$

We will also become used to writing, $(x - t)/c$ which is of course equivalent to $(1/c)x + (-t/c)$.

5.3.2 Application: Feature Scaling

Such vector-scalar operations and aggregation functions are the basis for the most commonly applied *feature scalers*, which can increase the interpretability of data points:

- standardisation,
- normalisation,
- min-max scaling and clipping,

bringing them onto a common, unitless scale. All of them are linear transforms of the form $y = cx + t$, which geometrically we can interpret as scaling (stretching or shrinking) and shifting (translating), see Figure 5.6 for an illustration.

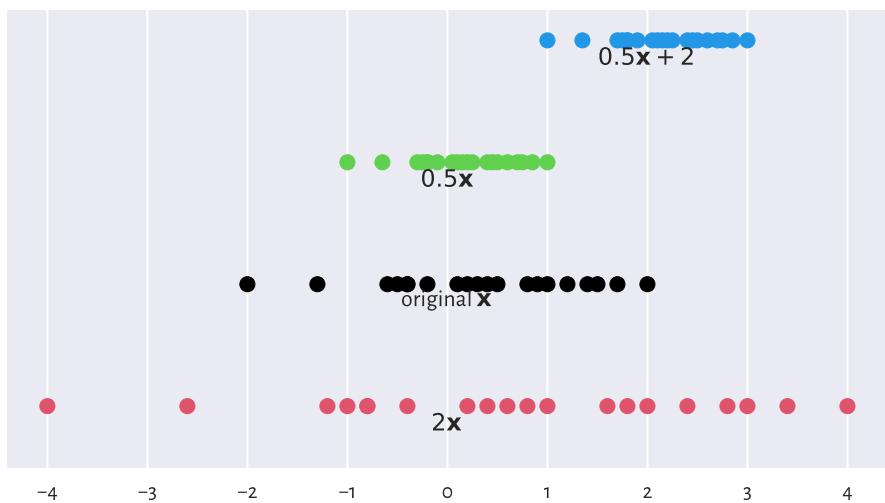


Figure 5.6: Scaled and shifted versions of a given vector

Note: Let $y = cx + t$ and let $\bar{x}, \bar{y}, s_x, s_y$ denote the vectors' arithmetic means and standard deviations. The following properties hold.

- the arithmetic mean and all the quantiles (including, of course, the median), are equivariant with respect to translation and scaling; it holds, for instance, $\bar{y} = c\bar{x} + t$;
- the standard deviation, the interquartile range, and the range are invariant to translations and equivariant to scaling; e.g., $s_y = cs_x$

As a by-product, for variance we get of course... $s_y^2 = c^2 s_x^2$.

Standardisation and Z-scores

Consider the female heights dataset:

```
heights = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_adult_female_height_2020.txt")
heights[-5:] # preview
## array([157. , 167.4, 159.6, 168.5, 147.8])
```

whose mean \bar{x} and standard deviation s are as follows:

```
np.mean(heights), np.std(heights)
## (160.13679222932953, 7.062021850008261)
```

Important: A *standardised* version of a vector $\mathbf{x} = (x_1, \dots, x_n)$ consists in subtracting, from each element, the sample arithmetic mean (which we call *centring*) and then dividing it by the standard deviation, i.e., $z = (\mathbf{x} - \bar{\mathbf{x}})/s$.

Thus, we transform each x_i so as to obtain:

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

With **numpy**, we simply apply 2 aggregation functions and 2 arithmetic operations:

```
heights_std = (heights-np.mean(heights))/np.std(heights)
heights_std[-5:] # preview
## array([-0.44417764,  1.02848843, -0.07601113,  1.18425119, -1.74692071])
```

Important: What we obtain in result is sometimes referred to as the *z-scores*.

Z-scores are nicely interpretable:

- z-score of 0 corresponds to an observation equal to the sample mean (perfectly average);
- z-score of 1 is obtained for a datum 1 standard deviation above the mean;
- z-score of -2 means that it is a value 2 standard deviations below the mean;

and so forth.

We should also note that because of the way they emerge, the mean of z-scores is always 0 and standard deviation is 1 (up to a tiny numerical error, as usual; see [Section 5.5.4](#)):

```
np.mean(heights_std), np.std(heights_std)
## (1.8920872660373198e-15, 1.0)
```

Moreover, z-scores are unitless (e.g., the original heights were measured in centimetres).

Important: Standardisation enables the comparison of measurements on different scales (think: height in cm vs weight in kg or apples vs oranges).

Exercise 5.8 We have a patient whose height z-score is 1 and weight z-score is -1. How to interpret this information?

Exercise 5.9 How about a patient whose weight z-score is 0 but BMI z-score is 2?

Note: (*) Standardisation makes most sense for bell-shaped distributions, in particular normally-distributed ones. Recalling the 2σ rule for the normal family, it is *expected* that 95% of observations should have z-scores between -2 and 2. Further, z-scores less than -3 and greater than 3 are highly unlikely.

Note: (*) Sometimes we might be interested in performing some form of *robust* standardisation (e.g., for skewed data or those that feature some outliers). In such a case, we can replace the mean with the median and the standard deviation with the IQR.

Min-Max Scaling and Clipping

A less frequently but still noteworthy transformation is called *min-max scaling* and involves subtracting the minimum and then dividing by the range.

```
x = np.array([-1.5, 0.5, 3.5, -1.33, 0.25, 0.8])
(x - np.min(x))/(np.max(x)-np.min(x))
## array([0.        , 0.4       , 1.        , 0.034, 0.35     , 0.46      ])
```

Here, the smallest value is mapped to 0 and the largest one is equal to 1. Note that 0.5 does not mean that the value is equal to the mean (unless we are very lucky!).

Also, *clipping* can be used to replace all values less than 0 with 0 and those greater than 1 with 1.

```
np.clip(x, 0, 1)
## array([0.        , 0.5       , 1.        , 0.        , 0.25     , 0.8      ])
```

The function is of course flexible; another popular choice is clipping to $[-1, 1]$. This can also be implemented manually by means of the vectorised pairwise minimum and maximum functions.

```
np.minimum(1, np.maximum(0, x))
## array([0. , 0.5 , 1. , 0. , 0.25, 0.8 ])
```

Normalisation (l_2 ; Dividing by Length)

Normalisation is the scaling of a given vector so that it is of *unit length*. Usually, by *length* we mean the square root of the sum of squares, i.e., the Euclidean (l^2) norm:

$$\|(x_1, \dots, x_n)\| = \sqrt{x_1^2 + x_2^2 + \dots + x_n^2} = \sqrt{\sum_{i=1}^n x_i^2},$$

Its special case for $n=2$ we know well from high school: the length of a vector (a, b) is $\sqrt{a^2 + b^2}$, e.g., $\|(1, 2)\| = \sqrt{5} \approx 2.236$. Also, it's good to program our brains so that when next time we see $\|\mathbf{x}\|^2$, we immediately think of the *sum of squares*.

We can thus write:

```
x = np.array([1, 5, -4, 2, 2.5])
x/np.sqrt(np.sum(x**2)) # x divided by the Euclidean norm of x
## array([ 0.13834289, 0.69171446, -0.55337157, 0.27668579, 0.34585723])
```

to mean the normalised vector

$$\frac{\mathbf{x}}{\|\mathbf{x}\|} = \left(\frac{x_1}{\|\mathbf{x}\|}, \frac{x_2}{\|\mathbf{x}\|}, \dots, \frac{x_n}{\|\mathbf{x}\|} \right).$$

Note: Note that normalisation is very similar to standardisation if data are already centred (when mean was subtracted). Actually, we can obtain one from the other via scaling by \sqrt{n} .

Important: A common confusion is that normalisation is supposed to make data more "normally" distributed. This is not the case, as we only scale (stretch or shrink) the observations here.

Normalisation (l_1 ; Dividing by Sum)

At other times, by *length* we can also mean the Manhattan (l^1) norm,

$$\|(x_1, \dots, x_n)\|_1 = |x_1| + |x_2| + \dots + |x_n| = \sum_{i=1}^n |x_i|,$$

being the sum of absolute values.

```
x / np.sum(np.abs(x))
## array([ 0.06896552,  0.34482759, -0.27586207,  0.13793103,  0.17241379])
```

l_1 normalisation is frequently applied on vectors of nonnegative values, whose normalised versions can be interpreted as *probabilities* or *proportions*: values between 0 and 1 which sum to 1 (or, equivalently, 100%). In particular, on binned data:

```
c, b = np.histogram(heights, [-np.inf, 150, 160, 170, np.inf])
print(c) # counts
## [ 306 1776 1773 366]
```

And now, converting the counts to empirical probabilities:

```
p = c/np.sum(c)
print(p)
## [0.07249467 0.42075338 0.42004264 0.08670931]
```

We did not apply `numpy.abs`, because the values were already nonnegative.

5.3.3 Vector-Vector Case

The arithmetic operators can also be applied on two vectors of equal lengths. In such a case, they will act *elementwisely*: taking each element from the first operand and combining it with the *corresponding* element from the second argument:

```
np.array([2, 3, 4, 5]) * np.array([10, 100, 1000, 10000])
## array([ 20,   300,  4000, 50000])
```

We see that the first element in the left operand (2) was multiplied by the first element in the right operand (10). Then, we computed $3 \cdot 100$ (the second elements), and so forth.

Such a behaviour of the binary operators is inspired by the usual convention in vector algebra where applying $+$ (or $-$) on $\mathbf{x} = (x_1, \dots, x_n)$ and $\mathbf{y} = (y_1, \dots, y_n)$ means exactly:

$$\mathbf{x} + \mathbf{y} = (x_1 + y_1, x_2 + y_2, \dots, x_n + y_n).$$

Using other operators this way (elementwisely) is less standard in mathematics (for instance multiplication might denote the dot product), but in `numpy` it is really convenient.

Example 5.10 Another example:

```
p = np.array([0.1, 0.3, 0.25, 0.15, 0.12, 0.08]) # example vector
-np.sum(p*np.log(p))
## 1.6790818544987114
```

computes the value of the expression $h = -(p_1 \log p_1 + \dots + p_n \log p_n)$, i.e., $h = -\sum_{i=1}^n p_i \log p_i$. Note that it involves the use of a unary vectorised minus (change sign), an aggregation function (sum), a vectorised mathematical function (log), and an elementwise multiplication.

Example 5.11 Let us assume that – for whatever the reason – we would like to plot two mathematical functions, the sine, $f(x) = \sin x$ and a polynomial of degree 7, $g(x) = x - x^3/6 + x^5/120 - x^7/5040$ for x in the interval $[-\pi, 3\pi/2]$.

To do this, we can probe the values off f and g at sufficiently many points using the vectorised operations discussed so far and then use the `matplotlib.pyplot.plot` function to draw what we see in Figure 5.7.

```
x = np.linspace(-np.pi, 1.5*np.pi, 1001) # many points in the said interval
yf = np.sin(x)
yg = x - x**3/6 + x**5/120 - x**7/5040
plt.plot(x, yf, 'r-', label="f(x)") # red solid line
plt.plot(x, yg, 'k:', label="g(x)") # black dotted line
plt.legend()
plt.show()
```

Note that decreasing the number of points in x will reveal that the plotting function merely draws a series of straight line segments.

Exercise 5.12 Based on the `nhanes_adult_female_height_202076` and `nhanes_adult_female_weight_202077` datasets (discussed in the part on histograms), using a single line of code, compute the vector of BMIs of all persons.

⁷⁶ https://github.com/gagolews/teaching_data/blob/master/marek/nhanes_adult_female_height_2020.txt

⁷⁷ https://github.com/gagolews/teaching_data/blob/master/marek/nhanes_adult_female_weight_2020.txt

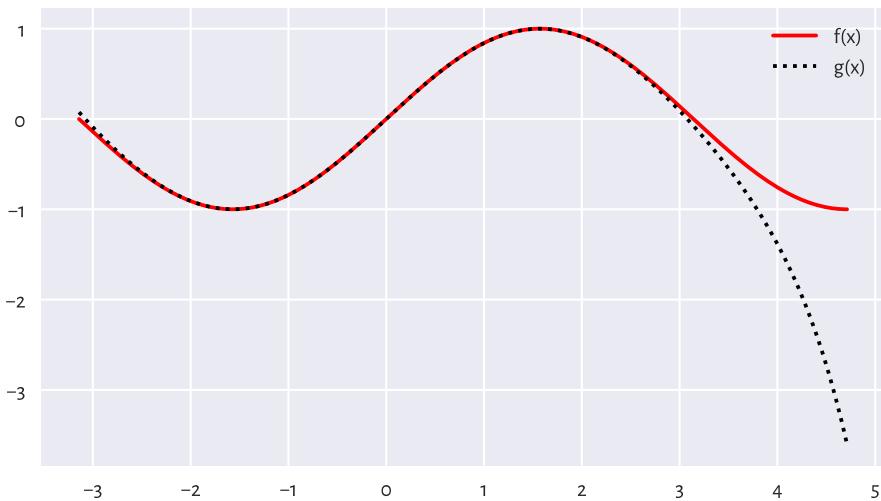


Figure 5.7: With vectorised functions, it is easy to generate plots such as this one

5.4 Vector Indexing

Recall that sequential objects in Python (lists, tuples, strings, ranges) support indexing using scalars and slices:

```
x = [10, 20, 30, 40, 50]
x[1] # scalar index - extract
## 20
x[1:2] # slice index - subset
## [20]
```

numpy vectors additionally support two other indexing schemes: using integer and boolean sequences.

5.4.1 Integer Indexing

Indexing with a single integer *extracts* a particular element:

```
x = np.array([10, 20, 30, 40, 50])
x[0], x[1], x[-1] # first, second, last
## (10, 20, 50)
```

We can also use lists of vector of integer indexes, which return a subvector with elements at the specified indices:

```
x[ [0] ], x[ [0, 1, -1] ], x[ [] ], x[ [0, 1, 0, 0] ]
## (array([10]), array([10, 20, 50]), array([]), array([10, 20, 40, 10]))
```

Note that we added some spaces between the square brackets, because, for example, `x[[0, 1, -1]]` might look slightly more enigmatic (What are these double square brackets? Nah, it is a list inside the index operator).

5.4.2 Logical Indexing

Subsetting using a vector of the same length as the indexed vector is possible too:

```
x[ [True, False, True, True, False] ]
## array([10, 30, 40])
```

Returned the 1st, 3rd, and 4th element (select 1st, don't select 2nd, select 3rd, select 4th, don't select 5th).

This is particularly useful as a *data filtering* technique. Knowing that the relational operators `<`, `<=`, `==`, `!=`, `>=`, and `>` on vectors are also performed elementwisely (just like `+`, `*`, etc.), for instance:

```
x >= 30
## array([False, False, True, True, True])
```

we can write:

```
x[ x >= 30 ]
## array([30, 40, 50])
```

to mean “select those elements in `x` which are not less than 30”.

Of course, the indexed vector and the vector used in comparisons do not have to be the same:

```
y = (x/10) % 2
y # 0 if a number is a multiply of 10 times an even number
## array([1., 0., 1., 0., 1.])
x[ y == 0 ]
## array([20, 40])
```

Important: If we would like to combine many logical vectors, unfortunately we cannot use the **and**, **or**, and **not** operators, because they are not vectorised (this is a limitation of our language per se).

numpy uses the `&`, `|`, and `~` operators, which unfortunately have lower order of precedence than `<`, `<=`, `==`, etc. Therefore, the bracketing of the comparisons is obligatory.

For example:

```
x[ (20 <= x) & (x <= 40) ] # check what happens if we skip the brackets
## array([20, 30, 40])
```

means “elements in x between 20 and 40” (greater than or equal to 20 and less than or equal to 40).

Exercise 5.13 Compute the BMIs only of the persons whose height is between 150 and 170 cm.

5.4.3 Slicing

Just as with ordinary lists, slicing with `:` can be used to fetch the elements at indexes in a given range `from:to` or `from:to:by`.

```
x[::-1], x[3:], x[1:4]
## (array([50, 40, 30, 20, 10]), array([40, 50]), array([20, 30, 40]))
```

Important: (*) For efficiency reasons, slicing returns a view on existing data – it does not make an independent copy of the subsetted elements.

In other words, both x and its sliced version share the same memory. This is important when we apply operations which modify a given vector in place, such as the `sort` method.

```
y = np.array([6, 4, 8, 5, 1, 3, 2, 9, 7])
y[::2].sort()
y
## array([1, 4, 2, 5, 6, 3, 7, 9, 8])
```

This sorted every second element in `y` (i.e., [6, 8, 1, 2, 7] was rearranged so as to obtain [1, 2, 6, 7, 8]).

Indexing with an integer or logical vector always returns a copy.

```
y[ [1, 3, 5, 7] ].sort()
y
## array([1, 4, 2, 5, 6, 3, 7, 9, 8])
```

This *did not* modify the original vector.

5.5 Other Operations

5.5.1 Sorting and Ranking

The `numpy.sort` function returns a sorted copy of the given vector, i.e., determines the order statistics.

```
x = np.array([10, 30, 50, 40, 20, 50])
np.sort(x)
## array([10, 20, 30, 40, 50, 50])
```

Recall that `x.sort()` sorts the vector in-place.

Next, `scipy.stats.rankdata` returns a vector of *ranks*, which is the inverse of `numpy.argsort`.

```
scipy.stats.rankdata(x)
## array([1., 3., 5.5, 4., 2., 5.5])
```

Element 10 is the smallest (“the winner”, say, the quickest racer), hence it has rank 1. Next is element 30, which is the 3rd on the podium, hence its rank is 3.

Exercise 5.14 Consult the manual page of `scipy.stats.rankdata` and test various methods for

dealing with tied elements, e.g., a situation where some values are nonunique (for instance, when two racers finished in exactly the same time).

Note: (*) There are many methods in nonparametric statistics (those that do not make any too particular assumptions about the underlying data distribution) that are based on ranks, e.g., the Spearman correlation coefficient which we cover later.

numpy.argsort returns a sequence of indexes that lead to an ordered version of a given vector (i.e., an ordering permutation).

```
np.argsort(x)
## array([0, 4, 1, 3, 2, 5])
```

Which means that the smallest element is at index 0, then the 2nd smallest is at index 4, 3rd smallest at index 1, etc. Therefore:

```
x[np.argsort(x)]
## array([10, 20, 30, 40, 50, 50])
```

is equivalent to **numpy.sort(x)**.

On a side note, **numpy.random.permutation** rearranges the elements in a given vector.

Note: (**) If there are tied observations in a vector **x**, **numpy.argsort(x, kind="stable")** will use a *stable* sorting algorithm (**timsort**⁷⁸, a variant of mergesort), which guarantees that the ordering permutation is unique: tied elements are placed in order of appearance

Note: (**) Readers with some background in discrete mathematics will be interested in the fact that calling **numpy.argsort** on a vector representing a permutation of elements in fact generates its inverse. In particular, **np.argsort(np.argsort(x, kind="stable"))+1** is equivalent to **scipy.stats.rankdata(x, method="ordinal")**.

5.5.2 Searching for Certain Indexes (Argmin, Argmax)

numpy.argmin and **numpy.argmax** return the index at which we can find the smallest and the largest observation in a given vector.

⁷⁸ <https://github.com/python/cpython/blob/3.7/Objects/listsort.txt>

```
x = np.array([10, 30, 50, 40, 20, 50])
np.argmin(x), np.argmax(x)
## (0, 2)
```

Note that if there are tied observations, the smallest index is returned.

Mathematically, for example, we write

$$i = \arg \min_j x_j$$

(read: i is the index of the smallest element in the sequence; it is the *argument of the minimum*, whenever

$$x_i = \min_j x_j$$

(read: the i -th element is the smallest).

We can use `numpy.flatnonzero` to fetch the indexes where a logical vector has elements equal to `True` (in Section 11.1.3 we note the a value equal to zero is treated as the logical `False`, and as `True` in all other cases). For example:

```
np.flatnonzero(x == np.max(x))
## array([2, 5])
```

This is a version of `numpy.argmax` that lets us decide what we would like to do with the tied maxima.

Exercise 5.15 Let x be a vector with possible ties. Write an expression that returns a randomly chosen index pinpointing one of the sample maximums.

5.5.3 Cumulative Sums and Iterated Differences

Recall that the `+` operator acts elementwisely on two vectors and that the `numpy.sum` function aggregates all values into a single one. We have one more similar function, but vectorised in a slightly different fashion. Namely, `numpy.cumsum` returns the vector of *cumulative sums*:

```
np.cumsum([5, 3, -4, 1, 1, 3])
## array([5, 8, 4, 5, 6, 9])
```

gave, in this order: the first element, the sum of first two elements, the sum of first three elements, ..., the sum of all elements.

Further, *iterative differences* are a somewhat inverse operation:

```
np.diff([5, 8, 4, 5, 6, 9])
## array([ 3, -4,  1,  1,  3])
```

returned the difference between the 2nd and 1st element, then the difference between the 3rd and the 2nd, and so forth. The resulting vector is 1 element shorter than the input one.

We often make use of cumulative sums and iterated differences when processing time series, e.g., stock exchange data (e.g., by how much the price changed since the previous day?; [Section 16.3.1](#)) or cumulative distribution functions ([Section 4.3.8](#)).

5.5.4 Dealing with Round-off and Measurement Errors

Mathematics tells us (the easy proof is left as an exercise to the reader) that a centred version of a given vector \mathbf{x} , $\mathbf{y} = \mathbf{x} - \bar{x}$, has arithmetic mean 0, i.e., $\bar{y} = 0$.

Of course it is also true on a computer. Or is it?

```
heights_centred = (heights - np.mean(heights))
np.mean(heights_centred) == 0
## False
```

Actually, the average is:

```
np.mean(heights_centred)
## 1.3359078775153175e-14
```

which is *almost* zero (0.0000000000000134), but not *exactly* zero (it's a zero for an engineer, not a mathematician). We have seen a similar behaviour when performing standardisation (which involves centring) in [Section 5.3.2](#).

Important: All floating-point operations on a computer (not only in Python) are performed with *finite* precision: they are performed with 15–17 decimal digits precision.

We know it from school – for example, some fractions cannot be represented as decimals, therefore when asked to add or multiply them, we will always apply some rounding that lead to precision loss; e.g., we know that $1/3 + 1/3 + 1/3 = 1$, but using decimal representation with 1 fractional digit, we get $0.3 + 0.3 + 0.3 = 0.9$; with 2 digits we

obtain $0.33 + 0.33 + 0.33 = 0.99$, and so forth. This sum will never be equal exactly to 1 when using a finite precision.

Moreover, errors induced in one operation will propagate onto further ones. Most often they cancel out, but in extreme cases they can lead to undesirable consequences (like for some model matrices in linear regression, see [Section 9.2.9](#)).

There is no reason to panic, though. The rule to remember is:

Important: As the floating-point values are precise up to a few decimal digits, we should refrain from comparing them using the `==` operator, because it tests exact equality.

When a comparison is needed, we should therefore take some error margin into account. Ideally, instead of testing $x == y$, we should either inspect the absolute error

$$|x - y| \leq \varepsilon$$

or, assuming $y \neq 0$, the relative error

$$\frac{|x - y|}{|y|} \leq \varepsilon,$$

where ε is some small error margin.

For instance, `numpy.allclose(x, y)` checks (by default) if for all corresponding elements in both vectors it holds `numpy.abs(x-y) <= 1e-8 + 1e-5*numpy.abs(y)`, which is a combination of both tests.

```
np.allclose(np.mean(heights_centred), 0)
## True
```

Also note that, to avoid sorrow surprises, even testing inequalities like $x \geq 0$ should rather be performed as, say, $x \geq 1e-8$.

Note: Our data is often imprecise by nature. When asked about people's heights, rarely will they give a non-integer answer (assuming they know how tall they are and are not lying about it, but it is a different story) – we get data rounded to 0 decimal digits. Actually, in our dataset the precision is higher:

```
heights[:6] # preview
## array([160.2, 152.7, 161.2, 157.4, 154.6, 144.7])
```

But still, there is an inherent *observational error*. Therefore, even if, for example, the mean thereof was computed exactly, the fact that the inputs themselves are not necessarily ideal makes the estimate *approximate* as well. We can only hope that these errors will more or less cancel out in the computations.

Exercise 5.16 Compute the BMIs of all females in the NHANES study. Determine their arithmetic mean. Compare it to the arithmetic mean computed for BMIs rounded to 1, 2, 3, 4, etc., decimal digits.

Note: (*) Another problem is related to the fact that floats on a computer use the binary base, not the decimal one. Therefore some fractional numbers that we *believe* to be representable exactly actually require an infinite number of bits therefore are subject to rounding.

```
0.1 + 0.1 + 0.1 == 0.3 # obviously
## False
```

This is because 0.1 , $0.1+0.1+0.1$, and 0.3 is actually represented as, respectively:

```
print(f"\{0.1:.20f\}, \{0.1+0.1+0.1:.20f\}, and \{0.3:.20f\}.")
## 0.1000000000000000555, 0.30000000000000004441, and 0.
˓→29999999999999890.
```

A good introductory reference to the topic of numerical inaccuracies is [[Gol91]], see also [[Higo2], [Knu97]] for a more comprehensive treatment of numerical analysis.

5.5.5 Vectorising Scalar Operations with List Comprehensions (*)

List comprehensions of the form `[expression for name in iterable]` are part of base Python. They allow us to create lists based on transformed versions of individual elements in a given iterable object. Hence, they might work in cases where a task at hand cannot be solved by means of vectorised `numpy` functions.

For example, here is a way to generate squares of 10 first natural numbers:

```
[ i**2 for i in range(1, 11) ]
## [1, 4, 9, 16, 25, 36, 49, 64, 81, 100]
```

The result can be passed to `numpy.array` to convert it to a vector.

And if we wish to filter our all elements that are not greater than 0, we can write:

```
np.random.seed(123) # make pseudorandom number generation reproducible
x = np.round(np.random.rand(10)*2-1, 2)
[ e for e in x if e > 0 ]
## [0.39, 0.1, 0.44, 0.96, 0.37]
```

Further, we can use the ternary operator of the form `x_true if cond else x_false` to return either `x_true` or `x_false` depending on the truth value of `cond`.

```
e = -2
e**0.5 if e >= 0 else (-e)**0.5
## 1.4142135623730951
```

Combined with a list comprehension, we can write, for instance:

```
[ round(e**0.5 if e >= 0 else (-e)**0.5, 2) for e in x ]
## [0.62, 0.66, 0.74, 0.32, 0.66, 0.39, 0.98, 0.61, 0.2, 0.47]
```

Exercise 5.17 Write equivalent versions of the above expressions using vectorised `numpy` functions.

Exercise 5.18 Write equivalent versions of the above expressions using base Python lists, the `for` loop and the `list.append` method (start from an empty list which will store the result).

Note: There is also a tool which vectorises a scalar function so that it can be used on `numpy` vectors:

```
def clip1(x):
    if x < 0:    return 0
    elif x > 1:  return 1
    else:        return x

clip = np.vectorize(clip1) # returns a function object
clip([0.3, -1.2, 0.7, 4, 9])
## array([0.3, 0. , 0.7, 1. , 1. ])
```

5.6 Exercises

Exercise 5.19 How can we interpret the different values of the arithmetic mean, median, standard deviation, interquartile range, and skewness?

Exercise 5.20 There is something scientific and magical about numbers that makes us approach them with some kind of respect. However, taking into account that there are many possible data aggregates, there is a risk that a party may be cherry-picking – reporting the one that portrays the analysed entity in a good or bad light. For instance, reporting the mean instead of the median or vice versa. Is there anything that can be done about it?

Exercise 5.21 Although – mathematically speaking – all measures can be computed on all data, it does not mean that it always makes sense. For instance, some distributions will yield skewness of 0, but we should not automatically assume that they are nicely symmetric and bell-shaped (e.g., this can be a bimodal distribution). It is thus best to always visualise your data. Give some examples of datasets and measures where we should be critical about the obtained results.

Exercise 5.22 Give some examples, where simple data preprocessing can drastically change the values of chosen sample aggregates.

Exercise 5.23 (**) Reflect on the famous⁷⁹ saying not everything that can be counted counts, and not everything that counts can be counted.

Exercise 5.24 (**) Being a data scientist can be a frustrating job, especially when you care for some causes. Reflect on: some things that count can be counted, but we will not count them, because there's no budget for it.

Exercise 5.25 (**) Being a data scientist can be a frustrating job, especially when you care for the truth. Reflect on: some things that count can be counted, but we will not count them, because some people might be offended.

Exercise 5.26 (**) Assume you were to establish your own nation on some island and become the benevolent dictator thereof. How would you measure if your people are happy or not? Let's say that you need to come up with 3 qualitative measures (key performance indicators). What would happen if your policy making were solely focused on optimising those KPIs? How about the same problem but with regards to your company and employees?

Exercise 5.27 Give the mathematical definitions, use cases, and interpretations of standardisation, normalisation, and min-max scaling.

Exercise 5.28 How are `numpy.log` and `numpy.exp` related to each other? How about `numpy.log`

⁷⁹ <https://quoteinvestigator.com/2010/05/26/everything-counts-einstein/>

vs `numpy.log10`, `numpy.cumsum` vs `numpy.diff`, `numpy.min` vs `numpy.argmax`, `numpy.sort` vs `numpy.argsort`, and `scipy.stats.rankdata` vs `numpy.argsort`?

Exercise 5.29 What is the difference between `numpy.trunc`, `numpy.floor`, `numpy.ceil`, and `numpy.round`?

Exercise 5.30 What happens when we apply `+` on two vectors of different lengths?

Exercise 5.31 List the four ways to index a vector.

Exercise 5.32 What is wrong with the expression `x[x >= 0 and x <= 1]`, where `x` is a numeric vector? How about `x[x >= 0 & x <= 1]`?

Exercise 5.33 (*) What does it mean that slicing returns a view on existing data?

6

Continuous Probability Distributions

Each successful data analyst will deal with hundreds or thousands of datasets in their lifetime. In the long run, at some level, most of them will be deemed *boring*. This is because a few common patterns will be occurring over and over again.

In particular, the previously mentioned bell-shapedness and right-skewness is quite prevalent in nature. But, surprisingly, this is exactly when things become scientific and interesting – allowing us to study various phenomena at an appropriate level of generality.

Mathematically, such idealised patterns in the histogram shapes can be formalised using the notion of a *probability distribution of a continuous, real-valued random variable*, and more precisely in this case, a *probability density function* of the corresponding random variable.

Intuitively⁸⁴, a *probability density function* is a nicely smooth curve that would arise if we drew a histogram for the whole *population* (e.g., all women living currently on Earth and beyond or otherwise an extremely large data sample obtained by independently querying the same underlying data generating process) in such a way that the total area of all the bars are equal to 1 and the bin sizes being very small.

As stated at the beginning, we do not intend this to be a course in probability theory and mathematical statistics, but a one that precedes and motivates them (e.g., [[Bil95], [DKLMos5], [Gen09], [Gen20]]), therefore our definitions are out of necessity simplified so that they are digestible. Hence, for the purpose of our illustrations, let us consider the following characterisation.

Important: (*) We call an integrable function $f : \mathbb{R} \rightarrow \mathbb{R}$ a *probability density function* (PDF) iff $f(x) \geq 0$ for all x and $\int_{-\infty}^{\infty} f(x) dx = 1$, i.e., it is nonnegative and normalised in such a way that the total area under the whole curve is 1.

⁸⁴ This intuition is of course theoretically grounded and is based on the asymptotic behaviour of the histograms as the estimators of the underlying probability density function, see, e.g., [[FD81]] and the many references therein.

For any $a < b$, we treat the area under the fragment of the $f(x)$ curve for x between a and b , i.e., $\int_a^b f(x) dx$, as the probability of the underlying real-valued random variable (theoretical data generating process) falling into the $[a, b]$ interval.

Some distributions appear more frequently than others and fit empirical data or parts thereof particularly well (or there is some established wishful thinking/delusion that they serve as their good-enough approximations; compare [[FEHP10]]). Let us thus review a few noteworthy probability distributions: the normal, log-normal, Pareto, and uniform families (in the course of this course we will also mention the chi-squared, Kolmogorov, and exponential ones).

6.1 Normal Distribution

A *normal distribution* is the one that has a prototypical, nicely symmetric, bell-shaped density. It is described by two parameters: $\mu \in \mathbb{R}$ (the expected value, at which the density is centred) and $\sigma > 0$ (the standard deviation, saying how much the distribution is dispersed around μ).

The probability density function of $N(\mu, \sigma)$ is given by:

$$f(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right).$$

6.1.1 Estimating Parameters

A course in statistics (which, again, this one is not, we are merely making an illustration here), may tell us that the sample arithmetic mean and standard deviation are natural, statistically well-behaving *estimators* of the said parameters: if all samples would really be drawn independently from $N(\mu, \sigma)$ each, the we *expect* the mean and standard deviation be equal to, more or less, μ and σ (the larger the sample size, the smaller the error).

Recall the `heights` (females from the NHANES study) dataset and its bell-shaped histogram in Figure 4.2.

```
heights = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_adult_female_height_2020.txt")
n = len(heights)
```

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```
n
## 4221
```

Let's estimate the said parameters for this sample:

```
mu = np.mean(heights)
sigma = np.std(heights, ddof=1)
mu, sigma
## (160.13679222932953, 7.062858532891359)
```

Mathematically, we will denote these two with $\hat{\mu}$ and $\hat{\sigma}$ (mu and sigma with a hat) to emphasise that they are merely guesstimates of the unknown respective parameters μ and σ . On a side note, we use `ddof=1` in the latter case, because this estimator has slightly better statistical properties.

Let's draw the fitted density function, i.e., the PDF of $N(160.1, 7.06)$, on top of the histogram, see [Figure 6.1](#). We pass `stat="density"` to `seaborn.histplot` so that the histogram bars are normalised (i.e., the total area of these rectangles sums to 1).

```
sns.histplot(heights, stat="density", color="lightgray")
x = np.linspace(np.min(heights), np.max(heights), 1000)
plt.plot(x, scipy.stats.norm.pdf(x, mu, sigma), "r--",
          label=f"PDF of N({mu:.1f}, {sigma:.2f})")
plt.legend()
plt.show()
```

At a first glance, this is a very nice match. Before proceeding with some ways of assessing the goodness of fit slightly more rigorously, let us praise the potential benefits of having an idealised *model* of our dataset at our disposal.

Important: (*) It might be the case that we will have to obtain the estimates of the probability distribution's parameters by numerical optimisation, for example, by minimising

$$\mathcal{L}(\mu, \sigma) = \sum_{i=1}^n \left(\frac{(x_i - \mu)^2}{\sigma^2} + \log \sigma^2 \right)$$

with respect to μ and σ (corresponding to the objective function in maximum likelihood estimation problem for the normal distribution family). In our case, however, we are lucky; there exist open-form formulae expressing the solution to the above in the form

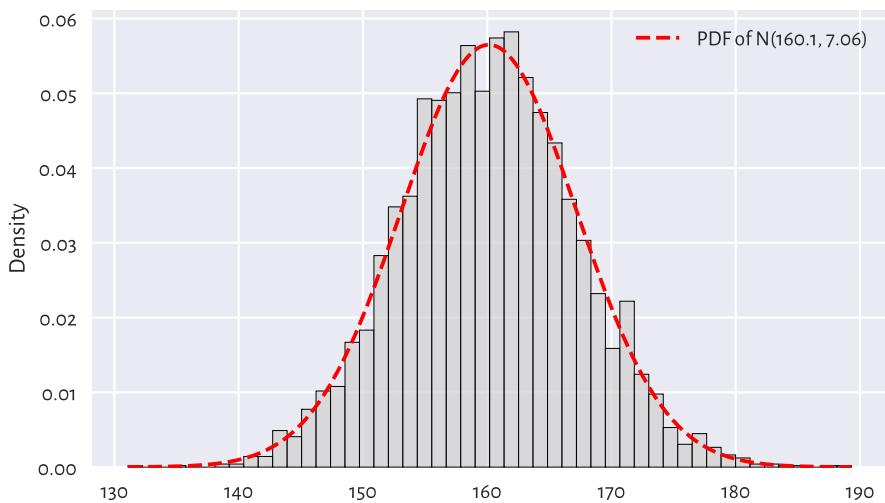


Figure 6.1: A histogram and the probability density function of the fitted normal distribution for the `heights` dataset

of the aforementioned sample mean and standard deviation. For other distributions things can get a little trickier, though.

Sometimes, we will have many options for point estimators to choose from, which might be more suitable if data aren't of top quality (e.g., contain outliers). For instance, in the normal model, it can be shown that we can also estimate μ and σ via the sample median and $IQR/1.349$.

6.1.2 Data Models Are Useful

If (provided that, assuming that, on condition that) our sample is a realisation of independent random variables following a given distribution, or a data analyst judges that such an approximation might be justified, then we have a set of many numbers *reduced* to merely few parameters.

In the above case, we might want to risk the statement that data follow the normal distribution (assumption 1) with parameters $\mu = 160.1$ and $\sigma = 7.06$ (assumption 2). Note that the choice of the distribution family is one thing, and the way we estimate the underlying parameters (in our case, we use $\hat{\mu}$ and $\hat{\sigma}$) is another.

This not only saves storage space and computational time, but also – based on what we can learn from a course in probability and statistics (by appropriately integrating the density function) – we can imply facts such as for normally distributed data:

- ca. 95% of (i.e., *most*) women are $\mu \pm 2\sigma$ tall (the 2σ rule),
- ca. 99.7% of (i.e., *almost all*) women are $\mu \pm 3\sigma$ tall (the 3σ rule).

Also, if we knew that the distribution of heights of men is also normal with some other parameters, we could be able to make some comparisons between the two samples. For example, what is the probability that a woman randomly selected from the crowd is taller than a male passerby.

Furthermore, there is a range of *parametric* (assuming some distribution family) of statistical methods that cannot be used if we don't assume the data normality, e.g., the *t*-test to compare the expected values. So many options.

Exercise 6.1 How different manufacturing industries can make use of such knowledge? Are simplifications necessary when dealing with complexity? What are the alternatives?

6.2 Assessing Goodness of Fit

6.2.1 Comparing Cumulative Distribution Functions

A better way of assessing the extent to which a sample deviates from a hypothesised distribution, is by comparing the theoretical *cumulative distribution function* (CDF) and the empirical one (\hat{F}_n , see [Section 4.3.8](#)).

Important: If f is a density function, then the corresponding theoretical CDF is defined as $F(x) = \int_{-\infty}^x f(t) dt$, i.e., the probability of the underlying random variable's taking a value not greater than x .

By definition⁸⁵, each CDF takes values in the unit interval ($[0, 1]$) and is nondecreasing.

For the normal distribution family, the values of the theoretical CDF can be computed by calling `scipy.stats.norm.cdf`; see [Figure 6.2](#).

⁸⁵ Actually, the probability distribution of any real-valued random variable X can be uniquely defined by means of a nondecreasing, right (upward) continuous function $F : \mathbb{R} \rightarrow [0, 1]$ such that $\lim_{x \rightarrow -\infty} F(x) = 0$ and $\lim_{x \rightarrow \infty} F(x) = 1$, in which case $\Pr(X \leq x) = F(x)$. The probability density function only exists for continuous random variables and is defined as the derivative of F .

```

x = np.linspace(np.min(heights), np.max(heights), 1001)
probs = scipy.stats.norm.cdf(x, mu, sigma) # sample the CDF at many points
plt.plot(x, probs, "r--", label="CDF of N({mu:.1f}, {sigma:.2f})")
heights_sorted = np.sort(heights)
plt.plot(heights_sorted, np.arange(1, n+1)/n,
         drawstyle="steps-post", label="Empirical CDF")
plt.xlabel("$x$")
plt.ylabel("Prob(height $\leq x$)")
plt.legend()
plt.show()

```

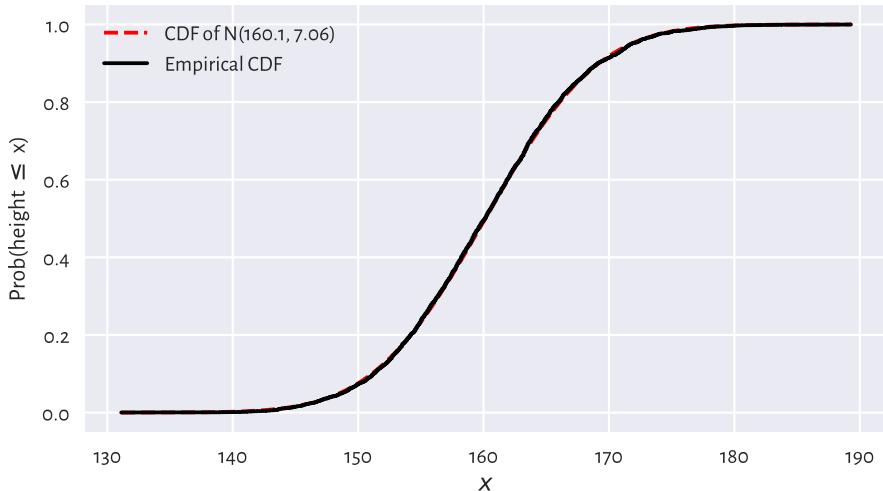


Figure 6.2: The empirical CDF and the fitted normal CDF for the `heights` dataset

This looks like a superb match.

Important: $F(b) - F(a) = \int_a^b f(t) dt$ is the probability of generating a value in the interval $[a, b]$.

Let us empirically verify the aforementioned 3σ rule:

`F = lambda x: scipy.stats.norm.cdf(x, mu, sigma)`

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```
F(mu+3*sigma) - F(mu-3*sigma)
## 0.9973002039367398
```

Indeed, almost all observations are within $[\mu - 3\sigma, \mu + 3\sigma]$, if data are normally distributed.

Note: A common way to summarise the discrepancy between the empirical and a given theoretical CDF is by computing the greatest absolute deviation between these two functions

$$\hat{D}_n = \sup_{t \in \mathbb{R}} |\hat{F}_n(t) - F(t)|.$$

Note that the supremum is a continuous version of the maximum.

It holds:

$$\hat{D}_n = \max_{k=1,\dots,n} \left\{ \max \left\{ \left| \frac{k-1}{n} - F(x_{(k)}) \right| \right\}, \max \left\{ \left| \frac{k}{n} - F(x_{(k)}) \right| \right\} \right\},$$

i.e., F needs to be probed only at the n points from the sorted input sample.

```
def compute_Dn(x, F): # equivalent to scipy.stats.kstest(x, F)[0]
    Fx = F(np.sort(x))
    n = len(x)
    k = np.arange(1, n+1) # 1, 2, ..., n
    Dn1 = np.max(np.abs((k-1)/n - Fx))
    Dn2 = np.max(np.abs(k/n - Fx))
    return max(Dn1, Dn2)

Dn = compute_Dn(heights, F)
Dn
## 0.010470976524201148
```

If the difference is *sufficiently small* (the larger the sample size, the less tolerant we should be with regards to the size of this disparity), then we can assume that a normal model describes data quite well. This is indeed the case here: we may estimate the probability of someone being as tall as any given height with error less than about 1%.

6.2.2 Comparing Quantiles

A Q-Q (quantile-quantile) plot is another graphical method for comparing two distributions. This time, instead of working with a cumulative distribution function F , we will be dealing with their (generalised) inverses, i.e., quantile functions.

Given a CDF F , the corresponding *quantile function* is defined for any $p \in (0, 1)$ as

$$Q(p) = \inf\{x : F(x) \geq p\},$$

i.e., the smallest x such that the probability of drawing a value not greater than x is at least p .

Important: If a CDF F is continuous, and this is the assumption in the current chapter, then Q is exactly its inverse, i.e., it holds $Q(p) = F^{-1}(p)$ for all $p \in (0, 1)$.

The theoretical quantiles can be generated by the `scipy.stats.norm.ppf` function. Here, `ppf` stands for the percent point function which is another (yet quite esoteric) name for the above Q .

For instance, given our $N(160.1, 7.06)$ -distributed NHANES dataset, $Q(0.9)$ is the height not exceeded by 90% of female population. In other words, only 10% of American women are taller than:

```
scipy.stats.norm.ppf(0.9, mu, sigma)
## 169.18820963937648
```

The sample quantiles that we have introduced in Section 5.1.1 are natural estimators of the theoretical quantile function. However, we have also mentioned that there are quite a few possible definitions thereof in the literature, compare [[HF96]].

A Q-Q plot draws a version of sample quantiles as a function of the corresponding theoretical quantiles. For simplicity, instead of using the `numpy.quantile` function, we will assume that the $\frac{i}{n+1}$ -quantile is equal to $x_{(i)}$, i.e., the i -th smallest value in a given sample (x_1, x_2, \dots, x_n) and consider only $i = 1, 2, \dots, n$.

Our simplified setting successfully avoids the problem which arises when the 0- or 1-quantile of the theoretical distribution, i.e., $Q(0)$ and $Q(1)$ is infinite (and this is the case for the normal distribution family).

```
n = len(heights)
q = np.arange(1, n+1)/(n+1) # 1/(n+1), 2/(n+2), ..., n/(n+1)
```

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```

heights_sorted = np.sort(heights)           # theoretical quantiles
quantiles = scipy.stats.norm.ppf(q, mu, sigma) # sample quantiles
plt.plot(quantiles, heights_sorted, "o")
plt.axline((heights_sorted[n//2], heights_sorted[n//2]), slope=1,
            linestyle=":", color="gray") # identity line
plt.xlabel(f"Quantiles of N({mu:.1f}, {sigma:.2f})")
plt.ylabel("Sample quantiles")
plt.show()

```

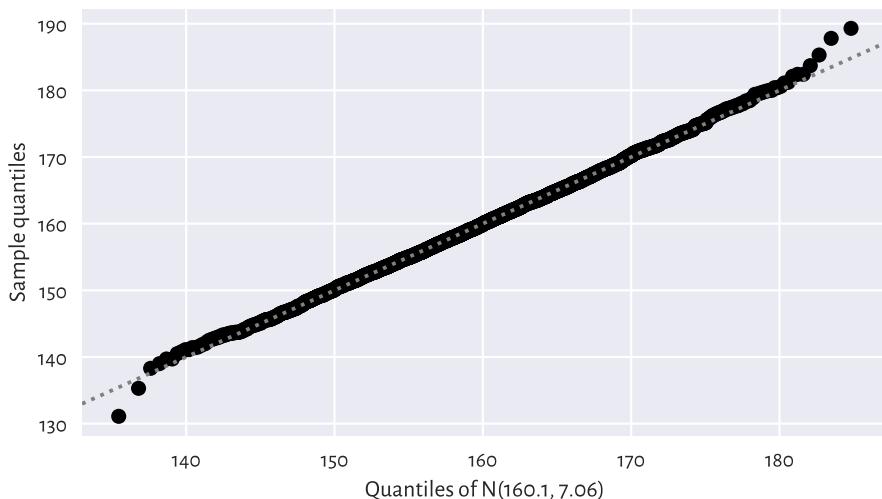


Figure 6.3: Q-Q plot for the heights dataset

Figure 6.3 depicts the Q-Q plot for our example dataset.

Ideally, the points should be arranged on the $y = x$ line (which was added for readability). This happens if the sample quantiles match the theoretical ones perfectly.

In our case, there are small discrepancies in the tails (e.g., the smallest observation was slightly smaller than expected, and the largest one was larger than expected), although it is quite *normal* a behaviour for small samples and certain distribution families

Overall, we can say that this is a very good fit.

6.2.3 Kolmogorov–Smirnov Test (*)

To be scientific, we should yearn for some more formal method that will enable us to test the null hypothesis stating that a given empirical distribution \hat{F}_n does not differ significantly from the theoretical one, F , against a two-sided alternative:

$$\begin{cases} H_0 : \hat{F}_n = F & \text{(null hypothesis)} \\ H_1 : \hat{F}_n \neq F & \text{(two-sided alternative)} \end{cases}$$

The popular goodness-of-fit test by Kolmogorov (and Smirnov) can give us a conservative interval of the acceptable values of \hat{D}_n as a function of n (within the framework of frequentist hypothesis testing).

Namely, if the *test statistic* \hat{D}_n is smaller than some *critical value* K_n , then we shall deem the difference insignificant. This is to take into account the fact that the reality might slightly deviate from the ideal; in [Section 6.4.4](#) we will note that even for samples which truly come from a hypothesised distribution, there is some inherent variability. We thus need to be somewhat tolerant.

Under the assumption that \hat{F}_n is the ECDF of a sample of n independent variables *really* generated from F , the random variable $\hat{D}_n = \sup_{t \in \mathbb{R}} |\hat{F}_n(t) - F(t)|$ follows the Kolmogorov distribution with parameter n (available via `scipy.stats.kstwo`).

In other words, if we generate many samples of length n from F , and compute \hat{D}_n s (again: the largest deviation between the empirical and theoretical CDF) for each of them, we expect it to be distributed like in [Figure 6.4](#).

```
p = np.linspace(0, 1, 1001)
_ns = [10, 100, n]
plt.subplot(121)
for _n in _ns: plt.plot(p, scipy.stats.kstwo.pdf(p, _n), label=f"$n={_n}$")
plt.legend()
plt.subplot(122)
for _n in _ns: plt.plot(p, scipy.stats.kstwo.cdf(p, _n))
plt.show()
```

The choice K_n involves a trade-off between our desire to reject the null hypothesis when it is true (data really come from F) and to reject it when it is false (data follow some other distribution, i.e., the difference is significant enough). These two needs are, unfortunately, mutually exclusive.

In practice, we assume some fixed upper bound (*significance level*) for making the former kind of mistake, the so-called *type-I error*. A nicely conservative (in a good way⁸⁶) value

⁸⁶ More details on that in [Section 12.2.6](#).

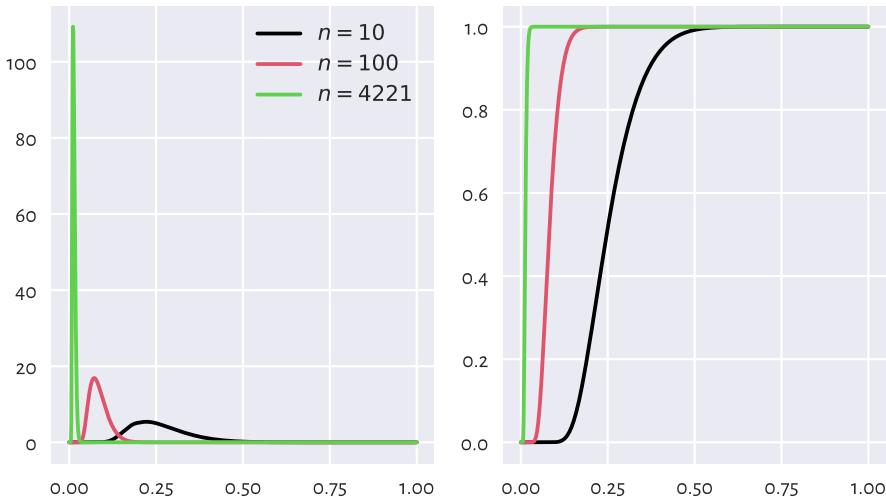


Figure 6.4: Density (left) and cumulative distribution function (right) of some Kolmogorov distributions; the greater the sample size, the smaller the acceptable deviations between the theoretical and empirical CDFs

that we suggest to employ is $\alpha = 0.001 = 0.1\%$, i.e., only 1 out of 1000 samples that really come from F will be rejected as not coming from F .

Such a K_n may be determined by considering the inverse of the CDF of the Kolmogorov distribution, Ξ_n . Namely, $K_n = \Xi_n^{-1}(1 - \alpha)$:

```
alpha = 0.001 # significance level
scipy.stats.kstwo.ppf(1-alpha, n)
## 0.029964456376393188
```

In our case $\hat{D}_n < K_n$, because $0.01047 < 0.02996$. Thus, we conclude that our empirical (heights) distribution does not differ significantly (at significance level 0.1%) from the assumed one ($N(\mu, \sigma)$). In other words, we do not have enough evidence against the statement that data are normally distributed (presumption of innocence).

We will go back to this discussion in [Section 6.4.4](#) and [Section 12.2.6](#).

6.3 Other Noteworthy Distributions

6.3.1 Log-normal Distribution

We say that a sample is *log-normally distributed*, if its logarithm is normally distributed.

In particular, it is sometimes observed that the income of most individuals (except the richest) is distributed, at least approximately, log-normally. Let us investigate whether this is the case for the UK taxpayers.

```
income = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/uk_income_simulated_2020.txt")
```

The plotting of the histogram for the logarithm of income is left as an exercise (we can pass `log_scale=True` to `seaborn.histplot`; we'll plot it soon anyway in a different way). We proceed directly with the fitting of a log-normal model, $\text{LN}(\mu, \sigma)$. The fitting process is similar to the normal case, but this time we determine the mean and standard deviation based on the logarithms of data, which we can compute using a vectorised mathematical function discussed in [Section 5.2](#).

```
lmu = np.mean(np.log(income))
lsigma = np.std(np.log(income), ddof=1)
lmu, lsigma
## (10.314409794364623, 0.5816585197803816)
```

[Figure 6.5](#) depicts the fitted probability density function together with the histograms on the log- and original scale. When creating this plot, there are two pitfalls, though. Firstly, `scipy.stats.lognorm` parametrises the distribution via the parameter s equal to σ and scale equal to e^μ , hence computing the PDF at different points must be done as follows:

```
x = np.linspace(np.min(income), np.max(income), 101)
fx = scipy.stats.lognorm.pdf(x, s=lsigma, scale=np.exp(lmu))
```

Second, passing both `log_scale=True` and `stat="density"` to `seaborn.histplot` does not normalise the values on the y-axis correctly. In order to make the histogram on the log-scale comparable with the true density, we need to turn the log-scale manually and pass manually generated bins that are equidistant on the logarithmic scale (via `numpy.geomspace`).

```
b = np.geomspace(np.min(income), np.max(income), 30)
```

And now:

```
plt.subplot(121)
sns.histplot(income, stat="density", bins=b, color="lightgray") # own bins!
plt.xscale("log")
plt.plot(x, fx, "r--")
print(plt.xlim())
plt.subplot(122)
sns.histplot(income, stat="density", color="lightgray")
plt.plot(x, fx, "r--", label=f"PDF of LN({lmu:.1f}, {lsigma:.2f})")
plt.legend()
plt.show()
```

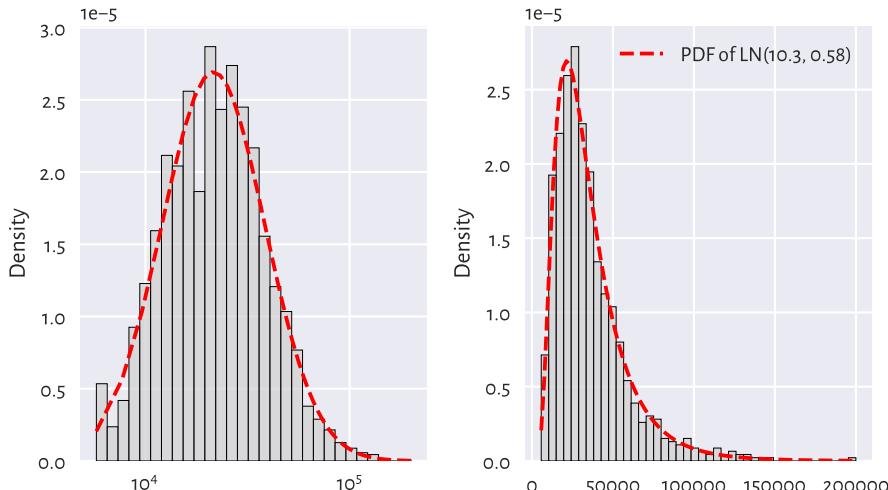


Figure 6.5: A histogram and the probability density function of the fitted log-normal distribution for the `income` dataset, on log- (left) and original (right) scale

Overall, this fit is not too bad. Note that we deal with only a sample of 1000 households

here; the original UK Office of National Statistics data⁸¹ could tell us more about the quality of this model in general, but it's beyond the scope of our simple exercise.

Exercise 6.2 Graphically compare the empirical CDF for `income` and the theoretical CDF of $LN(10.3, 0.58)$.

Furthermore, Figure 6.6 gives the quantile-quantile plot on a double-logarithmic scale for the above log-normal model. Additionally, we (empirically) verify the hypothesis of normality (using a “normal” normal distribution, not its “log” version).

```
n = len(income)
q = np.arange(1, n+1)/(n+1)
income_sorted = np.sort(income)

plt.subplot(121)
quantiles = scipy.stats.lognorm.ppf(q, s=lsigma, scale=np.exp(lmu))
plt.plot(quantiles, income_sorted, "o")
plt.axline((income_sorted[n//2], income_sorted[n//2]), slope=1,
           linestyle=":", color="gray")
plt.xlabel(f"Quantiles of LN({lmu:.1f}, {lsigma:.2f})")
plt.ylabel("Sample quantiles")
plt.xscale("log")
plt.yscale("log")

plt.subplot(122)
mu = np.mean(income)
sigma = np.std(income, ddof=1)
quantiles2 = scipy.stats.norm.ppf(q, mu, sigma)
plt.plot(quantiles2, income_sorted, "o")
plt.axline((income_sorted[n//2], income_sorted[n//2]), slope=1,
           linestyle=":", color="gray")
plt.xlabel(f"Quantiles of N({mu:.1f}, {sigma:.2f})")

plt.show()
```

We see that definitely the hypothesis that our data follow a normal distribution (the right subplot) is most likely false.

Exercise 6.3 (*) Perform the Kolmogorov-Smirnov goodness-of-fit test as in Section 6.2.3 to verify that the hypothesis of log-normality is not rejected at the $\alpha = 0.001$ significance level. At the same time, the income distribution significantly differs from a normal one.

⁸¹ <https://www.ons.gov.uk/peoplepopulationandcommunity/personalandhouseholdfinances/incomeandwealth/bulletins/householddisposableincomeandinequality/financialyear2020>

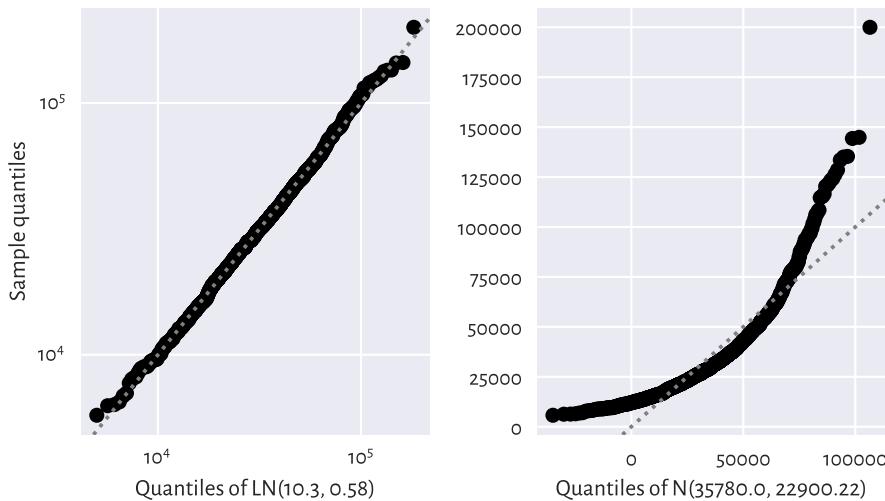


Figure 6.6: Q-Q plots for the `income` dataset vs a fitted log-normal (good fit; left) and normal (bad fit; right) distribution

The log-normal model (the left subplot), on the other hand, might be quite usable. It again reduced the whole dataset to merely two numbers, μ and σ , based on which (and probability theory), we may deduce that:

- the expected average (mean) income is $e^{\mu+\sigma^2/2}$,
- median is e^μ ,
- most probable one (mode) in $e^{\mu-\sigma^2}$,

etc.

Note: Recall again that for skewed distributions such as this one, reporting the mean might be misleading. This is why *most* people get angry when they read the news about the prospering economy – “yeah, I’d like to see that kind of money in my pocket”. Hence, it’s not only μ that matters, it’s also σ which quantifies the discrepancy between the rich and the poor (too much inequality is bad, but also too much uniformity is to be avoided).

Note that for a normal distribution the situation is very different, because, the mean,

median, and most probable outcomes tend to be the same – the distribution is symmetric around μ .

Exercise 6.4 (*) What is the fraction of people with earnings below the mean in our $\text{LN}(10.3, 0.58)$ model?

6.3.2 Pareto Distribution

Consider again the dataset⁸² on the populations of the US cities in the 2000 US Census:

```
cities = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/other/us_cities_2000.txt")
len(cities), sum(cities) # number of cities, total population
## (19447, 175062893.0)
```

Figure 6.7 gives the histogram of the city sizes with the populations on the log-scale. It kind-of looks like a log-normal distribution again, which the reader can inspect themselves when they are feeling playful.

```
sns.histplot(cities, bins=20, log_scale=True, color="lightgray")
plt.show()
```

We, however, this time will be interested in not what's *typical*, but what's in some sense *anomalous* or *extreme*. Let's take a look at the *truncated* version of the city size distribution by considering the cities with 10,000 or more inhabitants – i.e., we will only study the right tail the original data:

```
s = 10_000
large_cities = cities[cities >= s]
len(large_cities), sum(large_cities) # number of cities, total population
## (2696, 146199374.0)
```

Plotting the above on a double-logarithmic scale can be performed by passing `log_scale=(True, True)` to `seaborn.histplot`, which is left as an exercise. Anyway, doing so will lead to a similar picture as in Figure 6.8. This reveals something very interesting: the bar tops on the double-log-scale are arranged more or less on a straight line. There are many datasets which exhibit this behaviour; we say that they follow a *power law* (power in the arithmetic sense, not social one), see [[CSN09], [New05]] for discussion.

Let's introduce the *Pareto distribution* family which has a prototypical power law-like density. It is identified by two parameters:

⁸² <https://arxiv.org/abs/0706.1062v2>

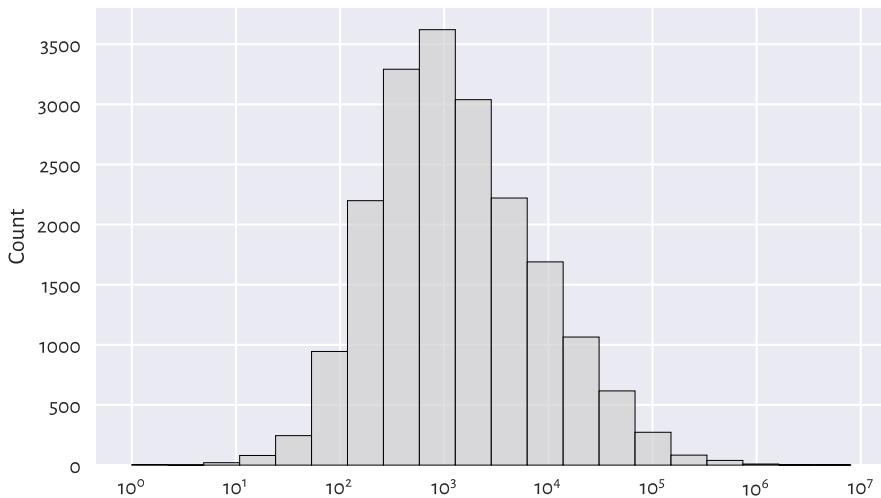


Figure 6.7: Histogram for the unabridged `cities` dataset

- the (what `scipy` calls it) scale parameter $s > 0$ is equal to the shift from 0 ,
- the shape parameter, $\alpha > 0$, controls the slope of the said line on the double-log-scale.

The probability density function of $P(\alpha, s)$ is given by:

$$f(x) = \frac{\alpha s^\alpha}{x^{\alpha+1}}$$

for $x \geq s$ and $f(x) = 0$ otherwise.

s is usually taken as the sample minimum (i.e., 10000 in our case). α can be estimated through the reciprocal of the mean of the scaled logarithms of our observations:

```
alpha = 1/np.mean(np.log(large_cities/s))
alpha
## 0.9496171695997675
```

Unfortunately, we have already noted that comparing the theoretical densities and an empirical histogram on a log-scale is quite problematic with `seaborn`, therefore we again must apply logarithmic binning manually in order to come up with what we see in Figure 6.8.

```
b = np.geomspace(s, np.max(large_cities), 21) # bins' boundaries
sns.histplot(large_cities, bins=b, stat="density", color="lightgray")
plt.plot(b, scipy.stats.pareto.pdf(b, alpha, scale=s), "r--",
         label=f"PDF of P({alpha:.3f}, {s})")
plt.xscale("log")
plt.yscale("log")
plt.legend()
plt.show()
```

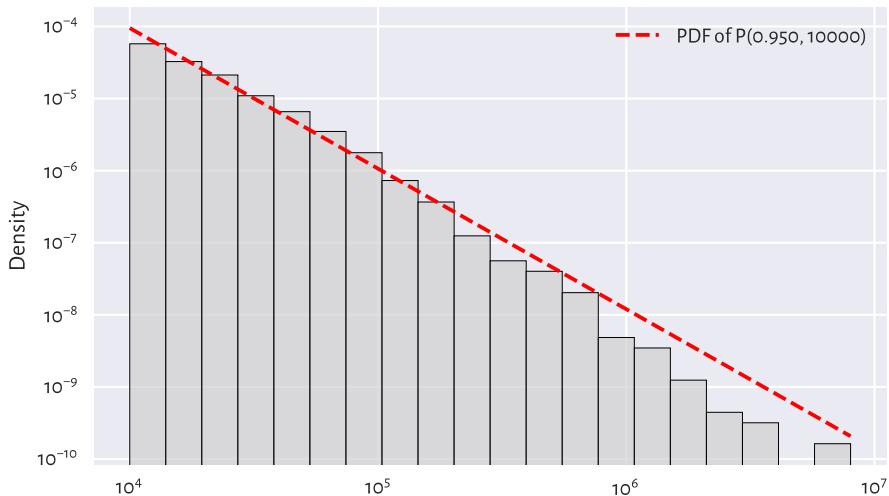


Figure 6.8: Histogram for the `large_cities` dataset and the fitted density on a double log-scale

Figure 6.9 gives the corresponding Q-Q plot on a double-logarithmic scale.

```
n = len(large_cities)
q = np.arange(1, n+1)/(n+1)
cities_sorted = np.sort(large_cities)
quantiles = scipy.stats.pareto.ppf(q, alpha, scale=s)
plt.plot(quantiles, cities_sorted, "o")
plt.axline((quantiles[n//2], cities_sorted[n//2]), slope=1,
            linestyle=":", color="gray")
plt.xlabel(f"Quantiles of P({alpha:.3f}, {s})")
```

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```
plt.ylabel("Sample quantiles")
plt.xscale("log")
plt.yscale("log")
plt.show()
```

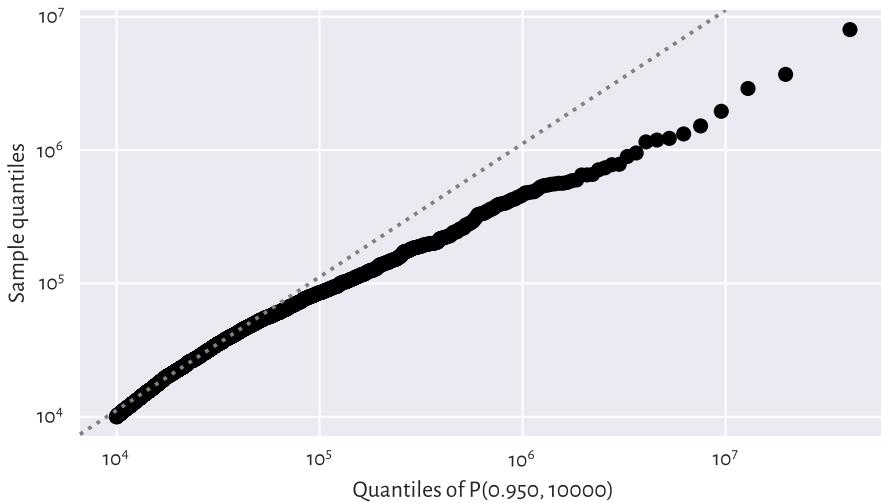


Figure 6.9: Q-Q plot for the `large_cites` dataset vs the fitted Paretian model

We see that the populations of the largest cities are overestimated. The model could be better, but the cities are still growing, right?

Example 6.5 (*) It might also be interesting to see how well can we predict the probability of a randomly selected city being at least a given size. Let us thus denote with $S(x) = 1 - F(x)$ the complementary cumulative distribution function (CCDF; sometimes referred to as the survival function) and with $\hat{S}_n(x) = 1 - \hat{F}_n(x)$ its empirical version. Figure 6.10 compares the empirical and the fitted CCDFs with probabilities on the linear- and log-scale.

```
x = np.geomspace(np.min(large_cities), np.max(large_cities), 1001)
probs = scipy.stats.pareto.cdf(x, alpha, scale=s)
for i in [1, 2]:
    plt.subplot(1, 2, i)
    plt.plot(x, 1-probs, "r--", label=f"CCDF of P({alpha:.3f}, {s})")
    plt.plot(cities_sorted, 1-np.arange(1, n+1)/n,
```

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```

    drawstyle="steps-post", label="Empirical Complementary CDF")
plt.xlabel("$x$")
plt.xscale("log")
plt.yscale(["linear", "log"][[i-1]])
if i == 1:
    plt.ylabel("Prob(city size > x)")
    plt.legend()
plt.show()

```

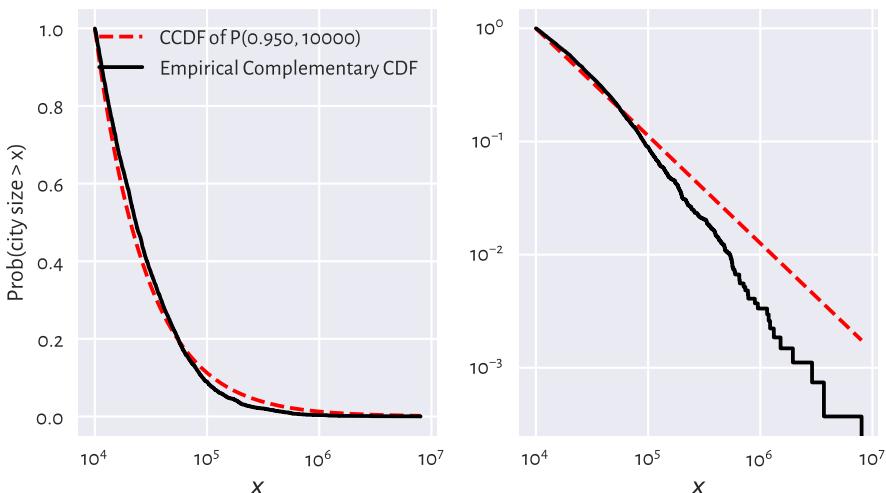


Figure 6.10: Empirical and theoretical complementary cumulative distribution functions for the `large_cities` dataset with probabilities on the linear- (left) and log-scale (right) and city sizes on the log-scale

In terms of the maximal absolute distance between the two functions, \hat{D}_n , the fit is looks pretty good (this can be seen on the left plot, note that the log-scale overemphasises the relatively small differences in the right tail and should not be used for judging the value of \hat{D}_n). However, that the Kolmogorov–Smirnov goodness-of-fit tests rejects the hypothesis of Pareitianity (at significance level 0.1%) is left as an exercise to the reader.

6.3.3 Uniform Distribution

Consider the Polish *Lotto* lottery, where 6 numbered balls $\{1, 2, \dots, 49\}$ are drawn without replacement from an urn. We have a data set that summarises the number of times each ball has been drawn in all the drawings in the period 1957–2016.

```
lotto = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/lotto_table.txt")
lotto
## array([720., 720., 714., 752., 719., 753., 701., 692., 716., 694.,
##        716., 668., 749., 713., 723., 693., 777., 747., 728., 734., 762.,
##        729., 695., 761., 735., 719., 754., 741., 750., 701., 744., 729.,
##        716., 768., 715., 735., 725., 741., 697., 713., 711., 744., 652.,
##        683., 744., 714., 674., 654., 681.])
```

Each event seems to occur more or less with the same probability. Of course, the numbers on the balls are integer, but in our idealised scenario we may try modelling this dataset using a continuous *uniform distribution*, which yields arbitrary real numbers on a given interval (a, b) , i.e., between some a and b . We denote such a distribution with $U(a, b)$. It has the probability density function given by

$$f(x) = \frac{1}{b - a},$$

for $x \in (a, b)$ and $f(x) = 0$ otherwise.

Note that `scipy.stats.uniform` uses parameters `a` and `scale` equal to $b - a$ instead.

In our case, it makes sense to set `a=1` and `b=50` and interpret an outcome like `49.1253` as representing the 49th ball (compare the notion of the floor function, $\lfloor x \rfloor$).

```
x = np.linspace(1, 50, 1001)
plt.bar(np.arange(1, 50), width=1, height=lotto/np.sum(lotto),
        color="lightgray", edgecolor="black", alpha=0.8, align="edge")
plt.plot(x, scipy.stats.uniform.pdf(x, 1, scale=49), "r--",
          label="PDF of U(1, 50)")
plt.legend()
plt.show()
```

Visually, see Figure 6.11, this model makes much sense, but again, some more rigorous statistical testing would be required to determine if someone hasn't been tampering with the lottery results, i.e., if data does not deviate from the uniform distribution significantly.

Exercise 6.6 Does playing lotteries and engaging in gambling make rational sense at all, from

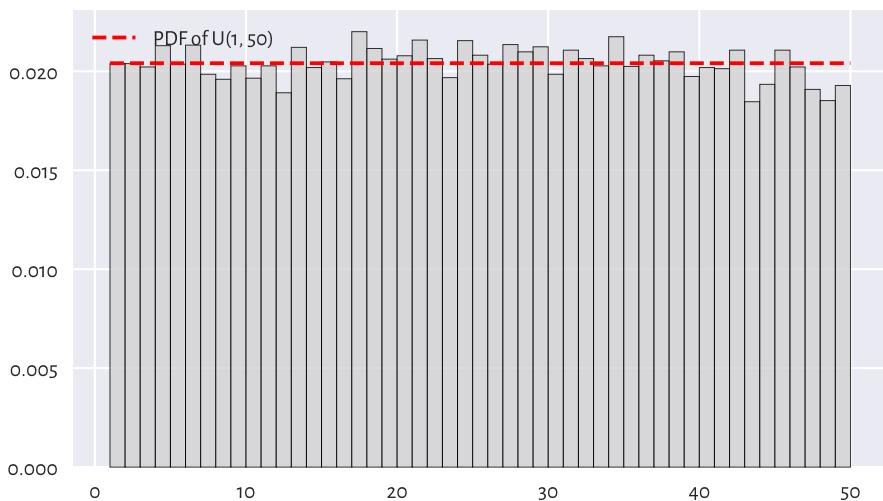


Figure 6.11: Histogram for the `lotto` dataset

the perspective of an individual player? Well, we see that 16 is the most frequently occurring outcome in Lotto, maybe there's some magic in it? Also, some people became millionaires after all, right?

Note: In data modelling (e.g., Bayesian statistics), sometimes a uniform distribution is chosen as a placeholder for “we know nothing about a phenomenon, so let’s just assume that every event is equally likely”. However, overall, it is quite fascinating that the real world tends to be structured after all; emerging patterns are plentiful and, furthermore, they are subject to qualitative analysis.

6.3.4 Distribution Mixtures (*)

Some datasets may fail to fit into simple models such as the ones described above. It may sometimes be due to their non-random behaviour: statistics gives just one means to create data idealisations, we also have partial differential equations, approximation theory, graphs and complex networks, agent-based modelling, and so forth, which might be worth giving a study (and then try).

Other reasons may be that what we observe is in fact a *mixture* (creative combination) of simpler processes.

The dataset representing the December 2021 hourly averages pedestrian counts⁸³ near the Southern Cross Station in Melbourne might be a good instance of such a scenario, compare Figure 4.6.

```
peds = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/southern_cross_station_peds_2019_dec.txt")
```

It might not be a bad idea to try to fit a probabilistic (convex) combination of three normal distributions f_1, f_2, f_3 , corresponding to the morning, lunch-time, and evening pedestrian count peaks. This yields the PDF

$$f(x) = w_1 f_1(x) + w_2 f_2(x) + w_3 f_3(x)$$

for some coefficients $w_1, w_2, w_3 \geq 0$ such that $w_1 + w_2 + w_3 = 1$.

Figure 6.12 depicts a mixture of $N(8, 1)$, $N(12, 1)$, and $N(17, 2)$ with the corresponding weights of 0.35, 0.1, and 0.55. This particular data set is quite coarse-grained (we only have 24 bar heights at our disposal), therefore these estimated parameters and coefficients should be taken with a pinch of chilli pepper.

```
plt.bar(np.arange(24), width=1, height=peds/np.sum(peds),
        color="lightgray", edgecolor="black", alpha=0.8)
x = np.arange(0, 25, 0.1)
p1 = scipy.stats.norm.pdf(x, 8, 1)
p2 = scipy.stats.norm.pdf(x, 12, 1)
p3 = scipy.stats.norm.pdf(x, 17, 2)
p = 0.35*p1 + 0.1*p2 + 0.55*p3 # weighted (convex) combination of 3
# densities
plt.plot(x, p, "r--", label="PDF of a normal mixture")
plt.legend()
plt.show()
```

Important: It will frequently be the case in data wrangling that more complex entities (models, methods) will be arising as combinations of simpler (primitive) components. This is why we should spend a great deal of time studying the *fundamentals*.

Note: Some data clustering techniques (in particular, the k -means algorithm that we briefly discuss later in this course) could be used to split a data sample into disjoint chunks corresponding to different mixture components.

⁸³ <http://www.pedestrian.melbourne.vic.gov.au/>

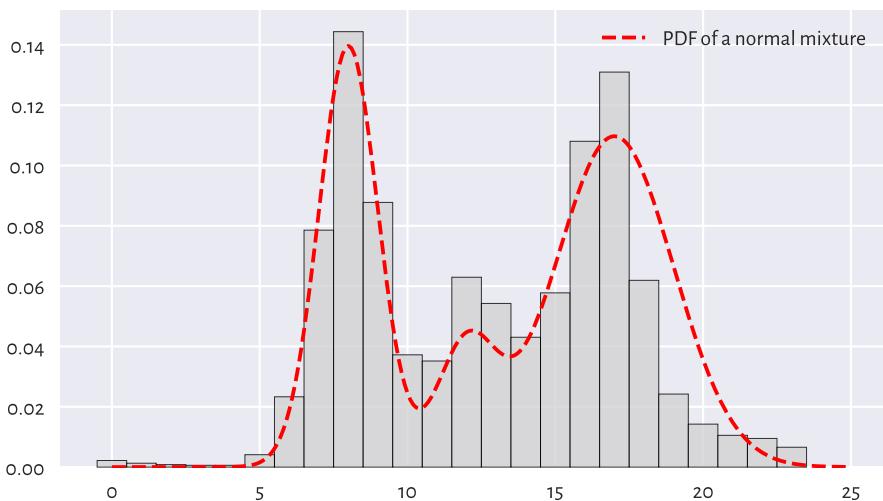


Figure 6.12: Histogram for the `peds` dataset and a guesstimated mixture of three normal distributions

Also, it might be the case that the mixture components can in fact be explained by another categorical variable which divides the dataset into natural groups, compare [Chapter 12](#).

6.4 Generating Pseudorandom Numbers

A probability distribution is useful not only for describing a dataset. It also enables us to perform many experiments on data that we don't currently have, but we might obtain in the future, to test various scenarios and hypotheses.

To do this, we can generate a random sample of independent (not related to each other) observations.

6.4.1 Uniform Distribution

When most people say *random*, they implicitly mean *uniformly distributed*. For example:

```
np.random.rand(5)
## array([0.69646919, 0.28613933, 0.22685145, 0.55131477, 0.71946897])
```

gives 5 observations sampled independently from the uniform distribution on the unit interval, i.e., $U(0, 1)$.

The same with **scipy**, but this time the support will be $(-10, 15)$.

```
scipy.stats.uniform.rvs(-10, scale=25, size=5) # from -10 to -10+25
## array([ 0.5776615 , 14.51910496, 7.12074346, 2.02329754, -0.19706205])
```

Which we could as well have generated by manually shifting and scaling the output the random number generator on the unit interval using the formula `np.random.rand(5)*25-10`.

6.4.2 Not Exactly Random

Actually, we are generating numbers using a computer, which is purely deterministic, hence we shall refer to them as *pseudorandom* or random-like ones (albeit they are non-distinguishable from truly random, when subject to rigorous tests for randomness).

To prove it, we can set the initial state of the number generator (the *seed*) to some number and see what values are output:

```
np.random.seed(123) # set seed
np.random.rand(5)
## array([0.69646919, 0.28613933, 0.22685145, 0.55131477, 0.71946897])
```

and then set the seed once again to the same number and see how “random” the next values are:

```
np.random.seed(123) # set seed
np.random.rand(5)
## array([0.69646919, 0.28613933, 0.22685145, 0.55131477, 0.71946897])
```

This enables us to perform completely *reproducible* numerical experiments, and this is a very good feature: truly scientific inquiries should lead to identical results in the same conditions.

Note: If we don't set the seed manually, it will be initialised based on the current wall time, which is different every... time – therefore the numbers will *seem* random to us.

Many Python packages that we will be using in the future, including `pandas` and `sklearn` rely on `numpy`'s random number generator, thus we'll be calling `numpy.random.seed` to make them predictable.

Additionally, many of them (e.g., `sklearn.model_selection.train_test_split` or `pandas.DataFrame.sample`) are equipped with the `random_state` argument, which can *temporarily* change the seed (for just one call to that function). For instance:

```
scipy.stats.uniform.rvs(size=5, random_state=123)
## array([0.69646919, 0.28613933, 0.22685145, 0.55131477, 0.71946897])
```

This gives the same sequence as above.

6.4.3 Sampling from Other Distributions

Of course, generating data from other distributions is possible too; there are many `rvs` methods implemented in `scipy.stats`. For example, here is a sample from $N(100, 16)$:

```
scipy.stats.norm.rvs(100, 16, size=3, random_state=50489)
## array([113.41134015, 46.99328545, 157.1304154 ])
```

On a side note, deviates from the *standard* normal distribution, i.e., $N(0, 1)$, can also be generated using `numpy.random.randn`. Therefore, as $N(100, 16)$ is a scaled and shifted version thereof, the above is equivalent to:

```
np.random.seed(50489)
np.random.randn(3)*16 + 100
## array([113.41134015, 46.99328545, 157.1304154 ])
```

Important: Conclusions based on simulated data are trustworthy, because they cannot be manipulated. Or can they?

The pseudorandom number generator's seed used above, 50489, is quite suspicious. It might suggest that someone wanted to *prove* some point (in this case, the violation of the 3σ rule).

This is why we recommend sticking to one and only seed most of the time, e.g., 123, or – when performing simulations – setting consecutive seeds for each iteration, 1, 2, ...

Exercise 6.7 Generate 1000 pseudorandom numbers from the log-normal distribution.

Note: (*) Having a good pseudorandom number generator from the uniform distribu-

tion on the unit interval is crucial, because sampling from other distributions usually involves transforming independent $U(0, 1)$ variates.

For instance, samples following any continuous cumulative distribution function F can be constructed by means of *inverse transform sampling*:

1. Generate a sample x_1, \dots, x_n independently from $U(0, 1)$;
2. Transform each x_i by applying the quantile function, $y_i = F^{-1}(x_i)$;
3. Now y_1, \dots, y_n follows the CDF F .

For more topics on random number generation, see [[Geno3], [RCO4]].

Exercise 6.8 (*) Generate 1000 pseudorandom numbers from the log-normal distribution using inverse transform sampling.

Exercise 6.9 (**) Generate 1000 pseudorandom numbers from the distribution mixture discussed in Section 6.3.4.

6.4.4 Natural Variability

Note that even a sample which we know that was generated from a specific distribution will deviate from it, sometimes considerably. Such effects usually disappear⁸⁷ when the availability of data increases, but definitely will be visible for small sample sizes.

For example, Figure 6.13 depicts the histogram of 9 different samples of size 100, all drawn independently from the normal distribution $N(0, 1)$.

```
plt.figure(figsize=(plt.rcParams["figure.figsize"][0], 2) # width=height
x = np.linspace(-4, 4, 1001)
fx = scipy.stats.norm.pdf(x) # PDF of N(0, 1)
for i in range(9):
    plt.subplot(3, 3, i+1)
    sample = scipy.stats.norm.rvs(size=100, random_state=i+1)
    sns.histplot(sample, stat="density", bins=10, color="lightgray")
    plt.plot(x, fx, "r--")
    plt.ylabel(None)
    plt.xlim(-4, 4)
    plt.ylim(0, 0.6)
plt.legend()
plt.show()
```

⁸⁷ Compare the Fundamental Theorem of Statistics (the Glivenko–Cantelli theorem).

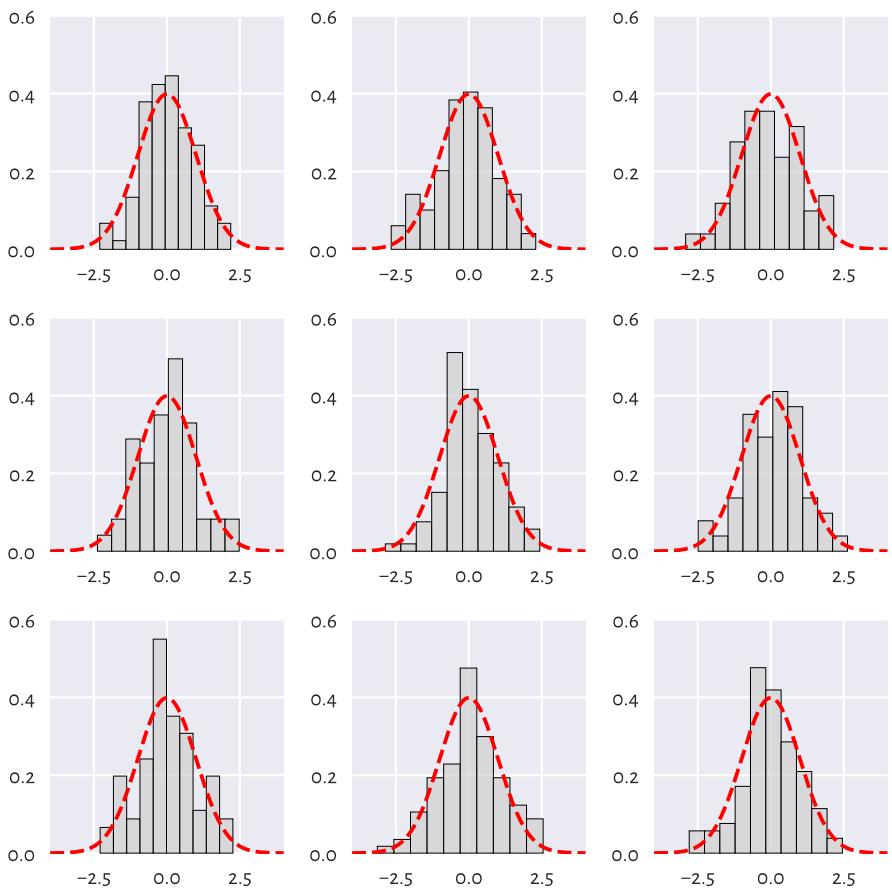


Figure 6.13: All 9 samples are normally distributed!

There is some ruggedness in the bars' sizes that a naïve observer might try to interpret as something meaningful; a competent data scientist must train their eye to ignore such impurities that are only due to random effects (but be always ready to detect those which are worth attention).

More specialist tools such as hypothesis tests enable us to tell if the deviation from the theoretical distribution is statistically significant or not. This is why, after finishing this introductory course, we should be yearning for more maths.

Exercise 6.10 Repeat the above experiment for samples of size 10, 1000, and 10000.

Example 6.11 (*) Using a simple Monte Carlo simulation, we can verify (approximately) that the Kolmogorov-Smirnov goodness-of-fit test introduced in Section 6.2.3 has been calibrated properly, i.e., that for samples which really follow the assumed distribution, the null hypothesis is rejected only in ca. 0.1% of the cases.

Let's say we are interested in the null hypothesis referencing the normal distribution $N(0, 1)$ and sample size $n = 100$. We need to generate many (we assume 10000 below) such samples for each of which we compute and store the maximal absolute deviation from the theoretical CDF, i.e., \hat{D}_n .

```
n = 100
distrib = scipy.stats.norm(0, 1) # assumed distribution - N(0, 1)
Dns = []
for i in range(10000): # increase this for better precision
    x = distrib.rvs(size=n, random_state=i+1) # really follows distrib
    Dns.append(compute_Dn(x, distrib.cdf))
Dns = np.array(Dns)
```

Now let us compute the proportion of cases which lead to \hat{D}_n greater than the critical value K_n :

```
len(Dns[Dns >= scipy.stats.kstwo.ppf(1-0.001, n)]) / len(Dns)
## 0.0016
```

In theory, this should be equal to 0.001, but we are relying on randomness above, therefore our values is approximate. Increasing the number of trials from 10000 to, say, 1000000 will make the above estimate more precise.

It is also worth checking out that the density histogram for Dns resembles the Kolmogorov distribution that we can compute via `scipy.stats.kstwo.pdf`.

Exercise 6.12 (*) It might also be interesting to check out the test's power, i.e., the probability that when the null hypothesis is false, it will actually be rejected. Modify the above code in such a way that x in the for loop is not generated from $N(0, 1)$ but from $N(0.1, 1)$, $N(0.2, 1)$, etc. and check the proportion of cases where we deem the sample's distribution different from $N(0, 1)$. Note that small differences in the location parameter μ are usually ignored, but that this improves with sample size n .

6.4.5 Adding Jitter (White Noise)

We have noted that measurements might be subject to observational error and rounding at data collection phase. In particular, our `heights` dataset has 1 fractional digits precision. However, in probability and statistics, when we say that data follow a continuous distribution, the probability of having two identical values in a sample is 0. Therefore,

some data analysis methods assume that there are no ties in the input vector, i.e., all values are unique.

The easiest way to deal with such numerical inconveniences is to add some white noise with expected value of 0, either uniformly or normally distributed.

For example, for `heights` it makes sense to add some jitter from $U[-0.05, 0.05]$:

```
heights_jitter = heights + (np.random.rand(len(heights))*0.1-0.05)
heights_jitter[:6] # preview
## array([160.21704623, 152.68870195, 161.24482407, 157.3675293 ,
##         154.61663465, 144.68964596])
```

Adding noise also might be performed for aesthetic reasons, e.g., when drawing scatterplots.

6.5 Exercises

Exercise 6.13 *Why is the notion of the mean income confusing the general public?*

Exercise 6.14 *When manually setting the seed of a random number generator makes sense?*

Exercise 6.15 *Given a log-normally distributed sample x , how can we turn it to a normally distributed one, i.e., $y=f(x)$, with f being... what?*

Exercise 6.16 *What is the 3σ rule for normally distributed data?*

Exercise 6.17 (*) *How we can verify graphically if a sample follows a hypothesised theoretical distribution?*

Exercise 6.18 (**) *Explain the meaning of: type I error, significance level, and a test's power.*

Part III

Multidimensional Data

Multidimensional Numeric Data at a Glance

From the perspective of structured datasets, a vector often represents n independent measurements of the same quantitative or qualitative property, e.g., heights of n different patients, incomes in n randomly chosen households, or age category brackets of n runners (we deal with categorical data in [Chapter 11](#)).

More generally, these are all instances of a bag of n points on the real line. By far (assuming we have solved all the suggested exercises) we should have become quite fluent with the methods for processing such one-dimensional arrays.

Let's increase the level of complexity by allowing each of the n entities be described by possibly more than one feature, let's say m of them. In other words, we will be dealing with n points in an m -dimensional space, \mathbb{R}^m .

We can arrange all the observations in a table with n rows and m columns (just like in spreadsheets). Such an object can be expressed with **numpy** as a two-dimensional array which we will refer to as *matrices*. Thanks to matrices, we can all keep n vectors of length m together in a single object and process them all at once (or m vectors of length n , depending how we want to look at it). Very convenient.

Important: Just like vectors, matrices were designed to store data of the same type. In [Chapter 10](#) we will cover *data frames*, which further increase the degree of complexity (and freedom) by not only allowing for mixed data types (e.g., numerical and categorical; this will enable us to perform data analysis in subgroups more easily) but also for the rows and columns be named.

Many data analysis algorithms convert data frames to matrices automatically and deal with them as such, and from the computational side, it is **numpy** which does most of the “mathematical” work. Our ambitions is to go way beyond very basic data wrangling (this is a university-level course after all), and that is why before proceeding with **pandas**, we are learning the former in detail.

7.1 Creating Matrices

7.1.1 Reading CSV Files

Tabular data are often stored and distributed in a very portable plain-text format called CSV (comma-separated values) or variants thereof.

`numpy.loadtxt`, which we have already been using, supports them quite well as long as they do not feature column names (comment lines are accepted, though). Unfortunately, for most CSV files the opposite is the case, and hence we suggest relying on a corresponding function from the `pandas` package (anticipating what's going to happen in Chapter 10):

```
body = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_adult_female_bmx_2020.csv",
    comment="#")
body = body.to_numpy() # data frames will be covered later
```

Note that we have converted the data frame to a `numpy` array by calling the `to_numpy` method. Here is a preview of a few first rows:

```
body[:6, :] # 6 first rows, all columns
## array([[ 97.1, 160.2, 34.7, 40.8, 35.8, 126.1, 117.9],
##        [ 91.1, 152.7, 33.5, 33. , 38.5, 125.5, 103.1],
##        [ 73. , 161.2, 37.4, 38. , 31.8, 106.2, 92. ],
##        [ 61.7, 157.4, 38. , 34.7, 29. , 101. , 90.5],
##        [ 55.4, 154.6, 34.6, 34. , 28.3, 92.5, 73.2],
##        [ 62. , 144.7, 32.5, 34.2, 29.8, 106.7, 84.8]])
```

This is an extended version of the National Health and Nutrition Examination Survey (**NHANES**⁸⁸ dataset), where we are given body measurements of adult females, in the following order:

1. weight (kg),
2. standing height (cm),
3. upper arm length (cm),
4. upper leg length (cm),
5. arm circumference (cm),

⁸⁸ <https://www.cdc.gov/nchs/nhanes/search/datapage.aspx>

6. hip circumference (cm),
7. waist circumference (cm).

Unfortunately, **numpy** matrices do not support column naming, so these should be noted down separately elsewhere. **pandas** data frames will have that capability, but – as we have said above – from the algebraic side, they are not as convenient for the purpose of scientific computing as matrices.

What we are dealing with is still a **numpy** array:

```
type(body)
## <class 'numpy.ndarray'>
```

however, this time a two-dimensional one:

```
body.ndim
## 2
```

which means that the `shape` slot is now a tuple of length 2:

```
body.shape
## (4221, 7)
```

The above gave the number of rows and columns, respectively.

7.1.2 Enumerating Elements

numpy.array can create a two-dimensional array based on a list of lists or vector-like objects of identical lengths. Each of them will constitute a separate row of the resulting matrix.

For example:

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

gives a 3-by-4 (3×4) matrix,

```
np.array([ [1], [2], [3] ])
## array([[1],
##        [2],
##        [3]])
```

yields a 3-by-1 one (we call it a *column vector*, but it is a special matrix — we'll soon learn that shapes can make a significant difference), and

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

produces a 1-by-4 array (a *row vector*).

Note: Note that an ordinary vector (a 1-dimensional array) only uses a single pair of square brackets:

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

7.1.3 Repeating Arrays

The previously mentioned `numpy.tile` and `numpy.repeat` can also generate some nice matrices. For instance,

```
np.repeat([[1, 2, 3]], 4, axis=0)
## array([[1, 2, 3],
##        [1, 2, 3],
##        [1, 2, 3],
##        [1, 2, 3]])
```

repeats a row vector rowwisely (i.e., over axis 0 – the first one).

Replicating a column vector columnwisely (i.e., over axis 1 – the second one) is possible as well:

```
np.repeat([[1], [2], [3], [4]], 3, axis=1)
## array([[1, 1, 1],
##        [2, 2, 2],
```

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```
##      [3, 3, 3],
##      [4, 4, 4])
```

Exercise 7.1 How to obtain matrices of the following kinds programmatically?

$$\left[\begin{array}{cc} 1 & 2 \\ 1 & 2 \\ 1 & 2 \\ 3 & 4 \\ 3 & 4 \\ 3 & 4 \\ 3 & 4 \end{array} \right], \quad \left[\begin{array}{ccccccc} 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \end{array} \right], \quad \left[\begin{array}{cccccccc} 1 & 1 & 1 & 2 & 2 & 2 & 2 & 2 \\ 3 & 3 & 3 & 4 & 4 & 4 & 4 & 4 \end{array} \right].$$

7.1.4 Stacking Arrays

`numpy.column_stack` and `numpy.row_stack` take a tuple of array-like objects and bind them column- or rowwisely to form a new matrix:

```
np.column_stack(([10, 20], [30, 40], [50, 60])) # a tuple of lists
## array([[10, 30, 50],
##        [20, 40, 60]])
np.row_stack(([10, 20], [30, 40], [50, 60]))
## array([[10, 20],
##        [30, 40],
##        [50, 60]])
np.column_stack(
    np.row_stack(([10, 20], [30, 40], [50, 60])),
    [70, 80, 90])
## array([[10, 20, 70],
##        [30, 40, 80],
##        [50, 60, 90]])
```

Exercise 7.2 Perform similar operations using `numpy.append`, `numpy.vstack`, `numpy.hstack`, `numpy.concatenate`, and (*) `numpy.c_`.

Exercise 7.3 Using `numpy.insert`, and a new row/column at the beginning, end, and in the middle of an array. Note that this function returns a new array.

7.1.5 Other Functions

Many built-in functions allow for generating arrays of arbitrary shapes (not only vectors). For example:

```
np.random.seed(123)
np.random.rand(3, 4) # not: rand((3, 4))
## array([[0.69646919, 0.28613933, 0.22685145, 0.55131477],
##        [0.71946897, 0.42310646, 0.9807642 , 0.68482974],
##        [0.4809319 , 0.39211752, 0.34317802, 0.72904971]])
```

The same with `scipy`:

```
np.random.seed(123)
scipy.stats.uniform.rvs(0, 1, size=(2, 5))
## array([[0.69646919, 0.28613933, 0.22685145, 0.55131477, 0.71946897],
##        [0.42310646, 0.9807642 , 0.68482974, 0.4809319 , 0.39211752]])
```

Note that the way we specify the output shapes might differ across functions and packages, therefore – as usual – it is always best to refer to their documentation.

Exercise 7.4 Check out the following functions: `numpy.eye`, `numpy.diag`, `numpy.zeros`, `numpy.ones`, and `numpy.empty`.

7.2 Reshaping Matrices

Let's take an example 3-by-4 matrix:

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

Internally, a matrix is represented using a *long* flat vector where elements are stored in the row-major order (sometimes referred to as a C-style array, as opposed to Fortran-style which is used in, e.g., R):

```
A.size # total number of elements
## 12
```

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```
A.ravel() # the underlying array
## array([ 1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12])
```

It is the `shape` slot that is causing the 12 elements to be treated as if they were arranged on a 3 by 4 grid, for example in different algebraic computations and during the printing thereof. It can be modified anytime without modifying the underlying array:

```
A.shape = (4, 3)
A
## array([[ 1,  2,  3],
##        [ 4,  5,  6],
##        [ 7,  8,  9],
##        [10, 11, 12]])
```

This way, we have obtained a different *view* on the same data.

For convenience, there is also the `reshape` method that returns a modified version of the object it is applied on:

```
A.reshape(-1, 6)
## array([[ 1,  2,  3,  4,  5,  6],
##        [ 7,  8,  9, 10, 11, 12]])
```

Here, “-1” means that `numpy` must deduce by itself how many rows we actually want in the result (12 elements are supposed to be arranged in 6 columns, so the maths behind it is not rocket science).

This way, generating row or column vectors is very easy:

```
np.linspace(0, 1, 5).reshape(1, -1)
## array([[0. , 0.25, 0.5 , 0.75, 1. ]])
np.array([9099, 2537, 1832]).reshape(-1, 1)
## array([[9099],
##        [2537],
##        [1832]])
```

We should also note that reshaping is not the same as matrix *transpose*, which also changes the order of elements in the underlying array:

```
A # to recall
## array([[ 1,  2,  3],
##        [ 4,  5,  6],
##        [ 7,  8,  9],
##        [10, 11, 12]])
A.T # transpose of A
## array([[ 1,  4,  7, 10],
##        [ 2,  5,  8, 11],
##        [ 3,  6,  9, 12]])
```

We see that the rows became columns and vice versa.

Note: (*) Higher-dimensional arrays are also possible. For example,

```
np.arange(24).reshape(2, 4, 3)
## array([[[ 0,  1,  2],
##           [ 3,  4,  5],
##           [ 6,  7,  8],
##           [ 9, 10, 11]],
##          [[12, 13, 14],
##           [15, 16, 17],
##           [18, 19, 20],
##           [21, 22, 23]]])
```

Is an array of “depth” 2, “height” 4, and “width” 3; we can see it as two 4-by-3 matrices stacked together. Theoretically, they can be useful for representing contingency tables for products of many factors, but in our application areas we are used to sticking with long data frames instead, see [Section 10.7](#) (more aesthetic display, better handling of sparse data).

7.3 Mathematical Notion

Here is some standalone mathematical notation that we shall be employing in the course of this course. A matrix with n rows and m columns (an n by m , $n \times m$ -matrix) \mathbf{X} can be

written as

$$\mathbf{X} = \begin{bmatrix} x_{1,1} & x_{1,2} & \cdots & x_{1,m} \\ x_{2,1} & x_{2,2} & \cdots & x_{2,m} \\ \vdots & \vdots & \ddots & \vdots \\ x_{n,1} & x_{n,2} & \cdots & x_{n,m} \end{bmatrix}.$$

Mathematically, we denote this as $\mathbf{X} \in \mathbb{R}^{n \times m}$. Looking at the above, if this makes us think of how data are displayed in spreadsheets, we are correct, because the latter were inspired by the former.

We see that $x_{i,j} \in \mathbb{R}$ denotes the element in the i -th row (e.g., the i -th *observation*) and the j -th column (e.g., the j -th *feature* or *variable*), for every $i = 1, \dots, n, j = 1, \dots, m$.

Important: Matrices like \mathbf{X} are a convenient means of representing many different kinds of data:

- n points in an m dimensional space (like n observations for which there are m measurements/features recorded, where each row describes a different object);
- m time series sampled at n points in time (e.g., m different stocks on n consecutive days);
- a single kind of measurement for data in m groups, each consisting of n subjects (e.g., heights of n males and n females); here, the order of elements in each column does not usually matter as observations are not *paired*; there is no relationship between $x_{i,j}$ and $x_{i,k}$ for $j \neq k$; a matrix is used merely as a convenient container for storing a few unrelated vectors of identical sizes; we will be dealing with a more generic case of possibly nonhomogeneous groups in Chapter 12;
- two-way contingency tables (see Section 11.2.2), where an element $x_{i,j}$ gives the number of occurrences of items at the i -th level of the first categorical variable and, at the same time, being at the j -th level of the second variable (e.g., blue-eyed *and* blonde-haired);
- graphs and other relationships between objects, e.g., $x_{i,j} = 0$ might denote that the i -th object is not connected⁹³ with the j -th one and $x_{k,l} = 0.2$ that there is a weak connection between k and l ;
- images, where $x_{i,j}$ represents the intensity of a colour component (e.g., red, green, blue or shades of grey or hue, saturation, brightness; compare Section 16.4) of a pixel in the $(n - i + 1)$ -th row and the j -th column.

⁹³ Such matrices are usually sparse, i.e., have many elements equal to 0. We have special, memory-efficient data structures for handling these data, see `scipy.sparse` for more detail as they go beyond the scope of our introductory course.

In this course, we are most often dealing with the first case, i.e., n independent points in an m dimensional space, \mathbb{R}^m , which we refer to as *multidimensional data*. The above body dataset is a typical example of such data.

Note: In practice, quite often more complex and less-structured data can be mapped to a tabular form. For instance, a set of audio recordings can be described by measuring overall loudness, timbre, and danceability of each song. Also, a collection of documents can be described by means of the degrees of belongingness to some automatically discovered topics (e.g., someone said that Joyce's *Ulysses* is 80% travel literature, 70% comedy, and 50% heroic fantasy, but let's not take it for granted).

7.3.1 Row and Column Vectors

Additionally, will sometimes use the following notation to emphasise that \mathbf{X} consists of n rows:

$$\mathbf{X} = \begin{bmatrix} \mathbf{x}_{1,\cdot} \\ \mathbf{x}_{2,\cdot} \\ \vdots \\ \mathbf{x}_{n,\cdot} \end{bmatrix}.$$

Here, $\mathbf{x}_{i,\cdot}$ is a *row vector* of length m , i.e., a $(1 \times m)$ -matrix:

$$\mathbf{x}_{i,\cdot} = [\ x_{i,1} \ x_{i,2} \ \cdots \ x_{i,m} \].$$

Also, recall that we are used to denoting a *vector* of length m with $\mathbf{x} = (x_1, \dots, x_m)$. A vector is a 1-dimensional array (not a 2-dimensional one), hence a slightly different notation in the case where ambiguity can lead to some trouble.

Important: In Chapter 8 we will see that often **numpy** automatically treats length- m vectors as if they were row vectors, i.e., matrices of size $1 \times m$. For the column vector behaviour, we will need to reshape them manually.

Alternatively, we can specify the m columns

$$\mathbf{X} = [\ \mathbf{x}_{\cdot,1} \ \mathbf{x}_{\cdot,2} \ \cdots \ \mathbf{x}_{\cdot,m} \],$$

where $\mathbf{x}_{\cdot,j}$ is a *column vector* of length n , i.e., an $(n \times 1)$ -matrix:

$$\mathbf{x}_{\cdot,j} = \begin{bmatrix} x_{1,j} & x_{2,j} & \cdots & x_{n,j} \end{bmatrix}^T = \begin{bmatrix} x_{1,j} \\ x_{2,j} \\ \vdots \\ x_{n,j} \end{bmatrix},$$

where \cdot^T denotes the transpose of a given matrix (thanks to which we can save some vertical space, we don't want this book be 1000 pages long, do we?).

7.3.2 Transpose

More generally, the *transpose* of a matrix $\mathbf{X} \in \mathbb{R}^{n \times m}$ is an $(m \times n)$ -matrix \mathbf{Y} given by:

$$\mathbf{Y} = \mathbf{X}^T = \begin{bmatrix} x_{1,1} & x_{2,1} & \cdots & x_{m,1} \\ x_{1,2} & x_{2,2} & \cdots & x_{m,2} \\ \vdots & \vdots & \ddots & \vdots \\ x_{1,n} & x_{2,n} & \cdots & x_{m,n} \end{bmatrix},$$

i.e., $y_{i,j} = x_{j,i}$.

Exercise 7.5 Compare the display of an example matrix A and its transpose $A.T$ above.

7.3.3 Identity and Other Diagonal Matrices

\mathbf{I} denotes the *identity matrix*, being a square $n \times n$ (with n most often clear from the context) matrix with 0s everywhere except on the main diagonal, where 1s lie.

```
np.eye(5)
## 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.]])
```

The identity matrix is a neutral element of matrix multiplication.

More generally, any diagonal matrix, $\text{diag}(a_1, \dots, a_n)$, can be constructed from a given sequence of elements by calling:

```
np.diag([1, 2, 3, 4])
## array([[1, 0, 0, 0],
```

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```
##      [0, 2, 0, 0],
##      [0, 0, 3, 0],
##      [0, 0, 0, 4]])
```

7.4 Visualising Multidimensional Data

Let us go back to our body dataset:

```
body[ :6, :] # preview
## array([[ 97.1, 160.2, 34.7, 40.8, 35.8, 126.1, 117.9],
##        [ 91.1, 152.7, 33. , 38.5, 125.5, 103.1],
##        [ 73. , 161.2, 37.4, 38. , 31.8, 106.2, 92. ],
##        [ 61.7, 157.4, 38. , 34.7, 29. , 101. , 90.5],
##        [ 55.4, 154.6, 34.6, 34. , 28.3, 92.5, 73.2],
##        [ 62. , 144.7, 32.5, 34.2, 29.8, 106.7, 84.8]])
```

This is an example of tabular (“structured”) data. The important property is that the elements in each row describe the same person; we can reorder all the columns at the same time (change the order of participants), but sorting a single column and leaving the others unchanged will be semantically invalid.

```
body.shape
## (4221, 7)
```

Mathematically, we consider the above as a set of 4221 points in a 7-dimensional space. Let us discuss how we can try visualising different natural *projections* thereof.

7.4.1 2D Data

A *scatterplot* can be used to visualise one variable against another one.

```
plt.scatter(body[:, 1], body[:, 3], c="#00000011")
plt.xlabel("standing height (cm)")
plt.ylabel("upper leg length (cm)")
plt.show()
```

Figure 7.1 depicts upper leg length (y axis) vs (versus; against; as a function of) standing

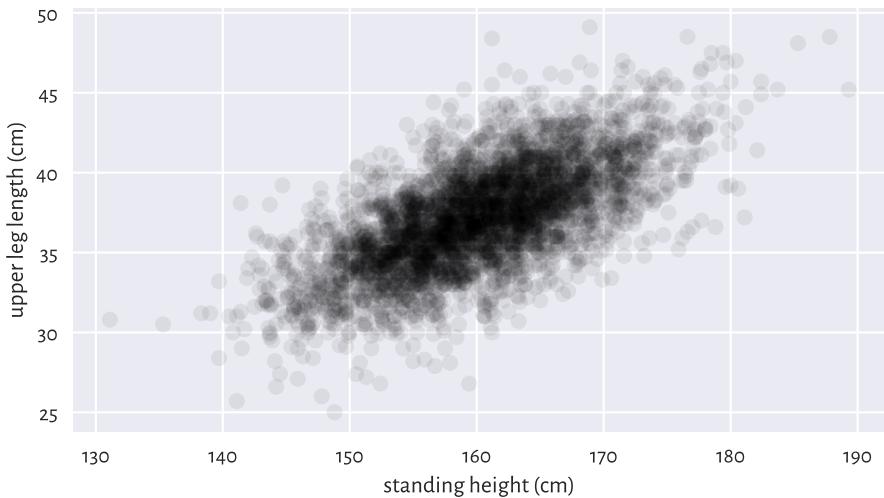


Figure 7.1: An example scatterplot

height (x axis) in the form of a point cloud with (x, y) coordinates like `(body[i, 1], body[i, 3])`.

For instance, here are the exact coordinates of the point corresponding to the person of the smallest height:

```
body[np.argmin(body[:, 1]), [1, 3]]
## array([131.1, 30.8])
```

and here is the one with the greatest upper leg length:

```
body[np.argmax(body[:, 3]), [1, 3]]
## array([168.9, 49.1])
```

As the points are plentiful, normally we cannot easily see *where* the majority of them is located. However, to remedy this, we applied the simple trick of plotting the points using a semi-transparent colour. Here, the colour specifier was of the form `#rrggbbaa`, giving the intensity of the red, green, blue, and alpha (opaqueness) channel in series of two hexadecimal digits (between `00` = 0 and `ff` = 255).

Overall, the plot reveals that there is a *general tendency* of small heights and small upper leg lengths to occur frequently together. The same with larger pairs. In Chapter 9

we will explore some measures of correlation that enable us to quantify the degree of association between variable pairs.

7.4.2 3D Data and Beyond

If we have more than 2 variables to visualise, we might be tempted to use, e.g., a 3-dimensional scatterplot like the one in Figure 7.2.

```
fig = plt.figure()
ax = fig.add_subplot(projection="3d")
ax.scatter(body[:, 1], body[:, 3], body[:, 0], color="#00000011")
ax.view_init(elev=30, azim=20, vertical_axis="y")
ax.set_xlabel("standing height (cm)")
ax.set_ylabel("upper leg length (cm)")
ax.set_zlabel("weight (kg)")
plt.show()
```

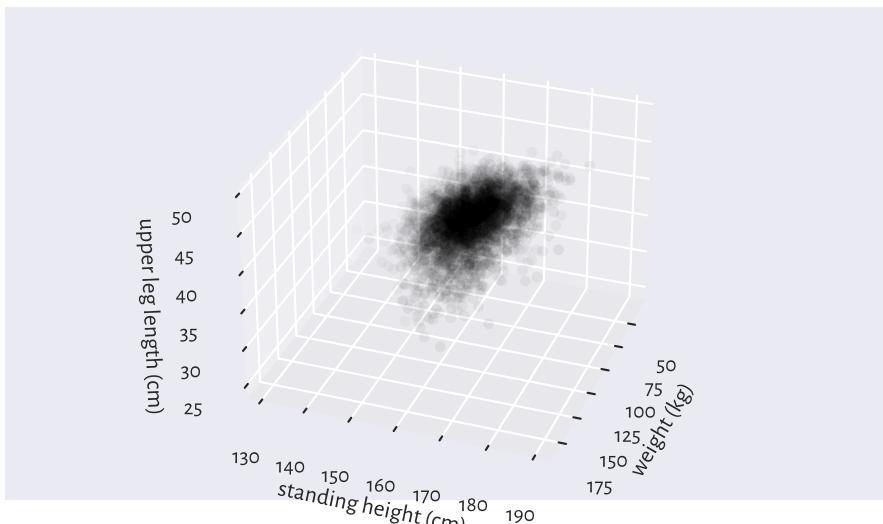


Figure 7.2: A three-dimensional scatterplot reveals almost nothing

However, infrequently will such a 3D plot provide us with readable results: we are projecting a three-dimensional reality onto a two-dimensional screen or page. Some information must inherently be lost. Also, what we see is relative to the position of the virtual camera.

Exercise 7.6 (*) Try finding an interesting elevation and azimuth angle by playing with the arguments passed to the `mpl_toolkits.mplot3d.axes3d.Axes3D.view_init` function. Also, depict arm circumference, hip circumference, and weight.

Note: (*) Sometimes there might be facilities available to create an interactive scatter-plot (e.g., running the above from the Python's console actually enables this), where the virtual camera can be freely repositioned. This can give some insight into our data. Also, there are means of creating animated sequences, where we can fly over the data scene. Some people find it cool, others find it annoying, but the biggest problem therewith is that they cannot be included in printed material. However, if we are only targeting the display for the Web (this includes mobile devices), we can try some Python libraries⁸⁹ that output HTML+CSS+JavaScript code to be rendered by a browser engine.

Example 7.7 Instead of drawing a 3D plot, it might be better to play with different marker colours (or sometimes sizes: think of them as bubbles). A suitable colour map⁹⁰, can be used to distinguish between low and high values of an additional variable, as in Figure 7.3.

```
from matplotlib import cm
plt.scatter(
    body[:, 4], # x
    body[:, 5], # y
    c=body[:, 0], # "z" - colours
    cmap=cm.get_cmap("copper"), # colour map
    alpha=0.5 # opaqueness level between 0 and 1
)
plt.xlabel("arm circumference (cm)")
plt.ylabel("hip circumference (cm)")
plt.axis("equal")
plt.rcParams["axes.grid"] = False
cbar = plt.colorbar()
plt.rcParams["axes.grid"] = True
cbar.set_label("weight (kg)")
plt.show()
```

We can see some tendency for the weight be greater as both the arm and the hip circumferences increase.

Exercise 7.8 Play around with different colour pallettes⁹¹.

⁸⁹ <https://wiki.python.org/moin/NumericAndScientific/Plotting>

⁹⁰ <https://matplotlib.org/stable/tutorials/colors/colormaps.html>

⁹¹ <https://matplotlib.org/stable/tutorials/colors/colormaps.html>

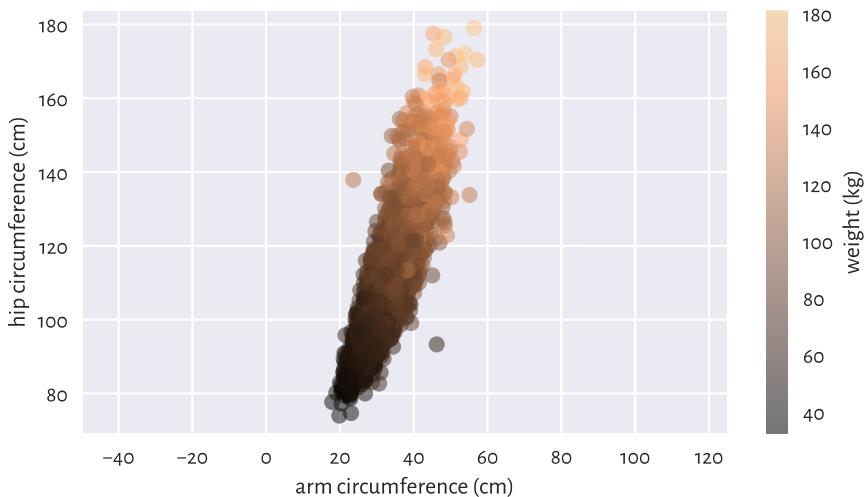


Figure 7.3: A two-dimensional scatter plot displaying 3 variables

However, be wary that ca. every 1 in 12 men (8%) and 1 in 200 women (0.5%) has colour vision deficiencies, especially in the red-green or blue-yellow spectrum, thence some diverging colour maps might be worse than others.

A piece of paper is 2-dimensional. We only have height and width. The world around us is 3-dimensional, we thus also understand the notion of depth. As far as the case of more-dimensional data is concerned, well, suffice it to say that we are 3-dimensional creatures and any attempts towards visualising them will simply not work, don't even trip.

Luckily, this is where mathematics comes to our rescue. With some more knowledge and intuitions, and this book lets us gain them, it will be as easy as imagining a generic m -dimensional space, and then assuming that, say, $m=7$ or 42 .

Pardon yours truly an old joke.

But, really, jokes aside, this is exactly why data science relies on automated methods for knowledge/pattern discovery – so that we are able to identify, describe, and analyse the structures that might be present in the data, but cannot be perceived with our imperfect senses.

Note: Linear and nonlinear dimensionality reduction techniques can be applied to visualise some aspects of high-dimensional data in form of 2D (or 3D) plots. In particular, the principal component analysis (PCA) finds an *interesting* angle at which to look at the data (so that most variance is along the first, and then second, etc., axis).

7.4.3 Scatterplot Matrix (Pairplot)

As a countermeasure, we may try depicting all (or most – ones we deem interesting) pairs of variables in the same drawing in form of a scatterplot matrix, see Figure 7.4.

```
sns.pairplot(data=pd.DataFrame(  
    body[:, [0, 1, 4, 5]],  
    columns=[  
        "weight (kg)", "standing height (cm)",  
        "arm circumference (cm)", "hip circumference (cm)"  
    ]  
)  
# plt.show() # not needed :/
```

As depicting a variable against itself is uninteresting (exercise: what would that be?), we have included histograms on the main diagonal to see how the one-dimensional projections are distributed (the *marginal distributions*).

In Chapter 9 we will be interested in describing and even modelling the possible relationships between variables. A scatterplot matrix can be a good tool for identifying interesting combinations of columns in our datasets.

Exercise 7.9 Draw a scatterplot matrix for the `fcps_chainlink`⁹² dataset. Note that we are only observing different 2-dimensional projections of this more complex domain – only those that are along the main axes. Create a 3D scatterplot to reveal the true shapes.

Exercise 7.10 (*) Use `matplotlib.pyplot.subplot` and other functions we have learned in the previous part to create a scatterplot matrix manually. Draw weight, arm circumference, and hip circumference on a logarithmic scale.

⁹² https://raw.githubusercontent.com/gagolews/teaching_data/master/clustering/fcps_chainlink.csv

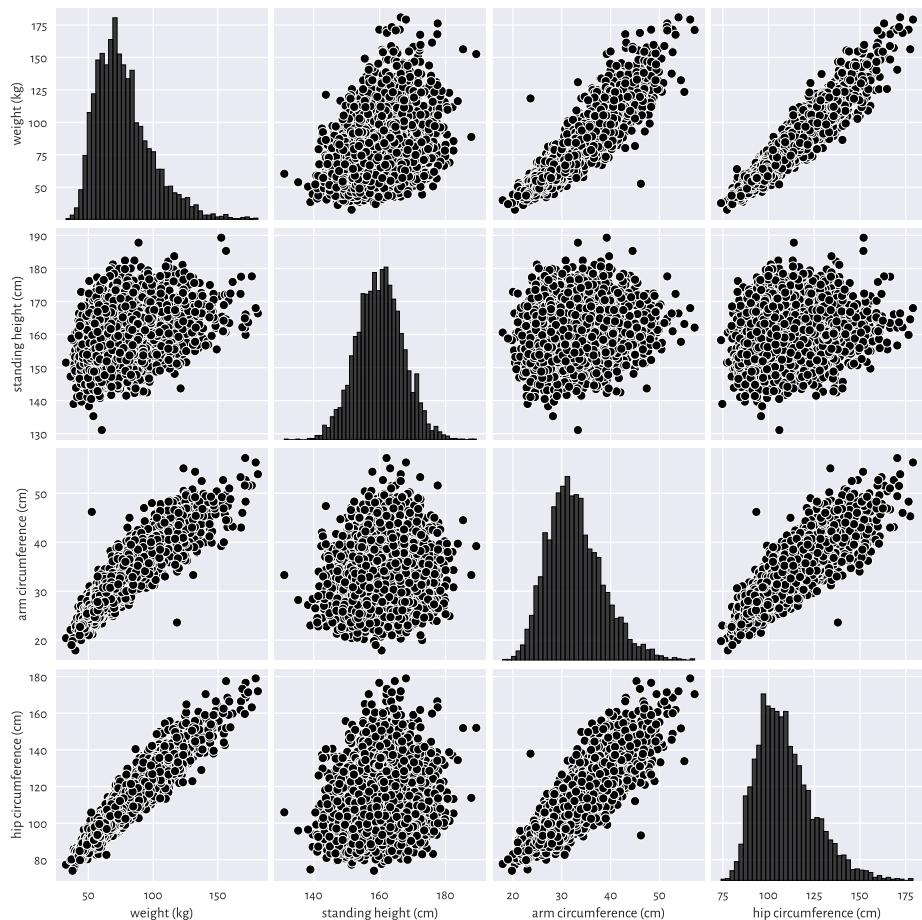


Figure 7.4: Scatterplot matrix for selected columns in the body dataset

7.5 Exercises

Exercise 7.11 What is the difference between `[1, 2, 3]`, `[[1, 2, 3]]` and `[[1], [2], [3]]` in the context of array creation?

Exercise 7.12 If A is a matrix with 5 rows and 6 columns, what is the difference between A , `reshape(6, 5)` and $A.T$?

Exercise 7.13 If A is a matrix with 5 rows and 6 columns, what is the meaning of: $A.\text{reshape}(-1)$, $A.\text{reshape}(3, -1)$, $A.\text{reshape}(-1, 3)$, $A.\text{reshape}(-1, -1)$, $A.\text{shape} = (3, 10)$, and $A.\text{shape} = (-1, 3)$?

Exercise 7.14 List some methods to add a new row to an existing matrix.

Exercise 7.15 Give some ways to visualise 3-dimensional data.

Exercise 7.16 How to and why set point opaqueness/transparency when drawing a scatter plot?

Processing Multidimensional Data

8.1 From Vectors to Matrices

First, let us study how the vector operations that we discussed in, amongst others, [Chapter 5](#) can be extended to matrices. In many cases, we'll end up applying the same transform either on every matrix element separately, or on each row or column. They are all a brilliant example of the *write less, do more* principle in practice.

8.1.1 Vectorised Mathematical Functions

Applying vectorised functions such as `numpy.round`, `numpy.log`, and `numpy.exp` returns an array of the same shape, with all elements transformed accordingly.

```
A = np.array([
    [0.2, 0.6, 0.4, 0.4],
    [0.0, 0.2, 0.4, 0.7],
    [0.8, 0.8, 0.2, 0.1]
]) # example matrix that we'll be using below
```

For example:

```
np.square(A)
## array([[0.04, 0.36, 0.16, 0.16],
##        [0. , 0.04, 0.16, 0.49],
##        [0.64, 0.64, 0.04, 0.01]])
```

takes the square of every element.

More generally, we will be denoting such operations with:

$$f(\mathbf{X}) = \begin{bmatrix} f(x_{1,1}) & f(x_{1,2}) & \cdots & f(x_{1,m}) \\ f(x_{2,1}) & f(x_{2,2}) & \cdots & f(x_{2,m}) \\ \vdots & \vdots & \ddots & \vdots \\ f(x_{n,1}) & f(x_{n,2}) & \cdots & f(x_{n,m}) \end{bmatrix}.$$

8.1.2 Componentwise Aggregation

Unidimensional aggregation functions (e.g., `numpy.mean`, `numpy.quantile`) can be applied to summarise:

- data in each row (`axis=1`),
- data in each column (`axis=0`),

as well as:

- all data into a single number (`axis=None`, being the default),

Here are the examples corresponding to the above cases:

```
np.mean(A)
## 0.3999999999999999
np.mean(A, axis=1)
## array([0.4 , 0.325, 0.475])
np.mean(A, axis=0)
## array([0.33333333, 0.53333333, 0.33333333, 0.4         ])
```

Important: Let us repeat, `axis=1` does not mean that we get the column means (even though columns constitute the 2nd axis, and we count starting at 0). It denotes the axis along which the matrix is sliced. Sadly, even yours truly sometimes does not get it right.

Exercise 8.1 Given the `nhanes_adult_female_bmx_2020`⁹⁴ dataset, compute the mean, standard deviation, minimum, and maximum of each body measurement.

We will get back to the topic of the aggregation of multidimensional data in Section 8.4.2 and Section 8.4.3.

⁹⁴ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/nhanes_adult_female_bmx_2020.csv

8.1.3 Arithmetic, Logical, and Comparison Operations

Recall that for vectors, binary operators such as `+`, `*`, `==`, `<=`, and `&` and similar elementwise functions (e.g., `numpy.minimum`) can be applied if both inputs are of the same length, for example:

```
np.array([1, 10, 100, 1000]) * np.array([7, -6, 2, 8])
## array([ 7, -60, 200, 8000])
```

Alternatively, one input can be a scalar:

```
np.array([1, 10, 100, 1000]) * -3
## array([-3, -30, -300, -3000])
```

More generally, a set of rules referred in the `numpy` manual to as *broadcasting*⁹⁵ describes how this package handles arrays of different shapes.

Important: Generally, for two matrices, their column/row numbers must match or be equal to 1. Also, if one operand is a 1-dimensional array, it will be promoted to a row vector.

Let us explore all the possible cases.

Matrix vs Scalar

If one operand is a scalar, then it is going to be propagated over all matrix elements, for example:

```
(-1)*A
## array([[-0.2, -0.6, -0.4, -0.4],
##        [-0. , -0.2, -0.4, -0.7],
##        [-0.8, -0.8, -0.2, -0.1]])
```

changes the sign of every element, which is, mathematically, an instance of multiplying a matrix \mathbf{X} by a scalar c

$$c\mathbf{X} = \begin{bmatrix} cx_{1,1} & cx_{1,2} & \cdots & cx_{1,m} \\ cx_{2,1} & cx_{2,2} & \cdots & cx_{2,m} \\ \vdots & \vdots & \ddots & \vdots \\ cx_{n,1} & cx_{n,2} & \cdots & cx_{n,m} \end{bmatrix}.$$

Furthermore:

⁹⁵ <https://numpy.org/devdocs/user/basics.broadcasting.html>

```
A**2
## array([[0.04, 0.36, 0.16, 0.16],
##        [0., 0.04, 0.16, 0.49],
##        [0.64, 0.64, 0.04, 0.01]])
```

takes the square of each element (this is not the same as matrix-multiply by itself which we cover in the matrix algebra section).

Also:

```
A >= 0.25
## array([[False, True, True, True],
##        [False, False, True, True],
##        [True, True, False, False]])
```

compares each element to 0.25.

Matrix vs Matrix

For two matrices of identical sizes, we will be acting on the corresponding elements:

```
B = np.tri(A.shape[0], A.shape[1]) # just an example
B # a lower triangular 0-1 matrix
## array([[1., 0., 0., 0.],
##        [1., 1., 0., 0.],
##        [1., 1., 1., 0.]])
```

And now:

```
A * B
## array([[0.2, 0., 0., 0.],
##        [0., 0.2, 0., 0.],
##        [0.8, 0.8, 0.2, 0.]])
```

multiples each $a_{i,j}$ by the corresponding $b_{i,j}$.

This extends on the idea from algebra that given **A**, **B** with n rows and m columns each, the result of + (or -) would be for instance:

$$\mathbf{A} + \mathbf{B} = \begin{bmatrix} a_{1,1} + b_{1,1} & a_{1,2} + b_{1,2} & \cdots & a_{1,m} + b_{1,m} \\ a_{2,1} + b_{2,1} & a_{2,2} + b_{1,2} & \cdots & a_{2,m} + b_{2,m} \\ \vdots & \vdots & \ddots & \vdots \\ a_{n,1} + b_{n,1} & a_{n,2} + b_{n,2} & \cdots & a_{n,m} + b_{n,m} \end{bmatrix}.$$

Thanks to the matrix-matrix and matrix-scalar operations we can perform various tests on an per-element basis, e.g.,

```
(A >= 0.25) & (A <= 0.75) # logical matrix & logical matrix
## array([[False,  True,  True,  True],
##        [False, False,  True,  True],
##        [False, False, False, False]])
```

Example 8.2 (*) Figure 8.1 depicts a (filled) contour plot of the Himmelblau's function, $f(x, y) = (x^2 + y - 11)^2 + (x + y^2 - 7)^2$, for $x \in [-5, 5]$ and $y \in [-4, 4]$. In order to draw it, we have probed 250 points from the two said ranges and called `numpy.meshgrid` to generate two matrices, both of shape 250 by 250, giving the x - and y -coordinates of all the points on the corresponding a two-dimensional grid. Thanks to this, we were able to use vectorised mathematical operations to compute the values off thereon.

```
x = np.linspace(-5, 5, 250)
y = np.linspace(-4, 4, 250)
xg, yg = np.meshgrid(x, y)
z = (xg**2 + yg - 11)**2 + (xg + yg**2 - 7)**2
plt.contourf(x, y, z, levels=20)
CS = plt.contour(x, y, z, levels=[1, 5, 10, 20, 50, 100, 150, 200, 250])
plt.clabel(CS, colors="black")
plt.show()
```

In order to understand the result generated by `numpy.meshgrid` better here are the outputs generated by it for a smaller number of probe points:

```
x = np.linspace(-5, 5, 3)
y = np.linspace(-4, 4, 5)
xg, yg = np.meshgrid(x, y)
xg
## array([[-5.,  0.,  5.],
##        [-5.,  0.,  5.],
##        [-5.,  0.,  5.],
##        [-5.,  0.,  5.],
##        [-5.,  0.,  5.]])
```

Here, each column is the same.

```
yg
## array([[-4., -4., -4.],
##        [-2., -2., -2.],
```

(continues on next page)

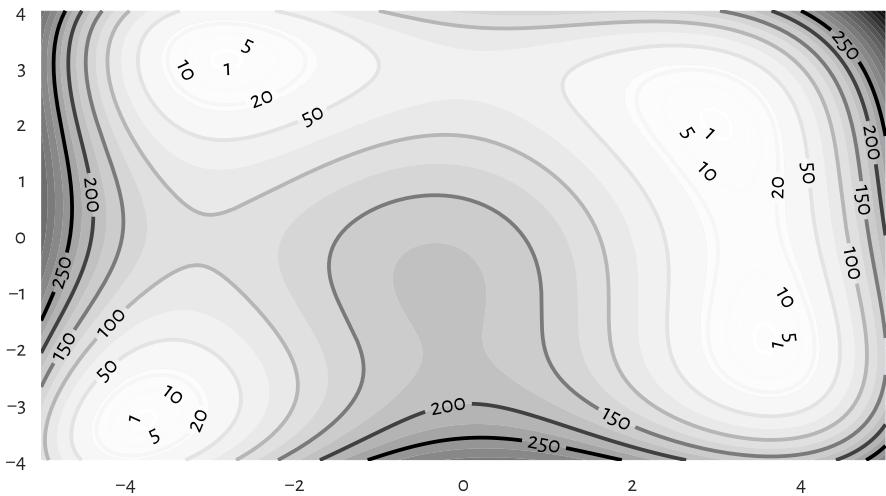


Figure 8.1: An example filled contour plot with additional labelled contour lines

(continued from previous page)

```
##      [,1] [,2] [,3]
## [1,]    0.   0.   0.
## [2,]    2.   2.   2.
## [3,]    4.   4.   4.]])
```

In this case, each row is identical. Thanks to this, calling:

```
(xg**2 + yg - 11)**2 + (xg + yg**2 - 7)**2
## array([[116., 306., 296.],
##        [208., 178., 148.],
##        [340., 170., 200.],
##        [320., 90., 260.],
##        [340., 130., 520.]])
```

gives a matrix \mathbf{Z} such that $z_{i,j}$ is generated by considering the i -th element in y and the j -th item in x , which is exactly what we have desired.

Matrix vs Any Vector

An $n \times m$ matrix can also be combined with an $n \times 1$ column vector:

```
A * np.array([1, 10, 100]).reshape(-1, 1)
## array([[ 0.2,  0.6,  0.4,  0.4],
##        [ 0. ,  2. ,  4. ,  7. ],
##        [80. ,  80. ,  20. ,  10. ]])
```

The above propagated the column vector over all columns (left to right).

Similarly, combining with an $1 \times m$ row vector:

```
A + np.array([1, 2, 3, 4]).reshape(1, -1)
## array([[1.2, 2.6, 3.4, 4.4],
##        [1. , 2.2, 3.4, 4.7],
##        [1.8, 2.8, 3.2, 4.1]])
```

recycles the row vector over all rows (top to bottom).

If one operand is a 1-dimensional array or a list of length m , it will be treated as a row vector.

```
np.round(A - np.mean(A, axis=0), 3)
## array([[-0.133,  0.067,  0.067, -0.    ],
##        [-0.333, -0.333,  0.067,  0.3   ],
##        [ 0.467,  0.267, -0.133, -0.3  ]])
```

This resulted in each column mean's being 0. An explicit `.reshape(1, -1)` was not necessary.

Mathematically, although it is not necessarily a standard notation, we will allow adding and subtracting row vectors from matrices of compatible sizes:

$$\mathbf{X} + \mathbf{t} = \begin{bmatrix} x_{1,1} + t_1 & x_{1,2} + t_2 & \dots & x_{1,m} + t_m \\ x_{2,1} + t_1 & x_{2,2} + t_2 & \dots & x_{2,m} + t_m \\ \vdots & \vdots & \ddots & \vdots \\ x_{n,1} + t_1 & x_{n,2} + t_2 & \dots & x_{n,m} + t_m \end{bmatrix}.$$

This corresponds to shifting (translating) every row in the matrix.

However, subtracting the row means already requires some extra labour:

```
A - np.mean(A, axis=1).reshape(-1, 1)
## array([[-0.2 ,  0.2 ,  0. ,  0.  ],
##        [-0.325, -0.125,  0.075,  0.375],
##        [ 0.325,  0.325, -0.275, -0.375]])
```

Note that `A - np.mean(A, axis=1)` would raise an exception.

Exercise 8.3 Standardise, normalise, and min-maxscale each column in the `nhanes_adult_female_bmx.csv`⁹⁶ dataset using a single line of code.

Row Vector vs Column Vector (*)

As a bonus, let us quickly mention that a row vector combined with a column vector results in an operation's being performed on each *combination of all* pairs of elements in the two arrays (i.e., the cross-product; not just the *corresponding* pairs).

```
np.arange(1, 8).reshape(1, -1) * np.array([1, 10, 100]).reshape(-1, 1)
## array([[ 1,   2,   3,   4,   5,   6,   7],
##        [ 10,  20,  30,  40,  50,  60,  70],
##        [100, 200, 300, 400, 500, 600, 700]])
```

Exercise 8.4 Check out that `numpy.nonzero` relies on similar shape broadcasting rules as the binary operators we have discussed here, however, not with regards to all the 3 arguments.

Example 8.5 Himmelblau's function in [Figure 8.1](#) is only defined by means of arithmetic operators, which all accept the kind of shape broadcasting that we discuss in this section. Therefore, calling `numpy.meshgrid` in that example was actually not necessary in order to evaluate f on a grid of points:

```
x = np.linspace(-5, 5, 3)
y = np.linspace(-4, 4, 5)
xg = x.reshape(1, -1)
yg = y.reshape(-1, 1)
(xg**2 + yg - 11)**2 + (xg + yg**2 - 7)**2
## array([[116., 306., 296.],
##        [208., 178., 148.],
##        [340., 170., 200.],
##        [320., 90., 260.],
##        [340., 130., 520.]])
```

See also the `sparse` parameter in `numpy.meshgrid` and [Figure 12.9](#) where this function turns out useful after all.

⁹⁶ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/nhanes_adult_female_bmx_2020.csv

8.1.4 Other Row and Column Transforms (*)

Some functions that we have already discussed in the previous part of this course are equipped with the `axis` argument, which allows to process each row or column independently, for example:

```
np.sort(A, axis=1)
## array([[0.2, 0.4, 0.4, 0.6],
##        [0. , 0.2, 0.4, 0.7],
##        [0.1, 0.2, 0.8, 0.8]])
```

sorts every row (separately). Moreover:

```
scipy.stats.rankdata(A, axis=0)
## array([[2. , 2. , 2.5, 2. ],
##        [1. , 1. , 2.5, 3. ],
##        [3. , 3. , 1. , 1. ]])
```

computes the ranks of elements in each column.

Also note that a few functions have the default argument `axis=-1`, which means that they are applied along the last (i.e., columns in the matrix case) axis:

```
np.diff(A) # axis=1 here
## array([[ 0.4, -0.2,  0. ],
##        [ 0.2,  0.2,  0.3],
##        [ 0. , -0.6, -0.1]])
```

However, the aforementioned `numpy.mean` is amongst the many exceptions to this rule.

Compare the above with:

```
np.diff(A, axis=0)
## array([[-0.2, -0.4,  0. ,  0.3],
##        [ 0.8,  0.6, -0.2, -0.6]])
```

which gives the iterated differences for each column separately (along the rows).

If a function (built-in or custom) is not equipped with the `axis` argument and – instead – it was designed to work with individual vectors, we can propagate it over all the rows or columns by calling `numpy.apply_along_axis`.

For instance, here is another (have we solved the suggested exercise?) way to compute the column z-scores:

```
def standardise(x):
    return (x-np.mean(x))/np.std(x)

np.round(np.apply_along_axis(standardise, 0, A), 2)
## array([[-0.39,  0.27,  0.71, -0.  ],
##        [-0.98, -1.34,  0.71,  1.22],
##        [ 1.37,  1.07, -1.41, -1.22]])
```

Note: (*) Matrices are of course iterable (in the sense of [Section 3.4](#)), but in an interesting way. Namely, an iterator traverses through each row in a matrix. Therefore, for example, writing

```
r1, r2, r3 = A # A has 3 rows
```

creates three variables, each representing a separate row in `A`, second of which being

```
r2
## array([0. , 0.2, 0.4, 0.7])
```

8.2 Matrix Indexing

Recall that for 1-dimensional arrays we have four possible choices of indexers (i.e., where performing filtering like `x[i]`):

- scalar (extracts a single element),
- slice (selects a regular subsequence, e.g., every 2nd element or the first 6 items; returns a view on existing data – it does not make an independent copy of the subsetted elements),
- integer vector (selects elements at given indices),
- logical vector (select elements that correspond to `True` in the indexer).

Matrices are two-dimensional arrays, and hence subsetting thereof will require two indexes: we will thus be writing `A[i, j]` to select rows given by `i` and columns given by `j`.

Both *i* and *j* can be one of the four above types, so we at least 10 different cases to consider (skipping the symmetric ones).

Important: Generally:

- each scalar indexer reduces the dimensionality of the subsetted object by 1;
 - slice-slice and slice-scalar indexing returns a view on the existing array, so we need to be careful when modifying the resulting object;
 - usually, indexing returns a submatrix (subblock), which is a combination of elements at given rows and columns, but two flat-vector indexers are vectorised elementwisely instead;
 - indexing with two integer or logical vectors at the same time should be avoided.
-

Let us look at all the possible scenarios in greater detail.

8.2.1 Slice-Based Indexing

Our favourite example matrix again:

```
A = np.array([
    [0.2, 0.6, 0.4, 0.4],
    [0.0, 0.2, 0.4, 0.7],
    [0.8, 0.8, 0.2, 0.1]
])
```

Indexing based on two slices selects a submatrix:

```
A[::2, 3:]
## array([[0.4],
##         [0.1]])
```

gives every second row and skips first three columns. Note that the result is still a matrix.

An empty slice selects all elements on the corresponding axis, therefore:

```
A[:, ::-1] # all rows, reversed columns
## array([[0.4, 0.4, 0.6, 0.2],
##        [0.7, 0.4, 0.2, 0. ],
##        [0.1, 0.2, 0.8, 0.8]])
```

simply reverses the order of columns.

8.2.2 Scalar-Based Indexing

Indexing by a scalar selects a given row or column, reducing the dimensionality of the output object.

```
A[1, :]
## array([0., 0.2, 0.4, 0.7])
```

selects the 2nd row and gives a flat vector.

```
A[0, -1]
## 0.4
```

yields the element in the first row and last column.

However, we can always use the `reshape` method to convert the resulting object back to a matrix.

8.2.3 Mixed Boolean/Integer Vector and Scalar/Slice Indexers

A logical and integer vector-like object can also be used for element selection. If the other indexer is a slice or a scalar, the result is quite predictable, for instance:

```
A[ [0, -1, 0], ::-1 ]
## array([[0.4, 0.4, 0.6, 0.2],
##        [0.1, 0.2, 0.8, 0.8],
##        [0.4, 0.4, 0.6, 0.2]])
```

selects the first, the last, and the first row again and reverses the order of columns.

```
A[ A[:, 0] > 0.1, : ]
## array([[0.2, 0.6, 0.4, 0.4],
##        [0.8, 0.8, 0.2, 0.1]])
```

selects rows such that in the first column the values are greater than 0.1.

```
A[np.mean(A, axis=1) > 0.35, :]
## array([[0.2, 0.6, 0.4, 0.4],
##        [0.8, 0.8, 0.2, 0.1]])
```

selects the rows whose mean is greater than 0.35.

```
A[np.argsort(A[:, 0]), :]
## array([[0., 0.2, 0.4, 0.7],
##        [0.2, 0.6, 0.4, 0.4],
##        [0.8, 0.8, 0.2, 0.1]])
```

orders the matrix with respect to the values in the first row (all rows permuted in the same way, together).

Exercise 8.6 In the `nhanes_adult_female_bmx_2020`⁹⁷ dataset, select all the participants whose heights is within their mean ± 2 standard deviations.

8.2.4 Two Vectors as Indexers (*)

With two vectors (logical or integer) things are a tad more horrible, as in this case not only some form *shape broadcasting* comes into play but also all the headache-inducing exceptions listed in the perhaps not the most clearly written Advanced Indexing⁹⁸ section of the `numpy` manual. Cheer up, however, things in `pandas` are much worse (see Section 10.5).

For the sake of our maintaining sanity, in practice it is best to stick only to the scenarios below and be extra careful when using two vector indexers.

For two flat integer indexers, we pick elementwisely:

```
A[ [0, -1, 0, 2, 0], [1, 2, 0, 2, 1] ]
## array([0.6, 0.2, 0.2, 0.2, 0.6])
```

yields `A[0, 1]`, `A[-1, 2]`, `A[0, 0]`, `A[2, 2]`, and `A[0, 1]`.

In order to select a submatrix using integer indexes, it is best to make sure that the first indexer is a column vector, and the second is a row vector (or some object like the two said ones, e.g., compatible lists of lists). Further, if indexing involves logical vectors, it is best to convert them to integer ones first (e.g., by calling `numpy.nonzero`).

The above transformations can be done automatically via the `numpy.ix_` function, which is always the safest choice:

```
A[ np.ix_(np.mean(A, axis=1) > 0.35, [0, 2, 3, 0]) ]
## array([[0.2, 0.4, 0.4, 0.2],
##        [0.8, 0.2, 0.1, 0.8]])
```

⁹⁷ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/nhanes_adult_female_bmx_2020.csv

⁹⁸ <https://numpy.org/doc/stable/user/basics.indexing.html>

Alternatively, we can always apply indexing twice instead (which we will anyway be forced to do in `pandas` whenever selecting rows by number and columns by names is required).

```
A[np.mean(A, axis=1) > 0.45, :][:, [0, 2, 3, 0]]
## array([[0.8, 0.2, 0.1, 0.8]])
```

8.2.5 Views on Existing Arrays (*)

Only indexing involving two slices or a slice and a scalar returns a `view`⁹⁹ on an existing array.

For example:

```
B = A[:, ::2]
B
## array([[0.2, 0.4],
##         [0., 0.4],
##         [0.8, 0.2]])
```

Now `B` and `A` share memory. Therefore, by modifying `B` in-place, e.g.,

```
B *= -1
```

the changes will be visible in `A` as well:

```
A
## array([[-0.2, 0.6, -0.4, 0.4],
##        [-0., 0.2, -0.4, 0.7],
##        [-0.8, 0.8, -0.2, 0.1]])
```

This is time and memory efficient, but might lead to some unexpected results if we are not focused enough. We have been warned.

8.2.6 Adding and Modifying Rows or Columns

With slice/scalar-based indexers, rows/columns/individual elements can be replaced by new content in a natural way:

⁹⁹ <https://numpy.org/devdocs/user/basics.copies.html>

```
A[:, 0] = A[:, 0]**2
```

With **numpy** arrays, however, brand new rows or columns cannot be added using the index operator. Instead, the whole array needs to be created from scratch using, for example, one of the functions discussed in [Section 7.1.4](#).

Here is an example where we add a new column to the `A` matrix being a function of the first column:

```
A = np.column_stack((A, np.sqrt(A[:, 0])))
A
## array([[ 0.04,  0.6 , -0.4 ,  0.4 ,  0.2 ],
##        [ 0. ,  0.2 , -0.4 ,  0.7 ,  0. ],
##        [ 0.64,  0.8 , -0.2 ,  0.1 ,  0.8 ]])
```

8.3 Matrix Multiplication, Dot Products, and the Euclidean Norm

Matrix algebra is at the core of most methods used in data analysis and matrix multiply is one of the most fundamental operations therein (e.g., [\[\[DFO20\]\]](#), [\[Gen17\]](#)).

Given $\mathbf{A} \in \mathbb{R}^{n \times p}$ and $\mathbf{B} \in \mathbb{R}^{p \times m}$, their *multiply* is a matrix $\mathbf{C} = \mathbf{AB} \in \mathbb{R}^{n \times m}$ such that $c_{i,j}$ is the sum of the i -th row in \mathbf{A} and the j -th column in \mathbf{B} multiplied elementwisely:

$$c_{i,j} = a_{i,1}b_{1,j} + a_{i,2}b_{2,j} + \cdots + a_{i,p}b_{p,j} = \sum_{k=1}^p a_{i,k}b_{k,j}$$

for $i = 1, \dots, n$ and $j = 1, \dots, m$.

For example:

```
A = np.array([
    [1, 0, 1],
    [2, 2, 1],
    [3, 2, 0],
    [1, 2, 3],
    [0, 0, 1],
])
B = np.array([
```

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```
[1, -1, 0, 0],
[0, 4, 1, 3],
[2, 0, 3, 1],
])
C = A @ B # or: A.dot(B)
C
## array([[ 3, -1,  3,  1],
##        [ 4,  6,  5,  7],
##        [ 3,  5,  2,  6],
##        [ 7,  7, 11,  9],
##        [ 2,  0,  3,  1]])
```

Mathematically, we can write the above as:

$$\begin{bmatrix} 1 & 0 & 1 \\ 2 & 2 & 1 \\ 3 & 2 & 0 \\ \textcolor{red}{1} & \textcolor{red}{2} & \textcolor{red}{3} \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} 1 & -1 & \textcolor{red}{0} & 0 \\ 0 & 4 & \textcolor{red}{1} & 3 \\ 2 & 0 & \textcolor{red}{3} & 1 \end{bmatrix} = \begin{bmatrix} 3 & -1 & 3 & 1 \\ 4 & 6 & 5 & 7 \\ 3 & 5 & 2 & 6 \\ 7 & 7 & \textcolor{red}{11} & 9 \\ 2 & 0 & 3 & 1 \end{bmatrix}.$$

For example, the element in the 4th row and 3rd column, $c_{4,3}$ takes the 4th row in the left matrix $\mathbf{a}_{4,\cdot} = [1\ 2\ 3]$ and the 3rd column in the right matrix $\mathbf{b}_{\cdot,3} = [0\ 1\ 3]^T$ (they are marked in red), multiplies the corresponding elements and computes their sum, i.e., $c_{4,3} = 1 \cdot 0 + 2 \cdot 1 + 3 \cdot 3 = 11$.

Important: Matrix multiplication can only be performed on two matrices of *compatible* sizes – the number of columns in the left matrix must match the number of rows in the right operand.

Another example:

```
A = np.array([
    [1, 2],
    [3, 4]
])
I = np.array([
    [1, 0],
    [0, 1]
])
```

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```
A @ I # or A.dot(I)
## array([[1, 2],
##         [3, 4]])
```

We matrix-multiplied **A** by the identity matrix **I**, which is a neutral element of the said operation, and hence the result is identical to **A**.

Important: In most textbooks, just like in this one, **AB** almost always denotes the matrix multiplication which is a very different operation to the elementwise multiplication.

Compare the above to:

```
A * I # elementwise multiplication
## array([[1, 0],
##         [0, 4]])
```

Exercise 8.7 Show that $\mathbf{A}^T \mathbf{A}$ gives the matrix that consists of the dot products of all the pairs of columns in **A** and $\mathbf{A} \mathbf{A}^T$ stores the dot products of all the pairs of rows.

Exercise 8.8 (*) Show that $(\mathbf{AB})^T = \mathbf{B}^T \mathbf{A}^T$. Also note that, typically, matrix multiplication is not commutative.

Note: Matrix multiplication gives a convenient means for denoting sums of products of corresponding elements in many pairs of vectors, which we refer to as dot products.

Given two vectors $\mathbf{x}, \mathbf{y} \in \mathbb{R}^p$, their *dot (or scalar) product* is given by

$$\mathbf{x} \cdot \mathbf{y} = \sum_{i=1}^p x_i y_i.$$

Thus, in matrix multiplication terms, if \mathbf{x} is a row vector and \mathbf{y}^T is a column vector, then the above can be written as \mathbf{xy}^T . Note that the result is a single number.

In particular, a dot product of a vector and itself,

$$\mathbf{x} \cdot \mathbf{x} = \sum_{i=1}^p x_i^2,$$

is the square of the Euclidean norm of \mathbf{x} , which – as we have said in [Section 5.3.2](#) – we

use to measure the *length* of a vector,

$$\|\mathbf{x}\| = \sqrt{\sum_{i=1}^p x_i^2} = \sqrt{\mathbf{x} \cdot \mathbf{x}} = \sqrt{\mathbf{x} \mathbf{x}^T}.$$

The Euclidean norm fulfils (amongst others) the condition that $\|\mathbf{x}\| = 0$ if and only if $\mathbf{x} = 0 = (0, 0, \dots, 0)$. The same of course holds for its square.

Note: To avoid notation clutter, we will often be implicitly promoting vectors like $\mathbf{x} = (x_1, \dots, x_p)$ to row vectors $\mathbf{x} = [x_1 \dots x_p]$, because this is the behaviour that `numpy` uses¹⁰⁰.

In Section 9.3.2 we will see that matrix multiplication can be used as a way to express certain geometrical transformations of points in a dataset, e.g., scaling and rotating.

Also, in Section 9.3.3 we briefly discuss the concept of the inverse of a matrix and in Section 9.3.4 its singular value decomposition.

8.4 Pairwise Distances and Related Methods

Many data analysis methods rely on the notion of *distances* between points, which quantify the extent to which two points (e.g., two rows in a matrix) are different from each other. Here we will be dealing with the most natural distance called the Euclidean metric. We know it from school, where we measured how two points are far away from each other with a ruler.

8.4.1 The Euclidean Metric

Given two vectors of length m , $\mathbf{u} = (u_1, \dots, u_m)$ and $\mathbf{v} = (v_1, \dots, v_m)$, the *Euclidean metric* is defined in terms of the corresponding Euclidean norm

$$\|\mathbf{u} - \mathbf{v}\| = \sqrt{(u_1 - v_1)^2 + (u_2 - v_2)^2 + \dots + (u_m - v_m)^2} = \sqrt{\sum_{i=1}^m (u_i - v_i)^2},$$

that is, it is the square root of the sum of squared differences between the corresponding vector components.

¹⁰⁰ However, some textbooks assume that all vectors are column vectors; in such a case, they would define the Euclidean norm as $\|\mathbf{x}\| = \sqrt{\mathbf{x}^T \mathbf{x}}$.

Exercise 8.9 Consider the following matrix $\mathbf{X} \in \mathbb{R}^{4 \times 2}$:

$$\mathbf{X} = \begin{bmatrix} 0 & 0 \\ 1 & 0 \\ -\frac{3}{2} & 1 \\ 1 & 1 \end{bmatrix}.$$

Calculate (by hand) $\|\mathbf{x}_{1,:} - \mathbf{x}_{2,:}\|$, $\|\mathbf{x}_{1,:} - \mathbf{x}_{3,:}\|$, $\|\mathbf{x}_{1,:} - \mathbf{x}_{4,:}\|$, $\|\mathbf{x}_{2,:} - \mathbf{x}_{4,:}\|$, $\|\mathbf{x}_{2,:} - \mathbf{x}_{3,:}\|$, $\|\mathbf{x}_{1,:} - \mathbf{x}_{1,:}\|$, and $\|\mathbf{x}_{2,:} - \mathbf{x}_{1,:}\|$.

Important: Note that for unidimensional data ($m = 1$) we have $\|u - v\| = |u - v|$.

The distances between all the pairs of rows in two matrices $\mathbf{X} \in \mathbb{R}^{n \times m}$ and $\mathbf{Y} \in \mathbb{R}^{k \times m}$ can be computed by calling `scipy.spatial.distance.cdist`. We need to be careful, though, because they result in a distance matrix of size $n \times k$, which can become quite large (e.g., for $n = k = 100000$ we would need ca. 80 GB of RAM to store it).

Here are the distances between all the pairs of points in the same dataset.

```
x = np.array([
    [0, 0],
    [1, 0],
    [-1.5, 1],
    [1, 1]
])
import scipy.spatial.distance
D = scipy.spatial.distance.cdist(x, x)
D
## array([[0.          , 1.          , 1.80277564, 1.41421356],
##        [1.          , 0.          , 2.6925824 , 1.          ],
##        [1.80277564, 2.6925824 , 0.          , 2.5         ],
##        [1.41421356, 1.          , 2.5         , 0.          ]])
```

Hence, $d_{i,j} = \|\mathbf{x}_{i,:} - \mathbf{x}_{j,:}\|$. That we have zeros on the diagonal is due to the fact that $\|u - v\| = 0$ if and only if $u = v$. Furthermore, $\|u - v\| = \|v - u\|$, which implies the symmetry of \mathbf{D} .

Figure 8.2 illustrates all the non-trivial pairwise distances. Note that our perception of distance is disturbed because of the aspect ratio (the ratio between the range of the x-axis to the range of the y-axis) is not 1:1. This is why it is very important, when judging spatial relationships between the points, to call `matplotlib.pyplot.axis("equal")` or set the axis limits manually (which is left as an exercise).

```
plt.plot(X[:, 0], X[:, 1], "ko")
for i in range(X.shape[0]-1):
    for j in range(i+1, X.shape[0]):
        plt.plot(X[[i,j], 0], X[[i,j], 1], "k-", alpha=0.2)
        plt.text(np.mean(X[[i,j], 0]), np.mean(X[[i,j], 1]), np.round(D[i, j], 2))
plt.show()
```

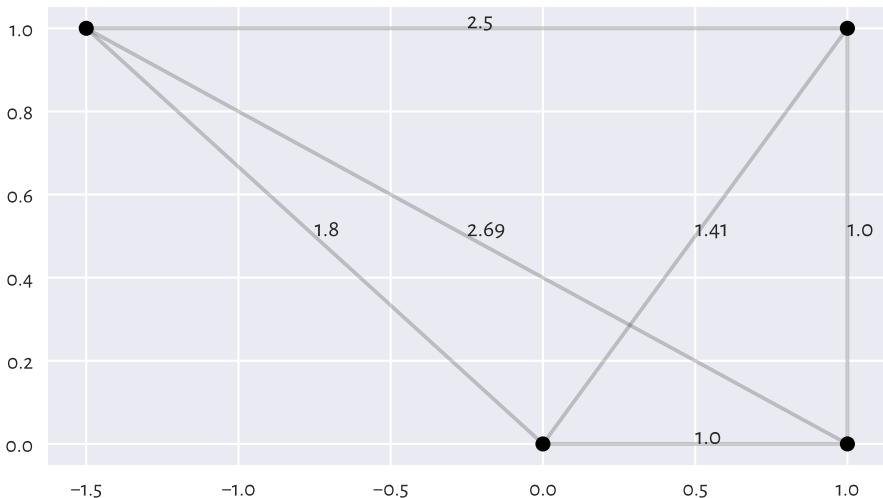


Figure 8.2: Distances between four example points. Their perception is disturbed because the aspect ratio is not 1:1

Note: There are many possible distances, allowing to measure the similarity of points not only in \mathbb{R}^m , but also character strings (e.g., the Levenshtein metric), ratings (e.g., cosine dissimilarity), etc.; there is even an encyclopedia of distances [[DD14]].

Important: There are many techniques in data science that rely on computing pairwise distances, including, but not limited to:

- multidimensional data aggregation (see below),
- k -means clustering (Section 12.4),

- k -nearest neighbour regression (Section 9.2.1) and classification (Section 12.3.1),
- density estimation (which we can use outlier detection, see Section 15.4),
- missing value imputation (Section 15.1).

In the sequel, whenever we apply them, we will be assuming that data have been appropriately preprocessed, in particular that columns are on the same scale (e.g., are standardised). Otherwise, computing their sums of squared differences might not make sense at all.

Note: Given two vectors of equal lengths $\mathbf{x}, \mathbf{y} \in \mathbb{R}^p$, the dot product of their difference,

$$(\mathbf{x} - \mathbf{y}) \cdot (\mathbf{x} - \mathbf{y}) = (\mathbf{x} - \mathbf{y})(\mathbf{x} - \mathbf{y})^T = \sum_{i=1}^p (x_i - y_i)^2$$

is nothing else than the square of the Euclidean distance between them.

8.4.2 Centroids

So far we have only been discussing ways to aggregate unidimensional data (for instance, each matrix column separately). It turns out that some summaries can be generalised to the multidimensional case.

For instance, it can be shown that the arithmetic mean of a vector (x_1, \dots, x_n) is a point c that minimises the sum of the *squared* 1-dimensional distances between itself and all the x_i s, i.e., $\sum_{i=1}^n \|x_i - c\|^2 = \sum_{i=1}^n (x_i - c)^2$.

Thus, we can define the *centroid* of a dataset $\mathbf{X} \in \mathbb{R}^{n \times m}$ as the point $\mathbf{c} \in \mathbb{R}^m$ to which the overall *squared* distance is the smallest

$$\text{minimise } \sum_{i=1}^n \|\mathbf{x}_{i,\cdot} - \mathbf{c}\|^2 \quad \text{w.r.t. } \mathbf{c}.$$

It can be shown that the solution to the above is

$$\mathbf{c} = \frac{1}{n} (\mathbf{x}_{1,\cdot} + \mathbf{x}_{2,\cdot} + \dots + \mathbf{x}_{n,\cdot}) = \frac{1}{n} \sum_{i=1}^n \mathbf{x}_{i,\cdot}$$

which is the componentwise arithmetic mean, i.e., its j component is

$$c_j = \frac{1}{n} \sum_{i=1}^n x_{i,j}.$$

For instance, the centroid of the above dataset is:

```
c = np.mean(X, axis=0)
c
## array([0.125, 0.5])
```

Centroids are, amongst others, a basis for the k -means clustering method that we discuss in Section 12.4.

8.4.3 Multidimensional Dispersion and Other Aggregates

Furthermore, as a measure of multidimensional dispersion, we can consider the natural generalisation of the standard deviation,

$$s = \sqrt{\frac{1}{n} \sum_{i=1}^n \|\mathbf{x}_{i,\cdot} - \mathbf{c}\|^2},$$

being the square root of the average squared distance to the centroid. Note that it is a single number.

```
np.sqrt(np.mean(scipy.spatial.distance.cdist(X, c.reshape(1, -1))**2))
## 1.1388041973930374
```

Note: (***) Generalising other aggregation functions is not a trivial task, because, amongst others, there is no natural linear ordering relation in the multidimensional space (see, e.g., [[PFBG19]]). For instance, any point on the convex hull of a dataset could serve as the analogue of the minimal and maximal observation. Furthermore, the componentwise median does not behave nicely (it may, for example, fall outside the convex hull). Thus, instead, we usually consider a different generalisation of the median being the point that minimises the sum of distances (not squared), $\sum_{i=1}^n \|\mathbf{x}_{i,\cdot} - \mathbf{c}\|$; sadly, it does not have an analytic solution (can be determined algorithmically).

Note: (***) A bag plot [[RT99]] is one of the possible multidimensional generalisations of the box-and-whisker plot. Unfortunately, its use is quite limited due its low popularity amongst practitioners.

8.4.4 Fixed-Radius and K-Nearest Neighbour Search

A number of data analysis techniques relies upon aggregating information about what is happening in the *local neighbourhoods* of the points. Let $\mathbf{X} \in \mathbb{R}^{n \times m}$ be a dataset and $\mathbf{y} \in \mathbb{R}^m$ be some point, not necessarily from \mathbf{X} . We basically have two options:

- *fixed-radius search*: for some radius $r > 0$, we seek the indices of all the points in \mathbf{X} whose distance to \mathbf{y} is not greater than r

$$B_r(\mathbf{y}) = \{i : \|\mathbf{x}_{i,\cdot} - \mathbf{y}\| \leq r\};$$

- *few nearest-neighbour search*: for some (usually small) integer $k \geq 1$, we seek the indices of the k points in \mathbf{X} which are the closest to \mathbf{y}

$$N_k(\mathbf{y}) = \{i_1, i_2, \dots, i_k\}$$

such that for all $j \notin \{i_1, \dots, i_k\}$

$$\|\mathbf{x}_{i_1,\cdot} - \mathbf{y}\| \leq \|\mathbf{x}_{i_2,\cdot} - \mathbf{y}\| \leq \dots \leq \|\mathbf{x}_{i_k,\cdot} - \mathbf{y}\| \leq \|\mathbf{x}_{j,\cdot} - \mathbf{y}\|.$$

Important: In \mathbb{R}^1 , $B_r(\mathbf{y})$ is an interval of length $2r$ centred at \mathbf{y} , i.e., $[y_1 - r, y_1 + r]$. In \mathbb{R}^2 , $B_r(\mathbf{y})$ is a circle of radius r centred at (y_1, y_2) . More generally, we call $B_r(\mathbf{y})$ an m -dimensional (Euclidean) ball or a solid hypersphere.

Here is an example dataset, consisting of some randomly generated points (see figure below).

```
np.random.seed(777)
X = np.random.randn(25, 2)
y = np.array([0, 0])
```

Local neighbourhoods can of course be determined by computing the distances between each point in \mathbf{X} and \mathbf{y} .

```
import scipy.spatial.distance
D = scipy.spatial.distance.cdist(X, y.reshape(1, -1))
```

For instance, here are the indices of the points in $B_{0.75}(\mathbf{y})$:

```
r = 0.75
B = np.flatnonzero(D <= r)
B
## array([ 1, 11, 14, 16, 24])
```

And here are the 11 nearest neighbours:

```
k = 11
N = np.argsort(D.reshape(-1))[::k]
N
## array([14, 24, 16, 11, 1, 22, 7, 19, 0, 9, 15])
```

See [Figure 8.3](#) for an illustration (note that the aspect ratio is set to 1:1 as otherwise the circle would look like an ellipse).

```
fig, ax = plt.subplots()
ax.add_patch(plt.Circle(y, r, color="red", alpha=0.1))
for i in range(k):
    plt.plot([y[0], X[N[i], 0]], [y[1], X[N[i], 1]], "r:", alpha=0.4)
plt.plot(X[:, 0], X[:, 1], "bo", alpha=0.1)
for i in range(X.shape[0]):
    plt.text(X[i, 0], X[i, 1], str(i), va="center", ha="center")
plt.plot(y[0], y[1], "rX")
plt.text(y[0], y[1], "$\\mathbf{y}$", va="center", ha="center")
plt.axis("equal")
plt.show()
```

8.4.5 Spatial Search with K-d Trees

For efficiency reasons, it is better to rely on dedicated spatial search data structures, especially if we have a large number of neighbourhood-related queries. `scipy` implements such a search algorithm based on the so-called K -dimensional trees (K -d trees; in our context, we should prefer referring to them as m -d trees, but let us stick with the traditional name).

Note: (*) In K -d trees, the data space is partitioned into hyperrectangles along the axes of the Cartesian coordinate system (standard basis). Thanks to such a representation, all subareas which are too far from the point of interest can be pruned to speed up the search.

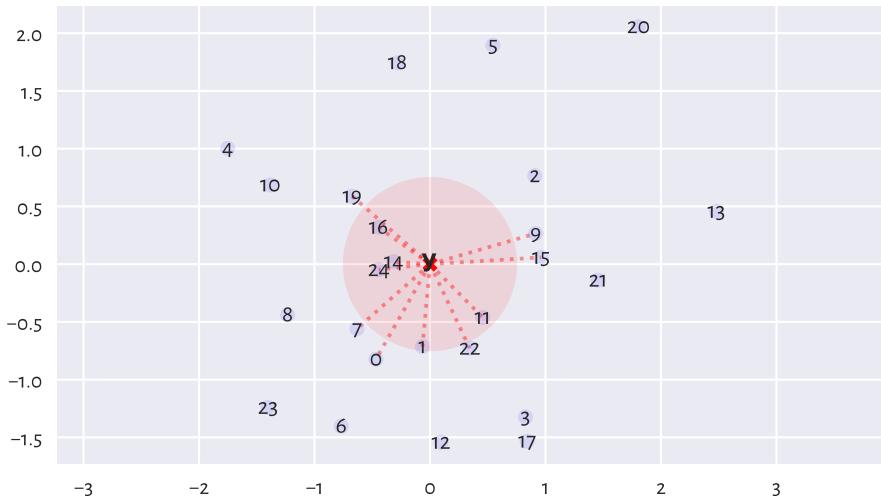


Figure 8.3: Fixed-radius vs few-nearest neighbour search

Let us create the data structure for searching within the above \mathbf{X} matrix.

```
import scipy.spatial
T = scipy.spatial.KDTree(X)
```

Assume we would like to make queries with regards to the 3 following pivot points.

```
Y = np.array([
    [0, 0],
    [2, 2],
    [2, -2]
])
```

Here are the results for the fixed radius searches:

```
T.query_ball_point(Y, r) # r was defined above
## array([list([1, 11, 14, 16, 24]), list([20]), list([])], dtype=object)
```

We see that the search was nicely vectorised; we have made a query about many points all at the same time. In result, we received a list-like object storing three lists representing the resulting indices, each for a different input point. Note that in the case of the 3rd

point, there are no elements in \mathbf{X} within the range (ball) of interest, hence the empty index list.

And here are the nearest neighbours:

```
T.query(Y, k) # k was defined above
## (array([[0.31457701, 0.44600012, 0.54848109, 0.64875661, 0.71635172,
##          0.80435675, 0.84401121, 0.89488218, 0.94671021, 0.95240875,
##          0.96257142],
##         [0.20356263, 1.45896222, 1.61587605, 1.64870864, 2.04640408,
##          2.2021443 , 2.20687238, 2.29585085, 2.90551519, 2.9678564 ,
##          3.02393202],
##         [1.2494805 , 1.35482619, 1.93984334, 1.95938464, 2.08926502,
##          2.17968448, 2.30592773, 2.43335828, 2.50319585, 2.51159254,
##          2.7345559 ]]), array([[14, 24, 16, 11, 1, 22, 7, 19, 0, 9, 15],
##          [20, 5, 13, 2, 9, 15, 21, 18, 11, 16, 19],
##          [17, 3, 21, 12, 22, 11, 15, 1, 13, 9, 0]]))
```

We obtained both the distances to the nearest neighbours as well as the indices, in the form of two separate matrices with 3 rows (corresponding to the number of pivot points) and 11 columns (the number of neighbours sought for).

Note: (***) We expect the K -d trees to be much faster than the brute-force approach (where we compute all pairwise distances) in low-dimensional spaces. However, due to the phenomenon called the *curse of dimensionality*, sometimes already for $m \geq 5$ the speed gains might be very small.

8.5 Exercises

Exercise 8.10 Does `numpy.mean(A, axis=0)` compute rowwise or columnwise means?

Exercise 8.11 How does shape broadcasting work? List the most common pairs of shape cases when performing arithmetic operations.

Exercise 8.12 What are the possible matrix indexing schemes and how do they behave?

Exercise 8.13 Which kinds of matrix indexers return a view on an existing array?

Exercise 8.14 (*) How to select a submatrix comprised of the first and the last row and the first and the last column?

Exercise 8.15 Why appropriate data preprocessing is required when computing the Euclidean distance between points?

Exercise 8.16 What is the relationship between the dot product, the Euclidean norm, and the Euclidean distance?

Exercise 8.17 What is a centroid? How is it defined by means of the Euclidean distance between the points in a dataset?

Exercise 8.18 When K-d trees or other spatial search data structures might be better than a brute-force search with `scipy.spatial.distance.cdist`?

Exploring Relationships Between Variables

Let's consider the National Health and Nutrition Examination Survey (NHANES study) excerpt again:

```
body = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_adult_female_bmx_2020.csv",
    comment="#")
body = body.to_numpy() # data frames will be covered later
body.shape
## (4221, 7)
body[:6, :] # 6 first rows, all columns
## array([[ 97.1, 160.2,  34.7,  40.8,  35.8, 126.1, 117.9],
##        [ 91.1, 152.7,  33.5,  33. ,  38.5, 125.5, 103.1],
##        [ 73. , 161.2,  37.4,  38. ,  31.8, 106.2,  92. ],
##        [ 61.7, 157.4,  38. ,  34.7,  29. , 101. ,  90.5],
##        [ 55.4, 154.6,  34.6,  34. ,  28.3,  92.5,  73.2],
##        [ 62. , 144.7,  32.5,  34.2,  29.8, 106.7,  84.8]])
```

We thus have $n=4221$ participants and 7 different features describing them, in this order:

1. weight (kg),
2. standing height (cm),
3. upper arm length (cm),
4. upper leg length (cm),
5. arm circumference (cm),
6. hip circumference (cm),
7. waist circumference (cm).

We expect the data in columns to be *related* to each other (e.g., a taller person *usually tends to weight more*). This is why in this chapter we are interested in quantifying the

degree of association and modelling functional relationships between the variables as well as finding new interesting combinations thereof.

9.1 Measuring Correlation

Scatterplots let us identify some simple patterns or structure in data. From Figure 7.4, we can note that higher hip circumferences *tend to* occur more often together with higher arm circumferences and that the latter does not really tell us anything about height.

Let's explore some basic means for measuring (expressing as a single number) the degree of association between a set of pairs of points.

9.1.1 Pearson's Linear Correlation Coefficient

First, the Pearson's *linear correlation* coefficient:

$$r(\mathbf{x}, \mathbf{y}) = \frac{1}{n} \sum_{i=1}^n \frac{x_i - \bar{x}}{s_x} \frac{y_i - \bar{y}}{s_y},$$

with s_x, s_y denoting the standard deviations and \bar{x}, \bar{y} being the means of $\mathbf{x} = (x_1, \dots, x_n)$ and $\mathbf{y} = (y_1, \dots, y_n)$, respectively.

Note: Look carefully: we are computing pairwise products of standardised versions of the two vectors. It is a normalised measure of how they *vary* together (co-variance).

(*) Furthermore, in Section 9.3.1 we will note that it is nothing else as the cosine of the angle between centred and normalised versions of the vectors.

Here is how we can compute it manually:

```
x = body[:, 4] # arm circumference
y = body[:, 5] # hip circumference
x_std = (x-np.mean(x))/np.std(x)
y_std = (y-np.mean(y))/np.std(y)
np.sum(x_std*y_std)/len(x)
## 0.8680627457873239
```

And here is a built-in function that implements the same formula:

```
scipy.stats.pearsonr(x, y)[0]
## 0.8680627457873241
```

Important: Basic properties of Pearson's r include:

1. $r(x,y) = r(y,x)$ (symmetric);
2. $|r(x,y)| \leq 1$ (bounded from below by -1 and from above by 1);
3. $r(x,y) = 1$ if and only if $y = ax + b$ for some $a > 0$ and b , (reaches the maximum when one variable is an increasing linear function of the other one);
4. $r(x,-y) = -r(x,y)$ (negative scaling (reflection) of one variable changes the sign of the coefficient);
5. $r(x,ay + b) = r(x,y)$ for any $a > 0$ and b (invariant to translation and scaling of inputs that does not change the sign of elements).

To get more insight, below we shall illustrate some interesting *correlations* using the following function that draws a scatter plot and prints out Pearson's r (and Spearman's ρ which we discuss below – let's ignore it by then):

```
def plot_corr(x, y):
    r = scipy.stats.pearsonr(x, y)[0]
    p = scipy.stats.spearmanr(x, y)[0]
    plt.scatter(x, y, label=f'r = {r:.3}\n\rho = {p:.3}')
    plt.legend()
    pass
```

Perfect Linear Correlation

First of all, note that the above properties imply that $r(x,y) = -1$ if and only if $y = ax + b$ for some $a < 0$ and b (reaches the minimum when one variable is a decreasing linear function of the other one) Furthermore, a variable is trivially perfectly correlated with itself $r(x,x) = 1$.

Hence, we get perfect *linear correlation* (-1 or 1) when one variable is a scaled and shifted version (linear function) of the other variable, see [Figure 9.1](#).

```
np.random.seed(123)
x = np.random.rand(100)
plt.subplot(121)
```

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```
plot_corr(x, -0.5*x+3) # negative slope
plt.axis("equal")
plt.subplot(122)
plot_corr(x, 3*x+10) # positive slope
plt.axis("equal")
plt.show()
```

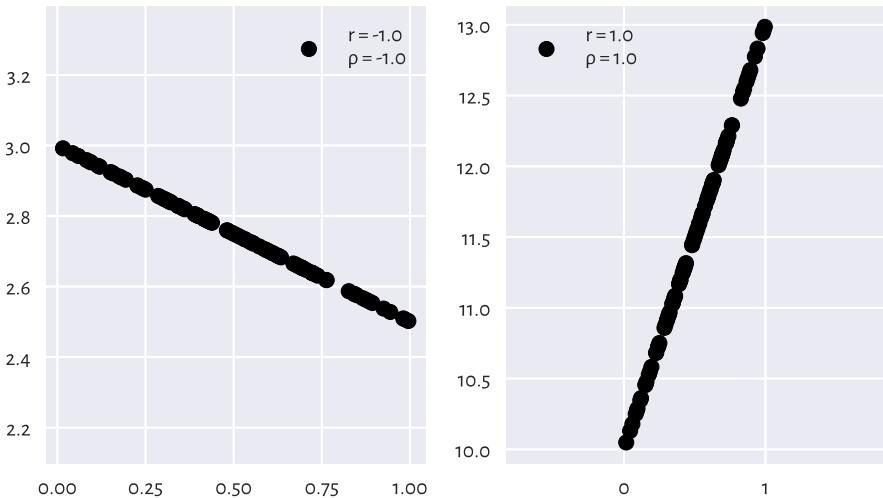


Figure 9.1: Perfect linear correlation (negative and positive)

Note that negative correlation means that when one variable increases, the other one decreases (like: a car's braking distance vs velocity).

Strong Linear Correlation

Next, if two variables are *more or less* linear functions of themselves, the correlations will be close to -1 or 1 , with the degree of association diminishing as the linear relationship becomes less and less present, see [Figure 9.2](#).

```
np.random.seed(123)
x = np.random.rand(100)
y = 0.5*x
e = np.random.randn(len(x)) # random white noise (of mean 0)
```

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```
plt.figure(figsize=(plt.rcParams["figure.figsize"])[0], )*2) # width=height
plt.subplot(221)
plot_corr(x, y)
plt.subplot(222)
plot_corr(x, y+0.05*e) # add some noise
plt.subplot(223)
plot_corr(x, y+0.1*e) # more noise
plt.subplot(224)
plot_corr(x, y+0.25*e) # even more noise
plt.show()
```

Note again that the arm and hip circumferences enjoy quite high positive degree of linear correlation.

Exercise 9.1 Draw a series of similar plots but for the case of negatively correlated point pairs.

Important: As a rule of thumb, linear correlation degree of 0.9 or greater (or -0.9 or smaller) is quite decent. Between -0.8 and 0.8 we probably shouldn't be talking about two variables being linearly correlated at all. Some textbooks are more lenient, but we have higher standards. In particular, it is not uncommon in social sciences to consider 0.6 a decent degree of correlation, but this is like building on sand. If a dataset at hand does not provide us with strong evidence, it is our ethical duty to refrain ourselves from publishing unjustified statements.

No Linear Correlation Does Not Imply Independence

We should stress that correlation close to 0 does not necessarily mean that two variables are not related to each other, although for two independent variables we definitely expect the correlation coefficient be approximately equal to 0. Pearson's r is a *linear* correlation coefficient, so we are only quantifying these types of relationships. See Figure 9.3 for an illustration of this fact.

```
np.random.seed(123)
plt.figure(figsize=(plt.rcParams["figure.figsize"])[0], )*2) # width=height
plt.subplot(221)
plot_corr(x, np.random.rand(100)) # independent (not correlated)
plt.subplot(222)
plot_corr(x, (2*x-1)**2-1) # quadratic dependence
plt.subplot(223)
```

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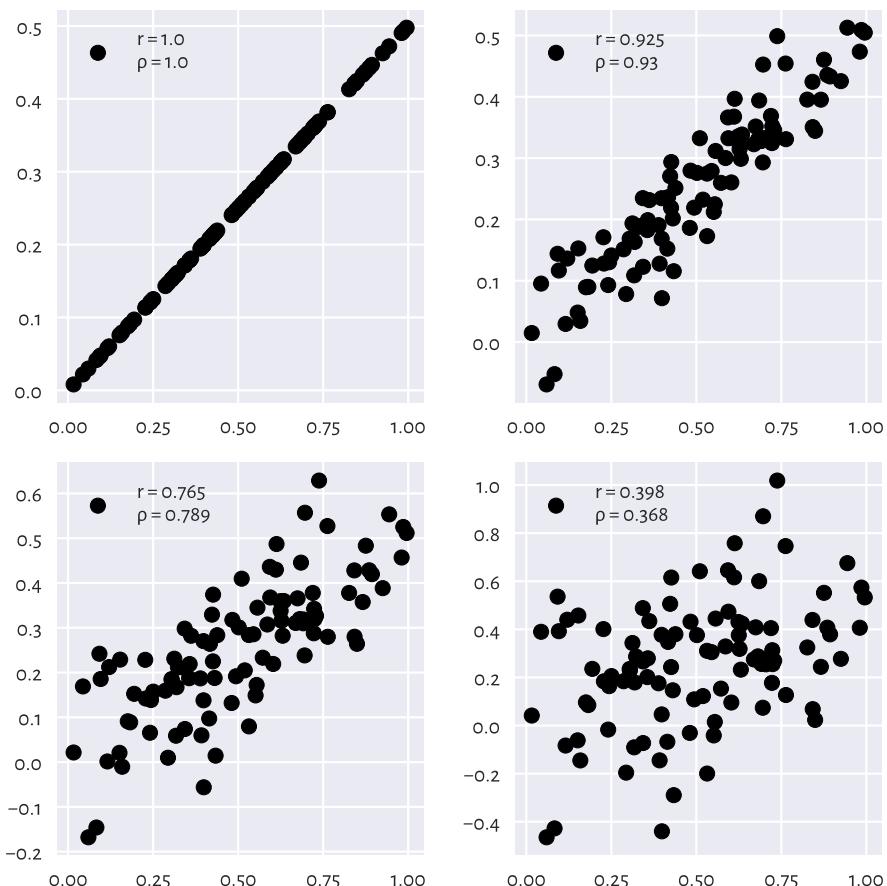


Figure 9.2: Linear correlation coefficients for data with different amounts of noise

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```
plot_corr(x, np.abs(2*x-1)) # another form of dependence
plt.subplot(224)
plot_corr(x, np.sin(10*np.pi*x)) # another
plt.show()
```

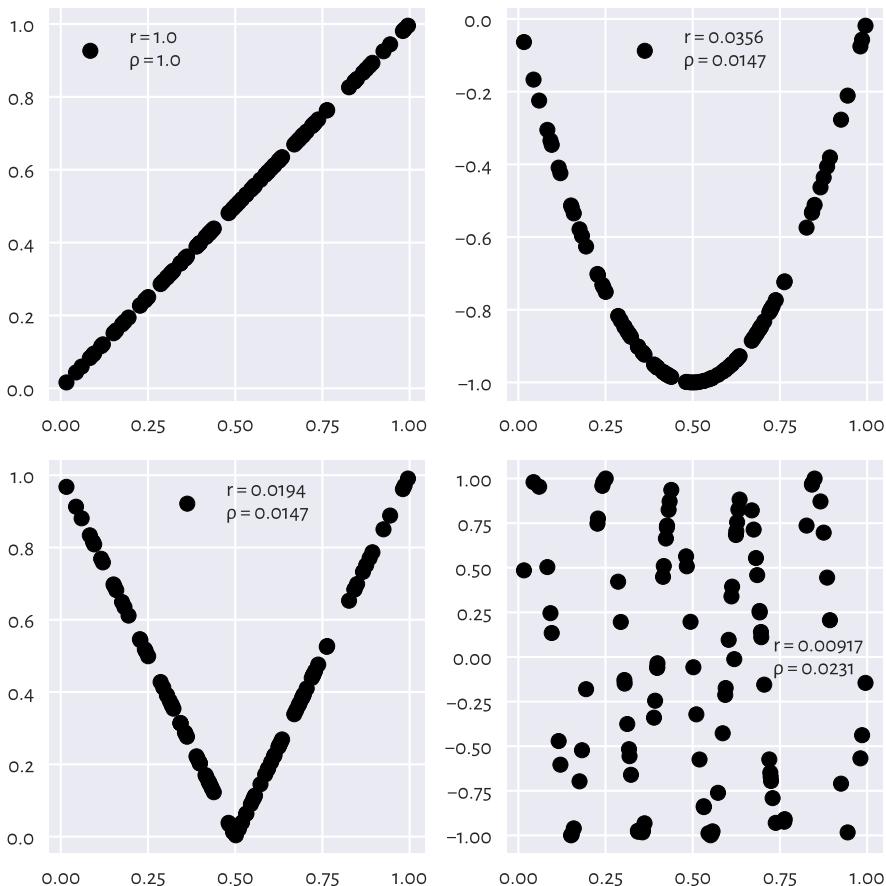


Figure 9.3: Are all of these really uncorrelated?

False Linear Correlations

What is more, sometimes we can detect *false* correlations – when data are functionally dependent, the relationship is not linear, but it kind of looks like linear. Refer to [Figure 9.4](#) for some examples.

```
np.random.seed(123)
plt.figure(figsize=(plt.rcParams["figure.figsize"])[0], )*2) # width=height
(continues on next page)
```

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```
plt.subplot(221)
plot_corr(x, np.sin(0.6*np.pi*x))
plt.subplot(222)
plot_corr(x, np.log(x+1))
plt.subplot(223)
plot_corr(x, np.exp(x**2))
plt.subplot(224)
plot_corr(x, 1/(x/2+0.2))
plt.show()
```

No single measure is perfect – we are trying to compress $2n$ data points into a single number — it is obvious that there will be many different datasets, sometimes very diverse, that will yield the same correlation value.

Correlation Is Not Causation

Note that high correlation degree (either positive or negative) does not mean that there is any *casual* relationship between the two variables. We cannot say that having large arm circumference affects hip size or the other way around. There might be some *latent* variable that influences these two (e.g., maybe also related to weight?).

Exercise 9.2 Quite often, medical advice is formulated based on correlations and similar association-measuring tools. We should know how to interpret them, as it is never a true cause-effect relationship; rather, it's all about detecting common patterns in larger populations. For instance, in “obesity increases the likelihood of lower back pain and diabetes” we does not say that one necessarily implies another or that if you are not obese, there is no risk of getting the two said conditions. It might also work the other way around, as lower back pain may lead to less exercise and then weight gain. Reality is complex. Find similar patterns related to other sets of conditions. Which are stronger than others?

Note: Measuring correlations can aid in constructing regression models, where we would like to identify the transformation that expresses one variable as a function of one or more other ones. When we say that y can be modelled by $ax + b$, regression analysis will identify some concrete a and b coefficients – see [Section 9.2.3](#) for more details.

In particular, we would like to include some variables that are correlated with the modelled variable but avoid modelling with the features that are highly correlated with each other, because they do not bring anything interesting to the table and can cause the solution to be numerically unstable.

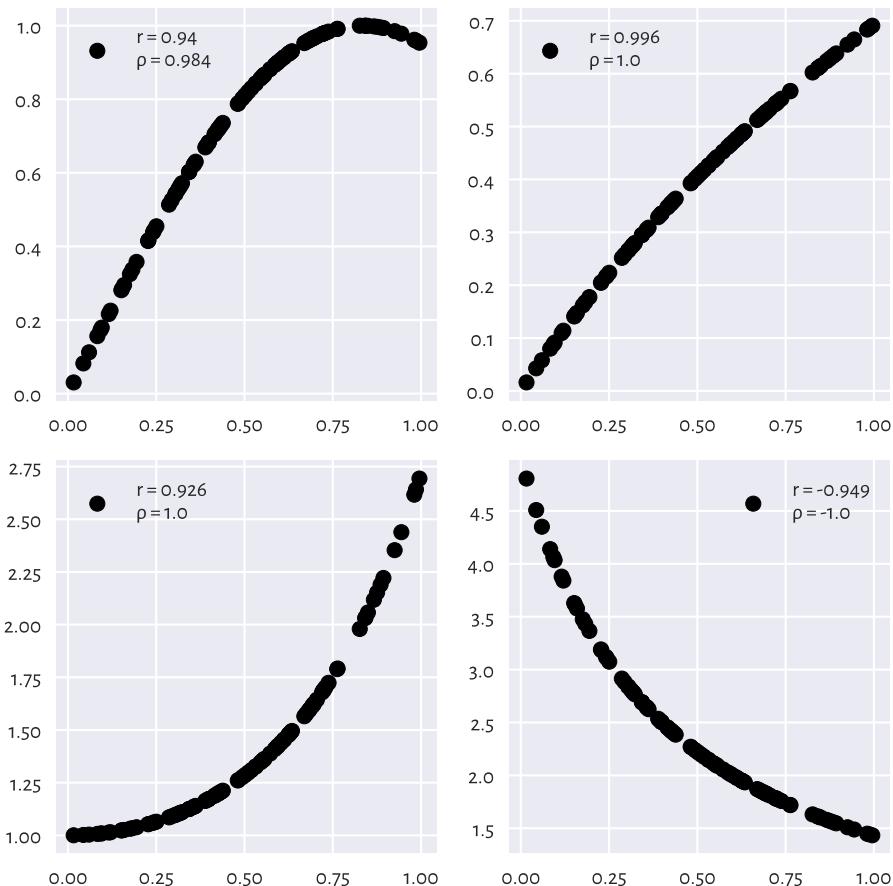


Figure 9.4: Example non-linear relationships look like linear to Pearson's r

9.1.2 Correlation Heatmap

Calling `numpy.corrcoef(body.T)` (note the matrix transpose) allows for determining the linear correlation coefficients between all pairs of variables.

We can nicely depict them on a heatmap, see Figure 9.5.

```
from matplotlib import cm
order = [4, 5, 6, 0, 2, 1, 3]
```

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```

cols = np.array(["weight", "height", "arm len",
                 "leg len", "arm circ", "hip circ", "waist circ"])
C = np.corrcoef(body.T)
sns.heatmap(
    C[np.ix_(order, order)],
    xticklabels=cols[order],
    yticklabels=cols[order],
    annot=True, fmt=".2f", cmap=cm.get_cmap("copper")
)
plt.show()

```

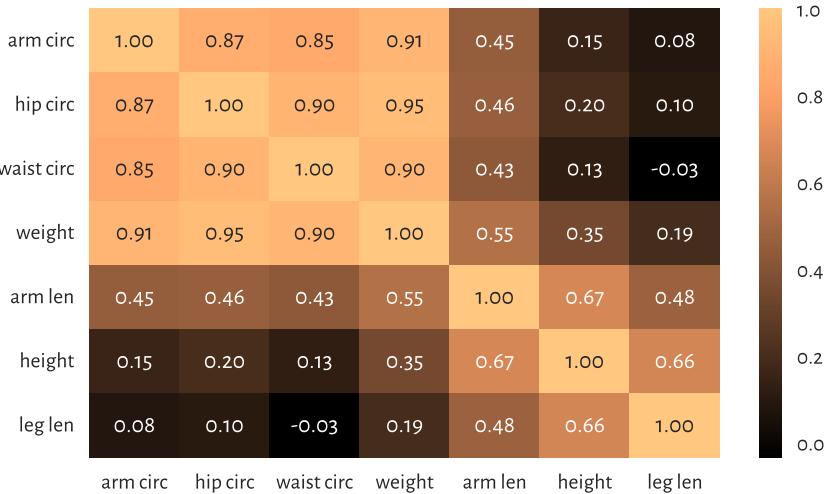


Figure 9.5: A correlation heatmap

Note that we have ordered the columns to reveal some naturally occurring variable clusters: for instance, arm, hip, waist circumference and weight are all quite strongly correlated.

Of course, we have 1.0s on the main diagonal because a variable is trivially correlated with itself. Also, note that this heatmap is symmetric which is due to the property $r(\mathbf{x}, \mathbf{y}) = r(\mathbf{y}, \mathbf{x})$.

Example 9.3 (*) To fetch the row and column index of the most correlated pair of variables (either

positively or negatively), we should first take the upper (or lower) triangle of the correlation matrix (see `numpy.triu` or `numpy.tril`) to ignore the irrelevant and repeating items:

```
Cu = np.triu(np.abs(C), 1)
np.round(Cu, 2)
## array([[0. , 0.35, 0.55, 0.19, 0.91, 0.95, 0.9 ],
##        [0. , 0. , 0.67, 0.66, 0.15, 0.2 , 0.13],
##        [0. , 0. , 0. , 0.48, 0.45, 0.46, 0.43],
##        [0. , 0. , 0. , 0. , 0.08, 0.1 , 0.03],
##        [0. , 0. , 0. , 0. , 0. , 0.87, 0.85],
##        [0. , 0. , 0. , 0. , 0. , 0. , 0.9 ],
##        [0. , 0. , 0. , 0. , 0. , 0. , 0. ]])
```

and then find the location of the maximum:

```
np.unravel_index(np.argmax(Cu), Cu.shape)
## (0, 5)
```

Thus, weight and hip circumference is the most strongly correlated.

Note that `numpy.argmax` returns an index in the flattened (unidimensional) array, therefore we had to use `numpy.unravel_index` to convert it to a two-dimensional one.

9.1.3 Linear Correlation Coefficients on Transformed Data

Pearson's coefficient can of course also be applied on nonlinearly transformed versions of variables, e.g., logarithms (remember incomes?), squares, square roots, etc.

Let's consider an excerpt from the 2020 CIA [World Factbook](#)¹⁰¹, where we have data on gross domestic product per capita (based on purchasing power parity) and life expectancy at birth in many countries.

```
world = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/world_factbook_2020_subset1.csv",
    comment="#")
world = world.to_numpy()
world[:6, :] # preview
## array([[ 2000. , 52.8],
##        [12500. , 79. ],
##        [15200. , 77.5],
```

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¹⁰¹ <https://www.cia.gov/library/publications/the-world-factbook/docs/rankorderguide.html>

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```
##      [11200. ,     74.8],
##      [49900. ,     83. ],
##      [ 6800. ,    61.3]])
```

Figure 9.6 depicts these data on a scatterplot.

```
plt.subplot(121)
plot_corr(world[:, 0], world[:, 1])
plt.xlabel("per capita GDP PPP")
plt.ylabel("life expectancy (years)")
plt.subplot(122)
plot_corr(np.log(world[:, 0]), world[:, 1])
plt.xlabel("log(per capita GDP PPP)")
plt.yticks()
plt.show()
```

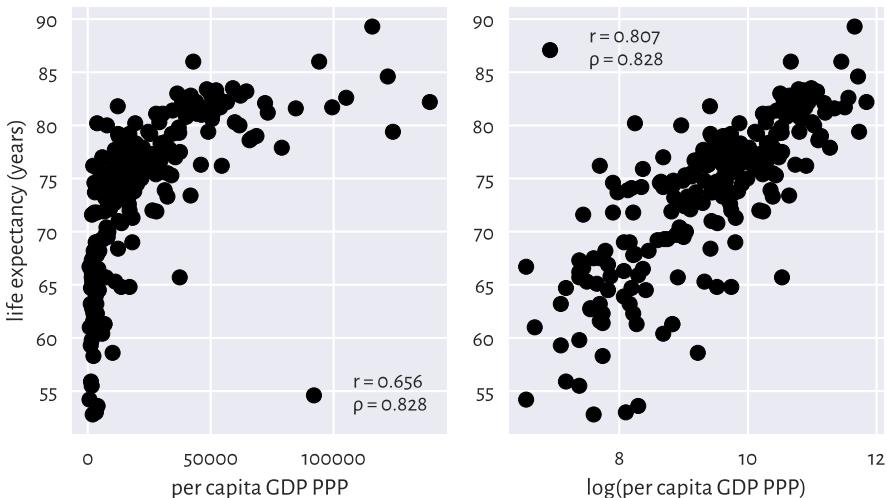


Figure 9.6: Scatterplots for life expectancy vs gross domestic product (purchasing power parity) on linear (left-) and log-scale (righthand side)

Computing Pearson's r between these two indicates a quite weak linear correlation:

```
scipy.stats.pearsonr(world[:, 0], world[:, 1])[0]
## 0.656471945486374
```

However, already the logarithm of GDP is slightly more strongly linearly correlated with life expectancy:

```
scipy.stats.pearsonr(np.log(world[:, 0]), world[:, 1])[0]
## 0.8066505089380016
```

which means that modelling our data via $y = a \log x + b$ can be an idea worth considering.

9.1.4 Spearman's Rank Correlation Coefficient

Sometimes we might be interested in measuring the degree of any kind of *monotonic* correlation – to what extent one variable is an increasing or decreasing function of another one (linear, logarithmic, quadratic over the positive domain, etc.).

Spearman's rank correlation coefficient is frequently used in such a scenario:

$$\rho(x, y) = r(R(x), R(y))$$

which is¹⁰⁵ the Pearson coefficient computed over vectors of the corresponding ranks of all the elements in x and y (denoted with $R(x)$ and $R(y)$).

Hence, the two following calls are equivalent:

```
scipy.stats.spearmanr(world[:, 0], world[:, 1])[0]
## 0.8275220380818622
scipy.stats.pearsonr(
    scipy.stats.rankdata(world[:, 0]),
    scipy.stats.rankdata(world[:, 1]))
#[0]
## 0.8275220380818621
```

Let us point out that this measure is invariant with respect to monotone transformations of the input variables (up to the sign):

```
scipy.stats.spearmanr(np.log(world[:, 0]), -np.sqrt(world[:, 1]))[0]
## -0.8275220380818622
```

¹⁰⁵ If a method Y is nothing else than X on transformed data, we should not consider it a totally new method.

Exercise 9.4 We have included the `ps` in all the outputs generated by our `plot_corr` functions. Review all the figures listed above.

Exercise 9.5 Apply `numpy.corrcoef` and `scipy.stats.rankdata` (with an appropriate axis argument) to compute the Spearman correlation matrix for all the variable pairs in `body`. Draw it on a heatmap.

Exercise 9.6 (*) Draw the scatterplots of the ranks of columns in the `world` and `body` datasets.

9.2 Regression Tasks

Given a *training* set of n points in an m -dimensional space represented as an $\mathbf{X} \in \mathbb{R}^{n \times m}$ matrix and a set of n reference numeric outputs $\mathbf{y} \in \mathbb{R}^n$, *regression* aims to find function between the m *independent/explanatory/predictor* variables and a chosen *dependent/response/predicted* variable:

$$\mathbf{y} = f(\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_m),$$

that *approximates* the given dataset in a *usable* way.

9.2.1 K-Nearest Neighbour Regression

A quite straightforward approach to regression relies on aggregating the reference outputs of the k nearest neighbours of the point tested (compare Section 8.4.4).

For a fixed $k \geq 1$ and a given $\mathbf{x}' \in \mathbb{R}^m$, $f(\mathbf{x}')$ is computed by averaging the reference outputs in the point's local neighbourhood.

1. Find the indices $N_k(\mathbf{y}) = \{i_1, \dots, i_k\}$ of the k points from \mathbf{X} closest to \mathbf{x}' , i.e., ones that fulfil for all $j \notin \{i_1, \dots, i_k\}$

$$\|\mathbf{x}_{i_1} - \mathbf{x}'\| \leq \dots \leq \|\mathbf{x}_{i_k} - \mathbf{x}'\| \leq \|\mathbf{x}_{j'} - \mathbf{x}'\|.$$

2. Return the arithmetic mean of $(y_{i_1}, \dots, y_{i_k})$ as the result, i.e., assign the average of the outputs corresponding to its k nearest neighbours.

Here is a straightforward implementation that generates the predictions for each point in `x_test`:

```
def knn_regress(X_test, X_train, y_train, k):
    t = scipy.spatial.KDTree(X_train.reshape(-1, 1))
    i = t.query(X_test.reshape(-1, 1), k)[1] # indices of NNs
    y = y_train[i] # corresponding reference outputs
    return np.mean(y, axis=1)
```

For example, let us try expressing weight (the 1st column) as a function of hip circumference (the 6th column) in our NHANES study (body dataset):

$$\text{weight} = f_1(\text{hip circumference}) \quad (+\text{some error}).$$

We will also model the life expectancy at birth in different countries (world dataset) as a function of their GDP per capita (PPP):

$$\text{life expectancy} = f_2(\text{GDP per capita}) \quad (+\text{some error}).$$

Figure 9.7 depicts the fitted functions for a few different k s.

We have obtained a *smoothed* version of the original dataset. The fact that we do not reproduce the data points in an exact manner is reflected by the (figurative) error term in the above equations. Its role is to emphasise the existence of some natural data variability; after all, one's weight is not purely determined by their hip size.

Let us note that for small k we adapt better to the data points, which can be a good thing unless data are very noisy. The greater the k , the smoother the approximation at the cost of losing fine detail and restricted usability at the domain boundary.

Usually, the number of neighbours is chosen by trial and error (just like the number of bins in a histogram; compare Section 4.3.4).

```
plt.subplot(121)
x = body[:, 5] # hip circumference
y = body[:, 0] # weight
plt.plot(x, y, "o", alpha=0.1)
_x = np.linspace(x.min(), x.max(), 1001)
for k in [5, 25, 100]:
    _y = knn_regress(_x, x, y, k)
    plt.plot(_x, _y, label=f"$k={k}$")
plt.legend()
plt.xlabel("hip circumference")
plt.ylabel("weight")
```

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```

plt.subplot(122)
x = world[:, 0] # GDP
y = world[:, 1] # life expectancy
plt.plot(x, y, "o", alpha=0.1)
_x = np.linspace(x.min(), x.max(), 1001)
for k in [5, 25, 100]:
    _y = knn_regress(_x, x, y, k)
    plt.plot(_x, _y, label=f"$k={k}$")
plt.legend()
plt.xlabel("per capita GDP PPP")
plt.ylabel("life expectancy (years)")

plt.show()

```

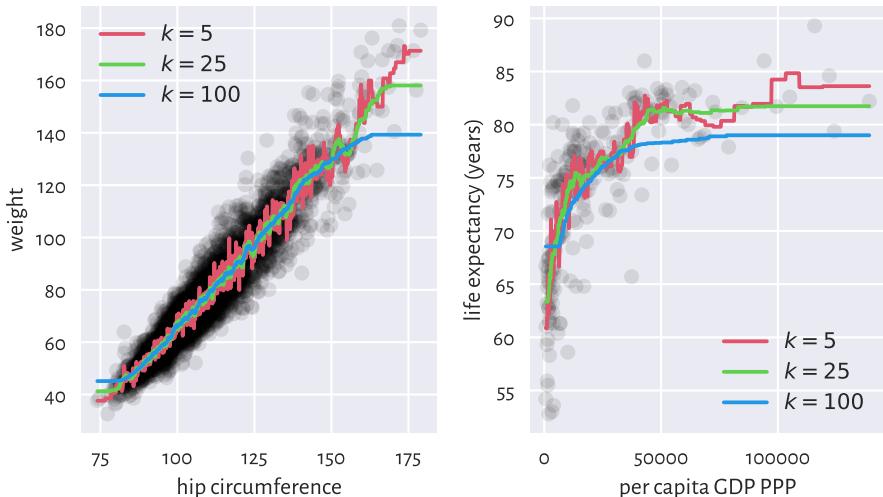


Figure 9.7: K -nearest neighbour regression curves for example datasets; the greater the k , the more coarse-grained the approximation

Note: (***) Some methods use weighted arithmetic means for aggregating the k reference outputs, with weights proportional to the actual distances to the neighbours (closer inputs are considered more important).

Also, instead of few nearest neighbours, we could easily implement some form of fixed-radius search regression (compare Section 8.4.4).

These are left as an enjoyable exercise to the skilled reader.

9.2.2 From Data To (Linear) Models

Unfortunately, in order to generate predictions for new data points, k -nearest neighbours regression requires that the training sample is available at all times. It does not *synthesise* or *simplify* the inputs; instead, it works as a kind of a black-box.

In many contexts we might prefer creating a data *model* instead, i.e., an easily interpretable mathematical function. A simple yet still quite flexible choice tackles regression problems via linear (affine) maps of the form:

$$y = f(x_1, x_2, \dots, x_m) = c_0 + c_1 x_1 + c_2 x_2 + \dots + c_m x_m,$$

or, in matrix multiplication terms,

$$y = c_0 + \mathbf{c} \mathbf{x}^T,$$

where $\mathbf{c} = [c_1 \ c_2 \ \dots \ c_m]$ and $\mathbf{x} = [x_1 \ x_2 \ \dots \ x_m]$.

For $m = 1$, the above simply defines a straight line, which we traditionally denote with

$$y = f(x) = ax + b$$

i.e., where we mapped $x \mapsto x_1$, $c_0 \mapsto b$ (intercept), and $c_1 \mapsto a$ (slope).

For $m > 1$, we obtain different hyperplanes (high-dimensional generalisations of the notion of a plane).

Note: As a separate intercept “ $c_0 +$ ” term in the defining equation can be quite inconvenient, notationwisely, we usually restrict ourselves to linear maps like

$$y = \mathbf{c} \mathbf{x}^T,$$

but where we can possibly have an explicit constant 1 component *inside* \mathbf{x} , for instance,

$$\mathbf{x} = [1 \ x_1 \ x_2 \ \dots \ x_m].$$

Together with $\mathbf{c} = [c_0 \ c_1 \ c_2 \ \dots \ c_m]$, as trivially $c_0 \cdot 1 = c_0$, this new setting is equivalent to the original one.

9.2.3 Least Squares Method

A linear model is uniquely¹⁰⁶ encoded using only the coefficients c_1, \dots, c_m . In order to find them, for each point $\mathbf{x}_{i,\cdot}$ from the input (training) set, we typically desire the *predicted value*

$$\hat{y}_i = f(x_{i,1}, x_{i,2}, \dots, x_{i,m}) = \mathbf{c}\mathbf{x}_{i,\cdot}^T$$

to be as *close* to the corresponding reference y_i as possible.

There can be many possible measures of *closeness* but the most popular one¹⁰⁷ uses the notion of the *sum of squared residuals* (true minus predicted outputs),

$$\text{SSR}(\mathbf{c}|\mathbf{X}, \mathbf{y}) = \sum_{i=1}^n (y_i - \hat{y}_i)^2 = \sum_{i=1}^n (y_i - (c_1 x_{i,1} + c_2 x_{i,2} + \dots + c_m x_{i,m}))^2,$$

which is a function of $\mathbf{c} = (c_1, \dots, c_m)$ (for fixed \mathbf{X}, \mathbf{y}).

And thus the *least squares* solution to the stated linear regression problem will be defined by the coefficient vector \mathbf{c} that minimises the SSR. Based on what we have said about matrix multiplication, this is equivalent to solving the optimisation task

$$\text{minimise } (\mathbf{y} - \mathbf{c}\mathbf{X}^T)(\mathbf{y} - \mathbf{c}\mathbf{X}^T)^T \quad \text{w.r.t. } (c_1, \dots, c_m) \in \mathbb{R}^m,$$

because $\hat{\mathbf{y}} = \mathbf{c}\mathbf{X}^T$ gives the predicted values as a row vector (the kind reader is encouraged to check that on a piece of paper now), $\mathbf{r} = \mathbf{y} - \hat{\mathbf{y}}$ computes all the n residuals, and $\mathbf{r} \mathbf{r}^T$ gives their sum of squares.

The method of least squares is one of the simplest and most natural approaches to regression analysis (curve fitting). Its theoretical foundations (calculus...) were developed more than 200 years ago by Gauss and then it was polished by Legendre.

Note: (*) Had the points lain on a hyperplane exactly (the interpolation problem), $\mathbf{y} = \mathbf{c}\mathbf{X}^T$ would have an exact solution, equivalent to solving the linear system of equations $\mathbf{y} - \mathbf{c}\mathbf{X}^T = \mathbf{0}$. However, in our setting we assume that there might be some measurement errors or other discrepancies between the reality and the theoretical model. Thus, to account for this, we are trying to solve a more general problem of finding a hyperplane for which $\|\mathbf{y} - \mathbf{c}\mathbf{X}^T\|^2$ is as small as possible.

¹⁰⁶ And thus in order to memorise the model for a further reference, we only need to serialise its m coefficients, e.g., in a JSON or CSV file.

¹⁰⁷ Due to computability and mathematical analysability, which we usually explore in more advanced courses on statistical data analysis, which this one is not.

Note: (*) The above can be solved analytically (compute the partial derivatives of SSR with respect to each c_1, \dots, c_m , equate them to 0, and solve a simple system of linear equations), which results in $\mathbf{c} = \mathbf{y}\mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}$, where \mathbf{A}^{-1} is the inverse of a matrix \mathbf{A} , i.e., the matrix such that $\mathbf{A}\mathbf{A}^{-1} = \mathbf{A}^{-1}\mathbf{A} = \mathbf{I}$. As inverting larger matrices directly is not too robust, numerically speaking, we prefer relying upon some more specialised algorithms to determine the solution.

The `scipy.linalg.lstsq` function provides a quite numerically stable procedure (which is based on the singular value decomposition of the model matrix, see below for discussion and common pitfalls).

Consider the above NHANES study excerpt one more time; let's say we would like to express weight (the 1st column) as a now linear function of hip circumference (the 6th column),

$$\text{weight} = a \cdot \text{hip circumference} + b \quad (+\text{some error}).$$

The error term corresponds to the residuals as by drawing a scatterplot (see the figure below) of the involved variables we can see that the data do not lie on a straight line perfectly: each model is an idealisation/simplification of the described reality.

The *design (model) matrix X* and reference *ys* are thus:

```
x_original = body[:, [5]]
X = x_original**[0, 1] # 1s, hip circumference
y_true = body[:, 0] # weight
```

Note that we have used the vectorised power operator to convert each x_i (the i -th hip circumference) to a pair $(x_i^0, x_i^1) = (1, x_i)$, which is a nice trick to prepend a column of 1s to X so that we can include the intercept term in the model. Here is a preview:

```
preview_indices = [4, 5, 6, 8, 12, 13]
X[preview_indices, :]
## array([[ 1. ,  92.5],
##        [ 1. , 106.7],
##        [ 1. ,  96.3],
##        [ 1. , 102. ],
##        [ 1. ,  94.8],
##        [ 1. ,  97.5]])
y_true[preview_indices]
## array([55.4, 62. , 66.2, 77.2, 64.2, 56.8])
```

Let us determine the least squares solution to our regression problem:

```
import scipy.linalg
res = scipy.linalg.lstsq(X, y_true)
```

The optimal coefficients vector (one that minimises the SSR) is:

```
c = res[0]
c
## array([-65.10087248,  1.3052463 ])
```

Therefore, the estimated model is:

$$\text{weight} = 1.305 \cdot \text{hip circumference} - 65.1 \quad (+\text{some error}).$$

Let us contemplate the fact that the model is nicely interpretable. For instance, with increasing hip circumference we expect the weights be greater. It does not mean that there is some *casual* relationship between the two (for instance, there can be some latent variables that affect both of them), but rather that there is some general tendency of how the data aligns in the sample space. For instance, that the “best guess” (according to the current model – there can be many, see below) weight for a person with hip circumference of 100 cm is 65.4 kg. Thanks to such models, we can understand certain phenomena better or find some proxies for different variables (especially if measuring them directly is tedious, costly, dangerous, etc.).

Let us determine the predicted weights and display them for the first 6 persons:

```
y_pred = c @ X.T
np.round(y_pred[preview_indices], 2)
## array([55.63, 74.17, 60.59, 68.03, 58.64, 62.16])
```

The scatterplot and the fitted regression line in Figure 9.8 indicates a quite good fit, but of course there is some natural variability.

```
_x = np.array([x_original.min(), x_original.max()]).reshape(-1, 1)
_y = c @ (_x**[0, 1]).T
plt.scatter(x_original, y_true, alpha=0.1)
plt.plot(_x, _y, "r-")
plt.xlabel("hip circumference")
plt.ylabel("weight")
plt.show()
```

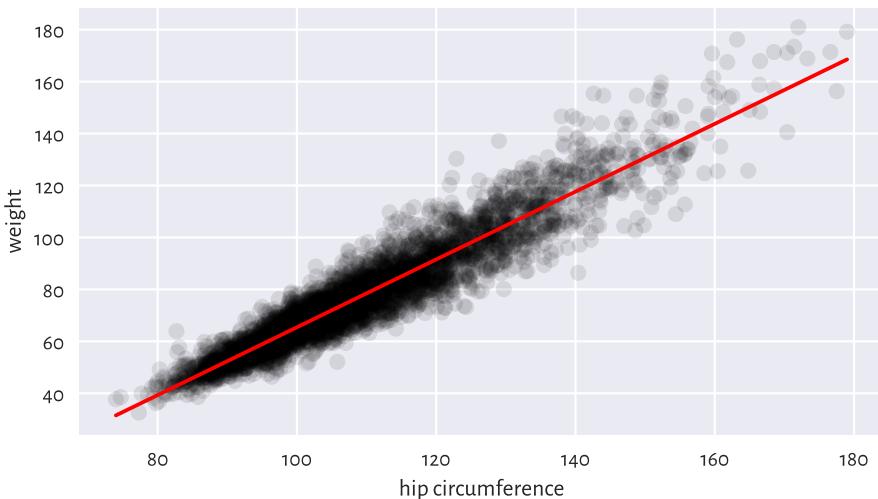


Figure 9.8: The least squares line for weight vs hip circumference

Exercise 9.7 The Anscombe quartet¹⁰² is a famous example dataset, where we have 4 pairs of variables having very similar means, variances, linear correlation coefficients, and which can be approximated by the same straight line, however, whose scatter plots are very different. Contemplate upon this toy example yourself.

9.2.4 Analysis of Residuals

The residuals, i.e., the estimation errors – what we expected vs what we get, for the chosen 6 observations are:

```
r = y_true - y_pred
np.round(r[preview_indices], 2)
## array([-0.23, -12.17,  5.61,  9.17,  5.56, -5.36])
```

These residuals are visualised in Figure 9.9.

We wanted the squared residuals (on average – across all the points) be as small as possible, and the least squares method assured that this is the case *relative to the chosen model*. However, it still does not mean that what we have obtained necessarily constitutes a good fit to the training data. Thus, we need to perform the analysis of residuals.

¹⁰² https://github.com/gagolews/teaching_data/blob/master/r/anscombe.csv

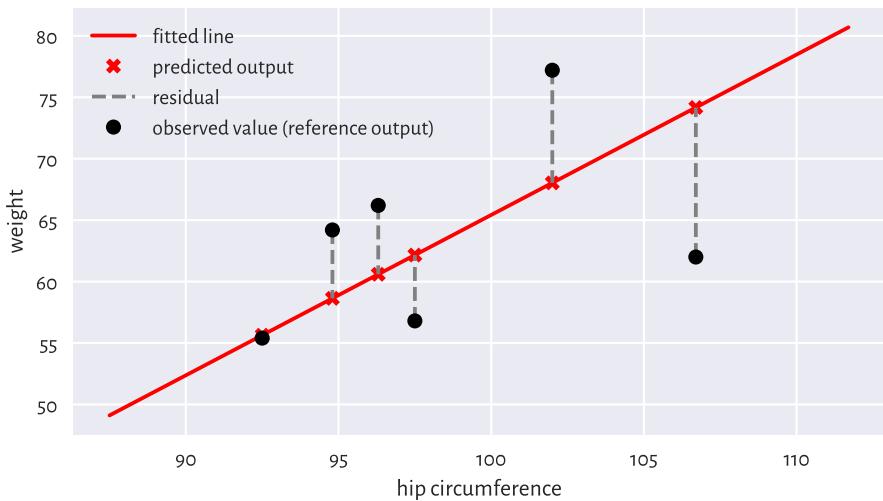


Figure 9.9: Example residuals in a simple linear regression task

Interestingly, the average of residuals is always zero:

$$\frac{1}{n} \sum_{i=1}^n (y_i - \hat{y}_i) = 0.$$

Therefore, if we want to summarise the residuals into a single number, we should rather use, for example, the root mean squared error (RMSE):

$$\text{RMSE}(c|\mathbf{X}, \mathbf{y}) = \sqrt{\frac{1}{n} \sum_{i=1}^n (y_i - \hat{y}_i)^2}.$$

```
np.sqrt(np.mean(r**2))
## 6.948470091176111
```

or the mean absolute error:

$$\text{MAE}(c|\mathbf{X}, \mathbf{y}) = \frac{1}{n} \sum_{i=1}^n |y_i - \hat{y}_i|.$$

```
np.mean(np.abs(r))
## 5.207073583769204
```

which is nicely interpretable, because it measures by how many kilograms do we err *on average*. Not bad.

Exercise 9.8 Fit a regression line explaining weight as a function of the waist circumference and compute the corresponding RMSE and MAE.

Note: Generally, fitting simple (involving one independent variable) linear models can only make sense for highly linearly correlated variables. Interestingly, if y and x are both standardised, and r is their Pearson's coefficient, then the least squares-fitted simple linear model will be given by $y = rx$.

In order to verify whether a fitted model is not extremely wrong (e.g., when we fit a liner model to data that clearly follows a different functional relationship), a plot of residuals against the fitted values can be of help; see Figure 9.10. Ideally, the points should be aligned totally at random (homoscedasticity) therein, without any dependence structure.

```
plt.scatter(y_pred, r, alpha=0.1)
plt.axhline(0, ls="--", color="red")
plt.xlabel("fitted values")
plt.ylabel("residuals")
plt.show()
```

Exercise 9.9 Compare¹⁰⁸ the RMSE and MAE for the k-nearest neighbour regression curves depicted in the lefthandside of Figure 9.7. Also, draw the residuals vs fitted plot.

For linear models fitted using the least squares method, it can be shown that

$$\frac{1}{n} \sum_{i=1}^n (y_i - \bar{y})^2 = \frac{1}{n} \sum_{i=1}^n (\hat{y}_i - \bar{\hat{y}})^2 + \frac{1}{n} \sum_{i=1}^n (y_i - \hat{y}_i)^2$$

that is, the variance of the dependent variable (left) can be decomposed as the variance of the predicted variables plus the averaged squared residuals. Multiplying the above by

¹⁰⁸ Note that in such an approach to regression we are not aiming to minimise anything in particular. If the model is good with respect to some metrics such as RMSE or MAE, we can consider ourselves lucky. However, there are some asymptotic results that guarantee the optimality of the results generated (e.g., consistency) for large sample sizes, see, e.g., [[DGL96]].

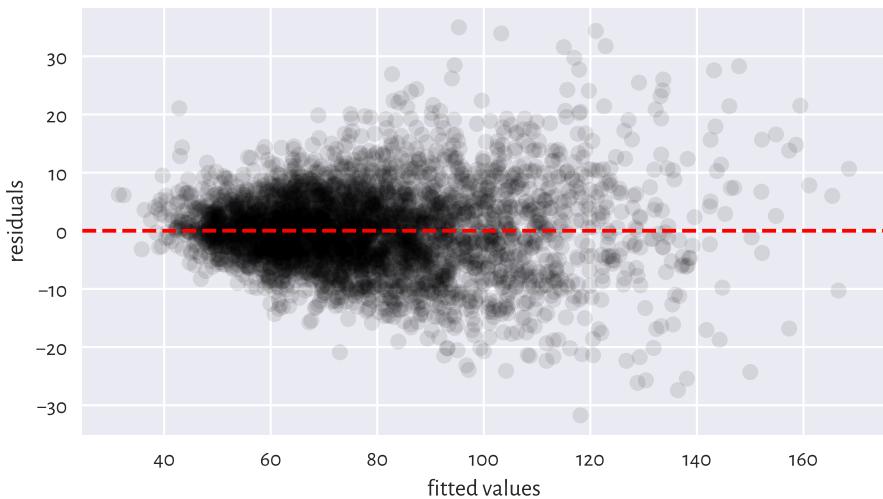


Figure 9.10: Residuals vs fitted values for the linear model explaining weight as a function of hip circumference; the variance of residuals slightly increases as \hat{y}_i increases, which is not ideal, but it could be much worse than this

n , we have that the *total* sum of squares (which we want to be as close to the former as possible) is equal to the *explained* sum of squares plus the *residual* sum of squares (which we want to be as small as possible):

$$\text{TSS} = \text{ESS} + \text{RSS}.$$

The *coefficient of determination* (unadjusted R-Squared, sometimes referred to as simply the *score*) is a popular normalised, unitless measure that is quite easy to interpret with no domain-specific knowledge of the modelled problem. Namely, it is given by:

$$R^2(c|\mathbf{X}, \mathbf{y}) = \frac{\text{ESS}}{\text{TSS}} = 1 - \frac{\text{RSS}}{\text{TSS}} = 1 - \frac{s_r^2}{s_y^2},$$

```
1 - np.var(y_true-y_pred)/np.var(y_true)
## 0.8959634726270759
```

The coefficient of determination in the current context¹⁰⁹ is thus the proportion of variance of the dependent variable explained by the independent variables in the model –

¹⁰⁹ Note that for models that are not generated via least squares, R-squared can also be negative, if they are

the closer it is to 1, the better. A dummy model that always returns the mean of y gives R-squared of 0.

In our case, $R^2 \approx 0.9$ is quite high, which indicates a moderately good fit.

Note: There are certain statistical results that can be relied upon provided that the residuals are independent random variables with expectation zero and the same variance (e.g., the Gauss–Markov theorem). Further, if they are normally distributed, then we have a number of hypothesis tests available (e.g., for the significance of coefficients). This is why various textbooks verify such assumptions. However, we do not go that far in this introductory course.

9.2.5 Multiple Regression

As another example, let us fit a model involving two independent variables, arm and hip circumference:

```
X = np.insert(body[:, [4, 5]], 0, 1, axis=1) # prepend a column of 1s
res = scipy.linalg.lstsq(X, y_true)
c = res[0]
np.round(c, 2)
## array([-63.38,    1.3 ,    0.9 ])
```

Thus, we have fitted the plane

$$\text{weight} = -63.38 + 1.3 \text{ arm circumference} + 0.9 \text{ hip circumference.}$$

We skip the visualisation part, because we do not expect it to result in a readable plot – these are multidimensional data after all. The coefficient of determination is

```
y_pred = c @ X.T
r = y_true - y_pred
1-np.var(r)/np.var(y_true)
## 0.9243996585518783
```

Root mean squared error:

extremely bad. Also note that this measure is dataset-dependent, therefore it should not be used for comparing between models explaining different dependent variables.

```
np.sqrt(np.mean(r**2))
## 5.923223870044694
```

Mean absolute error:

```
np.mean(np.abs(r))
## 4.431548244333894
```

Thus, it is a slightly better model than the previous one — we can predict the study participants' weights with better precision, at the cost of increased model complexity.

9.2.6 Variable Transformation and Linearisable Models (*)

We are of course not restricted merely to linear functions of the input variables, because by applying arbitrary transformations upon the design matrix columns, we can cover many interesting scenarios.

For instance, a polynomial model involving two variables:

$$g(v_1, v_2) = \beta_0 + \beta_1 v_1 + \beta_2 v_1^2 + \beta_3 v_1 v_2 + \beta_4 v_2 + \beta_5 v_2^2$$

can be obtained by substituting $x_1 = 1$, $x_2 = v_1$, $x_3 = v_1^2$, $x_4 = v_1 v_2$, $x_5 = v_2$, $x_6 = v_2^2$, and then fitting

$$f(x_1, x_2, \dots, x_6) = c_1 x_1 + c_2 x_2 + \dots + c_6 x_6.$$

The design matrix is made of rubber, it can handle anything (unless it carries highly correlated pairs of input variables). It will still be a linear model, but with respect to transformed data. The algorithm does not care. That is the beauty of the underlying mathematics.

A creative modeller can also turn models such as $u = ce^{av}$ into $y = ax + b$ by replacing $y = \log u$, $x = v$, and $b = \log c$. There are numerous possibilities here – we call them *linearisable models*.

As an example, let us model the life expectancy at birth in different countries as a function of their GDP per capita (PPP).

We will consider four different models:

1. $y = c_1 + c_2 x$ (linear),
2. $y = c_1 + c_2 x + c_3 x^2$ (quadratic),
3. $y = c_1 + c_2 x + c_3 x^2 + c_4 x^4$ (cubic),

4. $y = c_1 + c_2 \log x$ (logarithmic).

Here are the helper functions that create the model matrices:

```
def make_model_matrix1(x):
    return x.reshape(-1, 1)**[0, 1]

def make_model_matrix2(x):
    return x.reshape(-1, 1)**[0, 1, 2]

def make_model_matrix3(x):
    return x.reshape(-1, 1)**[0, 1, 2, 3]

def make_model_matrix4(x):
    return (np.log(x)).reshape(-1, 1)**[0, 1]

make_model_matrix1.__name__ = "linear model"
make_model_matrix2.__name__ = "quadratic model"
make_model_matrix3.__name__ = "cubic model"
make_model_matrix4.__name__ = "logarithmic model"

model_matrix_makers = [
    make_model_matrix1,
    make_model_matrix2,
    make_model_matrix3,
    make_model_matrix4
]
Xs = [ make_model_matrix(world[:, 0])
    for make_model_matrix in model_matrix_makers ]
```

Fitting the models:

```
y_true = world[:, 1]
cs = [ scipy.linalg.lstsq(X, y_true)[0]
    for X in Xs ]
```

Their coefficients of determination are equal to:

```
for i in range(len(Xs)):
    R2 = 1-np.var(y_true - cs[i] @ Xs[i].T)/np.var(y_true)
    print(f"{model_matrix_makers[i].__name__:20} R2={R2:.3f}")
## linear model           R2=0.431
```

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```
## quadratic model      R2=0.567
## cubic model         R2=0.607
## logarithmic model   R2=0.651
```

The logarithmic model is thus the best (out of the models we have considered). The four models are depicted in Figure 9.11.

```
plt.scatter(world[:, 0], world[:, 1], alpha=0.1)
_x = np.linspace(world[:, 0].min(), world[:, 0].max(), 101).reshape(-1, 1)
for i in range(len(model_matrix_makers)):
    _y = cs[i] @ model_matrix_makers[i](_x).T
    plt.plot(_x, _y, label=model_matrix_makers[i].__name__)
plt.legend()
plt.xlabel("per capita GDP PPP")
plt.ylabel("life expectancy (years)")
plt.show()
```

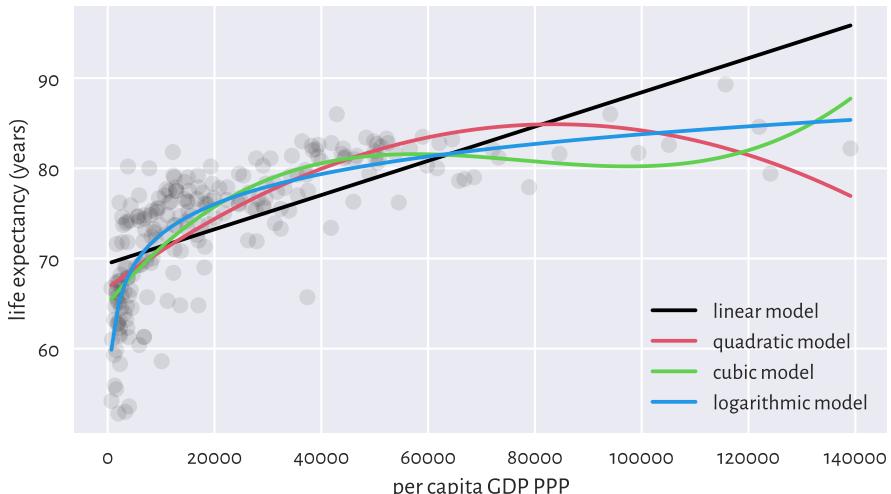


Figure 9.11: Different models for life expectancy vs GDP per-capita

Exercise 9.10 Draw boxplots and histograms of residuals for each model as well as the scatter-plots of residuals vs fitted values.

9.2.7 Descriptive vs Predictive Power (*)

We have *approximated* the life vs GDP relationship using a few different functions. Nevertheless, we see that the above quadratic and cubic models probably do not make much sense, semantically speaking. Sure, they do fit the data better, as far as individual points in the training set are concerned: after all, they have smaller mean squared errors (again: at these given points). However, looking at the way they behave, one does not need a university degree in economics/social policy to conclude that they probably are not the best *description* of how the reality behaves (on average).

Important: Naturally, a model's fit to observed data improves as the model's complexity increases. The Razor principle (by William of Ockham et al.) advises that if some phenomenon can be explained in many different ways, the simplest explanation should be chosen (*do not multiply entities* [here: introduce independent variables] *without necessity*).

In particular, the more independent variables we have in the model, the greater the R^2 coefficient will be. Thus, we can try correcting for this phenomenon by considering the *adjusted R²*

$$\bar{R}^2(\mathbf{c}|\mathbf{X}, \mathbf{y}) = 1 - (1 - R^2(\mathbf{c}|\mathbf{X}, \mathbf{y})) \frac{n - 1}{n - m - 1},$$

which, to some extent, penalises more complex models.

Note: (**) Model quality measures adjusted for the number of model parameters, m , can also be useful in automated variable selection. For example, the Akaike Information Criterion is given by $AIC(\mathbf{c}|\mathbf{X}, \mathbf{y}) = 2m + n \log(SSR(\mathbf{c}|\mathbf{X}, \mathbf{y})) - n \log n$ or the Bayes Information Criterion is defined via $BIC(\mathbf{c}|\mathbf{X}, \mathbf{y}) = m \log n + n \log(SSR(\mathbf{c}|\mathbf{X}, \mathbf{y})) - n \log n$. However, they are dependent on the scale of \mathbf{y} .

Further, we should also be interested in a model's *predictive power* – how well does it generalise to data points that we do not have now (or pretend we do not have), but might face in the future. After all, we observe the modelled reality only at a few different points – the question is how does the model perform when filling the gaps between them.

In particular, we should definitely be careful when *extrapolating* the model, i.e., making predictions outside of its usual domain. For example, the linear model predicts the following life expectancy for an imaginary country with \$500,000 per capita GDP PPP:

```
cs[0] @ model_matrix_makers[0](np.array([500000])).T
## array([164.3593753])
```

and the quadratic one gives:

```
cs[1] @ model_matrix_makers[1](np.array([500000])).T
## array([-364.10630778])
```

Nonsense.

Consider the following theoretical example. Let's assume that our true model is $y = 5 + 3x^3$.

```
def true_model(x):
    return 5 + 3*(x**3)
```

Next, we generate a sample from this model but which is – and such is life – subject to some measurement error:

```
np.random.seed(42)
x = np.random.rand(25)
y = true_model(x) + 0.2*np.random.randn(len(x))
```

Least-squares fitting of $y = c_1 + c_2x^3$ to the above gives:

```
X = x.reshape(-1, 1)**[0, 3]
c03 = scipy.linalg.lstsq(X, y)[0]
ssr03 = np.sum((y-c03 @ X.T)**2)
np.round(c03, 2)
## array([5.01, 3.13])
```

which is not very far, but still somewhat distant from the true coefficients, 5 and 3.

However, if we decided to fit a more flexible cubic polynomial, $y = c_1 + c_2x + c_3x^2 + c_4x^3$

```
X = x.reshape(-1, 1)**[0, 1, 2, 3]
c0123 = scipy.linalg.lstsq(X, y)[0]
ssr0123 = np.sum((y-c0123 @ X.T)**2)
np.round(c0123, 2)
## array([4.89, 0.32, 0.57, 2.23])
```

in terms of the SSR, the more complex model is of course better:

```
ssr03, ssr0123
## (1.061211154029558, 0.9619488226837543)
```

but it is farther away from the *truth* (which, when we perform the fitting task based only on given x and y , is unknown). We may thus say that the first model generalises better on yet-to-be-observed data, see Figure 9.12 for an illustration.

```
_x = np.linspace(0, 1, 101)
plt.plot(x, y, "o")
plt.plot(_x, true_model(_x), "--", label="true model")
plt.plot(_x, c0123 @ (_x.reshape(-1, 1)**[0, 1, 2, 3]).T,
         label="fitted model y=x**[0, 1, 2, 3]")
plt.plot(_x, c03 @ (_x.reshape(-1, 1)**[0, 3]).T,
         label="fitted model y=x**[0, 3]")
plt.legend()
plt.show()
```

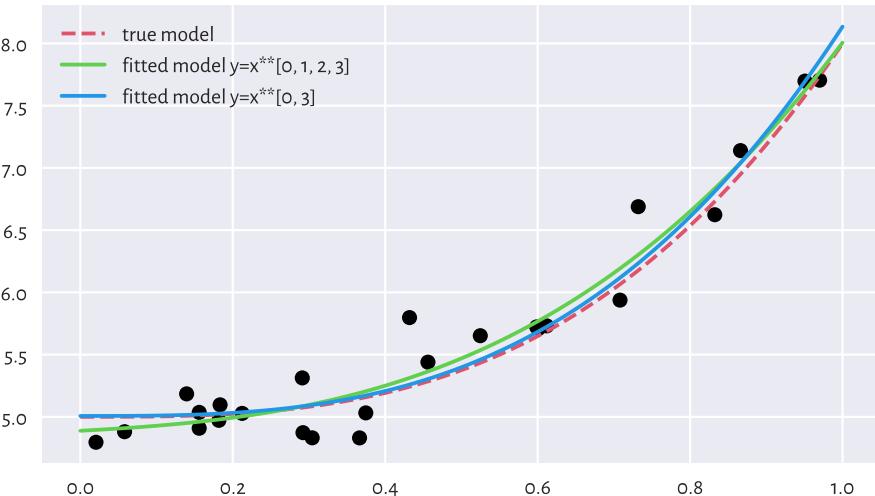


Figure 9.12: The true (theoretical) model vs some guesstimates (fitted from noisy data); more degrees of freedom does not necessarily reflect the truth better

Note that we have defined the sum of squared residuals (and its function, the root mean squared error) by means of the averaged deviation from the reference values, which in fact are themselves subject to error. They are our best-shot approximation of the truth, however, they should be taken with a degree of scepticism.

In our case, given the true (reference) model f defined over the domain D (in our case, $f(x) = 3x^3 + 5$ and $D = [0, 1]$) and an empirically fitted model \hat{f} , we can replace the

sample RMSE with the square root of the integrated squared error:

$$\text{RMSE}(\hat{f}|f) = \sqrt{\int_D (f(x) - \hat{f}(x))^2 dx}$$

which we can approximate numerically by sampling the above at sufficiently many points and applying the trapezoidal rule.

Let's fit a range of polynomial models of different degrees.

```
ps = np.arange(1, 10)
cs, rmse_train, rmse_test = [], [], []
for p in ps:
    c = scipy.linalg.lstsq(x.reshape(-1, 1)**np.arange(p+1), y)[0]
    cs.append(c)

    y_pred = c @ (x.reshape(-1, 1)**np.arange(p+1)).T
    rmse_train.append(np.sqrt(np.mean((y-y_pred)**2)))

    _y = c @ (_x.reshape(-1, 1)**np.arange(p+1)).T
    _r = (true_model(_x) - _y)**2
    rmse_test.append(np.sqrt(0.5*np.sum(
        np.diff(_x)*(_r[1:]+_r[:-1])
    )))

plt.plot(ps, rmse_train, label="RMSE (training set)")
plt.plot(ps, rmse_test, label="RMSE (theoretical)")
plt.legend()
plt.yscale("log")
plt.xlabel("model complexity (polynomial degree)")
plt.show()
```

From Figure 9.13 we see that a model's ability to make correct generalisations to unseen data, with the increased complexity initially improves, but then becomes worse. It is quite a typical behaviour. In fact, the model with the smallest RMSE on the training set, actually *overfits* to the input sample, see Figure 9.14.

```
plt.plot(x, y, "o")
plt.plot(_x, true_model(_x), "--", label="true model")
for i in [0, 1, 8]:
    plt.plot(_x, cs[i] @ (_x.reshape(-1, 1)**np.arange(ps[i]+1)).T,
            label=f"fitted degree-{ps[i]} polynomial")
```

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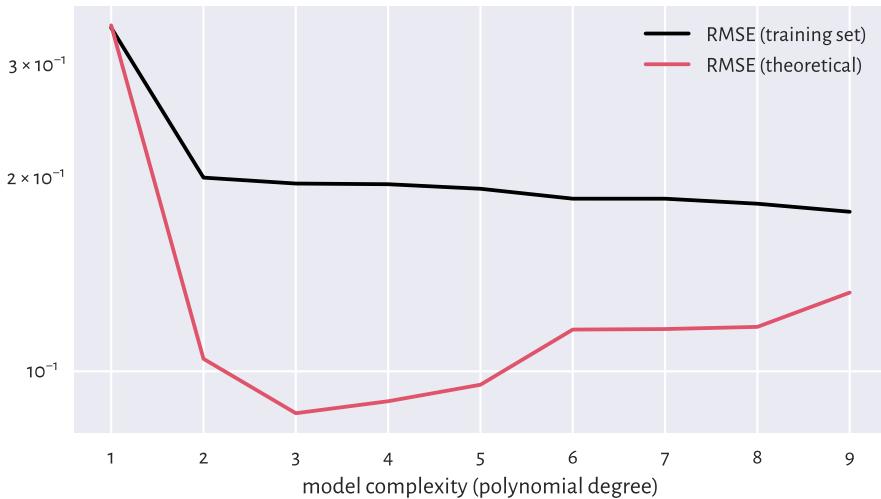


Figure 9.13: Good RMSE on training data does not necessarily imply good generalisation abilities

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```
plt.legend()  
plt.show()
```

Important: When evaluating a model's quality in terms of predictive power on unseen data, we should go beyond inspecting its behaviour merely on the points from the training sample. As the *truth* is usually not known (if it were, we would not need any guessing), a common approach in case where we have a data set of a considerable size is to divide it (randomly) into three parts:

- training sample (say, 60%) – used to fit a model,
- test sample (the remaining 40%) – used to assess its quality (e.g., by means of RMSE).

This might *emulate* an environment where some new data arrives later, see Section 12.3.3 for more details.

Furthermore, if model selection is required, we may apply a training-validation-test split (say, 60/20/20%; see Section 12.3.4) where many models are constructed on the

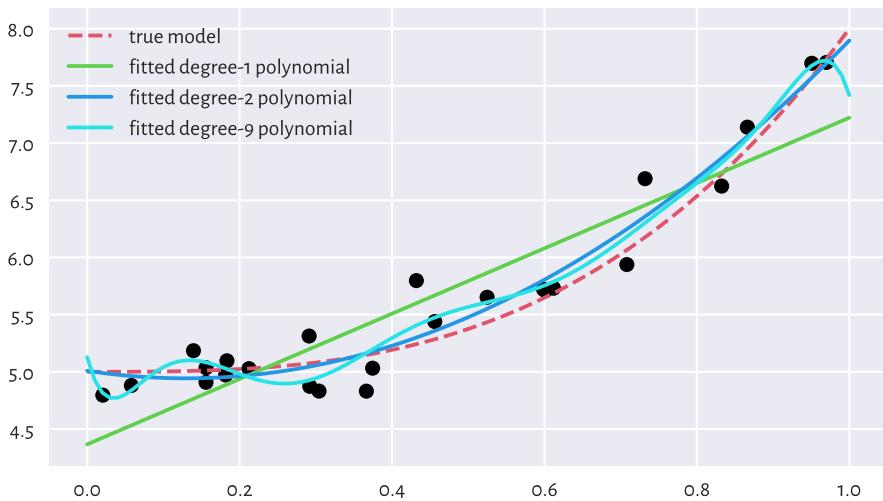


Figure 9.14: Under- and overfitting to training data

training set, the validation set is used to compute the metrics and choose the best model, and then the test set is employed to come up with the final valuation (because we do not want the model to overfit to the test set).

Overall, models should never be blindly trusted – common sense must always be applied. The fact that we have fitted something using a sophisticated procedure on a dataset that was hard to obtain does not mean we must glorify it. Bad models must be discarded and we should move on. Let us not think about them too much.

9.2.8 Fitting Regression Models with `scikit-learn` (**)

`scikit-learn`¹⁰³ (`sklearn`; [[PVG+11]]) is a huge Python package for machine learning built on top of `numpy`, `scipy`, and `matplotlib`. It has a nicely consistent API and implements or provides wrappers for many regression, classification, clustering, and dimensionality reduction algorithms (amongst others).

Important: `sklearn` is very convenient but allows for fitting models even if we do not understand the mathematics behind them. This is dangerous – it is like driving a

¹⁰³ <https://scikit-learn.org/stable/index.html>

manual without a driver's license only on an autopilot. Advanced students and practitioners will appreciate it, but if used by beginners, it needs to be handled with care; we should not mistake something's being easily accessible with its being safe to use. Too many bad models go into production and make our daily lives harder. Hence, as a rule, if given a function implementing some procedure and we are not able to provide its definition/mathematical properties/explain its idealised version using pseudocode, we should refrain from using it.

Because of the above, we shall only demo the package's API. Let us do that by fitting a multiple linear regression model for, again, weight as a function of arm and hip circumference:

```
X = body[:, [4, 5]]
y_true = body[:, 0]
import sklearn.linear_model
lm = sklearn.linear_model.LinearRegression(fit_intercept=True)
lm.fit(X, y_true)
lm.intercept_, lm.coef_
## LinearRegression()
## (-63.383425410947524, array([1.30457807, 0.8986582 ]))
```

In **scikit-learn**, once we construct an object representing the model to be fitted, the `fit()` method will determine the optimal parameters. We have obtained exactly the same solution – it is the same method, after all.

Computing the predicted values can be done by means of the `predict()` method. For example, we can calculate the coefficient of determination:

```
y_pred = lm.predict(X)
import sklearn.metrics
sklearn.metrics.r2_score(y_true, y_pred)
## 0.9243996585518783
```

This function is convenient, but do we remember the formula for the score? We should always do.

9.2.9 Ill-Conditioned Model Matrices (**)

Our approach to regression analysis relies on solving an optimisation problem (the method least squares). However, sometimes the “optimal” solution that the algorithm returns might have nothing to do with the *true* minimum. And this is despite the fact that we have the theoretical results (the objective is convex) stating that the solution is

unique (there are methods in statistical learning where there might be multiple local minima – this is even more difficult; see [Section 12.4.4](#)). The problem stems from our using the computer's finite-precision floating point arithmetic.

Let us fit a degree-4 polynomial to the life expectancy vs per capita GDP dataset.

```
X = world[:, [0]]**[0,1,2,3,4]
y_true = world[:, 1]
cs = dict()
```

We store the estimated model coefficients in a dictionary, because many methods will follow next. First, **scipy**:

```
res = scipy.linalg.lstsq(X, y_true)
cs["scipy_X"] = res[0]
cs["scipy_X"]
## array([ 2.33103950e-16,   6.31514064e-12,   1.34162021e-07, -2.33980973e-12,
##           1.03490968e-17])
```

If we drew the fitted polynomial (see the figure below), we would see that the fit is actually very very bad. The result returned by **lstsq** in this case is not at all optimal. It turns out that the fitting problem is very *ill-conditioned* (and it is not the algorithm's fault): GDPs range from very small to very large ones, and taking the powers of 4 thereof results in numbers of ever greater range. Finding the least squares solution involves some matrix inverse (not necessarily directly) and such a matrix might be close to singular.

As a measure of the model matrix's ill-conditioning, we often use the so-called condition number, being the ratio of the largest and smallest so-called *singular values*¹¹⁰ of \mathbf{X}^T , which are in fact returned by the **lstsq** method:

```
s = res[3]
s[0] / s[-1]
## 9.101246653543121e+19
```

As a rule of thumb, if the condition number is 10^k , we are losing k digits of precision when performing the computations. This is thus a very ill-conditioned problem, because the above number is very large.

Note: (***) The least squares regression problem can be solved by means of the singular value decomposition of the model matrix, see [Section 9.3.4](#). Let **USQ** be the SVD of \mathbf{X}^T .

¹¹⁰ Being themselves the square roots of eigenvalues of $\mathbf{X}^T \mathbf{X}$. Seriously, we really need linear algebra when we even remotely think about practising data science.

Then $\mathbf{c} = \mathbf{U}(1/\mathbf{S})\mathbf{Q}\mathbf{y}$, with $(1/\mathbf{S}) = \text{diag}(1/s_{1,1}, \dots, 1/s_{m,m})$. Interestingly, as $s_{1,1} \geq \dots \geq s_{m,m}$ gives the singular values of \mathbf{X}^T (square roots of the eigenvalues of $\mathbf{X}^T\mathbf{X}$), the aforementioned condition number can simply be computed as $s_{1,1}/s_{m,m}$.

Let us verify the approach used by **scikit-learn**, which fits the intercept separately (but still, it is merely a wrapper around **lstsq** with a different API), and so should be slightly better-behaving:

```
import sklearn.linear_model
lm = sklearn.linear_model.LinearRegression(fit_intercept=True)
lm.fit(X[:, 1:], y_true)
cs["sklearn"] = np.r_[lm.intercept_, lm.coef_]
cs["sklearn"]
## LinearRegression()
## array([ 6.92257641e+01,  5.05754568e-13,  1.38835855e-08, -2.18869526e-13,
##        9.09347414e-19])
```

Here is the condition number:

```
lm.singular_[0] / lm.singular_[-1]
## 1.4025984282521556e+16
```

The condition number is also huge – and **scikit-learn** did not warn us about it. Had we trusted the solution returned by it, we would end up with conclusions from our data analysis built on sand.

If the model matrix is almost singular, the computation of its inverse is prone to enormous numerical errors. One way of dealing with this is to remove highly correlated variables (the multicollinearity problem).

Interestingly, standardisation can *sometimes* make the fitting more numerically stable. Let \mathbf{Z} be a standardised version of the model matrix \mathbf{X} with the intercept part (the column of 1s) not included, i.e., with $\mathbf{z}_{:,j} = (\mathbf{x}_{:,j} - \bar{x}_j)/s_j$ with \bar{x}_j and s_j denoting the arithmetic mean and standard deviation of the j -th column in \mathbf{X} . If (d_1, \dots, d_{m-1}) is the least squares solution for \mathbf{Z} , then the least squares solution to the underlying original regression problem is

$$\left(\bar{y} - \sum_{j=1}^{m-1} \frac{d_j}{s_j} \bar{x}_j, \frac{d_1}{s_1}, \frac{d_2}{s_2}, \dots, \frac{d_{m-1}}{s_{m-1}} \right)$$

with the first term corresponding to the intercept.

Let us test this approach with **scipy.linalg.lstsq**.

```

means = np.mean(X[:, 1:], axis=0)
stds = np.std(X[:, 1:], axis=0)
Z = (X[:, 1:]-means)/stds
resZ = scipy.linalg.lstsq(Z, y_true)
c_scipyZ = resZ[0]/stds
cs["scipy_Z"] = np.r_[np.mean(y_true) - (c_scipyZ @ means.T), c_scipyZ]
cs["scipy_Z"]
## array([ 6.35946784e+01,  1.04541932e-03, -2.41992445e-08,  2.39133533e-13,
##        -8.13307828e-19])

```

The condition number is:

```

s = resZ[3]
s[0] / s[-1]
## 139.4279225737235

```

This is still not too good (we would prefer a value close to 1) but nevertheless way better.

Figure 9.15 depicts the three fitted models, each claiming to be *the* solution to the original regression problem.

```

plt.scatter(world[:, 0], world[:, 1], alpha=0.1)
_x = np.linspace(world[:, 0].min(), world[:, 0].max(), 101).reshape(-1, 1)
_X = _x**[0,1,2,3,4]
for lab, c in cs.items():
    ssr = np.sum((y_true-c @ X.T)**2)
    plt.plot(_x, c @ _X.T, label=f'{lab}:10 SSR={ssr:.2f}')
plt.legend()
plt.ylim(20, 120)
plt.xlabel("per capita GDP PPP")
plt.ylabel("life expectancy (years)")
plt.show()

```

Important: Always check the model matrix's condition number.

To be strict, if we read a paper in, say, social or medical sciences (amongst others) where the researchers fit a regression model but do not provide the model matrix's condition number, we should doubt the conclusions they make.

On a final note, we might wonder why the standardisation is not done automatically by

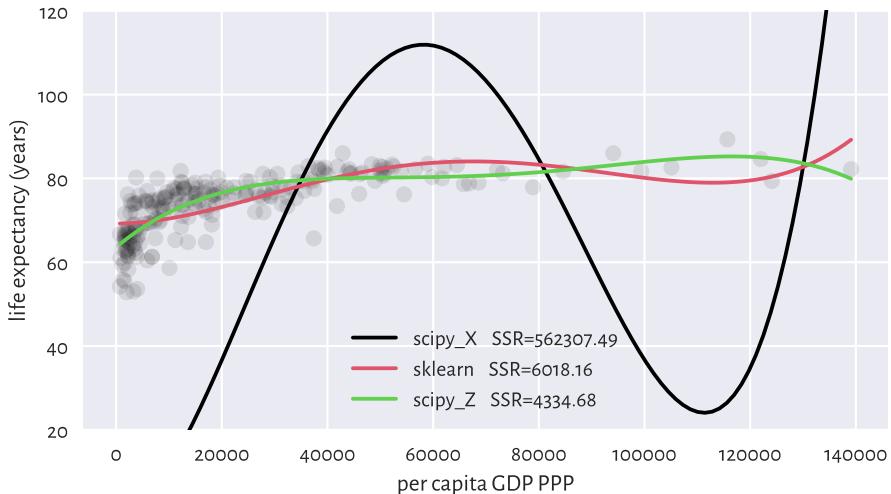


Figure 9.15: Ill-conditioned model matrix can result in the resulting models be very wrong

the least squares solver. As usual with most numerical methods, there is no one-fits-all solution: e.g., when there are columns of very small variance or there are outliers in data. This is why we need to study all the topics deeply: to be able to respond flexibly to many different scenarios ourselves.

9.3 Finding Interesting Combinations of Variables (*)

9.3.1 Dot Products, Angles, Collinearity, and Orthogonality

It turns out that the dot product (Section 8.3) has a nice geometrical interpretation:

$$\mathbf{x} \cdot \mathbf{y} = \|\mathbf{x}\| \|\mathbf{y}\| \cos \alpha,$$

where α is the angle between the two vectors. In other words, it is the product of the lengths of the two vectors and the cosine of the angle between them.

Note that we can get the cosine part by computing the dot product of the *normalised*

vectors, i.e., such that their lengths are equal to 1:

$$\cos \alpha = \frac{\mathbf{x} \cdot \mathbf{y}}{\|\mathbf{x}\| \cdot \|\mathbf{y}\|}.$$

For example, consider two vectors in \mathbb{R}^2 , $(1/2, 0)$ and $(\sqrt{2}/2, \sqrt{2}/2)$, which are depicted in Figure 9.16.

```
u = np.array([0.5, 0])
v = np.array([np.sqrt(2)/2, np.sqrt(2)/2])
```

Their dot product is equal to:

```
np.sum(u*v)
## 0.3535533905932738
```

The dot product of their normalised versions, i.e., the cosine of the angle between them is:

```
u_norm = u/np.sqrt(np.sum(u*u))
v_norm = v/np.sqrt(np.sum(v*v)) # BTW: this vector was already normalised
np.sum(u_norm*v_norm)
## 0.7071067811865476
```

The angle itself can be determined by referring to the inverse of the cosine function, i.e., arccosine.

```
np.arccos(np.sum(u_norm*v_norm)) * 180/np.pi
## 45.0
```

Note that we have converted the angle from radians to degrees.

Important: If two vectors are collinear (*codirectional*, one is a scaled version of another, angle 0°), then $\cos 0 = 1$. If they point to opposite directions (-180° degrees angle), then $\cos \pi = -1$. For *orthogonal* (perpendicular, 90° or -90° degree angle) vectors, we get $\cos(\pi/2) = \cos(-\pi/2) = 0$.

Note: (***) Note that the standard deviation s of a vector \mathbf{x} that has been centred (whose mean is 0) is a scaled version of the Euclidean norm (divided by the square root of the number of elements, n), i.e., $s = \|\mathbf{x}\|/\sqrt{n}$. Looking at the definition of the Pearson linear correlation coefficient, we see that it is the dot product of the standardised versions of

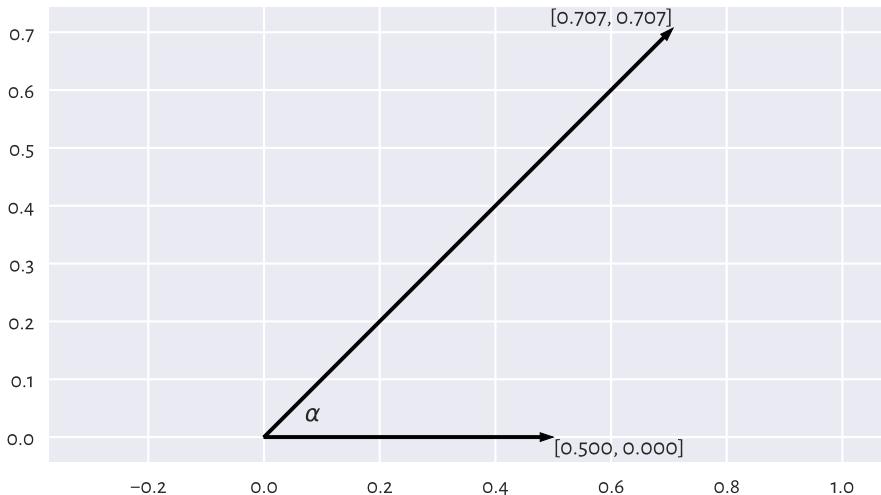


Figure 9.16: Example vectors and the angle between them

two vectors x and y divided by the number of elements therein. However, if the vectors are centred, we can rewrite the formula equivalently as $r(x, y) = \frac{x}{\|x\|} \cdot \frac{y}{\|y\|} = \cos \alpha$. It is not easy to imagine vectors in very high dimensional spaces, but at least the fact that r is bounded by -1 and 1 is implied from this observation.

9.3.2 Geometric Transformations of Points

For certain square matrices of size m by m , matrix multiplication can be thought of as an application of the corresponding geometrical transformation.

Let \mathbf{X} be a matrix of shape n by m , which we treat as representing the coordinates of n points in an m -dimensional space. For instance, if we are given a diagonal matrix:

$$\mathbf{S} = \text{diag}(s_1, s_2, \dots, s_m) = \begin{bmatrix} s_1 & 0 & \dots & 0 \\ 0 & s_2 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & s_m \end{bmatrix},$$

then \mathbf{XS} represents *scaling* (stretching) with respect to the axes of the coordinate system

in use, because:

$$\mathbf{XS} = \begin{bmatrix} s_1 x_{1,1} & s_2 x_{1,2} & \dots & s_m x_{1,m} \\ s_1 x_{2,1} & s_2 x_{2,2} & \dots & s_m x_{2,m} \\ \vdots & \vdots & \ddots & \vdots \\ s_1 x_{n-1,1} & s_2 x_{n-1,2} & \dots & s_m x_{n-1,m} \\ s_1 x_{n,1} & s_2 x_{n,2} & \dots & s_m x_{n,m} \end{bmatrix}.$$

Note that in **numpy** this can be implemented without actually referring to matrix multiplication; a notation like `X * np.array([s1, s2, ..., sm]).reshape(1, -1)` will suffice (elementwise multiplication and proper shape broadcasting).

Furthermore, if \mathbf{Q} is an *orthonormal* matrix, i.e., a square matrix whose columns and rows are unit vectors (normalised), all orthogonal to each other, then \mathbf{XQ} represents a combination of rotations and reflections.

Orthonormal matrices are sometimes simply referred to as orthogonal ones.

Important: By definition, a matrix \mathbf{Q} is *orthonormal* if and only if $\mathbf{Q}^T \mathbf{Q} = \mathbf{Q} \mathbf{Q}^T = \mathbf{I}$. It is due to the $\cos(\pi/2) = \cos(-\pi/2) = 0$ interpretation of the dot products of normalised orthogonal vectors.

In particular, for any angle α , the matrix representing rotations in \mathbb{R}^2 ,

$$\mathbf{R}(\alpha) = \begin{bmatrix} \cos \alpha & \sin \alpha \\ -\sin \alpha & \cos \alpha \end{bmatrix},$$

is orthonormal (which can be easily verified using the basic trigonometric equalities).

Furthermore,

$$\begin{bmatrix} 1 & 0 \\ 0 & -1 \end{bmatrix} \quad \text{and} \quad \begin{bmatrix} -1 & 0 \\ 0 & 1 \end{bmatrix}$$

represent the two reflections, one against the x- and the other against the y-axis, respectively. Both are orthonormal matrices as well.

Consider a data set \mathbf{X} in \mathbb{R}^2 :

```
np.random.seed(12345)
X = np.random.randn(10000, 2) * 0.25
```

and its scaled, rotated, and translated (shifted) version

$$\mathbf{Y} = \mathbf{X} \begin{bmatrix} 2 & 0 \\ 0 & 0.5 \end{bmatrix} \begin{bmatrix} \cos \frac{\pi}{6} & \sin \frac{\pi}{6} \\ -\sin \frac{\pi}{6} & \cos \frac{\pi}{6} \end{bmatrix} + [3 \ 2].$$

```
t = np.array([3, 2])
S = np.diag([2, 0.5])
S
## array([[2., 0.],
##        [0., 0.5]])
alpha = np.pi/6
Q = np.array([
    [np.cos(alpha), np.sin(alpha)],
    [-np.sin(alpha), np.cos(alpha)]
])
Q
## array([[ 0.8660254,  0.5       ],
##        [-0.5       ,  0.8660254]])
Y = X @ S @ Q + t
```

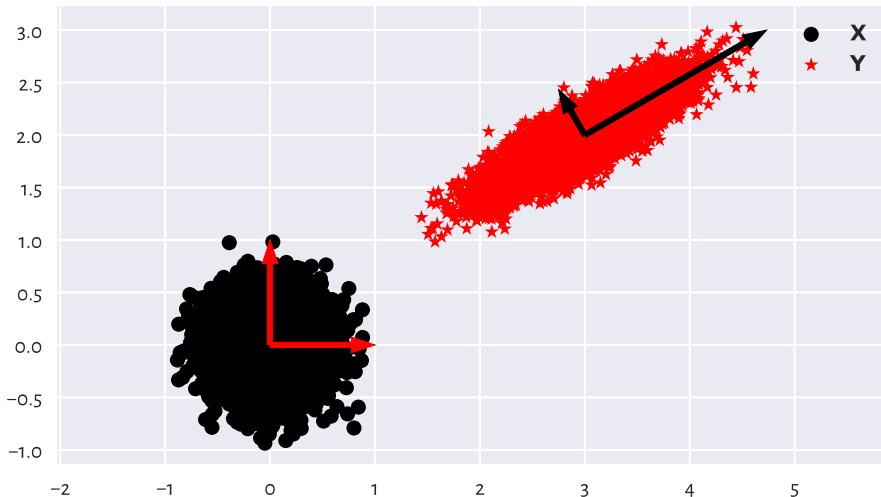


Figure 9.17: A dataset and its scaled, rotated, and shifted version

We can consider $\mathbf{Y} = \mathbf{X}\mathbf{S}\mathbf{Q} + \mathbf{t}$ a version of \mathbf{X} in a new coordinate system (basis), see

Figure 9.17. Each column in the transformed matrix is a shifted linear combination of the columns in the original matrix:

$$\mathbf{y}_{\cdot,j} = t_j + \sum_{k=1}^m (s_{k,k} q_{k,j}) \mathbf{x}_{\cdot,k}.$$

Computing such linear combinations of columns is natural during a dataset's pre-processing step, especially if they are on the same scale or they are unitless. Actually, we can note that standardisation itself is a form of scaling and translation.

Exercise 9.11 Assume that we have a dataset with two columns, giving the number of apples and the number of oranges in a fresh veggie market clients' baskets. What kind of orthonormal and scaling transforms should be applied to obtain a matrix bearing the total number of fruits and surplus apples (e.g., a row $(4, 7)$ should be converted to $(11, -3)$)?

9.3.3 Matrix Inverse

The *inverse* of a square matrix \mathbf{A} (if it exists) is denoted with \mathbf{A}^{-1} – it is the matrix fulfilling the identity

$$\mathbf{A}^{-1}\mathbf{A} = \mathbf{A}\mathbf{A}^{-1} = \mathbf{I}.$$

Noting that the identity matrix \mathbf{I} is the neutral element of the matrix multiplication, the above is thus the analogue of the inverse of a scalar: something like $3 \cdot 3^{-1} = 3 \cdot \frac{1}{3} = \frac{1}{3} \cdot 3 = 1$.

Important: For any invertible matrices of admissible shapes, it might be shown that the following noteworthy properties hold:

- $(\mathbf{A}^{-1})^T = (\mathbf{A}^T)^{-1}$,
- $(\mathbf{AB})^{-1} = \mathbf{B}^{-1}\mathbf{A}^{-1}$,
- a matrix equality $\mathbf{A} = \mathbf{BC}$ holds if and only if $\mathbf{AC}^{-1} = \mathbf{BC}\mathbf{C}^{-1} = \mathbf{B}$; this is also equivalent to $\mathbf{B}^{-1}\mathbf{A} = \mathbf{B}^{-1}\mathbf{BC} = \mathbf{C}$.

Matrix inverse allows us to identify the inverses of geometrical transformations. Knowing that $\mathbf{Y} = \mathbf{XSQ} + \mathbf{t}$, we can recreate the original matrix by applying:

$$\mathbf{X} = (\mathbf{Y} - \mathbf{t})(\mathbf{SQ})^{-1} = (\mathbf{Y} - \mathbf{t})\mathbf{Q}^{-1}\mathbf{S}^{-1}.$$

It is worth knowing that if $\mathbf{S} = \text{diag}(s_1, s_2, \dots, s_m)$ is a diagonal matrix, then its inverse is $\mathbf{S}^{-1} = \text{diag}(1/s_1, 1/s_2, \dots, 1/s_m)$.

Furthermore, the inverse of an orthonormal matrix \mathbf{Q} is always equal to its transpose, $\mathbf{Q}^{-1} = \mathbf{Q}^T$.

Luckilly, we will not be inverting other matrices in this introductory course.

Let us verify this numerically (testing equality up to some inherent round-off error):

```
np.allclose(X, (Y-t) @ Q.T @ np.diag(1/np.diag(S)))
## True
```

9.3.4 Singular Value Decomposition

It turns out that given any real n -by- m matrix \mathbf{Y} with $n \geq m$, we can find a very interesting scaling and orthonormal transforms that, when applied on a dataset whose columns are already normalised, yield exactly \mathbf{Y} .

Namely, the singular value decomposition (SVD in the so-called compact form) is a factorisation

$$\mathbf{Y} = \mathbf{U}\mathbf{S}\mathbf{Q},$$

where:

- \mathbf{U} is an n -by- m semi-orthonormal matrix (its columns are orthonormal vectors; it holds $\mathbf{U}^T\mathbf{U} = \mathbf{I}$);
- \mathbf{S} is an m -by- m diagonal matrix such that $s_{1,1} \geq s_{2,2} \geq \dots \geq s_{m,m} \geq 0$;
- \mathbf{Q} is an m -by- m orthonormal matrix.

Important: In data analysis, we usually apply the SVD on matrices that have already been centred (so that their column means are all 0).

```
import scipy.linalg
n = Y.shape[0]
Y_centred = Y - np.mean(Y, axis=0)
U, s, Q = scipy.linalg.svd(Y_centred, full_matrices=False)
```

And now:

```
U[:6, :] # preview first few rows
## array([[-0.00195072,  0.00474569,
```

(continues on next page)

(continued from previous page)

```

##      [-0.00510625, -0.00563582],
##      [ 0.01986719,  0.01419324],
##      [ 0.00104386,  0.00281853],
##      [ 0.00783406,  0.01255288],
##      [ 0.01025205, -0.0128136 ]])

```

The norms of all the columns in \mathbf{U} are all equal to 1 (and hence standard deviations are $1/\sqrt{n}$), thus they are on the same scale:

```

np.std(U, axis=0), 1/np.sqrt(n) # compare
## array([0.01, 0.01], 0.01)

```

Furthermore, they are orthogonal: their dot products are all equal to 0. Regarding what we have said about Pearson's linear correlation coefficients and its relation to dot products of normalised vectors, we imply that the columns in \mathbf{U} are not linearly correlated – they form *independent* dimensions.

Now $\mathbf{S} = \text{diag}(s_1, \dots, s_m)$, with the elements on the diagonal being

```

s
## array([49.72180455, 12.5126241 ])

```

is used to scale each column in \mathbf{U} . The fact that the elements on the diagonal are ordered decreasingly means that the first column in \mathbf{US} has the greatest standard deviation, the second column has the second greatest variability, and so forth.

```

S = np.diag(s)
US = U @ S
np.std(US, axis=0) # equal to s/np.sqrt(n)
## array([0.49721805, 0.12512624])

```

Multiplying \mathbf{US} by \mathbf{Q} simply rotates and/or reflects the dataset. This brings \mathbf{US} to a new coordinate system where, by construction, the dataset projected onto the direction determined by the first row in \mathbf{Q} , i.e., $\mathbf{q}_{1,:}$ has the largest variance, projection onto $\mathbf{q}_{2,:}$ has the second largest variance, and so on.

```

Q
## array([[ 0.86781968,  0.49687926],
##        [-0.49687926,  0.86781968]])

```

This is why we refer to the rows in \mathbf{Q} as *principal directions* or *components*. Their scaled versions (proportional to the standard deviations along them) are depicted in Figure 9.18.

Note that this way we have more or less recreated the steps needed to construct \mathbf{Y} from \mathbf{X} above (by the way we generated \mathbf{X} , we expect it to have linearly uncorrelated columns; yet note that \mathbf{X} and \mathbf{U} have different column variances).

```
plt.plot(Y_centred[:, 0], Y_centred[:, 1], "o")
plt.arrow(
    0, 0, Q[0, 0]*s[0]/np.sqrt(n), Q[0, 1]*s[0]/np.sqrt(n),
    width=0.02, color="red", length_includes_head=True, zorder=2)
plt.arrow(
    0, 0, Q[1, 0]*s[1]/np.sqrt(n), Q[1, 1]*s[1]/np.sqrt(n),
    width=0.02, color="red", length_includes_head=True, zorder=2)
plt.show()
```

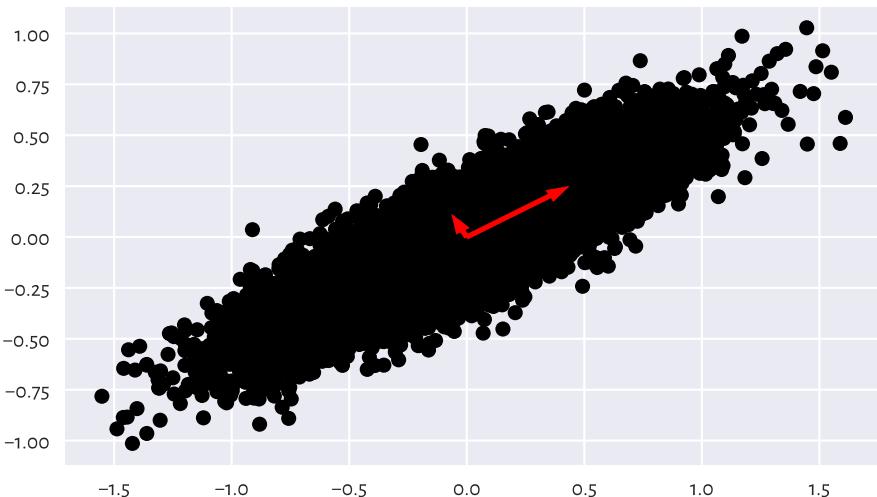


Figure 9.18: Principal directions of an example dataset (scaled so that they are proportional to the standard deviations along them)

9.3.5 Dimensionality Reduction with SVD

Let us consider the following example three dimensional dataset.

```
chainlink = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/clustering/fcps_chainlink.csv")
```

As we have told in [Section 7.4](#), plotting is always done on a 2-dimensional surface (be it the computer screen or book page), therefore we can look at the dataset only from one angle at a time.

In particular, a scatterplot matrix only depicts the dataset from the perspective of the axes of the Cartesian coordinate system (standard basis), see [Figure 9.19](#).

```
sns.pairplot(data=pd.DataFrame(chainlink))
# plt.show() # not needed :/
```

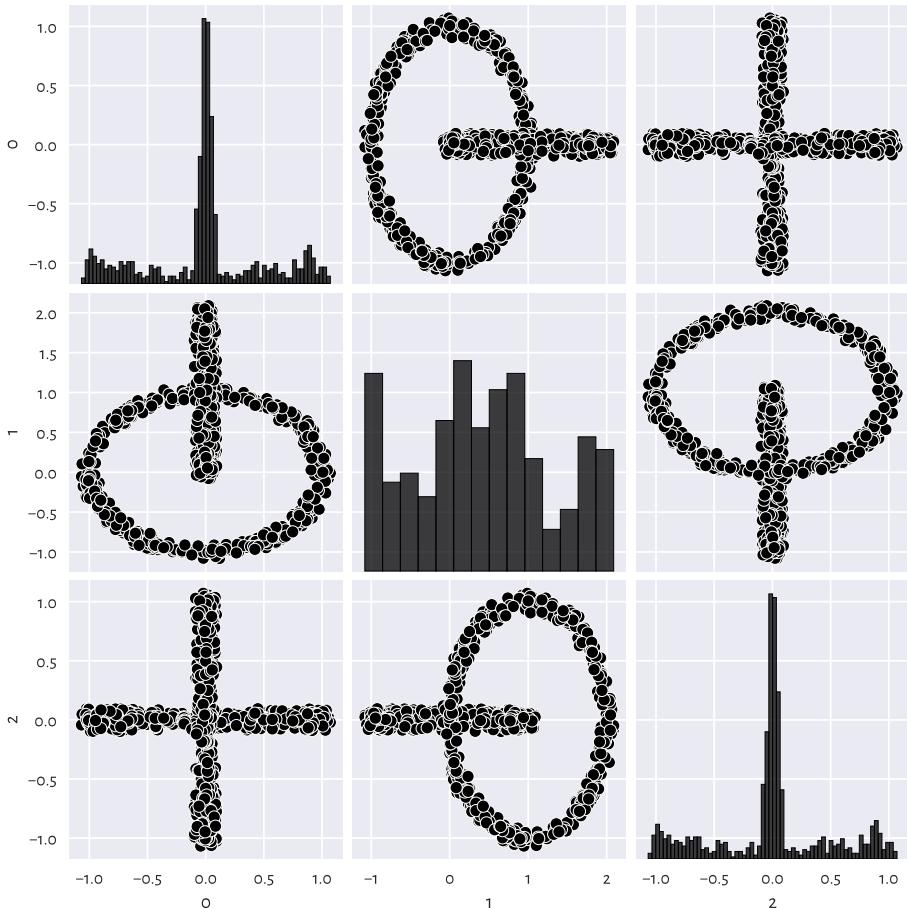


Figure 9.19: Views from the perspective of the main axes

These viewpoints by no means must reveal the true geometric structure of the dataset. We know that we can actually rotate the virtual camera and find some more *interesting* angle. It turns out that our dataset represents two nonintersecting rings, hopefully visible Figure 9.20.

```
fig = plt.figure()
ax = fig.add_subplot(131, projection="3d")
ax.scatter(chainlink[:, 0], chainlink[:, 1], chainlink[:, 2])
ax.view_init(elev=45, azim=45, vertical_axis="z")
ax = fig.add_subplot(132, projection="3d")
ax.scatter(chainlink[:, 0], chainlink[:, 1], chainlink[:, 2])
ax.view_init(elev=37, azim=0, vertical_axis="z")
ax = fig.add_subplot(133, projection="3d")
ax.scatter(chainlink[:, 0], chainlink[:, 1], chainlink[:, 2])
ax.view_init(elev=10, azim=150, vertical_axis="z")
plt.show()
```

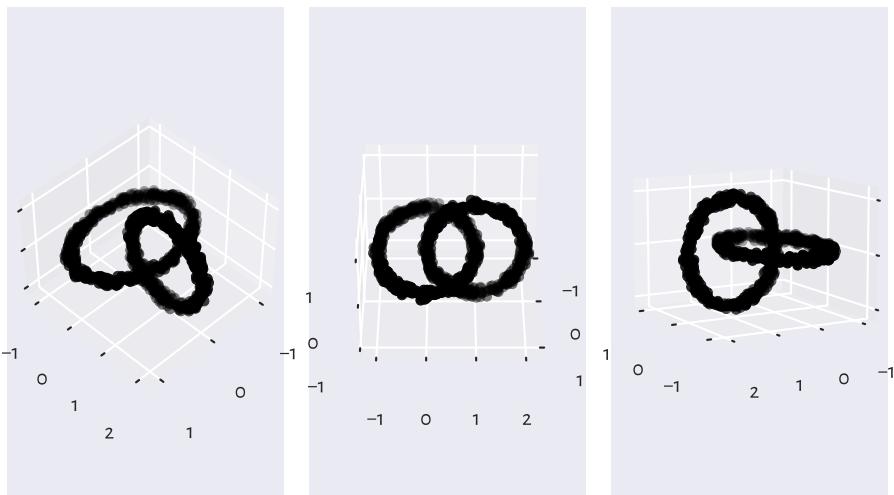


Figure 9.20: Different views

It turns out that we may find (one of the many) such an noteworthy viewpoint using the SVD. Namely, we can perform the decomposition of a centred dataset which we denote with \mathbf{Y} :

$$\mathbf{Y} = \mathbf{U}\mathbf{S}\mathbf{Q}$$

```
import scipy.linalg
Y_centered = chainlink-np.mean(chainlink, axis=0)
U, s, Q = scipy.linalg.svd(Y_centered, full_matrices=False)
```

Then, considering its rotated/reflected version

$$\mathbf{T} = \mathbf{YQ}^{-1} = \mathbf{US}$$

we know that its first column has the highest variance. Furthermore, the second column has the second highest variability, and so on. It might indeed be worth to look at that dataset from that *most informative* perspective.

Figure 9.21 gives the scatter plot for $\mathbf{t}_{:,1}$ and $\mathbf{t}_{:,2}$. Maybe this does not reveal the true geometric structure of the dataset (no single two-dimensional projection would do that here), but at least it is better than the initial ones (from the pairplot).

```
T2 = U[:, :2] @ np.diag(s[:2]) # the same as (U@np.diag(s))[:, :2]
plt.scatter(T2[:, 0], T2[:, 1])
plt.axis("equal")
plt.show()
```

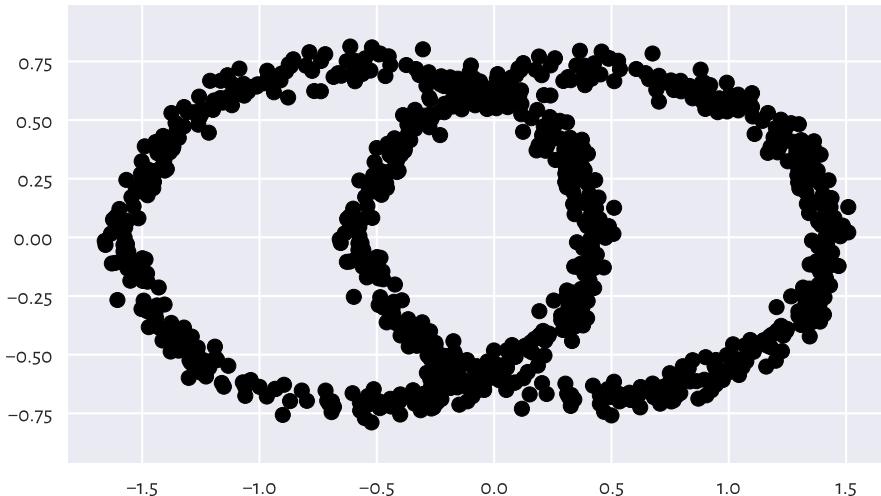


Figure 9.21: The view from the two principal axes

What we have thus done was a kind of *dimensionality reduction* – we have found a view-

point (in form of an orthonormal matrix, being a mixture of rotations and reflections) on \mathbf{Y} such that its orthonormal projection onto the first two axes of the Cartesian coordinate system is the most informative (in terms of having the highest variance, axis-wisely).

Note: (***) The Eckart–Young–Mirsky theorem states that $\mathbf{U}_{\cdot,:k}\mathbf{S}_{:k,:k}\mathbf{Q}_{:k,\cdot}$ (where “ $:k$ ” denotes “first k rows or columns”) is actually the best rank- k approximation of \mathbf{Y} with respect to both the Frobenius and spectral norms.

9.3.6 Principal Component Analysis

Principal component analysis (PCA) is a fancy name for the whole process of reflecting upon what happens along the projections onto the most variable dimensions. It can be used not only for data visualisation and deduplication, but also feature engineering (as in fact it creates new columns that are linear combinations of existing ones).

Let us consider a few chosen countrywise 2016 Sustainable Society Indices¹⁰⁴.

```
ssi = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/ssi_2016_indicators.csv",
    comment="#")
Y = ssi.iloc[:, [3, 5, 13, 15, 19]].to_numpy()
n = Y.shape[0]
Y[:6, :] # preview
## array([[ 9.32      ,  8.13333333,  8.386      ,  8.5757      ,
##          [ 8.74      ,  7.71666667,  7.346      ,  6.8426      ,
##          [ 5.11      ,  4.31666667,  8.788      ,  9.2035      ,
##          [ 9.61      ,  7.93333333,  5.97       ,  5.5232      ,
##          [ 8.95      ,  7.81666667,  8.032      ,  8.2639      ,
##          [10.        ,  8.65       ,  1.         ,  1.         ,  9.66401848]])
```

Each index is on the scale from 0 to 10. These are, in this order:

1. Safe Sanitation,
2. Healthy Life,
3. Energy Use,
4. Greenhouse Gases,

¹⁰⁴ <https://ssi.wi.th-koeln.de/>

5. Gross Domestic Product.

Note that above we have displayed the data corresponding to the 6 following countries:

```
countries = list(ssi.iloc[:, 0])
countries[:6] # preview
## ['Albania', 'Algeria', 'Angola', 'Argentina', 'Armenia', 'Australia']
```

This is a 5-dimensional dataset, thus we cannot easily visualise it. That the pairplot does not reveal too much is left as an exercise.

Let us thus perform the SVD decomposition of a standardised version of this dataset (recall that centring is necessary, at the very least).

```
Y_std = (Y - np.mean(Y, axis=0))/np.std(Y, axis=0)
U, s, Q = scipy.linalg.svd(Y_std, full_matrices=False)
```

The standard deviations of the data projected onto the consecutive principal components (columns in **US**) are:

```
s/np.sqrt(n)
## array([2.02953531, 0.7529221 , 0.3943008 , 0.31897889, 0.23848286])
```

It is customary to check the ratios of the variances explained by the consecutive principal components, which is a normalised measure of their importances. We can compute them by calling:

```
np.cumsum(s**2)/np.sum(s**2)
## array([0.82380272, 0.93718105, 0.96827568, 0.98862519, 1.])
```

Thus, we may say that the variability within the first two components covers 94% of the variability of the whole dataset. It might thus be a good idea to consider only a 2-dimensional projection of this dataset (actually, we are quite lucky here – or someone has selected these countrywise indices for us in a very clever fashion).

The rows in **Q** give us the so-called *loadings*. They give the coefficients defining the linear combinations of the rows in **Y** that correspond to the principal components.

Let us try to interpret them.

```
np.round(Q[0, :], 2)
## array([-0.43, -0.43, 0.44, 0.45, -0.47])
```

The first row in **Q** consists of similar values, but with different signs. We can consider them a scaled version of the average of Energy Use (column 3), Greenhouse Gases (4), and

MINUS Safe Sanitation (1), MINUS Healthy Life (2), MINUS Gross Domestic Product (5). Possibly some kind of a measure of a country's overall eco-unfriendliness?

```
np.round(Q[1, :], 2)
## array([ 0.52,  0.5 ,  0.52,  0.45, -0.02])
```

The second row in **Q** defines a scaled version of the average of Safe Sanitation (1), Healthy Life (2), Energy Use (3), and Greenhouse Gases (4), almost totally ignoring the GDP (5). Should we call it a measure of industrialisation? Something like this. But this naming is just for fun; mathematics – unlike the human brain – doesn't need our imperfect interpretations/fairy tales to function properly.

In Figure 9.22 is a scatter plot of the countries projected onto the said 2 principal directions. For readability, we only display a few chosen labels.

```
T2 = U[:, :2] @ np.diag(s[:2]) # == Y @ Q[:, :].T
plt.scatter(T2[:, 0], T2[:, 1], alpha=0.1)
which = [    # hand-crafted/artisan
    141, 117, 69, 123, 35, 80, 93, 45, 15, 2, 60, 56, 14,
    104, 122, 8, 134, 128, 0, 94, 114, 50, 34, 41, 33, 77,
    64, 67, 152, 135, 148, 99, 149, 126, 111, 57, 20, 63
]
for i in which:
    plt.text(T2[i, 0], T2[i, 1], countries[i], ha="center") #countries[i])
plt.axis("equal")
plt.xlabel("1st principal component (eco-unfriendliness?)")
plt.ylabel("2nd principal component (industrialisation?)")
plt.show()
```

This is merely a projection, but it might be an interesting one for some practitioners.

9.4 Further Reading

Some now-classic introductory text in statistical learning is [[HTF17]]. We recommend [[Biso06], [BHK20], [DGL96]] for more advanced students.

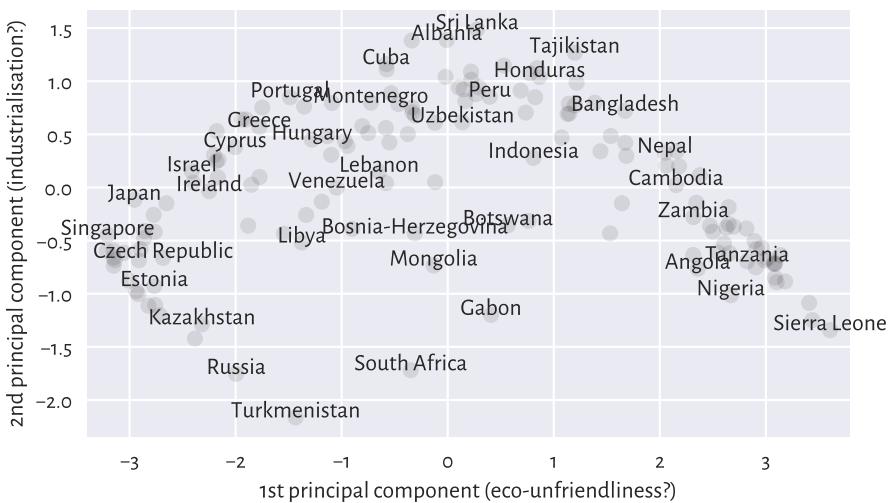


Figure 9.22: An example principal component analysis of countries

9.5 Exercises

Exercise 9.12 What does “correlation is not causation” mean?

Exercise 9.13 What does linear correlation of 0.9 mean? How about rank correlation of 0.9? And linear correlation of 0.0?

Exercise 9.14 How is the Spearman’s coefficient related to the Pearson’s one?

Exercise 9.15 How to write a linear model equation using the notion of the dot product?

Exercise 9.16 State the optimisation problem behind the least squares fitting of linear models.

Exercise 9.17 What are the different ways of the numerical summarising of residuals?

Exercise 9.18 Why is it important for the residuals to be homoscedastic?

Exercise 9.19 Is a more complex model always better?

Exercise 9.20 Why should extrapolation be handled with care?

Exercise 9.21 What is the difference between a train-test and a train-validate-test split?

Exercise 9.22 Why did we say that `scikit-learn` should be used carefully by novice users?

Exercise 9.23 What is a condition number of the model matrix and why it should always be checked?

Exercise 9.24 What is the geometrical interpretation of the dot product of two normalised vectors?

Exercise 9.25 How to verify if two vectors are orthogonal?

Exercise 9.26 What is an orthonormal projection? What is the inverse of an orthonormal matrix?

Exercise 9.27 What is the inverse of a diagonal matrix?

Exercise 9.28 Characterise the general properties of the three matrices obtained by performing the singular value decomposition of a given matrix of shape n-by-m.

Exercise 9.29 How to obtain the first principal component of a given centred matrix?

Exercise 9.30 How to compute the ratios of the variances explained by the consecutive principal components?

Part IV

Heterogeneous Data

Introducing Data Frames

numpy arrays are an extremely versatile tool for performing data analysis and other numerical computations computations of various kinds. Although theoretically possible otherwise, in practice we only store elements of the same type therein, most often numbers.

pandas¹¹¹ [[McK17]] is amongst over one hundred thousand¹¹² of open source packages and repositories that use **numpy** to provide additional data wrangling functionality. It was originally written by Wes McKinney and was heavily inspired by the `data.frame`¹²⁹ objects in S and R as well as tables in relational (think: SQL) databases and spreadsheets.

It is customary to load this package with the following alias:

```
import pandas as pd
```

The **pandas** package delivers a few classes, of which the most important are:

- `DataFrame` – for representing tabular data (matrix-like) with columns of possibly different types, in particular a mix of numerical and categorical variables,
- `Series` – vector-like objects for representing individual columns,
- `Index` – vector-like (usually) objects for labelling individual rows and columns of `DataFrames` and items in `Series` objects,

together with many methods for:

- transforming/aggregating/processing data, also in groups determined by categorical variables or products thereof,
- reshaping (e.g., from wide to long format) and joining datasets,
- importing/exporting data from/to various sources and formats, e.g., CSV and HDF5 files or relational databases,

¹¹¹ <https://pandas.pydata.org/>

¹¹² <https://libraries.io/pypi/numpy>

¹²⁹ Data frames were first introduced in the 1991 version of the S language [[CH91]].

- handling missing data,

which we introduce in this and further chapters.

10.1 Creating Data Frames

Important: Let us repeat: **pandas** is built on top of **numpy** and most objects therein can be processed by **numpy** functions as well. Other functions (e.g., in **seaborn** or **sklearn**) will be accepting both **DataFrame** and **ndarray** objects, but will be converting the former to the latter automatically to enable data processing using fast C/C++/Fortran routines. What we have learnt so far still applies. But there is of course more, hence this part.

Data frames can be created, amongst others, using the **DataFrame** class constructor, which can be fed, for example, with a **numpy** matrix:

```
np.random.seed(123)
pd.DataFrame(
    np.random.rand(4, 3),
    columns=["a", "b", "c"]
)
##           a         b         c
## 0  0.696469  0.286139  0.226851
## 1  0.551315  0.719469  0.423106
## 2  0.980764  0.684830  0.480932
## 3  0.392118  0.343178  0.729050
```

Note that rows and columns are labelled (and how readable that is).

A dictionary of vector-like objects of equal lengths is another common option:

```
np.random.seed(123)
pd.DataFrame(dict(
    u=np.round(np.random.rand(5), 2),
    v=[True, True, False, False, True],
    w=["A", "B", "C", "D", "E"],
    x=["spam", "spam", "bacon", "spam", "eggs"]
))
##           u         v         w         x
```

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```
## 0 0.70  True A  spam
## 1 0.29  True B  spam
## 2 0.23 False C bacon
## 3 0.55 False D  spam
## 4 0.72  True E  eggs
```

This illustrates the possibility of having columns of different types.

Exercise 10.1 Check out the `pandas.DataFrame.from_dict` and `pandas.DataFrame.from_records` methods in the documentation¹¹³. Use them to create some example data frames.

Further, data frames can be read from files in different formats, for instance, CSV:

```
body = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_adult_female_bmx_2020.csv",
    comment="#")
body.head() # display first few rows (5 by default)
##   BMXWT  BMXHT  BMXARML  BMXLEG  BMXARMC  BMXHIP  BMXWAIST
## 0  97.1   160.2     34.7    40.8     35.8    126.1    117.9
## 1  91.1   152.7     33.5    33.0     38.5    125.5    103.1
## 2  73.0   161.2     37.4    38.0     31.8    106.2     92.0
## 3  61.7   157.4     38.0    34.7     29.0    101.0     90.5
## 4  55.4   154.6     34.6    34.0     28.3    92.5     73.2
```

Reading from URLs and local files (compare Section 13.6.1) is of course supported.

Exercise 10.2 Check out the other `pandas.read_*` functions in the `pandas` documentation – some of which we shall be discussing later.

10.1.1 Data Frames are Matrix-Like

Data frames are modelled through `numpy` matrices, hence we can feel quite at home with them.

For example, given:

```
np.random.seed(123)
df = pd.DataFrame(dict(
    u=np.round(np.random.rand(5), 2),
    v=[True, True, False, False, True],
```

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¹¹³ <https://pandas.pydata.org/docs/>

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```
w=["A", "B", "C", "D", "E"],
x=["spam", "spam", "bacon", "spam", "eggs"]
))
df
##      u      v   w      x
## 0  0.70  True  A  spam
## 1  0.29  True  B  spam
## 2  0.23 False  C bacon
## 3  0.55 False  D  spam
## 4  0.72  True  E  eggs
```

it is easy to fetch the number of rows and columns:

```
df.shape
## (5, 4)
```

or the type of each column:

```
df.dtypes
## u      float64
## v        bool
## w      object
## x      object
## dtype: object
```

Recall that arrays are equipped with the `dtype` slot.

10.1.2 Series

There is a separate class for storing individual data frame columns: it is called `Series`.

```
s = df.loc[:, "u"] # extract the `u` column; alternatively: d.u
s
## 0    0.70
## 1    0.29
## 2    0.23
## 3    0.55
## 4    0.72
## Name: u, dtype: float64
```

Note that a data frame with one column is printed out slightly differently:

```
s.to_frame()  
##           u  
## 0    0.70  
## 1    0.29  
## 2    0.23  
## 3    0.55  
## 4    0.72
```

Indexing will of course be discussed later.

Important: It is crucial to know when we are dealing with a `Series` and when with a `DataFrame` object, because each of them defines a slightly different set of methods.

For example:

```
s.mean()  
## 0.4980000000000005
```

refers to `pandas.Series.mean` (which returns a scalar), whereas

```
df.mean(numeric_only=True)  
## u    0.498  
## v    0.600  
## dtype: float64
```

uses `pandas.DataFrame.mean` (which yields a `Series`).

Exercise 10.3 Look up the two methods in the `pandas` manual. Note that their argument list is slightly different.

`Series` are wrappers around `numpy` arrays.

```
s.values  
## array([0.7 , 0.29, 0.23, 0.55, 0.72])
```

Most importantly, `numpy` functions can be called directly on them:

```
np.mean(s)  
## 0.4980000000000005
```

Hence, what we have covered in the part dealing with vector processing still holds for data frame columns as well (there will be more, stay tuned).

`Series` can also be *named*.

```
s.name
## 'u'
```

This is convenient when we convert from/to a data frame.

```
s.rename("spam").to_frame()
##      spam
## 0  0.70
## 1  0.29
## 2  0.23
## 3  0.55
## 4  0.72
```

10.1.3 Index

Another important class is `Index`, which is used for encoding the row and column names in a data frame:

```
df.index # row labels
## RangeIndex(start=0, stop=5, step=1)
```

The above represents a sequence (0, 1, 2, 3, 4).

```
df.columns # column labels
## Index(['u', 'v', 'w', 'x'], dtype='object')
```

Also, we can label the individual elements in `Series` objects:

```
s.index
## RangeIndex(start=0, stop=5, step=1)
```

A quite frequent operation that we'll be applying to make a data frame column act as a vector of row labels is implemented in the `set_index` method for data frames:

```
df2 = df.set_index("x")
df2
##           u      v    w
## x
## spam    0.70  True   A
## spam    0.29  True   B
```

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```
## bacon  0.23  False  C
## spam   0.55  False  D
## eggs   0.72  True   E
```

Note that this `Index` object is named:

```
df2.index.name
## 'x'
```

which is handy when we decide that we want to convert the vector of row labels back to a standalone column:

```
df2.reset_index()
##      x      u      v      w
## 0  spam  0.70  True   A
## 1  spam  0.29  True   B
## 2 bacon  0.23  False  C
## 3  spam  0.55  False  D
## 4  eggs  0.72  True   E
```

There is also an option to get rid of the current `.index` and to replace it with the default label sequence, i.e., 0, 1, 2, ...:

```
df2.reset_index(drop=True)
##      u      v      w
## 0  0.70  True   A
## 1  0.29  True   B
## 2  0.23  False  C
## 3  0.55  False  D
## 4  0.72  True   E
```

Important: In due course, we will be calling `df.reset_index(drop=True)` quite frequently, sometimes more than once in a single chain of commands.

Exercise 10.4 Use the `pandas.DataFrame.rename` method to change the name of the `u` column in `df` to `spam`.

Also, a *hierarchical* index – one that is comprised of more than two levels – is possible:

```
df.sort_values("x", ascending=False).set_index(["x", "v"])
##           u   w
## x      v
## spam  True  0.70 A
##          True  0.29 B
##          False 0.55 D
## eggs  True  0.72 E
## bacon False  0.23 C
```

Note that a group of three consecutive `spams` does not have the labels repeated – this is for increased readability.

Important: We will soon see that hierarchical indexes might arise after aggregating data in groups (via the `groupby` method).

For example¹¹⁴:

```
nhanes = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_p_demo_bmx_2020.csv",
    comment="#")
res = nhanes.groupby(["RIAGENDR", "DMDEDUC2"])["BMXBMI"].mean()
res # BMI by gender and education
## RIAGENDR DMDEDUC2
## 1          1.0      28.765244
##          2.0      28.534737
##          3.0      29.637793
##          4.0      30.323158
##          5.0      28.689736
##          9.0      28.080000
## 2          1.0      30.489032
##          2.0      31.251247
##          3.0      30.969200
##          4.0      31.471476
##          5.0      28.891357
##          7.0      30.200000
##          9.0      33.950000
## Name: BMXBMI, dtype: float64
```

¹¹⁴ https://www.cdc.gov/Nchs/Nhanes/2017-2018/P_DEMO.htm

But let us fret not, as there is always:

```
res.reset_index()  
##   RIAGENDR DMDEDUC2    BMXBMI  
## 0         1     1.0 28.765244  
## 1         1     2.0 28.534737  
## 2         1     3.0 29.637793  
## 3         1     4.0 30.323158  
## 4         1     5.0 28.689736  
## 5         1     9.0 28.080000  
## 6         2     1.0 30.489032  
## 7         2     2.0 31.251247  
## 8         2     3.0 30.969200  
## 9         2     4.0 31.471476  
## 10        2     5.0 28.891357  
## 11        2     7.0 30.200000  
## 12        2     9.0 33.950000
```

10.2 Aggregating

Here is an example data frame:

```
np.random.seed(123)  
d = pd.DataFrame(dict(  
    u = np.round(np.random.rand(5), 2),  
    v = np.round(np.random.randn(5), 2),  
    w = ["spam", "bacon", "spam", "eggs", "sausage"]  
), index=["a", "b", "c", "d", "e"])  
d  
##      u      v      w  
## a  0.70  0.32    spam  
## b  0.29 -0.05   bacon  

```

First, all **numpy** functions can be applied directly on individual columns (i.e., objects of type `Series`), as the latter are, after all, vector-like.

```
np.quantile(d.loc[:, "u"], [0, 0.5, 1])
## array([0.23, 0.55, 0.72])
```

For more details on the `loc[...]`-type indexing, see below. By then, the meaning of the above should be clear from the context.

Most `numpy` functions also work if they are fed with data frames, but we will need to extract the numeric matrix columns manually.

```
np.quantile(d.loc[:, ["u", "v"]], [0, 0.5, 1], axis=0)
## array([[ 0.23, -1.62],
##        [ 0.55, -0.05],
##        [ 0.72,  1.98]])
```

Sometimes the results will automatically be coerced to a `Series` object with `index` slot set appropriately:

```
np.mean(d.loc[:, ["u", "v"]], axis=0)
## u    0.498
## v    0.086
## dtype: float64
```

Many operations, for convenience, have also been implemented as methods in the `Series` and `DataFrame` classes, e.g., `mean`, `median`, `min`, `max`, `quantile`, `var`, `std` (with `ddof=1` by default, interestingly), and `skew`.

```
d.loc[:, ["u", "v"]].mean(numeric_only=True)
## u    0.498
## v    0.086
## dtype: float64
d.loc[:, ["u", "v"]].quantile([0, 0.5, 1], numeric_only=True)
##      u      v
## 0.0  0.23 -1.62
## 0.5  0.55 -0.05
## 1.0  0.72  1.98
```

Also note the `describe` method, which returns a few statistics at the same time.

```
d.describe()
##              u            v
```

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```
## count  5.000000  5.000000
## mean   0.498000  0.086000
## std    0.227969  1.289643
## min    0.230000 -1.620000
## 25%    0.290000 -0.200000
## 50%    0.550000 -0.050000
## 75%    0.700000  0.320000
## max    0.720000  1.980000
```

Note: (*) Let us stress that above we see the corrected for bias (but still only asymptotically unbiased) version of standard deviation (`ddof=1`), given by $\sqrt{\frac{1}{n-1} \sum_{i=1}^n (x_i - \bar{x})^2}$, compare [Section 5.1](#).

Exercise 10.5 Check out the `pandas.DataFrame.agg` method that can apply all aggregating operations from a given list of functions. Write a call equivalent to `d.describe()`.

10.3 Transforming

By applying the already well-known vectorised mathematical `numpy` functions. we can transform each data cell and return an object of the same type as the input one.

```
np.exp(d.loc[:, "u"])
## a      2.013753
## b      1.336427
## c      1.258600
## d      1.733253
## e      2.054433
## Name: u, dtype: float64
np.exp(d.loc[:, ["u", "v"]])
##          u          v
## a  2.013753  1.377128
## b  1.336427  0.951229
## c  1.258600  0.818731
## d  1.733253  7.242743
## e  2.054433  0.197899
```

When applying the binary arithmetic, comparison, and logical operators on an object of class `Series` and a scalar or a `numpy` vector, the operations are performed elementwisely – a style with which we are already familiar.

For instance, here is a standardised version of the `u` column:

```
u = d.loc[:, "u"]
(u - np.mean(u)) / np.std(u)
## a    0.990672
## b   -1.020098
## c   -1.314357
## d    0.255025
## e    1.088759
## Name: u, dtype: float64
```

For two objects of class `Series`, the operators are vectorised somewhat differently from their `numpy` counterparts: they are applied on the pairs of elements having *identical labels* (i.e., labelwisely). Still, if we are transforming the columns that come from the same data frame (and thus having identical `index` slots; this is the most common scenario), there will be no surprises, because this is equivalent to elementwise action. For instance:

```
d.loc[:, "u"] > d.loc[:, "v"]
## a    True
## b    True
## c    True
## d   False
## e    True
## dtype: bool
```

For transforming many numerical columns at once, it is a good idea either to convert them to a numeric matrix explicitly and then use the basic `numpy` functions:

```
uv = d.loc[:, ["u", "v"]].values
uv = (uv-np.mean(uv, axis=0))/np.std(uv, axis=0)
uv
## array([[ 0.99067229,  0.20286225],
##        [-1.0200982 , -0.11790285],
##        [-1.3143573 , -0.24794275],
##        [ 0.25502455,  1.64197052],
##        [ 1.08875866, -1.47898717]])
```

or to use the `pandas.DataFrame.apply` method which invokes a given function on each column separately:

```
def standardise(x): return (x-np.mean(x))/np.std(x)
uv = d.loc[:, ["u", "v"]].apply(standardise)
uv
##           u            v
## a  0.990672  0.202862
## b -1.020098 -0.117903
## c -1.314357 -0.247943
## d  0.255025  1.641971
## e  1.088759 -1.478987
```

Note that, in both cases, we can then write:

```
d.loc[:, ["u", "v"]] = uv
```

to replace the old content with the transformed one.

Also, new columns can be added based on transformed versions of the existing ones:

```
d.loc[:, "uv_squared"] = (d.loc[:, "u"] * d.loc[:, "v"])**2
d
##           u            v            w      uv_squared
## a  0.990672  0.202862    spam   0.040389
## b -1.020098 -0.117903  bacon  0.014465
## c -1.314357 -0.247943    spam   0.106201
## d  0.255025  1.641971    eggs   0.175346
## e  1.088759 -1.478987  sausage 2.592938
```

10.4 Filtering Series Objects

Recall that each `DataFrame` and `Series` object is equipped with a slot called `index`, which is an object of class `Index` (or subclass thereof), giving the row and element labels, respectively. It turns out that we may apply the `index` operator, `[...]`, to subset these objects not only through the `indexers` known from the `numpy` part (e.g., numerical ones, i.e., by position) but also ones that pinpoint the items via their labels. That is quite a lot of index-ing.

Let us study different forms thereof in very detail.

In this section we play with two example objects of class `Series`:

```
np.random.seed(123)
b = pd.Series(np.round(np.random.uniform(0,1,10),2))
b.index = np.random.permutation(np.arange(0,10))
b
## 2    0.70
## 1    0.29
## 8    0.23
## 7    0.55
## 9    0.72
## 4    0.42
## 5    0.98
## 6    0.68
## 3    0.48
## 0    0.39
## dtype: float64
c = b.copy()
c.index = list("abcdefghij")
c
## a    0.70
## b    0.29
## c    0.23
## d    0.55
## e    0.72
## f    0.42
## g    0.98
## h    0.68
## i    0.48
## j    0.39
## dtype: float64
```

They consist of the same values, in the same order, but have different labels (`.index` slots). In particular, `b`'s labels are integers which *do not* match the physical element positions (where 0 would denote the first element, etc.).

Important: For `numpy` vectors, we had four different indexing schemes: by scalar (extracts an element at given position), slice, integer vector, and logical vector. `Series` objects are *additionally* labelled, therefore they can *additionally* be accessed taking into account the contents of the `.index` slot.

10.4.1 Do Not Use [...] Directly

Applying the index operator, [...], directly on `Series` is generally not a good idea:

```
b[0]  
## 0.39  
b[ [0] ]  
## 0    0.39  
## dtype: float64
```

both do not select the first item, but the item labelled 0.

However:

```
b[0:1] # slice - 0 only  
## 2    0.7  
## dtype: float64
```

and

```
c[0] # there is no label `0`  
## 0.7
```

fall back to position-based indexing.

Confusing? Well, with some self-discipline, the solution is easy. Namely:

Important: To stay away from potential problems, we should never apply [...] directly on `Series` objects.

10.4.2 loc[...]

To avoid ambiguity, which is what we want, we should be referring to `Series.loc[...]` and `Series.iloc[...]` for label- and position-based filtering, respectively.

And thus:

```
b.loc[0]  
## 0.39
```

returns the element labelled 0. On the other hand, `c.loc[0]` will raise a `KeyError`, because `c` consists of character labels only.

Next, we can use lists of labels to select a *subset*.

```
b.loc[ [0, 1, 0] ]
## 0    0.39
## 1    0.29
## 0    0.39
## dtype: float64
c.loc[ ["j", "b", "j"] ]
## j    0.39
## b    0.29
## j    0.39
## dtype: float64
```

The result is always of type `Series`.

Slicing behaves differently as the range is *inclusive* at both sides:

```
b.loc[1:7]
## 1    0.29
## 8    0.23
## 7    0.55
## dtype: float64
b.loc[0:4:-1]
## 0    0.39
## 3    0.48
## 6    0.68
## 5    0.98
## 4    0.42
## dtype: float64
c.loc["d":"g"]
## d    0.55
## e    0.72
## f    0.42
## g    0.98
## dtype: float64
```

return all elements between the two indicated labels.

Be careful that if there are repeated labels, then we will be returning all the matching items:

```
d = pd.Series([1, 2, 3, 4], index=["a", "b", "a", "c"])
```

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```
d.loc["a"]  
## a      1  
## a      3  
## dtype: int64
```

The result is not a scalar but a `Series` object.

10.4.3 `iloc[...]`

Here are some examples of position-based indexing:

```
b.iloc[0] # the same: c.iloc[0]  
## 0.7
```

returns the first element.

```
b.iloc[1:7] # the same: b.iloc[1:7]  
## 1      0.29  
## 8      0.23  
## 7      0.55  
## 9      0.72  
## 4      0.42  
## 5      0.98  
## dtype: float64
```

returns the 2nd, 3rd, ..., 7th element (not including `b.iloc[7]`, i.e., the 8th one).

10.4.4 Logical Indexing

Indexing using a logical vector-like object is also available.

We usually will be using `loc[...]` with either a `Series` object of identical `.index` slot as the subsetted object or a logical `numpy` vector.

```
b.loc[(b > 0.4) & (b < 0.6)]  
## 7      0.55  
## 4      0.42  
## 3      0.48  
## dtype: float64
```

For `iloc[...]`, the indexer must be unlabelled, like in, e.g., `b.loc[i.values]`.

10.5 Filtering Data Frames

10.5.1 loc[...] and iloc[...]

For data frames, `iloc` and `loc` can be used too, but they now require two arguments, serving as row and column selectors.

For example:

```
np.random.seed(123)
d = pd.DataFrame(dict(
    u = np.round(np.random.rand(5), 2),
    v = np.round(np.random.randn(5), 2),
    w = ["spam", "bacon", "spam", "eggs", "sausage"],
    x = [True, False, True, False, True]
), index=["a", "b", "c", "d", "e"])
```

And now:

```
d.loc[d.loc[:, "u"] > 0.5, "u":"w"]
##      u      v      w
## a  0.70  0.32    spam
## d  0.55  1.98    eggs
## e  0.72 -1.62  sausage
```

selects the rows where the values in the `u` column are greater than 0.5 and then returns all columns between `u` and `w`.

Furthermore,

```
d.iloc[:3, :].loc[:, ["u", "w"]]
##      u      w
## a  0.70    spam
## b  0.29   bacon
## c  0.23    spam
```

fetches the first 3 rows (by position – `iloc` is necessary) and then selects two indicated columns.

Important: We can write `d.u` as a shorter version of `d.loc[:, "u"]`. This improves the readability in contexts such as:

```
d.loc[(d.u >= 0.5) & (d.u <= 0.7), ["u", "w"]]
##      u      w
## a  0.70  spam
## d  0.55  eggs
```

However, this accessor is not universal: we can check this out by considering a data frame featuring a column named, e.g., `mean`.

Exercise 10.6 Use `pandas.DataFrame.drop` to select all columns but `v` in `d`.

Exercise 10.7 Use `pandas.Series.isin` (amongst others) to select all rows with `spam` and `bacon` on the `d`'s menu.

Exercise 10.8 In the `tips`¹¹⁵ dataset, select data on male customers where total bill was in the [10, 20] interval. Also, select data from Saturday and Sunday with tip greater than \$5 from `tips`.

10.5.2 Adding Rows and Columns

`loc[...]` can also used to add new columns to an existing data frame:

```
d.loc[:, "y"] = d.loc[:, "u"]**2 # or d.loc[:, "y"] = d.u**2
d
##      u      v      w      x      y
## a  0.70  0.32  spam  True  0.4900
## b  0.29 -0.05 bacon False  0.0841
## c  0.23 -0.20  spam  True  0.0529
## d  0.55  1.98  eggs False  0.3025
## e  0.72 -1.62 sausage  True  0.5184
```

Note that notation like “`d.new_column = ...`” will not work. As we have said, `loc` and `iloc` are universal, other accessors – not so much.

Exercise 10.9 Use `pandas.DataFrame.insert` to add a new column not necessarily at the end of `d`.

Exercise 10.10 Use `pandas.DataFrame.append` to add a few more rows to `d`.

10.5.3 Random Sampling

As a simple application of what we have covered so far, let us consider the case of randomly sampling a number of rows from an existing data frame.

¹¹⁵ https://raw.githubusercontent.com/gagolews/teaching_data/master/other/tips.csv

For the most basic use cases, we can use the `pandas.DataFrame.sample` method. It includes scenarios such as:

- randomly select 5 rows, without replacement,
- randomly select 20% rows, with replacement,
- randomly rearrange all the rows.

For example:

```
body = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_adult_female_bmx_2020.csv",
    comment="#")
body.sample(5, random_state=123) # 5 random rows without replacement
##      BMXWT  BMXHT  BMXARML  BMXLEG  BMXARMC  BMXHIP  BMXWAIST
## 4214   58.4  156.2    35.2    34.7    27.2    99.5    77.5
## 3361   73.7  161.0    36.5    34.5    29.0   107.6    98.2
## 3759   61.4  164.6    37.5    40.4    26.9    93.5    84.4
## 3733  120.4  158.8    33.5    34.6    40.5   147.2   129.3
## 1121  123.5  157.5    35.5    29.0    50.5   143.0   136.4
```

Note the `random_state` argument which controls the seed of the random number generator so that we get reproducible results. Alternatively, we could call `numpy.random.seed`.

Exercise 10.11 Show how the 3 aforementioned scenarios can be implemented manually using `iloc[...]` and `numpy.random.permutation` or `numpy.random.choice`.

In machine learning practice, as we shall see later, we are used to training and evaluating machine learning models on different (mutually disjoint) subsets of the whole data frame.

For instance, we might be interested in performing the so-called *train/test split*, where 80% (or 60% or 70%) of the randomly selected rows would constitute the first new data frame and the remaining 20% (or 40% or 30%) would go to the second one.

Given a data frame like:

```
x = body.head(10) # this is just an example
x
##      BMXWT  BMXHT  BMXARML  BMXLEG  BMXARMC  BMXHIP  BMXWAIST
## 0     97.1  160.2    34.7    40.8    35.8   126.1   117.9
## 1     91.1  152.7    33.5    33.0    38.5   125.5   103.1
## 2     73.0  161.2    37.4    38.0    31.8   106.2    92.0
## 3     61.7  157.4    38.0    34.7    29.0   101.0    90.5
```

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```
## 4 55.4 154.6 34.6 34.0 28.3 92.5 73.2
## 5 62.0 144.7 32.5 34.2 29.8 106.7 84.8
## 6 66.2 166.5 37.5 37.6 32.0 96.3 95.7
## 7 75.9 154.5 35.4 37.6 32.7 107.7 98.7
## 8 77.2 159.2 38.5 40.5 35.7 102.0 97.5
## 9 91.6 174.5 36.1 45.9 35.2 121.3 100.3
```

one way to perform the aforementioned split is to generate a random permutation of the set of row indices:

```
np.random.seed(123) # reproducibility matters
idx = np.random.permutation(x.shape[0])
idx
## array([4, 0, 7, 5, 8, 3, 1, 6, 9, 2])
```

And then to pick the first 80% of these indices to construct the data frame number one:

```
k = int(x.shape[0]*0.8)
x.iloc[idx[:k], :]
##   BMXWT BMXHT BMXARML BMXLEG BMXARMC BMXHIP BMXWAIST
## 4 55.4 154.6 34.6 34.0 28.3 92.5 73.2
## 0 97.1 160.2 34.7 40.8 35.8 126.1 117.9
## 7 75.9 154.5 35.4 37.6 32.7 107.7 98.7
## 5 62.0 144.7 32.5 34.2 29.8 106.7 84.8
## 8 77.2 159.2 38.5 40.5 35.7 102.0 97.5
## 3 61.7 157.4 38.0 34.7 29.0 101.0 90.5
## 1 91.1 152.7 33.5 33.0 38.5 125.5 103.1
## 6 66.2 166.5 37.5 37.6 32.0 96.3 95.7
```

and the remaining ones to generate the second dataset:

```
x.iloc[idx[k:], :]
##   BMXWT BMXHT BMXARML BMXLEG BMXARMC BMXHIP BMXWAIST
## 9 91.6 174.5 36.1 45.9 35.2 121.3 100.3
## 2 73.0 161.2 37.4 38.0 31.8 106.2 92.0
```

Exercise 10.12 In the `wine_quality_all`¹¹⁶ dataset, leave out all but the white wines. Partition the resulting data frame randomly into three data frames: `wines_train` (60% of the rows), `wines_validate` (another 20% of the rows), and `wines_test` (the remaining 20%).

¹¹⁶ https://raw.githubusercontent.com/gagolews/teaching_data/master/other/wine_quality_all.csv

Exercise 10.13 Consider the white wines dataset again. Write a function **kfold** which takes a data frame x and an integer $k > 1$ on input. Return a list of data frames resulting in randomly splitting x into k disjoint chunks of equal (or almost equal if that is not possible) sizes.

10.5.4 Hierarchical Indices (*)

Consider the following `DataFrame` object with a hierarchical index:

```
np.random.seed(123)
d = pd.DataFrame(dict(
    year = sorted([2023, 2024, 2025]*4),
    quarter = ["Q1", "Q2", "Q3", "Q4"]*3,
    data = np.round(np.random.rand(12), 2)
)).set_index(["year", "quarter"])
d
##                  data
## year quarter
## 2023 Q1      0.70
##       Q2      0.29
##       Q3      0.23
##       Q4      0.55
## 2024 Q1      0.72
##       Q2      0.42
##       Q3      0.98
##       Q4      0.68
## 2025 Q1      0.48
##       Q2      0.39
##       Q3      0.34
##       Q4      0.73
```

The index has both levels named, but this is purely for aesthetic reasons.

Indexing using `loc[...]` by default relates to the first level of the hierarchy:

```
d.loc[2023, :]
##                  data
## quarter
## Q1      0.70
## Q2      0.29
## Q3      0.23
## Q4      0.55
```

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```
d.loc[[2023, 2025], :]
##                  data
## year quarter
## 2023 Q1        0.70
##     Q2        0.29
##     Q3        0.23
##     Q4        0.55
## 2025 Q1        0.48
##     Q2        0.39
##     Q3        0.34
##     Q4        0.73
```

To access deeper levels, we can use tuples as indexers:

```
d.loc[(2023, "Q1"), :]
## data    0.7
## Name: (2023, Q1), dtype: float64
d.loc[((2023, "Q1"), (2024, "Q3"))]
##                  data
## year quarter
## 2023 Q1        0.70
## 2024 Q3        0.98
```

In certain scenarios, though, it will probably be much easier to subset a hierarchical index by using `reset_index` and `set_index` creatively (together with `loc[...]` and `pandas.Series.isin`, etc.).

Also, we should note that the `:` operator for slicing can be used only *directly* within square brackets, but we can always use the `slice` constructor to create them from within any context:

```
d.loc[(slice(None), ["Q1", "Q3"])]
##                  data
## year quarter
## 2023 Q1        0.70
##     Q3        0.23
## 2024 Q1        0.72
##     Q3        0.98
## 2025 Q1        0.48
##     Q3        0.34
```

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```
d.loc[(slice(None, None, -1), slice("Q2", "Q3")), :] # ::-1, "Q2":"Q3"
##           data
## year quarter
## 2025 Q3      0.34
##     Q2      0.39
## 2024 Q3      0.98
##     Q2      0.42
## 2023 Q3      0.23
##     Q2      0.29
```

10.6 Sorting

Let's consider another example dataset. Here are the yearly (for 2018) average air quality data¹¹⁷ in the Australian state of Victoria.

```
air = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/air_quality_2018_means.csv",
    comment="#")
air = (
    air.
    loc[air.param_id.isin(["BPM2.5", "NO2"])].
    reset_index(drop=True)
)
air
##           sp_name param_id      value
## 0       Alphington    BPM2.5  7.848758
## 1       Alphington        NO2  9.558120
## 2   Altona North        NO2  9.467912
## 3     Churchill    BPM2.5  6.391230
## 4   Dandenong        NO2  9.800705
## 5   Footscray    BPM2.5  7.640948
## 6   Footscray        NO2 10.274531
## 7 Geelong South    BPM2.5  6.502762
## 8 Geelong South        NO2  5.681722
```

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¹¹⁷ <https://discover.data.vic.gov.au/dataset/epa-air-watch-all-sites-air-quality-hourly-averages-yearly>

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```

## 9   Melbourne CBD    BPM2.5  8.072998
## 10          Moe    BPM2.5  6.427079
## 11 Morwell East    BPM2.5  6.784596
## 12 Morwell South    BPM2.5  6.512849
## 13 Morwell South      NO2  5.124430
## 14     Traralgon    BPM2.5  8.024735
## 15     Traralgon      NO2  5.776333

```

sort_values is a convenient means to order the rows with respect to one criterion:

```

air.sort_values("value", ascending=False)
##           sp_name param_id      value
## 6       Footscray      NO2  10.274531
## 4       Dandenong      NO2  9.800705
## 1     Alphington      NO2  9.558120
## 2   Altona North      NO2  9.467912
## 9   Melbourne CBD    BPM2.5  8.072998
## 14     Traralgon    BPM2.5  8.024735
## 0     Alphington    BPM2.5  7.848758
## 5       Footscray    BPM2.5  7.640948
## 11  Morwell East    BPM2.5  6.784596
## 12  Morwell South    BPM2.5  6.512849
## 7   Geelong South    BPM2.5  6.502762
## 10          Moe    BPM2.5  6.427079
## 3       Churchill    BPM2.5  6.391230
## 15     Traralgon      NO2  5.776333
## 8   Geelong South      NO2  5.681722
## 13  Morwell South      NO2  5.124430

```

Sorting with respect to more criteria is also possible:

```

air.sort_values(["param_id", "value"], ascending=[True, False])
##           sp_name param_id      value
## 9   Melbourne CBD    BPM2.5  8.072998
## 14     Traralgon    BPM2.5  8.024735
## 0     Alphington    BPM2.5  7.848758
## 5       Footscray    BPM2.5  7.640948
## 11  Morwell East    BPM2.5  6.784596
## 12  Morwell South    BPM2.5  6.512849
## 7   Geelong South    BPM2.5  6.502762

```

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```

## 10      Moe    BPM2.5  6.427079
## 3      Churchill    BPM2.5  6.391230
## 6      Footscray     NO2  10.274531
## 4      Dandenong     NO2  9.800705
## 1      Alphington     NO2  9.558120
## 2      Altona North     NO2  9.467912
## 15     Traralgon     NO2  5.776333
## 8      Geelong South     NO2  5.681722
## 13     Morwell South     NO2  5.124430

```

Note that here, in each group of identical parameters, we get a decreasing order with respect to the value.

Exercise 10.14 (*) Compare the ordering with respect to `param_id` and `value` vs `value` and then `param_id`.

Exercise 10.15 (**) Perform identical reorderings but using only `loc[...]`, `iloc[...]`, and `numpy.argsort`.

Note: (*) `DataFrame.sort_values` unfortunately uses a non-stable algorithm by default (a modified quicksort). If a data frame is sorted with respect to one criterion, and then we reorder it with respect to another one, tied observations are not guaranteed to be listed in the original order:

```

(pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
             "teaching_data/master/marek/air_quality_2018_means.csv",
             comment="#")
   .sort_values("sp_name")
   .sort_values("param_id")
   .set_index("param_id")
   .loc[['BPM2.5', 'NO2'], :]
   .reset_index())

```

| | param_id | sp_name | value |
|------|----------|---------------|----------|
| ## 0 | BPM2.5 | Melbourne CBD | 8.072998 |
| ## 1 | BPM2.5 | Moe | 6.427079 |
| ## 2 | BPM2.5 | Footscray | 7.640948 |
| ## 3 | BPM2.5 | Morwell East | 6.784596 |
| ## 4 | BPM2.5 | Churchill | 6.391230 |
| ## 5 | BPM2.5 | Morwell South | 6.512849 |
| ## 6 | BPM2.5 | Traralgon | 8.024735 |

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```

## 7   BPM2.5    Alphington  7.848758
## 8   BPM2.5    Geelong South 6.502762
## 9     NO2    Morwell South  5.124430
## 10    NO2    Traralgon  5.776333
## 11    NO2    Geelong South 5.681722
## 12    NO2    Altona North  9.467912
## 13    NO2    Alphington  9.558120
## 14    NO2    Dandenong  9.800705
## 15    NO2    Footscray  10.274531

```

We have lost the ordering based on station names in the two subgroups. To switch to a mergesort-like method (timsort), we should pass `kind="stable"`.

```

(pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
  "teaching_data/master/marek/air_quality_2018_means.csv",
  comment="#")
 .sort_values("sp_name")
 .sort_values("param_id", kind="stable") # !
 .set_index("param_id")
 .loc[[ "BPM2.5", "NO2"], :]
 .reset_index())
##   param_id      sp_name     value
## 0   BPM2.5    Alphington  7.848758
## 1   BPM2.5    Churchill  6.391230
## 2   BPM2.5    Footscray  7.640948
## 3   BPM2.5    Geelong South 6.502762
## 4   BPM2.5    Melbourne CBD 8.072998
## 5   BPM2.5        Moe  6.427079
## 6   BPM2.5    Morwell East 6.784596
## 7   BPM2.5    Morwell South 6.512849
## 8   BPM2.5    Traralgon  8.024735
## 9     NO2    Alphington  9.558120
## 10    NO2    Altona North  9.467912
## 11    NO2    Dandenong  9.800705
## 12    NO2    Footscray  10.274531
## 13    NO2    Geelong South 5.681722
## 14    NO2    Morwell South  5.124430
## 15    NO2    Traralgon  5.776333

```

10.7 Stacking and Unstacking

Let's discuss some further ways to transform data frames, that benefit from, make sense because of, or are possible due to their being able to store data of different types.

Note that the above `air` dataset is in the so-called *long* format, where all measurements are *stacked* one after/below another. Such a form is quite convenient for the purpose of storing data, but not necessarily for all processing tasks, compare [[[Wic14](#)]]. Recall from the matrix part that a more natural way would be to have a single *observation* (e.g., data for a measurement station) in each row.

We can *unstack* the `air` data frame (convert to the *wide* format) quite easily:

```
air.set_index(["sp_name", "param_id"]).unstack().loc[:, "value"]
## param_id      BPM2.5      NO2
## sp_name
## Alphington    7.848758  9.558120
## Altona North   Nan       9.467912
## Churchill     6.391230  NaN
## Dandenong     NaN       9.800705
## Footscray      7.640948  10.274531
## Geelong South  6.502762  5.681722
## Melbourne CBD  8.072998  NaN
## Moe            6.427079  NaN
## Morwell East   6.784596  NaN
## Morwell South  6.512849  5.124430
## Traralgon     8.024735  5.776333
```

Note that the missing values are denoted with `Nan`s (not-a-number) – we have a separate section devoted to their processing given a bit later. Interestingly, we got a hierarchical index in the columns, hence the `loc[...]` part.

Equivalently:

```
air_wide = air.pivot("sp_name", "param_id", "value").\
    rename_axis(index=None, columns=None)
air_wide
##                  BPM2.5      NO2
## Alphington    7.848758  9.558120
## Altona North   Nan       9.467912
```

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```
## Churchill      6.391230      NaN
## Dandenong      NaN      9.800705
## Footscray      7.640948 10.274531
## Geelong South  6.502762  5.681722
## Melbourne CBD  8.072998      NaN
## Moe            6.427079      NaN
## Morwell East   6.784596      NaN
## Morwell South  6.512849  5.124430
## Traralgon      8.024735  5.776333
```

The `rename_axis` part is there so as to get rid of the `name` parts of the `index` and `columns` slots.

The other way around, we can use the `stack` method:

```
air_wide.T.rename_axis(index="location", columns="param").\
  stack().rename("value").reset_index()
##   location      param     value
## 0    BPM2.5    Alphington  7.848758
## 1    BPM2.5    Churchill   6.391230
## 2    BPM2.5    Footscray   7.640948
## 3    BPM2.5  Geelong South  6.502762
## 4    BPM2.5  Melbourne CBD  8.072998
## 5    BPM2.5        Moe     6.427079
## 6    BPM2.5  Morwell East   6.784596
## 7    BPM2.5  Morwell South  6.512849
## 8    BPM2.5    Traralgon   8.024735
## 9      N02    Alphington  9.558120
## 10     N02  Altona North  9.467912
## 11     N02   Dandenong   9.800705
## 12     N02    Footscray  10.274531
## 13     N02  Geelong South  5.681722
## 14     N02  Morwell South  5.124430
## 15     N02    Traralgon   5.776333
```

We used the data frame transpose (`T`) to get a location-major order (less boring an outcome in this context).

10.8 Set-Theoretic Operations

Here are two not at all disjoint sets of imaginary persons:

```
A = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/some_birth_dates1.csv",
    comment="#")
```

A

| | Name | BirthDate |
|------|---------------------|------------|
| ## 0 | Paitoon Ornwimol | 26.06.1958 |
| ## 1 | Antónia Lata | 20.05.1935 |
| ## 2 | Bertoldo Mallozzi | 17.08.1972 |
| ## 3 | Nedeljko Bukv | 19.12.1921 |
| ## 4 | Micha Kitchen | 17.09.1930 |
| ## 5 | Mefodiy Shachar | 01.10.1914 |
| ## 6 | Paul Meckler | 29.09.1968 |
| ## 7 | Katarzyna Lasko | 20.10.1971 |
| ## 8 | Åge Trelstad | 07.03.1935 |
| ## 9 | Duchanee Panomyaong | 19.06.1952 |

and

```
B = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/some_birth_dates2.csv",
    comment="#")
```

B

| | Name | BirthDate |
|-------|---------------------|------------|
| ## 0 | Hushang Naigamwala | 25.08.1991 |
| ## 1 | Zhen Wei | 16.11.1975 |
| ## 2 | Micha Kitchen | 17.09.1930 |
| ## 3 | Jodoc Alwin | 16.11.1969 |
| ## 4 | Igor Mazal | 14.05.2004 |
| ## 5 | Katarzyna Lasko | 20.10.1971 |
| ## 6 | Duchanee Panomyaong | 19.06.1952 |
| ## 7 | Mefodiy Shachar | 01.10.1914 |
| ## 8 | Paul Meckler | 29.09.1968 |
| ## 9 | Noe Tae-Woong | 11.07.1970 |
| ## 10 | Åge Trelstad | 07.03.1935 |

In both datasets, there is a single column whose elements uniquely identify each record

(i.e., Name). In the language of relational databases, we would call it a *primary key*. In such a case, implementing the set-theoretic operations is relatively easy:

$A \cap B$ (intersection) – the rows that are both in A and in B:

```
A.loc[A.Name.isin(B.Name), :]
##           Name BirthDate
## 4      Micha Kitchen 17.09.1930
## 5    Mefodiy Shachar 01.10.1914
## 6      Paul Meckler 29.09.1968
## 7   Katarzyna Lasko 20.10.1971
## 8     Åge Trelstad 07.03.1935
## 9 Duchanee Panomyaong 19.06.1952
```

$A \setminus B$ (difference) – the rows that are in A but not in B:

```
A.loc[~A.Name.isin(B.Name), :]
##           Name BirthDate
## 0  Paitoon Ornwimal 26.06.1958
## 1  Antónia Lata 20.05.1935
## 2 Bertoldo Mallozzi 17.08.1972
## 3   Nedeljko Bukv 19.12.1921
```

$A \cup B$ (union) – the rows that exist in A or are in B:

```
pd.concat((A, B.loc[~B.Name.isin(A.Name), :]))
##           Name BirthDate
## 0  Paitoon Ornwimal 26.06.1958
## 1  Antónia Lata 20.05.1935
## 2 Bertoldo Mallozzi 17.08.1972
## 3   Nedeljko Bukv 19.12.1921
## 4      Micha Kitchen 17.09.1930
## 5    Mefodiy Shachar 01.10.1914
## 6      Paul Meckler 29.09.1968
## 7   Katarzyna Lasko 20.10.1971
## 8     Åge Trelstad 07.03.1935
## 9 Duchanee Panomyaong 19.06.1952
## 0   Hushang Naigamwala 25.08.1991
## 1       Zhen Wei 16.11.1975
## 3     Jodoc Alwin 16.11.1969
## 4      Igor Mazal 14.05.2004
## 9    Noe Tae-Woong 11.07.1970
```

Note that there are no duplicate rows in the output.

Exercise 10.16 Determine $(A \cup B) - (A \cap B) = (A - B) \cup (B - A)$ (symmetric difference).

Exercise 10.17 (*) Determine the union, intersection, and difference of the `wine_sample1`¹¹⁸ and `wine_sample2`¹¹⁹ datasets, where there is no column uniquely identifying the observations. Hint: consider using `pandas.DataFrame.duplicated` or `pandas.DataFrame.drop_duplicates`.

10.9 Joining (Merging)

In database design, it is common to normalise the datasets in order to avoid the duplication of information and pathologies stemming from them (e.g., [[`Data3`]])�

Example 10.18 The above air quality parameters are separately described in another data frame:

```
param = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/air_quality_2018_param.csv",
    comment="#")
param.rename(dict(param_std_unit_of_measure="unit"), axis=1)
##   param_id          param_name   unit   param_short_name
## 0      API     Airborne particle index   none  Visibility Reduction
## 1    BPM2.5      BAM Particles < 2.5 micron ug/m3            PM2.5
## 2        CO      Carbon Monoxide    ppm             CO
## 3     HPM10      Hivol PM10    ug/m3           NaN
## 4       NO2      Nitrogen Dioxide   ppb            NO2
## 5        O3        Ozone        ppb            O3
## 6     PM10      TEOM Particles <10micron ug/m3            PM10
## 7    PPM2.5      Partisol PM2.5   ug/m3           NaN
## 8      SO2      Sulfur Dioxide   ppb            SO2
```

We could have stored them alongside the `air` data frame, but that would be a waste of space.

Also, if we wanted to modify some datum (note, e.g., the annoying double space in `param_name` for `BPM2.5`), we would have to update all the relevant records.

Instead, we can always look the information up by `param_id` and join (merge) the two data frames only if we need it.

¹¹⁸ https://raw.githubusercontent.com/gagolews/teaching_data/master/other/wine_sample1.csv

¹¹⁹ https://raw.githubusercontent.com/gagolews/teaching_data/master/other/wine_sample2.csv

Let us discuss the possible join operations by studying the two following data sets:

```
A = pd.DataFrame({
    "x": ["a0", "a1", "a2", "a3"],
    "y": ["b0", "b1", "b2", "b3"]
})
A
##      x     y
## 0  a0  b0
## 1  a1  b1
## 2  a2  b2
## 3  a3  b3
```

and:

```
B = pd.DataFrame({
    "x": ["a0", "a2", "a2", "a4"],
    "z": ["c0", "c1", "c2", "c3"]
})
B
##      x     z
## 0  a0  c0
## 1  a2  c1
## 2  a2  c2
## 3  a4  c3
```

They both have one column somewhat *in common*, x.

The *inner (natural) join* returns the records that have a match in both datasets:

```
pd.merge(A, B, on="x")
##      x     y     z
## 0  a0  b0  c0
## 1  a2  b2  c1
## 2  a2  b2  c2
```

The *left join* of A with B guarantees to return all the records from A, even those which are not matched by anything in B.

```
pd.merge(A, B, how="left", on="x")
##      x     y     z
## 0  a0  b0  c0
```

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```
## 1 a1 b1 NaN
## 2 a2 b2 c1
## 3 a2 b2 c2
## 4 a3 b3 NaN
```

The *right join* of A with B is the same as the left join of B with A:

```
pd.merge(A, B, how="right", on="x")
##      x      y      z
## 0  a0    b0    c0
## 1  a2    b2    c1
## 2  a2    b2    c2
## 3  a4   NaN    c3
```

Finally, the *full outer join* is the set-theoretic union of the left and the right join:

```
pd.merge(A, B, how="outer", on="x")
##      x      y      z
## 0  a0    b0    c0
## 1  a1    b1   NaN
## 2  a2    b2    c1
## 3  a2    b2    c2
## 4  a3    b3   NaN
## 5  a4   NaN    c3
```

Exercise 10.19 Join `air_quality_2018_value`¹²⁰ with `air_quality_2018_point`¹²¹ and `air_quality`

Exercise 10.20 Normalise `air_quality_2018`¹²³ yourself so that you get the three data frames mentioned in the previous exercise (`value`, `point`, `param`).

Exercise 10.21 (*) In the National Health and Nutrition Examination Survey (NHANES) by the US Centres for Disease Control and Prevention, each participant is uniquely identified by their sequence number (`SEQN`), which is mentioned in numerous datasets, including:

- demographic variables¹²⁴;

¹²⁰ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/air_quality_2018_value.csv.gz

¹²¹ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/air_quality_2018_point.csv

¹²² https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/air_quality_2018_param.csv

¹²³ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/air_quality_2018.csv.gz

¹²⁴ https://www.cdc.gov/Nchs/Nhanes/2017-2018/P_DEMO.htm

- *body measures*¹²⁵;
- *audiometry*¹²⁶;
- *and many more*¹²⁷.

Join a few chosen datasets that are to your liking.

10.10 Further Reading

Looking at the list of methods for the `DataFrame` and `Series` classes in the `pandas` package's `documentation`¹²⁸, we can see that they are abundant. Together with the object-oriented syntax, we will often find ourselves appreciating the high readability of even quite complex operation chains such as `data.drop_duplicates().groupby(["year", "month"]).mean().reset_index()`.

Nevertheless, in fact, we should admit that the methods are too plentiful – they make an impression that someone was too generous by including a list of all the possible *verbs* related to data analysis, even if they can be easily expressed as a combination of 2-3 simpler operations. Therefore, in order to prevent the reader from being overloaded with too much new information, below we will be discussing only the most noteworthy features that often appear in data wrangling scenarios.

As strong advocates of minimalism (which is more environmentally friendly and sustainable), not rarely will we be more eager to fall back to the hand-crafted combinations of the more basic (universal) building blocks from `numpy` and `scipy` instead. This is also in line with our putting emphasis on developing *transferable* skills – as Python with `pandas` is not the only combo where we can work with data frames (e.g., base R allows that too).

10.11 Exercises

Exercise 10.22 How are data frames different from matrices?

¹²⁵ https://www.cdc.gov/Nchs/Nhanes/2017-2018/P_BMX.htm

¹²⁶ https://www.cdc.gov/Nchs/Nhanes/2017-2018/AUX_J.htm

¹²⁷ <https://www.cdc.gov/Nchs/Nhanes/continuousnhanes/default.aspx?BeginYear=2017>

¹²⁸ <https://pandas.pydata.org/pandas-docs/stable/reference/index.html>

Exercise 10.23 What are the use cases of the `name` slot in `Series` and `Index` objects?

Exercise 10.24 What is the purpose of `set_index` and `reset_index`?

Exercise 10.25 Why learning `numpy` is crucial when someone wants to become a proficient user of `pandas`?

Exercise 10.26 What is the difference between `iloc[...]` and `loc[...]`?

Exercise 10.27 Why applying the index operator `[...]` directly on a `Series` or `DataFrame` object is not necessarily a good idea?

Exercise 10.28 What is the difference between `.index`, `Index`, and `.columns`?

Exercise 10.29 How to compute the arithmetic mean and median of all the numeric columns in a data frame, using a single line of code?

Exercise 10.30 What is a train/test split and how to perform it using `numpy` and `pandas`?

Exercise 10.31 What is the difference between stacking and unstacking? Which one yields a wide (as opposed to long) format?

Exercise 10.32 Name different data frame join (merge) operations and explain how they work.

Exercise 10.33 How does sorting with respect to more than one criterion work?

Exercise 10.34 Name the basic set-theoretic operations on data frames.

Handling Categorical Data

So far we have been mostly dealing with *quantitative* (numeric) data – real numbers on which we can apply various mathematical operations, such as computing the arithmetic mean or taking the square thereof. Of course, not every transformation thereof must always make sense in every context (e.g., multiplying temperatures – what does it mean when we say that it's twice as hot today as compared to yesterday?), but still, the possibilities were plenty.

Qualitative data (also known as categorical data, factors, enumerated types), on the other hand, take a small number of unique values and support a very limited set of admissible operations. Usually, we can only determine where two entities are equal to each other or not (think: eye colour, blood type, or a flag whether a patient is ill).

In datasets involving many features, which we shall cover in [Chapter 12](#), categorical variables are often used for observation *grouping* (e.g., so that we can compute the best and average time for marathoners in each age category or draw boxplots for finish times of men and women separately). Also, they may serve as target variables in statistical classification tasks (e.g., so that we can determine if an email is “spam” or “not spam”).

Also, sometimes we might additionally be able to *rank* the observations (Australian school grades are *linearly ordered* like F (fail) < P (pass) < C (credit) < D (distinction) < HD (high distinction), some questionnaires use Likert-type scales such as “strongly disagree” < “disagree” < “neutral” < “agree” < “strongly agree”, etc.).

11.1 Representing and Generating Categorical Data

Common ways to represent a categorical variable with l distinct levels $\{L_1, L_2, \dots, L_l\}$ is by storing it as:

- a vector of strings,
- a vector of integers between 0 (inclusive) and l (exclusive).

These two are easily interchangeable.

Furthermore, for $l = 2$ (binary data), another convenient representation is by means of logical vectors. This can be extended to a so-called one-hot encoded representation using a logical vector of length l .

Let's consider the data on the original whereabouts of the top 16 marathoners (the 37th PZU Warsaw Marathon dataset):

```
marathon = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/37_pzu_warsaw_marathon_simplified.csv",
    comment="#")
cntrs = np.array(marathon.loc[:, "country"], dtype="str")
cntrs16 = cntrs[:16]
cntrs16
## array(['KE', 'KE', 'KE', 'ET', 'KE', 'KE', 'ET', 'MA', 'PL', 'IL',
##        'PL', 'KE', 'KE', 'PL', 'PL'], dtype='<U2')
```

These are two-letter ISO 3166 country codes, encoded of course as strings (note the `dtype="str"` argument).

Calling `numpy.unique` allows us to determine the set of distinct categories:

```
cat_cntrs16 = np.unique(cntrs16)
cat_cntrs16
## array(['ET', 'IL', 'KE', 'MA', 'PL'], dtype='<U2')
```

Hence, `cntrs16` is a categorical vector of length $n=16$ (`len(cntrs16)`) with data assuming one of $l = 5$ different levels (`len(cat_cntrs16)`).

Important: `numpy.unique` sorts the distinct values lexicographically. In other words, they are not listed in the order of appearance, which might be something desirable in certain contexts.

11.1.1 Encoding and Decoding Factors

In order to *encode* a label vector through a set of consecutive nonnegative integers, we pass the `return_inverse=True` argument to `numpy.unique`:

```
cat_cntrs16, codes_cntrs16 = np.unique(cntrs16, return_inverse=True)
cat_cntrs16
## array(['ET', 'IL', 'KE', 'MA', 'PL'], dtype='<U2')
codes_cntrs16
## array([2, 2, 2, 0, 2, 2, 0, 3, 4, 4, 1, 4, 2, 2, 4, 4])
```

Note that the code sequence $2, 2, 2, 0, \dots$ corresponds to the 3rd, 3rd, 3rd, 1st, ... level in `cat_cntrs16`, i.e., Kenya, Kenya, Kenya, Ethiopia,

The values between 0 and $l - 1 = 4$ can be used to index a given array of length $l = 5$. Hence, in order to *decode* our factor, we can write:

```
cat_cntrs16[codes_cntrs16]
## array(['KE', 'KE', 'KE', 'ET', 'KE', 'KE', 'ET', 'MA', 'PL', 'PL',
##        'IL', 'PL', 'KE', 'KE', 'PL', 'PL'], dtype='<U2')
```

We can use any other set of labels now:

```
np.array(["Ethiopia", "Israel", "Kenya", "Morocco", "Poland"])[codes_cntrs16]
## array(['Kenya', 'Kenya', 'Kenya', 'Ethiopia', 'Kenya', 'Kenya',
##        'Ethiopia', 'Morocco', 'Poland', 'Poland', 'Israel', 'Poland',
##        'Kenya', 'Kenya', 'Poland', 'Poland'], dtype='<U8')
```

This is an instance of the *recoding* of a categorical variable.

Important: Despite the fact that we can *represent* categorical variables using a set of integers, it does not mean that they become instances of a quantitative type. Arithmetic operations thereon do not really make sense.

Note: When we represent categorical data using numeric codes, it is possible to introduce non-occurring levels. Such information can be useful, e.g., we could explicitly indicate that there were no runners from Australia in the top 16.

Exercise 11.1 (***) Determine the set of unique values in `cntrs16` in the order of appearance (and not sorted lexicographically). Then, encode `cntrs16` using this level set.

Hint: check out the `return_index` argument to `numpy.unique` and the `numpy.searchsorted` function.

11.1.2 Categorical Data in pandas

pandas includes¹³⁰ a special dtype for storing categorical data. Namely, we can write:

```
cntrs16_series = marathon.iloc[:16, :].loc[:, "country"].astype("category")
cntrs16_series
## 0      KE
## 1      KE
## 2      KE
## 3      ET
## 4      KE
## 5      KE
## 6      ET
## 7      MA
## 8      PL
## 9      PL
## 10     IL
## 11     PL
## 12     KE
## 13     KE
## 14     PL
## 15     PL
## Name: country, dtype: category
## Categories (5, object): ['ET', 'IL', 'KE', 'MA', 'PL']
```

or, equivalently in our case, `pd.Series(cntrs16, dtype="category")`. This yields a Series object displayed as if it was represented using string labels, however, in fact it is encoded using the numeric representation. This can be revealed by accessing:

```
cntrs16_series.cat.codes.to_numpy()
## array([2, 2, 2, 0, 2, 2, 0, 3, 4, 4, 1, 4, 2, 2, 4, 4], dtype=int8)
cntrs16_series.cat.categories
## Index(['ET', 'IL', 'KE', 'MA', 'PL'], dtype='object')
```

exactly matching what we have obtained with `numpy.unique`. Most often, however, categorical data in data frames will be stored as ordinary strings.

11.1.3 Binary Data and Logical Vectors

Binary data is a special case of the qualitative setting, where we only have two categories.

¹³⁰ https://pandas.pydata.org/pandas-docs/stable/user_guide/categorical.html

For convenience, we usually encode the two classes as integers:

- 0 (or logical `False`, e.g., healthy/fail/off/non-spam/absent/...) and
- 1 (or `True`, e.g., ill/success/on/spam/present/...).

Important: When converting logical to numeric, `False` becomes 0 and `True` becomes 1. Conversely, 0 is converted to `False` and anything else (including -0.326) to `True`.

For example:

```
np.array([True, False, True, True, False]).astype(int)
## array([1, 0, 1, 1, 0])
```

The other way around:

```
np.array([-2, -0.326, -0.000001, 0.0, 0.1, 1, 7643]).astype(bool)
## array([ True,  True,  True, False,  True,  True,  True])
```

or, equivalently:

```
np.array([-2, -0.326, -0.000001, 0.0, 0.1, 1, 7643]) != 0
## array([ True,  True,  True, False,  True,  True,  True])
```

Exercise 11.2 Given a numeric vector x , create a vector of the same length as x whose i -th element is equal to "yes" if $x[i]$ is in the unit interval and to "no" otherwise. Use `numpy.where`, which can act as a vectorised version of the `if` statement.

11.1.4 One-Hot Encoding (*)

Let x be vector of n integers in $\{0, \dots, l-1\}$. Its *one-hot* encoded version is a 0-1 (or, equivalently, logical) matrix \mathbf{R} of shape n by l such that $r_{i,j} = 1$ if and only if $x_i = j$.

For example, if $x = (0, 1, 2, 1)$ and $l = 4$, then:

$$\mathbf{R} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \end{bmatrix}.$$

Such a representation is useful when solving a multiclass classification problem by means of l binary classifiers. For example, if *spam*, *bacon*, and *hot dogs* are on the menu, then *spam* is encoded as $(1, 0, 0)$, i.e., yeah-spam, nah-bacon, and nah-hot dog. We can

build three binary classifiers, each specialising in telling whether what it encounters is a given food or something else.

Example 11.3 Write a function to one-hot encode a given categorical vector.

Example 11.4 Write a function to decode a one-hot encoded matrix.

11.1.5 Binning Numeric Data (Revisited)

Numerical data can be converted to categorical via binning (quantisation). This results in information (precision) loss, however, it also opens some new possibilities. In fact, this is what we needed to do in order to draw all the histograms in [Chapter 4](#). Also, reporting observation counts in each bin instead of raw data enables us to include them in printed reports (in form of a table).

Note: As strong proponents of openness and transparency, we always encourage all entities (governments, universities, non-for-profits, corporations, etc.) to share (e.g., under the Creative Commons CC-BY-SA-4.0 license) unabridged versions of their datasets to enable public scrutiny and getting the most of the possibilities they can bring for the public good.

Of course, sometimes the sharing of unprocessed information can violate the privacy of the subjects. In such a case, it might be a good idea to communicate them in a binned form.

Consider the 16 best marathon finish times (in minutes):

```
mins = marathon.loc[:, "mins"].to_numpy()
mins16 = mins[:16]
mins16
## array([129.32, 130.75, 130.97, 134.17, 134.68, 135.97, 139.88, 143.2 ,
##        145.22, 145.92, 146.83, 147.8 , 149.65, 149.88, 152.65, 152.88])
```

`numpy.searchsorted` can be used to determine the interval where each value in `mins` falls.

```
bins = [130, 140, 150]
codes_mins16 = np.searchsorted(bins, mins16)
codes_mins16
## array([0, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 3])
```

By default, the intervals are of the form $(a, b]$ (not including a , including b). Code o cor-

responds to values less than the first bin bound, whereas code 3 – greater than or equal to the last bound:

pandas.cut us another interface to the same binning method. It returns a vector-like object of dtype "category", with very readable labels generated automatically (and ordered, see [Section 11.4.7](#)):

```
cut_mins16 = pd.Series(pd.cut(mins16, [-np.inf, 130, 140, 150, np.inf]))
cut_mins16
## 0      (-inf, 130.0]
## 1      (130.0, 140.0]
## 2      (130.0, 140.0]
## 3      (130.0, 140.0]
## 4      (130.0, 140.0]
## 5      (130.0, 140.0]
## 6      (130.0, 140.0]
## 7      (140.0, 150.0]
## 8      (140.0, 150.0]
## 9      (140.0, 150.0]
## 10     (140.0, 150.0]
## 11     (140.0, 150.0]
## 12     (140.0, 150.0]
## 13     (140.0, 150.0]
## 14     (150.0, inf]
## 15     (150.0, inf]
## dtype: category
## Categories (4, interval[float64, right]): [(-inf, 130.0] < (130.0, 140.0]
## < (140.0, 150.0] <
##                               (150.0, inf]]
cut_mins16.cat.categories.astype("str")
## Index(['(-inf, 130.0]', '(130.0, 140.0]', '(140.0, 150.0]', '(150.0, inf]')
##       , dtype='object')
```

Exercise 11.5 (*) Check out the **numpy.histogram_bin_edges** function which tries to determine some informative interval bounds automatically based on a range of simple heuristics. Also, note that **numpy.linspace** and **numpy.geomspace** which we have covered in [Chapter 4](#) can be useful for generating equidistant bounds on linear and logarithmic scale, respectively.

Example 11.6 (**) We can create a set of the corresponding categories manually, for example, as follows:

```
bins2 = np.r_[-np.inf, bins, np.inf]
```

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```
cat_mins16 = np.array(
    [f"{{bins2[{i-1}]}, {bins2[i]}]}" for i in range(1, len(bins2))]
)
cat_mins16
## array(['(-inf, 130.0]', '(130.0, 140.0]', '(140.0, 150.0]',
##        '(150.0, inf]'], dtype='<U14')
```

Recall from Section 5.5.5 that list comprehensions are a convenient substitute for a `for` loop and the `list.append` method. Recoding based on the above yields:

```
cat_mins16[codes_mins16]
## array(['(-inf, 130.0]', '(130.0, 140.0]', '(130.0, 140.0]',
##        '(130.0, 140.0]', '(130.0, 140.0]', '(130.0, 140.0]',
##        '(130.0, 140.0]', '(140.0, 150.0]', '(140.0, 150.0]',
##        '(140.0, 150.0]', '(140.0, 150.0]', '(140.0, 150.0]',
##        '(140.0, 150.0]', '(140.0, 150.0]', '(150.0, inf]', '(150.0, inf]'
##       ],
##      dtype='<U14')
```

11.1.6 Generating Pseudorandom Labels

It is worth knowing that `numpy.random.choice` allows us to create a pseudorandom sample with categories picked with any probabilities:

```
np.random.seed(123)
np.random.choice(
    a=["spam", "bacon", "eggs", "tempeh"],
    p=[ 0.7,     0.1,   0.15,    0.05],
    replace=True,
    size=16
)
## array(['spam', 'spam', 'spam', 'spam', 'bacon', 'spam', 'tempeh', 'spam',
##        'spam', 'spam', 'spam', 'bacon', 'spam', 'spam', 'spam', 'bacon'],
##      dtype='<U6')
```

Hence, if we generate a sufficiently large sample, we will expect "spam" to occur ca. 70% times, and "tempeh" to be drawn in 5% of the cases, etc.

11.2 Frequency Distributions

11.2.1 Counting

For arbitrary categorical data, we can call:

```
cat_cntrs16, counts_cntrs16 = np.unique(cntrs16, return_counts=True)
cat_cntrs16, counts_cntrs16
## (array(['ET', 'IL', 'KE', 'MA', 'PL'], dtype='|<U2'), array([2, 1, 7, 1, 5]))
```

to get both the set of unique categories and the *corresponding* number of occurrences. For instance, there were 7 runners from Kenya amongst the top 16.

Also, note that if we *already* have an array of integer codes between 0 and $l - 1$, there is no need to call `numpy.unique`, as `numpy.bincount` can return the number of times each code appears therein.

```
np.bincount(codes_cntrs16)
## array([2, 1, 7, 1, 5])
```

Of course, a vector of counts can easily be turned into a vector of proportions (fractions):

```
counts_cntrs16 / np.sum(counts_cntrs16)
## array([0.125, 0.0625, 0.4375, 0.0625, 0.3125])
```

Hence, almost 31.25% of the top runners were from Poland (it is a marathon in Warsaw after all...). Note that we can of course multiply the above by 100 to get the percentages.

We can output a nice *frequency table* by storing both objects in a single data frame (or a `Series` object with an appropriate vector of row labels):

```
table = pd.DataFrame({
    "Country": cat_cntrs16,
    "%": 100 * counts_cntrs16 / np.sum(counts_cntrs16)
})
table
##   Country      %
## 0      ET  12.50
## 1      IL   6.25
## 2      KE  43.75
```

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```
## 3      MA    6.25
## 4      PL   31.25
```

Example 11.7 (*) In Section 14.3 we will discuss `IPython.display.Markdown` as a means to embed arbitrary Markdown code inside IPython/Jupyter reports. In the meantime, let us just note that nicely formatted tables can be created from data frames by calling:

```
import IPython.display
IPython.display.Markdown(table.to_markdown(index=False))
```

| Country | % |
|---------|-------|
| ET | 12.5 |
| IL | 6.25 |
| KE | 43.75 |
| MA | 6.25 |
| PL | 31.25 |

`pandas.Series.value_counts` is even more convenient, as it returns a `Series` object equipped with a readable index (element labels):

```
marathon.iloc[:16, :].loc[:, "country"].value_counts()
## KE     7
## PL     5
## ET     2
## MA     1
## IL     1
## Name: country, dtype: int64
```

Note that by default data are ordered with respect to the counts, decreasingly.

Exercise 11.8 In Chapter 4 we have mentioned the `numpy.histogram` function which applies the binning of a numeric vector and then counts the number of occurrences. This is merely a helper function: the same result can be obtained by means of the more basic `numpy.searchsorted`, `numpy.bincount`, and `numpy.histogram_bin_edges`. Apply `numpy.histogram` on the whole `37_pzu_warsaw_marathon_mins` dataset.

Exercise 11.9 Using `numpy.argsort`, sort `counts_cntrs16` increasingly together with the corresponding items in `cat_cntrs16`.

11.2.2 Two-Way Contingency Tables: Factor Combinations

Some datasets may feature many categorical columns, each having possibly different levels. Let us now consider the whole `marathon` dataset:

```
marathon.loc[:, "age"] = marathon.category.str.slice(1) # first two chars
marathon.loc[marathon.age >= "60", "age"] = "60+" # too few runners aged 70+
marathon = marathon.loc[:, ["sex", "age", "country"]]
marathon.head()
##   sex age country
## 0   M  20      KE
## 1   M  20      KE
## 2   M  20      KE
## 3   M  20      ET
## 4   M  30      KE
```

The three columns are: sex, age (in 10-year brackets), and country. We can of course analyse the data distribution in each column individually, however, some interesting patterns might also arise when we study the *combinations* of levels of different variables.

Here are the levels of the sex and age variables:

```
np.unique(marathon.loc[:, "sex"])
## array(['F', 'M'], dtype=object)
np.unique(marathon.loc[:, "age"])
## array(['20', '30', '40', '50', '60+'], dtype=object)
```

We thus have 10 different possible combinations thereof.

A two-way *contingency table* is a matrix which gives the number of occurrences of each pair of values:

```
v = marathon.loc[:, ["sex", "age"]].value_counts().unstack(fill_value=0)
v
## age    20     30     40     50    60+
## sex
## F      240    449    262    43    19
## M      879   2200   1708   541   170
```

Hence, for example, there were 19 women aged 60 and over amongst the marathoners. Nice.

Note that the *marginal* (one dimensional) frequency distributions can be recreated by computing the rowwise and columnwise sums.

```
np.sum(v, axis=1)
## sex
## F      1013
## M      5498
## dtype: int64
np.sum(v, axis=0)
## age
## 20     1119
## 30     2649
## 40     1970
## 50      584
## 60+    189
## dtype: int64
```

11.2.3 Combinations of Even More Factors

`pandas.DataFrame.value_counts` can also be used with a combination of more than 2 categorical variables:

```
marathon.loc[:, ["sex", "age", "country"]].value_counts().\
    rename("count").reset_index()
##      sex   age country  count
## 0     M    30      PL  2081
## 1     M    40      PL  1593
## 2     M    20      PL   824
## 3     M    50      PL   475
## 4     F    30      PL   422
## ..
## 189   M    30      SI     1
## 190   F   60+      EE     1
## 191   F   60+      FI     1
## 192   M    30      PE     1
## 193   F    20      BE     1
##
## [194 rows x 4 columns]
```

Of course, the display will be in the *long* format (compare Section 10.7) here, as high-dimensional arrays are not nicely printable.

11.3 Visualising

Methods for visualising categorical data are by no means fascinating (unless we use them as grouping variables in more complex datasets, but this is a topic that we cover in [Chapter 12](#)).

11.3.1 Bar Plots

Bar plots are self-explanatory and hence will do the trick most of the time, see [Figure 11.1](#).

```
ind = np.arange(len(cat_cntrs16))
plt.bar(ind, height=counts_cat_cntrs16,
        color="lightgray", edgecolor="black", alpha=0.8)
plt.xticks(ind, cat_cntrs16)
plt.show()
```

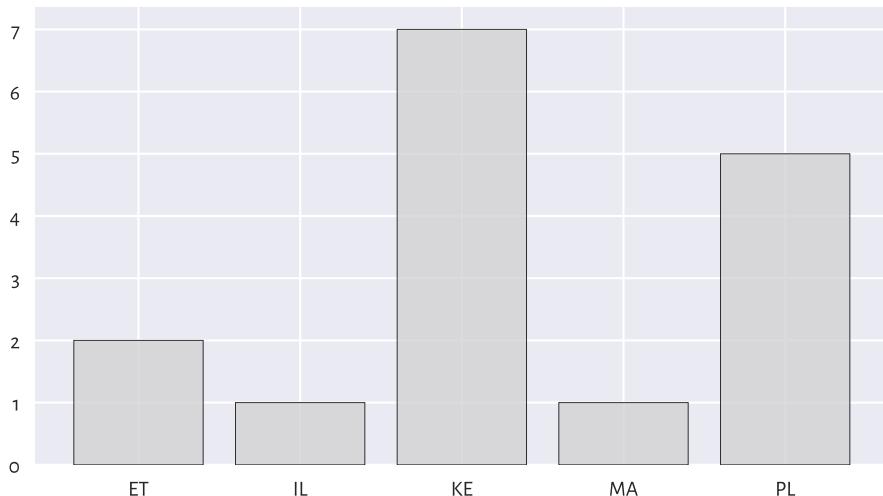


Figure 11.1: Bar plot for the top 16 marathoners' countries

The `ind` vector gives the x-coordinates of the bars, here: consecutive integers. By calling `matplotlib.pyplot.xticks` we assign them readable labels.

Exercise 11.10 Assign a different colour to each bar.

Exercise 11.11 Draw a bar plot which features percentages instead of counts, so that the total bar height is 100%.

Exercise 11.12 Print the frequency table and draw a bar plot for the top 100 marathoners' countries.

Exercise 11.13 (*) Print the frequency table and draw a bar plot all the marathoners (not just the elite ones), ordered from the highest to the lowest counts. There will be too many bars, therefore replace the few last bars with a single one, labelled "All other".

A bar plot is a versatile tool for visualising the counts also in the two-variable case, see Figure 11.2:

```
v = marathon.loc[:, ["sex", "age"]].value_counts().\
    rename("count").reset_index()
sns.barplot(x="age", hue="sex", y="count", data=v)
plt.show()
```

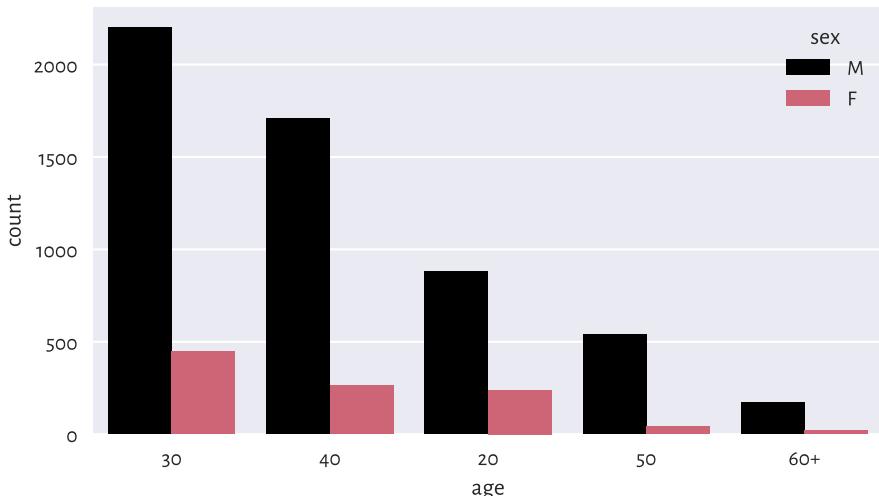


Figure 11.2: Number of runners by age category and sex

Exercise 11.14 (*) Draw a similar chart using `matplotlib.pyplot.bar`.

Exercise 11.15 (***) Create a stacked bar plot similar to the one in [Figure 11.3](#), where we have horizontal bars for data that have been normalised so that for each sex their sum is 100%.

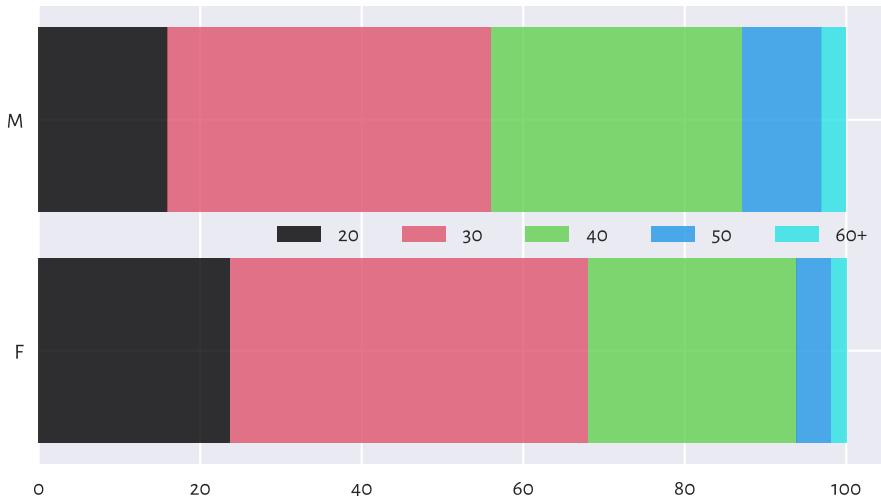


Figure 11.3: Example stacked bar plot: Age distribution for different sexes amongst all the runners

11.3.2 Political Marketing and Statistics

Even such a simple plot can be manipulated. For example, presidential elections were held in Poland in 2020. In the second round, Andrzej Duda had won against Rafał Trzaskowski. In [Figure 11.4](#) we have the official results that might be presented by one of the infamous Polish TV conglomerate:

```
plt.bar([1, 2], height=[51.03, 48.97], width=0.25,
       color="lightgray", edgecolor="black", alpha=0.8)
plt.xticks([1, 2], ["Duda", "Trzaskowski"])
plt.ylabel("%")
plt.xlim(0, 3)
plt.ylim(48.9, 51.1)
plt.show()
```

Such a great victory! Wait... it was a close vote after all! We should just take a look at the y-axis tick marks.

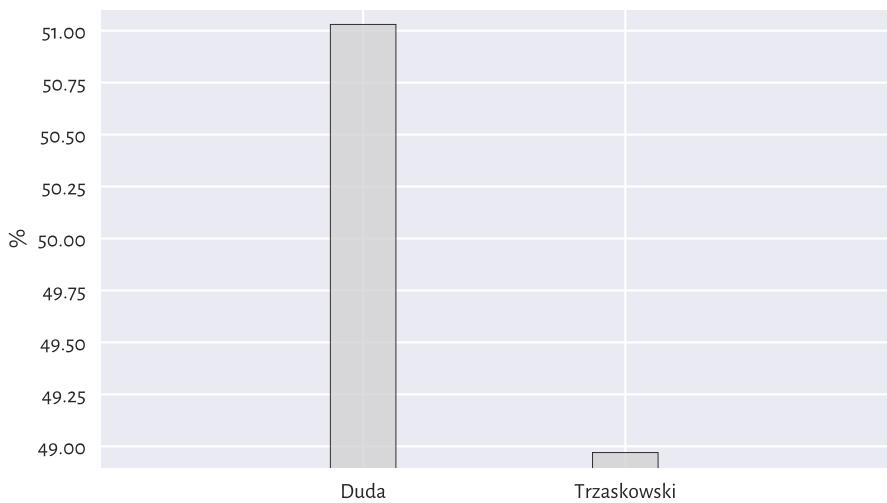


Figure 11.4: Flawless victory!

Another media outlet could have reported it like in Figure 11.5:

```
plt.bar([1, 2], height=[51.03, 48.97], width=0.25,
        color="lightgray", edgecolor="black", alpha=0.8)
plt.xticks([1, 2], ["Duda", "Trzaskowski"])
plt.ylabel("%")
plt.xlim(0, 3)
plt.ylim(0, 250)
plt.yticks([0, 100])
plt.show()
```

The moral of the story is:

Important: Always read the y-axis tick marks. And when drawing own bar plots, do not trick the reader; this is unethical.

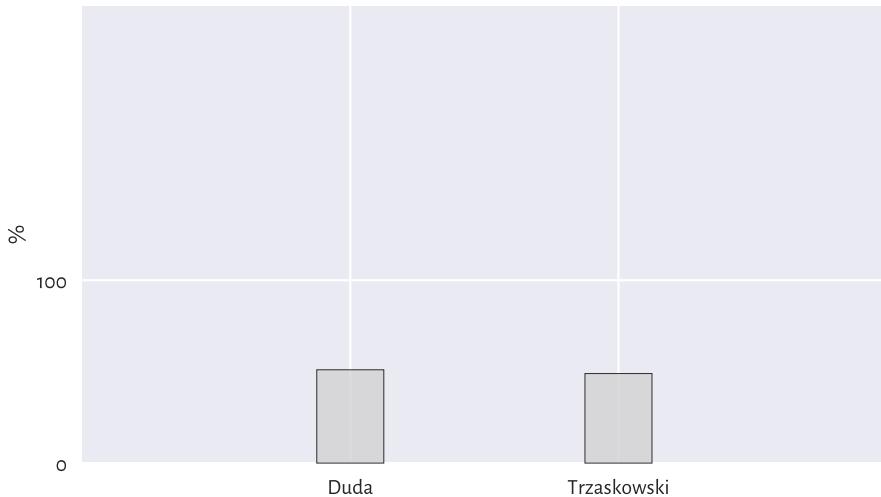


Figure 11.5: It was a draw, so close!

11.3.3 Pie Cha... Don't Even Trip

We are definitely not going to discuss the infamous pie charts, because their use in data analysis has been widely criticised for a long time (it's difficult to judge the ratios of areas of their slices). Case closed. Good morning.

11.3.4 Pareto Charts (*)

As a general (empirical) rule, it is usually the case that most instances of something's happening (usually 70–90%) are due to only few causes (10–30%). This is known as the *Pareto rule* (with 80% vs 20% being an often cited rule of thumb).

Example 11.16 In *Chapter 6* we modelled the US cities' population dataset using the Pareto distribution (the very same Pareto, but a different, yet related object). We discovered that only ca. 14% of the settlements (those with 10,000 or more inhabitants) is home to as much as 84% of the population. Hence, we may say that this data domain follows the Pareto rule.

Here is a dataset¹³¹ fabricated by the Clinical Excellence Commission in New South Wales, Australia, listing the most frequent causes for medication errors:

¹³¹ <https://www.cec.health.nsw.gov.au/CEC-Academy/quality-improvement-tools/pareto-charts>

```

cat_med = np.array([
    "Unauthorised drug", "Wrong IV rate", "Wrong patient", "Dose missed",
    "Underdose", "Wrong calculation", "Wrong route", "Wrong drug",
    "Wrong time", "Technique error", "Duplicated drugs", "Overdose"
])
counts_med = np.array([1, 4, 53, 92, 7, 16, 27, 76, 83, 3, 9, 59])
np.sum(counts_med) # total number of medication errors
## 430

```

Let's order the dataset with respect to the counts, decreasingly:

```

o = np.argsort(counts_med)[::-1] # ordering permutation (decreasing)
cat_med = cat_med[o] # order categories based on counts
counts_med = counts_med[o] # equivalent to np.sort(counts_med)[::-1]
pd.DataFrame(dict(
    category=cat_med,
    count=counts_med
)) # nicer display
##           category  count
## 0          Dose missed    92
## 1          Wrong time    83
## 2          Wrong drug    76
## 3          Overdose      59
## 4          Wrong patient   53
## 5          Wrong route     27
## 6          Wrong calculation  16
## 7          Duplicated drugs   9
## 8          Underdose       7
## 9          Wrong IV rate     4
## 10         Technique error     3
## 11         Unauthorised drug     1

```

Pareto charts are tools which may aid in visualising the Pareto-ruled datasets. They are based on bar plots, but feature some extras:

- bars are listed in a decreasing order,
- the cumulative percentage curve is added.

The plotting of the Pareto chart is a little tricky, because it involves using two different Y axes (as usual, fine-tuning of the figure and studying the manual of the `matplotlib` package is left as an exercise.)

```

x = np.arange(len(cat_med)) # 0, 1, 2, ...
p = 100.0*counts_med/np.sum(counts_med) # percentages

fig, ax1 = plt.subplots()
ax1.set_xticks(x-0.5, cat_med, rotation=60)
ax1.set_ylabel("%")
ax1.bar(x, height=p)
ax2 = ax1.twinx() # creates a new coordinate system with a shared x-axis
ax2.plot(x, np.cumsum(p), "ro-")
ax2.grid(visible=False)
ax2.set_ylabel("cumulative %")

fig.tight_layout()
plt.show()

```

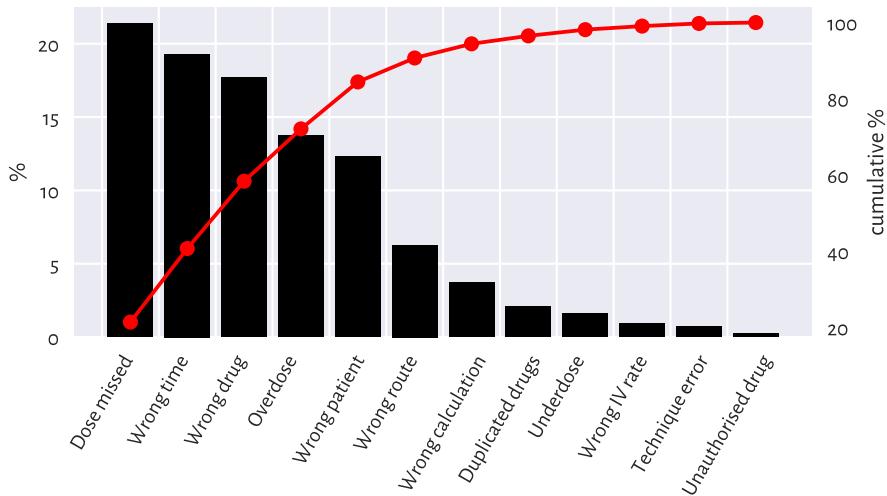


Figure 11.6: The most frequent causes for medication errors

From Figure 11.6, we can read that 5 causes (less than 40%) correspond to ca. 85% of the medication errors. More precisely,

```
pd.DataFrame({
    "category": cat_med,
```

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```

  "cumulative %": np.round(np.cumsum(p), 1)
})
##           category   cumulative %
## 0      Dose missed       21.4
## 1      Wrong time        40.7
## 2      Wrong drug        58.4
## 3      Overdose          72.1
## 4      Wrong patient      84.4
## 5      Wrong route         90.7
## 6      Wrong calculation    94.4
## 7      Duplicated drugs     96.5
## 8      Underdose          98.1
## 9      Wrong IV rate       99.1
## 10     Technique error      99.8
## 11     Unauthorised drug     100.0

```

Note that there is an explicit assumption here that a single error is only due to a single cause. Also, we presume that each medication error has a similar degree of severity.

Policy makers and quality controllers often rely on such simplifications, therefore they most probably are going to be addressing only the top causes. If we have ever wondered why some processes (mal)function the way they do, there is a hint above. However, coming up with something more effective yet so simple at the same time requires much more effort.

11.3.5 Heat Maps

Two-way contingency tables can be depicted by means of a heatmap, where each count affects the corresponding cell's colour intensity, see Figure 11.7.

```

from matplotlib import cm
v = marathon.loc[:, ["sex", "age"]].value_counts().unstack(fill_value=0)
sns.heatmap(v, annot=True, fmt="d", cmap=cm.get_cmap("copper"))
plt.show()

```

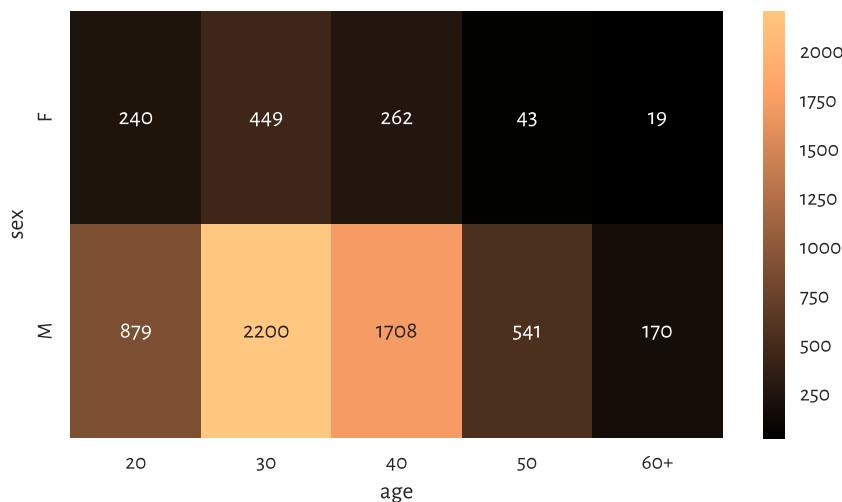


Figure 11.7: Heatmap for the marathoners' sex and age category

11.4 Aggregating and Comparing

11.4.1 A Mode

As we have already said, the only operation on categorical data that we can rely on is counting (because we have an equivalence relation on the set of labels and nothing more). Therefore, as far as qualitative data aggregation is concerned, what we are left with is the *mode*, i.e., the most frequently occurring value.

```
cat_cntrs16, counts_cntrs16 = np.unique(cntrs16, return_counts=True)
cat_cntrs16[np.argmax(counts_cntrs16)]
## 'KE'
```

Recall that if `i` is `numpy.argmax(counts)` (*argument maximum*, i.e., where is it?), then `counts[i]` is the same as `numpy.max(counts)` and `cat[i]` is the category with the greatest counts.

Important: A mode might be ambiguous.

For instance, amongst the fastest 22 runners, there is a tie between Kenya and Poland – both meet our definition of a mode:

```
cat_cntrs22, counts_cntrs22 = np.unique(cntrs[:22], return_counts=True)
cat_cntrs22[np.where(counts_cntrs22 == np.max(counts_cntrs22))]
## array(['KE', 'PL'], dtype='<U2')
```

To avoid any bias, it would be best to report both of them as potential mode candidates. Alternatively, we can pick one at random (calling `numpy.random.choice`).

11.4.2 Binary Data as Logical Vectors

Perhaps the most useful arithmetic operation on logical vectors is the sum.

```
cntrs16 = cntrs[:16]
cntrs16 # recall
## array(['KE', 'KE', 'KE', 'ET', 'KE', 'KE', 'ET', 'MA', 'PL', 'PL', 'IL',
##        'PL', 'KE', 'KE', 'PL', 'PL'], dtype='<U2')
np.sum(cntrs16 == "PL")
## 5
```

is the number of elements in `cntrs16` that are equal to "PL" (because the sum of 0s and 1s is equal to the number of 1s in the sequence). Note that (`cntrs16 == "PL"`) is a logical vector that represents a binary categorical variable with levels: not-Poland (`False`) and Poland (`True`).

If we divide the above result by the length of the vector, we will get the proportion:

```
np.mean(cntrs16 == "PL")
## 0.3125
```

Hence, 31.25% amongst the top 16 runners are from Poland.

Exercise 11.17 What is the meaning of `numpy.all`, `numpy.any`, `numpy.min`, `numpy.max`, `numpy.cumsum`, and `numpy.cumprod` applied on logical vectors?

Note: (***) Having the 0/1 (or zero/nonzero) vs `False/True` correspondence allows us to perform some logical operations using integer arithmetic. In particular, assuming that `p` and `q` are logical values and `a` and `b` are numeric ones, we have, what follows:

- `p+q != 0` means that at least one value is `True` and `p+q == 0` if and only if both are `False`;

- more generally, $p+q == 2$ if both elements are True, $p+q == 1$ if only one is True (we call it exclusive-or, XOR), and $p+q == 0$ if both are False;
 - $p*q != 0$ means that both values are True and $p*q == 0$ holds whenever at least one is False;
 - $1-p$ corresponds to negation of p ;
 - $p*a + (1-p)*b$ is equal to a if p is True and equal to b otherwise.
-

11.4.3 Pearson's Chi-Squared Test (*)

The Kolmogorov–Smirnov test that we described in Section 6.2.3 verifies whether a given sample differs significantly from a hypothesised *continuous* distribution, i.e., it works for *numeric* data.

For binned/categorical data, we can use a classical and easy-to-understand test developed by Karl Pearson in 1900. It is supposed to judge whether the difference between the observed proportions $\hat{p}_1, \dots, \hat{p}_l$ and the theoretical ones p_1, \dots, p_l is significantly large or not:

$$\begin{cases} H_0 : \hat{p}_i = p_i \text{ for all } i = 1, \dots, l & \text{(null hypothesis)} \\ H_1 : \hat{p}_i \neq p_i \text{ for some } i = 1, \dots, l & \text{(alternative hypothesis)} \end{cases}$$

Having such a test is beneficial, e.g., when the data we have at hand are based on small surveys that are supposed to serve as estimates of what might be happening in a larger population.

Going back to our political example from Section 11.3.2, it turns out that one of the pre-election polls indicated that $c = 516$ out of $n = 1017$ people would vote for the first candidate. We have $\hat{p}_1 = 50.74\%$ (Duda) and $\hat{p}_2 = 49.26\%$ (Traskowski). If we would like to test whether the observed proportions are significantly different from each other, we could test them against the theoretical distribution $p_1 = 50\%$ and $p_2 = 50\%$, stating that there is a tie between the competitors (up to a sampling error).

As a natural test statistic is based on the relative squared differences:

$$\hat{T} = n \sum_{i=1}^l \frac{(\hat{p}_i - p_i)^2}{p_i}.$$

`c, n = 516, 1017`

`p_observed = np.array([c, n-c]) / n`

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```
p_expected = np.array([0.5, 0.5])
T = n * np.sum( (p_observed-p_expected)**2 / p_expected )
T
## 0.2212389380530986
```

Similarly to the continuous case in [Section 6.2.3](#), we should reject the null hypothesis, if

$$\hat{T} \geq K,$$

where the critical value K is based on the fact that, if the null hypothesis is true, \hat{T} follows the χ^2 (chi-squared, hence the name of the test) distribution with $l - 1$ degrees of freedom, see `scipy.stats.chi2`.

```
alpha = 0.001 # significance level
scipy.stats.chi2.ppf(1-alpha, len(p_observed)-1)
## 10.827566170662733
```

As $\hat{T} < K$ (because $0.22 < 10.83$), we cannot deem the two proportions significantly different from each other. In other words, this poll did not indicate (at significance level 0.1%) any of the candidates as a clear winner.

Exercise 11.18 Determine the smallest c , i.e., the number of respondents indicating they would vote for Duda, that leads to the rejection of the null hypothesis.

11.4.4 Two-Sample Pearson's Chi-Squared Test (*)

Let's consider the data depicted in [Figure 11.3](#) and test whether the runners' age distributions differ significantly between females and males.

We have $l = 5$ categories. First, denote the total number of observations in both groups with n' and n'' .

```
d = marathon.loc[:, ["sex", "age"]].value_counts().unstack(fill_value=0)
c1, c2 = d.to_numpy() # first row, second row
n1 = c1.sum()
n2 = c2.sum()
n1, n2
## (1013, 5498)
```

The observed proportions in the first group (females), denoted as $\hat{p}'_1, \dots, \hat{p}'_l$, are, respectively:

```
p1 = c1/n1
p1
## array([0.23692004, 0.44323791, 0.25863771, 0.04244817, 0.01875617])
```

Here are the proportions in the second group (males), $\hat{p}_1'', \dots, \hat{p}_l''$:

```
p2 = c2/n2
p2
## array([0.15987632, 0.40014551, 0.31065842, 0.09839942, 0.03092033])
```

We would like to verify whether the corresponding proportions are equal to each other (up to some sampling error):

$$\begin{cases} H_0 : \hat{p}'_i = \hat{p}''_i \text{ for all } i = 1, \dots, l & \text{(null hypothesis)} \\ H_1 : \hat{p}'_i \neq \hat{p}''_i \text{ for some } i = 1, \dots, l & \text{(alternative hypothesis)} \end{cases}$$

In other words, we are interested whether the categorical data in the two groups come from the same discrete probability distribution.

Taking the estimated expected proportions,

$$\bar{p}_i = \frac{c'_i + c''_i}{n' + n''},$$

for all $i = 1, \dots, l$, the test statistic this time is equal to:

$$\hat{T} = n' \sum_{i=1}^l \frac{(\hat{p}'_i - \bar{p}_i)^2}{\bar{p}_i} + n'' \sum_{i=1}^l \frac{(\hat{p}''_i - \bar{p}_i)^2}{\bar{p}_i},$$

which is a variation on the one-sample theme presented in [Section 11.4.4](#).

```
pp = (c1+c2)/(n1+n2)
T = n1 * np.sum( (p1-pp)**2 / pp ) + n2 * np.sum( (p2-pp)**2 / pp )
T
## 75.31373854741857
```

It can be shown that, if the null hypothesis is true, the test statistic *approximately* follows the χ^2 distribution with $l - 1$ degrees of freedom¹³⁷. The critical value K is equal to:

¹³⁷ Note that [[PTVF07]] in Section 14.3 suggests l degrees of freedom, but do not agree with the reasoning therein. Also, simple Monte Carlo simulations suggests that $l - 1$ is a better candidate.

```
alpha = 0.001 # significance level
scipy.stats.chi2.ppf(1-alpha, len(c1)-1)
## 18.46682695290317
```

As $\hat{T} \geq K$ (because $75.31 \geq 18.47$), we reject the null hypothesis. And so, the age distribution differs across sexes (at significance level 0.1%).

11.4.5 Measuring Association (*)

Let us consider Australian Bureau of Statistics' National Health Survey 2018¹³² data on the prevalence of certain medical conditions as a function of age. Here is the extracted contingency table:

```
l = [
    "Arthritis", "Asthma", "Back problems", "Cancer (malignant neoplasms)",
    "Chronic obstructive pulmonary disease", "Diabetes mellitus",
    "Heart, stroke and vascular disease", "Kidney disease",
    "Mental and behavioural conditions", "Osteoporosis"],
    ["15-44", "45-64", "65+"]
]

C = 1000*np.array([
    [ 360.2,      1489.0,      1772.2],
    [1069.7,       741.9,       433.7],
    [1469.6,      1513.3,      955.3],
    [  28.1,       162.7,       237.5],
    [ 103.8,       207.0,       251.9],
    [ 135.4,       427.3,       607.7],
    [  94.0,       344.4,       716.0],
    [ 29.6,        67.7,        123.3],
    [2218.9,      1390.6,      725.0],
    [  36.1,       312.3,       564.7],
]).astype(int)

pd.DataFrame(C, index=l[0], columns=l[1])
##                                     15-44     45-64     65+
## Arthritis                      360000  1489000  1772000
## Asthma                         1069000   741000   433000
## Back problems                   1469000  1513000  955000
## Cancer (malignant neoplasms)  28000    162000   237000
```

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¹³² <https://www.abs.gov.au/statistics/health/health-conditions-and-risks-national-health-survey-first-results/2017-18>

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| | | | |
|---|----------------------|----------------------|---------------------|
| <code>## Chronic obstructive pulmonary disease</code> | <code>103000</code> | <code>207000</code> | <code>251000</code> |
| <code>## Diabetes mellitus</code> | <code>135000</code> | <code>427000</code> | <code>607000</code> |
| <code>## Heart, stroke and vascular disease</code> | <code>94000</code> | <code>344000</code> | <code>716000</code> |
| <code>## Kidney disease</code> | <code>29000</code> | <code>67000</code> | <code>123000</code> |
| <code>## Mental and behavioural conditions</code> | <code>2218000</code> | <code>1390000</code> | <code>725000</code> |
| <code>## Osteoporosis</code> | <code>36000</code> | <code>312000</code> | <code>564000</code> |

Cramer's V is one of a few ways to measure the degree of association between two categorical variables. It is equal to 0 (lowest possible value) if the two variables are independent (there is no association between them) and 1 (highest possible value) if they are tied.

```
scipy.stats.contingency.association(C)
## 0.316237999724298
```

The above means that there might be a small association between age and the prevalence of certain conditions. In other words, it might be the case that some conditions are more prevalent in different age groups than others.

Given a two-way contingency table C with n rows and m columns and assuming that

$$T = \sum_{i=1}^n \sum_{j=1}^m \frac{(c_{i,j} - e_{i,j})^2}{e_{i,j}},$$

where

$$e_{i,j} = \frac{\sum_{k=1}^m v_{i,k} \sum_{k=1}^n c_{k,j}}{\sum_{i=1}^n \sum_{j=1}^m c_{i,j}}$$

the Cramer coefficient is given by

$$V = \sqrt{\frac{T}{\min\{n-1, m-1\} \sum_{i=1}^n \sum_{j=1}^m c_{i,j}}}.$$

Note that $c_{i,j}$ gives the actually observed counts and $e_{i,j}$ denotes the number that we would expect if the two variables were actually independent.

Exercise 11.19 Compute the Cramer V using only `numpy` functions.

Exercise 11.20 (***) Actually we can easily verify the hypothesis whether V does not differ significantly from 0, i.e., whether the variables are independent. Looking at T , we see that this is actually the test statistic in Pearson's chi-squared goodness-of-fit test.

```
E = C.sum(axis=1).reshape(-1, 1) * C.sum(axis=0).reshape(1, -1) / C.sum()
T = np.sum((C-E)**2 / E)
T
## 3715440.465191512
```

If the data are really independent, T follows the chi-squared distribution $n + m - 1$, hence the critical value is equal to

```
alpha = 0.001 # significance level
scipy.stats.chi2.ppf(1-alpha, C.shape[0] + C.shape[1] - 1)
## 32.90949040736021
```

as it is greater than T , we conclude (at significance level 0.1%) that the conditions are not independent of age.

Exercise 11.21 (*) Take a look at Table 19: Comorbidity of selected chronic conditions of the National Health Survey 2018¹³³, where we clearly see that many disorders co-occur. Visualise them on some heatmaps and bar plots (including data grouped by sex and age).

11.4.6 Binned Numeric Data

Note that generally modes do not work for continuous data, where repeated values are – at least theoretically – highly unlikely (unless someone does not report them with full digit precision). It might make sense to compute it on binned data, though.

Looking at a histogram, the mode is the interval corresponding to the highest bar (hopefully assuming there is only one). If we would like to obtain a single number, we can choose for example the middle of this interval as the mode.

Of course, for numeric data, the mode will heavily depend on the binning (recall that we can also apply logarithmic binning). Thus, the question “what is the most popular income” is overall quite difficult to answer.

Exercise 11.22 Compute some potentially informative modes for the 2020 UK income¹³⁴ data. Play around with different numbers of bins for linear and logarithmic binning and see how it affects the mode.

¹³³ <https://www.abs.gov.au/statistics/health/health-conditions-and-risks/national-health-survey-first-results/2017-18>

¹³⁴ https://raw.githubusercontent.com/gagolews/%5Cteaching_data/master/marek/uk_income_simulated_2020.txt

11.4.7 Ordinal Data (*)

The case where the categories can be linearly ordered, is called *ordinal data*. This gives a few more options as except for the mode, thanks to the existence of order statistics, we can also easily define sample quantiles. However, the standard methods for resolving ties will not work, hence we need to be careful.

For example, median of a sample of student grades (P, P, C, D, HD) is C, but (P, P, C, D, HD, HD) is either C or D - we can choose one at random or just report that the solution is ambiguous.

Another option, of course, is to treat ordinal data as numbers (e.g., F=0, P=1, ..., HD=4). In the latter example, the median would be equal to 2.5.

There are some cases, though, where the conversion of labels to consecutive integers is far from optimal – because it gives the impression that the “distance” between different levels is always equal (linear).

Exercise 11.23 (**) The `grades_results`¹³⁵ represents the grades (F, P, C, D, HD) of 100 students attending an imaginary course in a virtual Australian university. You can load it in form of an ordered categorical Series by calling:

```
grades = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/grades_results.txt", dtype="str")
grades = pd.Series(pd.Categorical(grades,
    categories=["F", "P", "C", "D", "HD"], ordered=True))
grades
## 0      F
## 1      F
## 2      F
## 3      F
## 4      F
##
## ...
## 118    HD
## 119    HD
## 120    HD
## 121    HD
## 122    HD
## Length: 123, dtype: category
## Categories (5, object): ['F' < 'P' < 'C' < 'D' < 'HD']
```

How would you determine the average grade represented as a number between 0 and 100, tak-

¹³⁵ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/grades_results.txt

ing into account that for a P you need at least 50%, C is given for $\geq 60\%$, D for $\geq 70\%$, and HD for only 80% of the points. Come up with a pessimistic, optimistic, and a best-shot estimate and then compare your result to the true corresponding scores listed in the `grades_scores`¹³⁶ dataset.

11.5 Exercises

Exercise 11.24 Does it make sense to compute the arithmetic mean of a categorical variable?

Exercise 11.25 Name the basic use cases for categorical data.

Exercise 11.26 (*) What is a Pareto chart?

Exercise 11.27 How to deal with the case of the mode being nonunique?

Exercise 11.28 What is the meaning of `numpy.mean((x > 0) & (x < 1))`, where `x` is a numeric vector?

Exercise 11.29 What is the meaning of the sum and mean for binary data (logical vectors)?

Exercise 11.30 List some ways to visualise multidimensional categorical data.

Exercise 11.31 (*) State the null hypotheses verified by the one- and two-sample chi-squared tests.

Exercise 11.32 (*) How is Cramer's V defined and what values does it take?

¹³⁶ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/grades_scores.txt

Processing Data in Groups

Let's consider (again) a subset of the US Centres for Disease Control and Prevention National Health and Nutrition Examination Survey data, this time carrying some body measures (`P_BMX`¹³⁸) and demographics (`P_DEMO`¹³⁹).

```

nhanes = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_p_demo_bmx_2020.csv",
    comment="#")
nhanes = (
    nhanes
    .loc[
        (nhanes.loc[:, "DMDBORN4"] <= 2) & (nhanes.loc[:, "RIDAGEYR"] >= 18),
        ["RIDAGEYR", "BMXWT", "BMXHT", "BMXBMI", "RIAGENDR", "DMDBORN4"]
    ]
    .rename({
        "RIDAGEYR": "age",
        "BMXWT": "weight",
        "BMXHT": "height",
        "BMXBMI": "bmival",
        "RIAGENDR": "gender",
        "DMDBORN4": "usborn"
    }, axis=1)
    .dropna()
    .reset_index(drop=True)
)

nhanes.loc[:, "usborn"] = nhanes.loc[:, "usborn"].astype("category").\
    cat.rename_categories(["yes", "no"]).astype("str")

nhanes.loc[:, "gender"] = nhanes.loc[:, "gender"].astype("category").\
    cat.rename_categories(["male", "female"])

```

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¹³⁸ https://www.cdc.gov/Nchs/Nhanes/2017-2018/P_BMX.htm

¹³⁹ https://www.cdc.gov/Nchs/Nhanes/2017-2018/P_DEMO.htm

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```

cat.rename_categories(["male", "female"]).astype("str")

nhanes.loc[:, "bmicat"] = pd.cut(nhanes.loc[:, "bmival"],
    bins=[0, 18.5, 25, 30, np.inf],
    labels=["underweight", "normal", "overweight", "obese"])
)

nhanes.head()
##   age  weight  height  bmival gender usborn      bmicat
## 0   29     97.1   160.2    37.8 female    no       obese
## 1   49     98.8   182.3    29.7 male     yes  overweight
## 2   36     74.3   184.2    21.9 male     yes      normal
## 3   68    103.7   185.3    30.2 male     yes       obese
## 4   76     83.3   177.1    26.6 male     yes  overweight

```

We consider only the adult (at least 18 years old) participants, whose country of birth (the US or not) is well-defined.

We have a mix of categorical (gender, US born-ness, BMI category) and numerical (age, weight, height, BMI) variables. Unless we had encoded qualitative variables as integers, this would not be possible with plain matrices.

In this section, we will treat the qualitative columns as grouping variables, so that we can, e.g., summarise or visualise the data *in each group* separately, because it is likely that data distributions vary across different factor levels. This is much like having many data frames stored in one object.

`nhanes` is thus an example of heterogeneous data at their best.

12.1 Basic Methods

`DataFrame` and `Series` objects are equipped with the `groupby` methods, which assist in performing a wide range of popular operations in data groups defined by one or more data frame columns (compare [[[Wic11](#)]])�.

They return objects of class `DataFrameGroupBy` and `SeriesGroupby`:

```
type(nhanes.groupby("gender"))
```

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```
## <class 'pandas.core.groupby.generic.DataFrameGroupBy'>
type(nhanes.groupby("gender").height) # or (...)["height"]
## <class 'pandas.core.groupby.generic.SeriesGroupBy'>
```

Important: `DataFrameGroupBy` and `SeriesGroupBy` inherit from (extend) the `GroupBy` class, hence they have many methods in common. Knowing that they are separate types is useful in exploring the list of possible methods and slots in the **pandas** manual.

Exercise 12.1 Skim through the documentation¹⁴⁰ of the said classes.

For example, the `size` method determines the number of observations in each group:

```
nhanes.groupby("gender").size()
## gender
## female    4514
## male      4271
## dtype: int64
```

This returns an object of type `Series`.

Another example, this time with grouping with respect to a combination of levels in two qualitative columns:

```
nhanes.groupby(["gender", "bmicat"]).size()
## gender  bmicat
## female  underweight    93
##          normal        1161
##          overweight     1245
##          obese         2015
## male    underweight     65
##          normal        1074
##          overweight    1513
##          obese         1619
## dtype: int64
```

This yielded a `Series` with a hierarchical index (row labels). We can always use `reset_index` to convert it to standalone columns:

¹⁴⁰ <https://pandas.pydata.org/pandas-docs/stable/reference/groupby.html>

```
nhanes.groupby(["gender", "bmicat"]).size().rename("counts").reset_index()
##   gender      bmcat  counts
## 0  female  underweight    93
## 1  female       normal  1161
## 2  female  overweight  1245
## 3  female      obese  2015
## 4   male  underweight    65
## 5   male       normal  1074
## 6   male  overweight  1513
## 7   male      obese  1619
```

Note the `rename` part thanks to which we have obtained a readable column name.

Exercise 12.2 Unstack the above data frame (i.e., convert it from the long to the wide format).

Exercise 12.3 (*) Note the difference between `pandas.GroupBy.count` and `pandas.GroupBy.size` methods.

12.1.1 Aggregating Data in Groups

The `DataFrameGroupBy` and `SeriesGroupBy` classes are equipped with a number of well-known aggregation functions, for example:

```
nhanes.groupby("gender").mean().reset_index()
##   gender      age     weight     height     bmival
## 0  female  48.956580  78.351839 160.089189 30.489189
## 1   male  49.653477  88.589932 173.759541 29.243620
```

Note that the arithmetic mean was computed only on numeric columns. Further, a few common aggregates are generated by `describe`:

```
nhanes.groupby("gender").height.describe().reset_index()
##   gender  count      mean       std      min     25%     50%     75%     max
## 0  female  4514.0 160.089189  7.035483 131.1 155.3 160.0 164.8 189.3
## 1   male  4271.0 173.759541  7.702224 144.6 168.5 173.8 178.9 199.6
```

But we can always apply a custom list of functions using `aggregate`:

```
(
  nhanes.
  loc[:, ["gender", "height", "weight"]].
  groupby("gender").
```

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```

aggregate([np.mean, np.median, len]).
reset_index()
)
##   gender      height           weight
##           mean median   len       mean median   len
## 0  female  160.089189  160.0  4514  78.351839  74.1  4514
## 1    male  173.759541  173.8  4271  88.589932  85.0  4271

```

Note that the result's `columns` slot is a hierarchical index.

Own functions can of course be passed as well, e.g., arbitrary inline *lambda expressions*:

```

(
  nhanes.
  loc[:, ["gender", "height", "weight"]].
  groupby("gender").
  aggregate(lambda x: (np.max(x)-np.min(x))/2).
  reset_index()
)
##   gender height weight
## 0  female   29.1 110.85
## 1    male   27.5 102.90

```

Note: (***) The column names in the output object are generated by reading the applied functions' `__name__` slots, see, e.g., `print(np.mean.__name__)`.

```

mr = lambda x: (np.max(x)-np.min(x))/2
mr.__name__ = "midrange"
(
  nhanes.
  loc[:, ["gender", "height", "weight"]].
  groupby("gender").
  aggregate([np.mean, mr]).
  reset_index()
)
##   gender      height           weight
##           mean midrange       mean midrange
## 0  female  160.089189     29.1  78.351839  110.85
## 1    male  173.759541     27.5  88.589932  102.90

```

12.1.2 Transforming Data in Groups

We can easily transform individual columns relative to different data groups by means of the `transform` method for `GroupBy` objects.

```
def standardise(x):
    return (x-np.mean(x, axis=0))/np.std(x, axis=0, ddof=1)

nhanes[ "height_std" ] = (
    nhanes.
    loc[:, [ "height", "gender" ]].
    groupby( "gender" ).
    transform(standardise)
)
(
    nhanes.
    loc[:, [ "gender", "height", "height_std" ]].
    groupby( "gender" ).
    aggregate([np.mean, np.std])
)
##           height          height_std
##      mean      std      mean   std
## gender
## female  160.089189  7.035483 -1.353518e-15  1.0
## male    173.759541  7.702224  3.155726e-16  1.0
```

The new column gives the *relative z-scores*: a woman with relative z-score of 0 has height of 160.1 cm, whereas a man with the same z-score has height of 173.8 cm.

Exercise 12.4 Create a data frame comprised of 5 tallest men and 5 tallest women.

12.1.3 Manual Splitting Into Subgroups (**)

It turns out that `GroupBy` objects and their derivatives are *iterable* (compare [Section 3.4](#)), therefore the grouped data frames and series can be easily processed manually in case where the built-in methods are insufficient (i.e., not so rarely).

Let us consider a small sample of our data frame.

```
grouped = nhanes.loc[:5, ["gender", "weight", "height"]].groupby("gender")
list(grouped)
## [('female',    gender weight height
## 0   female    97.1   160.2
## 5   female   91.1   152.7), ('male',    gender weight height
## 1   male     98.8   182.3
## 2   male     74.3   184.2
## 3   male    103.7   185.3
## 4   male    83.3   177.1)]
```

Therefore, when iterating through a `GroupBy` object, we get access to pairs giving all the levels of the grouping variable and the subsets of the input data frame corresponding to these categories.

```
for level, df in grouped:
    # df is a data frame - we can do whatever we want
    print(f"There are {df.shape[0]} subjects with gender={level}'.")
## There are 2 subjects with gender='female'.
## There are 4 subjects with gender='male'.
```

Let us also demonstrate that the splitting can be done manually without the use of `pandas`. Calling `numpy.split(arr, ind)` returns a list with `arr` (being an array-like object, e.g., a matrix, a vector, or a data frame) split rowwisely into `len(ind)+1` chunks at indices given by `ind`.

For example:

```
np.split(np.arange(10)*10, [3, 7])
## [array([ 0, 10, 20]), array([30, 40, 50, 60]), array([70, 80, 90])]
```

To split a data frame into groups defined by a categorical column, we can first sort it with respect to the criterion of interest, for instance, the gender data:

```
nhanes_srt = nhanes.sort_values("gender", kind="stable")
```

Then, we can use `numpy.unique` to fetch the indices of first occurrences of each series of identical labels:

```
levels, where = np.unique(nhanes_srt.loc[:, "gender"], return_index=True)
levels, where
## (array(['female', 'male'], dtype=object), array([ 0, 4514]))
```

This can now be used for dividing the sorted data frame into chunks:

```
nhanes_grp = np.split(nhanes_srt, where[1:])
```

We obtained a list of data frames split at rows specified by `where[1:]`. Here is a preview of the first and the last row in each chunk:

```
for i in range(len(levels)):
    print(f"level='{levels[i]}'; preview:")
    print(nhanes_grp[i].iloc[ [0, -1], : ])
    print("")
```

level='female'; preview:

| | age | weight | height | bmival | gender | usborn | bmicat | height_std |
|---------|-----|--------|--------|--------|--------|--------|--------|------------|
| ## 0 | 29 | 97.1 | 160.2 | 37.8 | female | no | obese | 0.015750 |
| ## 8781 | 67 | 82.8 | 147.8 | 37.9 | female | no | obese | -1.746744 |

##

level='male'; preview:

| | age | weight | height | bmival | gender | usborn | bmicat | height_std |
|---------|-----|--------|--------|--------|--------|--------|------------|------------|
| ## 1 | 49 | 98.8 | 182.3 | 29.7 | male | yes | overweight | 1.108830 |
| ## 8784 | 74 | 59.7 | 167.5 | 21.3 | male | no | normal | -0.812693 |

We can apply any operation on each subgroup we have learned so far, our imagination is the only limiting factor, e.g., aggregate some columns:

```
nhanes_agg = [
    dict(
        level=t.loc[:, "gender"].iloc[0],
        height_mean=np.mean(t.loc[:, "height"]),
        weight_mean=np.mean(t.loc[:, "weight"]))
    )
    for t in nhanes_grp
]
nhanes_agg
## [{"level": 'female', 'height_mean': 160.0891891892, 'weight_mean': 78.
#-35183872396988}, {"level": 'male', 'height_mean': 173.75954109107937,
#-weight_mean': 88.58993210021072}]
```

Finally, the results may be combined, e.g., to form a data frame:

```
pd.DataFrame(nhanes_agg)
##      level  height_mean  weight_mean
```

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```
## 0   female  160.089189  78.351839  
## 1     male  173.759541  88.589932
```

We see that manual splitting is very powerful but quite tedious in case where we would like to perform the basic operations such as computing some basic aggregates. These scenarios are very common, no wonder why the **pandas** developers came up with an additional, convenience interface in the form of the **pandas.DataFrame.groupby** and **pandas.Series.groupby** methods and the **DataFrameGroupBy** and **SeriesGroupby** classes. However, it is still worth knowing the low-level way to perform splitting in case of more ambitious tasks.

Exercise 12.5 (***) Using **numpy.split** and **matplotlib.pyplot.boxplot**, draw a box-and-whisker plot of heights grouped by BMI category (four boxes side by side).

Exercise 12.6 (***) Using **numpy.split**, compute the relative z-scores of the height column separately for each BMI category.

Note: (**) A simple trick to allow grouping with respect to more than one column is to apply **numpy.unique** on a string vector that combines the levels of the grouping variables, e.g., by concatenating them like `nhanes_srt.gender + " " + nhanes_srt.bmicat` (assuming that `nhanes_srt` is ordered with respect to these two criteria).

12.2 Plotting Data in Groups

The **seaborn** package is particularly convenient for plotting grouped data – it's highly interoperable with **pandas**.

12.2.1 Series of Box Plots

For example, Figure 12.1 depicts a boxplot with four boxes side by side:

```
sns.boxplot(x="bmival", y="gender", hue="usborn",  
            data=nhanes, palette="Set2")  
plt.show()
```

Let us contemplate for a while how easy it is now to compare the BMI distribution in

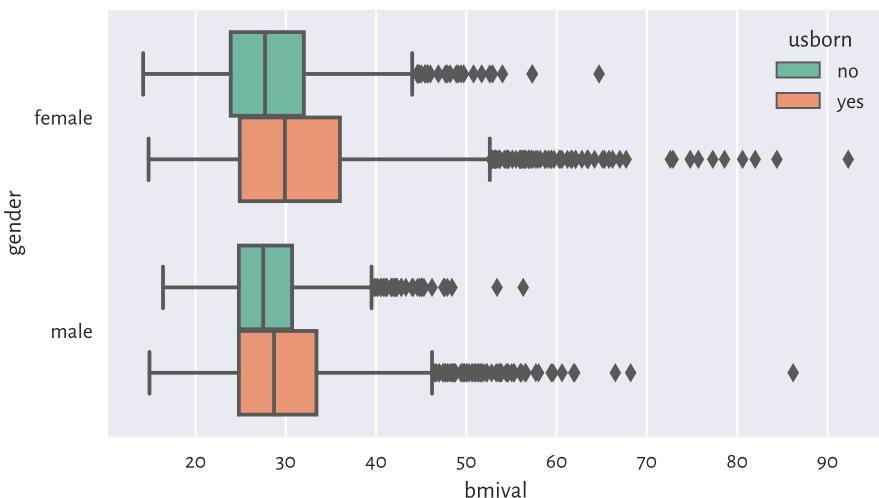


Figure 12.1: The distribution of BMIs for different genders and countries of birth

different groups. Note that we have two grouping variables, as specified by the `y` and `hue` arguments.

Exercise 12.7 Create a similar series of violin plots.

Exercise 12.8 Add the average BMIs in each group to the above box plot.

12.2.2 Series of Bar Plots

In Figure 12.2, on the other hand, we have a bar plot representing a two way contingency table (obtained in a different way than in Chapter 11):

```
sns.barplot(
    y="counts",
    x="gender",
    hue="bmicat",
    palette="Set2",
    data=(nhanes.
          groupby(["gender", "bmicat"]).
          size().
```

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```

        rename("counts").
        reset_index()
    )
plt.show()

```

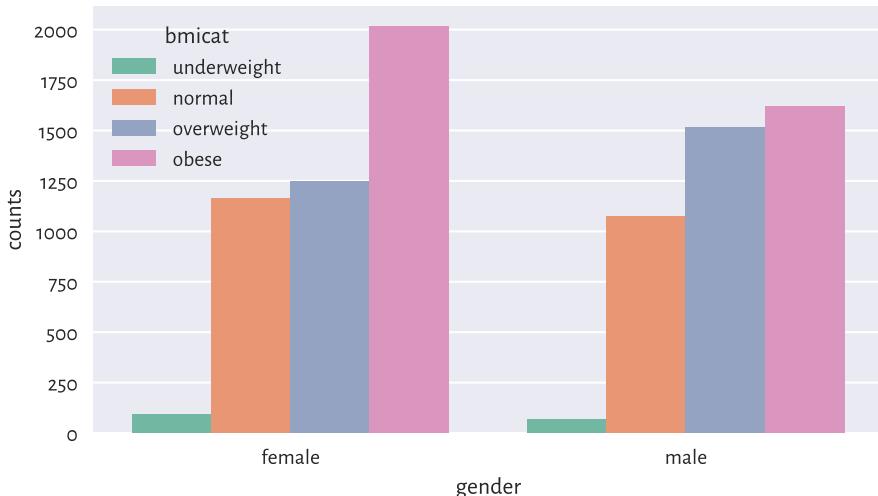


Figure 12.2: Number of persons for each gender and BMI category

Exercise 12.9 Draw a similar bar plot where the bar heights sum to 100% for each gender.

Exercise 12.10 Using the two-sample chi-squared test, verify whether the BMI category distributions differ significantly from each other across genders.

12.2.3 Semitransparent Histograms

Figure 12.3 illustrates that playing with semitransparent objects can make comparisons easy. Note that by passing `common_norm=False` we have scaled each density histogram separately, which is the behaviour we desire as samples are of different lengths.

```

sns.histplot(data=nhanes, x="weight", hue="usborn",
             element="step", stat="density", common_norm=False)
plt.show()

```

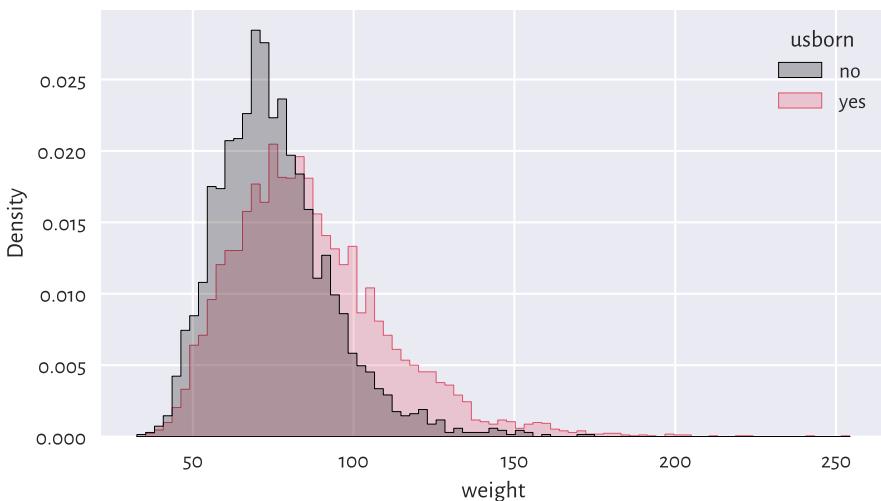


Figure 12.3: Clearly, the weight distribution of the US-born participants has higher mean and variance

12.2.4 Scatterplots with Group Information

Scatterplots for grouped data can display category information using points of different shapes or colours, compare Figure 12.4.

```
sns.scatterplot(x="height", y="weight", hue="gender", data=nhanes, alpha=0.1)
plt.show()
```

12.2.5 Grid (Trellis) Plots

Grid plot (also known as trellis, panel, or lattice plots) are a way to visualise data separately for each factor level. All the plots share the same coordinate ranges which makes them easily comparable. For instance, Figure 12.5 depicts a series of histograms for weights grouped by a combination of two categorical variables.

```
grid = sns.FacetGrid(nhanes, col="gender", row="usborn")
grid.map(sns.histplot, "weight", stat="density", color="lightgray")
# plt.show() # not required...
```

Exercise 12.11 Pass `hue="bmcat"` additionally to `seaborn.FacetGrid`.

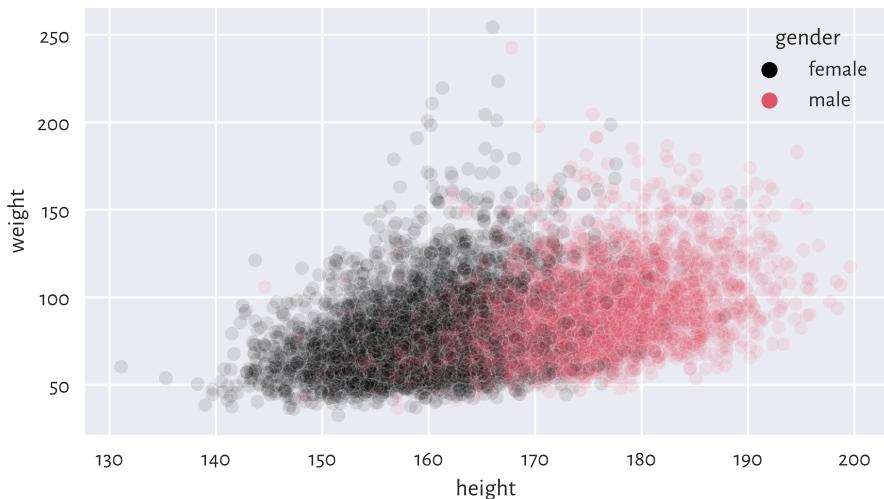


Figure 12.4: Weight vs height grouped by gender

Important: Grid plots can bear any kind of data visualisation we have discussed so far (e.g., histograms, bar plots, scatterplots).

Exercise 12.12 Draw a trellis plot with scatterplots of weight vs height grouped by BMI category and gender.

12.2.6 Comparing ECDFs with the Two-Sample Kolmogorov–Smirnov Test (*)

Figure 12.6 compares the empirical cumulative distribution functions of the weight distributions for US and non-US born participants.

```
sns.ecdfplot(data=nhanes, x="weight", hue="usborn")
plt.show()
```

A two-sample Kolmogorov–Smirnov test can be used to check whether two empirical cumulative distribution functions \hat{F}'_n (e.g., weight of the US-born participants) and \hat{F}''_m

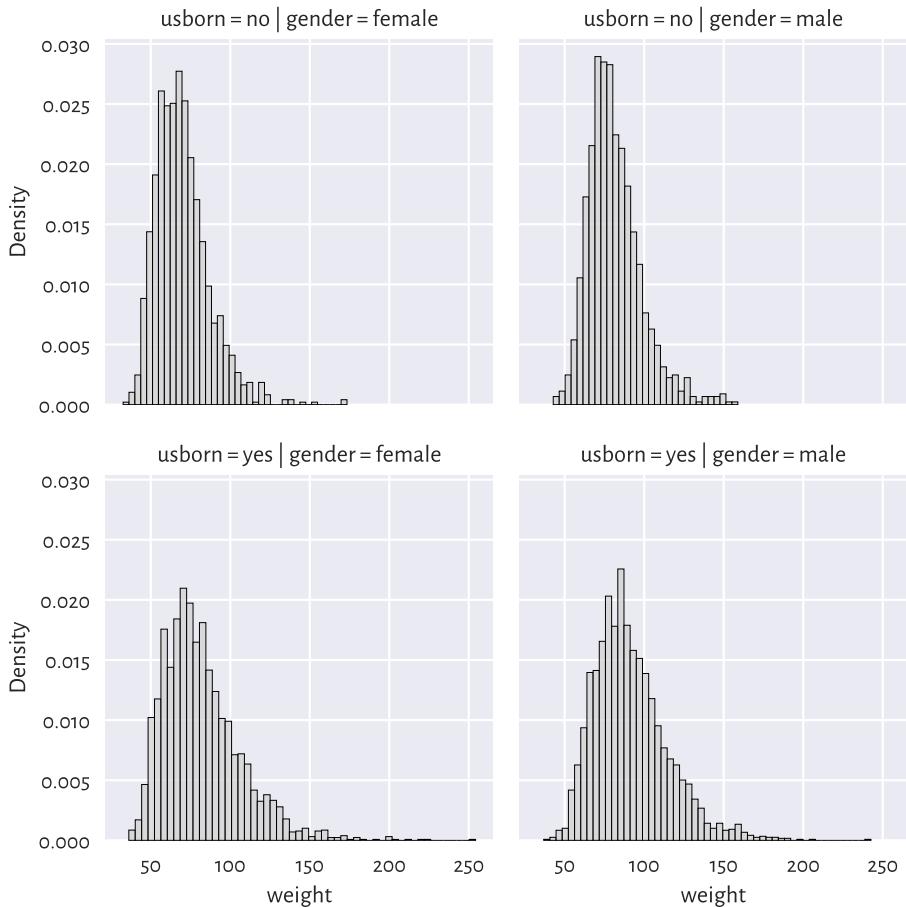


Figure 12.5: Distribution of weights for different genders and countries of birth

(e.g., weight of non-US-born persons) are significantly different or not from each other:

$$\begin{cases} H_0 : \hat{F}'_n = \hat{F}''_n & \text{(null hypothesis)} \\ H_1 : \hat{F}'_n \neq \hat{F}''_n & \text{(two-sided alternative)} \end{cases}$$

The test statistic is a variation of the one-sample variant discussed in [Section 6.2.3](#). Namely, let

$$\hat{D}_{n,m} = \sup_{t \in \mathbb{R}} |\hat{F}'_n(t) - \hat{F}''_m(t)|.$$

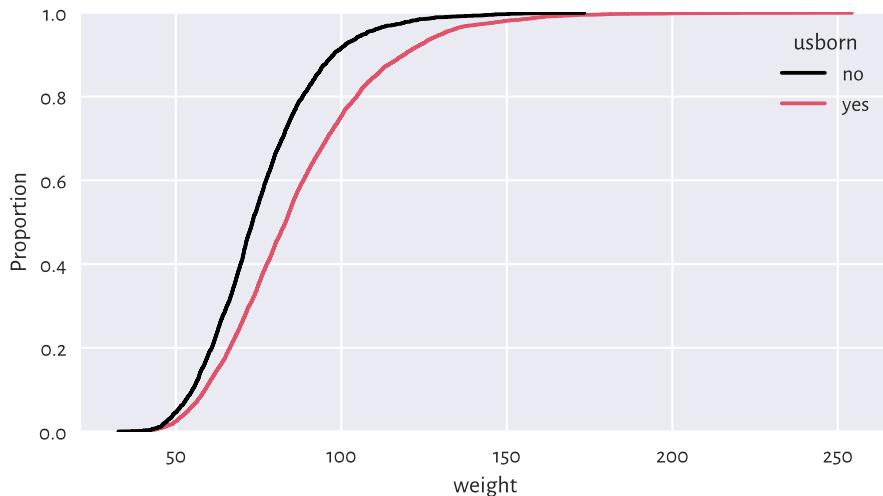


Figure 12.6: Empirical cumulative distribution functions of weight distributions for different birthplaces

Computing the above is slightly trickier than in the previous case, but luckily an appropriate procedure is already implemented in **scipy**:

```
x12 = nhanes.set_index("usborn").weight
x1 = x12.loc["yes"]
x2 = x12.loc["no"]
Dnm = scipy.stats.ks_2samp(x1, x2)[0]
Dnm
## 0.22068075889911914
```

Assuming significance level $\alpha = 0.001$, the critical value is approximately (for larger n and m) equal to

$$K_{n,m} = \sqrt{-\frac{\log(\alpha/2)(n+m)}{2nm}},$$

```
alpha = 0.001
np.sqrt(-np.log(alpha)/2) * (len(x1)+len(x2)) / (2*len(x1)*len(x2)))
## 0.04607410479813944
```

As usual, we reject the null hypothesis when $\hat{D}_{n,m} \geq K_{n,m}$, which is exactly the case here (at significance level 0.1%). In other words, weights of US- and non-US-born participants differ significantly.

Important: Frequentist hypothesis testing only takes into account the deviation between distributions that is explainable due to sampling effects (the assumed randomness of the data generation process). For large sample sizes, even very small deviations¹⁴⁷ will be deemed *statistically significant*, but it does not mean that we should consider them as *practically significant*. For instance, if a very costly, environmentally unfriendly, and generally inconvenient for everyone upgrade leads to a process' improvement such that we reject the null hypothesis stating that two distributions are equal, but it turns out that the gains are ca. 0.5%, the good old common sense should be applied.

Exercise 12.13 Compare ECDFs of weights of males who are between 18 and 25 years old. Determine whether they are significantly different.

Important: Some statistical textbooks and many research papers in the social sciences (amongst many others) employ the significance level of $\alpha = 5\%$, which is often criticised as too high (and for similar reasons we do not introduce the notion of *p*-values, which most practitioners misunderstand anyway). As many stakeholders aggressively push towards constant improvements in terms of inventing bigger, better, faster, more efficient things, larger α allows for generating more *sensational* discoveries, because it considers smaller differences as already significant, and thus possibly adding to what we call the reproducibility crisis in the empirical sciences.

We, on the other hand, claim that it is better to err on the side of being cautious – which, in the long run, is more sustainable, and eco-friendly.

12.2.7 Comparing Quantiles

Plotting quantiles in two samples against each other can also give us some further (informal) insight with regards to the possible distributional differences. Figure 12.7 depicts an example Q-Q plot (compare Section 6.2.2 for a one-sample version), where we see that the distributions have similar shapes (points more or less lie on a straight line), but they are shifted and/or scaled (if they were, they would be on the identity line).

¹⁴⁷ Including those that are merely due to round-off errors, in very large samples.

```
x = nhanes.weight.loc[nhanes.usborn == "yes"]
y = nhanes.weight.loc[nhanes.usborn == "no"]
xd = np.sort(x)
yd = np.sort(y)
if len(xd) > len(yd): # interpolate between quantiles in a longer sample
    xd = np.quantile(xd, np.arange(1, len(yd)+1)/(len(yd)+1))
else:
    yd = np.quantile(yd, np.arange(1, len(xd)+1)/(len(xd)+1))
plt.plot(xd, yd, "o")
plt.axline((xd[len(xd)//2], xd[len(xd)//2]), slope=1,
           linestyle=":", color="gray") # identity line
plt.xlabel(f"Sample quantiles (weight; usborn=yes)")
plt.ylabel(f"Sample quantiles (weight; usborn=no)")
plt.show()
```

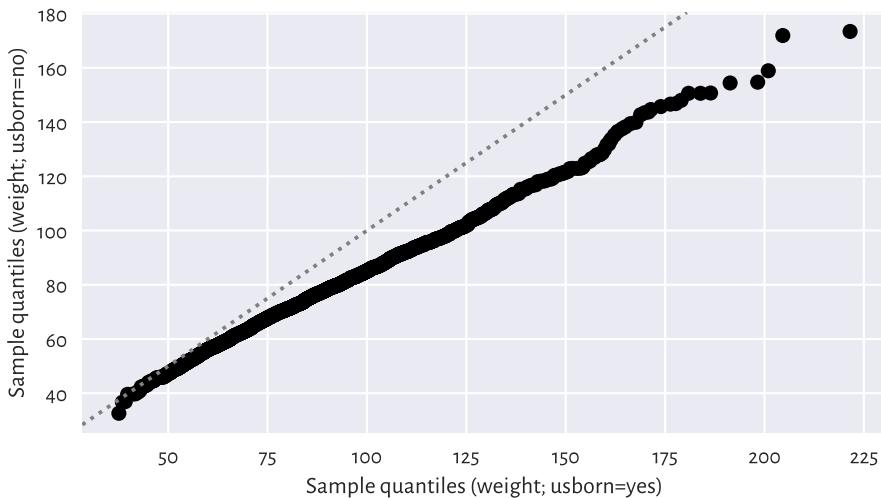


Figure 12.7: A two-sample Q-Q plot

Note that we interpolated between the quantiles in a larger sample to match the length of the shorter vector.

12.3 Classification Tasks

Let us consider a small sample of white, rather sweet wines from a much larger `wine quality`¹⁴¹ dataset.

```
wine_train = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/other/sweetwhitewine_train2.csv",
    comment="#")
wine_train.head()
##      alcohol      sugar  bad
## 0  10.625271  10.340159   0
## 1   9.066111  18.593274   1
## 2  10.806395   6.206685   0
## 3  13.432876   2.739529   0
## 4   9.578162   3.053025   0
```

We are given each wine's alcohol and residual sugar content, as well as a binary categorical variable stating whether a group of sommeliers deem a given beverage quite bad (1) or not (0). Figure 12.8 reveals that bad wines are rather low in... alcohol and, to some extent, sugar.

```
sns.scatterplot(x="alcohol", y="sugar",
    data=wine_train, hue="bad", palette=["black", "red"], alpha=0.5)
plt.xlabel("alcohol")
plt.ylabel("sugar")
plt.legend(title="bad")
plt.show()
```

Someone answer the door! We have just received a delivery: quite a few new wine bottles whose alcohol and sugar contents have, luckily, been given on their respective labels.

```
wine_test = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/other/sweetwhitewine_train2.csv",
    comment="#").iloc[:, :-1]
wine_test.head()
##      alcohol      sugar
## 0  10.625271  10.340159
## 1   9.066111  18.593274
```

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¹⁴¹ <http://archive.ics.uci.edu/ml/datasets/Wine+Quality>

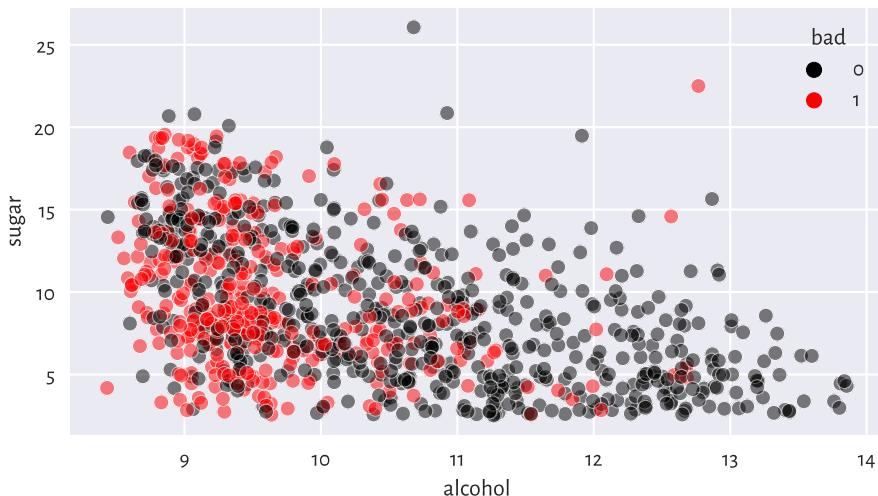


Figure 12.8: Scatterplot for sugar vs alcohol content for white, rather sweet wines, and whether they are considered bad (1) or drinkable (0) by some experts

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```
## 2 10.806395 6.206685
## 3 13.432876 2.739529
## 4 9.578162 3.053025
```

We would like to determine which of the wines from the test set might be not-bad without asking an expert for their opinion. In other words, we would like to exercise a *classification* task. More formally:

Important: Assume we are given a set of training points $\mathbf{X} \in \mathbb{R}^{n \times m}$ and the corresponding reference outputs $\mathbf{y} \in \{L_1, L_2, \dots, L_l\}^n$ in form of a categorical variable with l distinct levels. The aim of a *classification* algorithm is to predict what the outputs for each point from a possibly different dataset $\mathbf{X}' \in \mathbb{R}^{n' \times m}$, i.e., $\hat{\mathbf{y}}' \in \{L_1, L_2, \dots, L_l\}^{n'}$, might be.

In other words, we are asked to fill the gaps in a categorical variable. Recall that in a regression problem (Section 9.2), the reference outputs were numerical.

Exercise 12.14 Which of the following are instances of classification problems and which are regression tasks?

- Detect email spam;
- Predict a market stock price;
- Predict the likeability of a new advertising piece;
- Assess credit risk;
- Detect tumour tissues in medical images;
- Predict time-to-recovery of cancer patients;
- Recognise smiling faces on photographs;
- Detect unattended luggage in airport security camera footage;
- Turn on emergency braking to avoid a collision with pedestrians in autonomous vehicle.

What kind of data should you gather in order to tackle them?

12.3.1 K-Nearest Neighbour Classification

One of the simplest approaches to classification – good enough for such an introductory course – is based on the information about a test point's nearest neighbours (compare Section 8.4.4) living in the training sample.

Fix $k \geq 1$. Namely, to classify some $\mathbf{x}' \in \mathbb{R}^m$:

1. Find the indices $N_k(\mathbf{y}) = \{i_1, \dots, i_k\}$ of the k points from \mathbf{X} closest to \mathbf{x}' , i.e., ones that fulfil for all $j \notin \{i_1, \dots, i_k\}$

$$\|\mathbf{x}_{i_1, \cdot} - \mathbf{x}'\| \leq \dots \leq \|\mathbf{x}_{i_k, \cdot} - \mathbf{x}'\| \leq \|\mathbf{x}_{j, \cdot} - \mathbf{x}'\|.$$

2. Classify \mathbf{x}' as $y' = \text{mode}(y_{i_1}, \dots, y_{i_k})$, i.e., assign it the label that most frequently occurs amongst its k nearest neighbours. If a mode is nonunique, resolve the ties, for example, at random.

It is thus a very similar algorithm to k -nearest neighbour regression (Section 9.2.1), where we replaced the quantitative mean with the qualitative mode.

This is a variation on the theme: if you do not know what to do in a given situation, try to mimic what most of the other people around you are doing. Or, if you do not know what to think about a particular wine, but amongst the 5 similar ones (in terms of alcohol and sugar content) three were said to be awful, say that you don't like it because it's not sweet enough. Thanks to this, others will think you are a very sophisticated wine taster.

Let us apply a 5-nearest neighbour classifier on the standardised version of the dataset: as we are about to use a technique based on pairwise distances, it would be best if the variables were on the same scale.

```
k = 5
y_train = wine_train.bad.to_numpy()
```

Computing the z-scores for the train set:

```
X_train = wine_train.loc[:, ["alcohol", "sugar"]].to_numpy()
means = np.mean(X_train, axis=0)
sds = np.std(X_train, axis=0)
Z_train = (X_train-means)/sds
```

The z-scores for the test set (note that they are based on the aggregates computed for the train set):

```
Z_test = (wine_test.loc[:, ["alcohol", "sugar"]].to_numpy()-means)/sds
```

Making the predictions:

```
def knn_class(X_test, X_train, y_train, k):
    nnis = scipy.spatial.KDTree(X_train).query(X_test, k)[1]
    nnls = y_train[nnis] # same as: y_train[nnis.reshape(-1)].reshape(-1, k)
    return scipy.stats.mode(nnls.reshape(-1, k), axis=1)[0].reshape(-1)

y_pred = knn_class(Z_test, Z_train, y_train, k)
y_pred[:10] # preview
## array([0, 1, 0, 0, 1, 0, 0, 0, 0, 0])
```

First, we have fetched the indices of each test point's nearest neighbours (amongst the points in the training set). Then, we have fetched their corresponding labels; they are stored in a matrix with k columns. Finally, we computed the modes in each row, and hence classified each point in the test set.

Note: Unfortunately, `scipy.stats.mode` does not resolve the possible ties at random. Nevertheless, in our case, k is odd and the number of possible classes is $l = 2$, therefore the mode is always unique.

Figure 12.9 shows how nearest neighbour classification categorises different regions of a section of the two-dimensional plane. The greater the k , the smoother the decision

boundaries. Naturally, in regions corresponding to few training points we do not expect the classification accuracy to be good enough.

```
x1 = np.linspace(Z_train[:, 0].min(), Z_train[:, 0].max(), 100)
x2 = np.linspace(Z_train[:, 1].min(), Z_train[:, 1].max(), 100)
xg1, xg2 = np.meshgrid(x1, x2)
Xg12 = np.column_stack((xg1.reshape(-1), xg2.reshape(-1)))
ks = [5, 25]
for i in range(len(ks)):
    plt.subplot(1, len(ks), i+1)
    yg12 = knn_class(Xg12, Z_train, y_train, ks[i])
    plt.scatter(Z_train[:, 0], Z_train[:, 1],
                c=np.array(["black", "red"])[y_train], alpha=0.5)
    plt.contourf(x1, x2, yg12.reshape(len(x2), len(x1)),
                  cmap="RdGy_r", alpha=0.5)
    plt.title(f"$k={ks[i]}$")
    plt.xlabel("alcohol")
    plt.ylabel("sugar")
plt.show()
```

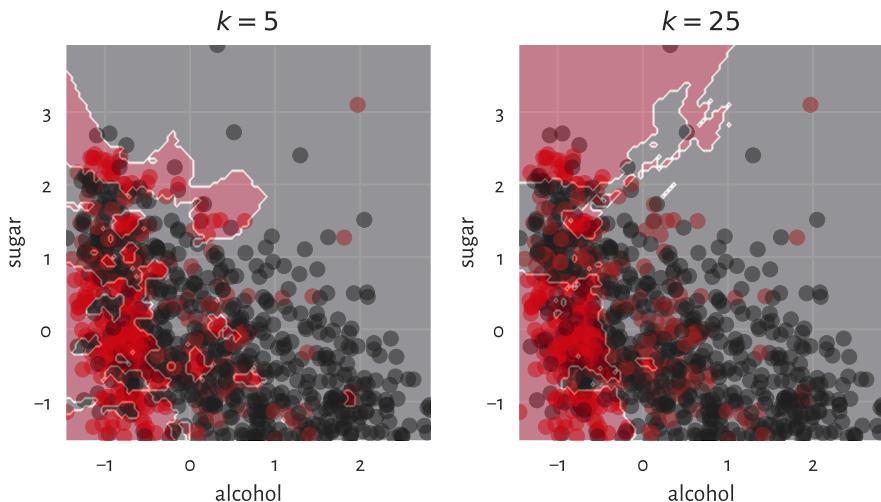


Figure 12.9: K -nearest neighbour classification of a whole, dense, two-dimensional grid of points for different k

Example 12.15 (***) The same with the **scikit-learn** package:

```
import sklearn.neighbors
knn = sklearn.neighbors.KNeighborsClassifier(k)
knn.fit(Z_train, y_train)
y_pred2 = knn.predict(Z_test)
```

We can verify that the results are identical to the ones above by calling:

```
np.all(y_pred2 == y_pred)
## True
```

12.3.2 Assessing the Quality of Predictions

It is time to reveal the truth: our test wines, it turns out, have already been assessed by some experts.

```
y_test = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/other/sweetwhitewine_train2.csv",
    comment="#").iloc[:, -1].to_numpy()
y_test[:10] # preview
## array([0, 1, 0, 0, 0, 1, 0, 0, 0, 1])
```

The *accuracy* score is the most straightforward measure of the similarity between these true labels (denoted y') and the ones predicted by the classifier (denoted \hat{y}'). It is defined as a ratio of the correctly classified instances to all the instances.

```
np.mean(y_test == y_pred)
## 0.788
```

Thus, 79% of the wines were correctly classified with regards to their true quality. Before we get too enthusiastic, let us note that our dataset is slightly imbalanced:

```
pd.Series(y_test).value_counts() # contingency table
## 0    639
## 1    361
## dtype: int64
```

It turns out that 639 out of 1000 wines in our sample are (truly) good. Therefore, a classifier which labels all the wines as great would have accuracy of ca. 64%. Thus, our machine learning approach to wine quality assessment is not that usable after all.

Thus, it is always good to analyse the corresponding *confusion matrix*, which is a two-way contingency table summarising the correct decisions and errors we make.

```
C = pd.DataFrame(
    dict(y_pred=y_pred, y_test=y_test)
).value_counts().unstack(fill_value=0)
C
## y_test      0      1
## y_pred
## 0          548   121
## 1          91    240
```

In the binary classification case ($l = 2$) such as this one, its entries are usually referred to as what is given in the table below. Note that the terms *positive* and *negative* refer to the output predicted by a classifier, i.e., they indicate whether some \hat{y}' is equal to 1 and 0, respectively.

Table 12.1: The different cases of true vs predicted labels in a binary classification task

| $(l = 2)$ | $y' = 0$ | $y' = 1$ |
|----------------|-------------------------------|--------------------------------|
| $\hat{y}' = 0$ | True Negative | False Negative (Type II error) |
| $\hat{y}' = 1$ | False Positive (Type I error) | True Positive |

Ideally, the number of false positives and false negatives should be as low as possible. The accuracy score only takes the raw number of true negatives (TN) and true positives (TP) into account and thus might not be a good metric in imbalanced classification problems.

There are, fortunately, some more meaningful measures in the case where class 1 less frequently occurring and where mispredicting it is considered more hazardous than making an inaccurate prediction with respect to class 0 (most will agree that it's better to be surprised by a vino mis-labelled as bad, than be disappointed with a highly recommended product where we have already built some expectations around it; not getting diagnosed with COVID-19 where we actually are sick can be more dangerous for the people around us than being forced to stay at home where it turned out to be only some mild headache after all; and so forth).

- *Precision* answers the question: If the classifier outputs 1, what is the probability that this is indeed true?

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}}.$$

```
C = C.to_numpy()
C[1,1]/(C[1,1]+C[1,0]) # Precision
## 0.7250755287009063
```

Thus, in 73% cases, when a classifier labels a vino as bad, it is actually undrinkable.

- *Recall* (sensitivity, hit rate, or true positive rate) – If the true class is 1, what is the probability that the classifier will detect it?

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}}.$$

```
C[1,1]/(C[1,1]+C[0,1]) # Recall
## 0.6648199445983379
```

Only 66% of the really bad wines will be filtered out by the classifier.

- *F-measure* (or F_1 -measure), is the harmonic mean of precision and recall in the case where we had rather have them aggregated into a single number

$$F = \frac{1}{\frac{1}{\text{Precision}} + \frac{1}{\text{Recall}}} = \left(\frac{1}{2} \left(\text{Precision}^{-1} + \text{Recall}^{-1} \right) \right)^{-1} = \frac{\text{TP}}{\text{TP} + \frac{\text{FP} + \text{FN}}{2}}.$$

```
C[1,1]/(C[1,1]+0.5*C[0,1]+0.5*C[1,0]) # F
## 0.6936416184971098
```

Overall, we can conclude that our classifier is subpar.

Exercise 12.16 Would you use precision or recall in each of the following settings?

- *Medical diagnosis;*
- *Medical screening;*
- *Suggestions of potential matches in a dating app;*
- *Plagiarism detection;*
- *Wine recommendation.*

12.3.3 Train-Test Set Split

The training set, that we have been provided with, was used as a source of knowledge about our problem domain.

Important: The k -nearest neighbour classifier is technically *model-free*, therefore in order to generate a new prediction, we need to be able to query all the points in the database – they must be at hand all the time.

Most statistical/machine learning algorithms, however, by construction, generalise the patterns discovered in the dataset in form of mathematical functions (oftentimes, very complicated ones), that are fitted by minimising some error metric. Linear regression analysis by means of the least squares approximation uses exactly this kind of approach.

Either way, we have used a separate *test set* to verify the quality of our classifier on so-far *unobserved* data, i.e., its *predictive* capabilities. After all, we do not want our model to overfit to training data and be completely useless when filling the gaps between the points we were exposed to. This is like being a student who can only repeat what the teacher says, and when faced with a slightly different real-world problem, they panic and say complete gibberish.

In the above example, the train and test sets were created by yours truly. Normally, however, it is the data scientist who splits a single data frame into two parts themselves. This way, they can *mimic* the situation where some *test* observations become available after the learning phase is complete.

Here is an example data frame:

```
XY = pd.DataFrame(dict(  
    x=np.round(np.random.rand(10), 1),  
    y=np.round(np.random.rand(10), 1)  
) # whatever  
XY  
##      x      y  
## 0  0.7  0.3  
## 1  0.3  0.7  
## 2  0.2  0.4  
## 3  0.6  0.1  
## 4  0.7  0.4  
## 5  0.4  0.7  
## 6  1.0  0.2  
## 7  0.7  0.2  
## 8  0.5  0.5  
## 9  0.4  0.5
```

Let us generate its 60/40% partition. To avoid bias, it is best to allocate the rows into

the training and test sets at random. One way to do so is to create a vector of randomly rearranged row indices:

```
np.random.seed(123) # assure reproducibility
n = XY.shape[0]
idx = np.arange(n)
np.random.shuffle(idx) # modifies idx in place
idx
## array([4, 0, 7, 5, 8, 3, 1, 6, 9, 2])
```

and now the train set can be created by picking the rows at the first 60% of these indices:

```
XY_train = XY.iloc[idx[:int(0.6*n)], :]
XY_train
##      x     y
## 4  0.7  0.4
## 0  0.7  0.3
## 7  0.7  0.2
## 5  0.4  0.7
## 8  0.5  0.5
## 3  0.6  0.1
```

and the test set can utilise the remaining 40%:

```
XY_test = XY.iloc[idx[int(0.6*n):], :]
XY_test
##      x     y
## 1  0.3  0.7
## 6  1.0  0.2
## 9  0.4  0.5
## 2  0.2  0.4
```

It is easy to verify that the union of these two sets gives the original data frame and that they have no rows in common.

12.3.4 Validating Many Models (Parameter Selection)

When trying to come up with a good solution to a given task, there usually are many *hyperparameters* that should be tweaked, for example:

- which independent variables should be used for model building,
- how they should be preprocessed; e.g., which of them should be standardised,

- if an algorithm has some tunable parameters, what is the best combination thereof; for instance, which k should we use in for the k -nearest neighbours search.

At initial stages of data analysis, we usually tune them up by trial and error. Later, but this is already beyond the scope of this introductory course, we are used to exploring all the possible combinations thereof (exhaustive grid search) or making use of some local search-based heuristics (e.g., greedy optimisers such as hill climbing).

These always involve verifying the performance of *many* different classifiers, for example, 1-, 3-, 9, and 15-nearest neighbours-based ones. For each of them, we need to compute separate quality metrics, e.g., F -measures. Then, the classifier which yields the highest score is picked as the best. Unfortunately, if we do it recklessly, this can lead to *overfitting* to the test set – the obtained metrics might be too optimistic and can poorly reflect the real performance of the solution on future data.

Assuming that our dataset carries a decent number of observations, in order to overcome this problem, we can perform a random *train-validation-test split*:

- *training sample* (e.g., 60% of randomly chosen rows) – for model construction,
- *validation sample* (e.g., 20%) – used to tune the hyperparameters of many classifiers and to choose the best one,
- *test sample* (e.g., the remaining 20%) – used to assess the goodness of fit of the best classifier.

Important: Test sample must neither be used in the training nor in the validation phase (no cheating). After all, we would like to obtain a good estimate of a classifier's performance on previously unobserved data.

Of course, in the same way we can validate different regression models – this common-sense approach is not limited to classification.

Exercise 12.17 Determine the best parameter setting for the k -nearest neighbour classification of the *color* variable based on standardised versions of some physicochemical features (chosen columns) of wines in the *wine_quality_all*¹⁴² dataset. Create a 60/20/20% dataset split. For each $k = 1, 3, 5, 7, 9$, compute the corresponding F-measure on the validation test. Evaluate the quality of best classifier on the test set.

Note: (*) We can use various *cross-validation* techniques instead of a train-validate-test split, especially on smaller datasets. For instance, in a *5-fold cross-validation*, we split the

¹⁴² https://github.com/gagolews/teaching_data/blob/master/other/wine_quality_all.csv

original train set randomly into 5 disjoint parts: A, B, C, D, E (more or less of the same size). We use each combination of 4 chunks as training sets and the remaining part as the validation set, for which we generate the predictions and then compute, say, the F-measure:

| train set | validation set | F-measure |
|--------------------------|----------------|-----------|
| $B \cup C \cup D \cup E$ | A | F_A |
| $A \cup C \cup D \cup E$ | B | F_B |
| $A \cup B \cup D \cup E$ | C | F_C |
| $A \cup B \cup C \cup E$ | D | F_D |
| $A \cup B \cup C \cup D$ | E | F_E |

At the end we can compute the average F-measure, $(F_A + F_B + F_C + F_D + F_E)/5$, as a basis for assessing different classifiers' quality.

Exercise 12.18 (***) Redo the above exercise (assessing the wine colour classifiers), but this time maximising the F-measure obtained by a 5-fold cross-validation.

12.4 Clustering Tasks

So far we have been implicitly assuming that either each dataset comes from a single homogeneous distribution or we have a categorical variable that naturally defines the groups that we can split the dataset into. However, it might be the case that we are given a sample coming from a distribution mixture, where some subsets behave differently, but a grouping variable has not been provided at all (e.g., we have height and weight data but no information about the subjects' sexes).

Clustering (also known as segmentation, or quantisation) methods can be used to partition a dataset into groups based only on the spatial structure of the points' relative densities. In the k -means method, which we discuss below, the cluster structure is determined based on the proximity to k carefully chosen group centroids (compare Section 8.4.2).

12.4.1 The K-Means Method

Fix $k \geq 2$. In the k -means method¹⁴⁸, we seek k pivot points, $\mathbf{c}_1, \mathbf{c}_2, \dots, \mathbf{c}_k \in \mathbb{R}^m$ whose total squared distance thereto is minimised

$$\text{minimise } \sum_{i=1}^n \min \{\|\mathbf{x}_{i,\cdot} - \mathbf{c}_1\|^2, \|\mathbf{x}_{i,\cdot} - \mathbf{c}_2\|^2, \dots, \|\mathbf{x}_{i,\cdot} - \mathbf{c}_k\|^2\} \quad \text{w.r.t. } \mathbf{c}_1, \mathbf{c}_2, \dots, \mathbf{c}_k,$$

however, for each point in the dataset this time we take into account only the closest pivot.

Let us introduce the *label vector* ℓ such that

$$\ell_i = \arg \min_j \|\mathbf{x}_{i,\cdot} - \mathbf{c}_j\|^2,$$

i.e., it is the index of the pivot closest to $\mathbf{x}_{i,\cdot}$.

We will consider all the points $\mathbf{x}_{i,\cdot}$ with i such that $\ell_i = j$ as belonging to the same, j th, *cluster* (point group). This way, ℓ defines a *partition* of the original dataset into k nonempty, mutually disjoint subsets.

Now, the above optimisation task can be equivalently rewritten as:

$$\text{minimise } \sum_{i=1}^n \|\mathbf{x}_{i,\cdot} - \mathbf{c}_{\ell_i}\|^2 \quad \text{w.r.t. } \mathbf{c}_1, \mathbf{c}_2, \dots, \mathbf{c}_k$$

And this is why we refer to the above objective function as the (total) *within-cluster sum of squares* (WCSS). This problems looks easier, but let us not be tricked; ℓ_i s depend on \mathbf{c}_j s and thus they vary together. We have just made it less explicit.

It can be shown that given a fixed label vector ℓ representing a partitioning, \mathbf{c}_j must be the centroid ([Section 8.4.2](#)) of the points assigned thereto:

$$\mathbf{c}_j = \frac{1}{n_j} \sum_{i:\ell_i=j} \mathbf{x}_{i,\cdot},$$

where $n_j = |\{i : \ell_i = j\}|$ gives the number of i s such that $\ell_i = j$, i.e., how many points are assigned to \mathbf{c}_j .

Here is an example dataset (see below for a scatterplot):

¹⁴⁸ Of course we do not have to denote the number of clusters with k : we could be speaking about the 2-means, 3-means, c -means, or ϵ -means method too. Nevertheless, some mainstream practitioners consider k -means as a kind of a brand name, let us thus refrain from adding to their confusion.

```
X = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/blobs1.txt", delimiter=",")
```

We can call `scipy.cluster.vq.kmeans2` to find $k = 2$ clusters:

```
import scipy.cluster.vq
c, l = scipy.cluster.vq.kmeans2(X, 2)
```

The discovered cluster centres are stored in a matrix with k rows and m columns, i.e., the j -th row gives \mathbf{c}_j .

```
c
## array([[ 0.99622971,  1.052801  ],
##        [-0.90041365, -1.08411794]])
```

The label vector is

```
l
## array([1, 1, 1, ..., 0, 0, 0], dtype=int32)
```

As usual in Python, indexing starts at 0, therefore for $k = 2$ we only obtain the labels 0 and 1.

[Figure 12.10](#) depicts the two clusters (painted in different colours) together with the cluster centroids (black crosses). Note that in the code we use `l` as a colour selector in `my_colours[l]` (this is a clever instance of the integer vector-based indexing). It looks like we have correctly discovered the very natural partitioning of this dataset into two clusters.

```
plt.scatter(X[:, 0], X[:, 1], c=np.array(["black", "red"])[l])
plt.plot(c[:, 0], c[:, 1], "yX")
plt.axis("equal")
plt.show()
```

Here are the cluster sizes:

```
np.bincount(l) # or, e.g., pd.Series(l).value_counts()
## array([1017, 1039])
```

The label vector `l` can be added as a new column in the dataset; here is a preview:

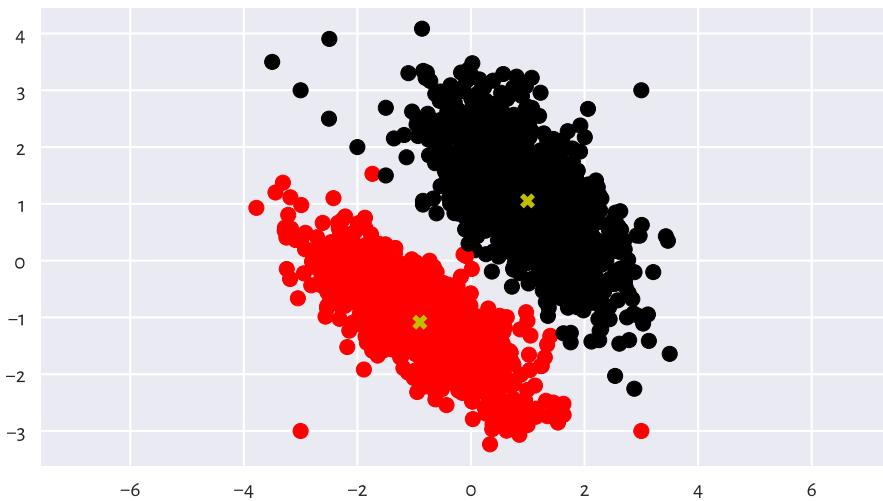


Figure 12.10: The two clusters discovered by the k -means method; cluster centroids are marked in black

```
Xl = pd.DataFrame(dict(X1=X[:, 0], X2=X[:, 1], l=l))
Xl.sample(5, random_state=42) # some randomly chosen rows
##           X1         X2   l
## 184 -0.973736 -0.417269  1
## 1724  1.432034  1.392533  0
## 251 -2.407422 -0.302862  1
## 1121  2.158669 -0.000564  0
## 1486  2.060772  2.672565  0
```

We can now enjoy all the techniques for processing data in groups that we have discussed so far. In particular, computing the columnwise means gives nothing else than the above cluster centroids:

```
Xl.groupby("l").mean()
##           X1         X2
## l
## 0  0.996230  1.052801
## 1 -0.900414 -1.084118
```

The label vector \mathbf{l} can of course be recreated by referring to the distances of all the points to the centroids and picking the index of the closest pivot:

```
np.argmin(scipy.spatial.distance.cdist(X, C), axis=1)
## array([1, 1, 1, ..., 0, 0, 0])
```

Important: By construction (and its relation to Voronoi diagrams), the k -means method can only detect clusters of convex shapes (such as Gaussian blobs).

Exercise 12.19 Perform the clustering of the `wut_isolation`¹⁴³ dataset and note how non-sensical, geometrically speaking, the returned clusters are.

Note: Determine a clustering of the `wut_twospashes`¹⁴⁴ dataset and display the results on a scatterplot. Compare the results to those obtained on the standardised version thereof. Recall what we have said about the Euclidean distance and its perception being disturbed when a plot's aspect ratio is not 1:1.

Note: (*) An even simpler classifier than the k -nearest neighbours one described above builds upon the concept of the nearest centroids. Namely, it first determines the centroids (componentwise arithmetic means) of the points in each class. Then, a new point (from the test set) is assigned to the class whose centroid is the closest thereto. The implementation of such a classifier is left as a rather straightforward exercise to the reader. As an application, we recommend using it to extrapolate the results generated by the k -means method to previously unobserved data.

12.4.2 Solving k -means is Hard

Unfortunately, the k -means method – the identification of label vectors/cluster centres that minimise the total within-cluster sum of squares – relies on solving a computationally hard combinatorial optimisation problem (e.g., [[Lee11]]). In other words, search for the *truly* (i.e., globally) optimal solution takes impractically long time for larger n and k .

Therefore, we must rely on some approximate algorithms which all have the same drawback: whatever they return can actually be a *suboptimal*, and hence possibly meaningless, solution.

¹⁴³ https://github.com/gagolews/teaching_data/blob/master/clustering/wut_isolation.csv

¹⁴⁴ https://github.com/gagolews/teaching_data/blob/master/clustering/wut_twospashes.csv

The documentation of `scipy.cluster.vq.kmeans2` is honest about it (after all, it is a package made by people with PhDs in STEM, not working for marketing divisions of some greedy corporations), stating that the method *attempts to minimise the Euclidean distance between observations and centroids*. Further, `sklearn.cluster.KMeans`, implementing a similar algorithm, mentions that the procedure *is very fast [...], but it falls in local minima. That's why it can be useful to restart it several times.*

To understand what it all means, it will thus be very educational to study this issue in more detail, as certainly the discussed approach to clustering is not the only hard problem in data science (selecting an optimal set of independent variables with respect to AIC or BIC in linear regression being another example).

12.4.3 Lloyd's Algorithm

Technically, there is no such thing as *the k-means* algorithm. There many procedures, based on many different heuristics, which attempt to solve the *k-means* problem. Unfortunately, neither of them is of course perfect (because it is not possible).

Perhaps the most widely know (and easy to understand) method is based on fixed-point iteration and is traditionally attributed to Lloyd [[Llo2]]. For a given $\mathbf{X} \in \mathbb{R}^{n \times m}$ and $k \geq 2$:

1. Pick initial cluster centres $\mathbf{c}_1, \dots, \mathbf{c}_k$, for example, randomly.
2. For each point in the dataset, $\mathbf{x}_{i,\cdot}$, determine its closest centre ℓ_i :

$$\ell_i = \arg \min_j \|\mathbf{x}_{i,\cdot} - \mathbf{c}_j\|^2,$$

3. Compute the centroids of the clusters defined by the label vector ℓ , i.e., for every $j = 1, 2, \dots, k$,

$$\mathbf{c}_j = \frac{1}{n_j} \sum_{i:\ell_i=j} \mathbf{x}_{i,\cdot},$$

where $n_j = |\{i : \ell_i = j\}|$ gives the size of the j -th cluster.

4. If the objective function (total within-cluster sum of squares) has not changed significantly (say, the absolute value of the difference is less than 10^{-9}) since the last iteration, stop and return the current $\mathbf{c}_1, \dots, \mathbf{c}_k$ as the result. Otherwise, go to Step 2.

Exercise 12.20 (*) Implement the Lloyd's algorithm in the form of a function `kmeans(X, C)`, where X is the data matrix (n-by-m) and where the rows in C , being an k-by-m matrix, give the initial cluster centres.

12.4.4 Local Minima

By the way the above algorithm is constructed, we have, what follows.

Important: Lloyd's method guarantees that the centres c_1, \dots, c_k it returns cannot be improved any further, at least not significantly. However, it does not necessarily mean that they yield the *globally* optimal (the best possible) WCSS. We might as well get stuck in a *local* minimum, where there is no better positioning thereof in the *neighbourhood* of the current cluster centres (compare Figure 12.11). Yet, had we looked beyond that, we could have found a superior solution.

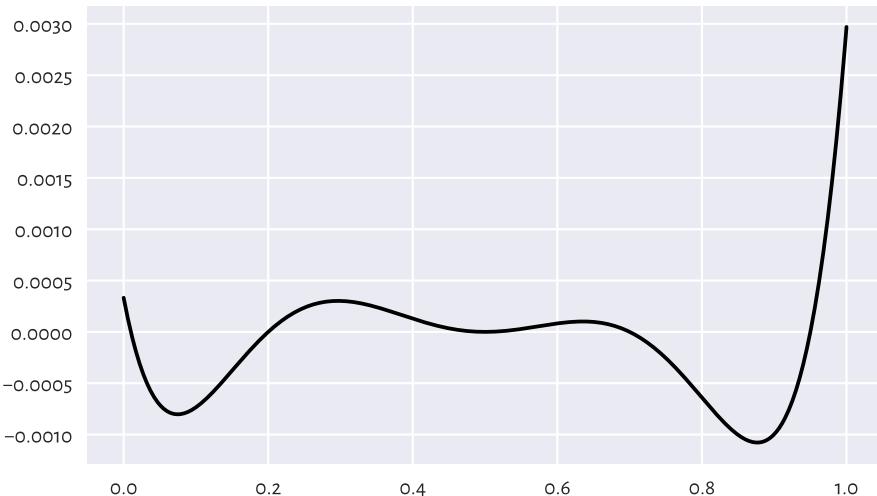


Figure 12.11: An example function (of only one variable; our problem is much higher-dimensional) with many local minima; how can we be sure there is no better minimum outside of the depicted interval?

A variant of the Lloyd's method is implemented in `scipy.cluster.vq.kmeans2`, where the initial cluster centres are picked at random. Let us test its behaviour by analysing three chosen country-wise categories from the 2016 Sustainable Society Indices¹⁴⁵ dataset.

```
ssi = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
(continues on next page)
```

¹⁴⁵ <https://ssi.wi.th-koeln.de/>

(continued from previous page)

```

"teaching_data/master/marek/ssi_2016_categories.csv",
comment="#")
X = ssi.set_index("Country").loc[:, [
    "PersonalDevelopmentAndHealth", "WellBalancedSociety", "Economy"]
]
n = X.shape[0]
X.loc[["Australia", "Germany", "Poland", "United States"], :] # preview
##          PersonalDevelopmentAndHealth  WellBalancedSociety   Economy
## Country
## Australia                  8.590927      6.105539  7.593052
## Germany                   8.629024      8.036620  5.575906
## Poland                    8.265950      7.331700  5.989513
## United States              8.357395      5.069076  3.756943

```

Thus, it is a three-dimensional dataset, where each point corresponds to a different country. Let us find a partition into $k = 3$ clusters.

```

k = 3
np.random.seed(123) # reproducibility matters
C1, l1 = scipy.cluster.vq.kmeans2(X, k)
C1
## array([[7.99945084, 6.50033648, 4.36537659],
##        [7.6370645 , 4.54396676, 6.89893746],
##        [6.24317074, 3.17968018, 3.60779268]])

```

The objective function (total within-cluster sum of squares) at the returned cluster centres is equal to:

```

import scipy.spatial.distance
def get_wcss(X, C):
    D = scipy.spatial.distance.cdist(X, C)**2
    return np.sum(np.min(D, axis=1))

get_wcss(X, C1)
## 446.5221283436733

```

Is it good or not necessarily? We are unable to tell. What we can do, however, is to run the algorithm again, this time from a different starting point:

```
np.random.seed(1234) # different seed - different initial centres
```

(continues on next page)

(continued from previous page)

```
C2, l2 = scipy.cluster.vq.kmeans2(X, k)
C2
## array([[7.80779013, 5.19409177, 6.97790733],
##        [6.31794579, 3.12048584, 3.84519706],
##        [7.92606993, 6.35691349, 3.91202972]])
get_wcss(X, C2)
## 437.51120966832775
```

It is a better solution (we are lucky; it might as well have been worse). But is it the best possible? Again, we cannot tell, alone in the dark.

Does a potential suboptimality affect the way the data points are grouped? It is indeed the case here. Let us take a look at the contingency table for the two label vectors:

```
pd.DataFrame(dict(l1=l1, l2=l2)).value_counts().unstack(fill_value=0)
## l2    0    1    2
## l1
## 0     8    0   43
## 1    39    6    0
## 2     0   57    1
```

Important: Clusters are actually unordered. The label vector (1, 1, 2, 2, 1, 3) represents the same clustering as the label vectors (3, 3, 2, 2, 3, 1) and (2, 2, 3, 3, 2, 1).

By looking at the contingency table, we see that clusters 0, 1, and 2 in l1 correspond, respectively, to clusters 2, 0, and 1 in l2 (by a form of majority voting). Therefore, we can relabel the elements in l1 to get a more readable result:

```
l1p = np.array([2, 0, 1])[l1]
pd.DataFrame(dict(l1p=l1p, l2=l2)).value_counts().unstack(fill_value=0)
## l2    0    1    2
## l1p
## 0     39    6    0
## 1      0   57    1
## 2      8    0   43
```

It turns out that 8+6+1 countries are categorised differently. We would definitely not want to initiate any diplomatic crisis because of our not knowing that the above algorithm might return suboptimal solutions.

Exercise 12.21 (*) Determine which countries are affected.

12.4.5 Random Restarts

There will never be any guarantees, but we can increase the probability of generating a good solution by simply restarting the method many times from many randomly chosen points and picking the best¹⁴⁹ solution (the one with the smallest WCSS) identified as the result.

Let us make 1000 such *restarts*:

```
wcss, Cs = [], []
for i in range(1000):
    C, l = scipy.cluster.vq.kmeans2(X, k, seed=i)
    Cs.append(C)
    wcss.append(get_wcss(X, C))
## /usr/local/lib/python3.9/dist-packages/scipy/cluster/vq.py:607:□
  ↵UserWarning: One of the clusters is empty. Re-run kmeans with a different□
  ↵initialization.
##     warnings.warn("One of the clusters is empty. "
```

The best of the local minima (no guarantee that it is the global one, again) is:

```
np.min(wcss)
## 437.51120966832775
```

It corresponds to the cluster centres:

```
Cs[np.argmin(wcss)]
## array([[7.80779013, 5.19409177, 6.97790733],
##        [7.92606993, 6.35691349, 3.91202972],
##        [6.31794579, 3.12048584, 3.84519706]])
```

Actually, it is the same as `C2`, `l2` above (up to a permutation of labels). We were lucky, after all.

It is very educational to take a look at the distribution of the objective function at the

¹⁴⁹ If we have many different heuristics, each aiming to approximate a solution to the k -means problem, from the practical point of view it does not really matter which one returns the best solution – they are merely our tools to achieve a higher goal. Ideally, we should run all of them a few times and just get the result that corresponds to the smallest WCSS. What matters is that we have *did our best* to find the optimal set of cluster centres – and of course more approaches tested improve the chance of success.

identified local minima to see that, proportionally, in the case of this dataset it is not rare to end up in a quite bad solution; see [Figure 12.12](#).

```
plt.hist(wcss, bins=100)  
plt.show()
```

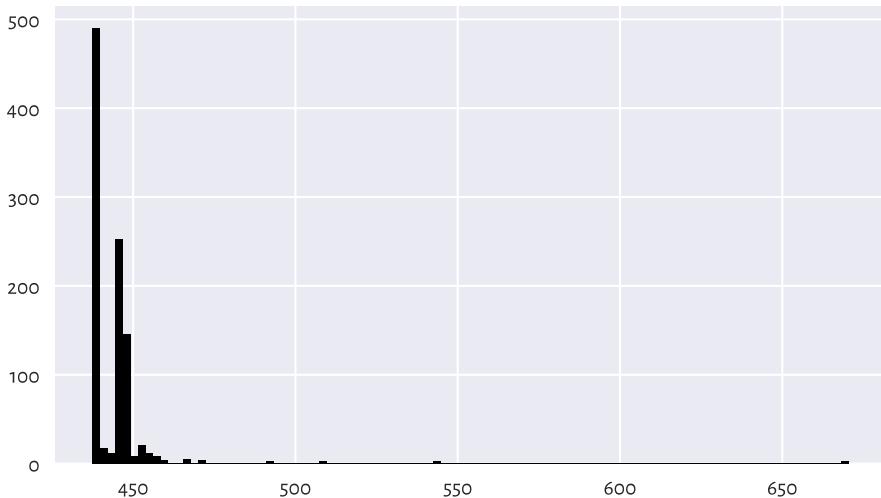


Figure 12.12: Within-cluster sum of squares at the results returned by different runs of the k -means algorithm; sometimes we might be very unlucky

Also, [Figure 12.13](#) depicts all the cluster centres that the algorithm converged to. We see that we should not be trusting the results generated by a single run of a heuristic solver to the k -means problem.

Example 12.22 (*) The `scikit-learn` package implements an algorithm that is similar to the Lloyd's one. The method is equipped with the `n_init` parameter (which defaults to 10) which automatically applies the aforementioned restarting. Still there are no guarantees:

```
import sklearn.cluster  
np.random.seed(123)  
km = sklearn.cluster.KMeans(k) # KMeans(k, n_init=10)  
km.fit(X)  
## KMeans(n_clusters=3)  
km.inertia_ # WCSS  
## 437.5467188958929
```

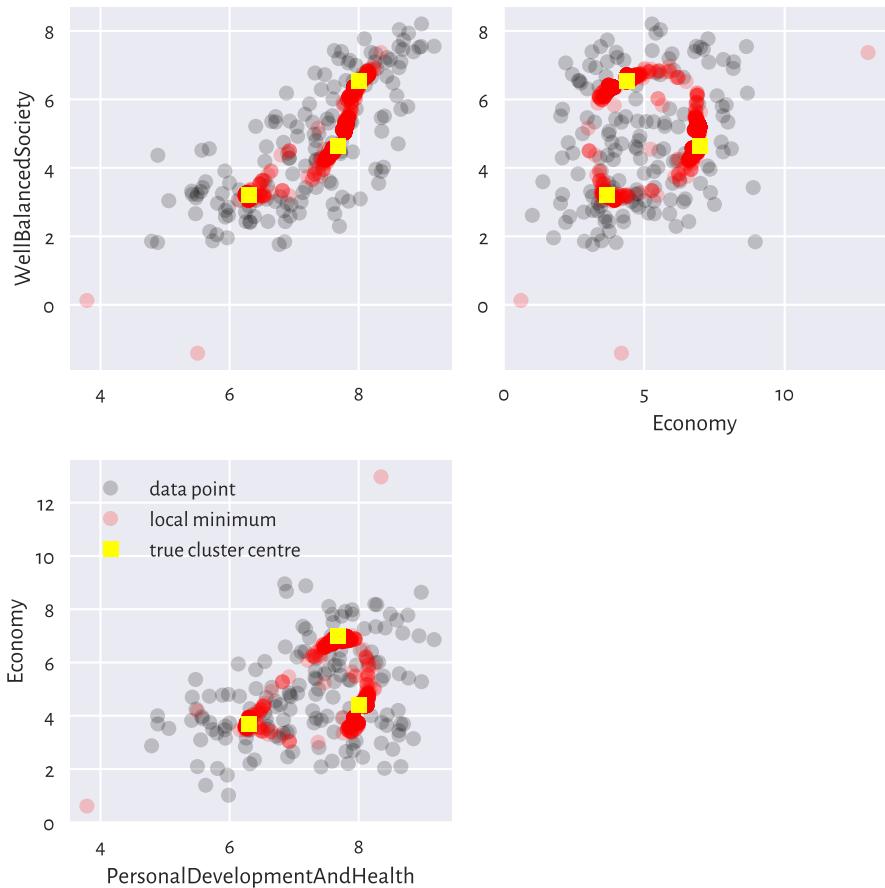


Figure 12.13: Different cluster centres our k-means algorithm converged to; some are definitely not optimal, and therefore the method must be restarted a few times in order to increase the likelihood of pinpointing the true solution

In this case, the solution is suboptimal too. As an exercise, we suggest the reader to pass `n_init=100`, `n_init=1000`, and `n_init=10000` and determine the best WCSS.

Note: It is theoretically possible that a developer from the `scikit-learn` team, when they see the above result, will make a tweak in the algorithm so that after an update to the package, the returned minimum will be better. This cannot be deemed a bug fix, though, as there are no bugs here. Improving the behaviour of the method on this example will lead to its degradation on others. There is no free lunch in optimisation.

Note: Some datasets are more well-behaving than others. The k -means method is overall quite usable, but we should always be cautious.

Exercise 12.23 Run the k -means method, $k = 8$, on the `sipu_unbalance`¹⁴⁶ dataset numerous times and note the value of the total within-cluster sum of squares. Also, plot the cluster centres discovered. Do they make sense? Compare these to the case where you start the method from the following cluster centres which are close to the global minimum.

$$\mathbf{C} = \begin{bmatrix} -15 & 5 \\ -12 & 10 \\ -10 & 5 \\ 15 & 0 \\ 15 & 10 \\ 20 & 5 \\ 25 & 0 \\ 25 & 10 \end{bmatrix}$$

12.5 Further Reading

An overall good introduction to classification is [[HTF17]] and [[Biso06]]. However, as we have said earlier, we recommend going through a solid course in matrix algebra and probability and statistics first, e.g., [[DFO20], [Gen17]] and [[DKLM05], [Gen09], [Gen20]].

For advanced theoretical (probabilistic, information-theoretic) results, see, e.g., [[BHK20], [DGL96]].

¹⁴⁶ https://github.com/gagolews/teaching_data/blob/master/clustering/sipu_unbalance.csv

12.6 Exercises

Exercise 12.24 Name the data type of an object that the `DataFrame.groupby` method returns.

Exercise 12.25 What is the relationship between `GroupBy`, `DataFrameGroupBy`, and `SeriesGroupBy`?

Exercise 12.26 What are relative z-scores and how can we compute them?

Exercise 12.27 Why and when the accuracy score might not be the best way to quantify a classifier's performance?

Exercise 12.28 What is the difference between recall and precision, both in terms of how they are defined and where they are the most useful?

Exercise 12.29 Explain how a k-nearest neighbour classification algorithm works. Why do we say that is is model-free?

Exercise 12.30 In the context of k-nearest neighbour classification, why it might be important to resolve the potential ties at random when computing the mode of the neighbours' labels?

Exercise 12.31 What is the purpose of a train-test and train-validation-test set splits?

Exercise 12.32 What is the difference between the fixed-radius and few-nearest-neighbours search?

Exercise 12.33 Give the formula for the total within-cluster sum of squares.

Exercise 12.34 Are there any cluster shapes that cannot be detected by the k-means method?

Exercise 12.35 Why do we say that solving the k-means problem is hard?

Exercise 12.36 Why restarting Lloyd's algorithm a few times is usually necessary?

Accessing Databases

pandas is convenient for working with data that fit into memory and which can be stored in individual CSV files. However, larger information banks, possibly in a shared environment, will often be made available to us via relational (structured) databases such us PostgreSQL or MariaDB, or a wide range of commercial products.

Most commonly, we will be using SQL (structured query language) to express the data chunks we need for analysis, fetching them from the database driver, and importing them to a **pandas** data frame to perform the already well-known operations.

Below we give a quick introduction to the basics of SQL using **SQLite**¹⁵⁰, which is a light-weight, flat-file, and server-less database management system. Overall, SQLite is sensible for data of even hundreds or thousands of gigabytes in size that fit on a single computer's disk (making it a good choice for playing with our own data science projects or prototyping more complex solutions).

Important: The syntax of SQL is very readable – it is modelled after the natural (English) language. In this introduction, we merely assume that we wish to learn how to read the basic SQL queries, not to write our own. The latter should be covered by a separate course on databases.

13.1 Example Database

In the course of this section, we will be working with a simplified data dump of the Q&A site **Travel Stack Exchange**¹⁵¹, which we have downloaded¹⁵² on 2017-10-31.

¹⁵⁰ <https://sqlite.org>

¹⁵¹ <http://travel.stackexchange.com>

¹⁵² <https://archive.org/details/stackexchange>

Exercise 13.1 Before continuing, make yourself familiar with the Travel Stack Exchange¹⁵³ site.

For example, Tags gives, amongst others, topic categories (TagName) and how many questions mention them (Count):

```
Tags = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/travel_stackexchange_com_2017/Tags.csv.gz",
    comment="#")
Tags.head(3)
##   Count  ExcerptPostId  Id      TagName  WikiPostId
## 0    104          2138.0  1  cruising       2137.0
## 1     43          357.0   2 caribbean      356.0
## 2     43          319.0   4 vacations      318.0
```

Users provides information on the registered users. In particular, the Id column uniquely identifies each member.

```
Users = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/travel_stackexchange_com_2017/Users.csv.gz",
    comment="#")
Users.head(3)
##   AccountId  Age           CreationDate ... Reputation  UpVotes □
##  ↵Views
## 0      -1.0  NaN  2011-06-21T15:16:44.253 ...        1.0  2472.0   0.
##  ↵0
## 1      2.0  40.0  2011-06-21T20:10:03.720 ...      101.0     1.0   31.
##  ↵0
## 2    7598.0  32.0  2011-06-21T20:11:02.490 ...      101.0     1.0   14.
##  ↵0
## 
## [3 rows x 11 columns]
```

Badges recall all rewards given to the users (UserId) for their engaging in various praiseworthy activities:

```
Badges = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/travel_stackexchange_com_2017/Badges.csv.gz",
    comment="#")
Badges.head(3)
##   Class           Date  Id      Name  TagBased  UserId
## 
## (continues on next page)
```

¹⁵³ <http://travel.stackexchange.com>

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```
## 0      3 2011-06-21T20:16:48.910    1 Autobiographer    False     2
## 1      3 2011-06-21T20:16:48.910    2 Autobiographer    False     3
## 2      3 2011-06-21T20:16:48.910    3 Autobiographer    False     4
```

`Posts` (note again that `Id` is the unique identifier of each record in every data frame) lists all the questions and answers (the latter don't have `ParentId` set to `NaN`).

```
Posts = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
  "teaching_data/master/travel_stackexchange_com_2017/Posts.csv.gz",
  comment="#")
Posts.head(3)
##   AcceptedAnswerId ... ViewCount
## 0            393.0 ...      419.0
## 1             NaN ...     1399.0
## 2             NaN ...       NaN
##
## [3 rows x 17 columns]
```

`Votes` list all the up-votes (`VoteTypeId` equal to 2) and down-votes (`VoteTypeId` of 3) to all the posts. For privacy reasons, all `UserIds` are missing (which is encoded with a not-a-number, compare [Chapter 15](#)).

```
Votes = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
  "teaching_data/master/travel_stackexchange_com_2017/Votes.csv.gz",
  comment="#")
Votes.head(3)
##   BountyAmount        CreationDate  Id  PostId UserId VoteTypeId
## 0      NaN 2011-06-21T00:00:00.000  1      1     NaN         2
## 1      NaN 2011-06-21T00:00:00.000  2      1     NaN         2
## 2      NaN 2011-06-21T00:00:00.000  3      2     NaN         2
```

Exercise 13.2 See the `README154` file for the detailed description of each column.

¹⁵⁴ https://github.com/gagolews/teaching_data/blob/master/travel_stackexchange_com/README.md

13.2 Exporting Data

Let us establish a connection with the to-be SQLite database. In our case, that will be an ordinary file stored on the computer's disk:

```
import tempfile, os.path
dbfile = os.path.join(tempfile.mkdtemp(), "travel.db")
print(dbfile)
## /tmp/tmpzzlzoj8x/travel.db
```

The above gives the file path (compare Section 13.6.1) where the database is going to be stored. We use a randomly generated filename inside the local filesystem's (we are on Linux) temporary directory, `/tmp`, because this is just a simple exercise and we will not be using this database afterwards.

And now:

```
import sqlite3
conn = sqlite3.connect(dbfile)
```

We are thus “connected”. The database might now be queried: new tables can be added, new records inserted, and information fetched.

Important: At the end, we should not forget about the call to `conn.close()`.

We already have our data in form of `pandas` data frames, therefore exporting them to the database is straightforward. All we have to do is to perform a bunch of calls to the `pandas.DataFrame.to_sql` method.

```
Tags.to_sql("Tags", conn, index=False)
Users.to_sql("Users", conn, index=False)
Badges.to_sql("Badges", conn, index=False)
Posts.to_sql("Posts", conn, index=False)
Votes.to_sql("Votes", conn, index=False)
```

Note: (*) It is possible to export data that do not fit into memory by reading them in chunks of considerable, but not too large, sizes. In particular `pandas.read_csv` has the `nrows` argument that lets us read a number of rows from a file buffer; see `help("open")`.

Then, `pandas.DataFrame.to_sql(..., if_exists="append")` can be used to append new rows to an existing table.

Exporting data can of course be done without `pandas` as well, e.g., when they are to be fetched from XML or JSON files (compare [Section 13.5](#)) and processed manually, row by row. Intermediate-level SQL users can call `conn.execute("CREATE TABLE t...")`, `conn.executemany("INSERT INTO t VALUES(?, ?, ?)", l)` followed by `conn.commit()` to create a new table (here: named `t`) populated by a list of records (e.g., in form of tuples or `numpy` vectors). For more details, see the [manual¹⁵⁵](#) of the `sqlite3` package.

13.3 Exercises on SQL vs pandas

We can use `pandas` to fetch the results generated by executing any SQL query, for example:

```
pd.read_sql_query("""
    SELECT * FROM Tags LIMIT 3
""", conn)
##   Count  ExcerptPostId  Id      TagName  WikiPostId
## 0    104          2138.0  1  cruising        2137.0
## 1     43          357.0  2 caribbean       356.0
## 2     43          319.0  4  vacations       318.0
```

Fetches all columns (`SELECT *`) and the first 3 rows (`LIMIT 3`) from the `Tags` table.

Exercise 13.3 For the above and all the following SQL queries, write the equivalent Python code using `pandas` functions and methods that generates exactly the same result. In each case, there might be more than one equally fine solution.

Note again that the SQL syntax is very readable, hence no explanations should be necessary for the queries below. In case of any doubt, though, refer to the [manual¹⁵⁶](#).

Example solutions are provided at the end of this section.

Example 13.4 For instance, here is the reference result:

```
res1a = pd.read_sql_query("""

```

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¹⁵⁵ <https://docs.python.org/3/library/sqlite3.html>

¹⁵⁶ <https://sqlite.org/lang.html>

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```
SELECT * FROM Tags LIMIT 3
""", conn)
```

Our example equivalent **pandas** implementation of the above operation might look like:

```
res1b = Tags.head(3)
```

To verify if the results are identical, we can call:

```
pd.testing.assert_frame_equal(res1a, res1b)
```

Sometimes, however the results generated by **pandas** will be the same up to the reordering of rows. In such a case, before calling **pandas.testing.assert_frame_equal**, it might thus be a good idea to call **DataFrame.sort_values** on both data frames to sort them with respect to 1 or 2 chosen columns. The good thing about the **assert_frame_equal** function is that it ignores small round-off errors introduced by some operations.

13.3.1 Filtering

Exercise 13.5 Fetch all tag data for tags whose name contain "europe" as substring:

```
res2a = pd.read_sql_query("""
    SELECT * FROM Tags WHERE TagName LIKE '%europe%'
""", conn)
res2a
```

| ## | Count | ExcerptPostId | Id | TagName | WikiPostId |
|------|-------|---------------|------|------------------|------------|
| ## 0 | 681 | 286.0 | 30 | europe | 285.0 |
| ## 1 | 27 | 2384.0 | 174 | eastern-europe | 2383.0 |
| ## 2 | 12 | 6403.0 | 512 | southeast-europe | 6402.0 |
| ## 3 | 20 | 4513.0 | 669 | central-europe | 4512.0 |
| ## 4 | 36 | 16392.0 | 1950 | western-europe | 16391.0 |

Hint: use `Tags.TagName.str.contains("europe")` to obtain the same result with **pandas**.

Exercise 13.6 From `Tags`, select two columns `TagName` and `Count` and rows for which `TagName` is equal to one of the three choices provided.

```
res3a = pd.read_sql_query("""
    SELECT TagName, Count
    FROM Tags
    WHERE TagName IN ('poland', 'australia', 'china')
""", conn)
```

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```
"""", conn)
res3a
##      TagName  Count
## 0      china    443
## 1  australia   411
## 2     poland   139
```

Hint: use `pandas.Series.isin`.

Exercise 13.7 Select a number of columns from `Posts` whose rows fulfil given conditions:

```
res4a = pd.read_sql_query("""
SELECT Title, Score, ViewCount, FavoriteCount
FROM Posts
WHERE PostTypeId=1 AND
      ViewCount>=10000 AND
      FavoriteCount BETWEEN 35 AND 100
""", conn)
res4a
##                                     Title  Score  ViewCount
## 0  When traveling to a country with a different c...    136  16838.0
## 1  How can I do a "broad" search for flights?      95  33554.0
## 2  Tactics to avoid getting harassed by corrupt p...    156  13220.0
## 3  Flight tickets: buy two weeks before even duri...    109  49440.0
## 4  OK we're all adults here, so really, how on ea...    306  73808.0
## 5  How to intentionally get denied entry to the U...    219  63873.0
## 6  How do you know if Americans genuinely/literal...    254  30312.0
## 7  OK, we are all adults here, so what is a bidet...    140  52265.0
## 8  How to cope with too slow Wi-Fi at hotel?       82  16380.0
```

13.3.2 Ordering

Exercise 13.8 Select the `Title` and `Score` columns from `Posts` where `ParentId` is missing (i.e., the post is actually a question) and `Title` is well-defined; then, sort the result by the `Score` column, decreasingly (descending order); finally, return only first 5 rows (e.g., top 5 scoring questions):

```
res5a = pd.read_sql_query("""
    SELECT Title, Score
    FROM Posts
    WHERE ParentId IS NULL AND Title IS NOT NULL
    ORDER BY Score DESC
    LIMIT 5
""", conn)
res5a
##                                     Title  Score
## 0  OK we're all adults here, so really, how on ea...  306
## 1  How do you know if Americans genuinely/literal...  254
## 2  How to intentionally get denied entry to the U...  219
## 3  Why are airline passengers asked to lift up wi...  210
## 4  Why prohibit engine braking?                   178
```

Hint: use `pandas.DataFrame.sort_values` and `numpy.isnan` or `pandas.isnull`.

13.3.3 Removing Duplicates

Exercise 13.9 Get all unique badge names for the user with `Id=23`.

```
res6a = pd.read_sql_query("""
    SELECT DISTINCT Name
    FROM Badges
    WHERE UserId=23
""", conn)
res6a
##             Name
## 0      Supporter
## 1        Student
## 2       Teacher
## 3     Scholar
## 4       Beta
## 5  Nice Question
## 6      Editor
```

(continues on next page)

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```
## 7      Nice Answer
## 8      Yearling
## 9 Popular Question
## 10     Taxonomist
## 11 Notable Question
```

Hint: use `pandas.DataFrame.drop_duplicates`.

Exercise 13.10 For each badge given to the user with `Id=23`, get the year it was given and store it in a new column named `Year`. Then, select all unique pairs (`Name`, `Year`).

```
res7a = pd.read_sql_query("""  
SELECT DISTINCT  
    Name,  
    CAST(strftime('%Y', Date) AS FLOAT) AS Year  
FROM Badges  
WHERE UserId=23  
""", conn)  
  
res7a  
##          Name    Year  
## 0      Supporter 2011.0  
## 1      Student 2011.0  
## 2      Teacher 2011.0  
## 3      Scholar 2011.0  
## 4      Beta 2011.0  
## 5  Nice Question 2011.0  
## 6      Editor 2012.0  
## 7  Nice Answer 2012.0  
## 8      Yearling 2012.0  
## 9  Nice Question 2012.0  
## 10  Nice Question 2013.0  
## 11      Yearling 2013.0  
## 12 Popular Question 2014.0  
## 13      Yearling 2014.0  
## 14  Taxonomist 2014.0  
## 15 Notable Question 2015.0  
## 16  Nice Question 2017.0
```

Hint: use `Badges.Date.astype("datetime64").dt.strftime("%Y").astype("float")`.

13.3.4 Grouping and Aggregating

Exercise 13.11 Count how many badges of each type the user with $Id=23$ has received. Also, for each badge type, return the minimal, average, and maximal receiving year. Return only the top 4 badges (with respect to the counts).

```
res8a = pd.read_sql_query("""
    SELECT
        Name,
        COUNT(*) AS Count,
        MIN(CAST(strftime('%Y', Date) AS FLOAT)) AS MinYear,
        AVG(CAST(strftime('%Y', Date) AS FLOAT)) AS MeanYear,
        MAX(CAST(strftime('%Y', Date) AS FLOAT)) AS MaxYear
    FROM Badges
    WHERE UserId=23
    GROUP BY Name
    ORDER BY Count DESC, MeanYear ASC
    LIMIT 4
""", conn)
res8a
##          Name  Count  MinYear  MeanYear  MaxYear
## 0      Nice Question     4  2011.0   2013.25  2017.0
## 1      Yearling       3  2012.0   2013.00  2014.0
## 2 Popular Question     3  2014.0   2014.00  2014.0
## 3 Notable Question     2  2015.0   2015.00  2015.0
```

Exercise 13.12 Similarly to the above, but now count how many unique combinations of pairs ($Name$, $Date$) are there; then, return only the rows having $Count$ greater than 1 and order the results by $Count$ decreasingly.

```
res9a = pd.read_sql_query("""
    SELECT
        Name,
        CAST(strftime('%Y', Date) AS FLOAT) AS Year,
        COUNT(*) AS Count
    FROM Badges
    WHERE UserId=23
    GROUP BY Name, Year
    HAVING Count > 1
    ORDER BY Count DESC
""", conn)
```

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(continued from previous page)

```
res9a
##           Name   Year Count
## 0 Popular Question 2014.0     3
## 1 Notable Question 2015.0     2
```

Note that *WHERE* is performed before *GROUP BY*, and *HAVING* is applied thereafter.

13.3.5 Joining

Exercise 13.13 Join (merge) *Tags*, *Posts*, and *Users* for all posts with *OwnerUserId* not equal to -1 (i.e., the tags which were created by “alive” users). Return the top 6 records with respect to *Tags.Count*.

```
res10a = pd.read_sql_query("""
    SELECT Tags.TagName, Tags.Count, Posts.OwnerUserId,
           Users.Age, Users.Location, Users.DisplayName
      FROM Tags
     JOIN Posts ON Posts.Id=Tags.WikiPostId
     JOIN Users ON Users.AccountId=Posts.OwnerUserId
     WHERE OwnerUserId != -1
    ORDER BY Tags.Count DESC, Tags.TagName ASC
    LIMIT 6
""", conn)
res10a
##           TagName  Count OwnerUserId   Age          Location
## 0         canada    802      101.0  34.0  Mumbai, India
## 1        hitec      681      583.0  35.0 Philadelphia, PA
## 2   europe-refusals    554     1737.0  34.0  New York, NY
## 3        tuttle      411      101.0  34.0  Mumbai, India
## 4       pollack      204      583.0  35.0 Philadelphia, PA
## 5  new-york-city      204      101.0  34.0  Mumbai, India
```

Exercise 13.14 First, create an auxiliary (temporary) table named *UpVotesTab*, where we store

the information about the number of up-votes (`VoteTypeId=2`) that each post has received. Then, join (merge) this table with `Posts` and fetch some details about the 5 questions (`PostTypeId=1`) with the most up-votes:

```
res11a = pd.read_sql_query("""
    SELECT UpVotesTab.*, Posts.Title FROM
    (
        SELECT PostId, COUNT(*) AS UpVotes
        FROM Votes
        WHERE VoteTypeId=2
        GROUP BY PostId
    ) AS UpVotesTab
    JOIN Posts ON UpVotesTab.PostId=Posts.Id
    WHERE Posts.PostTypeId=1
    ORDER BY UpVotesTab.UpVotes DESC LIMIT 5
""", conn)
res11a
##   PostId  UpVotes                                Title
## 0    3080      307  OK we're all adults here, so really, how on ea...
## 1    38177     254  How do you know if Americans genuinely/literal...
## 2    24540     221  How to intentionally get denied entry to the U...
## 3    20207     211  Why are airline passengers asked to lift up wi...
## 4    96447      178                                Why prohibit engine braking?
```

13.3.6 Solutions to Exercises

Below are example solutions to the above exercises.

Example 13.15

```
Tags.
loc[Tags.TagName.str.contains("europe"), :].
reset_index(drop=True)
)
res2b
##   Count  ExcerptPostId     Id      TagName  WikiPostId
## 0    681          286.0    30       europe      285.0
## 1     27          2384.0   174  eastern-europe      2383.0
## 2     12          6403.0   512 southeast-europe      6402.0
## 3     20          4513.0   669 central-europe      4512.0
## 4     36         16392.0  1950 western-europe      16391.0
pd.testing.assert_frame_equal(res2a, res2b)
```

Example 13.16

```

Tags.
loc[
    Tags.TagName.isin(["poland", "australia", "china"]),
    ["TagName", "Count"]
].
reset_index(drop=True)
)
res3b
##      TagName  Count
## 0      china    443
## 1  australia    411
## 2     poland    139
pd.testing.assert_frame_equal(res3a, res3b)

```

Example 13.17

```

Posts.
loc[
    (Posts.PostTypeId == 1) & (Posts.ViewCount >= 10000) &
    (Posts.FavoriteCount >= 35) & (Posts.FavoriteCount <= 100),
    ["Title", "Score", "ViewCount", "FavoriteCount"]
].
reset_index(drop=True)
)
res4b
##                                     Title  Score  ViewCount
~-FavoriteCount
## 0  When traveling to a country with a different c...      136   16838.0
~-      35.0
## 1  How can I do a "broad" search for flights?      95   33554.0
~-      49.0
## 2  Tactics to avoid getting harassed by corrupt p...     156   13220.0
~-      42.0
## 3  Flight tickets: buy two weeks before even duri...     109   49440.0
~-      36.0
## 4  OK we're all adults here, so really, how on ea...     306   73808.0
~-      79.0
## 5  How to intentionally get denied entry to the U...     219   63873.0
~-      53.0
## 6  How do you know if Americans genuinely/literal...     254   30312.0
~-      79.0
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```

```
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## 7 OK, we are all adults here, so what is a bidet...      140      52265.0  □
↳      38.0
## 8           How to cope with too slow Wi-Fi at hotel?     82      16380.0  □
↳      41.0
pd.testing.assert_frame_equal(res4a, res4b)
```

Example 13.18

```
Posts.
loc[
    Posts.ParentId.isna() & (~Posts.Title.isna()),
    ["Title", "Score"]
].
sort_values("Score", ascending=False).
head(5).
reset_index(drop=True)
)
res5b
##                                     Title  Score
## 0  OK we're all adults here, so really, how on ea...    306
## 1  How do you know if Americans genuinely/literal...    254
## 2  How to intentionally get denied entry to the U...    219
## 3  Why are airline passengers asked to lift up wi...    210
## 4                           Why prohibit engine braking?    178
pd.testing.assert_frame_equal(res5a, res5b)
```

Example 13.19

```
Badges.
loc[Badges.UserId == 23, ["Name"]].
drop_duplicates().
reset_index(drop=True)
)
res6b
##          Name
## 0      Supporter
## 1      Student
## 2      Teacher
## 3      Scholar
## 4        Beta
## 5  Nice Question
```

(continues on next page)

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```
## 6           Editor
## 7       Nice Answer
## 8       Yearling
## 9 Popular Question
## 10      Taxonomist
## 11 Notable Question
pd.testing.assert_frame_equal(res6a, res6b)
```

Example 135 `Badges.copy()`

```
Badges2.loc[:, "Year"] = (
    Badges2.Date.astype("datetime64").dt.strftime("%Y").astype("float")
)
res7b = (
    Badges2.
        loc[Badges2.UserId == 23, ["Name", "Year"]].
        drop_duplicates().
        reset_index(drop=True)
)
res7b
##          Name    Year
## 0   Supporter  2011.0
## 1     Student  2011.0
## 2    Teacher  2011.0
## 3   Scholar  2011.0
## 4      Beta  2011.0
## 5  Nice Question  2011.0
## 6      Editor  2012.0
## 7  Nice Answer  2012.0
## 8     Yearling  2012.0
## 9  Nice Question  2012.0
## 10  Nice Question  2013.0
## 11     Yearling  2013.0
## 12 Popular Question  2014.0
## 13     Yearling  2014.0
## 14  Taxonomist  2014.0
## 15 Notable Question  2015.0
## 16  Nice Question  2017.0
pd.testing.assert_frame_equal(res7a, res7b)
```

```
Example-13B Badges.copy()
Badges2.loc[:, "Year"] = (
    Badges2.Date.astype("datetime64").dt.strftime("%Y").astype("float")
)
res8b = (
    Badges2.
    loc[Badges2.UserId == 23, ["Name", "Year"]].
    groupby(["Name"])["Year"].
    aggregate([len, np.min, np.mean, np.max]).
    sort_values(["len", "mean"], ascending=[False, True]).
    head(4).
    reset_index()
)
res8b.columns = ["Name", "Count", "MinYear", "MeanYear", "MaxYear"]
res8b
##          Name  Count  MinYear  MeanYear  MaxYear
## 0      Nice Question      4  2011.0   2013.25  2017.0
## 1      Yearling        3  2012.0   2013.00  2014.0
## 2  Popular Question      3  2014.0   2014.00  2014.0
## 3  Notable Question      2  2015.0   2015.00  2015.0
```

Note that had we not converted `Year` to `float`, we would obtain meaningless average year, without any warning.

```
pd.testing.assert_frame_equal(res8a, res8b)
```

```
Example-13B Badges.copy()
Badges2.loc[:, "Year"] = (
    Badges2.Date.astype("datetime64").dt.strftime("%Y").astype("float")
)
res9b = (
    Badges2.
    loc[ Badges2.UserId == 23, ["Name", "Year"] ].
    groupby(["Name", "Year"]).
    size().
    rename("Count").
    reset_index()
)
res9b = (
    res9b.
```

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```

loc[ res9b.Count > 1, : ].
sort_values("Count", ascending=False).
reset_index(drop=True)
)
res9b
##           Name   Year  Count
## 0  Popular Question  2014.0      3
## 1  Notable Question  2015.0      2

```

Note that the HAVING part is performed after WHERE and GROUP BY.

```
pd.testing.assert_frame_equal(res9a, res9b)
```

Example 13.23 `merge(Posts, Tags, left_on="Id", right_on="WikiPostId")`

```

res10b = pd.merge(Posts, Tags, left_on="Id", right_on="WikiPostId")
res10b = (
    res10b.
    loc[
        (res10b.OwnerUserId != -1) & (~res10b.OwnerUserId.isna()),
        ["TagName", "Count", "OwnerUserId", "Age", "Location", "DisplayName"]
    ].
    sort_values(["Count", "TagName"], ascending=[False, True]).
    head(6).
    reset_index(drop=True)
)
res10b
##           TagName  Count  OwnerUserId     Age          Location  DisplayName
## 0            canada    802       101.0   34.0  Mumbai, India
## 1             hitec    681      583.0   35.0  Philadelphia, PA
## 2  visa-refusals    554     1737.0   34.0  New York, NY
## 3            Pollack    411       101.0   34.0  Mumbai, India
## 4            europa    204      583.0   35.0  Philadelphia, PA
## 5  new-york-city    204       101.0   34.0  Mumbai, India

```

Note that in SQL, “not equals to -1” implies that “IS NOT NULL”.

```
pd.testing.assert_frame_equal(res10a, res10b)
```

Example 13.24 To obtain *res11b*, we first create an auxiliary data frame that corresponds to the subquery.

```
UpVotesTab = (
    Votes.
    loc[Votes.VoteTypeId==2, :].
    groupby("PostId").
    size().
    rename("UpVotes").
    reset_index()
)
```

And now:

```
res11b = pd.merge(UpVotesTab, Posts, left_on="PostId", right_on="Id")
res11b = (
    res11b.
    loc[res11b.PostTypeId==1, ["PostId", "UpVotes", "Title"]].
    sort_values("UpVotes", ascending=False).
    head(5).
    reset_index(drop=True)
)
res11b
##   PostId  UpVotes          Title
## 0    3080     307  OK we're all adults here, so really, how on ea...
## 1    38177     254  How do you know if Americans genuinely/literal...
## 2    24540     221  How to intentionally get denied entry to the U...
## 3    20207     211  Why are airline passengers asked to lift up wi...
## 4    96447     178                      Why prohibit engine braking?
pd.testing.assert_frame_equal(res11a, res11b)
```

13.4 Closing the Database Connection

We have said we should not forget about:

```
conn.close()
```

This gives some sense of closure. Such a relief.

13.5 Common Data Serialisation Formats for the Web

CSV files are an all-round way to exchange *tabular* data between different programming and data analysis environments.

For unstructured or non-tabularly-structured data, XML as well as JSON (and its superset, YAML) are the common formats of choice, especially for communicating with different Web APIs.

Important: It is recommended that we solve some of the following exercises to make sure we can fetch data in these formats. Warning: often, this will quite tedious labour, neither art nor science; see also [[vdLdJ18]] and [[DJ03]]. Good luck.

Exercise 13.25 Consider the Web API for [accessing¹⁵⁷](#) the on-street parking bay sensor data in Melbourne, VIC, Australia. Using, for example, the `json` package, convert the [data¹⁵⁸](#) in the JSON format to a `pandas` data frame.

Exercise 13.26 Australian Radiation Protection and Nuclear Safety Agency publishes¹⁵⁹ UV data for different Aussie cities. Using, for example, the `xml` package, convert [this XML dataset¹⁶⁰](#) to a `pandas` data frame.

Exercise 13.27 (*) Check out the English Wikipedia article featuring a [list of 20th-century classical composers¹⁶¹](#). Using `pandas.read_html`, convert the Climate Data table included therein to a data frame.

Exercise 13.28 (*) Using, for example, the `lxml` package, write a function that converts each bullet list featured in a given Wikipedia article (e.g., [this one¹⁶²](#)), to a list of strings.

¹⁵⁷ <https://data.melbourne.vic.gov.au/Transport/On-street-Parking-Bay-Sensors/vh2v-4nfs>

¹⁵⁸ <https://data.melbourne.vic.gov.au/resource/vh2v-4nfs.json>

¹⁵⁹ <https://www.arpansa.gov.au/our-services/monitoring/ultraviolet-radiation-monitoring/ultraviolet-radiation-data-information>

¹⁶⁰ <https://uvdata.arpansa.gov.au/xml/uvvalues.xml>

¹⁶¹ https://en.wikipedia.org/wiki/List_of_20th-century_classical_composers

¹⁶² https://en.wikipedia.org/wiki/Category:Fr%C3%A9d%C3%A9ric_Chopin

Exercise 13.29 (***) Import an archived version of a Stack Exchange¹⁶³ site that you find interesting and store it in an SQLite database. You can find the relevant data dumps here¹⁶⁴.

Exercise 13.30 (**) Download¹⁶⁵ and then import an archived version of one of the wikis hosted by the Wikimedia Foundation¹⁶⁶ (e.g., the whole English Wikipedia) so that it can be stored in an SQLite database.

13.6 Working with Many Files

For the mass-processing of many files, it is worth knowing of the most basic functions for dealing with file paths, searching for files, etc. Usually we will be looking up ways to complete specific tasks at hand, e.g., how to read data from a ZIP archive, on the internet.

13.6.1 File Paths

UNIX-like operating systems, including GNU/Linux and macOS, use slashes, `/`, as path separators, e.g., `/home/marek/file.csv`. Windows, however, uses backslashes, `\`, which have a special meaning in character strings (escape sequences, see [Section 2.1.3](#)), therefore they should be input as, e.g., "c:\\users\\marek\\file.csv" or r"c:\\users\\marek\\file.csv" (note the r prefix).

When constructing file paths programmatically, it is thus best to rely on `os.path.join`, which takes care of the system-specific nuances.

```
import os.path
os.path.join("~", "Desktop", "file.csv") # we're on GNU/Linux
## '~/Desktop/file.csv'
```

Note that the tilde, `~`, denotes the current user's home directory.

Note: For storing auxiliary data, we will often be using the system's temporary directory. See the `tempfile` module for functions that generate appropriate file paths therein.

¹⁶³ <https://stackexchange.com/>

¹⁶⁴ <https://archive.org/details/stackexchange>

¹⁶⁵ https://meta.wikimedia.org/wiki/Data_dumps

¹⁶⁶ <https://wikimediafoundation.org/>

For instance, a subdirectory inside the temporary directory can be created via a call to `tempfile.mkdtemp`.

Important: We will frequently be referring to file paths relative to the working directory of the currently executed Python session (e.g., from which IPython/Jupyter notebook server was started). The latter can be read by calling `os.getcwd`.

And thus, all non-absolute file names (ones that do not start with `~`, `/`, `c:\\`, and the like), for example, "filename.csv" or `os.path.join("subdir", "filename.csv")` are always relative to the current working directory.

For instance, if the working directory is "/home/marek/projects/python", then "filename.csv" refers to "/home/marek/projects/python/filename.csv".

Also, `..` denotes the current working directory's parent directory. Thus, ".../filename2.csv" resolves to "/home/marek/projects/filename2.csv".

Exercise 13.31 Print the result output by `os.getcwd`. Next, download the file `air_quality_2018_param.csv`¹⁶⁷ and save it in the current Python session's working directory (e.g., in your web browser, right-click on the web page's canvas and select Save Page As...). Load it as a `pandas` data frame by passing simply "`air_quality_2018_param.csv`" as the input path.

Exercise 13.32 (*) Download the aforementioned file programmatically (if you have not done so) using the `requests` module.

13.6.2 File Search

`glob.glob` and `os.listdir` can generate a list of files in a given directory (and possibly all its subdirectories).

`os.path.isdir` and `os.path.isfile` can be used to determine the type of a given object in the file system.

Exercise 13.33 Write a function that computes the total size of all the files in a given directory and all its subdirectories.

¹⁶⁷ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/air_quality_2018_param.csv

13.7 Exercises

Exercise 13.34 Find an example of an XML and JSON file. Which one is more human-readable? Do they differ in terms of capabilities?

Exercise 13.35 What is wrong with constructing file paths like "`~" + "||" + "filename.csv`"?

Exercise 13.36 What are the benefits of using a SQL-supporting relational database management system in data science activities?

Exercise 13.37 (***) How to populate a database with gigabytes of data read from many CSV files?

Part V

Other Types of Data

14

Text Data

In [[Gag22]] it is noted that effective processing of character strings is required at various stages of data analysis pipelines: from data cleansing and preparation, through information extraction, to report generation. Pattern searching, string collation and sorting, normalisation, transliteration, and formatting are ubiquitous in text mining, natural language processing, and bioinformatics. Means for the handling of string data should be included in each statistician's or data scientist's repertoire to complement their numerical computing and data wrangling skills.

Diverse data cleansing and preparation operations (compare, e.g., [[vdLdJ18]] and [[DJo3]]) need to be applied before an analyst can begin to enjoy an orderly and meaningful data frame, matrix, or spreadsheet being finally at their disposal. Activities related to information retrieval, computer vision, bioinformatics, natural language processing, or even musicology can also benefit from including them in data processing pipelines.

In this part we discuss the most basic string operations in base Python, together with their vectorised versions in **numpy** and **pandas**.

14.1 Basic String Operations

Recall that the `str` class represents individual character strings:

```
x = "spam"  
type(x)  
## <class 'str'>
```

There are a few binary operators overloaded for strings, e.g., `+` stands for string concatenation:

```
x + " and eggs"  
## 'spam and eggs'
```

`*` duplicates a given string:

```
x * 3
## 'spamspamspam'
```

Further, `str` is a sequential type, therefore we can extract individual code points and create substrings using the index operator:

```
x[-1] # last letter
## 'm'
```

Recall that strings are immutable. However, parts of strings can always be reused in conjunction with the concatenation operator:

```
x[:2] + "cial"
## 'special'
```

14.1.1 Unicode as the Universal Encoding

It is worth knowing that all strings in Python (from version 3.0) use Unicode(<https://www.unicode.org>) which is a universal encoding capable of representing ca. 150,000 characters covering letters and numbers in contemporary and historic alphabets/scripts, mathematical, political, phonetic, and other symbols, emojis, etc. It is thus a very powerful representation.

Note: Despite the wide support for Unicode, sometimes our own or other readers' display (e.g., web browsers when viewing a HTML version of the output report) might not be able to *render* all code points properly (e.g., due to missing fonts). However, we should rest assured that they are still there, and are processed correctly if string functions are applied thereon.

Note: (***) More precisely, Python strings are `UTF-8`¹⁶⁸-encoded. Most web pages and API data are nowadays served in UTF-8. However, occasionally we can encounter files encoded in ISO-8859-1 (Western Europe), Windows-1250 (Eastern Europe), Windows-1251 (Cyrillic), GB18030 and Big5 (Chinese), EUC-KR (Korean), Shift-JIS and EUC-JP (Japanese), amongst others; they can be converted using the `str.decode` method.

¹⁶⁸ <https://www.ietf.org/rfc/rfc3629.txt>

14.1.2 Normalising Strings

Dirty text data are a pain, especially if similar (semantically) tokens are encoded in many different ways. For the sake of string matching, we might want, e.g., the German "groß", "GROSS", and "gross" to compare all equal.

`str.strip` removes whitespaces (spaces, tabs, newline characters) at both ends of strings (see also `str.lstrip` and `str.rstrip` for their nonsymmetric versions).

`str.lower` and `str.upper` change letter case. For caseless comparison/matching, `str.casefold` might be a slightly better option as it unfolds many more code point sequences:

```
"Groß".lower(), "Groß".upper(), "Groß".casefold()
## ('groß', 'GROSS', 'gross')
```

Important: (***) More advanced string transliteration can be performed by means of the `ICU`¹⁶⁹ library, which the `PyICU` package provides wrappers for.

For instance, converting all code points to ASCII (English) might be necessary when identifiers are expected to miss some diacritics that would normally be included (as in "Gągolewski" vs "Gagolewski"):

```
import icu # PyICU package
icu.Transliterator.createInstance("Lower; Any-Latin; Latin-ASCII").
  transliterate(
    "Xaípετε! Groß gżegżółka – © La Niña – köszönöm – Gągolewski"
)
## 'chairete! gross gzeugolka - (c) la nina - koszonom - gagolewski'
```

Converting between different `Unicode Normalisation Forms`¹⁷⁰ (also available in the `unicodedata` package and via `pandas.Series.str.normalize`) might be used for the removal of some formatting nuances:

```
icu.Transliterator.createInstance("NFKD; NFC").transliterate("%q{r2{")
## '%qr2{'
```

¹⁶⁹ <https://icu.unicode.org/>

¹⁷⁰ <https://www.unicode.org/faq/normalization.html>

14.1.3 Substring Searching and Replacing

Determining if a string features a particular fixed substring can be done in a number of different ways.

For instance:

```
food = "bacon, spam, spam, eggs, and spam"
"spam" in food
## True
```

verifies whether a particular substring exists,

```
food.count("spam")
## 3
```

counts the number of occurrences of a substring,

```
food.find("spam")
## 7
```

locates the first pattern occurrence (see also `str.rfind` as well as `str.index` and `str.rindex`),

```
food.replace("spam", "veggies")
## 'bacon, veggies, veggies, eggs, and veggies'
```

replaces matching substrings with another string.

Exercise 14.1 Read the manual of the following methods: `str.startswith`, `str.endswith`, `str.removeprefix`, `str.removesuffix`.

The splitting of long strings at specific fixed delimiter strings can be done via:

```
food.split(", ")
## ['bacon', 'spam', 'spam', 'eggs', 'and spam']
```

see also `str.partition`. The `str.join` method implements the inverse operation:

```
", ".join(["spam", "bacon", "eggs", "spam"])
## 'spam, bacon, eggs, spam'
```

Important: In Section 14.4, we will discuss pattern matching with regular expressions,

which can be useful in, amongst others, extracting more abstract data chunks (numbers, URLs, email addresses, IDs) from within strings.

14.1.4 Locale-Aware Services in ICU (*)

Recall that relational operators such as `<` and `>= perform lexicographic comparing of strings:

```
"spam" > "egg"
## True
```

We have: "a" < "aa" < "aaaaaaaaaaaa" < "ab" < "aba" < "abb" < "b" < "ba" < "baaaaaaa" < "bb" < "Spanish inquisition".

Lexicographic ordering (character-by-character, from left to right) is, however, not necessarily appropriate for strings featuring numerals:

```
"a9" < "a123"
## False
```

Also, it only takes into account the [numeric codes¹⁷¹](#) corresponding to each Unicode character, therefore does not work well with non-English alphabets:

```
"MIELONECZKĄ" < "MIELONECZKI"
## False
```

In Polish, *A with ogonek* (A) should sort after *A* and before *B*, let alone *I*. However, their corresponding numeric codes in the Unicode table are: 260 (A), 65 (A), 66 (B), and 73 (I), therefore the resulting ordering is incorrect, natural language processing-wisely.

It is best to perform string collation using the services provided by **ICU**. Here is an example of German phone book-like collation where "ö" is treated the same as "oe":

```
c = icu.Collator.createInstance(icu.Locale("de_DE@collation=phonebook"))
c.setStrength(0)
c.compare("Löwe", "loewe")
## 0
```

A result of 0 means that the strings are deemed equal.

¹⁷¹ <https://www.unicode.org/charts/>

In some languages, contractions occur, e.g., in Slovak and Czech, two code points "ch" are treated as a single entity and are sorted after "h":

```
icu.Collator.createInstance(icu.Locale("sk_SK")).compare("chladný", "hladný")
## 1
```

i.e., we have "chladný" > "hladný" (the 1st argument is greater than the 2nd one). Compare the above to something similar in Polish:

```
icu.Collator.createInstance(icu.Locale("pl_PL")).compare("chłodny", "hardy")
## -1
```

i.e., "chłodny" < "hardy" (the first argument is less than the 2nd one).

Also, with **ICU**, numeric collation is possible:

```
c = icu.Collator.createInstance()
c.setAttribute(icu.UCollAttribute.NUMERIC_COLLATION, icu.UCollAttributeValue.
    ON)
c.compare("a9", "a123")
## -1
```

Which is the correct result: "a9" is less than "a123" (compare the above to the example which was using using `<`).

14.1.5 String Operations in pandas

String sequences in `Series` are by default¹⁷² using the broadest possible `object` data type:

```
pd.Series(["spam", "bacon", "spam"])
## 0      spam
## 1    bacon
## 2      spam
## dtype: object
```

which basically means that we deal with a sequence of Python objects of arbitrary type (here, are all of class `str`). This allows for the encoding of missing values by means of the `None` object.

¹⁷² https://pandas.pydata.org/pandas-docs/stable/user_guide/text.html

Vectorised versions of base string operations are available¹⁷³ via the `pandas.Series.str` accessor, which we usually refer to by calling `x.str.method_name()`, for instance:

```
x = pd.Series(["spam", "bacon", None, "buckwheat", "spam"])
x.str.upper()
## 0      SPAM
## 1      BACON
## 2      None
## 3      BUCKWHEAT
## 4      SPAM
## dtype: object
```

We thus have `pandas.Series.str.strip`, `pandas.Series.str.split`, `pandas.Series.str.find`, and so forth.

But there is more. For example, a function to compute the length of each string:

```
x.str.len()
## 0    4.0
## 1    5.0
## 2    NaN
## 3    9.0
## 4    4.0
## dtype: float64
```

Concatenating all items into a single string:

```
x.str.cat(sep="; ")
## 'spam; bacon; buckwheat; spam'
```

Vectorised string concatenation:

```
x + " and spam"
## 0      spam and spam
## 1      bacon and spam
## 2      None and spam
## 3      buckwheat and spam
## 4      spam and spam
## dtype: object
```

Conversion to numeric:

¹⁷³ <https://numpy.org/doc/stable/reference/routines.char.html>

```
pd.Series(["1.3", "-7", None, "3523"]).astype(float)
## 0      1.3
## 1     -7.0
## 2      NaN
## 3    3523.0
## dtype: float64
```

Selecting substrings:

```
x.str.slice(2, -1) # like x.iloc[i][2:-1] for all i
## 0      a
## 1     co
## 2     None
## 3   ckwhea
## 4      a
## dtype: object
```

Replacing substrings:

```
x.str.slice_replace(0, 2, "tofu") # like x.iloc[i][2:-1] = "tofu"
## 0      tofuam
## 1     tofucon
## 2     None
## 3   tofuckwheat
## 4      tofuam
## dtype: object
```

Exercise 14.2 Consider the `nasaweather_glaciers`¹⁷⁴ data frame. All glaciers are assigned 11/12-character unique identifiers. The ID number is assigned to the glacier as defined by the WGMS convention that forms the glacier ID number by combining the following five elements. Extract all of them and store them as independent columns in the data frame.

1. 2-character political unit,
2. 1-digit continent code,
3. 4-character drainage code,
4. 2-digit free position code,
5. 2- or 3-digit local glacier code.

¹⁷⁴ https://github.com/gagolews/teaching_data/blob/master/other/nasaweather_glaciers.csv

14.1.6 String Operations in numpy (*)

There is a huge overlap between the **numpy** and **pandas** capabilities for string handling, with the latter being more powerful. Still, some readers will find the following useful.

As mentioned in our introduction to **numpy** vectors, objects of type `ndarray` can store not only numeric and logical data, but also character strings. For example:

```
x = np.array(["spam", "bacon", "egg"])
x
## array(['spam', 'bacon', 'egg'], dtype='<U5')
```

Here, the data type "<U5" (compare also `x.dtype`) means that we deal with Unicode strings of length no greater than 5. Thus, unfortunately, replacing elements with too long a content will result in truncated strings:

```
x[2] = "buckwheat"
x
## array(['spam', 'bacon', 'buckw'], dtype='<U5')
```

In order to remedy this, we first need to recast the vector manually:

```
x = x.astype("<U10")
x[2] = "buckwheat"
x
## array(['spam', 'bacon', 'buckwheat'], dtype='<U10')
```

Conversion from/to numeric is also possible:

```
np.array(["1.3", "-7", "3523"]).astype(float)
## array([ 1.300e+00, -7.000e+00,  3.523e+03])
np.array([1, 3.14, -5153]).astype(str)
## array(['1.0', '3.14', '-5153.0'], dtype='<U32')
```

The **numpy.char**¹⁷⁵ module includes a number of vectorised versions of string routines, most of which we have discussed above. For example:

```
x = np.array([
    "spam", "spam, bacon, and spam",
    "spam, eggs, bacon, spam, spam, and spam"
])
```

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¹⁷⁵ <https://numpy.org/doc/stable/reference/routines.char.html>

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```
np.char.split(x, " ")
## array([list(['spam']), list(['spam', 'bacon', 'and spam']),
##        list(['spam', 'eggs', 'bacon', 'spam', 'spam', 'and spam'])],
##       dtype=object)
np.char.count(x, "spam")
## array([1, 2, 4])
```

Operations that we would normally perform via the use of binary operators (i.e., `+`, `*`, `<`, etc.) are available through standalone functions:

```
np.char.add(["spam", "bacon"], " and spam")
## array(['spam and spam', 'bacon and spam'], dtype='<U14')
np.char.equal(["spam", "bacon", "spam"], "spam")
## array([ True, False,  True])
```

Also the function that returns the length of each string is noteworthy:

```
np.char.str_len(x)
## array([ 4, 21, 39])
```

14.2 Working with String Lists

Series can also consist of lists of strings of varying lengths. They can not only be input manually (via the `pandas.Series` constructor), but also through string splitting. For instance:

```
x = pd.Series([
    "spam",
    "spam, bacon, spam",
    None,
    "spam, eggs, bacon, spam, spam"
])
xs = x.str.split(", ", regex=False)
xs
## 0                  [spam]
## 1              [spam, bacon, spam]
## 2                  None
```

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```
## 3      [spam, eggs, bacon, spam, spam]
## dtype: object
```

and now, e.g., looking at the last element:

```
xs.iloc[-1]
## ['spam', 'eggs', 'bacon', 'spam', 'spam']
```

reveals that it is indeed a list of strings.

There are a few vectorised operations that enable us to work with such variable length lists, such as concatenating all strings:

```
xs.str.join("; ")
## 0                  spam
## 1      spam; bacon; spam
## 2                  None
## 3      spam; eggs; bacon; spam; spam
## dtype: object
```

selecting, say, the first string in each list:

```
xs.str.get(0)
## 0    spam
## 1    spam
## 2    None
## 3    spam
## dtype: object
```

or slicing:

```
xs.str.slice(0, -1) # like xs.iloc[i][0:-1] for all i
## 0          []
## 1      [spam, bacon]
## 2          None
## 3      [spam, eggs, bacon, spam]
## dtype: object
```

Exercise 14.3 (*) Using `pandas.merge`, join the following datasets: `countries`¹⁷⁶, `world_factbook_2020`¹⁷⁷,

¹⁷⁶ https://github.com/gagolews/teaching_data/blob/master/other/countries.csv

¹⁷⁷ https://github.com/gagolews/teaching_data/blob/master/marek/world_factbook_2020.csv

and `ssi_2016_dimensions`¹⁷⁸ based on the country names. Note that some manual data cleansing will be necessary.

Exercise 14.4 (***) Given a `Series` object featuring lists of strings:

1. determine the list of all unique strings (e.g., for `xs` above we have: `["spam", "bacon", "eggs"]`), let's call it `xu`;
 2. create a data frame `x` with `xs.shape[0]` rows and `len(xu)` columns such that `x.iloc[i, j]` is equal to 1 if `xu[j]` is amongst `xs.loc[i]` and equal to 0 otherwise;
 3. given `x` (and only `x`: neither `xs` nor `xu`), perform the inverse operation.
-

14.3 Formatted Outputs

When preparing reports from data analysis (e.g., using Jupyter Notebooks or writing directly to Markdown files which we later compile to PDF or HTML using `pandoc`¹⁷⁹) it is important to be able to output nicely formatted content programmatically.

14.3.1 Formatting Strings

Recall that string formatting for inclusion of data stored in existing objects can easily be done using f-strings (formatted string literals) of the type `f" ...{expression}... "`. For instance:

```
pi = 3.14159265358979323846
f"n = {pi:.2f}"
## 'n = 3.14'
```

creates a string including the variable `pi` formatted as a float rounded to two places after the decimal separator.

Note: (***) Similar functionality can be achieved using the `str.format` method as well as the `%` operator overloaded for strings, which uses `sprintf`-like value placeholders known to some readers from other programming languages (such as C):

¹⁷⁸ https://github.com/gagolews/teaching_data/blob/master/marek/ssi_2016_dimensions.csv

¹⁷⁹ <https://pandoc.org/>

```
"n = {:.2f}".format(pi), "n = %.2f" % pi  
## ('n = 3.14', 'n = 3.14')
```

14.3.2 str and repr

The `str` and `repr` functions can create string representations of a number of objects, with the former being more human-readable and latter slightly more technical.

```
x = np.array([1, 2, 3])  
str(x), repr(x)  
## ('[1 2 3]', 'array([1, 2, 3])')
```

Note that `repr` often returns an output that can be interpreted as executable Python code literally (with no or few adjustments, however, `pandas` objects are one of the many exceptions).

14.3.3 Justifying Strings

`str.center`, `str.ljust`, `str.rjust` can be used to centre, left-, or-right justify a string so that it's of at least given width, which might make the display thereof more aesthetic. Very long strings, possibly containing whole text paragraphs can be dealt with using the `wrap` and `shorten` functions from the `textwrap` package.

14.3.4 Direct Markdown Output in Jupyter

Further, note that with IPython/Jupyter, we can output strings that will be directly interpreted as Markdown-formatted:

```
import IPython.display  
x = 2+2  
out = f"*Result*: $2^2=2+2={x}$."  
IPython.display.Markdown(out)
```

Result: $2^2 = 2 + 2 = 4$.

Recall that `Markdown`¹⁸⁰ is a very flexible markup language, allowing us to insert itemised and numbered lists, mathematical formulae, tables, images, etc.

¹⁸⁰ <https://daringfireball.net/projects/markdown/syntax>

14.3.5 Manual Markdown File Output

We can also generate Markdown code programmatically in form of standalone .md files:

```
f = open("/tmp/test-report.md", "w") # open for writing (overwrite if exists)
f.write("## Yummy Foods** include, but are not limited to:\n\n")
x = ["spam", "bacon", "eggs", "spam"]
for e in x:
    f.write(f"* {e}\n")
f.write("\nAnd now for something completely different:\n\n")
f.write("Rank | Food\n")
f.write("----|----\n")
for i in range(len(x)):
    f.write(f"{i+1:4} | {x[i][-10:]}\n")
f.close()
## 50
## 7
## 8
## 7
## 7
## 46
## 12
## 12
## 18
## 18
## 18
## 18
## 18
```

Here is the resulting raw Markdown source file:

```
with open("/tmp/test-report.md", "r") as f:
    out = f.read()
print(out)
## ## Yummy Foods** include, but are not limited to:
##
## * spam
## * bacon
## * eggs
## * spam
##
```

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```
## And now for something completely different:  
##  
## Rank / Food  
## ----- / -----  
##   1 | maps  
##   2 | nocab  
##   3 | sgge  
##   4 | maps
```

We can run it through the `pandoc`¹⁸¹ tool to convert it to a number of formats, including HTML, PDF, EPUB, and ODT. We may also render it directly into our report:

```
IPython.display.Markdown(out)
```

Yummy Foods include, but are not limited to:

- spam
- bacon
- eggs
- spam

And now for something completely different:

| Rank | Food |
|------|-------|
| 1 | maps |
| 2 | nocab |
| 3 | sgge |
| 4 | maps |

Note: Figures created in `matplotlib` can be exported to PNG, SVG, or PDF files using the `matplotlib.pyplot.savefig` function.

Note: Data frames can be nicely prepared for display in a report using `pandas.DataFrame.to_markdown`.

¹⁸¹ <https://pandoc.org/>

14.4 Regular Expressions (*)

Note that this section contains large excerpts from yours truly's other work [[Gag22]].

Regular expressions (regexes) provide us with a concise grammar for defining systematic patterns which can be sought in character strings. Examples of such patterns include: specific fixed substrings, emojis of any kind, stand-alone sequences of lower-case Latin letters (“words”), substrings that can be interpreted as real numbers (with or without fractional parts, also in scientific notation), telephone numbers, email addresses, or URLs.

Theoretically, the concept of regular pattern matching dates back to the so-called regular languages and finite state automata [[Kle51]], see also [[RS59]] and [[HU79]]. Regexes in the form as we know today have already been present in one of the pre-Unix implementations of the command-line text editor `qed` [[RT70]] (the predecessor of the well-known `sed`).

14.4.1 Regex Matching with `re`

In Python, the `re` module implements a regular expression matching engine that accepts patterns following a similar syntax to the ones available in the Perl language.

Before we proceed with a detailed discussion on how to read and write regexes, let us first review the methods for identifying the matching substrings. Below we use the `r"\bni+\b"` regex as an example, which catches "`n`" followed by at least one "`i`" that begins and ends at a *word boundary*, i.e., which may be considered standalone words.

In particular, `re.findall` extracts all non-overlapping matches to a given regex:

```
import re
x = "We're the knights who say ni! niiiii! ni! niiiiiiii!"
re.findall(r"\bni+\b", x)
## ['ni', 'niiiii', 'ni', 'niiiiiiii']
```

Note that the order of arguments is *look for what, where*, not the other way around.

Important: Note that we used the `r"..."` prefix when entering a string so that `\b` is not treated as a escape sequence denoting the backspace character. Otherwise, the above would have to be input as "`\\\bni+\\b`".

Hadn't we insisted on matching at the word boundaries (i.e., if we used "`ni+`" instead), we would also match the "`ni`" in "`knight`s".

The `re.search` function returns an object of class `re.Match` that enables us to get some more information about the first match:

```
r = re.search(r"\bni+\b", x)
r.start(), r.end(), r.group()
## (26, 28, 'ni')
```

The above includes the start and end position (index) and the match itself. If the regex contains *capture groups* (see below for more details), we can also pinpoint the matches thereto.

Moreover, `re.finditer` returns an iterable object that includes the same details, but now about all the matches:

```
rs = re.finditer(r"\bni+\b", x)
for r in rs:
    print((r.start(), r.end(), r.group()))
## (26, 28, 'ni')
## (30, 36, 'niiiii')
## (38, 40, 'ni')
## (42, 52, 'niiiiiiii')
```

`re.split` divides a string into chunks separated by matches to a given regex:

```
re.split(r"!|\s+", x)
## ["We're the knights who say ni", 'niiiii', 'ni', 'niiiiiiii!']
```

The `r"!|\s*"` regex matches the exclamation mark followed by one or more whitespace characters.

`re.sub` replaces each match with a given string:

```
re.sub(r"\bni+\b", "nu", x)
## "We're the knights who say nu! nu! nu! nu!"
```

Note: (***) More flexible replacement strings can be generated by passing a custom function as the second argument:

```
re.sub(r"\bni+\b", lambda m: "n" + "u"*(m.end()-m.start()-1), x)
## "We're the knights who say nu! nuuuuu! nu! nuuuuuuuu!"
```

14.4.2 Regex Matching with pandas

The `pandas.Series.str` accessor also defines a number of vectorised functions that utilise the `re` package's matcher.

Example Series object:

```
x = pd.Series(["ni!", "niiii, ni, nii!", None, "spam, bacon", "nii, ni!"])
x
## 0           ni!
## 1      niiii, ni, nii!
## 2           None
## 3      spam, bacon
## 4           nii, ni!
## dtype: object
```

Here are the most notable functions; their names are self-explanatory, so let's just get the picture instead of the words' abundance.

```
x.str.contains(r"\bni+\b")
## 0    True
## 1    True
## 2   None
## 3   False
## 4    True
## dtype: object
x.str.count(r"\bni+\b")
## 0    1.0
## 1    3.0
## 2    NaN
## 3    0.0
## 4    2.0
## dtype: float64
x.str.replace(r"\bni+\b", "nu", regex=True)
## 0        nu!
## 1    nu, nu, nu!
```

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```
## 2      None
## 3  spam, bacon
## 4      nu, nu!
## dtype: object
x.str.findall(r"\bni+\b")
## 0      [ni]
## 1  [niiii, ni, nii]
## 2      None
## 3      []
## 4  [nii, ni]
## dtype: object
x.str.split(r",\s+") # a comma, one or more whitespaces
## 0      [ni!]
## 1  [niiii, ni, nii!]
## 2      None
## 3  [spam, bacon]
## 4  [nii, ni!]
## dtype: object
```

In the two last cases, we get lists of strings in result.

Also, later we will mention `pandas.Series.str.extract` and `pandas.Series.str.extractall` which work with regexes that include capture groups.

Note: (*) If we intend to seek matches to the same pattern in different strings without the use of `pandas`, it might be a good to pre-compile a regex first and then use the `re.Pattern.findall` method instead or `re.findall`:

```
p = re.compile(r"\bni+\b") # returns an object of class `re.Pattern`
p.findall("We're the knights who say ni! ni! niiii! nininiiiiii!")
## ['ni', 'ni', 'niiii']
```

14.4.3 Matching Individual Characters

Most programming languages and text editors (including [Kate¹⁸²](#), [Eclipse¹⁸³](#), and [VSCode¹⁸⁴](#)) support finding or replacing patterns with regexes. Therefore, they should be amongst the instruments at every data scientist's disposal. One general introduction to regexes is [[Frio6]]. The `re` module flavour is summarised in the official [manual¹⁸⁵](#), see also [[Kuc22]]. In the following sections we review the most important elements of the regex syntax as we did in [[Gag22]].

We begin by discussing different ways to define character sets. In this part, determining the length of all matching substrings will be quite straightforward.

Important: The following characters have special meaning to the regex engine:

. \ | () [] > { } ^ \$ * + ?

Any regular expression that contains none of the above behaves like a fixed pattern:

```
re.findall("spam", "spam, eggs, spam, bacon, sausage, and spam")
## ['spam', 'spam', 'spam']
```

There are hence 3 occurrences of a pattern that is comprised of 4 code points, “s” followed by “p”, then by “a”, and ending with “m”.

If we wish to include a special character as part of a regular expression – so that it is treated literally – we'll need to escape it with a backslash, “\”.

```
re.findall(r"\.", "spam...")
```

```
## ['.', '.', '.']
```

¹⁸² <https://kate-editor.org/>

¹⁸³ <https://www.eclipse.org/ide/>

¹⁸⁴ <https://code.visualstudio.com/>

¹⁸⁵ <https://docs.python.org/3/library/re.html>

Matching Any Character

The (unesCAPed) dot, “.”, matches any code point except the newline.

```
x = "Spam, ham,\njam, SPAM, eggs, and spam"  
re.findall(..am", x, re.IGNORECASE)  
## ['Spam', 'ham', 'SPAM', 'spam']
```

The above matches non-overlapping length-4 substrings that end with “am”, case insensitively.

The dot’s insensitivity to the newline character is motivated by the need to maintain the compatibility with tools such as **grep** (when searching within text files in a line-by-line manner). This behaviour can be altered by setting the **DOTALL** flag.

```
re.findall(..am", x, re.DOTALL|re.IGNORECASE)  
## ['Spam', 'ham', '\njam', 'SPAM', 'spam']
```

Defining Character Sets

Sets of characters can be introduced by enumerating their members within a pair of square brackets. For instance, “[abc]” denotes the set {a, b, c} – such a regular expression matches one (and only one) symbol from this set. Moreover, in:

```
re.findall([hj]am", x)  
## ['ham', 'jam']
```

the “[hj]am” regex matches: “h” or “j”, followed by “a”, followed by “m”. In other words, “ham” and “jam” are the only two strings that are matched by this pattern (unless matching is done case-insensitively).

Important: The following characters, if used within square brackets, may be treated non-literally:

\ [] ^ - & ~ |

Therefore, to include them as-is in a character set, the backslash-escape must be used. For example, “[\\[\\]]” matches a backslash or a square bracket.

Complementing Sets

Including “^” (the caret) after the opening square bracket denotes the set complement. Hence, “[^abc]” matches any code point except “a”, “b”, and “c”. Here is an example where we seek any substring that consists of 3 non-spaces.

```
x = "Nobody expects the Spanish Inquisition!"  
re.findall("[^ ][^ ][^ ]", x)  
## ['Nob', 'ody', 'exp', 'ect', 'the', 'Spa', 'nis', 'Inq', 'uis', 'iti',  
#  'on!']
```

Defining Code Point Ranges

Each Unicode code point can be referenced by its unique numeric identifier for more details. For instance, “a” is assigned code U+0061 and “z” is mapped to U+007A. In the pre-Unicode era (mostly with regards to the ASCII codes, \leq U+007F, representing English letters, decimal digits, some punctuation characters, and a few control characters), we were used to relying on specific code ranges; e.g., “[a-z]” denotes the set comprised of all characters with codes between U+0061 and U+007A, i.e., lowercase letters of the English (Latin) alphabet.

```
re.findall("[0-9A-Za-z]", "Gągolewski")
## [ 'G', 'ą', 'g', 'o', 'ł', 'e', ' ', 's', 'k', 'i' ]
```

The above pattern denotes a union of 3 code ranges: digits and ASCII upper- and lower-case letters.

Nowadays, in the processing of text in natural languages, this notation should rather be avoided. Note the missing “*a*” (Polish “*a*” with ogonek) in the result.

Using Predefined Character Sets

Some other noteworthy Unicode-aware code point classes include the “word characters”:

decimal digits:

```
re.findall(r"\d", x)
## ['1', '2', '3', '4', '5']
```

and whitespaces:

```
re.findall(r"\s", x)
## [' ', '\t', '\n']
```

Moreover, e.g., “\W” is equivalent to “[^\w]”, i.e., denotes its complement.

14.4.4 Alternating and Grouping Subexpressions

Alternation Operator

The alternation operator, “|” (the pipe or bar), matches either its left or its right branch, for instance:

```
x = "spam, egg, ham, jam, algae, and an amalgam of spam, all al dente"
re.findall("spam|ham", x)
## ['spam', 'ham', 'spam']
```

Grouping Subexpressions

“|” has a very low precedence. Therefore, if we wish to introduce an alternative of subexpressions, we need to group them using the “(?:...)” syntax. For instance, “(?:sp|h)am” matches either “spam” or “ham”.

Note that the bare use of the round brackets, “(...)” (i.e., without the “?:”) part, has the side-effect of creating new capturing groups, see below for more details.

Also, matching is always done left-to-right, on a first-come, first-served basis. Hence, if the left branch is a subset of the right one, the latter will never be matched. In particular, “(?:al|alga|algae)” can only match “al”. To fix this, we can write “(?:algae|alga|al)”.

Non-grouping Parentheses

Some parenthesised subexpressions – those in which the opening bracket is followed by the question mark – have a distinct meaning. In particular, “(?#...)” denotes a free-format comment that is ignored by the regex parser:

```
re.findall(
  "(?# match 'sp' or 'h')(:sp|h)(?# and 'am')am|(?# or match 'egg')egg",
  x)
```

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```
)
## ['spam', 'egg', 'ham', 'spam']
```

This is just horrible. Luckily, constructing more sophisticated regexes by concatenating subfragments thereof is more readable:

```
re.findall(
    "(?:sp|h)" +      # match either 'sp' or 'h'
    "am" +            # followed by 'am'
    "|" +           # ...
    "egg",          # just match 'egg'
    x
)
## ['spam', 'egg', 'ham', 'spam']
```

What is more, e.g., “(?i)” enables the case-insensitive mode.

```
re.findall("(?i)spam", "Spam spam SPAMITY spAm")
## ['Spam', 'spam', 'SPAM', 'spAm']
```

14.4.5 Quantifiers

More often than not, a variable number of instances of the same subexpression needs to be captured or its presence should be made optional. This can be achieved by means of the following quantifiers:

- “?” matches 0 or 1 times;
- “*” matches 0 or more times;
- “+” matches 1 or more times;
- “{n,m}” matches between n and m times;
- “{n,}” matches at least n times;
- “{n}” matches exactly n times.

These operators are applied onto the directly preceding atoms. For example, “ni+” captures “ni”, “nii”, “niii”, etc., but neither “n” alone nor “ninini” altogether.

By default, the quantifiers are greedy – they match the repeated subexpression as many times as possible. The “?” suffix (hence, quantifiers such as “??”, “*?”, “+?”, and so forth) tries with as few occurrences as possible (to obtain a match still).

Greedy:

```
x = "sp(AM)(maps)(SP)am"
re.findall(r"\(.+\)", x)
## ['(AM)(maps)(SP)']
```

Lazy:

```
re.findall(r"\(.+?\)", x)
## ['(AM)', '(maps)', '(SP)']
```

Greedy (but clever):

```
re.findall(r"\([^\)]+\)", x)
## ['(AM)', '(maps)', '(SP)']
```

The first regex is greedy: it matches an opening bracket, then as many characters as possible (including ")") that are followed by a closing bracket. The two other patterns terminate as soon as the first closing bracket is found.

More examples:

```
x = "spamamamnomnomnomnomammmmmmm"
re.findall("sp(?:am|nom)+", x)
## ['spamamamnomnomnomnom']
re.findall("sp(?:am|nom)+?", x)
## ['spam']
```

And:

```
re.findall("sp(?:am|nom)+?m*", x)
## ['spam']
re.findall("sp(?:am|nom)+?m+", x)
## ['spamamamnomnomnomnomammmmmmm']
```

Let's stress that the quantifier is applied to the subexpression that stands directly before it. Grouping parentheses can be used in case they are needed.

```
x = "12, 34.5, 678.901234, 37...629, ..."
re.findall(r"\d+\.\d+", x)
## ['34.5', '678.901234']
```

matches digits, a dot, and another series of digits.

```
re.findall(r"\d+(?:\.\d+)?", x)
## ['12', '34.5', '678.901234', '37', '629']
```

finds digits which are possibly (but not necessarily) followed by a dot and a digit sequence.

Exercise 14.5 Write a regex that extracts all #hashtags from a string `#omg #SoEasy`.

14.4.6 Capture Groups and References Thereto

Round-bracketed subexpressions (without the ":" prefix) form the so-called *capture groups* that can be extracted separately or be referred to in other parts of the same regex.

Extracting Capture Group Matches

The above is evident when we use `re.findall`:

```
x = "name='Sir Launcelot', quest='Seek the Grail', favecolour='blue'"
re.findall(r"(\w+)=(.+?)'", x)
## [('name', 'Sir Launcelot'), ('quest', 'Seek the Grail'), ('favecolour',
    ↴ 'blue')]
```

Simply returned the matches to the capture groups, not the whole matching substring.

`re.find` and `re.finditer` can pinpoint each component:

```
r = re.search(r"(\w+)=(.+?)'", x)
print("all (0):", (r.start(), r.end(), r.group()))
print("      1 :", (r.start(1), r.end(1), r.group(1)))
print("      2 :", (r.start(2), r.end(2), r.group(2)))
## all (0): (0, 20, "name='Sir Launcelot'")
##      1 : (0, 4, 'name')
##      2 : (6, 19, 'Sir Launcelot')
```

Here is a vectorised version of the above from `pandas`, returning the first match:

```
y = pd.Series([
    "name='Sir Launcelot'",
    "quest='Seek the Grail'",
    "favecolour='blue', favecolour='yel.. Aaargh!'"
])
```

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```
y.str.extract(r"(\w+)='(.*?)'")
```

| | 0 | 1 |
|------|------------|----------------|
| ## 0 | name | Sir Launcelot |
| ## 1 | quest | Seek the Grail |
| ## 2 | favecolour | blue |

We see that the findings are presented in a data frame form. The first column gives the matches to the first capture group, and so forth.

All matches are available too:

```
y.str.extractall(r"(\w+)='(.*?)'")
```

| | 0 | 1 |
|--------|------------|----------------|
| ## 0 | match | |
| ## 0 0 | name | Sir Launcelot |
| ## 1 0 | quest | Seek the Grail |
| ## 2 0 | favecolour | blue |
| ## 1 | favecolour | yel.. Aaargh! |

Recall that if we just need the grouping part of “(...)\”, i.e., without the capturing feature, “(?:...)” can be applied.

Also, named capture groups defined like “(?P<name>...)” are supported.

```
y.str.extract("(?:\w+)='(?P<value>.+)')")
```

| | value |
|------|----------------|
| ## 0 | Sir Launcelot |
| ## 1 | Seek the Grail |
| ## 2 | blue |

Replacing with Capture Group Matches

Matches to particular capture groups can be recalled in replacement strings when using **re.sub** and **pandas.Series.str.replace**. Here, the match in its entirety is denoted with “\g<0>”, then “\g<1>” stores whatever was caught by the first capture group, “\g<2>” is the match to the second capture group, etc.

```
re.sub(r"(\w+)='(.*?)'", r"\g<2> is a \g<1>", x)
## 'Sir Launcelot is a name, Seek the Grail is a quest, blue is a favecolour'
```

Named capture groups can be referred to too:

```
re.sub(r"(?P<key>\w+)=(?P<value>.+?)",
      r"\g<value> is a \g<key>", x)
## 'Sir Launcelot is a name, Seek the Grail is a quest, blue is a favecolour'
```

Back-Referencing

Matches to capture groups can also be part of the regexes themselves. For example, "\1" denotes whatever has been consumed by the first capture group.

Even though, in general, parsing HTML code with regexes is not recommended, let's consider the following examples:

```
x = "<strong><em>spam</em></strong><code>eggs</code>"\nre.findall(r"<[a-z]+>.*?</[a-z]+>", x)\n## ['<strong><em>spam</em>', '<code>eggs</code>']\nre.findall(r"(<[a-z]+>.*?</2>)", x)\n## [('<strong><em>spam</em></strong>', 'strong'), ('<code>eggs</code>', 'code')]"]
```

The second regex guarantees that the match will include all characters between the opening `<tag>` and the corresponding (not: any) closing `</tag>`. Named capture groups can be referenced using the `(?P=name)` syntax (the angle brackets are part of the token):

```
re.findall(r"(<(?P<tagname>[a-z]+)>.*?</?P=>tagname>)", x)\n## [('<strong><em>spam</em></strong>', 'strong'), ('<code>eggs</code>', 'code')]"]
```

14.4.7 Anchoring

Lastly, let's mention the ways to match a pattern at a given abstract position within a string.

Matching at the Beginning or End of a String

`"^"` and `"$"` match, respectively, start and end of the string (or each line within a string, if the `re.MULTILINE` flag is set).

```
x = pd.Series(["spam egg", "bacon spam", "spam", "egg spam bacon", "sausage\n"])
rs = ["spam", "^spam", "spam$", "spam$|^spam", "^spam$"]
```

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```
pd.concat([x.str.contains(r) for r in rs], axis=1, keys=rs)
##      spam  ^spam  spam$  spam$/^spam  ^spam$
## 0    True   True  False       True  False
## 1    True  False   True       True  False
## 2    True   True   True       True   True
## 3    True  False  False      False  False
## 4   False  False  False      False  False
```

The 5 regular expressions match “spam”, respectively, anywhere within the string, at the beginning, at the end, at the beginning or end, and in strings that are equal to the pattern itself.

Exercise 14.6 Write a regex that does the same job as `str.strip`.

Matching at Word Boundaries

Furthermore, “\b” matches at a “word boundary”, e.g., near spaces, punctuation marks, or at the start/end of a string (i.e., wherever there is a transition between a word, “\w”, and a non-word character, “\W”, or vice versa).

In the following example, we match all stand-alone numbers (this regular expression is provided for didactic purposes only):

```
re.findall(r"[+-]?\b\d+(?:\.\d+)?\b", "+12, 34.5, -5.3243")
## ['+12', '34.5', '-5.3243']
```

Looking Behind and Ahead

There are also ways to guarantee that a pattern occurrence begins or ends with a match to some subexpression: “(?<=...)...” is the so-called look-behind, whereas “...(?=...)” denotes the look-ahead. Moreover, “(?<!...)...” and “...(?!...)” are their negated (“negative look-behind/ahead”) versions.

```
x = "I like spam, spam, eggs, and spam."
re.findall(r"\b\w+\b(?:=[,.])", x)
## ['spam', 'spam', 'eggs', 'spam']
re.findall(r"\b\w+\b(?:![,.])", x)
## ['I', 'like', 'and']
```

The first regex captures words that end with “,” or “.”. The second one matches words that end neither with “,” nor “.”.

Exercise 14.7 Write a regex that extracts all standalone numbers accepted by Python, including 12.123, -53, +1e-9, -1.2423e10, 4. and .2.

Exercise 14.8 Write a regex that matches all email addresses.

Exercise 14.9 Write a regex that matches all URLs starting with `http://` or `https://`.

Exercise 14.10 Cleanse the `warsaw_weather`¹⁸⁶ dataset so that it contains analysable numeric data.

14.5 Exercises

Exercise 14.11 List some ways to normalise character strings.

Exercise 14.12 (**) What are the challenges of processing non-English text?

Exercise 14.13 What are the problems with the "[A-Za-z]" and "[A-z]" character sets?

Exercise 14.14 Name the two ways to turn on case-insensitive regex matching.

Exercise 14.15 What is a word boundary?

Exercise 14.16 What is the difference between the "^" and "\$" anchors?

Exercise 14.17 When we would prefer using "[0-9]" instead of "\d"?

Exercise 14.18 What is the difference between the "?", "??", "*", "*?", "+", and "+?" quantifiers?

Exercise 14.19 Does ". " match all the characters?

Exercise 14.20 What are named capture groups and how to refer to the matches thereto in `re.sub`?

¹⁸⁶ https://github.com/gagolews/teaching_data/blob/master/marek/warsaw_weather.csv

15

Missing, Censored, and Questionable Data

So far we have been assuming that observations are of “decent quality”, i.e., trustworthy. It would be nice if in reality that was always the case, but it is not.

In this section we briefly address the most basic methods for dealing with “suspicious” observations: outliers, missing, censored, and incorrect data.

15.1 Missing Data

Consider the `nhanes_p_demo_bmx_2020` dataset being another excerpt from the National Health and Nutrition Examination Survey by the US Centres for Disease Control and Prevention:

```
nhanes = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/nhanes_p_demo_bmx_2020.csv",
    comment="#")
nhanes.head(3)
##      SEQN BMDSTATS BMXWT  BMIWT ...      WTMECPRP SDMVPSU SDMVSTRA
## 0 109263        4     NaN     NaN ...  8951.815567      3       156
## 1 109264        1    42.2     NaN ... 12271.157043      1       155
## 2 109265        1    12.0     NaN ... 16658.764203      1       157
## [3 rows x 50 columns]
```

Some of the columns feature `NaN` (not-a-number) values, which are used here to encode *missing data*.

The reasons behind why some items are missing might be numerous, for instance:

- a participant doesn't know the answer to a given question;
- a patient refused to answer a given question;
- a participant does not take part in the study anymore (attrition, death, etc.);
- an item is not applicable (e.g., number of minutes spent cycling weekly when someone answered they don't like bikes at all);
- a piece of information was not collected, e.g., due to the lack of funding or equipment failure.

15.1.1 Representing and Detecting Missing Values

Sometimes missing values will be specially encoded, especially in CSV files, e.g., with `-1`, `0`, `9999`, `numpy.inf`, `-numpy.inf`, or `None`, strings such as "NA", "N/A", "Not Applicable", "----" – we should always inspect our datasets carefully.

Generally, we will be converting them to `NaN` (as in: `numpy.nan`) in numeric (floating-point) columns or to Python's `None` otherwise, to assure consistent representation.

Vectorised functions such as `numpy.isnan` (or, more generally, `numpy.isfinite`) and `pandas.isnull` as well as `isna` methods in the `DataFrame` and `Series` classes can be used to verify whether an item is missing or not.

For instance, here are the counts and proportions of missing values in each column (we will display only the top 5 columns to save space):

```
nhanes_na_stats = nhanes.isna().apply([np.sum, np.mean]).T
nhanes_na_stats.nlargest(5, "sum")
##           sum      mean
## BMIHEAD    14300.0  1.000000
## BMIRECUM   14257.0  0.996993
## BMIHT     14129.0  0.988042
## BMXHEAD    13990.0  0.978322
## BMIHIP     13924.0  0.973706
```

Looking at the column descriptions¹⁸⁷, `BMIHEAD` stands for “Head Circumference Com-
ment”, whereas `BMXHEAD` is “Head Circumference (cm)”, but it is only applicable for in-
fants.

¹⁸⁷ https://www.cdc.gov/Nchs/Nhanes/2017-2018/P_BMX.htm

Exercise 15.1 Read the column descriptions (refer to the comments in the CSV file for the relevant URLs) to identify the possible reasons for some of the NHANES data being missing.

Exercise 15.2 Study the `pandas` manual to learn about the difference between the `DataFrameGroupBy.size` and `DataFrameGroupBy.count` methods.

15.1.2 Computing with Missing Values

Our use of `NaN` to denote a missing piece of information is actually an ugly (but still functioning) hack. The original use case for not-a-number is to represent the results of incorrect operations, e.g., logarithms of negative numbers or subtracting two infinite entities. Therefore, we need extra care when handling them. On a side note, e.g., the R environment has a built-in, seamless support for missing values.

Generally, arithmetic operations on missing values yield a result that is undefined as well:

```
np.nan + 2 # "don't know" + 2 == "don't know"  
## nan  
np.mean([1, np.nan, 2, 3])  
## nan
```

There are versions of certain aggregation functions that ignore missing values whatsoever: `numpy.nanmean`, `numpy.nanmin`, `numpy.nanmax`, `numpy.nanpercentile`, `numpy.std`, etc.

```
np.nanmean([1, np.nan, 2, 3])  
## 2.0
```

However, running aggregation functions directly on `Series` objects ignores missing entities by default. Compare an application of `numpy.mean` on a `Series` instance vs on a vector:

```
x = nhanes.loc[:6, "BMXHT"] # some example Series, whatever  
np.mean(x), np.mean(x.to_numpy())  
## (148.5, nan)
```

This is quite an unfortunate behaviour, because this way we might miss (sic!) the presence of missing values. This is why it is very important always to pre-inspect a dataset carefully.

Also, due to `NaN`'s being of floating-point type, it cannot be present in, amongst others, logical vectors. By convention, comparisons against missing values yield `False` (instead of the more semantically valid missing value):

```

x # preview
## 0      NaN
## 1    154.7
## 2     89.3
## 3   160.2
## 4      NaN
## 5   156.0
## 6   182.3
## Name: BMXHT, dtype: float64
y = (x > 40)
y
## 0    False
## 1     True
## 2     True
## 3     True
## 4    False
## 5     True
## 6     True
## Name: BMXHT, dtype: bool

```

Note: (*) If we want to retain the missingness information (we don't know if a missing value is greater than 40), we need to do it manually:

```

y = y.astype("object") # required for numpy vectors, not for pandas Series
y[np.isnan(x)] = None
y
## 0    None
## 1     True
## 2     True
## 3     True
## 4    None
## 5     True
## 6     True
## Name: BMXHT, dtype: object

```

Exercise 15.3 Read the `pandas` manual¹⁸⁸ for more technical details on missing value handling.

¹⁸⁸ https://pandas.pydata.org/pandas-docs/stable/user_guide/missing_data.html

15.1.3 Missing at Random or Not?

At a general level (from the mathematical modelling perspective), we may distinguish between different missingness patterns (as per Rubin's [[Rub76]]):

- *missing completely at random*: reasons are unrelated to data and probabilities of cases being missing are all the same;
- *missing at random*: there are different probabilities of being missing within different groups (e.g., males might systematically refuse to answer specific questions);
- *missing not at random*: due to reasons unknown to us (e.g., data was collected at different times, there might be systematic differences but within the groups that we cannot easily identify, e.g., amongst participants with data science background where we did not ask about education or occupation).

It is important to try to determine the reason for missingness, because this will usually imply the kinds of techniques that are more or less suitable in specific cases.

15.1.4 Discarding Missing Values

We may try removing (discarding) the rows or columns that feature at least one, some, or too many missing values.

However, for this we need to be “rich enough” – such a scheme will obviously not work for small datasets, where each observation is precious (but on the other hand, if we want to infer from too small datasets, we should ask ourselves whether this is a good idea at all... it might be better to simply refrain from any data analysis than to come up with conclusions that are likely to be unjustified).

Also, we should not exercise data removal in situations where missingness is conditional (e.g., data only available for infants) or otherwise group-dependent (not-completely at random; e.g., it might result in an imbalanced dataset).

Exercise 15.4 With the `nhanes_p_demo_bmx_2020`¹⁸⁹ dataset:

1. remove all columns that are comprised of missing values only,
2. remove all columns that are made of more than 20% missing values,
3. remove all rows that only consist of missing values,
4. remove all rows that feature at least one missing value,
5. remove all columns that feature at least one missing value.

¹⁸⁹ https://github.com/gagolews/teaching_data/blob/master/marek/nhanes_p_demo_bmx_2020.csv

Hint: `pandas.DataFrame.dropna` might be useful in the simplest cases, and `numpy.isnan` or `pandas.DataFrame.isna` with `loc[...]` or `iloc[...]` otherwise.

15.1.5 Mean Imputation

When we cannot afford or it is inappropriate/inconvenient to proceed with the removal of missing observations or columns, we might try applying some missing value *imputation* techniques. Although, let us be clear – this is merely a replacement thereof by some hopefully useful guesstimates.

Important: Whatever we decide to do with the missing values, we need to be explicit about the way we have handled them in all the reports from data analysis, as sometimes they might strongly affect the results.

Let's consider an example vector with missing values, comprised of heights of the adult participants of the NHANES study.

```
x = nhanes.loc[nhanes.loc[:, "RIDAGEYR"] >= 18, "BMXHT"]
```

The simplest approach is to replace each missing value with the corresponding column's mean (for each column separately). This does not change the overall average (but decreases the variance).

```
xi = x.copy()
xi[np.isnan(xi)] = np.nanmean(xi)
```

Similarly, we could have considered replacing missing values with the median, or – in case of categorical data – the mode.

Our height data are definitely not missing completely at random – in particular, we expect heights to differ, on average, between sexes. Therefore, another basic imputation option is to replace the missing values with the corresponding within-group averages:

```
xg = x.copy()
g = nhanes.loc[nhanes.loc[:, "RIDAGEYR"] >= 18, "RIAGENDR"]
xg[np.isnan(xg) & (g == 1)] = np.nanmean(xg[g == 1]) # male
xg[np.isnan(xg) & (g == 2)] = np.nanmean(xg[g == 2]) # female
```

Unfortunately, whichever imputation method we choose, it will artificially distort the data distribution (and hence introduce some kind of bias), see [Figure 15.1](#).

```

plt.subplot(131)
sns.histplot(x, binwidth=1, binrange=[130, 200], color="lightgray")
plt.ylim(0, 500)
plt.title("Original")
plt.subplot(132)
sns.histplot(xi, binwidth=1, binrange=[130, 200], color="lightgray")
plt.ylim(0, 500)
plt.title("Replace by mean")
plt.subplot(133)
sns.histplot(xg, binwidth=1, binrange=[130, 200], color="lightgray")
plt.ylim(0, 500)
plt.title("Replace by group mean")
plt.show()

```

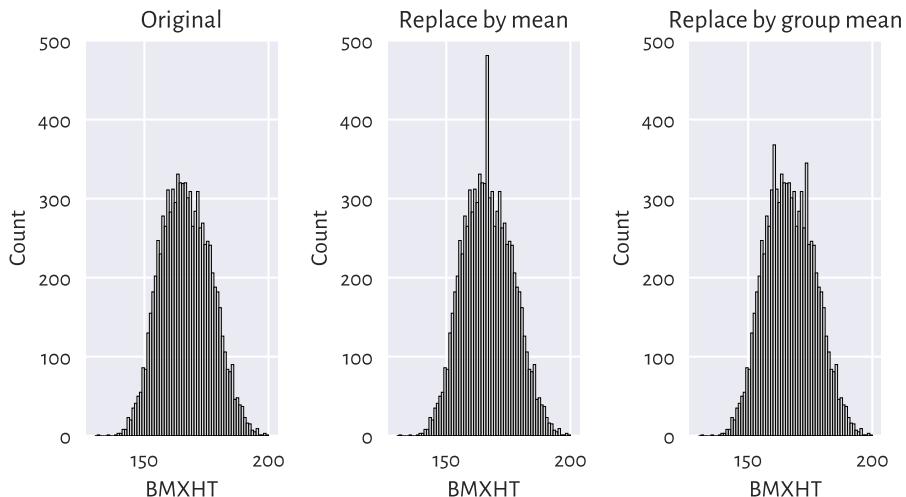


Figure 15.1: Mean imputation distorts the data distribution

Note that these effects might not be visible if we increase the bin widths, but they are still there. After all, we have added to the sample many identical values.

Exercise 15.5 With the `nhanes_p_demo_bmx_2020`¹⁹⁰ dataset:

1. for each numerical column, replace all missing values with the column averages,

¹⁹⁰ https://github.com/gagolews/teaching_data/blob/master/marek/nhanes_p_demo_bmx_2020.csv

2. for each categorical column, replace all missing values with the column modes,
3. for each numerical column, replace all missing values with the averages corresponding to a patient's sex (as given by the RIAGENDR column).

Note: (*) We can easily implement a missing value imputer based on averaging data from an observation's non-missing nearest neighbours, compare {numref}`sec:knn`. This is an extension of the simple idea of finding the most "similar" observation (with respect to chosen criteria) to a given one and "borrowing" missing measurements from it. More generally, different regression or classification models can be built on non-missing data and then the missing observations can be replaced by the values predicted by those models.

Note: (***) Rubin (e.g., [[LR02]]) suggests the use of a procedure called *multiple imputation* (see also [[VB18]]), where copies of the original datasets are created, missing values are imputed by sampling from some estimated distributions, inference is made, and then the results are aggregated. An example implementation of such an algorithm is available in `sklearn.impute.IterativeImputer`.

15.2 Censored and Interval Data (*)

Censored data frequently appear in the context of reliability, risk analysis, and biostatistics, where the observed objects might "fail" (e.g., break down, die, withdraw), compare, e.g., [[MKK16]]. Our introductory course can't obviously cover everything, but a beginner analyst should at least be aware of such data being a thing, in particular:

- right-censored data: we only know that the actual value is above the recorded one (e.g., we stopped the experiment on the reliability of light bulbs after 1000 hours, so those which still work will not have a time-of-failure precisely known);
- left-censored data: the actual observation is below the recorded one, e.g., we observe a component's failure, but we don't know for how long it has been in operation before the study has started.

Hence, in such cases, the recorded datum of, say, 1000, can actually mean $[1000, \infty)$, $[0, 1000]$, or $(-\infty, 1000]$.

There might also be instances where we know that a value is in some interval $[a, b]$. There

are numerical libraries that deal with *interval computations*, and some data analysis methods exist in such a case.

15.3 Incorrect Data

Missing data might already be present in a given sample but also we might be willing to mark some existing values as missing, e.g., when they are simply incorrect.

For example:

- for text data, misspelled words;
- for spatial data, GPS coordinates of places out of this world, non-existing zip codes, or invalid addresses;
- for date-time data, misformatted date-time strings, incorrect dates such as “29 February 2011”, an event’s start date being after the end date;
- for physical measurements, observations that do not meet specific constraints, e.g., negative ages, or heights of people over 300 centimetres;
- IDs of entities that simply do not exist (e.g., unregistered or deleted clients’ accounts);

and so forth.

In order to be able to identify and handle incorrect data, we need specific knowledge valid for a particular domain. Optimally, basic data validation techniques should already be employed on the data collection stage, for instance when a user submits an online form.

There can be many tools that can assist us with identifying erroneous observations, e.g., spell checkers such as [hunspell](#)¹⁹¹.

For smaller datasets, observations can also be manually inspected. However, sometimes we will have to develop our own algorithms for detecting “bugs” in data.

Exercise 15.6 Given some data frame with numeric columns only, perform what follows.

1. Check if all numeric values in each column are between 0 and 1000.
2. Check if all values in each column are unique.

¹⁹¹ <https://hunspell.github.io/>

3. Verify that all the rowwise sums add up to 1.0 (up to a small numeric error).
4. Check if the data frame consists of 0s and 1s only. If that is the case, verify that for each row, if there is a 1 in the first column, then all the remaining columns are filled with 1s too.

Many data validation methods can be reduced to operations on strings. They may be as simple as writing a single regular expression or checking if a label is in a dictionary of possible values and as difficult as writing your own parser for a custom context-sensitive grammar.

15.3.1 Exercises on Validating Data

Once we have imported the data fetched from different sources, it will usually be the case that relevant information will have to be extracted from raw text, e.g., strings like "1" should be converted to floating-point numbers. Below we suggest a number of tasks that aid in developing data validation skills involving some operations on textual information.

Exercise 15.7 Given an example data frame with text columns (manually invented, be creative), perform what follows.

1. Remove trailing and leading whitespaces from each string.
2. Check if all strings can be interpreted as numbers, e.g., "23.43".
3. Verify if a date string in YYYY-MM-DD format is correct.
4. Determine if a date-time string in YYYY-MM-DD hh:mm:ss format is correct.
5. Check if all strings are of the form (+NN) NNN-NNN-NNN or (+NN) NNNN-NNN-NNN, where N denotes any digit (valid telephone numbers).
6. Inspect whether all strings are valid country names.
7. Given a person's date of birth, sex, and their Polish ID number PESEL¹⁹², check if that PESEL is correct.
8. Determine if a string represents a correct International Bank Account Number (IBAN¹⁹³) (note that IBANs feature two check digits).
9. Transliterate text to ASCII, e.g., "żółty" to "zolty (C)".
10. Using an external spell checker, determine if every string is a valid English word.
11. Using an external spell checker, ascertain that every string is a valid English noun in singular form.

¹⁹² <https://en.wikipedia.org/wiki/PESEL>

¹⁹³ https://en.wikipedia.org/wiki/International_Bank_Account_Number

12. Resolve all abbreviations by means of a custom dictionary, e.g., "Kat." → "Katherine", "Gr." → "Grzegorz".
-

15.4 Outliers

Another group of inspectionworthy observations consists of *outliers*, which we may define as the samples that reside at areas of substantially lower density than their neighbours.

Outliers might be present due to an error, or their being otherwise anomalous, but they may also simply be interesting, original, or novel. After all, statistics does not give any meaning to data items; humans do.

What we do with outliers is a separate decision. We can get rid of them, correct them, replace them with a missing value (and then possibly impute), etc.

15.4.1 The 3/2 IQR Rule for Normally-Distributed Data

For unidimensional data (or individual columns in matrices and data frames), usually the first few smallest and largest observations should be inspected manually. It might be, for instance, the case that someone accidentally entered a patient's height in metres instead of centimetres – such cases are easily detectable. A data scientist is like a detective.

Recall that in the section on box-and-whisker plots (Section 5.1.4), one heuristic definition of an outlier that is particularly suited for data that are expected to come from a normal distribution, was to consider everything that does not fall into the interval $[Q_1 - 1.5\text{IQR}, Q_3 + 1.5\text{IQR}]$.

This is merely a rule of thumb. It is based on quartiles, and thus should not be affected by potential outliers (they are robust aggregates, see below). Plus, the magic constant 1.5, is nicely round and thus easy to memorise (good for some practitioners). It is not too small and not too large; for the normal distribution $N(\mu, \sigma)$, the above interval corresponds to roughly $[\mu - 2.698\sigma, \mu + 2.698\sigma]$ and thus the probability of obtaining a value outside of it is ca. 0.7%. In other words, for a sample size 1000 that is *truly* normally distributed (and thus not contaminated by anything), only 7 observations will be marked as suspicious; thus, it is not a problem to inspect them by hand.

Note: (*) We can of course choose a different threshold. For instance, for the normal distribution $N(10, 1)$, the probability of observing a value ≥ 15 is theoretically non-

zero, hence whether we consider 15 an outlier is a matter of taste (or, to be precise, the threshold we impose). Nevertheless, this probability is smaller than 0.000029%, and thus it is simply rational to treat this observation as suspicious. On the other hand, we don't want to mark too many observations as outliers because inspecting them manually will be too labour-intense.

Exercise 15.8 For each column in `nhanes_p_demo_bmx_2020`¹⁹⁴, inspect a few smallest and largest observations and see if they make sense. Draw a histogram to verify if the data are perhaps multimodal.

Exercise 15.9 Perform the above separately for data in each group as defined by the `RIAGENDR` column.

15.4.2 Robust Aggregates

In Section 5.1.1 we have noted that the arithmetic mean (and hence standard deviation and skewness) are very fragile when exposed to significantly smaller or larger observations than the rest.

For example:

```
x = np.array([1, 2, 3, 4, 5])
np.mean(x)
## 3.0
```

And now:

```
x[-1] = 5000 # oopsie, someone made a typo
np.mean(x)
## 1002.0
```

The sample median is an example of a *robust* aggregate — it ignores almost all but 1-2 middle observations (we'd say it has a high *breakdown point*). Some measures of central tendency that are in-between the mean-median extreme include:

- *trimmed means* – the arithmetic mean of all the observations except a number of, say p , the smallest and the greatest ones,
- *winsorised means* – the arithmetic mean with p smallest and p greatest observations replaced with the $(p+1)$ -smallest the $(p+1)$ -largest one.

¹⁹⁴ https://github.com/gagolews/teaching_data/blob/master/marek/nhanes_p_demo_bmx_2020.csv

As far as spread measures are concerned, the interquartile range (IQR) is a robust statistic. If need be, standard deviation might be replaced with:

- mean absolute deviation from the mean: $\frac{1}{n} \sum_{i=1}^n |x_i - \bar{x}|$,
- mean absolute deviation from the median: $\frac{1}{n} \sum_{i=1}^n |x_i - m|$,
- median absolute deviation from the median: the median of $(|x_1 - m|, |x_2 - m|, \dots, |x_n - m|)$.

15.4.3 Unidimensional Density Estimation (*)

For skewed distributions such as the ones representing incomes, there might be nothing wrong, at least statistically speaking, with very large isolated observations.

For well-separated multimodal distributions on the real line, outliers may sometimes also fall in-between the areas of high density.

Example 15.10 That neither box plots themselves, nor the 1.5IQR rule might not be ideal tools for multimodal data is exemplified in Figure 15.2, where we have a mixture of $N(10, 1)$ and $N(25, 1)$ samples and 4 potential outliers at 0, 15, 45, and 50.

```
x = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/blobs2.txt")
plt.subplot(121)
sns.boxplot(data=x, orient="h", color="lightgray")
plt.subplot(122)
sns.histplot(x, binwidth=1, color="lightgray")
plt.show()
```

Fixed-radius search techniques that we have discussed in Section 8.4 can be used for estimating the underlying probability density function. Given a data sample $\mathbf{x} = (x_1, \dots, x_n)$, let us consider¹⁹⁵

$$\hat{f}_r(z) = \frac{1}{2rn} \sum_{i=1}^n |B_r(z)|,$$

where $|B_r(z)|$ denotes the number of observations from \mathbf{x} whose distance to z is not greater than r , i.e., fall into the interval $[z - r, z + r]$.

```
n = len(x)
r = 1 # radius
```

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¹⁹⁵ This is an instance of a kernel density estimator, with the simplest kernel – a rectangular one.

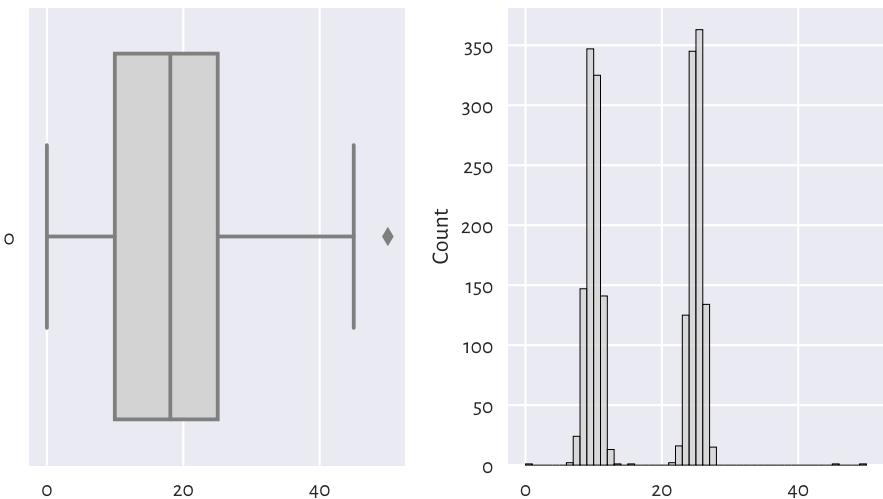


Figure 15.2: With box plots, we may fail to detect some outliers

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```
import scipy.spatial
t = scipy.spatial.KDTree(x.reshape(-1, 1))
dx = pd.Series(t.query_ball_point(x.reshape(-1, 1), r)).str.len() / (2*r*n)
dx[:6] # preview
## 0    0.000250
## 1    0.116267
## 2    0.116766
## 3    0.166667
## 4    0.076098
## 5    0.156188
## dtype: float64
```

Then, points in the sample lying in low-density regions (i.e., all x_i such that $\hat{f}_r(x_i)$ is small) can be marked for further inspection as potential outliers:

```
x[dx < 0.001]
## array([ 0.          , 13.57157922, 15.          , 45.          , 50.          ,])
```

See Figure 15.3 for an illustration of \hat{f}_r . Of course, r should be chosen with care – just like the number of bins in a histogram.

```

sns.histplot(x, binwidth=1, stat="density", color="lightgray")
z = np.linspace(np.min(x)-5, np.max(x)+5, 1001)
dz = pd.Series(t.query_ball_point(z.reshape(-1, 1), r)).str.len() / (2*r*n)
plt.plot(z, dz, label=f"density estimator ($r={r}$)")
plt.show()

```

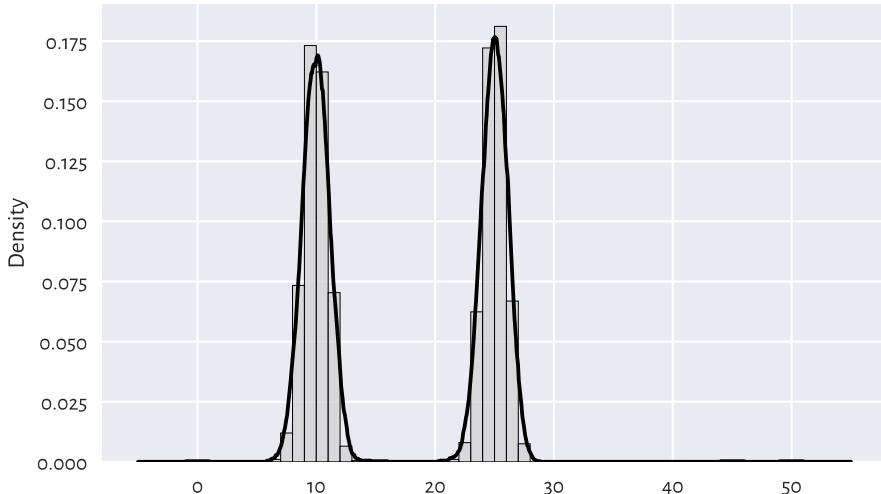


Figure 15.3: Density estimation based on fixed-radius search

15.4.4 Multidimensional Density Estimation (*)

By far we should have got used to the fact that unidimensional data projections might lead to our losing too much information: some values might seem perfectly fine when they are considered in isolation, but already plotting them in 2D reveals the truth.

Consider the following example dataset and the depiction of the distributions of its two natural projections in Figure 15.4.

```

X = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/blobs1.txt", delimiter=",")
plt.figure(figsize=(plt.rcParams["figure.figsize"][0], )*2) # width=height
plt.subplot(221)
sns.boxplot(data=X[:, 0], orient="h", color="lightgray")

```

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```
plt.subplot(222)
sns.histplot(X[:, 0], bins=20, color="lightgray")
plt.title("X[:, 0]")
plt.subplot(223)
sns.boxplot(data=X[:, 1], orient="h", color="lightgray")
plt.subplot(224)
sns.histplot(X[:, 1], bins=20, color="lightgray")
plt.title("X[:, 1]")
plt.show()
```

There is nothing suspicious here. Or is there?

The scatterplot in Figure 15.5 already reveals that the data consist of two quite well-separable blobs:

```
plt.scatter(X[:, 0], X[:, 1])
plt.axis("equal")
plt.show()
```

Also, there are a few observations that we might consider outliers. Yours truly included 8 junk points at the very end of the dataset:

```
X[-8:, :]
## array([[-3. ,  3. ],
##        [ 3. ,  3. ],
##        [ 3. , -3. ],
##        [-3. , -3. ],
##        [-3.5,  3.5],
##        [-2.5,  2.5],
##        [-2. ,  2. ],
##        [-1.5,  1.5]])
```

Thus, handling multidimensional data requires slightly more sophisticated methods. A quite straightforward approach is to check if there are any points within an observation's radius of some assumed size $r > 0$. If that is not the case, we may consider it an outlier. This is a variation on the aforementioned 1-dimensional density estimation approach.

Example 15.11 Consider the following code chunk:

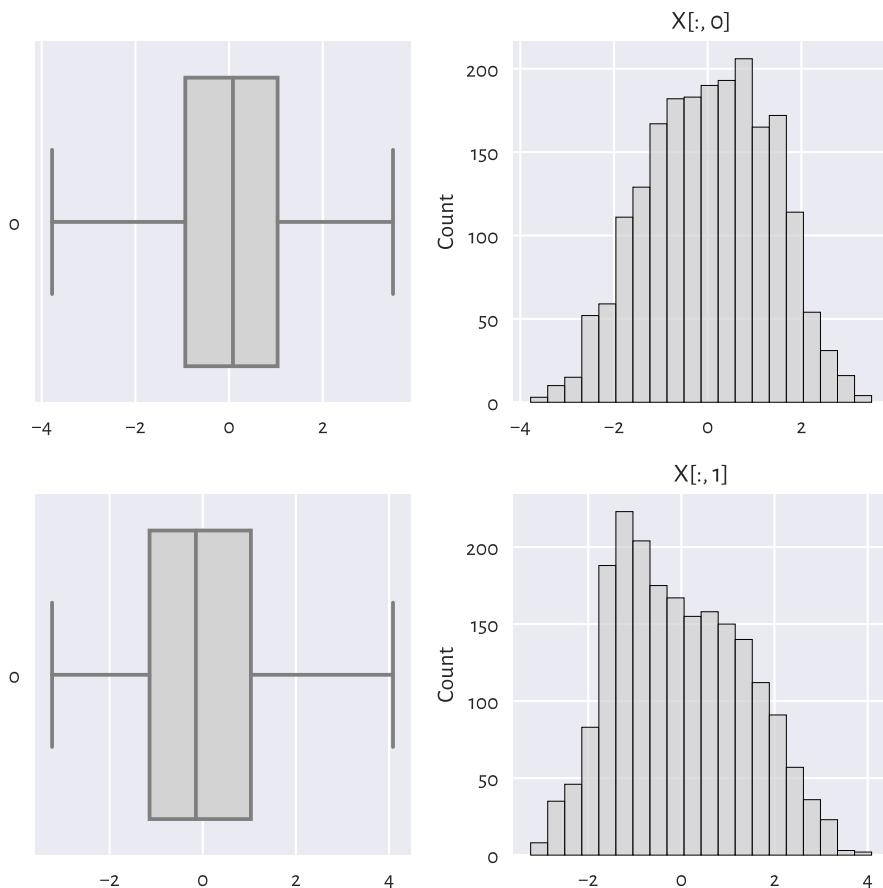


Figure 15.4: One-dimensional projections of the blobs1 dataset

```
t = scipy.spatial.KDTree(X)
n = t.query_ball_point(X, 0.2) # r=0.2 (radius)
c = pd.Series(n).str.len().to_numpy()
c[[0, 1, -2, -1]] # preview
## array([42, 30, 1, 1])
```

$c[i]$ gives the number of points within $X[i, :]$'s r -radius (with respect to the Euclidean distance),

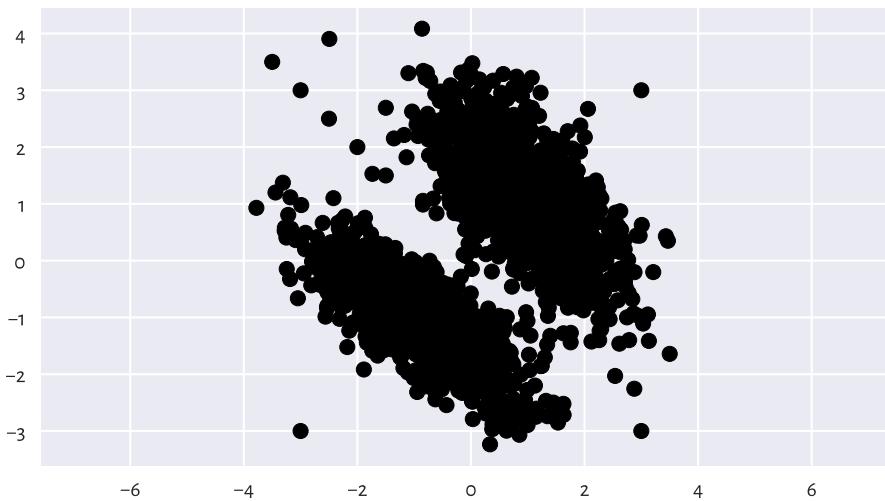


Figure 15.5: Scatterplot of the `blobs1` dataset

including the point itself. Therefore, `c[i]==1` denotes a potential outlier, see [Figure 15.6](#) for an illustration.

```
plt.scatter(X[c > 1, 0], X[c > 1, 1], label="normal point")
plt.scatter(X[c == 1, 0], X[c == 1, 1], marker="v", label="outlier")
plt.axis("equal")
plt.legend()
plt.show()
```

15.5 Exercises

Exercise 15.12 How can missing values be represented in `numpy` and `pandas`?

Exercise 15.13 Explain some basic strategies for dealing with missing values in numeric vectors.

Exercise 15.14 Why we should be very explicit about the way we have handled missing and other suspicious data? Is it a good idea to mark as missing or remove completely the observations that we

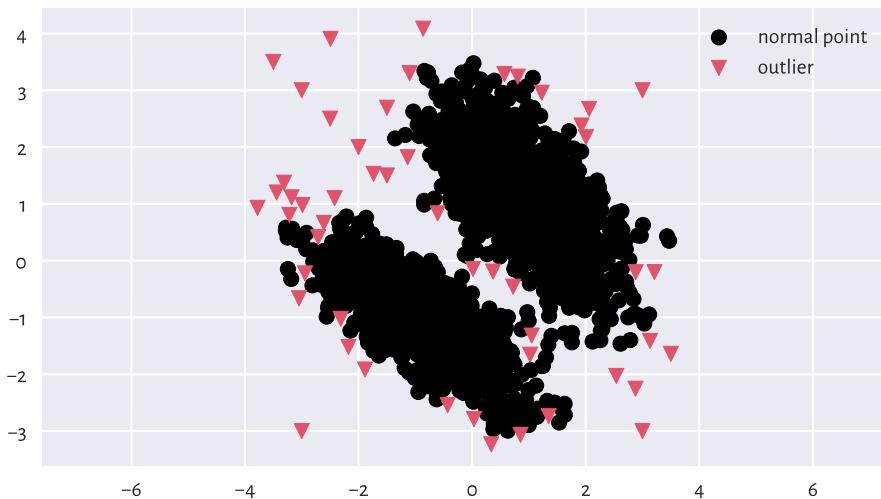


Figure 15.6: Outlier detection based on a fixed-radius search for the `blobs1` dataset

don't like or otherwise deem inappropriate, controversial, dangerous, incompatible with our political views, etc.?

Exercise 15.15 Is replacing missing values with the sample arithmetic mean for income data (as in, e.g., `uk_income_simulated_2020.txt`) a sensible strategy?

Exercise 15.16 What are the differences between data missing completely at random, missing at random, and missing not at random (according to Rubin's [[Rub76]] classification)?

Exercise 15.17 List some basic strategies for dealing with data that might contain outliers.

16

Time Series

So far we have been using **numpy** and **pandas** mostly for storing:

- *independent* measurements, e.g., where each element is a height record of a different subject; we often consider these a sample of a representative subset of one or more populations, each recorded at a particular point in time;
- frequency distributions, i.e., count data and the corresponding categories or labels,
- data to report (as in: tables, figures, heatmaps, etc.).

In this part we'll explore the most basic concepts related to the wrangling of *time series* data – signals indexed by discrete time. Usually a time series is a sequence of measurements sampled at equally spaced moments, e.g., a patient's heart rate probed every second, daily opening stock market prices, or average monthly temperatures recorded in some location.

16.1 Temporal Ordering and Line Charts

Consider the midrange daily temperatures in degrees Celsius at Spokane International Airport (Spokane, WA, US) between 1889-08-01 (first observation) and 2021-12-31 (last observation). Note that midrange, being the mean of the lowest and highest observed temperature on a given day, is not a particularly good estimate of the average daily reading, however, we must work with the data we have.

```
temps = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
 "teaching_data/master/marek/spokane_temperature.txt")
```

Let us preview the December 2021 data:

```
temps[-31:] # last 31 days
## array([-11.9, -5.8, -0.6,  0.8, -1.9, -4.4, -1.9,  1.4, -1.9,
# (continues on next page)
```

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```
##      -1.4,    3.9,    1.9,    1.9,   -0.8,   -2.5,   -3.6,  -10. ,   -1.1,
##     -1.7,   -5.3,   -5.3,   -0.3,    1.9,   -0.6,   -1.4,   -5. ,   -9.4,
##    -12.8,  -12.2,  -11.4,  -11.4])
```

Here are some data aggregates – the popular quantiles:

```
np.quantile(temp, [0, 0.25, 0.5, 0.75, 1])
## array([-26.9,    2.2,    8.6,   16.4,  33.9])
```

as well as the arithmetic mean and standard deviation:

```
np.mean(temp), np.std(temp)
## (8.990273958441023, 9.16204388619955)
```

and a graphical summary of the data distribution in [Figure 16.1](#):

```
sns.violinplot(data=temp, orient="h", color="lightgray")
plt.show()
```

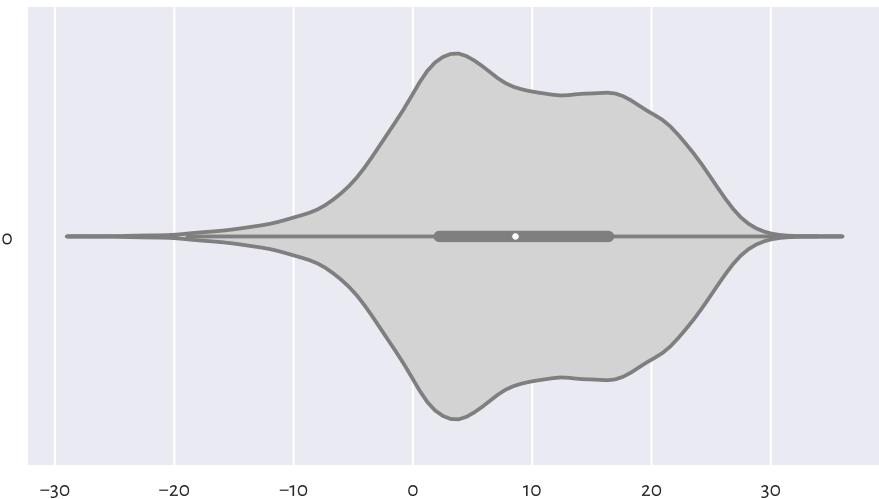


Figure 16.1: Distribution of the midrange daily temperatures in Spokane in the period 1889–2021; observations are treated as a bag of unrelated items (temperature on a “randomly chosen day” in a version of planet Earth where there is no climate change)

Important: Contrary to the *independent* measurements case, we do not have to treat vectors representing time series simply as mixed bags of unrelated items (note that when computing data aggregates or plotting histograms, the order of elements does not matter).

Instead, in time series, for any given item x_i , its neighbouring elements x_{i-1} and x_{i+1} denote the recordings occurring directly before and after it. We can use this *temporal ordering* to model how consecutive measurements *depend* on each other, describe how they change over time, forecast future values, detect long-time trends, and so forth.

Here are the data for 2021, plotted as a function of time:

```
plt.plot(temp[ -365 : ])
plt.xticks([0, 181, 364], ["2021-01-01", "2021-07-01", "2021-12-31"])
plt.show()
```

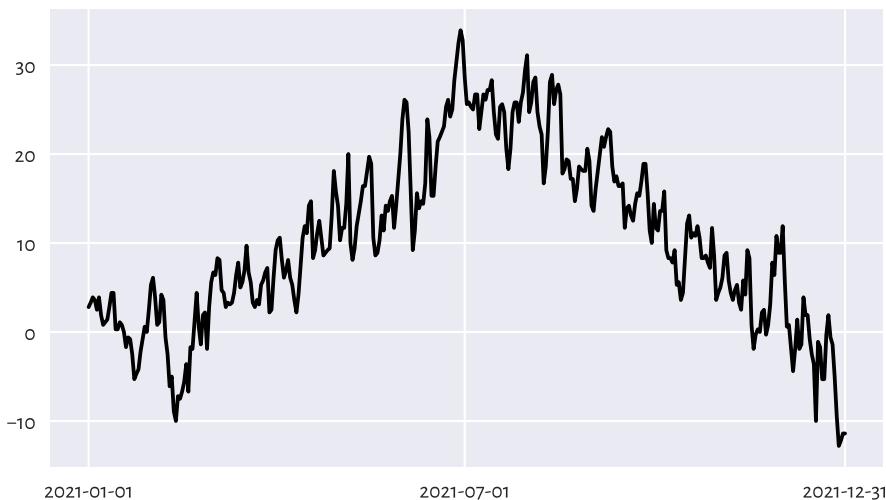


Figure 16.2: Line chart of midrange daily temperatures in Spokane for 2021; plotting data as a function of the time variable reveals some seasonal pattern

What we see in Figure 16.2 is often referred to as a *line chart* – data points are connected by straight line segments. There are some visible seasonal variations, such as that, well, obviously, winter is colder than summer.

16.2 Working with Datetimes and Timedeltas

16.2.1 Representation: The UNIX Epoch

`numpy.datetime64`¹⁹⁶ is a type to represent datetimes. Usually, we'll be creating dates from strings, for instance:

```
d = np.array([
    "1889-08-01", "1970-01-01", "2021-12-31", "today"
], dtype="datetime64")
d
## array(['1889-08-01', '1970-01-01', '2021-12-31', '2022-06-13'],
##       dtype='datetime64[D]')
```

Similarly with datetimes:

```
dt = np.array(["1970-01-01T02:01:05", "now"], dtype="datetime64")
dt
## array(['1970-01-01T02:01:05', '2022-06-13T04:56:53'],
##       dtype='datetime64[s]')
```

Important: Internally, the above are represented as the number of days or seconds since the so-called *Unix Epoch*, 1970-01-01T00:00:00 in the UTC time zone.

Let's verify that:

```
d.astype(float)
## array([-29372.,      0.,   18992.,   19156.])
dt.astype(float)
## array([7.26500000e+03, 1.65509621e+09])
```

Which, when we think about it for a while, is exactly what we expected.

Exercise 16.1 Write a regular expression that extract all dates in the YYYY-MM-DD format from a (possibly long) string and converts them to `datetime64`.

¹⁹⁶ <https://numpy.org/doc/stable/reference/arrays.datetime.html>

16.2.2 Time Differences

Computing datetime differences is possible thanks to the `numpy.timedelta64` objects:

```
d = np.timedelta64(1, "D") # minus 1 Day
## array(['1889-07-31', '1969-12-31', '2021-12-30', '2022-06-12'],
##        dtype='datetime64[D]')
dt + np.timedelta64(12, "h") # plus 12 hours
## array(['1970-01-01T14:01:05', '2022-06-13T16:56:53'],
##        dtype='datetime64[s]')
```

Also, `numpy.arange` (and `pandas.date_range`) can be used to generate sequences of equidistant datetimes:

```
dates = np.arange("1889-08-01", "2022-01-01", dtype="datetime64[D]")
dates[:3] # preview
dates[-3:] # preview
## array(['1889-08-01', '1889-08-02', '1889-08-03'], dtype='datetime64[D]')
## array(['2021-12-29', '2021-12-30', '2021-12-31'], dtype='datetime64[D]')
```

16.2.3 Datetimes in Data Frames

Dates and datetimes can of course be emplaced in `pandas` data frames:

```
spokane = pd.DataFrame(dict(
    date=np.arange("1889-08-01", "2022-01-01", dtype="datetime64[D]"),
    temp=temps
))
spokane.head()
##      date   temp
## 0 1889-08-01  21.1
## 1 1889-08-02  20.8
## 2 1889-08-03  22.2
## 3 1889-08-04  21.7
## 4 1889-08-05  18.3
```

Interestingly, if we ask the `date` column to become the data frame's `.index` (i.e., row labels), we will be able select date ranges quite easily with `loc[...]` and string slices (refer to the manual of `pandas.DateTimeIndex` for more details).

```
spokane.set_index("date").loc["2021-12-25":, :].reset_index()
##      date   temp
```

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```
## 0 2021-12-25 -1.4
## 1 2021-12-26 -5.0
## 2 2021-12-27 -9.4
## 3 2021-12-28 -12.8
## 4 2021-12-29 -12.2
## 5 2021-12-30 -11.4
## 6 2021-12-31 -11.4
```

Example 16.2 Based on the above, we can plot the data for the last 5 years quite easily, see Figure 16.3.

```
x = spokane.set_index("date").loc["2017-01-01":, "temp"]
plt.plot(x)
plt.show()
```

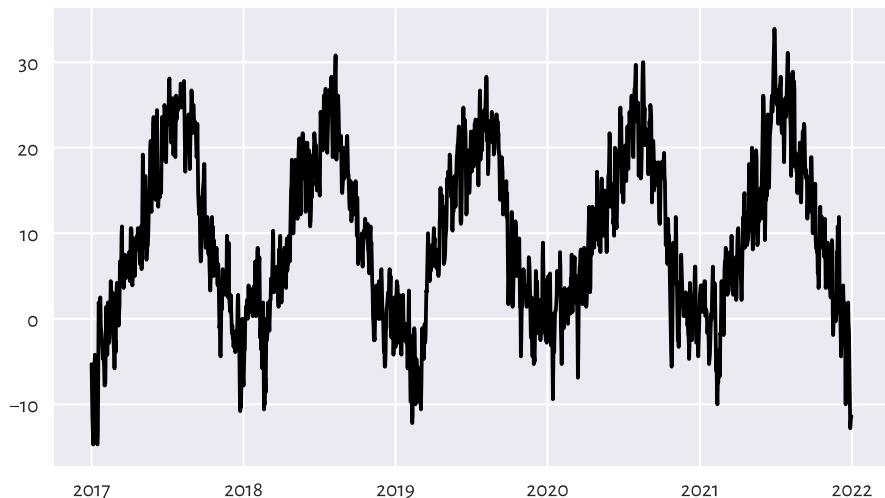


Figure 16.3: Line chart of midrange daily temperatures in Spokane for 2017–2021

Note that now the x-axis labels have been generated automatically.

Note that `pandas.to_datetime` can be used to convert strings to datetime objects:

```
dates = ["1991-04-05", "2021-09-12", "2042-12-31"]
```

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```
dates = pd.Series(pd.to_datetime(dates))
dates
## 0    1991-04-05
## 1    2021-09-12
## 2    2042-12-31
## dtype: datetime64[ns]
```

Exercise 16.3 From the `birth_dates`¹⁹⁷ dataset, select all people less than 18 years old (as of the current day). The `pandas.to_datetime` function can also convert arbitrarily formatted date strings, e.g., "MM/DD/YYYY" or DD.MM.YYYY to `Series` of `datetime64`s.

A number of datetime functions and related properties can be referred to via the `pandas.Series.dt` accessor (similarly to `pandas.Series.str` discussed in Chapter 14). In particular, they are are a convenient means for extracting different date or time fields, such as:

```
dates_ymd = pd.DataFrame(dict(
    year = dates.dt.year,
    month = dates.dt.month,
    day = dates.dt.day
))
dates_ymd
##   year  month  day
## 0  1991      4    5
## 1  2021      9   12
## 2  2042     12   31
```

Interestingly, `pandas.to_datetime` can also convert data frames with columns named `year`, `month`, `day`, etc. back to datetime objects directly:

```
pd.to_datetime(dates_ymd)
## 0    1991-04-05
## 1    2021-09-12
## 2    2042-12-31
## dtype: datetime64[ns]
```

Example 16.4 For instance, we can extract the month and year parts of dates to compute the average monthly temperatures it the last 50-ish years:

¹⁹⁷ https://github.com/gagolews/teaching_data/blob/master/marek/birth_dates.csv

```

x = spokane.set_index("date").loc["1970":, ].reset_index()
mean_monthly_temps = x.groupby([
    x.date.dt.year.rename("year"),
    x.date.dt.month.rename("month")
]).temp.mean().unstack()
mean_monthly_temps.head().round(1)
## month   1   2   3   4   5   6   7   8   9   10  11  12
## year
## 1970 -3.4  2.3  2.8  5.3 12.7 19.0 22.5 21.2 12.3  7.2  2.2 -2.4
## 1971 -0.1  0.8  1.7  7.4 13.5 14.6 21.0 23.4 12.9  6.8  1.9 -3.5
## 1972 -5.2 -0.7  5.2  5.6 13.8 16.6 20.0 21.7 13.0  8.4  3.5 -3.7
## 1973 -2.8  1.6  5.0  7.8 13.6 16.7 21.8 20.6 15.4  8.4  0.9  0.7
## 1974 -4.4  1.8  3.6  8.0 10.1 18.9 19.9 20.1 15.8  8.9  2.4 -0.8

```

Figure 16.4 depicts these data on a heatmap:

```

sns.heatmap(mean_monthly_temps)
plt.show()

```

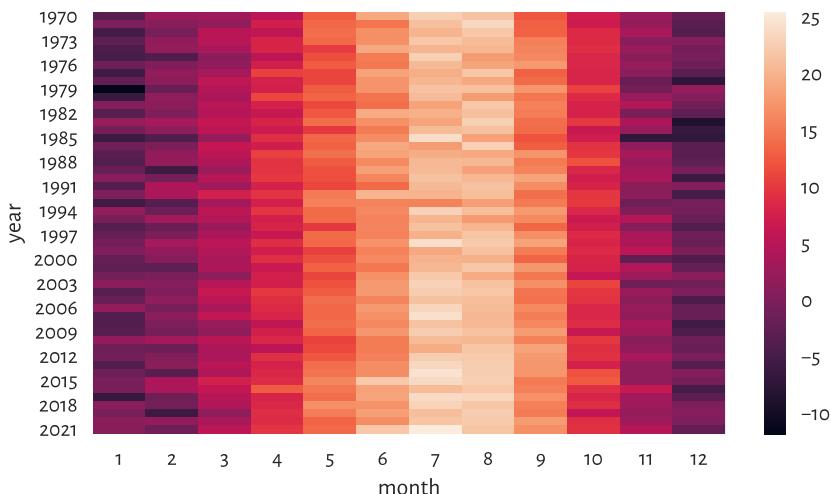


Figure 16.4: Average monthly temperatures

Again we discover the ultimate truth that winters are cold, whereas in the summertime the living is easy, what a wonderful world.

16.2.4 Modelling Event Times with an Exponential Distribution (**)

The exponential distribution family is frequently used for modelling times between different events (i.e., deltas) under the assumption that a system generates on average a constant number of events and that they occur independently of each other.

This may be the case for the times between requests to a cloud service during peak hours, wait times for the next pedestrian to appear at a crossing near the Southern Cross Station in Melbourne, or the amount of time it takes a bank teller to interact with a customer (note that there is a whole branch of applied mathematics – or should we refer to it more fashionably: data science – called queuing theory that deals with this type of modelling).

An exponential family is identified by the scale parameter $s > 0$, being at the same time its expected value. The probability density function of $\text{Exp}(s)$ is given by

$$f(x) = \frac{1}{s} e^{-x/s}$$

for $x \geq 0$ and $f(x) = 0$ otherwise. We should be careful: some textbooks choose the parametrisation by $\lambda = 1/s$ instead of s ; also **scipy** uses this convention.

Here is a pseudorandom sample where there are 5 events per minute on average:

```
np.random.seed(123)
λ = 60/5 # 5 events per 60 seconds on average
d = scipy.stats.expon.rvs(size=1200, scale=λ)
np.round(d[:8], 3) # preview
## array([14.307, 4.045, 3.087, 9.617, 15.253, 6.601, 47.412, 13.856])
```

This gave us the wait times between the events (deltas), in seconds.

A natural sample estimator of the scale parameter is of course:

```
np.mean(d)
## 11.839894504211724
```

Which is close to what we *expect*, i.e., 12 seconds between the events.

We can convert the above to datetime (starting at a fixed calendar date), e.g., as follows:

```
t0 = np.array("2022-01-01T00:00:00", dtype="datetime64[ms]")
d_ms = np.round(d*1000).astype(int) # in milliseconds
t = t0 + np.array(np.cumsum(d_ms), dtype="timedelta64[ms]")
```

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```
t[:8], t[-2:] # preview
## (array(['2022-01-01T00:00:14.307', '2022-01-01T00:00:18.352',
##          '2022-01-01T00:00:21.439', '2022-01-01T00:00:31.056',
##          '2022-01-01T00:00:46.309', '2022-01-01T00:00:52.910',
##          '2022-01-01T00:01:40.322', '2022-01-01T00:01:54.178'],
##         dtype='datetime64[ms]'), array(['2022-01-01T03:56:45.312', '2022-01-
-01T03:56:47.890'],
##         dtype='datetime64[ms]'))
```

W converted the deltas to milliseconds so that we didn't lose precision; `datetime64` is based on integers, not floating-point numbers.

As an exercise, let's apply binning and count how many events occur in each hour:

```
b = np.arange(
    "2022-01-01T00:00:00", "2022-01-01T05:00:00",
    1000*60*60, # number of milliseconds in 1 hour
    dtype="datetime64[ms]"
)
np.histogram(t, bins=b)
## (array([305, 300, 274, 321]), array(['2022-01-01T00:00:00.000', '2022-01-
-01T01:00:00.000',
##          '2022-01-01T02:00:00.000', '2022-01-01T03:00:00.000',
##          '2022-01-01T04:00:00.000'], dtype='datetime64[ms]'))
```

We expect 5 events per second, hence, 300 of them per hour. On a side note, from a course in statistics we know that for exponential inter-event times, the number of events per unit of time follows a Poisson distribution.

Exercise 16.5 (***) Consider the `wait_times`¹⁹⁸ dataset that gives the times between consecutive events, in seconds. Estimate the event rate per hour. Draw a histogram representing the number of events per hour.

¹⁹⁸ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/wait_times.txt

16.3 Basic Operations

16.3.1 Iterative Differences and Cumulative Sums Revisited

Recall the `numpy.diff` function and its almost-inverse, `numpy.cumsum`. The former can turn a time series into a vector of *relative changes* (also called *deltas*, $\Delta_i = x_{i+1} - x_i$).

```
x = temps[-7:] # last 7 days
x
## array([-1.4, -5. , -9.4, -12.8, -12.2, -11.4, -11.4])
```

The iterative differences (deltas) are:

```
d = np.diff(x)
d
## array([-3.6, -4.4, -3.4,  0.6,  0.8,  0. ])
```

For instance, between the second and the first day of the last week, the midrange temperature dropped by -3.6°C .

The other way around, here the cumulative sums of the deltas:

```
np.cumsum(d)
## array([-3.6, -8. , -11.4, -10.8, -10. , -10. ])
```

This turned deltas back to a shifted version of the original series. However, we will need the first (root) observation therefrom to restore the dataset in full.

```
x[0] + np.append(0, np.cumsum(d))
## array([-1.4, -5. , -9.4, -12.8, -12.2, -11.4, -11.4])
```

Exercise 16.6 Consider the `euraud-20200101-20200630-no-na`¹⁹⁹ dataset which lists daily EUR/AUD exchange rates in the first half of 2020 (remember COVID-19?), with missing observations removed. Using `numpy.diff`, compute the minimal, median, average, and maximal daily price changes. Also, draw a box and whisker plot for these deltas.

Exercise 16.7 (*) Consider the `btcusd_ohlcv_2021_dates`²⁰⁰ dataset which gives the daily BTC/USD exchange rates in 2021:

¹⁹⁹ https://raw.githubusercontent.com/gagolews/teaching_data/master/marek/euraud-20200101-20200630-no-na.txt

²⁰⁰ https://github.com/gagolews/teaching_data/blob/master/marek/btcusd_ohlcv_2021_dates.csv

```

btc = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/btcusd_ohlcv_2021_dates.csv",
    comment="#").loc[:, ["Date", "Close"]]
btc["Date"] = btc["Date"].astype("datetime64[D]")
btc.head(12)
##           Date      Close
## 0 2021-01-01 29374.152
## 1 2021-01-02 32127.268
## 2 2021-01-03 32782.023
## 3 2021-01-04 31971.914
## 4 2021-01-05 33992.430
## 5 2021-01-06 36824.363
## 6 2021-01-07 39371.043
## 7 2021-01-08 40797.609
## 8 2021-01-09 40254.547
## 9 2021-01-10 38356.441
## 10 2021-01-11 35566.656
## 11 2021-01-12 33922.961

```

Convert it to a “lagged” representation, being a convenient form for some machine learning algorithms:

1. Add the *Change* column giving by how much the price changed since the previous day.
2. Add the *Dir* column indicating if the change was positive or negative.
3. Add the *Lag1*, ..., *Lag5* columns which give the *Changes* in the 5 preceding days.

The first few rows of the resulting data frame should look like this (assuming we do not want any missing values):

```

##           Date      Close     Change Dir      Lag1      Lag2      Lag3      Lag4      Lag5
## 2021-01-07 39371  2546.68 inc  2831.93  2020.52 -810.11  654.76 2753.12
## 2021-01-08 40798  1426.57 inc  2546.68  2831.93  2020.52 -810.11  654.76
## 2021-01-09 40255 -543.06 dec  1426.57  2546.68  2831.93  2020.52 -810.11
## 2021-01-10 38356 -1898.11 dec -543.06  1426.57  2546.68  2831.93  2020.52
## 2021-01-11 35567 -2789.78 dec -1898.11 -543.06  1426.57  2546.68  2831.93
## 2021-01-12 33923 -1643.69 dec -2789.78 -1898.11 -543.06  1426.57  2546.68

```

Note that in the 6th row (representing 2021-01-12), *Lag1* corresponds to *Change* on 2021-01-11, *Lag2* gives the *Change* on 2021-01-10, and so forth.

To spice things up, make sure your code can generate any number, say *k* of lagged variables.

16.3.2 Smoothing with Moving Averages

With time series it makes sense to consider batches of consecutive points as there is a time dependence between them. In particular, we can consider computing different aggregates inside *rolling windows* of a particular size.

For example, given sequence (x_1, x_2, \dots, x_n) and some $k \leq n$, the k -moving average is a vector $(y_1, y_2, \dots, y_{n-k+1})$ such that

$$y_i = \frac{1}{k} \sum_{j=1}^k x_{i+j-1},$$

i.e., the arithmetic mean of k consecutive observations starting at x_i .

For example, here are the temperatures in the last 7 days of December 2011:

```
x = spokane.set_index("date").iloc[-7:, :]
x
##           temp
## date
## 2021-12-25 -1.4
## 2021-12-26 -5.0
## 2021-12-27 -9.4
## 2021-12-28 -12.8
## 2021-12-29 -12.2
## 2021-12-30 -11.4
## 2021-12-31 -11.4
```

The 3-moving average:

```
x.rolling(3, center=True).mean().round(2)
##           temp
## date
## 2021-12-25    NaN
## 2021-12-26 -5.27
## 2021-12-27 -9.07
## 2021-12-28 -11.47
## 2021-12-29 -12.13
## 2021-12-30 -11.67
## 2021-12-31    NaN
```

We get, in this order: the mean of the first 3 observations; the mean of the 2nd, 3rd, and

4th items; then the mean of the 3rd, 4th, and 5th; and so forth. Note that we have centred the observations in such a way that we have the same number of missing values at the start and end of the series. This way, we treat the first 3-day moving average (the average of the temperatures on the first 3 days) as representative for the 2nd day.

And now for something completely different; the 5-moving average:

```
x.rolling(5, center=True).mean().round(2)
##                      temp
## 2021-12-25      NaN
## 2021-12-26      NaN
## 2021-12-27 -8.16
## 2021-12-28 -10.16
## 2021-12-29 -11.44
## 2021-12-30      NaN
## 2021-12-31      NaN
```

Applying the moving average has the nice effect of *smoothing* out all kinds of broadly-conceived noise. To illustrate this, compare the temperature data for the last 5 years in Figure 16.3 and in Figure 16.5.

```
x = spokane.set_index("date").loc["2017-01-01":, "temp"]
x30 = x.rolling(30, center=True).mean()
x100 = x.rolling(100, center=True).mean()
plt.plot(x30, label="30-day moving average")
plt.plot(x100, "r--", label="100-day moving average")
plt.legend()
plt.show()
```

Exercise 16.8 (*) Other aggregation functions can be applied in rolling windows too. Draw, in the same figure, the plots of the 1-year moving minimums, medians, and maximums.

16.3.3 Detecting Trends and Seasonal Patterns

Thanks to windowed aggregation, we can also detect general trends (when using longish windows). For instance, below we compute (but plot later) 10-year moving averages for the last 50-odd years worth of data:

```
x = spokane.set_index("date").loc["1970-01-01":, "temp"]
x10y = x.rolling(3653, center=True).mean()
```

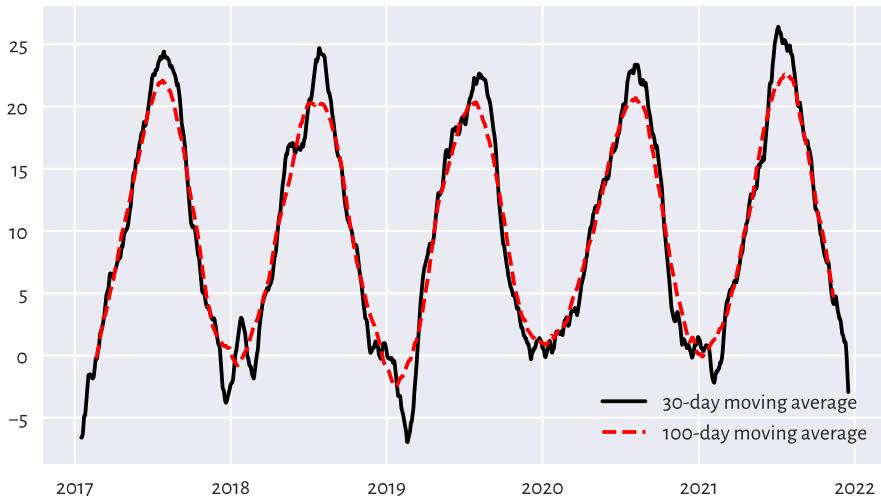


Figure 16.5: Line chart of 30- and 100-moving averages of the midrange daily temperatures in Spokane for 2017-2021

Based on this, we can compute detrended series:

```
xd = x - x10y
```

Seasonal patterns can be revealed by smoothening out the detrended version of the data, e.g., using a 1-year moving average:

```
xd1y = xd.rolling(365, center=True).mean()
```

See Figure 16.6 for an illustration:

```
plt.plot(x10y, label="trend")
plt.plot(xd1y, "r--", label="seasonal pattern")
plt.legend()
plt.show()
```

Also, if we know the length of the seasonal pattern (in our case, 365-ish days), we can draw a seasonal plot, where we have a separate curve for each season (here: year) and all series share the same x-axis (here: day of year), see Figure 16.7.

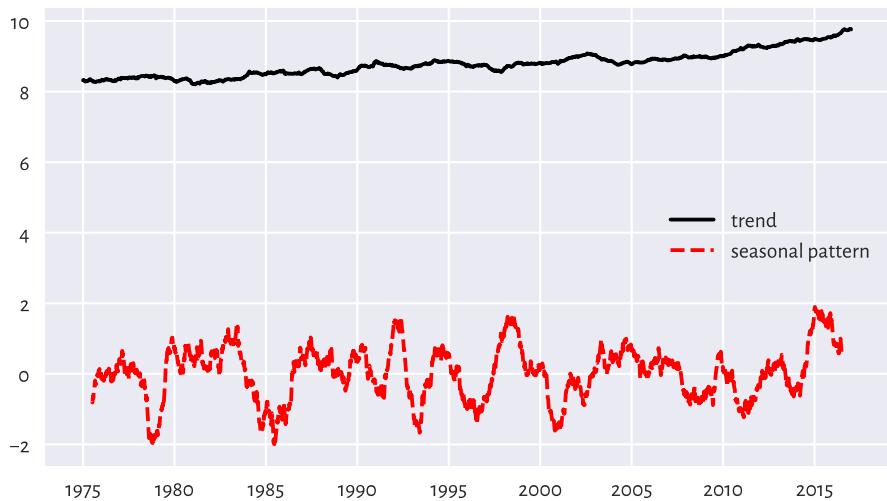


Figure 16.6: Trend and seasonal pattern for the Spokane temperatures in recent years

```
from matplotlib import cm
cmap=cm.get_cmap("coolwarm")
x = spokane.set_index("date").loc["1970-01-01":, :].reset_index()
for year in range(1970, 2022, 5):
    y = x.loc[x.date.dt.year == year, :]
    plt.plot(y.date.dt.day_of_year, y.temp,
              c=cmap((year-1970)/(2021-1970)), alpha=0.3,
              label=year if year % 10 == 0 else None)
avex = x.temp.groupby(x.date.dt.day_of_year).mean()
plt.plot(avex.index, avex, "g-", label="Average")
plt.legend()
plt.xlabel("Day of year")
plt.ylabel("Temperature")
plt.show()
```

16.3.4 Imputing Missing Values

Missing values in time series can use the information from the neighbouring non-missing observations. After all, it is usually the case that, e.g., today's weather is "similar" to yesterday's and tomorrow's.

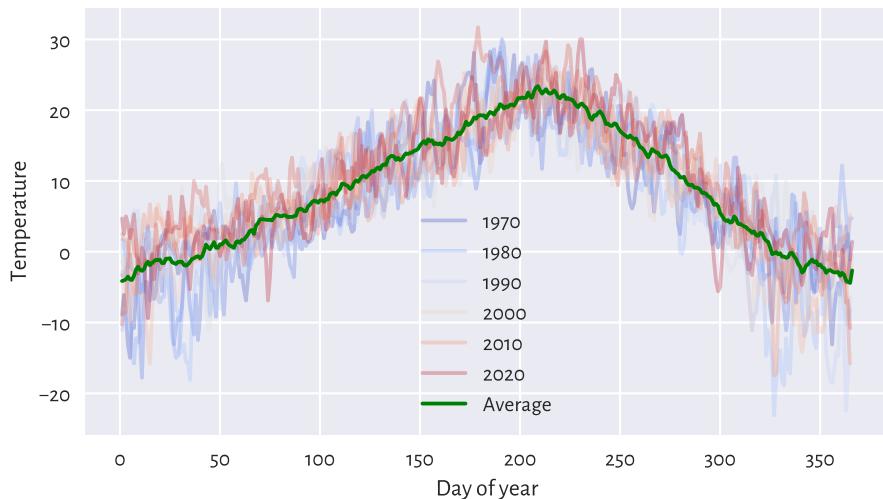


Figure 16.7: An example seasonal plot: Spokane temperatures vs day of year between 1970 and 2021

The most straightforward ways for dealing with missing values in time series are:

- *forward-fill* – propagate the last non-missing observation,
- *backward-fill* – get the next non-missing value,
- *linearly interpolate between two adjacent non-missing values* – in particular, a single missing value will be replaced by the average of its neighbours.

Example 16.9 The classic `air_quality_1973`²⁰¹ dataset gives some daily air quality measurements in New York, between May and September 1973. As an example, let's impute a first few observations in the solar radiation column:

```
air = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/r/air_quality_1973.csv",
    comment="#")
x = air.loc[:, "Solar.R"].iloc[:12]
pd.DataFrame(dict(
    original=x,
```

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²⁰¹ https://github.com/gagolews/teaching_data/blob/master/r/air_quality_1973.csv

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```

ffilled=x.fillna(method="ffill"),
bfilled=x.fillna(method="bfill"),
interpolated=x.interpolate(method="linear"))

##      original    ffilled    bfilled  interpolated
## 0      190.0      190.0      190.0     190.000000
## 1      118.0      118.0      118.0     118.000000
## 2      149.0      149.0      149.0     149.000000
## 3      313.0      313.0      313.0     313.000000
## 4       NaN      313.0      299.0     308.333333
## 5       NaN      313.0      299.0     303.666667
## 6      299.0      299.0      299.0     299.000000
## 7       99.0       99.0       99.0      99.000000
## 8       19.0       19.0       19.0      19.000000
## 9      194.0      194.0      194.0     194.000000
## 10      NaN      194.0      256.0     225.000000
## 11      256.0      256.0      256.0     256.000000

```

Exercise 16.10 (*) With the `air_quality_2018`²⁰² dataset:

1. Based on the hourly observations, compute the daily mean PM2.5s for Melbourne CBD and Morwell South.

For Melbourne CBD, if some hourly measurement is missing, linearly interpolate between the preceding and following non-missing data, e.g., a PM2.5 sequence of `[..., 10, NaN, NaN, 40, ...]` (you need to manually add the `NaN` rows to the dataset) should be transformed to `[..., 10, 20, 30, 40, ...]`.

For Morwell South, impute the reading as an average of the records in the nearest air quality stations, located in Morwell East, Moe, Churchill, or Traralgon.

2. Present the daily mean PM2.5 measurements for Melbourne CBD and Morwell South on a single plot. The x-axis labels should be human-readable and intuitive.
3. For the Melbourne data, count on how many days the average PM2.5 was greater than in the preceding day.
4. Find 5 most air-polluted days for Melbourne.

²⁰² https://github.com/gagolews/teaching_data/blob/master/marek/air_quality_2018.csv.gz

16.3.5 Plotting Multidimensional Time Series

Multidimensional time series stored in form of an n -by- m matrix are best viewed as m time series – possibly but not necessarily somehow related to each other – all sampled at the same n points in time (e.g., m different stocks on n consecutive days).

Consider the currency exchange rates for the first half of 2020:

```
eurxxx = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/eurxxx-20200101-20200630-no-na.csv",
    delimiter=",")
eurxxx[:6, :] # preview
## array([[1.6006 , 7.7946 , 0.84828, 4.2544 ],
##        [1.6031 , 7.7712 , 0.85115, 4.2493 ],
##        [1.6119 , 7.8049 , 0.85215, 4.2415 ],
##        [1.6251 , 7.7562 , 0.85183, 4.2457 ],
##        [1.6195 , 7.7184 , 0.84868, 4.2429 ],
##        [1.6193 , 7.7011 , 0.85285, 4.2422 ]])
```

This gives EUR/AUD (how many Australian Dollars we pay for 1 Euro), EUR/CNY (Chinese Yuans), EUR/GBP (British Pounds), and EUR/PLN (Polish Złotys), in this order. Let's draw the four time series, see Figure 16.8.

```
dates = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/euraud-20200101-20200630-dates.txt",
    dtype="datetime64")
labels = ["AUD", "CNY", "GBP", "PLN"]
styles = ["solid", "dotted", "dashed", "dashdot"]
for i in range(eurxxx.shape[1]):
    plt.plot(dates, eurxxx[:, i], ls=styles[i], label=labels[i])
plt.legend()
plt.show()
```

Unfortunately, they are all on different scales, hence the plot is not necessarily readable. It would be better to draw these time series on 4 separate plots (compare the trellis plots in Section 12.2.5).

Another idea is to depict the currency exchange rates *relative* to the prices on some day, say, the first one; see Figure 16.9.

```
for i in range(eurxxx.shape[1]):
    plt.plot(dates, eurxxx[:, i]/eurxxx[0, i],
              ls=styles[i], label=labels[i])
```

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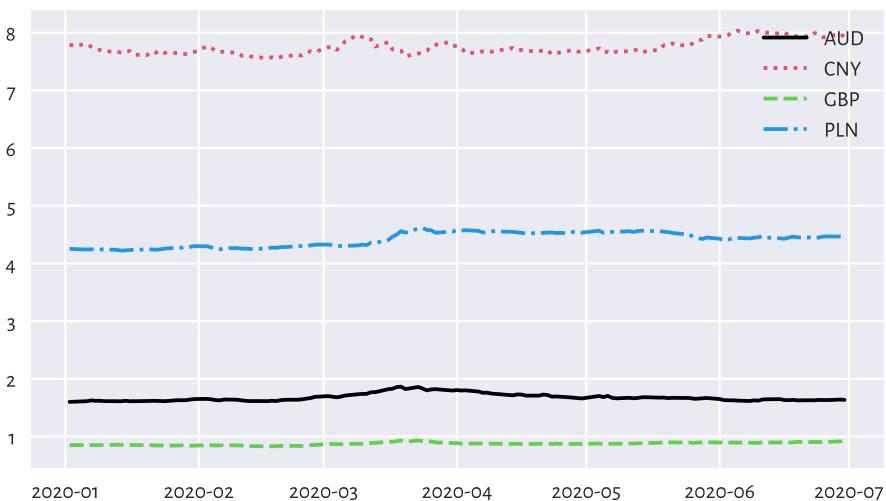


Figure 16.8: EUR/AUD, EUR/CNY, EUR/GBP, and EUR/PLN exchange rates in the first half of 2020

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```
plt.legend()  
plt.show()
```

This way, e.g., relative EUR/AUD rate of ca. 1.15 in mid-March denotes means that if an Australian bought some Euros on the first day and then sold them three-ish months later, they would have 15% more currency (the Euro became 15% stronger relative to AUD).

Exercise 16.11 Based on EUR/AUD and EUR/PLN rates, compute and plot the AUD/PLN as well as PLN/AUD ones.

Exercise 16.12 (*) Draw the EUR/AUD and EUR/GBP rates on a single plot, but with each series having its own²⁰³ y axis.

Exercise 16.13 (*) Draw the EUR/xxx rates for your favourite currencies over a larger period of

²⁰³ https://matplotlib.org/stable/gallery/subplots_axes_and_figures/secondary_axis.html

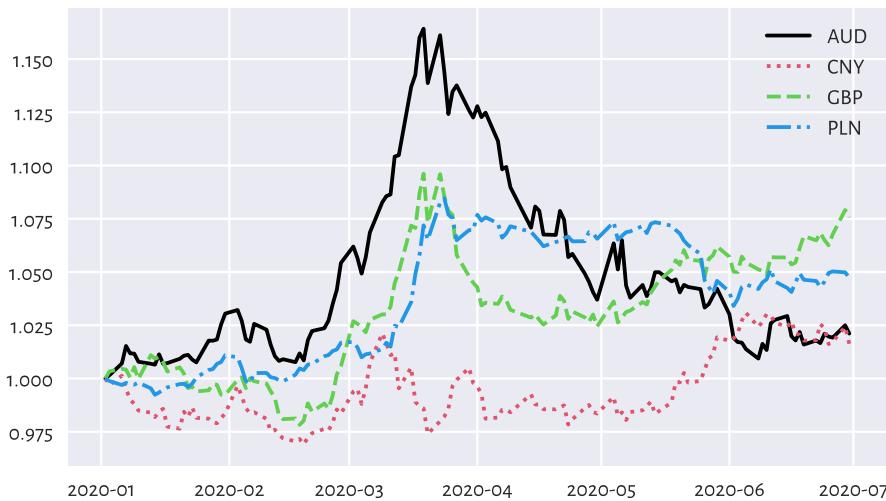


Figure 16.9: EUR/AUD, EUR/CNY, EUR/GBP, and EUR/PLN exchange rates relative to the prices on the first day

time. Use [data²⁰⁴](#) downloaded from the European Central Bank. Add a few moving averages. For each year, identify the lowest and the highest rate.

16.3.6 Candlestick Plots (*)

Consider the BTC/USD data for 2021:

```
btcusd = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
    "teaching_data/master/marek/btcusd_ohlcv_2021.csv",
    delimiter=",")
btcusd[:6, :4] # preview
## array([[28994.01, 29600.627, 28803.586, 29374.152],
##        [29376.455, 33155.117, 29091.182, 32127.268],
##        [32129.408, 34608.559, 32052.316, 32782.023],
##        [32810.949, 33440.219, 28722.756, 31971.914],
##        [31977.041, 34437.59, 30221.188, 33992.43],
##        [34013.613, 36879.699, 33514.035, 36824.363]])
```

²⁰⁴ https://www.ecb.europa.eu/stats/policy_and_exchange_rates/euro_reference_exchange_rates/html/index.en.html

This gives the open, high, low, close prices on the 365 consecutive days (we skipped the marked volume column for readability), which is a common way to summarise daily rates.

The `mplfinance`²⁰⁵ package (**matplotlib-finance**) features a few functions related to the plotting of financial data. Here, let us briefly mention the candlestick plot.

```
import mplfinance as mpf
dates = np.arange("2021-01-01", "2022-01-01", dtype="datetime64[D]")
mpf.plot(pd.DataFrame(
    btcusd,
    columns=["Open", "High", "Low", "Close", "Volume"])
.set_index(dates).iloc[:31, :], type="candle", style="charles")
# plt.show() # not needed...
```



Figure 16.10: Candlestick plot for the BTC/USD exchange rates in January 2021

Figure 16.10 depicts the January 2021 data. Note that this is not a box and whisker plot.

²⁰⁵ <https://github.com/matplotlib/mplfinance>

The candlestick body denotes the difference in the market opening and the closing price. The wicks (shadows) give the range (high to low).

Green candlesticks represent bullish days – where the closing rate is greater than the opening one (uptrend). Red candles are bearish (decline)

Exercise 16.14 Draw the BTC/USD rates for the whole year and add the 10-day moving averages.

Exercise 16.15 (*) Draw a candlestick plot manually, without using the `mplfinance` package. `matplotlib.pyplot.fill` might be helpful.

Exercise 16.16 (*) Using `matplotlib.pyplot.fill_between` add a semi-transparent polygon that fills the area bounded between the Low and High prices on all the days.

16.4 Notes on Signal Processing (Audio, Image, Video) (*)

Data science classically deals with information that is or can be represented in tabular form and where particular observations (which can be multidimensional) are usually independent from but still somewhat similar to each other. We often treat them as samples from different larger populations which we would like to describe or compare at some level of generality (think: health data on patients being subject to two treatment plans that we wish to evaluate).

From this perspective, time series which we have briefly touched upon above are already quite distinct, because there is some dependence observed in the time domain: a price of a stock that we observe today is influenced by what was happening yesterday. There might also be some seasonal patterns or trends under the hood. Still, for data of this kind, employing statistical modelling techniques (*stochastic processes*) still can make sense.

Signals such as audio, images, and video, are slightly different, because *structured randomness* does not play dominant role there (unless it's noise that we would like to filter out). Instead, what is happening in the frequency (think: perceiving pitches when listening to music) or spatial (seeing green grass and sky on a photo) domain will play key role there.

Signal processing thus requires a quite distinct set of tools, e.g., Fourier analysis and finite impulse response (discrete convolution) filters. This course obviously cannot be about everything (also because it requires some more advanced calculus skills that we didn't assume the reader to have at this time). Therefore, see, e.g., [[Smio2]], [Ste96].

Nevertheless, we should keep in mind that these are not completely independent domains. For example, we can extract various features of audio signals (e.g., overall loudness, timbre, and danceability of each recording in a large song database) and then treat them as tabular data to be analysed using the techniques described in this course. Moreover, machine learning (e.g., deep convolutional neural networks) algorithms may also be used for tasks such as object detection on images or optical character recognition.

Note: Some Python packages for signal processing worth inspecting include:

- `scipy.signal` and `scipy.ndimage`,
 - `pillow`²⁰⁶ (PIL),
 - `scikit-image`²⁰⁷,
 - `OpenCV`²⁰⁸ (a C++ library for image and video processing with Python bindings).
-

16.5 Further Reading

Note that due to limited spacetime, we merely touched upon the most basic methods for dealing with time series. The reader is encouraged to take a look at the broad literature concerning statistical analysis of time series (e.g., issues in forecasting, [[HA21], [OFK17]]) as well as on signal processing (e.g., [[Smio2], [Ste96]]); their toolkits somewhat overlap.

For probabilistic modelling, see textbooks on stochastic processes, e.g., [[Tij03]].

16.6 Exercises

Exercise 16.17 Let's say we have a time series with n observations. What is a 1- and an n -moving average? Which one is smoother, an $(0.01n)$ - or a $(0.1n)$ - one?

²⁰⁶ <https://pillow.readthedocs.io>

²⁰⁷ <https://scikit-image.org/>

²⁰⁸ <https://www.opencv.org>

Exercise 16.18 *What is the Unix Epoch?*

Exercise 16.19 *How can we recreate the original series when we are given its `numpy.diff`-transformed version?*

Exercise 16.20 (*) *In your own words, describe the key elements of a candlestick plot.*

Part VI

Appendix

A

Changelog

Important: This book is still a work in progress. It is already quite readable, but there will be more, especially related to the processing of multidimensional data. Stay tuned. Any bug/typos reports/fixes²⁰⁹ are appreciated.

Below is the list of the most noteworthy changes.

- **2022-06-13 (v0.5.1):**

- The Kolmogorov–Smirnov Test (one and two sample).
- The Pearson Chi-Squared Test (one and two sample and for independence).
- Dealing with round-off and measurement errors.
- Adding white noise (jitter).
- Lambda expressions.
- Matrices are iterable.

- **2022-05-31 (v0.4.1):**

- The Rules.
- Matrix multiplication, dot products.
- Euclidean distance, few-nearest-neighbour and fixed-radius search.
- Aggregation of multidimensional data.
- Regression with k -nearest neighbours.
- Least squares fitting of linear regression models.
- Geometric transforms; orthonormal matrices.
- SVD and dimensionality reduction/PCA.

²⁰⁹ https://github.com/gagolews/datawranglingpy/blob/master/CODE_OF_CONDUCT.md

- Classification with k -nearest neighbours.
 - Clustering with k -means.
 - Text Processing and Regular Expression chapters were merged.
 - Unidimensional Data Aggregation and Transformation chapters were merged.
 - `pandas.GroupBy` objects are iterable.
 - Semitransparent histograms.
 - Contour plots.
 - Argument unpacking and variadic arguments (`*args, **kwargs`).
- 2022-05-23 (v0.3.1):
 - More lightweight mathematical notation.
 - Some equalities related to the mathematical functions we rely on (the natural logarithm, cosine, etc.).
 - A way to compute the most correlated pair of variables.
 - A note on modifying elements in an array and on adding new rows and columns.
 - An example seasonal plot in the time series chapter.
 - Solutions to the SQL exercises added; using `pandas.testing.assert_frame_equal` instead of `pandas.DataFrame.equals` to ignore small round-off errors.
 - More details on file paths.
 - 2022-04-12 (v0.2.1):
 - Many chapters merged or relocated.
 - Added captions to all figures.
 - Improved formatting of elements (information boxes such as *note*, *important*, *exercise*, *example*).
 - 2022-03-27 (v0.1.1):
 - First public release – most chapters are drafted, more or less.
 - Using `Sphinx` for building.
 - 2022-01-05 (v0.0.0):
 - Project started (lecture notes for my students at Deakin).

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