Minimalist Data Wrangling with Python [DRAFTvo.1]

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Marek Gagolewski

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Minimalist Data Wrangling with Python is a very-early-and-rough-draft of the forthcoming (ETA 2023) textbook by Marek Gagolewski¹. It is distributed in the hope that it will be useful. If you detect any bugs or typos, please share them by email². 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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You can access this book at:

- https://datawranglingpy.gagolewski.com/ (a browser-friendly version)
- https://datawranglingpy.gagolewski.com/datawranglingpy.pdf (PDF)
- https://github.com/gagolews/datawranglingpy (source code)

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/



Preface

0.1 The Art of Data Wrangling

The broadly-conceived data science 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.

Here are some application domains where data-driven decision making, modelling, and prediction has already proven itself very useful:

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

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.

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. There are NGOs. Finally, 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.

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., text, time series) gathered from structured and unstructured sources,
- cleaning data by identifying outliers,
- · handling missing data,
- transforming, selecting, and extracting features, dimensionality reduction,
- identifying naturally occurring data clusters,
- applying sampling techniques,
- data modelling using basic machine learning algorithms,
- maintaining data privacy and exercising ethics in data manipulation.

0.2 Aims and Scope

Most of the time during the course of this course, we will be writing code in Python⁵. The 2021 StackOverflow Developer Survey⁶ 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

⁵ https://www.python.org/

⁶ https://insights.stackoverflow.com/survey/2021#technology-most-popular-technologies

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data wrangling techniques. This is possible thanks to the famous⁷ high quality packages written by the devoted community of open source programmers, including but not limited to numpy⁸, scipy⁹, pandas¹⁰, matplotlib¹¹, seaborn¹², and sklearn¹³.

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 became a qualified and respected engineer by simply *reading* online tutorials or books.

Of course, Python and third-party packages written therein is amongst many software tools which can help gain new knowledge from data. Other open source choices include, e.g., \mathbb{R}^{14} and Julia¹⁵. There are also some commercial solutions available on the market, but we believe that ultimately all software should be free¹⁶.

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 *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 specialists¹⁷. Money does not bring joy, but luckily it is a very interesting domain anyway!

All that we shall learn can be used for improving different processes, in research, helping NGOs, debunking false news or wishful thinking, maintaining quality of various

⁷ https://insights.stackoverflow.com/survey/2021#other-frameworks-and-libraries

⁸ https://numpy.org/

⁹ https://scipy.org/

¹⁰ https://pandas.pydata.org/

¹¹ https://matplotlib.org/

¹² https://seaborn.pydata.org/

¹³ https://scikit-learn.org/

¹⁴ https://www.r-project.org/

¹⁵ https://julialang.org/

¹⁶ https://www.gnu.org/philosophy/free-sw.en.html

¹⁷ https://insights.stackoverflow.com/survey/2021#other-frameworks-and-libraries

industrial processes, and doing any other good deeds for the advancement of humanity.

We're 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 should thus be too.

0.3 About the Author

I, Marek Gagolewski¹⁸ (pronounced like Mark Gaggle-Eve-Ski), am 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 Faculty of Mathematics and Information Science, Warsaw University of Technology, Poland.

I'm actively involved in developing *usable* free (libre, independent) and open source software, with particular focus on data science and machine learning. He is the main author and maintainer of stringi¹⁹ – one of the most often downloaded R packages that aims at natural language and string processing as well as the Python and R package genieclust²⁰ implementing the fast and robust hierarchical clustering algorithm *Genie* with noise point detection.

I'm an author of over 80 publications on machine learning and optimisation algorithms, data aggregation and clustering, statistical modelling, and scientific computing. I taught various courses related to R and Python programming, algorithms, data science, and machine learning in Australia, Poland, and Germany.

¹⁸ https://www.gagolewski.com

¹⁹ https://stringi.gagolewski.com

²⁰ https://genieclust.gagolewski.com

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0.4 Acknowledgements

This book has been prepared with TeX (XeLaTeX) and Sphinx. Python code chunks have been processed with the R package **knitr**. A little help of Makefiles and custom shell scripts dotted the j's and crossed the f's.

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. It has also been battle-tested at Warsaw University of Technology, Data Science Retreat (Berlin), and Deakin University (Melbourne) – I thank my students for the feedback given over the last 7 or so years.

Part I Introducing Python

Getting Started with Python and JupyterLab

1.1 Installing Python

We will be using the reference implementation of the Python language (called CPython²¹). Python 3.8 (not: 2.x!) or later will be required.

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, and jupyter, etc.).

Exercise 1.1 Download and install the latest version of Anaconda Individual Edition from https: //www.anaconda.com/products/individual. If you run into any troubles, consult the official product documentation available at https://docs.anaconda.com/anaconda/install/.

Note: Slightly more advanced users of Unix-like operating systems (GNU/Linux, FreeBSD, etc.), just like yours truly, might prefer downloading Python via their native package manager (e.g., sudo apt install python3 in Debian and Ubuntu). Then, installing²² additional Python packages can either be done by the said manager or directly from the Python Package Index (PyPI²³) via the **pip** tool.

GNU/Linux is the language of choice of machine learning engineers and data scientists both on the desktop and in the cloud. Switching to a free system at some point cannot be recommended highly enough.

²¹ https://www.python.org

²² https://packaging.python.org/en/latest/tutorials/installing-packages/

²³ https://pypi.org/

1.2 What is JupyterLab?

JupyterLab²⁴ is a web-based development environment supporting numerous²⁵ programming languages, including of course Python; see Figure 1.1.

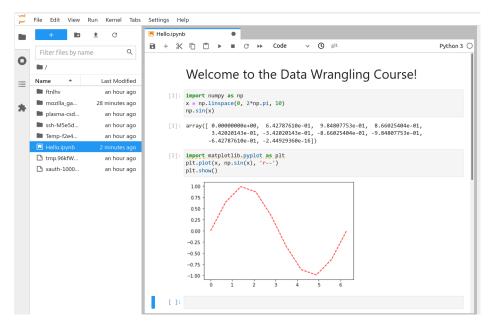


Figure1.1: JupyterLab at a glance

In JupyterLab, we can work with:

- Jupyter notebooks²⁶ .ipynb documents combining code, text, plots, and other rich
 outputs; importantly, code chunks can be created, modified, and run interactively;
 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);

²⁴ https://jupyterlab.readthedocs.io/en/stable/

²⁵ https://github.com/jupyter/jupyter/wiki/Jupyter-kernels

²⁶ https://jupyterlab.readthedocs.io/en/stable/user/notebook.html

• source files for many different languages – with syntax highlighting and the ability to send code to the associated consoles;

and many more.

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.).

Exercise 1.2 Head to the official documentation of the JupyterLab project located at https://jupyterlab.readthedocs.io/en/stable/index.html and watch the introductory video linked in the Overview section.

Note: (**) If you are a more advanced student, you can consider **jupytext**²⁷ as a means to create .ipynb files directly from Markdown files.

1.3 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 Navigator²⁸, which can be accessed through the Start menu/application launcher. Read more in the official manual²⁹.
- 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.

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

²⁷ https://jupytext.readthedocs.io/en/latest/

²⁸ https://docs.anaconda.com/anaconda/navigator/getting-started/#navigator-starting-navigator

²⁹ https://docs.anaconda.com/anaconda/user-guide/getting-started/#run-python-in-a-jupyter-notebook

them are provided gratis, there are always strings attached). It is best to run our applications locally, where we are free³⁰ to be in full control over the software environment.

1.4 First Jupyter/IPython Notebook

- 1. From JupyterLab, create a new notebook running a Python 3 kernel (for example, by selecting File \rightarrow New \rightarrow Notebook in the web app menu).
- 2. Select File \rightarrow 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.

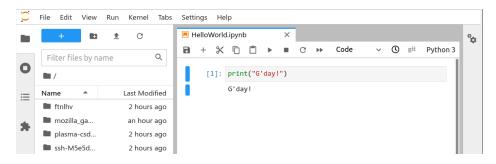


Figure1.2: "Hello World" in a Jupyter Notebook

³⁰ https://www.youtube.com/watch?v=Ag1AKIl_2GM

1.5 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.

1.6 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.

1.7 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

(continued from previous page)

```
## Subsection
This ~~was~~ *is* **really** nice.

* one
* two
    1. aaa
    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 introduction to the Markdown syntax located at https://daringfireball.net/projects/markdown/syntax.

**Exercise 1.4** Follow the interactive tutorial at https://commonmark.org/help/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.

#### 1.8 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<sup>31</sup> command line tool.

More generally, pandoc<sup>32</sup> 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.

#### 1.9 Questions

**Exercise 1.6** What is the difference between the Edit and the Command Mode in Jupyter?

**Exercise 1.7** What is Markdown?

**Exercise 1.8** How to format a table in Markdown?

<sup>31</sup> https://pypi.org/project/nbconvert/

<sup>32</sup> https://pandoc.org/

### Scalar Types in Python

Python<sup>33</sup> was designed and implemented by a Dutch programmer Guido van Rossum in the late 1980s. It is a very popular<sup>34</sup> object-oriented programming language that is quite suitable for rapid prototyping. Its name is a tribute to the funniest British comedy troupe<sup>35</sup> ever, therefore we will surely be having a jolly good laugh along our journey.

In this part we quickly introduce the 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 About Scalar Types

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

- bool logical (Boolean) values: True and False;
- 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 infrequently used in our applications);
- str character strings (which we can also classify as sequential types).

In this part, we'll also cover the if statement and ways to define own simple functions.

<sup>33</sup> https://www.python.org/

<sup>34</sup> https://insights.stackoverflow.com/survey/2021#technology-most-popular-technologies

<sup>35</sup> https://en.wikipedia.org/wiki/Monty\_Python

**Important.** Python is case-sensitive. Writing TRUE or true instead of True will result in an error.

**Exercise.** 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.

#### 2.2 Arithmetic Operators

Here is the list of arithmetic operators available:

```
1 + 2
 # addition
3
 # subtraction
1 - 7
-6
4 * 0.5 # multiplication
2.0
7 / 3
 # float division (the result is always of type float)
2.3333333333333333
7 // 3 # integer division
2
7 % 3
 # division remainder
2 ** 4
 # exponentiation
16
```

The precedence of these operators is quite predictable<sup>36</sup>, e.g., exponentiation has higher priority than multiplication and division which in turn binds more strongly than addition and subtraction. Hence:

<sup>&</sup>lt;sup>36</sup> https://docs.python.org/3/reference/expressions.html#operator-precedence

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

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

#### 2.3 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)
2.33333333333333333
```

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

**Exercise.** Create two named variables height and width. Based on them, determine your  $BMI^{37}$ .

<sup>37</sup> https://en.wikipedia.org/wiki/Body\_mass\_index

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

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

#### 2.4 Character Strings

Strings, which can consist of arbitrary text, are created using either double quotes or apostrophes:

```
print("spam, spam, #, bacon, and spam")
print("DD Cześć DD ¿Qué tal? Привет DDDD")

spam, spam, #, bacon, and spam

DDD Cześć DD ¿Qué tal? Привет DDDD

print('"G\'day, how ya goin\'," he asked.\n"Quite well, thanks," I responded.

--')

"G'day, how ya goin'," he asked.

"Quite well, thanks," I responded.
```

Above, "\'" (a way to include an apostrophe in an apostrophe-delimited string) and "\n" (newline character) are examples of escape sequences<sup>38</sup>.

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\'sD
\subseteq Flying Circuseses are a must\nsorry not sorry\ntasty\t"spam"\nlovely\t\
\subseteq 'spam\'\n'
```

<sup>38</sup> https://docs.python.org/3/reference/lexical\_analysis.html#string-and-bytes-literals

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

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

```
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<sup>39</sup> 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.

```
n = 3.14159265358979323846
e = 2.71828182845904523536
print(f"""
n = {n:10.8f}
e = {e:10.8f}
""")
##
n = 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.

**Important.** There are many string operations available – related for example to formatting, pattern searching, extracting chunks; they are very

<sup>&</sup>lt;sup>39</sup> https://docs.python.org/3/reference/lexical\_analysis.html#f-strings

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 a bit later.

#### 2.5 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.

**Exercise.** Call help("round") or ?round (this is 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.

#### 2.5.1 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
```

(continues on next page)

(continued from previous page)

```
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.

#### 2.5.2 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.sin(math.pi)) # sin(pi) equals 0 (with some numeric error)
1.2246467991473532e-16
print(math.floor(-7.33)) # the floor function
-8
```

See https://docs.python.org/3/library/math.html for its official documentation and the comprehensive list of objects defined therein. Also, we assume that the reader is familiar with basic mathematical objects such as the said floor function. If not, please consult the English Wikipedia which is overall a reliable source of knowledge on topics from our discipline.

#### 2.6 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'>
```

Classes define the following kinds of attributes:

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

**Exercise.** 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).

#### 2.7 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</pre>
```

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</pre>
```

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</pre>
```

Note that not 100 <= 3 is equivalent to 100 > 3. Also, via the de Morgan's laws<sup>40</sup>, not (1 > 2 and 2 < 3) is true if and only if 1 <= 2 or 2 >= 3 holds.

**Exercise.** 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>=b and b>=c and a>=c),
(a>b and a<c) or (a<c and a>d).
```

<sup>40</sup> https://en.wikipedia.org/wiki/De\_Morgan%27s\_laws

# 2.8 Controlling Program Flow

#### 2.8.1 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!")
0.815116830285657</pre>
```

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 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
ham!
I'd rather eat spam!
more spam!</pre>
```

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!") # :(</pre>
```

**Exercise.** For a given BMI<sup>41</sup> (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 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.** (\*) 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.

### 2.8.2 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:
```

<sup>41</sup> https://en.wikipedia.org/wiki/Body\_mass\_index

```
count = count + 1
print(count)
68
```

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

# 2.9 Defining Own Simple 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</pre>
```

#### 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
```

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)
0.305
```

**Exercise.** Write a function named bmi which computes and returns BMI<sup>42</sup> given 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:</pre>
```

<sup>42</sup> https://en.wikipedia.org/wiki/Body\_mass\_index

```
m = b
if c < m: # be careful! no `else` or `elif` here - it's a separate `if`
 m = c
return m</pre>
```

#### 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.** Write a function max3 which determines the maximum of 3 given values.

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

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

# 2.10 Questions

- 1. What does import xxxxxx as x mean?
- 2. What is the difference between if and while?
- 3. Name the scalar types we have introduced here.
- 4. What is a docstring and how to create and access it?
- 5. What are keyword arguments?

# Sequential and Other Types in Python

#### 3.1 Sequential Types

Sequential objects store data items that we can access 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:

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

**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.

Lists are *mutable* and hence their state may be changed arbitrarily:

```
x = [
[1, 2, 3, 4],
[5, 6, 7, 8]
```

```
] # a list of lists
x.append([9, 10, 11, 12])
print(x)
[[1, 2, 3, 4], [5, 6, 7, 8], [9, 10, 11, 12]]
```

#### 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 often we can drop the round brackets and still get a tuple:

```
1, 2, 3 # the same as `(1, 2, 3)`
(1, 2, 3)
1, # i.e., `(1,)` - note it's not the same as simply `1` or `(1)`
(1,)
```

**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.).

### 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

Recall that we have discussed character strings in the previous part.

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

#### 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, ..., n-2, n-1, where n is the length of the sequence.

**Note.** 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)
```

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.

# 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
```

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

**Exercise.** 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.** 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!'}
```

(\*) Here is a more advanced example: in the sequel, we will frequently be reading JSON<sup>43</sup> 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']
```

<sup>43</sup> https://en.wikipedia.org/wiki/JSON

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

**Exercise.** 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.** (\*) 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.
 """
 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</pre>
```

**Exercise.** Write your own basic versions (using the for loop) of the builtin max, sum, any, and all functions.

(\*) Exercise. 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
```

For example, knowing that the items method for a dictionary 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 also 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']
```

(\*\*) 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.

#### 3.5 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]
```

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

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
[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

This 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 be elaborating on many other language elements and its standard library in the course of this course (list comprehensions, lambda expressions, exception handling, string formatting, argument unpacking, variadic arguments like \*args and \*\*kwargs, regular expressions, file handling, etc.).

We have also 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 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.

The official Python 3 tutorial is available at https://docs.python.org/3/tutorial/index. html. We encourage at some point to skim through at least the following chapters:

- 3. An Informal Introduction to Python<sup>44</sup>,
- 4. More Control Flow Tools<sup>45</sup>,
- 5. Data Structures<sup>46</sup>.

#### 3.7 Questions

- 1. Name the sequential objects we have introduced.
- 2. Is every iterable object sequential?
- 3. Is dict an instance of a sequential type?
- 4. What is the meaning of + and \* operations on strings and lists?
- 5. 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?
- 6. (\*) How to make an object copy and when we should do so?
- 7. What is the difference between x[0] and x[:0], where x is a sequential object?

<sup>44</sup> https://docs.python.org/3/tutorial/introduction.html

<sup>45</sup> https://docs.python.org/3/tutorial/controlflow.html

<sup>46</sup> https://docs.python.org/3/tutorial/datastructures.html

# Part II Unidimensional Data

# *Introduction to Vectors in numpy*

numpy 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 history<sup>47</sup> and stands on the shoulders of many giants (e.g., concepts from the [APL](https://en.wikipedia.org/wiki/APL\_(programming\_language) and Fortran<sup>48</sup> 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*, *pandas*, and *sklearn*), 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 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).

**Technical 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

<sup>&</sup>lt;sup>47</sup> https://scipy.github.io/old-wiki/pages/History\_of\_SciPy

<sup>48</sup> https://en.wikipedia.org/wiki/Fortran

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
np.__version__ # FYI
'1.22.2'
```

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

# 4.1 Creating Vectors

# 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 themself.

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')</pre>
```

The in 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 later, 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.** Call help(np.linspace) and study the meaning of the endpoint argument. Also, find the same documentation page at the *numpy* project's website<sup>49</sup>. 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 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:

<sup>49</sup> https://numpy.org/doc/stable/reference/index.html

```
np.random.rand(5)
array([0.25176841, 0.56452847, 0.8526928 , 0.67202392, 0.36498808])
and picking values from a given set:
np.random.choice(np.arange(1, 10), 3, replace=False)
array([2, 7, 5])
```

This gave 3 values from the set {1, 2, ..., 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, being the topic we shall cover later, but it is worth mentioning that, for example, numpy.loadtxt can read text files where numeric values are stored in separate text lines.

**Exercise.** Use loadtxt to read the dataset located at https://github.com/gagolews/teaching\_data/blob/master/marek/population\_largest\_cities\_unnamed.txt (click *Raw* to get access to its contents).

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

### 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*,  $\infty$ .

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 Further Reading

The *numpy* project's website, https://numpy.org/doc/stable/reference/index.html.

# 4.3 Questions

- 1. What are some benefits of using a *numpy* vector over an ordinary Python list? What are the drawbacks?
- 2. What is the difference between numpy.arange and numpy.linspace?
- 3. (\*) 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.)

4. (\*) What happens when we convert a numeric vector to a logical one?

# Inspecting the Distribution of Numeric Data

Let's assume that we have dozens of data points at hand, representing some measurements, such as heights or weights of 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<sup>50</sup> called National Health and Nutrition Examination Survey (NHANES<sup>51</sup>) conducted by the US Centres for Disease Control and Prevention.

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

Let's preview a few randomly chosen observations:

```
np.random.choice(heights, 24, replace=False)
array([144.8, 163.8, 157.5, 173.8, 161.4, 166.5, 159.1, 160.2, 160.8,
166. , 152.9, 168.3, 154.7, 153.1, 145.1, 157.4, 159.3, 164.1,
153.6, 162. , 159.7, 154.8, 161.1, 166.6])
```

This is an example of *quantitative* (numeric) data – as opposed to, e.g., *qualitative* (categorical) data which we shall cover later – we are dealing with a series of numbers on which it makes sense to apply various mathematical operations, such as subtraction, taking logarithms, etc.

Looking at the numbers themselves (luckily there are not that many of them) tells us nothing. They're gibberish. Thus, we yearn for methods that could extract some meaning from them.

<sup>50</sup> https://en.wikipedia.org/wiki/Longitudinal\_study

<sup>51</sup> https://wwwn.cdc.gov/nchs/nhanes/search/datapage.aspx

#### 5.1 Histograms

 $seaborn^{52}$  is a nice package for data visualisation written by Michael Waskom. It is build on top of  $matplotlib^{53}$ , which we will be using frequently.

Let's import both packages and set its traditional aliases:

```
import matplotlib.pyplot as plt
import seaborn as sns
plt.style.use("seaborn")
sns.__version__ # FYI
'0.11.2'
```

A histogram<sup>54</sup> is one of the most intuitive tools for depicting the empirical distribution of a data sample:

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

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 later) – the most typical (*normal*) observations are somewhere in the middle, and the probability mass decreases quickly. For instance, observations outside the (more or less) [139, 181] interval are very rare (less than 1% probability).

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 strong mathematical result saying that the sum or average of many observations, assuming that they are independent and follow the same (any!) distribu-

<sup>52</sup> https://seaborn.pydata.org

<sup>53</sup> https://matplotlib.org/

<sup>54</sup> https://en.wikipedia.org/wiki/Histogram

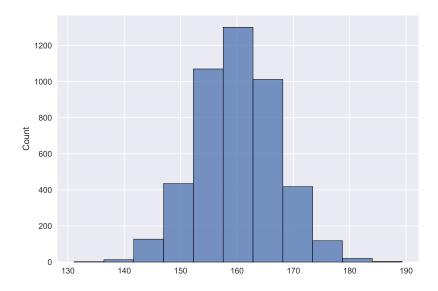


Figure 5.1: plot of chunk 220-histogram-4

tion with finite variance, is approximately normally distributed (the central limit theorem). This is a very strong result.

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

Let us therefore consider another dataset. Below is a simulated sample of disposable income (financial year ending 2020) of 1000 randomly chosen UK households, in  $\pounds$  (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 report<sup>55</sup>):

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

<sup>&</sup>lt;sup>55</sup> https://www.ons.gov.uk/peoplepopulationandcommunity/personalandhouseholdfinances/incomeandwealth/bulletins/householddisposableincomeandinequality/financialyear2020

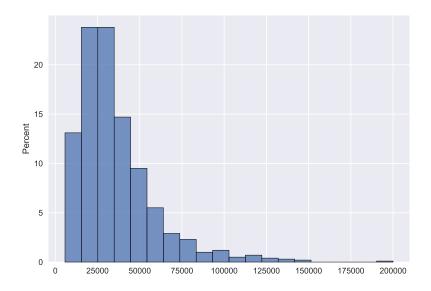


Figure 5.2: plot of chunk 220-histogram-5

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 £16,500 (it is an educated guess) 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 just due to the 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.

**Exercise.** There is also a nhanes\_adult\_female\_weight\_2020.txt dataset in the above folder, giving weights (in kgs) of the participants. Draw a histogram. Does its shape resemble the income or heights distribution more?

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

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

```
marathon[:5] # preview top 5 (data are 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:

```
sns.histplot(marathon[marathon < 180])
plt.show()</pre>
```

reveals that the data are highly left-skewed.

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

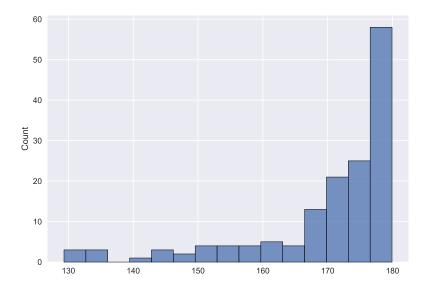


Figure 5.3: plot of chunk 220-histogram-8

## 5.2 Binning

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.

Consider the income dataset again:

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

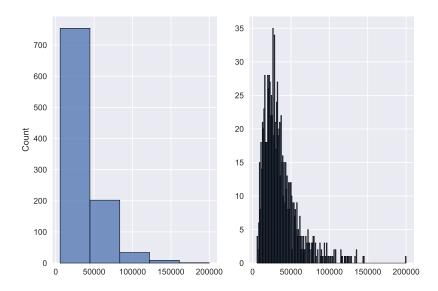


Figure 5.4: plot of chunk 220-histogram-9

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.

As usual, the "truth" is probably somewhere in-between. When preparing a histogram for publication (e.g., in a report or on a webpage), you might be tempted to thing "I need to choose one and only one bin count". The truth is that you 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 you 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 you cannot request access to the original data, best thing you 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.** 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.

(\*) 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.

(\*) 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. We will discuss it in more detail in the section on categorical data processing. 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).

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

Sometimes data we get access to have already been binned by somebody else. For instance, here are the December 2021 hourly averages pedestrian counts<sup>56</sup> near the Southern Cross Station in Melbourne:

<sup>56</sup> http://www.pedestrian.melbourne.vic.gov.au/

#### (continued from previous page)

```
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:

```
plt.bar(np.arange(0, 24), width=1, height=peds, edgecolor="black")
plt.show()
<BarContainer object of 24 artists>
```

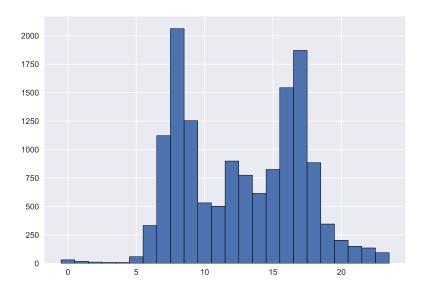


Figure5.5: plot of chunk 220-histogram-11

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).

Here is 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, edgecolor="black")
plt.show()
<BarContainer object of 71 artists>
```

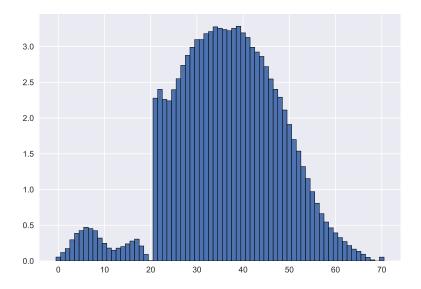


Figure 5.6: plot of chunk 220-histogram-12

This gives the distribution<sup>57</sup> of the 2019 Matura<sup>58</sup> exam scores in Poland (in %) – Polish literature at basic level.

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,

<sup>&</sup>lt;sup>57</sup> https://cke.gov.pl/images/\_EGZAMIN\_MATURALNY\_OD\_2015/Informacje\_o\_wynikach/2019/sprawozdanie/Sprawozdanie%202019%20-%20J%C4%99zyk%20polski.pdf

<sup>58</sup> https://en.wikipedia.org/wiki/Matura

• 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.

### 5.3 Cumulative Counts

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:

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

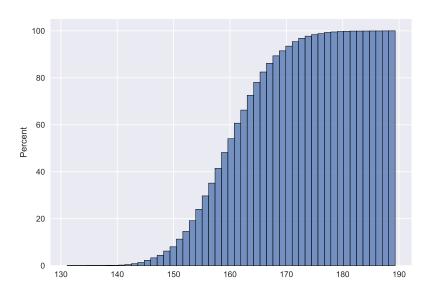


Figure 5.7: plot of chunk 220-histogram-13

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 we denote as  $\hat{F}_n$ :

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

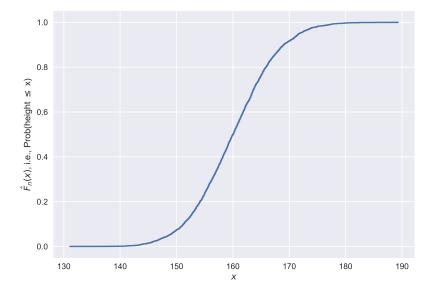


Figure 5.8: plot of chunk 220-histogram-14

At any given point x,  $\hat{F}_n(x)$  is a step function (we cannot see the steps here, because the points are too plentiful) that gives the proportion of observations in our sample that are not greater than x.

Note that drawing the ECDF does not involve binning – we only need to arrange the ob-

servations in an ascending order. Then, the arithmetic progression 1/n, 2/n, ... n is plotted against them.

### 5.4 Log-scale

Consider the dataset<sup>59</sup> 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:] # data are sorted
array([1517550., 1953633., 2896047., 3694742., 8008654.])
```

The histogram:

```
sns.histplot(large_cities, bins=20)
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<sup>60</sup>:

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

The log-scale on the x axis does not increase linearly – based on steps of equal sizes

<sup>59</sup> https://arxiv.org/abs/0706.1062v2

<sup>60</sup> https://en.wikipedia.org/wiki/Logarithmic\_scale

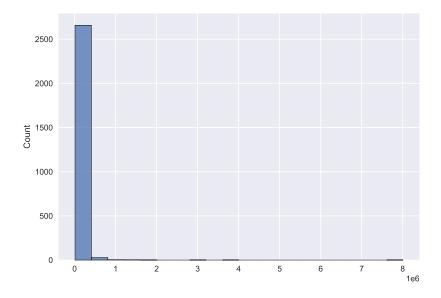


Figure 5.9: plot of chunk 220-histogram-18

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. (\*) Later we will discuss the Pareto distribution family which yields similar histograms.

**Exercise.** Draw the histogram of income on the logarithmic scale. Does is resemble a bell-shaped distribution?

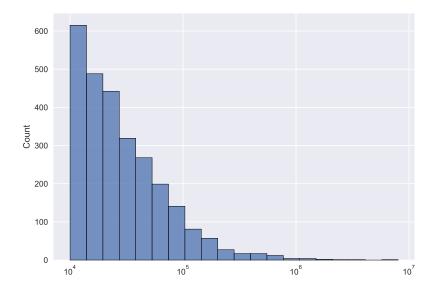


Figure 5.10: plot of chunk 220-histogram-19

(\*) **Exercise.** 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.

## 5.5 Questions

- 1. What is a bell-shaped distribution?
- 2. What is a right-skewed distribution?
- 3. What is a heavy-tailed distribution?
- 4. What is a multi-modal distribution?
- 5. (\*) When does logarithmic binning make sense?

# Descriptive Statistics for Continuous 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:

```
import numpy as np
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] # bin□
-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
```

And a graphical representation:

```
import matplotlib.pyplot as plt
import seaborn as sns
plt.style.use("seaborn")
sns.histplot(income)
plt.show()
```

Instead of dealing with a large dataset, we obtained just a few counts.

Generally, the process of binning and its textual or visual depictions are useful in de-

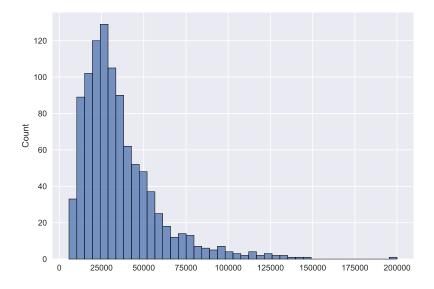


Figure 6.1: plot of chunk 230-aggregate-2

termining 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, to 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.

In the sequel, 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.

#### 6.1 Mathematical Notation

From now on we will denote the sample to be aggregated with  $x = (x_1, x_2, ..., x_n)$ , 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 x is not an atomic entity (x), but rather a collection thereof.

For brevity, instead of saying "let x be a real-valued sequence (or a vector – in many contexts this is synonymous) of length n", we shall write "let  $x \in \mathbb{R}^n$ ". Here, the " $\in$ " symbol stand for "is in" or "is a member of" and  $\mathbb{R}$  denotes the set of real numbers.

Mathematical notation is pleasantly *abstract* (general) in the sense that x can be anything, e.g., the above income vector.

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

Furthermore, by  $x_{(i)}$  (note the bracket) we will denote the *i*-th smallest value in x. In particular,  $x_{(1)}$  is the minimum and  $x_{(n)}$  is the maximum.

```
income_sorted = np.sort(income)
income_sorted[0], income_sorted[-1] # the minimum and the maximum
(5750.0, 199969.0)
```

This gave us the smallest and largest income, which are already data aggregates of some kind.

Below we will also be using the heights dataset as an illustration:

```
heights = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
 "teaching_data/master/marek/nhanes_adult_female_height_2020.txt")
heights_sorted = np.sort(heights)
heights_sorted[0], heights_sorted[-1]
(131.1, 189.3)

Let's draw its histogram again:
sns.histplot(heights)
plt.show()
```

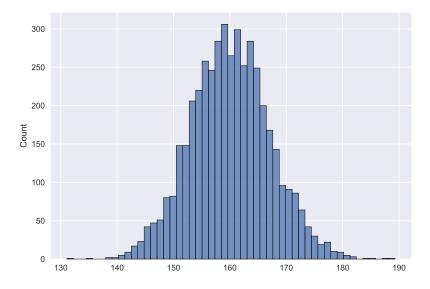


Figure 6.2: plot of chunk 230-aggregate-5

## 6.2 Measures of Location

#### 6.2.1 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)
(160.08245186988268, 160.0)
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.

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 totally ignores most 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.

**Exercise.** Compute the arithmetic mean and median for the 37\_pzu\_warsaw\_marathon\_m dataset mentioned in the previous part.

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

(\*) On a side 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]
(160.08245186988268, 160.08245186988268, 160.08245186988268)
```

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

## 6.2.2 Quantiles

Quantiles<sup>61</sup> generalise the notion of the sample median.

For any p between 0 and 1, a p-quantile, denoted  $q_p$ , is a value dividing the sample in such a way that:

- 100p% of observations are not greater than  $q_p$ ,
- the remaining 100(1-p)% are not less than  $q_p$ .

Quantiles appear under many different names, but they all refer to the same concept. In

<sup>61</sup> https://en.wikipedia.org/wiki/Quantile

particular, the we can speak about 100p-th percentiles, e.g., the 0.5-quantile is the same as the 50th percentile.

#### Furthermore:

- o-quantile  $(q_0)$  = the minimum (also: numpy.min),
- 25-quantile  $(q_{0.25})$  = the 1st quartile (denoted  $Q_1$ ),
- 50-quantile  $(q_{0.5})$  = the 2nd quartile a.k.a. median,
- 75-quantile  $(q_{0.75})$  = the 3rd quartile (denoted  $Q_3$ ),
- 100-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. , 164.75, 189.3])
```

**Exercise.** Compute some quantiles for the whole 37\_pzu\_warsaw\_marathon\_mins dataset. In particular, does the minimum and maximum make sense? Or maybe there are some errors in the dataset that require further inspection?

**Exercise.** What is the income bracket for 95% of the "most typical" tax-payers? In other words, determine the 2.5- and 97.5-percentiles.

is in the detail – there are many definitions of quantiles across statistical software, although most of them fall into our (broad) definition; they have been nicely summarised in the article R.J. Hyndman and Y. Fan, Sample Quantiles in Statistical Packages, *American Statistician* **50**(4), 361-365 (1996). doi:10.2307/2684934.

**Exercise.** 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.

## 6.3 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.

The noteworthy dispersion measures include:

• the standard deviation (\*\* in the so-called uncorrected for bias version), being the

average distance to the arithmetic mean:

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

the interquartile range (IQR), being the difference between the 3rd and the 1st quartile:

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

Computing the above is almost effortless:

```
np.std(income), np.quantile(income, 0.75)-np.quantile(income, 0.25)
(22888.77122437908, 23454.0)
np.std(heights), np.quantile(heights, 0.75)-np.quantile(heights, 0.25)
(7.035238940603155, 9.44999999999999)
```

The IQR has an appealing interpretation, because we may say that this is the range comprised of the 50% most typical values.

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. 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's might come across the variance every now and then as well.

The *range* (or support) is simply the difference between the maximal and minimal observation.

## 6.4 Box (and Whisker) Plots

The box and whisker plot<sup>62</sup> (or the box plot for short) depicts some of the most noteworthy features of a data sample.

Box plots will be particularly useful for comparing data samples with each other (e.g., heights of men and women separately).

```
plt.subplot(211) # 2 rows, 1 column, 1st subplot
sns.boxplot(data=income, orient="h")
plt.title("income")

plt.subplot(212) # 2 rows, 1 column, 2nd subplot
sns.boxplot(data=heights, orient="h")
plt.title("heights")

plt.show()
```

Each box plot consists of:

• the box, which spans between the 1st and the 3rd quartile:

<sup>62</sup> https://en.wikipedia.org/wiki/Box plot

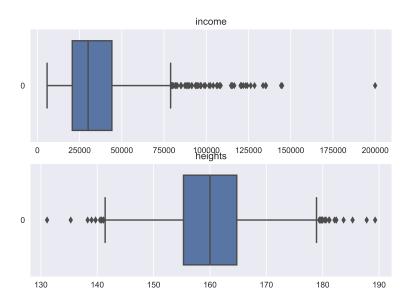


Figure6.3: plot of chunk 230-aggregate-15

- 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 span between
  - the smallest observation (the minimum) or  $Q_1$  1.5IQR (the left side of the box minus 3/2 of its width), whichever is larger,
  - the largest observation (the maximum) or  $Q_3 + 1.5$ IQR (the right side of the box plus 3/2 of its width), whichever is smaller.

Additionally, all observations that are less than  $Q_1-1.5{\rm IQR}$  (if any) or greater than  $Q_3+1.5{\rm IQR}$  (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 in such a way that we expect there to be no or only few outliers if the data are normally distributed. For skewer distributions, there will naturally be many outliers on either side.

**Important.** Most of the statistical packages *do not* include the arithmetic mean in the figure. If they do, it is marked with a special symbol.

**Exercise.** Call plt.plot(np.mean(..data..), 0, "wX") after seaborn. boxplot to mark the arithmetic mean with a white cross.

(\*) We may also sometimes be interested in a *violin plot*, which combines the box plot (although with no outliers marked) and the so-called kernel density estimator<sup>63</sup> (which is a smoothened version of a histogram):

```
sns.violinplot(data=income, orient="h")
plt.show()
```

## 6.5 Measures of Shape (\*)

Note that from a histogram or a box plot we can easily deduce if a dataset is symmetric or skewed.

<sup>63</sup> https://en.wikipedia.org/wiki/Kernel\_density\_estimator

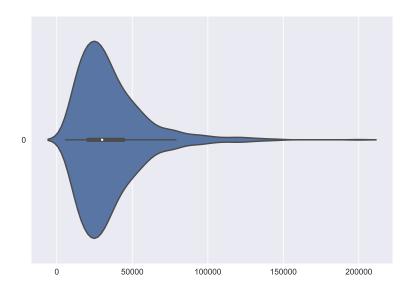


Figure 6.4: plot of chunk 230-aggregate-16

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:

import scipy.stats
scipy.stats.skew(heights)
## 0.08279841283619495

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.

## 6.6 Some Other Measures (\*)

We have said that the arithmetic mean is very sensitive to extreme observations. In a farther part, 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*<sup>64</sup> and *geometric*<sup>65</sup> 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*<sup>66</sup>, 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. It is normalised so that it takes values in the unit interval. An index of o reflects the situation where all values in a sample are the same (o 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.

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.

<sup>64</sup> https://en.wikipedia.org/wiki/Harmonic\_mean

<sup>65</sup> https://en.wikipedia.org/wiki/Geometric\_mean

<sup>66</sup> https://en.wikipedia.org/wiki/Gini\_coefficient

## 6.7 Further Reading

- M. Gagolewski, Spread measures and their relation to aggregation functions, *European Journal of Operational Research* **241**(2), 469–477, 2015, doi:10.1016/j.ejor.2014.08.034
- M. Grabisch, J.-L. Marichal, R. Mesiar, and E. Pap, Aggregation functions, Cambridge University Press, 2009
- R.J. Hyndman and Y. Fan, Sample Quantiles in Statistical Packages, *American Statistician* **50**(4), 361-365, 1996. doi:10.2307/2684934

## 6.8 Questions

- 1. How can we interpret the different values of the arithmetic mean, median, standard deviation, interquartile range, skewness, and the Gini index?
- 2. 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?
- 3. 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.
- 4. Give some examples, where simple data preprocessing can drastically change the values of chosen sample aggregates.
- 5. (\*\*) Reflect on the famous<sup>67</sup> saying not everything that can be counted counts, and not everything that counts can be counted.
- 6. (\*\*) Being a data scientist can be a frustrating job, especially when you care for some

<sup>67</sup> https://quoteinvestigator.com/2010/05/26/everything-counts-einstein/

- causes. Reflect on: some things that count can be counted, but we will not count them, because there's no budget for it.
- 7. (\*\*) 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 be focused on optimising those KPIs? How about the same problem but with regards to your company and employees?

# Transforming and Filtering Continuous 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).

The first topic has already been covered in a previous part, time for the two remaining ones. Also, we will be discussing basic techniques for handling missing data and outliers.

**Important.** The same operations we are going to be applying on individual data frame columns.

import numpy as np

### 7.1 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,
- exponential function: numpy.exp,
- logarithms: numpy.log (the natural logarithm, i.e., base e), numpy.log10 (base 10), etc.,
- trigonometric functions: numpy.sin, numpy.cos, numpy.tan, etc.,
- rounding and truncating: numpy.round, numpy.floor, numpy.ceil, numpy.trunc (when in doubt about their definitions, we should, as usual, refer to the official manual).

All these functions are *vectorised*: if we apply them on a vector of length n, they return a sequence of the same size, with all elements transformed.

Thanks to this, our code can not only be more readable, but it runs faster – as otherwise we would have to employ a while or for loop to traverse through each element in a given sequence.

For example:

```
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.

Other examples:

and so forth.

## 7.2 Arithmetic Operators

We can apply the standard binary (two-argument) arithmetic operators +, -, \*, /, \*\*, %, // on vectors too.

#### 7.2.1 Vector-Scalar Case

Often we will be applying 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, this use case behaves just like the vectorised mathematical functions discussed above.

## 7.2.2 Application: Feature Scaling

Vector-scalar operations and aggregation functions are the basis for the most commonly applied feature scalers<sup>68</sup>, which can increase the interpretability of data points:

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

#### Standardisation

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:

<sup>68</sup> https://en.wikipedia.org/wiki/Feature\_scaling

```
np.mean(heights), np.std(heights)
(160.08245186988268, 7.035238940603155)
```

A standardised version of a vector  $(x_1, \dots, x_n)$  consists in subtracting from each element the sample arithmetic mean (which we call *centring*) and then dividing it by the standard deviation.

Mathematically, 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([-0.43814459, 1.04012788, -0.06857647, 1.19648362, -1.74584715])
```

What we obtain in result is sometimes referred to as the *z-scores*. They are nicely interpretable:

- z-score of o 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;

all right, we get the point.

We should also note that because of the way they emerge, the mean of z-scores is always o and standard deviation is 1 (up to a tiny numerical error, as usual):

```
np.mean(heights_std), np.std(heights_std)
(6.0252262965981495e-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).

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<b>Exercise.</b> We have a patient whose height z-score is 1 and weight z-score is -1. How to interpret this information?	
<b>Exercise.</b> How about a patient whose weight z-score is 0 but BMI z-score is 2?	
(*) <b>Note.</b> Standardisation makes most sense for bell-shaped distributions, in particular normally-distributed ones. Recalling the 2σ rule for the normal family, it is <i>expected</i> 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.	
(*) <b>Note.</b> Sometimes we might be interested in performing some form of <i>robust</i> 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 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 (\*)

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 norm:

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

whose 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.,  $\|(1, 2)\| = \sqrt{5} \simeq 2.236$ .

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])
```

(\*\*) Note that normalisation is pretty similar to standardisation if data are already centred (when mean was subtracted). Actually, we can obtain one from the other by scaling by  $\sqrt{n-1}$ .

At other times, by *length* we can also mean the Manhattan 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])
```

This is frequently applied on vectors of nonnegative values, whose normalised versions can be interpreted as *probabilities*: values between 0 and 1 which additionally add up 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
[330 1918 1890 381]
```

And now, converting the counts to empirical probabilities:

```
p = c/np.sum(c)
print(p)
[0.07302501 0.42443018 0.41823412 0.08431069]
```

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

### 7.2.3 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\*100 (the second elements), and so forth.

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  $h = -(p_1 \log p_1 + p_2 \log p_2 + \dots + p_n \log p_n) = -\sum_{i=1}^n p_i \log p_i$ . 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.

Yet another example: let's say we would like to plot two mathematical functions:  $f(x) = \sin x \cos^2 \frac{x}{3}$  and  $g(x) = \frac{\sin(-2x)}{x^2+1}$  for x in the interval  $[-2\pi, 4\pi]$ .

To do this, we can probe the values of f and g at sufficiently many points using the vectorised operations discussed so far and then use the matplotlib.pyplot.plot function:

```
import matplotlib.pyplot as plt
plt.style.use("seaborn")
x = np.linspace(-2*np.pi, 4*np.pi, 1001) # many points in the said interval
yf = np.sin(x)*np.cos(x/3)**2
yg = np.sin(-2*x)/(x**2+1)
plt.plot(x, yf, 'r-', label="f(x)") # red solid line
plt.plot(x, yg, 'b:', label="g(x)") # blue dotted line
plt.legend()
plt.show()
```

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

**Exercise.** Based on the nhanes\_adult\_female\_height\_2020.txt and nhanes\_adult\_femaltxt datasets (discussed in the part on histograms), using a single line of code, compute the vector of BMIs of all persons.

## 7.3 Vector Indexing

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

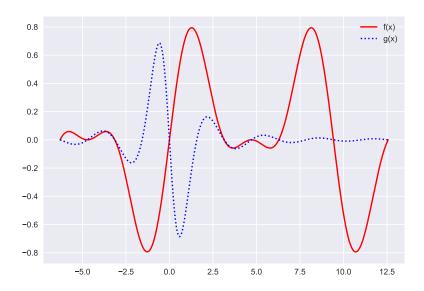


Figure 7.1: plot of chunk 240-transform-uni-20

```
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.

## 7.3.1 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([], dtype=int64), array([10, 20, 0]
-10, 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).

### 7.3.2 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 does 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])
```

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).

Instead, *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. Based on the nhanes\_adult\_female\_height\_2020.txt and nhanes\_adult\_female\_weightxt datasets, compute the BMIs of the persons only whose height is between 150 and 170 cm.

## 7.3.3 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]))
```

(\*) **Note.** 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 ([6, 8, 1, 2, 7]  $\rightarrow$  [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.

## 7.4 Other Operations

## 7.4.1 Sorting and Ranking

The numpy.sort function returns a sorted copy of the given vector.

```
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<sup>69</sup>, which is the inverse of numpy. argsort.

```
import scipy.stats
scipy.stats.rankdata(x)
array([1. , 3. , 5.5, 4. , 2. , 5.5])
```

<sup>69</sup> https://en.wikipedia.org/wiki/Ranking

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.** 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*<sup>70</sup> sorting algorithm (timsort<sup>71</sup>, 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 argsort on a vector representing a permutation of elements in fact generates its [inverse](https://en.wikipedia.org/wiki/Inversion\_(discrete\_mathematics). In particular, np.argsort(np.argsort(x, kind="stable"))+1 is equivalent to scipy.stats.rankdata(x, method="ordinal").

## 7.4.2 Searching for Certain Indexes

numpy.argmin and numpy.argmax return the index at which we can find the smallest and the largest observation in a given vector.

```
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.

We can use numpy where to get the indexes where a logical vector has elements equal to True. For example:

```
np.where(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.

<sup>70</sup> https://en.wikipedia.org/wiki/Sorting\_algorithm#Stability

<sup>71</sup> https://github.com/python/cpython/blob/3.7/Objects/listsort.txt

**Exercise.** Let x be a vector with possible ties. Write an expression that returns a randomly chosen index pinpointing the sample maximum.

**Exercise.** *numpy.where* can also act as a vectorised version of the if statement. Consult its documentation

### 7.4.3 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.

(\*) Note that this operation is useful when preparing cumulative histograms discussed earlier.

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?).

### 7.4.4 Vectorising Scalar Operations (\*)

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.** Write equivalent versions of the above expressions using vectorised *numpy* functions.

**Exercise.** 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).

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.])
```

## 7.5 Questions

- 1. Give the mathematical definitions, use cases, and interpretations of standardisation, normalisation, and min-max scaling.
- 2. How are numpy.log and numpy.exp related to each other? How about numpy.log vs numpy.log10, numpy.cumsum vs numpy.diff, numpy.min vs numpy.argmin, numpy.sort vs numpy.argsort, and scipy.stats.rankdata vs numpy.argsort?
- 3. What is the difference between numpy.trunc, numpy.floor, numpy.ceil, and numpy.round?
- 4. What happens when we apply + on two vectors of different lengths?
- 5. List four ways to index a vector.
- 6. 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 ]?
- 7. (\*) What does it mean that slicing returns a view on existing data?

# 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 patterns in the histogram shapes can be formalised using the notion of a continuous probability distribution, and more precisely, a probability density function of the corresponding random variable.

Unfortunately, we do not intend this to be a course in probability theory, therefore we shall provide the curious reader with a digestible intuition only, and encourage them to delve into this magical world on their own at some other time.

A density function is a nicely smooth curve that would arise if we drew a probability histogram (i.e., one whose bars' total sum are equal to 1) given the whole population (e.g., all women living currently on Earth and beyond) or otherwise an extremely (infinitely even) large data sample.

(\*\*) Mathematically, it is a continuous function f (fulfilling  $f(x) \ge 0$  for all x and  $\int_{-\infty}^{\infty} f(x) \, dx = 1$  – these are probabilities after all) such that  $\int_a^b f(x) \, dx$  gives the probability of obtaining a result in any [a, b] interval. This is a continuous equivalent of the concept of binning and determining the fraction of values falling therein.

The so-called *kerned density estimators* (KDEs), although based on finite data samples, can give us the taste of the said objects:

```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
plt.style.use("seaborn")
```

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```
heights = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
 "teaching_data/master/marek/nhanes_adult_female_height_2020.txt")
sns.histplot(heights, stat="density", kde=True)
plt.show()
```

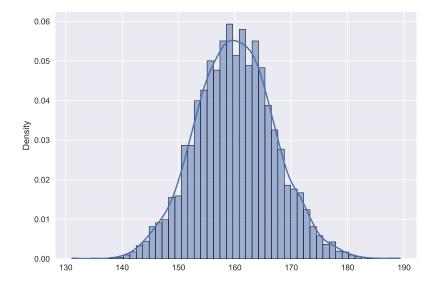


Figure 8.1: plot of chunk 250-distribution-uni-2

stat="density" means exactly that the total area of all the bars are normalised so that they sum to 1.

Some distributions appear more frequently than others and fit empirical data or parts thereof particularly well. Let us thus review a few noteworthy probability distributions: the normal, log-normal, Pareto, and uniform families. In the sequel, we will be using the *scipy* package, which is built on top of *numpy*:

import scipy.stats

(\*) **Note.** There are many other useful continuous probability distributions that we usually study in a course in statistics: the exponential, beta, gamma, chi-square, Cauchy, Snedecor's F, Student's t, and other families, just to name a few.

### 8.1 Normal Distribution

A normal distribution  $^{72}$  yields a prototypical bell-shaped density. It is described by two parameters:  $\mu$  (the expected value, at which the density is centred) and  $\sigma$  (the standard deviation, saying how much is the distribution dispersed around  $\mu$ ).

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,  $\mu$  and  $\sigma$  (the more the samples are, the smaller the error).

Let's estimate these parameters in the case of the heights dataset:

```
\mu = np.mean(heights) # an estimator of expected value \sigma = np.std(heights, ddof=1) # an estimator of standard deviation \mu, \sigma ## (160.08245186988268, 7.03601747642589)
```

We use ddof=1, because this estimator has slightly better statistical properties.

Next, we can draw the density function of the N(160.1, 7.04) distribution on top of the histogram:

```
sns.histplot(heights, stat="density", kde=True)
x = np.linspace(np.min(heights), np.max(heights), 1000)
plt.plot(x, scipy.stats.norm.pdf(x, μ, σ), "r:") # a dotted red curve
plt.show()
```

This yields a very nice fit! (Of course, formally, this of course needs to be verified more rigorously using some statistical hypothesis testing – which yours truly did on the side, hence his enthusiasm.)

<sup>72</sup> https://en.wikipedia.org/wiki/Normal\_distribution

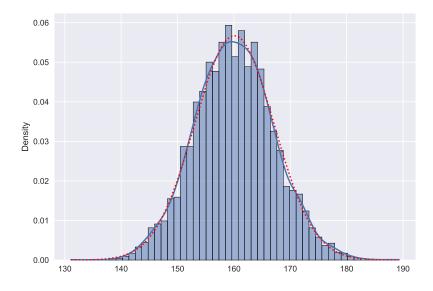


Figure 8.2: plot of chunk 250-distribution-uni-5

Instead of working with a few thousands data points, an analyst may instead decide that they will use the above *idealisation* as the data *model*. Note that the whole sample has been *reduced* to merely two parameters.

This not only saves storage space and computational time, but – based on some facts that can be proven mathematically and be found in good textbooks in probability and statistics – we can imply things such as:

- 95% of (i.e., most) women are  $\mu\pm2\sigma$  tall (the  $2\sigma$  rule),
- 99.7% of (i.e., almost all) women are  $\mu\pm3\sigma$  tall (the  $3\sigma$  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, etc.

knowledge? Are simplifications necessary when dealing with complexity? What are the alternatives?

## 8.2 Comparing Cumulative Distribution Functions

One way of visually assessing the extent to which a sample deviates from a hypothesised distribution, is by plotting the empirical and the theoretical *cumulative distribution* function (CDF) on one plot.

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 obtaining a value not greater than x. For the normal distribution family, this can be computed by calling scipy.stats.norm.cdf.

This is a superb match.

Of course, visual inspection does not replace statistical goodness-of-fit tests. However, it is worth noting that the popular Kolmogorov–Smirnov<sup>73</sup> test relies on assessing the greatest absolute deviation between the two functions.

<sup>73</sup> https://en.wikipedia.org/wiki/Kolmogorov%E2%80%93Smirnov\_test

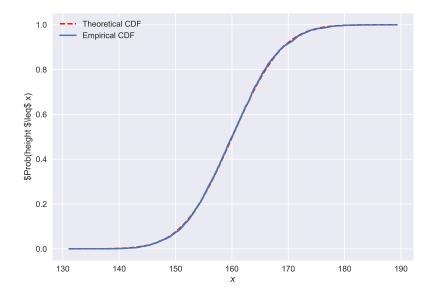


Figure 8.3: plot of chunk 250-distribution-uni-6

## 8.3 Q-Q plots

A Q-Q<sup>74</sup> (quantile-quantile) plot is another graphical method for comparing two distributions. This time, instead of working with cumulative distribution functions, we will be dealing with their inverses, i.e., quantile functions.

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 simply assume that the  $\frac{i}{n+1}$ -quantile is equal to  $x_{(i)}$ , i.e., the i-th smallest value in the given sample  $(x_1, x_2, \ldots, x_n)$  and consider only i=1, 2, ..., n.

The theoretical quantiles can be generated by the scipy.stats.norm.ppf function, where ppf stands for the percent point function (but most statisticians call it the quantile function).

<sup>74</sup> https://en.wikipedia.org/wiki/Q%E2%80%93Q\_plot

Our simplified setting successfully avoids the problem which arises when the 0- or 1-quantile of the theoretical distribution 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)
heights_sorted = np.sort(heights) # theoretical quantiles
quantiles = scipy.stats.norm.ppf(q, μ, σ) # sample quantiles
plt.plot(quantiles, heights_sorted, "o")
plt.axline((heights_sorted[n//2], heights_sorted[n//2]), slope=1)
plt.xlabel("Theoretical quantiles")
plt.ylabel("Sample quantiles")
plt.show()
```

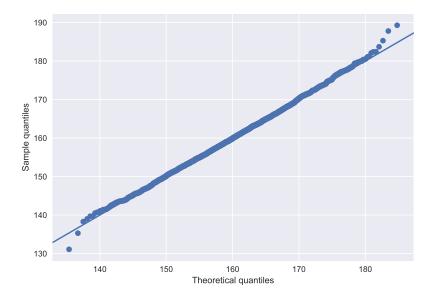


Figure 8.4: plot of chunk 250-distribution-uni-7

Ideally, the points should be arranged on the y=x line (which was added for readability) – which would happen if the sample quantiles matched 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.

Overall, we can say that this is a very good fit.

## 8.4 Log-normal Distribution

We say that a sample is log-normally distributed<sup>75</sup>, if its logarithm is normally distributed. It is sometimes observed that the income of most individuals (except the richest) is distributed, at least approximately, log-normally.

Let us depict the distribution of the logarithm of income:

```
income = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
 "teaching_data/master/marek/uk_income_simulated_2020.txt")
sns.histplot(income, stat="density", kde=True, log_scale=True)
plt.show()
```

This indeed resembles a normal distribution (note again the log scale on the x-axis).

It might thus make sense to fit a log-normal model. The fitting process is similar to the normal case, but this time we the compute mean and standard deviation based on the logarithm of data:

```
μ = np.mean(np.log(income))
σ = np.std(np.log(income), ddof=1)
μ, σ
(10.314409794364623, 0.5816585197803816)
```

Let's draw the probability density function (on the original, not log-scale now):

```
sns.histplot(income, stat="density", kde=True)
x = np.linspace(np.min(income), np.max(income), 1000)
plt.plot(x, scipy.stats.lognorm.pdf(x, s=\sigma, scale=np.exp(\mu)), "r:")
plt.show()
```

This fit is not too bad. It slightly underestimates the proportion of households with extremely small income and overestimates the fraction of the quite small-income ones, hence it might be considered too optimistic (note that we deal with only a sample of

<sup>75</sup> https://en.wikipedia.org/wiki/Log-normal\_distribution

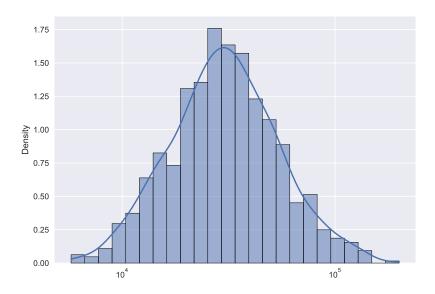


Figure 8.5: plot of chunk 250-distribution-uni-8

1000 households here; the original UK Office of National Statistics data<sup>76</sup> could tell us more about the quality of the model in general, but it's beyond the scope of our simple exercise).

Here is the quantile-quantile plot on a double-logarithmic scale for both the above log-normal model and an estimated normal one.

 $<sup>^{76}\</sup> https://www.ons.gov.uk/people$ population and community/personal and household finances/income and we alth/bulletins/household disposable income and in equality/financial year 2020

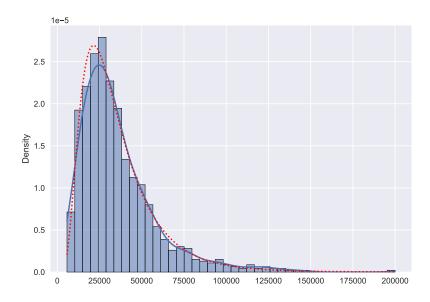


Figure 8.6: plot of chunk 250-distribution-uni-10

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```
plt.xlabel("Log-normal heoretical quantiles")
plt.ylabel("Sample quantiles")
plt.xscale("log")
plt.yscale("log")

plt.subplot(122)
quantiles2 = scipy.stats.norm.ppf(
 q, np.mean(income), np.std(income_sorted, ddof=1)
)
plt.plot(quantiles2, income_sorted, "o")
plt.axline((income_sorted[n//2], income_sorted[n//2]), slope=1)
plt.xlabel("Normal theoretical quantiles")
```

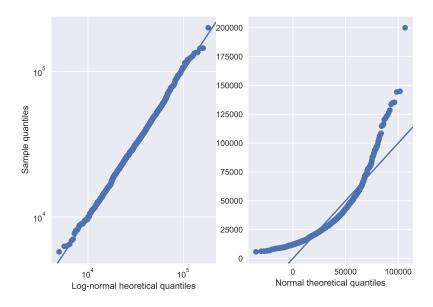


Figure 8.7: plot of chunk 250-distribution-uni-11

We see that definitely the hypothesis that our data follow a normal distribution (the right subplot) is most likely false.

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,  $\mu$  and  $\sigma$ , based on which (and probability theory), we may deduce<sup>77</sup> that:

- the expected average (mean) income is  $e^{\mu+\sigma^2/2}$ ,
- median is  $e^{\mu}$ ,
- most probable one (mode) in  $e^{\mu \sigma^2}$ ,

#### etc.

Recall again that for skewed distributions such as this one, reporting the mean might mislead some of us. 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,

<sup>77</sup> https://en.wikipedia.org/wiki/Log-normal\_distribution

it's not only  $\mu$  that matters, it's also  $\sigma$  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  $^{78}$  distribution the situation is very different, because, the mean, median, and most probable outcomes tend to be the same – the distribution is symmetric around  $\mu$ .

**Exercise.** Compare the empirical and theoretical CDFs for the income dataset and its log-normal model.

(\*) **Exercise.** What is the fraction of people with earnings below the mean?

### 8.5 Pareto Distribution

Consider again the dataset<sup>79</sup> 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)
```

Here is the histogram with the populations on the log-scale:

```
sns.histplot(cities, bins=20, log_scale=True)
plt.show()
```

<sup>&</sup>lt;sup>78</sup> https://en.wikipedia.org/wiki/Normal\_distribution

<sup>79</sup> https://arxiv.org/abs/0706.1062v2

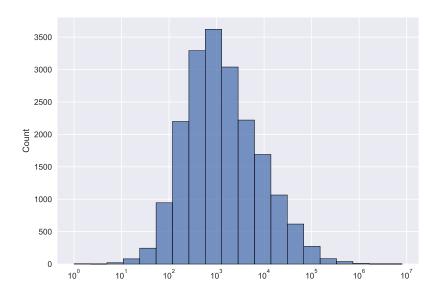


Figure 8.8: plot of chunk 250-distribution-uni-13

This kind-of looks like a log-normal distribution again, which the reader can inspect themself.

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:

```
min_size = 10_000
large_cities = cities[cities >= min_size]
len(large_cities), sum(large_cities) # number of cities, total population
(2696, 146199374.0)
```

Plotting the above on a double-logarithmic scale:

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

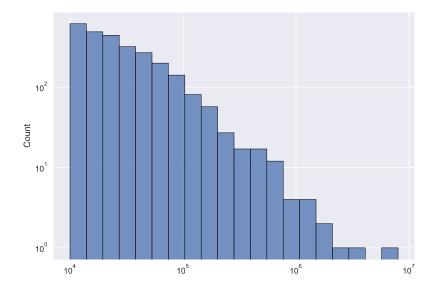


Figure 8.9: plot of chunk 250-distribution-uni-15

reveals something 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 this paper and this one for discussion.

(\*\*) Let's fit a Pareto distribution to our dataset. This is a little tricky; the reader is free to skip the following and just take a look at the final plot.

The Pareto distribution family is also identified by two parameters: the (what *scipy* calls it) scale parameter is equal to the shift from 0, and is usually taken as the sample minimum (i.e., 10,000 in our case). The shape parameter,  $\alpha$ , which controls the slope of the said line on the double-log-scale, can be estimated through the reciprocal of the mean of the scaled logarithms of our observations:

(continues on next page)

<sup>80</sup> https://arxiv.org/pdf/0706.1062v2.pdf

<sup>81</sup> https://www.cs.cornell.edu/courses/cs6241/2019sp/readings/Newman-2005-distributions.pdf

(continued from previous page)

```
a
0.9496171695997675
```

Unfortunately, comparing the theoretical densities and an empirical histogram on a log-scale is quite problematic, therefore we will have to implement the whole drawing manually.

First, we apply logarithmic binning on the dataset and normalise the counts so that they add to 1.

```
b = np.geomspace(min_size, np.max(large_cities), 21) # bins' boundaries
c = np.histogram(large_cities, bins=b)[0] # apply binning
c = c/np.sum(c) # normalise so that it adds to 1
```

Next, we compute the probabilities of a random variable's from our Pareto distribution falling into each bin:

```
p = np.diff(scipy.stats.pareto.cdf(b, a, scale=min_size))
p = p/np.sum(p) # normalise so that it adds to 1
```

This is based on the cumulative distribution function. We have that for any b[i], cdf(b[i]) is the probability that we observe a value  $\leq b[i]$ . Therefore, cdf(b[i]) - cdf(b[i-1]), which we ultimately get by applying numpy.diff, is the probability of observing a value between b[i-1] and b[i].

Now we can depict the counts and the probabilities on the same plot:

```
midb = 0.5*(b[:-1]+b[1:]) # mid-bins
plt.bar(midb, width=np.diff(b), height=c, edgecolor="black")
plt.plot(midb, p, "r:")
plt.xscale("log")
plt.yscale("log")
plt.show()
<BarContainer object of 20 artists>
```

This is an okayish fit, although the populations of the largest cities are overestimated.

Here is 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)
```

(continues on next page)

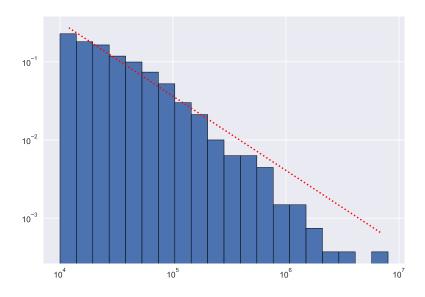


Figure 8.10: plot of chunk 250-distribution-uni-19

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```
quantiles = scipy.stats.pareto.ppf(q, a, scale=min_size)
plt.plot(quantiles, cities_sorted, "o")
plt.axline((quantiles[n//2], cities_sorted[n//2]), slope=1)
plt.xlabel("Theoretical quantiles")
plt.ylabel("Sample quantiles")
plt.xscale("log")
plt.yscale("log")
plt.yscale("log")
```

It could be better, but the cities are still growing, right?

(\*\*) **Exercise.** Compare the empirical and theoretical CDFs for the large\_cities dataset and its Paretian model.

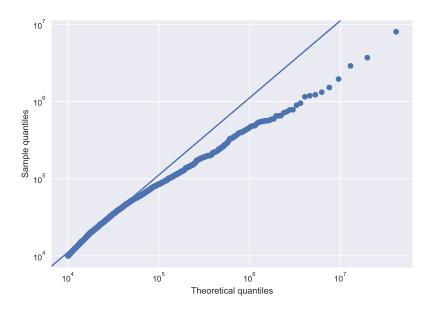


Figure 8.11: plot of chunk 250-distribution-uni-20

### 8.6 Uniform Distribution

Consider the Polish *Lotto* lottery, where 6 numbered balls {1,2,...,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")
plt.bar(np.arange(1, 50), width=1, height=lotto, edgecolor="black")
plt.show()
<BarContainer object of 49 artists>
```

Here, we see that each event occurs more or less with the same probability. Of course,

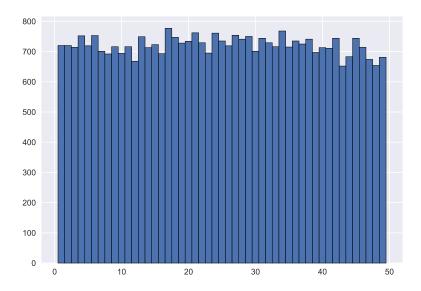


Figure 8.12: plot of chunk 250-distribution-uni-21

the numbers on the balls are integer, but in our idealised scenario we may try modelling this dataset using a continuous  $uniform^{82}$  distribution (there is its discrete version too), which yields arbitrary real numbers on a given interval (a, b), i.e., between some a and b.

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<sup>83</sup> function).

```
x = np.arange(1, 50)
plt.bar(x, width=1, height=lotto/np.sum(lotto), edgecolor="black")
plt.plot(x, scipy.stats.uniform.pdf(x, 1, 49), "r:")
plt.show()
<BarContainer object of 49 artists>
```

Visually, this model makes much sense, but again, some more rigorous statistical test-

<sup>82</sup> https://en.wikipedia.org/wiki/Continuous\_uniform\_distribution

<sup>83</sup> https://en.wikipedia.org/wiki/Floor\_and\_ceiling\_functions

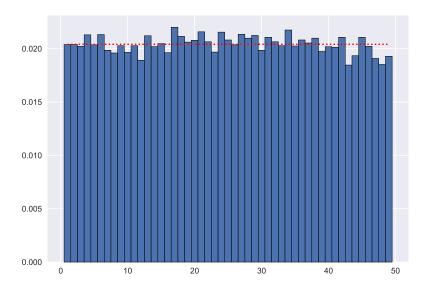


Figure 8.13: plot of chunk 250-distribution-uni-22

ing 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.** Does playing lotteries<sup>84</sup> and engaging in gambling make *rational* sense at all? 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?

<sup>84</sup> https://en.wikipedia.org/wiki/Lottery

**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 and that the emerging patterns are plentiful and subject to qualitative analysis. "Why there is something rather than nothing" being the fundamental question of metaphysics, is left for the reader to figure out once and for all when they go for their next stroll (or millions thereof) in the park.

## 8.7 Generating Pseudorandom Numbers

A probability distribution is useful not only for describing a dataset. It also enables performing some 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 any numbers of independent (not related to each other) observations.

When most people say *random*, they implicitly mean *uniformly distributed*. For example:

```
np.random.rand(5)
array([0.64690469, 0.57709702, 0.11913463, 0.10785634, 0.30480813])
```

gives 5 deviates from the uniform distribution on the (0, 1) interval.

The same with *scipy*, but this time the support will be (-10, 15).

```
scipy.stats.uniform.rvs(-10, 25, size=5) # from -10 to -10+25
array([4.70983568, -8.64842379, 2.65283952, 2.6988176 , -0.97321071])
```

Actually, we are generating numbers using a computer, which is purely deterministic, hence we shall refer to them as pseudorandom<sup>86</sup> or random-like ones (albeit they are non-distinguishable from truly random, when subject to rigorous tests for randomness).

<sup>85</sup> https://en.wikipedia.org/wiki/Why\_there\_is\_anything\_at\_all

<sup>86</sup> https://en.wikipedia.org/wiki/Pseudorandom\_number\_generator

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.

Of course, generating data from other distributions is possible too. For example, here is a normally distributed sample:

```
sample = scipy.stats.norm.rvs(100, 16, size=250, random_state=12641)
sns.histplot(sample, stat="density", kde=True)
x = np.linspace(36, 164, 1001)
plt.plot(x, scipy.stats.norm.pdf(x, 100, 16), "r:")
plt.show()
```

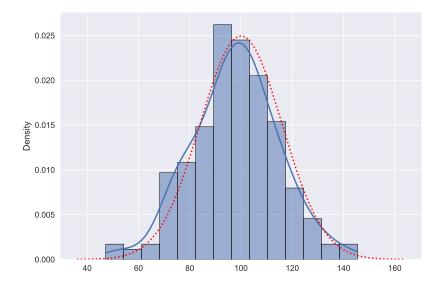


Figure 8.14: plot of chunk 250-distribution-uni-28

Note that even a sample which we know that was generated from a specific distribution will deviate from it, sometimes considerably. Such effects usually disappear when the sample size increases (compare the Fundamental Theorem of Statistics<sup>87</sup>).

**Exercise.** Conclusions based on simulated data are trustworthy, because they cannot be manipulated. Or can they? The above pseudorandom number generator's seed, 12641, is quite suspicious. It might suggest

<sup>87</sup> https://en.wikipedia.org/wiki/Glivenko%E2%80%93Cantelli\_theorem

that someone wanted to *prove* some point. This is why yours truly recommends sticking to one and only seed most of the time, e.g., 123.

**Exercise.** Generate many samples from the standard normal distribution of different sizes (e.g., 100 and 10000) and plot histograms for them. Note how often there will be some ruggedness in the bars' sizes that a naïve observer would 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 do detect those which are worth attention).

### 8.8 Distribution Mixtures

Some datasets may fail to fit into simple models such as the ones describe 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 try.

Other reasons may be that what we observe is in fact a *mixture* of simpler processes.

The December 2021 hourly averages pedestrian counts<sup>88</sup> near the Southern Cross Station in Melbourne data might be a good instance of such a scenario:

```
peds = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
 "teaching_data/master/marek/southern_cross_station_peds_2019_dec.txt")
plt.bar(np.arange(0, 24), width=1, height=peds, edgecolor="black")
plt.show()
<BarContainer object of 24 artists>
```

This particular data set is quite coarse-grained (we only have 24 bar heights at our dis-

<sup>88</sup> http://www.pedestrian.melbourne.vic.gov.au/

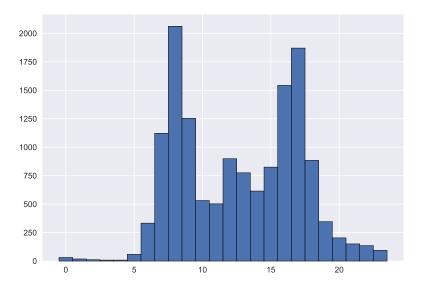


Figure 8.15: plot of chunk 250-distribution-uni-29

posal), but otherwise it might not be a bad idea to try to fit a probabilistic combination<sup>89</sup> of three normal distributions, corresponding to the morning, lunch-time, and evening pedestrian count peak.

For example (below are lucky guesstimates only):

(continues on next page)

<sup>89</sup> https://en.wikipedia.org/wiki/Mixture\_distribution

plt.show()
## <BarContainer object of 24 artists>

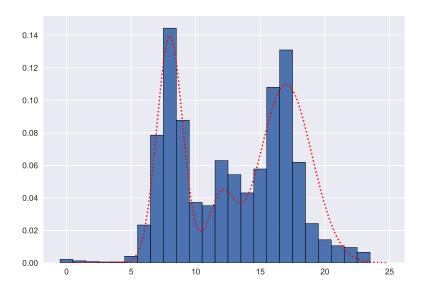


Figure 8.16: plot of chunk 250-distribution-uni-30

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.

It will frequently be the case in data modelling that more complex entities 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.

(\*) **Exercise.** Generate 1000 pseudorandom numbers from the above mixture.

### 8.9 Further Reading

 $James\ E.\ Gentle, \textit{Theory of Statistics}, draft\ https://mason.gmu.edu/~jgentle/books/MathStat.pdf and the statistics of the statistic$ 

A. Clauset, C.R. Shalizi, and M.E.J. Newman, Power-law distributions in empirical data, SIAM Review 51(4), 661-703 (2009). (arXiv:0706.1062) https://arxiv.org/pdf/0706.1062v2.pdf

M.E.J. Newman, Power laws, Pareto distributions and Zipf's law, *Contemporary Physics* **46**, 323 (2005). https://www.cs.cornell.edu/courses/cs6241/2019sp/readings/Newman-2005-distributions.pdf

### 8.10 Questions

- 1. Why is the notion of the mean income confusing?
- 2. When manually setting the seed of a random number generator makes sense?
- 3. 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 = ...?

# Handling Categorical Data

So far we have been dealing with *quantitative* (numeric) data – real numbers on which we can apply various mathematical operations, such as computing the arithmetic mean and standard deviation or binning. 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 are 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 the part on data frames, 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<sup>90</sup>-type scales such as "strongly disagree" < "disagree" < "neutral" < "agree" < "strongly agree", etc.).

### 9.1 Representing Categorical Data

Two common ways to represent a categorical variable with k distinct levels is by storing it as:

<sup>90</sup> https://en.wikipedia.org/wiki/Likert\_scale

- · a vector of strings,
- a vector of integers between 0 (inclusive) and k (exclusive).

These two are easily interchangeable.

For instance, consider the data on where the top 16 marathoners come from:

```
import numpy as np
countries = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
 "teaching_data/master/marek/37_pzu_warsaw_marathon_country.txt",
 dtype="str")
x = countries[:16]
x
array(['KE', 'KE', 'KE', 'ET', 'KE', 'ET', 'MA', 'PL', 'PL', 'IL',
'PL', 'KE', 'KE', 'PL', 'PL'], dtype='<U2')</pre>
```

These are two-letter ISO 3166<sup>91</sup> country codes, encoded of course as strings (note the dtype="str" argument).

Calling numpy.unique allows us to determine the set of distinct categories:

```
np.unique(x)
array(['ET', 'IL', 'KE', 'MA', 'PL'], dtype='<U2')</pre>
```

They have been sorted automatically.

### 9.1.1 Encoding and Decoding Factors

In order to *encode* x through a set of consecutive nonnegative integers, we pass the return inverse=True argument to numpy.unique:

Note that the code sequence 2, 2, 2, 0, ... corresponds to the 3rd, 3rd, 3rd, 1st, ... level in categories, i.e., Kenya, Kenya, Kenya, Ethiopia, ....

The values between 0 and k-1=4 can be used to index a given an array of length k=5. Hence, in order to *decode* our factor, we can write:

<sup>91</sup> https://en.wikipedia.org/wiki/List\_of\_ISO\_3166\_country\_codes

#### categories[codes]

```
array(['KE', 'KE', 'KE', 'KE', '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]
array(['Kenya', 'Kenya', 'Ethiopia', 'Kenya', 'Kenya',
'Ethiopia', 'Morocco', 'Poland', 'Poland', 'Israel', 'Poland',
'Kenya', 'Kenya', 'Poland', 'Poland'], dtype='<U8')</pre>
```

This is an instance of the *recoding* of a categorical variable.

**Important.** Despite the fact that we can *represent* a categorical variables using a set of integers, it does not make them become instances of a numerical type. Arithmetic operations do not make sense on them.

(\*\*) **Exercise.** Determine the set of unique values in x in the order of appearance (and not sorted lexicographically). Then, encode x using this level set. Hint: check out the return\_index argument to numpy.unique and the numpy.searchsorted function.

### 9.1.2 Binning Numeric Data

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 a histogram.

Also, reporting counts 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 (government, research, non-for-profits, NGOs, 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.

**Note.** 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 distribute them in binned or otherwise aggregated form.

Consider the 16 best marathon finish times (in minutes):

numpy.searchsorted can be used to determine the interval where each value in t falls.

```
bins = [130, 140, 150]
codes = np.searchsorted(bins, t)
codes
array([0, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 2, 3, 3])
```

By default, the intervals are of the form (*a*, *b*] (not including *a*, including *b*). Code 0 corresponds to values less than the first bin bound, whereas code 3 – greater than or equal to the last bound:

(\*) **Exercise.** 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 can be useful for generating equidistant bounds on linear and logarithmic scale, respectively.

(\*) We can create a set of the corresponding categories, for example, as follows:

```
bins2 = np.r_[-np.inf, bins, np.inf]
categories = np.array(
 [f"({bins2[i-1]}, {bins2[i]}]" for i in range(1, len(bins2))]
)
categories
array(['(-inf, 130.0]', '(130.0, 140.0]', '(140.0, 150.0]',
'(150.0, inf]'], dtype='<U14')</pre>
```

This uses the so-called *list comprehension* which is a convenient substitute for a for loop and the list.append method.

And now recoding:

```
categories[codes]
```

# 9.1.3 Generating Pseudorandom Labels

numpy.random.choice allows us to create a pseudorandom sample of with categories picked with any probabilities:

```
np.random.seed(123)
np.random.choice(
 ["spam", "bacon", "eggs", "tempeh"], p=[0.7, 0.1, 0.15, 0.05],
 replace=True, size=16
```

```
(continued from previous page)
```

```
)
array(['spam', 'spam', 'spam', 'bacon', 'spam', 'tempeh', 'spam',
'spam', 'spam', 'spam', 'bacon', '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.

## 9.2 Frequency Distributions

### 9.2.1 Counting

For arbitrary categorical data, we can call:

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.

If we already have an array of integer codes between 0 and k-1, numpy. bincount will return the number of times each code appears therein.

```
categories, codes = np.unique(x, return_inverse=True)
counts = np.bincount(codes)
counts
array([2, 1, 7, 1, 5])
```

We can output a nice frequency table as follows:

```
for category, count in zip(categories, counts):
 print(f"{category:4}: {count:5}")
ET : 2
IL : 1
KE : 7
```

```
MA : 1
PL : 5
```

Note that a vector of counts can easily be turned into a vector of proportions (fractions):

```
counts/np.sum(counts)
array([0.125 , 0.0625, 0.4375, 0.0625, 0.3125])
```

Hence, almost 31.25% of the top players were from Poland.

Recall that in the part on histograms, 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.

**Exercise.** Apply numpy.histogram on the 37\_pzu\_warsaw\_marathon\_mins data.

## 9.2.2 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 later).

First of all, we are definitely not going to be discussing the infamous pie charts<sup>92</sup>, because their use in data analysis has been widely criticised for a long time (it's difficult to judge the ratios of areas).

#### **Bar Plots**

Bar plots will do the trick most of the time (matplotlib.pyplot.bar):

```
import matplotlib.pyplot as plt
plt.style.use("seaborn")
```

<sup>92</sup> https://en.wikipedia.org/wiki/Pie\_chart

```
ind = np.arange(len(categories))
plt.bar(ind, height=counts)
plt.xticks(ind, categories)
plt.show()
<BarContainer object of 5 artists>
([<matplotlib.axis.XTick object at 0x7fdd659cb2b0>, <matplotlib.axis.
-XTick object at 0x7fdd659cb280>, <matplotlib.axis.XTick object at[]
-0x7fdd659b0e20>, <matplotlib.axis.XTick object at 0x7fdd646bc700>,
-<matplotlib.axis.XTick object at 0x7fdd646bcc10>], [Text(0, 0, 'ET'), []
-Text(1, 0, 'IL'), Text(2, 0, 'KE'), Text(3, 0, 'MA'), Text(4, 0, 'PL')]])
```

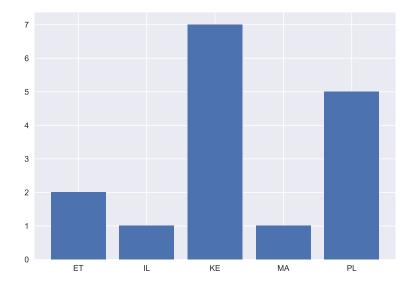


Figure 9.1: plot of chunk 260-categorical-uni-15

**Exercise.** Assign a different colour to each bar.

**Exercise.** Draw a bar plot which features proportions instead of counts, so that the total bar height is 100% (or 1).

**Exercise.** Print the frequency table and draw a bar plot for all the marathoners' countries (not just the top 16).

#### Don't Let Them Trick You

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. Here are the official results that might be presented by one of the infamous Polish TV conglomerate:

Such a great victory! Wait... it was a close vote after all!

Another media source could have reported it like this:

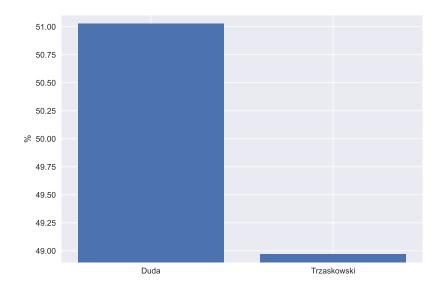


Figure 9.2: plot of chunk 260-categorical-uni-16

```
plt.bar([1, 2], height=[51.03, 48.97])
plt.xticks([1, 2], ["Duda", "Trzaskowski"])
plt.ylabel("%")
plt.ylim(0, 250)
plt.yticks([0, 100])
plt.show()
<BarContainer object of 2 artists>
([<matplotlib.axis.XTick object at 0x7fdd57c949d0>, <matplotlib.axis.
-XTick object at 0x7fdd57c94d90>], [Text(1, 0, 'Duda'), Text(2, 0,
-'Trzaskowski')])
(0.0, 250.0)
([<matplotlib.axis.YTick object at 0x7fdd57c31910>, <matplotlib.axis.
-YTick object at 0x7fdd57c31d00>], [Text(0, 0, ''), Text(0, 0, '')])
```

The moral of the story is: always read the axis tick marks.

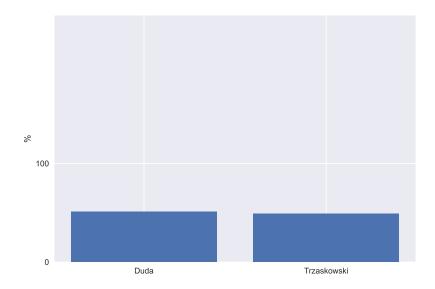


Figure9.3: plot of chunk 260-categorical-uni-17

## Error Bars (\*\*)

Occasionally, the data we have at hand are based on small surveys and are supposed to serve as estimates of what might be happening in a larger population.

For instance, one of the pre-election polls indicated that 516 out of 1017 people would vote for Duda. This is ca. 50.74%, but this number is subject to sampling error.

If we asked a statistician for the error estimates, they could provide us with, for example, 95% confidence intervals for the true proportions (scipy.stats.binomtest has a procedure implementing this). For both candidates, they are within ca.  $\pm 3.1\%$  from the sample estimates. It would be nice to inform the reader of the figure that we are uncertain about the truth. *Error bars* can serve this purpose.

To recall, the winner scored 51.03% on the election day, where 20,458,911 valid votes were cast in total.

```
c, n = 516, 1017
plt.bar([1, 2], height=[c/n, (n-c)/n])
```

```
plt.errorbar([1, 2], [c/n, (n-c)/n], yerr=0.031, fmt="r")
plt.xticks([1, 2], ["Duda", "Trzaskowski"])
plt.ylabel("%")
plt.show()
<BarContainer object of 2 artists>
<ErrorbarContainer object of 3 artists>
([<matplotlib.axis.XTick object at 0x7fdd57c31550>, <matplotlib.axis.

_XTick object at 0x7fdd57c31220>], [Text(1, 0, 'Duda'), Text(2, 0,
_'Trzaskowski')])
```

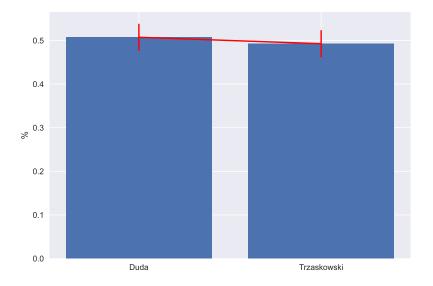


Figure 9.4: plot of chunk 260-categorical-uni-18

Note that in order to improve the estimate, we would of course have to poll more people, e.g., a sample of size 10,000 would give errors of  $\pm 0.1\%$  (assuming people don't change their minds in the meantime).

(continues on next page)

### 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 80–20% being an often cited rule of thumb).

For instance, in the part where we modelled the US cities' population dataset using the Pareto distribution (the very same Pareto, but a different, yet related object), where 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.

Here is a dataset<sup>93</sup> fabricated by the Clinical Excellence Commission in New South Wales, Australia, listing the most frequent causes for medication errors:

```
categories = np.array([
 "Unauthorised drug", "Wrong IV rate", "Wrong patient", "Dose missed",
 "Under dose", "Wrong calculation","Wrong route", "Wrong drug",
 "Wrong time", "Technique error", "Duplicated drugs", "Over dose"
])
counts = np.array([1, 4, 53, 92, 7, 16, 27, 76, 83, 3, 9, 59])
np.sum(counts) # total number of medication errors
430
```

Let's order the dataset with respect to the counts, decreasingly:

```
o = np.arqsort(counts)[::-1] # ordering permutation (reversed = decreasing)
categories = categories[o] # order categories based on counts
counts = counts[o] # equivalent to np.sort(counts)[::-1]
for category, count in zip(categories, counts):
 print(f"{category:20}: {count:2}")
Dose missed
 : 92
Wrona time
 : 83
Wrong drug
 : 76
Over dose
 : 59
Wrong patient
 : 53
Wrong route
 : 27
Wrong calculation : 16
Duplicated drugs : 9
Under dose
 : 7
Wrong IV rate
```

<sup>93</sup> https://www.cec.health.nsw.gov.au/CEC-Academy/quality-improvement-tools/pareto-charts

```
Technique error : 3
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:

```
x = np.arange(len(categories)) # 0, 1, 2, ...
p = 100.0*counts/np.sum(counts) # percentages

fig, ax1 = plt.subplots()
ax1.set_xticks(x-0.5, categories, rotation=60)
ax1.set_ylabel("%")
ax1.bar(x, height=p)

ax2 = ax1.twinx() # this creates a new coordinate system with a shared XL
-axis
ax2.plot(x, np.cumsum(p), "ro-")
ax2.grid(visible=False)
ax2.set_ylabel("cumulative %")

fig.tight_layout()
plt.show()
<BarContainer object of 12 artists>
```

As usual, fine-tuning of the figure and studying the manual of the *matplotlib* package is left as an exercise.

From the figure, we can read that 5 causes (less than 40%) correspond to ca. 85% of the medication errors:

```
for category, cumprob in zip(categories, np.round(np.cumsum(p), 1)):
 print(f"{category:20}: {cumprob:5}%")

Dose missed : 21.4%

Wrong time : 40.7%

Wrong drug : 58.4%
```

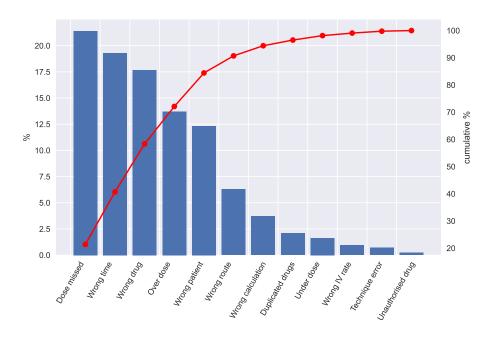


Figure 9.5: plot of chunk 260-categorical-uni-21

```
Over dose
 72.1%
Wrong patient
 84.4%
Wrona route
 90.7%
Wrona calculation
 : 94.4%
Duplicated drugs
 : 96.5%
Under dose
 98.1%
Wrong IV rate
 : 99.1%
Techniaue error
 : 99.8%
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, above there is a hint. However, com-

ing up with something more effective yet so simple at the same time requires much more thinking.

## 9.2.3 Aggregating

As we have already said, the only operation on categorical data that we can rely on is counting. Therefore, as far as qualitative data aggregation is concerned, what we are left is the *mode*, i.e., the most frequently occurring value.

### Categorical Data

There is one more measure of central tendency worth mentioning. Namely, a *mode* is a most frequently occurring value.

```
categories, counts = np.unique(countries, return_counts=True)
categories[np.argmax(counts)]
'P|'
```

Recall that if i is argmax(counts) (argument maximum), then counts[i] is the same as max(counts) and categories[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:

```
categories2, counts2 = np.unique(countries[:22], return_counts=True)
categories2[np.where(counts2 == np.max(counts2))]
array(['KE', 'PL'], dtype='<U2')</pre>
```

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).

#### **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.** Compute some potentially informative modes for the 2020 UK income<sup>94</sup> data. Play around with different numbers of bins for linear and logarithmic binning and see how it affects the mode.

### Ordinal Data (\*)

In case where the categories can be linearly ordered, i.e., ordinal data, except for the mode, we can also define sample quantiles, although the standard methods for resolving ties will not work.

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=1, P=2, ..., HD=5). In the latter example, the median would be equal to 3.5.

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).

<sup>94</sup> https://raw.githubusercontent.com/gagolews/%5Cteaching\_data/master/marek/uk\_income\_simulated\_2020.txt

(\*\*) **Exercise.** The grades\_results<sup>95</sup> represents the grades (F, P, C, D, HD) of 100 students attending an imaginary course in a virtual Australian university. How would you determine the *average* grade represented as a number between 0 and 100, taking 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<sup>96</sup> dataset.

### 9.3 Binary Data and Logical Vectors

Binary data is a special case of the qualitative setting, where we only have two categories.

For convenience, we usually encode the two classes as integer 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 -0.327) to True.

### For example:

or, equivalently:

```
np.array([True, False, True, True, False]).astype(int)
array([1, 0, 1, 1, 0])
np.array([-2, -0.326, -0.000001, 0.0, 0.1, 1, 7643]).astype(bool)
array([True, True, True, False, True, True, True])
```

<sup>95</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/marek/grades\_results.txt

<sup>&</sup>lt;sup>96</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/marek/grades\_scores.txt

```
np.array([-2, -0.326, -0.000001, 0.0, 0.1, 1, 7643]) != 0 ## array([True, True, True, False, True, True, True])
```

Perhaps the most useful arithmetic operation on logical vectors is the sum.

```
x = countries[:16]
x # recall
array(['KE', 'KE', 'ET', 'KE', 'KE', 'ET', 'MA', 'PL', 'PL', 'IL',
'PL', 'KE', 'KE', 'PL', 'PL'], dtype='<U2')
np.sum(x == "KE")
7</pre>
```

is the number of elements in x that are equal to "KE" (because the sum of os and 1s is equal to the number of 1s in the sequence). Note that (x == "KE") is a logical vector that represents a binary categorical variable with levels: not-Kenya (False) and Kenya (True).

If we divide the above result by the length of the vector, we will get the proportion:

```
np.mean(x == "KE")
0.4375
```

Hence, almost 44% amongst the top 16 runners are from Kenya.

**Exercise.** What is the meaning of numpy.all, numpy.any, numpy.min, numpy.max, numpy.cumsum, and numpy.cumprod applied on logical vectors?

(\*\*) Having the O/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.

## 9.4 Questions

- 1. Does it make sense to compute the arithmetic mean of a categorical variable?
- 2. Name the basic use cases for categorical data.
- 3. (\*) What is a Pareto chart?
- 4. How to deal with the case of the mode being nonunique?
- 5. What is the meaning of numpy.mean((x > 0) & (x < 1)), where x is a numeric vector?
- 6. What is the meaning of the sum and mean for binary data (logical vectors)?

# **Processing Time Series**

So far we have been using *numpy* vectors 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 a population recorded at a particular point in time;
- frequency distributions, i.e., count data and the corresponding categories or labels.

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.

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.

Here are some data aggregates – the popular quantiles:

```
np.quantile(temps, [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(temps), np.std(temps)
(8.990273958441023, 9.16204388619955)
```

and a graphical summary of the data distribution:

```
import matplotlib.pyplot as plt
import seaborn as sns
plt.style.use("seaborn")
sns.violinplot(data=temps, orient="h")
plt.show()
```

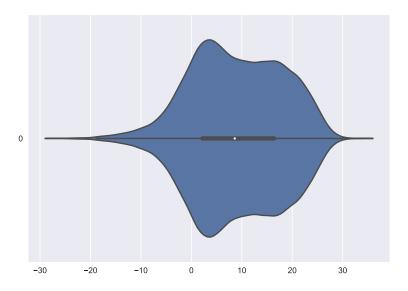


Figure 10.1: plot of chunk 270-time-uni-4

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:

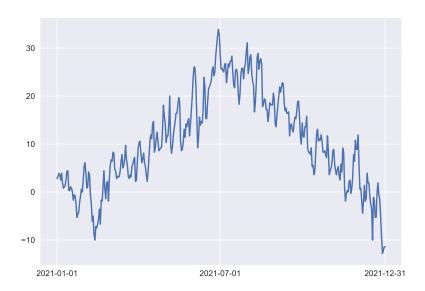


Figure 10.2: plot of chunk 270-time-uni-5

We call this a *line chart* – data points are connected by straight line segments. There are some visible trends, such as that, well, obviously, winter is colder than summer, duh.

# 10.1 Working with Datetimes and Timedeltas

numpy.datetime6497 is a type to represent datetimes.

Usually, we'll be creating datetimes from strings, for instance:

```
d = np.array(["1889-08-01", "1970-01-01", "2021-12-31"], dtype="datetime64")
d
array(['1889-08-01', '1970-01-01', '2021-12-31'], dtype='datetime64[D]')
dt = np.array(["1970-01-01T02:01:05"], dtype="datetime64")
dt
array(['1970-01-01T02:01:05'], dtype='datetime64[s]')
```

**Note.** In a farther part, we'll be dealing with datetimes in nonstandard formats, e.g., "08/31/1996".

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:

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'], dtype='datetime64[D]')
dt+np.timedelta64(12, "h") # plus 12 hours
array(['1970-01-01T14:01:05'], dtype='datetime64[s]')
d-dt
array([-2537748065, -7265, 1640901535], dtype='timedelta64[s]')
```

<sup>97</sup> https://numpy.org/doc/stable/reference/arrays.datetime.html

numpy.arange can be used to generate sequences of equidistant datetimes:

Based on this, we can plot the data for the last 5 years quite easily:

```
which = (dates >= np.datetime64("2017-01-01"))
dates5, temps5 = dates[which], temps[which]
plt.plot(dates5, temps5)
plt.show()
```

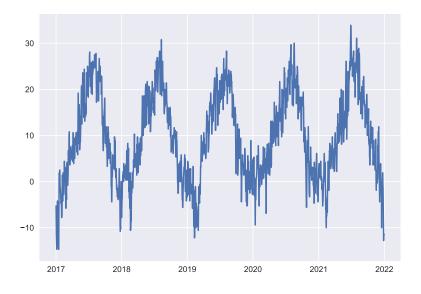


Figure 10.3: plot of chunk 270-time-uni-14

### 10.2 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[-5:] # last 5 days
x
array([-9.4, -12.8, -12.2, -11.4, -11.4])
```

The iterative differences (deltas) are:

```
d = np.diff(x)
d
array([-3.4, 0.6, 0.8, 0.])
```

For instance, between the second and the first day, the midrange temperature dropped by -3.4°C.

The other way around, the cumulative sums of the deltas:

```
np.cumsum(d)
array([-3.4, -2.8, -2. , -2.])
```

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([-9.4, -12.8, -12.2, -11.4, -11.4])
```

**Exercise.** Consider the euraud-20200101-20200630-no-na<sup>98</sup> 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.

<sup>98</sup> https://raw.githubusercontent.com/gagolews/%5Cteaching\_data/master/marek/euraud-20200101-20200630-no-na.txt

### 10.3 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  $(x_1, x_2, ..., x_n)$  and some  $k \le n$ , the k-moving average is a vector  $(y_1, y_2, ..., y_{n-k+1})$  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:

```
x = np.array([3, 5, 4, -3, 6, 9, 11, 7, 2])
```

Here is the 3-moving average:

```
from numpy.lib.stride_tricks import sliding_window_view
np.round(np.mean(sliding_window_view(x, 3), axis=-1), 2)
array([4. , 2. , 2.33, 4. , 8.67, 9. , 6.67])
```

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.

And now for something completely different: the 5-moving average:

```
np.round(np.mean(sliding_window_view(x, 5), axis=-1), 2)
array([3. , 4.2, 5.4, 6. , 7.])
```

Applying the moving average has the nice effect of *smoothing* out all kinds of broadly-conceived noise. To illustrate this, consider the temperature data for the 5 last years:

```
plt.plot(dates5[50:-49], temps5_ma100, "r--", label="100-day moving average")
plt.legend()
plt.show()
```

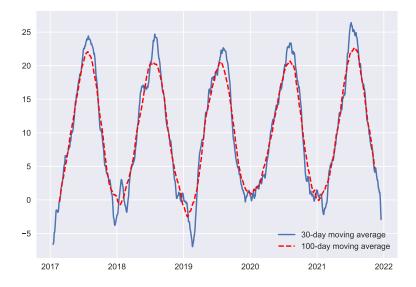


Figure 10.4: plot of chunk 270-time-uni-22

Note that computing the moving averages results in a shorter series, therefore, the corresponding dates needed to be adjusted. We have centred them by removing a similar number of values from both sides. This way, we treat the first 30-day moving average (the average of the first 30 days) as representative for the 15th day.

**Exercise.** Compute the 1-year and 10-year moving averages for the complete temps dataset. This will reveal some long-term trends.

Thanks to windowed aggregation, we can be detecting seasonal patterns (using shortish windows) and general trends (longish windows); the former can be revealed by subtracting the latter from the original series.

**Exercise.** Draw the plot of the 1-year moving average from which the 10-year average was subtracted.

(\*) Also, note that other aggregation functions (such as the median, min, or max) can be applied in rolling windows too.

(\*) **Exercise.** Draw, in the same figure, the plots of the 1-year moving minimums, medians, and maximums.

**Exercise.** Compute the 3-, 5-, and 10-day moving average averages for the EUR/AUD exchange rates and draw them on a single plot.

### 10.4 A Note on Nonuniform Sampling (\*)

Data do not have to be recorded at equispaced moments in time. In fact, our EUR/AUD exchange rates are given only on 126 out of 161 days in the first half of 2020.

**Exercise.** Load the euraud-20200101-20200630-dates<sup>99</sup> dataset and plot the currency rates as a function of now nonequidistant time.

### 10.4.1 Dealing with Nonequispaced Series

A times series is recorded at unequally spaced points in time may complicate our analysis.

In some contexts, it might be safe to ignore the real event time and merely treat them as consecutive samples (day 1, day 2, day 3, ..., day 126). This approach, however, in some contexts can make the results we obtain less valid.

If data are generally equispaced but some measurements are not present, we can add them to our dataset, mark them as missing values, and use one of the imputation techniques that we describe in a different part of our course.

Otherwise, we can consider creating an interpolated version of the original signal and resampling it at equally spaced intervals, e.g., using a Fourier method (scipy.signal.resample).

# 10.4.2 Modelling Event Times with an Exponential Distribution (\*\*)

An exponential distribution<sup>100</sup> 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<sup>101</sup> 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 (but be careful: some textbooks choose the parameter  $\lambda=1/s$  instead; also *scipy* uses this convention).

Here is a pseudorandom sample where there are 5 events per minute on average:

 $<sup>^{99}\</sup> https://raw.githubusercontent.com/gagolews/%5Cteaching_data/master/marek/euraud-20200101-20200630-dates.txt$ 

<sup>100</sup> https://en.wikipedia.org/wiki/Exponential\_distribution

<sup>101</sup> https://en.wikipedia.org/wiki/Queueing\_theory

```
import scipy.stats
np.random.seed(123)
\[\lambda = 60/5 # 5 events per 60 seconds on average \]
\[d = scipy.stats.expon.rvs(size=1200, scale=\lambda) \]
\[np.round(d[:8], 3) # preview \]
\[## array([14.307, 4.045, 3.087, 9.617, 15.253, 6.601, 47.412, 13.856]) \]
```

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]")
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-
##
→01T03:56:47.890'7.
 dtvpe='datetime64[ms7'))
##
```

Note that we converted the deltas to milliseconds so that we didn't lose precision; date-time64 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'], '(continues on next page)
```

```
'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.** Consider the wait\_times<sup>102</sup> 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.

# 10.5 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) as well as on signal processing (which can be used for the processing of audio); their toolkits somewhat overlap.

For probabilistic modelling, see textbooks on stochastic processes.

# 10.6 Questions

- 1. 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 (0.01*n*)- or a (0.1*n*)- one?
- 2. What is the Unix Epoch?

<sup>102</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/marek/wait\_times.txt

3. How can we recreate the original series when we are given its numpy.diff-transformed version?

# Part III Multidimensional Data

# *Introduction to Matrices in numpy*

From the perspective of structured datasets, a vector often represents a single feature: n measurements of the same quantitative or qualitative property, e.g., heights of n different patients, age category brackets of n runners, or prices of some stock at n consecutive days.

By far (assuming we have solved all the suggested exercises) we should have become quite fluent with the methods for processing of such one-dimensional arrays.

The time has come to increase the level of complexity – slightly – by allowing each of the n entities be described by possibly more than one, let's say m, features. We can arrange all the observations in a table with n rows and m columns (just like in spreadsheets).

Such objects can be expressed with numpy as two-dimensional arrays which we will refer to as matrices. Thanks to matrices, we can all keep m vectors of length n together in a single object and process them all at once (or n vectors of length m, depending how we want to look at it). Very convenient.

**Important.** Just like vectors, matrices were designed to store data of the same type. Later we will cover *data frames*, which further increase the complexity (and freedom) degree by allowing for mixed data types (e.g., numerical and categorical; this will enable us to perform data analysis in subgroups more easily) and 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 this is why before proceeding with *pandas*, we are learning the former in detail.

#### 11.1 Creating Matrices

#### 11.1.1 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 (just raw data). Unfortunately, most CSV files do, and hence it will be better if we rely on a corresponding function from the *pandas* package:

```
import numpy as np
import pandas as pd
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[: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<sup>103</sup> 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),
- 6. hip circumference (cm),
- 7. waist circumference (cm).

<sup>103</sup> https://wwwn.cdc.gov/nchs/nhanes/search/datapage.aspx

Unfortunately, *numpy* matrices do not support column naming, so these should be noted down separately elsewhere.

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 will now be a tuple of length 2:

```
body.shape ## (4221, 7)
```

this gives the number of rows and columns, respectively.

#### 11.1.2 Enumerating Elements

numpy.array can create a two-dimensional array based on a list of lists or vectors 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],
##
 Γ 9, 10, 11, 1277)
##
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 still a 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).

#### 11.1.3 Repeating Arrays

The previously mentioned numpy.tile and numpy.repeat can also generate some nice matrices. Consider the following examples:

Axis 0 (the first one) is the rowwise one. Axis 1 (the second one) refers to the columns:

Note the double square brackets which mean that we are replicating a row or a column vector, not a flat vector.

Exercise. How to obtain matrices of following kind programmatically?

$$\begin{bmatrix} > 1 & 2 \\ > 1 & 2 \\ > 1 & 2 \\ > 3 & 4 \\ > 3 & 4 \\ > 3 & 4 \\ > 3 & 4 \end{bmatrix}, \qquad > \begin{bmatrix} > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 & 1 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > > 1 & 2 & 1 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 & 1 \\ > 2 & 2 & 1 & 2 & 1 \\ > 2 & 2 & 1 & 2 & 1 \\ > 2 & 2 & 1 & 2 & 1 \\ > 2 & 2 & 1 & 2 & 1 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 1 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ > 2 & 2 & 2 \\ >$$

#### 11.1.4 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 single matrix:

```
np.column_stack(([10, 20], [30, 40], [50, 60]))
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.** Perform similar operations using numpy.append, numpy.vstack, numpy.hstack, numpy.concatenate, and (\*) numpy.c\_.

**Exercise.** Using numpy.insert, and a new row/column at the beginning, end, and in the middle of an array.

#### 11.1.5 Other Functions

Many built-in functions allow for generating arrays of arbitrary shapes (not only vectors). For example:

```
np.random.seed(12345678)
np.random.rand(3, 4) # not: rand((3, 4))
array([[0.24580423, 0.59642861, 0.35879163, 0.37891011],
[0.02445137, 0.23830957, 0.38793433, 0.68054104],
[0.83934083, 0.76073689, 0.2217416 , 0.06344161]])
```

Similarly with scipy:

```
import scipy.stats
scipy.stats.uniform.rvs(-1, 1, size=(2, 5))
array([[-0.22055625, -0.27825863, -0.80586116, -0.48853833, -0.93119693],
[-0.60585732, -0.01827233, -0.69509149, -0.218041 , -0.26529402]])
```

**Exercise.** Check out the following functions: numpy.eye, numpy.diag, numpy.zeros, numpy.ones, numpy.empty.

#### 11.2 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 Fortranstyle):

```
A.size # total number of elements
12
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 be treated if they were arranged on a 3 by 4 grid. We can change it anytime without modifying the underlying 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 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).

Another example:

We should also note that reshaping is not the same as matrix *transpose*, which also changes the order of elements:

```
A.T # transpose
array([[0., 0.5, 1., 1.5],
[0.1, 0.6, 1.1, 1.6],
[0.2, 0.7, 1.2, 1.7],
[0.3, 0.8, 1.3, 1.8],
[0.4, 0.9, 1.4, 1.9]])
```

Here, the rows became columns and vice versa.

#### 11.3 Further Reading

https://numpy.org/devdocs/user/basics.creation.html

#### 11.4 Questions

- 1. What is the difference between [1, 2, 3], [[1, 2, 3]] and [[1], [2], [3]] in the context of array creation?
- 2. If A is a matrix with 5 rows and 6 columns, what is the difference between A. reshape(6, 5) and A.T?
- 3. If A is a matrix with 5 rows and 6 columns, what is the meaning of: A.reshape(-1), A.reshape(3, -1), A.reshape(-1, 3), A.reshape(-1, -1), A.shape = (3, 10), and A.shape = (-1, 3)?
- 4. List some methods to add a new row to an existing matrix.

# Transforming, Aggregating, and Filtering Multidimensional Data

Below we will study how the vector operations we have already discussed have been extended to matrices. In many cases, we'll see that they apply the same transform either on every matrix element separately, or on each row or column. Thus, they allow us to exercise the write less, do more principle.

import numpy as np

#### 12.1 Mathematical Notion

First, however, some standalone mathematical notation. 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, ..., n, j = 1, ..., m.

Additionally, will sometimes use the following notations to emphasise that X consists of n rows or m columns:

$$\mathbf{X} = \begin{bmatrix} \mathbf{x}_{.,1} & \mathbf{x}_{.,2} & \cdots & \mathbf{x}_{.,m} \end{bmatrix} = \begin{bmatrix} \mathbf{x}_{1,.} \\ \mathbf{x}_{2,.} \\ \vdots \\ \mathbf{x}_{n,.} \end{bmatrix} = \begin{bmatrix} \mathbf{x}_{1,.} & \mathbf{x}_{2,.} & \cdots & \mathbf{x}_{n,.} \end{bmatrix}^T,$$

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?).

Here,  $\mathbf{x}_{i,\cdot}$  is a row vector of length m, i.e., a (1×m)-matrix:

$$\mathbf{x}_{i,\cdot} = \left[ \begin{array}{ccc} x_{i,1} & x_{i,2} & \cdots & x_{i,m} \end{array} \right].$$

Moreover,  $\mathbf{x}_{..i}$  is a *column vector* of length n, i.e., an  $(n \times 1)$ -matrix:

$$\mathbf{x}_{\cdot,j} = \begin{bmatrix} x_{1,j} & x_{2,j} & \cdots & x_{n,j} \end{bmatrix}^T = \begin{bmatrix} x_{1,j} \\ x_{2,j} \\ \vdots \\ x_{n,j} \end{bmatrix}.$$

Also, recall that we are used to denoting a *vector* of length m with  $\mathbf{x} = (x_1, \dots, x_m)$ . A vector is 1-, not 2-dimensional, hence a slightly different notation in the case where ambiguity can lead to some trouble.

**Important.** We will see that often *numpy* will automatically treat 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.

#### 12.2 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
np.square(A)
array([[0.04, 0.36, 0.16, 0.16],
```

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```
[0., 0.04, 0.16, 0.49],
[0.64, 0.64, 0.04, 0.01]])
```

takes the square of every element.

#### 12.3 Aggregation Functions

Aggregation functions (e.g., np.mean, np.quantile) can summarise:

- all data into a single number (axis=None, being the default),
- data in each row (axis=1),
- data in each column (axis=0).

For example:

```
np.mean(A)
0.3999999999997
np.mean(A, axis=1)
array([0.4 , 0.325, 0.475])
np.mean(A, axis=0)
array([0.333333333, 0.533333333, 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 means the axis *along* which the matrix is sliced. Sadly, even yours truly sometimes does not get it right (e.g., the apply function in the R language follows a more natural convention).

**Exercise.** Given the nhanes\_adult\_female\_bmx\_2020.csv<sup>104</sup> dataset, compute the mean, standard deviation, minimum, and maximum of each body measurement.

#### 12.4 Arithmetic, Logical, and Comparison Operations

Recall that for vectors, binary operators such as +, \*, ==, <=, and & and similar element-wise functions (e.g., numpy.minimum) can either be applied if both inputs are of the same length or if one is a scalar.

For example:

```
np.array([1, 10, 100, 1000]) * np.array([7, -6, 2, 8])
array([7, -60, 200, 8000])
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*<sup>105</sup> describes how this package handles arrays of different shapes.

**Important.** Generally, for two matrices, their column/row numbers much 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.

<sup>104</sup> https://raw.githubusercontent.com/gagolews/%5Cteaching\_data/master/marek/nhanes\_adult\_female\_bmx\_2020.csv

<sup>105</sup> https://numpy.org/devdocs/user/basics.broadcasting.html

#### 12.4.1 Matrix vs Scalar

If one operand is a scalar, then it is going to be propagated over all matrix elements, for example:

```
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
```

And now:

# 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.

```
(-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.

```
A >= 0.25

array([[False, True, True, True],

[False, False, True, True],

[True, True, False, False]])
```

compares each element to 0.25.

#### 12.4.2 Matrix vs Matrix

For two matrices of identical sizes, we will be combining 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.]])
```

multiplies each  $a_{i,j}$  by the corresponding  $b_{i,j}$ .

Thanks to this and the matrix-scalar operations we can perform various tests on an perelement basis, e.g.,

```
(A >= 0.25) & (A <= 0.75) # logical matrix & logical matrix
array([[False, True, True],
[False, False, True, True],
[False, False, False, False]])</pre>
```

#### 12.4.3 Matrix vs Any Vector

An *n*×*m* matrix can also be combined with an *n*×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.]])
```

propagates the column vector over all columns (left to right).

Similarly, combining with an 1×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.],
```

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```
[-0.333, -0.333, 0.067, 0.3],
[0.467, 0.267, -0.133, -0.3]])
```

results in each column mean's being 0 and there is no need for an explicit .reshape(1, -1).

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.** Standardise, normalise, and min-max scale each column in the nhanes adult female bmx 2020.csv<sup>106</sup> dataset using a single line of code.

#### 12.4.4 Row Vector vs Column Vector (\*)

As a bonus, let's 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. Check out that numpy. where relies on similar shape broad-

casting rules as the binary operators we have discussed here, however, not with regards to all the 3 arguments.

#### 12.5 Other Row and Column Transforms (\*)

Some functions that we have already discussed 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. Moreover:

computes the ranks of elements in each column.

Also note that some functions have the default argument axis=-1, which means that they are applied along the last (i.e., columns in the matrix case) axis:

compare it with:

which gives the iterated differences for each column separately (along the rows).

If a function (built-in or custom) in 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 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]])
```

#### 12.6 Filtering

Recall that for 1-dimensional arrays we have 4 possible choices of an indexer (i.e., where performing filtering like x[i]):

- scalar (extracts a single element),
- slice (selects a regular subsequence, e.g., every 2ndelement 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).

#### 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.

Let us look at all the possible scenarios in greater detail.

#### 12.6.1 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 at 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.

#### 12.6.2 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.

```
A[0, -1]
0.4
```

yields the element in the first row and last column.

We can always use the reshape method to convert the resulting object back to a matrix.

#### 12.6.3 Mixing Vectors with Scalars or Slices

A logical and integer vector can also be used as an indexer. If the other indexer is a slice or a scalar, the result is quite predictable.

selects the first, the last, and the first row again and reverses the order of columns.

```
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 those rows whose mean is greater than 0.35.

**Exercise.** In the nhanes\_adult\_female\_bmx\_2020.csv $^{107}$  dataset, select all participants whose height is within mean  $\pm 2$  standard deviations.

#### 12.6.4 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 quite badly written Advanced Indexing<sup>108</sup> section of the *numpy* manual.

<sup>107</sup> https://raw.githubusercontent.com/gagolews/%5Cteaching\_data/master/marek/nhanes\_adult\_female\_bmx\_2020.csy

<sup>108</sup> https://numpy.org/doc/stable/user/basics.indexing.html

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.where).

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]])
```

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]])
```

#### 12.6.5 Views on Existing Arrays

Only indexing involving two slices or a slice and a scalar returns a view 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]])
```

Which is time and memory efficient, but might lead to some unexpected results if we are not focused enough.

#### 12.7 Further Reading

https://numpy.org/devdocs/user/basics.broadcasting.html https://numpy.org/doc/stable/user/basics.indexing.html https://numpy.org/devdocs/user/basics.copies.html

#### 12.8 Questions

- 1. Does numpy.mean(A, axis=0) compute rowwise or columnwise means?
- 2. How does shape broadcasting work? List the most common shape cases when performing arithmetic operations.
- 3. What are the possible matrix indexing schemes and how do they behave?
- 4. Which kinds of matrix indexers return a view on an existing array?
- 5. (\*) How to select a submatrix comprised of the first and the last row and the first and the last column?

### Multivariate Categorical and Relational Data

Some datasets may feature many categorical columns, each having possibly different levels.

Let us consider the data on the top 1000 marathoners (held in Warsaw in 2015):

The three columns are: sex, age category (in 10-year brackets), and country. We can of course analyse the data distribution in each column individually (based on the tools discussed in the section on the processing of unidimensional categorical data), however, some interesting patterns might also arise when we study the *combinations* of levels of different variables.

#### 13.1 Two-Way Contingency Tables

Here are the levels of the first two variables:

```
np.unique(marathon[:, 0])
array(['F', 'M'], dtype='<U2')</pre>
```

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```
np.unique(marathon[:, 1])
array(['20', '30', '40', '50', '60'], dtype='<U2')</pre>
```

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:

This is not quite readable, hence we have written our own function to print it out much more nicely:

```
import marek
marek.print_labelled_array(l, v)
20 30 40 50 60
F 17 23 8 1 0
```

M 158 433 278 73 9

Hence, for example, there were 9 men aged 60-69 amongst the top 1000 runners. Nice.

Note that the *marginal* (one dimensional) frequency distributions can be recreated by computing the rowwise and columnwise sums.

```
marek.print_labelled_array(l[0], np.sum(v, axis=1))
F M
49 951
marek.print_labelled_array(l[1], np.sum(v, axis=0))
20 30 40 50 60
175 456 286 74 9
```

#### 13.2 Visualising

#### 13.2.1 Heat Map

Two-way contingency tables can be depicted by means of a heatmap, where the element value affects the corresponding cell's colour intensity.

```
import matplotlib.pyplot as plt
import seaborn as sns
plt.style.use("seaborn")
from matplotlib import cm
sns.heatmap(
 v, xticklabels=l[1], yticklabels=l[0],
 annot=True, fmt="d", cmap=cm.get_cmap("copper")
)
plt.show()
```

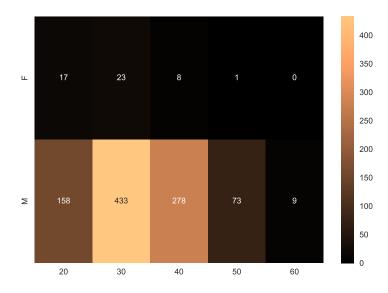


Figure13.1: plot of chunk 330-categorical-multi-8

#### 13.2.2 Bar Plot

A good old bar plot is a versatile tool for visualising counts also in the two-variable case:

```
ind = np.arange(len(l[1]))
plt.bar(ind-0.25, height=v[0, :], width=0.4, label=l[0][0])
plt.bar(ind+0.25, height=v[1, :], width=0.4, label=l[0][1])
plt.xticks(ind, l[1])
plt.legend()
plt.legend()
plt.show()
<BarContainer object of 5 artists>
([<matplotlib.axis.XTick object at 0x7fe14c18d160>, <matplotlib.axis.
-XTick object at 0x7fe14c18dd00>, <matplotlib.axis.XTick object at 0x7fe14c05a3d0>, <matplotlib.axis.XTick object at 0x7fe14c068b20>,
-<matplotlib.axis.XTick object at 0x7fe14c0da760>], [Text(0, 0, '20'),]
-Text(1, 0, '30'), Text(2, 0, '40'), Text(3, 0, '50'), Text(4, 0, '60')])
```

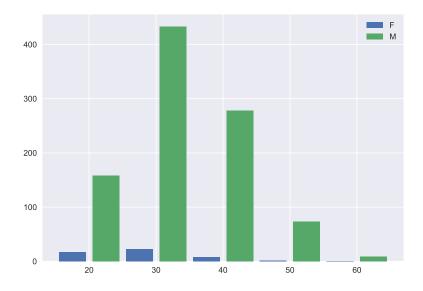


Figure 13.2: plot of chunk 330-categorical-multi-9

We can also create stacked bar plots. Here, we are drawing horizontal bars for data that have been normalised so that for each sex they sum to 100%.

```
ind = np.arange(len(l[0]))
p_sex = v/np.sum(v, axis=1).reshape(-1, 1)*100.0 # normalise each row (100%)
c_sex = np.insert(np.cumsum(p_sex, axis=1), 0, 0, axis=1) # prepend column[]
for j in range(p sex.shape[1]):
 plt.barh(ind, left=c sex[:, j], width=p sex[:, j], label=l[1][j])
plt.yticks(ind, l[0])
plt.legend(ncol=len(l[1]))
plt.show()
<BarContainer object of 2 artists>
([<matplotlib.axis.YTick object at 0x7fe155168d30>, <matplotlib.axis.
→YTick object at 0x7fe14c14ad30>], [Text(0, 0, 'F'), Text(0, 1, 'M')])
```

#### 13.3 Higher-Order Contingency Tables (\*)

*Numpy* also supports higher-dimensional arrays. They often arise when we create contingency tables for more than 2 variables.

For example, let's introduce another variable based on the *country* column: Poland, Kenya, and Other (because there are too many countries in the database).

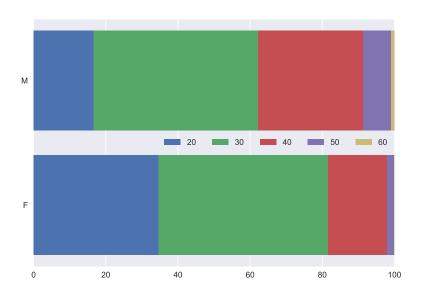


Figure 13.3: plot of chunk 330-categorical-multi-10

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```
l, v
((array(['KE', 'PL', 'XX'], dtype='<U2'), array(['F', 'M'], dtype='<U2'), [
→array(['20', '30', '40', '50', '60'], dtype='<U2')), array([[[0, 2, □
 0, 07,
 [4, 2, 0, 0, 0]],
##
##
##
 [[13, 17, 6, 1, 0],
 [142, 391, 251, 65, 9]],
##
##
 [[4, 4, 2, 0, 0],
##
 [12, 40, 27, 8, 0]]]))
##
```

This gave us a 3-dimensional array (which in our case can be thought of as three matrices stacked together). The same in a slightly more readable form:

```
marek.print_labelled_array(l, v)
KE, :, :
##
 20
 30
 40
 50
 0
##
 2
 0
 0
 0
##
 4
PL, :, :
 20
##
 30
 40
##
 F 13 17
 1
 6
 M 142 391 251
##
XX, :, :
##
 20
 30
 40
 50
##
 F 4
 4 2
 0
 M 12 40
 27
```

It is worth noting that most vectorisation schemes that we have covered for matrix data naturally translate to higher dimensions. For instance, indexing: v[1, 0, 2] denotes the number of Polish females aged 40-49 (i.e., 6 persons). Also, we can aggregate data along different axes:

```
marek.print_labelled_array((l[0], l[1]), np.sum(v, axis=2))
##
 2
 6
##
 KE
##
 PL
 37 858
 XX 10 87
##
marek.print labelled array([0], np.sum(v, axis=(1, 2)))
 KE PL
 XX
##
 8 895
##
 97
```

#### 13.4 Measuring Association (\*)

Let us consider Australian Bureau of Statistics' National Health Survey 2018<sup>109</sup> data on the prevalence of certain conditions as a function of age. Here is the extracted contingency table:

<sup>109</sup> https://www.abs.gov.au/statistics/health/health-conditions-and-risks/national-health-survey-first-results/2017-18

```
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+"]
1
v = 1000*np.array([
 360.2,
 1489.0,
 1772.2],
 [1069.7,
 741.9,
 433.7],
 1469.6,
 955.3],
 1513.3,
 28.1,
 162.7,
 237.5],
 207.0,
 103.8,
 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)
marek.print_labelled_array(l, v)
##
 15-44
 45-64
 65+
 ##
 Arthritis
 360000
 1489000
 1772000
 Asthma
 П
##
 1069000
 741000
 433000
 Back problems
 1513000
 ##
 1469000
 955000
 Cancer (malignant neo
 ##
 28000
 162000
 237000
##
 Chronic obstructive p
 103000
 207000
 251000
4
 Diabetes mellitus
 ##
 135000
 427000
 607000
Heart, stroke and vas
 94000
 344000
 716000
##
 Kidnev disease
 29000
 67000
 123000
```

(continued from previous page)

Cramer's  $V^{110}$  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(v)
0.316237999724298
```

The above means that there is 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).

It is defined via:

$$\chi^2 = \sum_{i=1}^n \sum_{j=1}^m \frac{(v_{i,j} - v_{i,\cdot} v_{\cdot,j}/c)^2}{v_{i,\cdot} v_{\cdot,j}/c},$$

where  $c = \sum_{i=1}^n \sum_{j=1}^m v_{i,j}, v_{i,\cdot} = \sum_{j=1}^m v_{i,j}, v_{\cdot,j} = \sum_{i=1}^n v_{i,j}$ , and then

$$V = \sqrt{\frac{\chi^2/c}{\min\{n-1, m-1\}}}.$$

Note that  $v_{i,j}$  is what we observe and  $v_{i,\cdot}v_{\cdot,j}/c$  denotes what we would expect if the two variables were independent.

Here is how to compute it manually:

<sup>110</sup> https://en.wikipedia.org/wiki/Cramer%27s V

(\*) **Exercise.** Take a look at *Table 19: Comorbidity of selected chronic conditions* of the National Health Survey 2018<sup>111</sup>, where we clearly see that many disorders co-occur. Visualise them on some heatmaps and bar plots (including data grouped by sex and age).

#### 13.5 Questions

- 1. List some ways to visualise multidimensional categorical data.
- 2. (\*) How is Cramer's V defined and what values does it take?

 $<sup>^{111}\,</sup>https://www.abs.gov.au/statistics/health/health-conditions-and-risks/national-health-survey-first-results/2017-18$ 

# Visualising Multidimensional Data and Measuring Correlation

Let **X** be a numeric matrix with *n* rows and *m* columns. Such matrices 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 the data frame chapter;
- two-way contingency tables, where an element x<sub>i,j</sub> 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 connected 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) of a pixel in the (n-i+1)-th row and the j-th column.

In this part we will be dealing with the first case, i.e., n points in an m dimensional space,  $\mathbb{R}^m$ , which we refer to as multidimensional data.

The National Health and Nutrition Examination Survey (NHANES study) excerpt is a typical example of such data:

```
import numpy as np
import pandas as pd
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
bodv.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).

Such kind of tabular ("structured") data are the most prevalent.

The important property it 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.

Thus, we expect that the data in columns will somewhat be *correlated* which each other (e.g., a taller person *usually tends to* weight more). We will also be interested in quantifying the degree of association between variables.

data can be mapped to a tabular form. For instance, a set of audio recordings<sup>112</sup> 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., Joyce's *Ulysses* is 40% travel literature, 70% comedy, and 50% heroic fantasy, but do not take it for granted).

#### 14.1 Scatterplots

#### 14.1.1 2D Data

A scatterplot can be used to visualise one variable against another one. For example:

```
import matplotlib.pyplot as plt
import seaborn as sns
plt.style.use("seaborn")
plt.scatter(body[:, 1], body[:, 3]) # x=body[:, 1], y=body[:, 3]
plt.xlabel("standing height (cm)")
plt.ylabel("upper leg length (cm)")
plt.show()
```

gives a depiction of upper leg length (y axis) vs standing 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])
```

<sup>112</sup> http://millionsongdataset.com/

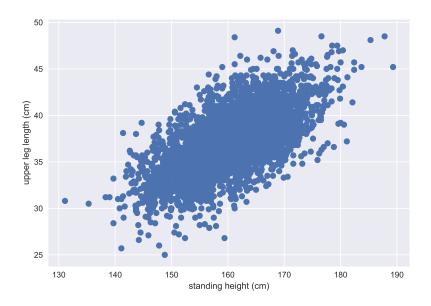


Figure 14.1: plot of chunk 330-visualise-multi-3

As the points are plentiful, we do not necessarily see *where* the majority of them is located. A simple trick to remedy this is to plot the points using a semi-transparent colour:

```
plt.scatter(body[:, 1], body[:, 3], c="#00000011")
plt.plot(np.mean(body[:, 1]), np.mean(body[:, 3]), "rX") # the centroid
plt.xlabel("standing height (cm)")
plt.ylabel("upper leg length (cm)")
plt.axis("equal")
plt.show()
(128.19, 192.21, 23.795, 50.305)
```

Here, the colour specifier is of the form  $\#rrggbbaa^{113}$ , giving the intensity of the red, green, blue, and alpha (opaqueness) channel in series of two hexadecimal<sup>114</sup> digits (between 00 = 0 and ff = 255).

We have also, but more for the sake of an exercise, marked the point corresponding

<sup>113</sup> https://en.wikipedia.org/wiki/RGBA\_color\_model

<sup>114</sup> https://en.wikipedia.org/wiki/Hexadecimal

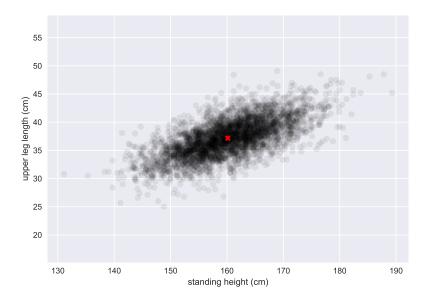


Figure14.2: plot of chunk 330-visualise-multi-6

to the *centroid*, which is simply the componentwise arithmetic mean. Furthermore, we asked for the axes to use the same scale.

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. Later we will explore some measures of correlation that enable us to quantify the degree of association between variable pairs.

(\*) **Exercise.** Check out seaborn. jointplot for a two-dimensional version of a histogram, a density heatmap. Instead of bar heights, the number of classes in each bin can be encoded by colour intensities. This function can also depict 2D kernel density estimators (KDEs) in the form of nice level curve plots. Note the marginal distributions depicted in the top and right pane.

#### 14.1.2 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.

```
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()
```

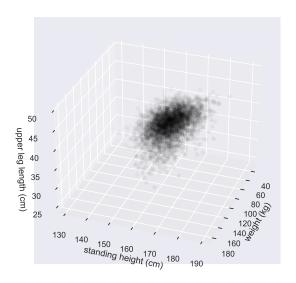


Figure 14.3: plot of chunk 330-visualise-multi-7

However, infrequently will it 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.** 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 scatterplot (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 in 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 libraries<sup>115</sup> that output HTML+CSS+JavaScript code to be rendered by a browser engine. Still, there are people who want to keep JavaScript disabled/blocked, therefore we are not big fans of such solutions. Less is better.

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.

<sup>115</sup> https://wiki.python.org/moin/NumericAndScientific/Plotting

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 2-, or 3-dimensional 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).

As some form of a workaround, we can play with marker colours (or sometimes sizes: think of them as bubbles). A suitable colour map<sup>116</sup>, can be used to distinguish between low and high values of an additional variable:

```
from matplotlib import cm
plt.scatter(
 body[:, 4],
 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()
(15.9349999999999, 59.16500000000006, 68.75, 184.25)
```

<sup>116</sup> https://matplotlib.org/stable/tutorials/colors/colormaps.html

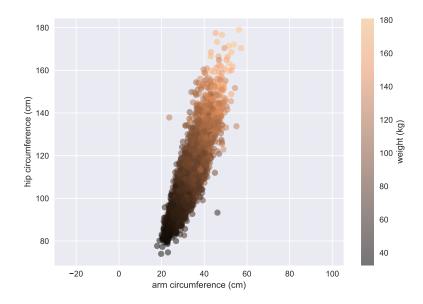


Figure14.4: plot of chunk 330-visualise-multi-8

We can see some tendency for the weight be greater as both the arm and the hip circumferences increase.

**Exercise.** Play around with different colour pallettes  $^{117}$ .

**Important.** We should be wary that ca. every 1 in 12 men (8%) and 1 in 200 women (0.5%) has colour vision deficiencies<sup>118</sup>, especially in the

<sup>117</sup> https://matplotlib.org/stable/tutorials/colors/colormaps.html

<sup>118</sup> https://en.wikipedia.org/wiki/Color\_blindness

red-green or blue-yellow spectrum, thence some diverging colour maps might be worse than others.

#### 14.1.3 Scatterplot Matrix (Pairplot)

As a countermeasure, we may try depicting all (or most – ones we deem interesting) pairs of variables in the same figure in form of a scatterplot matrix.

```
sns.pairplot(data=pd.DataFrame(
 body[:, [0, 1, 4, 5]],
 columns=[
 "weight (kg)", "standing height (cm)",
 "arm circumference (cm)", "hip circumference (cm)"
]
))
plt.show()
```

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*).

**Exercise.** Draw a scatterplot matrix for the fcps\_chainlink<sup>119</sup> 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. Use matplotlib.pyplot.subplot and other functions we

 $<sup>^{119}\</sup> https://raw.githubusercontent.com/gagolews/\%5Cteaching\_data/master/clustering/fcps\_chainlink.csv$ 

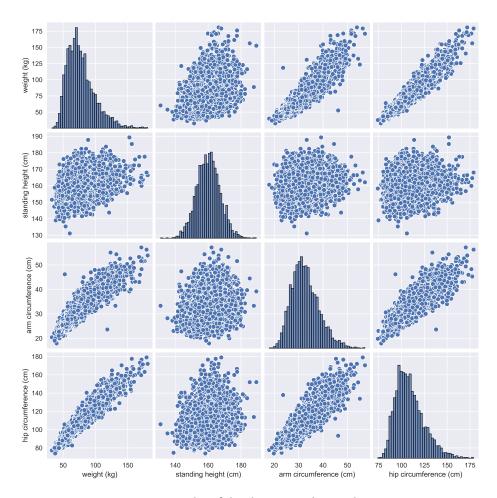


Figure14.5: plot of chunk 330-visualise-multi-9

```{figure} 330-visualise-multi-figures/330-visualise-multi-9-10.\* plot of chunk 330-visualise-multi-9

have learned in the previous part to create a scatterplot matrix manually. Draw weight, arm circumference, and hip circumference on a logarithmic scale.

14.2 Measuring Correlation

Scatterplots let us identify some simple patterns or structure in data: we 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 the two most popular means for measuring (expressing as a single number) the degree of association between a set of pairs of points.

14.2.1 Pearson's Linear Correlation Coefficient

First, the Pearson's linear correlation coefficient¹²⁰:

$$r(x,y) = \frac{1}{n-1} \sum_{i=1}^{n} \frac{x_i - \bar{x}}{s_x} \frac{y_i - \bar{y}}{s_y},$$

with s_x, s_y denoting the standard deviations and \bar{x}, \bar{y} being the means of $x = (x_1, \dots, x_n)$ and $y = (y_1, \dots, y_n)$, 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).

Here is how we can compute it manually:

¹²⁰ https://en.wikipedia.org/wiki/Pearson_correlation_coefficient

```
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)-1)
## 0.8682684478597853
```

And here is a built-in function that implements the same formula:

```
import scipy.stats
scipy.stats.pearsonr(x, y)[0] # returns more than we ask for
## 0.8680627457873241
```

To get more insight, we'll illustrate some interesting cases 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}\np = {p:.3}")
    plt.legend()
```

Here are the basic properties of Pearson's r:

- 1. r(x, y) = r(y, x) (symmetric);
- 2. r(x, y) is always between -1 and 1 (bounded from below and above);
- 3. r(x, y) = 1 if and only if y = ax + b for some a > 0 and b;
- 4. r(x, y) = -1 if and only if y = ax + b for some a < 0 and b;

Hence, we get perfect *linear correlation* (-1 or 1) when one variable is a scaled and shifted version (linear function) of the other variable.

```
np.random.seed(123)
x = np.random.rand(100)
plt.subplot(121)
plot_corr(x, -0.5*x+3) # negative slope
plt.axis("equal")
plt.subplot(122)
plot_corr(x, 3*x+10) # positive slope
```

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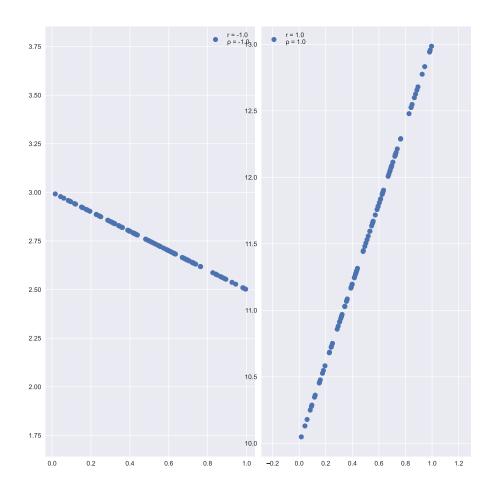


Figure 14.6: plot of chunk 330-visualise-multi-13

Note that negative correlation means that when one variable increases, the other one decreases (like: a car's braking distance vs velocity).

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.

```
x = np.random.rand(100)
y = 0.5*x
e = np.random.randn(len(x)) # random white noise (of mean 0)
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. Draw a series of similar plots but for the case of negatively correlated point pairs.

We should stress that correlation close to 0 does not necessarily mean that two variables are not related to each other. It is a *linear* correlation coefficient, so we are only quantifying those types of relationships.

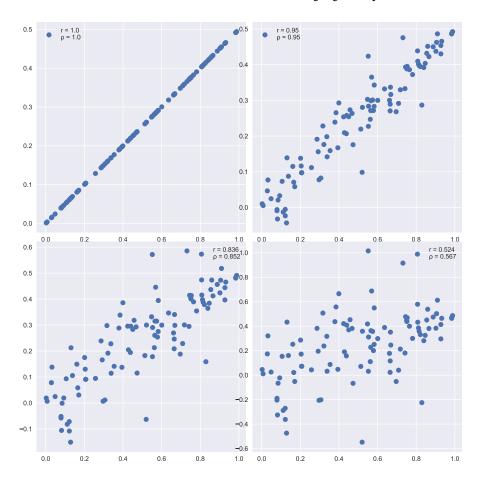


Figure 14.7: plot of chunk 330-visualise-multi-14

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```
plt.subplot(224)
plot_corr(x, 0.25*np.sin(8*np.pi*x)) # another
plt.show()
```

What's more, sometimes we can detect *false* correlations – when data are functionally dependent, but the relationship is not linear, but it kind of looks like linear.

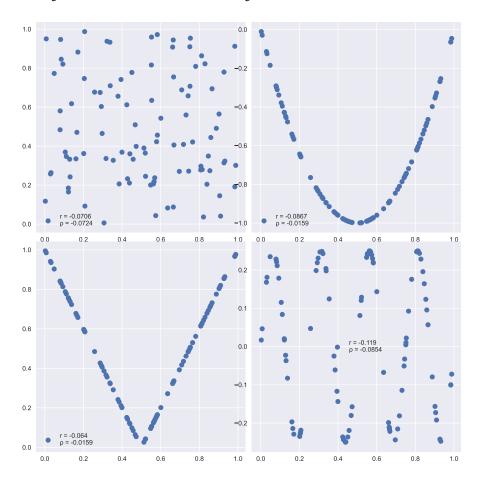


Figure14.8: plot of chunk 330-visualise-multi-15

```
plt.subplot(221)
plot_corr(x, 0.7*np.sin(2*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)
```

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plot_corr(x, 1/x)
plt.show()

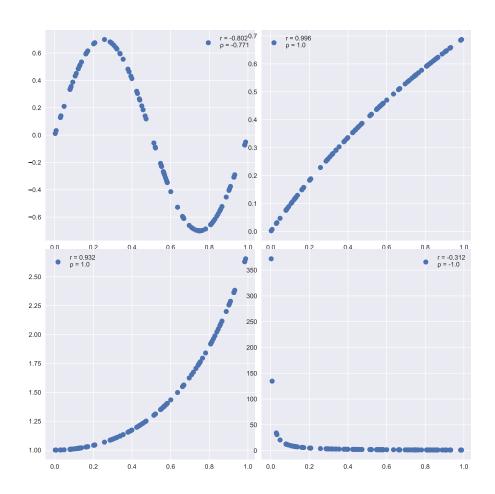


Figure14.9: plot of chunk 330-visualise-multi-16

No single measure is perfect – we are trying to compress 2*n* 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.

Important. Note that high correlation degree (either positive or negative) does not mean that there is any *casual* relationship between the two variables ("correlation is not causation"). 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. 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 with identify the concrete a and b coefficients). 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.

14.2.2 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.

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(x,y) = r(y,x).

14.2.3 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 the 2020 CIA World Factbook¹²¹, where we have data on gross domestic product¹²² per capita (based on purchasing power parity¹²³) 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()
    (continues on next page)
```

¹²¹ https://www.cia.gov/library/publications/the-world-factbook/docs/rankorderguide.html

¹²² https://en.wikipedia.org/wiki/Gross_domestic_product

¹²³ https://en.wikipedia.org/wiki/Purchasing_power_parity

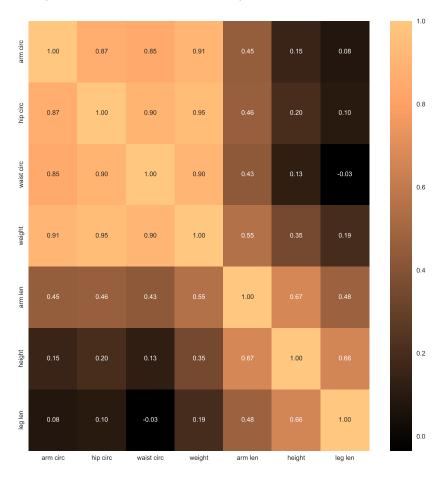


Figure14.10: plot of chunk 330-visualise-multi-17

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```
world[:6, :] # preview
## array([[ 2000. ,
                       52.87,
                       79. ],
##
          [12500.,
          [15200.,
                       77.5],
##
          [11200.,
                       74.8],
##
          [49900.,
                       83. ],
##
          [ 6800. ,
                       61.3]])
##
```

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.

Here are the scatterplots:

```
plt.subplot(121)
plot_corr(world[:, 0], world[:, 1])
plt.subplot(122)
plot_corr(np.log(world[:, 0]), world[:, 1])
plt.show()
```

14.2.4 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 coefficient¹²⁴ is frequently used in such a scenario:

$$\rho(x,y) = r(R(x),R(y))$$

which is 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]),
```

(continues on next page)

¹²⁴ https://en.wikipedia.org/wiki/Spearman%27s_rank_correlation_coefficient

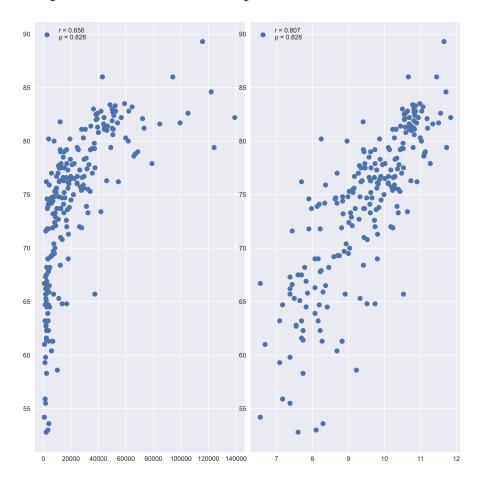


Figure14.11: plot of chunk 330-visualise-multi-21

```
(continued from previous page)
```

```
scipy.stats.rankdata(world[:, 1])
)[0]
## 0.8275220380818621
```

Let's 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
```

Exercise. We have included the ρ s in all the outputs generated by our plot_corr functions. Review all the figures listed above.

(*) **Exercise.** Draw the scatterplots of the ranks of columns in the world and body datasets.

14.3 Further Reading

Another interesting rank correlation coefficient: Kendall's τ^{125} .

14.4 Questions

- 1. What does "correlation is not causation" mean?
- 2. Give some ways to visualise 3-dimensional data.
- 3. How to and why set point opaqueness/transparency when drawing a scatter plot?
- 4. What does linear correlation of 0.9 mean?
- 5. What does rank correlation of 0.9 mean?

https://en.wikipedia.org/wiki/Kendall_rank_correlation_coefficient

- 6. What does linear correlation of 0.0 mean?
- 7. How is the Spearman's coefficient related to the Pearson's one?

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).

Let us make a few additions to what we have covered whilst discussing the unidimensional case.

```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
plt.style.use("seaborn")
```

15.1 Basic Plotting

Consider the currency exchange rates for the first half of 2020:

This gives EUR/AUD, EUR/CNY, EUR/GBP, and EUR/PLN, in this order.

Let's draw the four time series:

```
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()
```

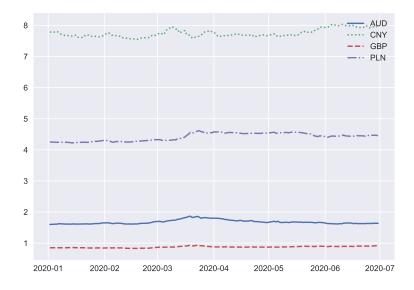


Figure15.1: plot of chunk 350-time-multi-3

Unfortunately, they are all on different scales, hence the plot is not necessarily readable. Let's draw the currency exchange rates *relative* to the prices on 2020-03-19.

(continues on next page)

(continued from previous page)

plt.legend()
plt.show()

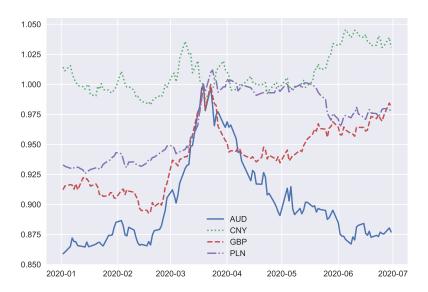


Figure 15.2: plot of chunk 350-time-multi-4

This way, e.g., relative rate of 1.05 denotes the rate 5% higher than on the reference day.

Exercise. Based on EUR/AUD and EUR/PLN rates, compute and plot the AUD/PLN as well as PLN/AUD ones.

(*) **Exercise.** Draw the EUR/AUD and EUR/GBP rates on a single plot, but with each series having its own¹²⁶ y axis.

(*) **Exercise.** Draw the EUR/xxx rates for your favourite currencies over a larger period of time. Use data¹²⁷ downloaded from the European Central Bank. Add a few moving averages. For each year, identify the lowest and the highest rate.

15.2 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]])
```

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.

¹²⁶ https://matplotlib.org/stable/gallery/subplots_axes_and_figures/secondary_axis.html

¹²⁷ https://www.ecb.europa.eu/stats/policy_and_exchange_rates/euro_reference_exchange_rates/html/index.en.html

The mplfinance¹²⁸ package (*matplotlib-finance*) features a few functions related to the plotting of financial data.

Here, let us briefly mention the candlestick plot¹²⁹. Unfortunately, the package requires the data to be fed as a *pandas* data frame (which we cover later). However, we are now only interested in getting to know the meaning of the basic plot elements.

```
import mplfinance as mpf
import pandas as pd
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()
```

This depicts the January 2021 data.

Note that this is not a box and whisker plot. 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. Draw the BTC/USD rates for the whole year and add the 10-day moving averages.

(*) **Exercise.** Draw a candlestick plot manually, without using the *mplfinance* package. matplotlib.pyplot.fill might be helpful.

¹²⁸ https://github.com/matplotlib/mplfinance

¹²⁹ https://en.wikipedia.org/wiki/Candlestick_chart



Figure15.3: plot of chunk 350-time-multi-6

```
```{figure} 350-time-multi-figures/350-time-multi-6-6.* plot of chunk 350-time-multi-6
```

(\*) **Exercise.** 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.

# 15.3 Questions

1. (\*) In your own words, describe the key elements in a candlestick plot.

# 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 different treatment plans that we wish to evaluate).

From this perspective, time series which we have briefly touched upon previously, are already quite different, 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 periodic 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 different 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 and thus we have decided that this topic must be treated separately elsewhere (also because it requires some more advanced calculus skills that we didn't assume the reader to have at this time).

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.

## 16.1 Representing Images

In order to demonstrate that signals are *some kinds of data* after all and that – at some basic level – there is nothing particularly mysterious behind them, let us briefly discuss how images are usually represented.

The *pillow*<sup>130</sup> (*PIL*) package provides a number of functions for basic image processing.

Let's load the very small example image that we can download from our example data repository<sup>131</sup> (the file needs to be fetched manually).

It is a bitmap of height 8 and width 8 pixels.

Converting to a numpy matrix:

```
im = np.array(im.getdata()).reshape(im.size)
im
array([[255, 255, 255, 0, 0, 255, 255, 255],
 [255, 255, 255, 255, 255, 255, 255],
##
 [119, 255, 119, 255, 119, 255, 119, 255],
##
 [255, 119, 255, 119, 255, 119, 255, 119],
##
##
 [194, 119, 194, 119, 194, 119, 194, 119],
 [194, 194, 194, 194, 194, 194, 194],
##
 [255, 255, 255, 255, 255, 255, 255],
##
 Γ 0. 255. 0. 255. 0. 0. 255.
##
 011)
```

The image is in 8-bit greyscale: the values represent 256 shades of grey between 0 (black) and 255 (white).

And here is its plot:

<sup>130</sup> https://pillow.readthedocs.io

<sup>&</sup>lt;sup>131</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/images/grayscale\_demo\_8x8. png

```
import matplotlib.pyplot as plt
plt.style.use("seaborn")
plt.rcParams["axes.grid"] = False
plt.imshow(im, cmap="gray")
plt.rcParams["axes.grid"] = True
plt.show()
```

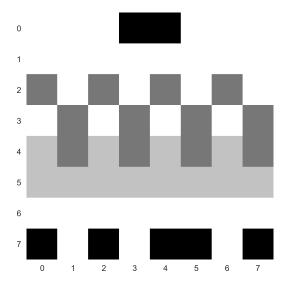


Figure16.1: plot of chunk 360-image-3

**Note.** Machine learning algorithms will often be expecting flat vectors on inputs – instead of an 8x8 matrix, they'd rather be fed with a sequence of 64 elements. Call im.flatten() to get such a form.

**Exercise.** Scale the brightness values from 0-255 to the [0, 1] interval, which is another common option (as we can read from the matplotlib. pyplot.imshow manual).

(\*\*) **Exercise.** Write a program that imports and visualises chosen example images in the famous MNIST<sup>132</sup> and Fashion-MNIST<sup>133</sup> datasets which are frequently used for benchmarking classification algorithms.

#### 16.2 Colour Models

There are quite a few colour models<sup>134</sup> in use, including:

- RBG<sup>135</sup> (red-green-blue),
- RGBA<sup>136</sup> (RGB with the alpha channel governing the pixel transparency/opaqueness),
- HSV<sup>137</sup> (hue-saturation-value),
- CMY<sup>138</sup> (cyan-magenta-yellow) usually used for printing.

They require each pixel be described by 3 (or 4 if the alpha channel is included) values. Thus, instead of a  $h \times w$  matrix, we well be dealing with three- dimensional arrays of size  $h \times w \times 3$  (or 4).

<sup>132</sup> http://yann.lecun.com/exdb/mnist/

<sup>133</sup> https://github.com/zalandoresearch/fashion-mnist

<sup>134</sup> https://en.wikipedia.org/wiki/Color\_model

<sup>135</sup> https://en.wikipedia.org/wiki/RGB\_color\_model

<sup>136</sup> https://en.wikipedia.org/wiki/RGBA\_color\_model

<sup>137</sup> https://en.wikipedia.org/wiki/HSL\_and\_HSV

<sup>138</sup> https://en.wikipedia.org/wiki/CMY\_color\_model

**Exercise.** Load and display some larger PNG or JPEG file downloaded from the internet.

## 16.3 Further Reading

Python packages worth inspecting:

- scipy.signal and scipy.ndimage
- pillow<sup>139</sup>
- scikit-image<sup>140</sup>
- OpenCV (it's a C++ library for image and video processing with Python bindings)

#### Literature:

- Ken Steiglitz, A Digital Signal Processing Primer: With Applications to Digital Audio and Computer Music, Pearson, 1996.
- Steven W. Smith, The Scientist and Engineer's Guide to Digital Signal Processing, Newnes, 2002. https://www.dspguide.com/

## 16.4 Questions

- 1. What colours do the following RGB hex triples<sup>141</sup> represent? #ff0000, #808000, #cccccc, #00aaff?
- 2. What are some other  $^{142}$  popular colour models?

<sup>139</sup> https://pillow.readthedocs.io

<sup>140</sup> https://scikit-image.org/

<sup>141</sup> https://en.wikipedia.org/wiki/Web\_colors

<sup>142</sup> https://en.wikipedia.org/wiki/Color\_model

# Part IV Heterogeneous Data

# Introduction to Data Frames in pandas

numpy arrays are an extremely versatile tool for performing data analysis and other numerical computations computations of various kinds. Although theoretically possible otherwise, however, we only store elements of the same type therein, most often numbers.

Pandas<sup>143</sup> is amongst over one hundred thousand<sup>144</sup> 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 objects in S and R as well as tables in relational (think: SQL) databases and spreadsheets.

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 objects for labelling individual rows and columns of DataFrames and items in Series objects,

together with many methods for:

- transforming/aggregating/processing data in groups determined by categorical variables or Cartesian 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,
- handling missing data.

<sup>143</sup> https://pandas.pydata.org/

<sup>144</sup> https://libraries.io/pypi/numpy

**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.

```
import numpy as np
import pandas as pd
pd.set_option("display.notebook_repr_html", False) # disable "rich" output
pd.__version__ # FYI
'1.4.1'
```

## 17.1 Creating Data Frames

Data frames can be created, amongst others, using the DataFrame class constructor, which can be fed, for example, with a *numpy* matrix:

Note that rows and columns are labelled (and how readable that finally 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"]
))
##
 И
 W
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.

Check out the pandas. DataFrame.from\_dict and pandas. DataFrame.from\_records methods in the pandas documentation 145. 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
 73.0 161.2
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
 73.2
4
 55.4 154.6
 34.6
 34.0
 28.3 92.5
```

<sup>145</sup> https://pandas.pydata.org/docs/

Check out the other pandas.read\_\* functions in the *pandas* documentation – some of which we shall be discussing later.

## 17.2 Representing Data Frames

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],
 w=["A", "B", "C", "D", "E"],
 x=["spam", "spam", "bacon", "spam", "eggs"]
))
df
 И
 V W
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.

#### 17.2.1 Series

There is a separate class for storing individual data frame columns: it is called Series.

```
s = df.loc[:, "u"] # extract the `u` column
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:

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()
0.49800000000000005
```

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.** 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)
0.49800000000000005
```

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.

#### 17.2.2 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, ..., 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:

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:

### 

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.** 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:

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 example 146:
```

```
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
##
 1.0
 30.489032
2
##
 2.0
 31.251247
 3.0
 30.969200
##
```

(continues on next page)

<sup>146</sup> https://wwwn.cdc.gov/Nchs/Nhanes/2017-2018/P\_DEMO.htm

##		4.0		31.471476
##		5.0		28.891357
##		7.0		30.200000
##		9.0		33.950000
##	Name:	BMXBMI,	dtype:	float64

But let us fret not, as there is always:

#### res.reset\_index()

##	RIAGENDR	DMDEDUC2	BMXBMI
## (	9 1	1.0	28.765244
## 3	1 1	2.0	28.534737
## 2	2 1	3.0	29.637793
## 3	3 1	4.0	30.323158
## 4	4 1	5.0	28.689736
## 3	5 1	9.0	28.080000
## (	5 2	1.0	30.489032
## 7	7 2	2.0	31.251247
## 8	8 2	3.0	30.969200
## 9	9 2	4.0	31.471476
## 2	10 2	5.0	28.891357
## 2	11 2	7.0	30.200000
## 2	12 2	9.0	33.950000

First things first, though – in the next part we shall discuss some more basic operations.

## 17.3 Further Reading

McKinney W. Python for Data Analysis: Data Wrangling with Pandas, NumPy, and IPython, O'Reilly, 2017.

Data frames were first introduced in the 1991 version of the S language (Chambers J.M., Hastie T.J., *Statistical Models in S*, Pacific Grove, CA, USA: Wadsworth & Brooks/Cole, 1991).

## 17.4 Questions

- 1. How are data frames different from matrices?
- 2. What are the use cases of the name slot in Series and Index objects?
- 3. What is the purpose of set\_index and reset\_index?

# Basic Operations on Data Frames

Looking at the list of methods for the DataFrame and Series classes in the *pandas* package's documentation<sup>147</sup>, 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).

```
import numpy as np
import pandas as pd
pd.set_option("display.notebook_repr_html", False) # disable "rich" output
```

## 18.1 Aggregating

Here is an example data frame:

<sup>147</sup> https://pandas.pydata.org/pandas-docs/stable/reference/index.html

```
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"])
##
 u v
a 0.70 0.32
 SDAM
b 0.29 -0.05
 bacon
c 0.23 -0.20
 spam
d 0.55 1.98
 eggs
e 0.72 -1.62 sausage
```

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.

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) skew, kurt.

Also let us note the describe method, which returns a few statistics at the same time.

#### d.describe()

```
u v v
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
```

(\*) Let us stress that above we see the corrected version of standard deviation, given by  $\sqrt{\frac{1}{n-1}}$ ...

**Exercise.** 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().

## 18.2 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"])
 2.013753
b
 1.336427
c 1.258600
 1.733253
d
e 2.054433
Name: u, dtype: float64
np.exp(d.loc[:, ["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:

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:

or to use the pandas.DataFrame.apply method which invokes a given function on each column separately:

Note that, in both cases, we can then write d.loc[:, ["u", "v"]] = uv to replace the old content with the transformed one.

## 18.3 Filtering

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.

#### 18.3.1 Series

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.r [0:10])
Ь
2
 0.70
1
 0.29
8
 0.23
 0.55
7
9
 0.72
 0.42
4
 0.98
5
 0.68
6
3
 0.48
0
 0.39
dtype: float64
c = b.copy()
c.index = list("abcdefghij")
a
 0.70
b
 0.29
C
 0.23
 0.55
d
 0.72
e
f
 0.42
```

(continues on next page)

```
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.).

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.

#### 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.

**Important.** To stay away from potential problems, we should never apply [...] directly on Series objects.

#### 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
 0.39
0
dtvpe: float64
c.loc[["j", "b", "j"]]
j
 0.39
b
 0.29
 0.39
j
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
```

(continues on next page)

```
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:

The result is not a scalar but a Series object.

#### 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).

## **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].

#### 18.3.2 DataFrame

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 local local results as a second results.
```

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,

fetches the first 3 rows (by position – iloc is necessary) and then selects two indicated columns.

On a side note, we can write d.u as a shorter version of d.loc[:, "u"], but this accessor is not universal: we can check this out by considering a data frame featuring a column named, e.g., mean.

**Exercise.** Use pandas.DataFrame.drop to select all columns but v in d.

**Exercise.** Use pandas. Series.isin (amongst others) to select all rows with spam and bacon on the d's menu.

**Exercise.** In the tips<sup>148</sup> 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.

 $<sup>^{148}\</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/other/tips.csv$ 

## 18.3.3 Adding Rows and Columns

loc[...] can also used to add new columns to an existing data frame:

**Exercise.** Use pandas.DataFrame.insert to add a new column not necessarily at the end of d.

**Exercise.** Use pandas. DataFrame. append to add a few more rows to d.

## 18.3.4 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.

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
 58.4 156.2
 35.2
 34.7
 27.2
 99.5
 77.5
4214
 36.5
 73.7 161.0
 34.5
 29.0
 107.6
 98.2
3361
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.** 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
х
##
 BMXWT BMXHT
 BMXARML
 BMXLEG
 BMXARMC
 BMXHIP
 BMXWAIST
 97.1 160.2
 35.8
 117.9
0
 34.7
 40.8
 126.1
 91.1 152.7
 33.5
 33.0
 38.5 125.5
 103.1
1
 73.0 161.2
 37.4
 31.8 106.2
 92.0
 38.0
2
3
 61.7 157.4
 38.0
 34.7
 29.0 101.0
 90.5
 55.4 154.6
 92.5
 34.6
 34.0
 28.3
 73.2
4
```

(continues on next page)

```
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
 97.5
8
 77.2 159.2
 38.5
 40.5
 35.7
 102.0
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
 31.8
 92.0
 37.4
 38.0
 106.2
```

Exercise. In the wine\_quality\_all<sup>149</sup> dataset, leave out all but the white

<sup>149</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/other/wine\_quality\_all.csv

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%).

**Exercise.** 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.

### 18.3.5 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
 0.29
##
 02
 03
 0.23
##
 0.55
##
 04
2024 01
 0.72
##
 02
 0.42
 Q3
 0.98
##
##
 04
 0.68
2025 01
 0.48
##
 02
 0.39
 0.34
##
 03
##
 04
 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
 0.29
Q2
 0.23
Q3
Q4
 0.55
d.loc[[2023, 2025], :]
##
 data
year quarter
2023 Q1
 0.70
##
 Q2
 0.29
##
 Q3
 0.23
##
 04
 0.55
2025 01
 0.48
 0.39
##
 02
##
 Q3
 0.34
 0.73
##
 04
```

To access deeper levels, we can use tuples as indexers:

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"]), :] # `:`, ["Q1", "Q3"]
##
 data
year quarter
 0.70
2023 Q1
##
 03
 0.23
 0.72
2024 01
 0.98
##
 03
2025 01
 0.48
 0.34
##
 03
d.loc[(slice(None, None, -1), slice("Q2", "Q3")), :] # ::-1, "Q2":"Q3"
 data
##
year quarter
2025 Q3
 0.34
 0.39
##
 02
2024 03
 0.98
 02
 0.42
##
2023 Q3
 0.23
 0.29
 02
##
```

## 18.4 Further Reading

McKinney W. Python for Data Analysis: Data Wrangling with Pandas, NumPy, and IPython, O'Reilly, 2017.

## 18.5 Questions

- 1. Why learning *numpy* is crucial when someone wants to become a proficient user of *pandas*?
- 2. What is the difference between iloc[...] and loc[...]?
- 3. Why applying the index operator [...] directly on a Series or DataFrame object is not necessarily a good idea?
- 4. What is the difference between .index, Index, and .columns?

5. How to compute the arithmetic mean and median of all the numeric columns in a data frame, using a single line of code?

## Reshaping and Fusing Datasets

In this part we 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 heterogeneous data.

```
import numpy as np
import pandas as pd
pd.set_option("display.notebook_repr_html", False) # disable "rich" output
```

## 19.1 Sorting

Let's consider another example dataset. Here are the yearly (for 2018) average air quality data<sup>150</sup> 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", "CO"]), :].
 reset index(drop=True)
)
air
##
 sp name param id
 value
0
 Alphington
 BPM2.5 7.848758
 Alphington
 CO 0.210884
1
 Alphington
2
 NO2
 9.558120
3
 Altona North
 N02
 9.467912
```

(continues on next page)

<sup>150</sup> https://discover.data.vic.gov.au/dataset/epa-air-watch-all-sites-air-quality-hourly-averages-yearly

##	4	Churchill	BPM2.5	6.391230
##	5	Dandenong	NO2	9.800705
##	6	Footscray	BPM2.5	7.640948
##	7	Footscray	CO	0.139754
##	8	Footscray	NO2	10.274531
##	9	Geelong South	BPM2.5	6.502762
##	10	Geelong South	CO	0.142473
##	11	Geelong South	NO2	5.681722
##	12	Melbourne CBD	BPM2.5	8.072998
##	13	Мое	BPM2.5	6.427079
##	14	Morwell East	BPM2.5	6.784596
##	15	Morwell East	CO	0.140836
##	16	Morwell South	BPM2.5	6.512849
##	17	Morwell South	CO	0.151979
##	18	Morwell South	NO2	5.124430
##	19	Traralgon	BPM2.5	8.024735
##	20	Traralgon	CO	0.159212
##	21	Traralgon	NO2	5.776333

sort\_values is a convenient means to order the rows with respect to one:

## air.sort\_values("value", ascending=False)

##	sp_name	param_id	value
## 8	Footscray	NO2	10.274531
## 5	Dandenong	NO2	9.800705
## 2	Alphington	NO2	9.558120
## 3	Altona North	NO2	9.467912
## 12	Melbourne CBD	BPM2.5	8.072998
## 19	Traralgon	BPM2.5	8.024735
## 0	Alphington	BPM2.5	7.848758
## 6	Footscray	BPM2.5	7.640948
## 14	Morwell East	BPM2.5	6.784596
## 16	Morwell South	BPM2.5	6.512849
## 9	Geelong South	BPM2.5	6.502762
## 13	Moe	BPM2.5	6.427079
## 4	Churchill	BPM2.5	6.391230
## 21	Traralgon	NO2	5.776333
## 11	Geelong South	NO2	5.681722
## 18	Morwell South	NO2	5.124430

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```
Alphington
1
 CO
 0.210884
 Traralgon
20
 CO
 0.159212
17
 Morwell South
 CO
 0.151979
 Geelona South
10
 CO 0.142473
15
 Morwell East
 0.140836
 CO
7
 Footscray
 0.139754
 CO
```

### or more criteria:

```
air.sort_values(["param_id", "value"], ascending=[True, False])
```

```
sp name param id
##
 value
12
 Melbourne CBD
 BPM2.5
 8.072998
19
 Traralgon
 BPM2.5
 8.024735
0
 Alphington
 BPM2.5 7.848758
 BPM2.5 7.640948
 Footscray
6
 Morwell East
14
 BPM2.5
 6.784596
 Morwell South
 BPM2.5
 6.512849
16
9
 Geelong South
 BPM2.5
 6.502762
 6.427079
13
 Moe
 BPM2.5
 Churchill
 BPM2.5
 6.391230
4
 Alphington
 0.210884
1
 CO
20
 Traralgon
 CO
 0.159212
 Morwell South
17
 CO
 0.151979
10
 Geelong South
 CO
 0.142473
 Morwell East
15
 0.140836
 CO
7
 Footscray
 CO
 0.139754
 Footscray
 10.274531
8
 N02
5
 Dandenong
 N02
 9.800705
2
 Alphington
 N02
 9.558120
3
 Altona North
 N02
 9.467912
 Traralgon
21
 N02
 5.776333
 Geelong South
11
 NO2
 5.681722
 Morwell South
18
 N02
 5.124430
```

Note that in the latter example, in each group of identical parameters, we get a decreasing order with respect to the value.

(\*) **Exercise.** Compare the ordering with respect to param\_id and value vs value and then param\_id.

(\*\*) **Exercise.** Perform identical reorderings but using only iloc[...], loc[...], and numpy.argsort.

## 19.2 Stacking and Unstacking

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. 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
sp name
Alphington
 7.848758 0.210884
 9.558120
Altona North
 9.467912
 NaN
 NaN
Churchill
 6.391230
 NaN
 NaN
Dandenong
 NaN
 NaN
 9.800705
Footscray
 7.640948 0.139754
 10.274531
Geelong South
 6.502762 0.142473
 5.681722
Melbourne CBD
 8.072998
 NaN
 NaN
Moe
 6.427079
 NaN
 NaN
 6.784596 0.140836
Morwell East
 NaN
 5.124430
Morwell South 6.512849 0.151979
Traralgon
 5.776333
 8.024735 0.159212
```

Note that the missing values are denoted with NaNs (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
 CO
 NO2
Alphington
 7.848758
 0.210884
 9.558120
Altona North
 9.467912
 NaN
 NaN
Churchill
 6.391230
 NaN
 NaN
Dandenong
 9.800705
 NaN
 NaN
 7.640948
Footscrav
 0.139754
 10.274531
Geelong South 6.502762
 0.142473
 5.681722
Melbourne CBD 8.072998
 NaN
 NaN
Moe
 6.427079
 NaN
 NaN
Morwell East
 6.784596
 0.140836
 NaN
Morwell South 6.512849
 0.151979
 5.124430
Traralgon
 8.024735 0.159212
 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
##
 рагат
 BPM2.5
 Alphington 7.848758
0
 BPM2.5
1
 Churchill 6.391230
 BPM2.5
 Footscray 7.640948
2
3
 BPM2.5 Geelong South 6.502762
 BPM2.5 Melbourne CBD 8.072998
4
5
 BPM2.5
 Moe 6.427079
 BPM2.5
 Morwell East 6.784596
6
 BPM2.5 Morwell South 6.512849
7
 BPM2.5
 Traralgon 8.024735
8
 CO
 Alphington 0.210884
9
 Footscray 0.139754
 CO
10
11
 CO Geelong South
 0.142473
 Morwell East 0.140836
12
 CO
```

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```
Morwell South
13
 0.151979
14
 CO
 Traralgon
 0.159212
15
 N02
 Alphington
 9.558120
16
 Altona North 9.467912
 NO2
17
 NO2
 Dandenong
 9.800705
18
 N02
 Footscray 10.274531
 Geelong South
19
 NO2
 5.681722
 Morwell South
20
 NO2
 5.124430
21
 N02
 Traralgon
 5.776333
```

We used the data frame transpose (T) to get a location-major order (less boring an outcome in this context).

# 19.3 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="#")
Α
##
 Name BirthDate
0
 Paitoon Ornwimol 26.06.1958
1
 Antónia Lata 20.05.1935
2
 Bertoldo Mallozzi 17.08.1972
3
 Nedeliko Bukv 19.12.1921
4
 Micha Kitchen 17.09.1930
5
 Mefodiy Shachar 01.10.1914
6
 Paul Meckler 29.09.1968
7
 Katarzvna Lasko 20.10.1971
8
 Åge Trelstad 07.03.1935
9
 Duchanee Panomyaong 19.06.1952
```

B = pd.read csv("https://raw.githubusercontent.com/gagolews/" +

```
and
```

```
"teaching_data/master/marek/some_birth_dates2.csv",
(continues on next page)
```

(continued from previous page)

```
comment="#")
В
 BirthDate
##
 Name
 Hushang Naigamwala
 25.08.1991
0
1
 Zhen Wei
 16.11.1975
 Micha Kitchen 17.09.1930
2
 Jodoc Alwin 16.11.1969
3
 Igor Mazał 14.05.2004
4
 Katarzyna Lasko 20.10.1971
5
 Duchanee Panomvaona 19.06.1952
6
 Mefodiy Shachar 01.10.1914
7
 Paul Meckler 29.09.1968
8
 Noe Tae-Woong
 11.07.1970
9
10
 Age 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 Panomyaona 19.06.1952
```

*A B* (difference) – the rows that are in *A* but not in *B*:

### A.loc[~A.Name.isin(B.Name), :]

```
Name BirthDate
0 Paitoon Ornwimol 26.06.1958
1 Antónia Lata 20.05.1935
2 Bertoldo Mallozzi 17.08.1972
3 Nedeliko Buky 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
 Paitoon Ornwimol 26.06.1958
0
1
 Antónia Lata 20.05.1935
2
 Bertoldo Mallozzi 17.08.1972
3
 Nedeljko Bukv 19.12.1921
 Micha Kitchen 17.09.1930
4
5
 Mefodiy Shachar 01.10.1914
6
 Paul Meckler 29.09.1968
7
 Katarzyna Lasko 20.10.1971
8
 Age Trelstad 07.03.1935
 Duchanee Panomyaong 19.06.1952
9
0
 Hushang Naigamwala 25.08.1991
 Zhen Wei 16.11.1975
1
 Jodoc Alwin 16.11.1969
3
4
 Igor Mazał 14.05.2004
9
 Noe Tae-Woong 11.07.1970
```

Not that there are no duplicate rows in the output.

**Exercise.** Determine  $(A \cup B)$   $(A \cap B) = (A \ B) \cup (B \ A)$  (symmetric difference).

(\*) **Exercise.** Determine the union, intersection, and difference of the wine\_sample1<sup>151</sup> and wine\_sample2<sup>152</sup> datasets, where there is no column uniquely identifying the observations. Hint: consider using pandas. DataFrame.duplicated or pandas.DataFrame.drop duplicates.

<sup>151</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/other/wine\_sample1.csv 152 https://raw.githubusercontent.com/gagolews/teaching\_data/master/other/wine\_sample2.csv

# 19.4 Joining (Merging)

In database design, it is common to normalise<sup>153</sup> the datasets in order to avoid the duplication of information and pathologies stemming from them.

For example, 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
 Visibility Reduction
0
 API
 Airborne particle index none
1
 BPM2.5
 BAM Particles < 2.5 micron ua/m3
 PM2.5
 Carbon Monoxide
2
 CO
 DDM
3
 HPM10
 Hivol PM10 ua/m3
 NaN
 NO2
 Nitroaen Dioxide
4
 ppb
 NO2
5
 0.3
 Ozone
 DDb
 0.3
 PM10
 TEOM Particles <10micron ua/m3
6
 PM10
 Partisol PM2.5 ua/m3
7
 PPM2.5
 NaN
 Sulfur Dioxide
 502
 502
8
 ppb
```

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.

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
```

(continues on next page)

<sup>153</sup> https://en.wikipedia.org/wiki/Database\_normalization

##

x y

(continued from previous page)

```
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"]
})
В
##
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:

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*.

The right join of *A* with *B* is the same as the left join of *B* with *A*:

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")
##
 У
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.** Join air\_quality\_2018\_value $^{154}$  with air\_quality\_2018\_point $^{155}$  and air\_quality\_2018\_param $^{156}$ .

**Exercise.** Normalise air\_quality\_2018<sup>157</sup> yourself so that you get the three data frames mentioned in the previous exercise (value, point, param).

<sup>154</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/marek/air\_quality\_2018\_value.

<sup>&</sup>lt;sup>155</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/marek/air\_quality\_2018\_point.csv

<sup>&</sup>lt;sup>156</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/marek/air\_quality\_2018\_param.csv

<sup>157</sup> https://raw.githubusercontent.com/gagolews/teaching\_data/master/marek/air\_quality\_2018.csv.gz

- (\*) **Exercise.** 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 variables<sup>158</sup>
- body measures<sup>159</sup>
- audiometry<sup>160</sup>

and many more<sup>161</sup>. Join a few chosen datasets that are to your liking.

## 19.5 Further Reading

McKinney W. Python for Data Analysis: Data Wrangling with Pandas, NumPy, and IPython, O'Reilly, 2017.

Wickham H. Tidy Data. Journal of Statistical Software, 59 (10):1–23. 2014. ht-tps://doi.org/10.18637/jss.v059.i10.

## 19.6 Questions

- 1. What is a train/test split and how to perform it using *numpy* and *pandas*?
- 2. What is the difference between stacking and unstacking? Which one yields a wide (as opposed to long) format?
- 3. Name different data frame join (merge) operations and explain how they work.
- 4. How does sorting with respect to more than one criterion work?

<sup>158</sup> https://wwwn.cdc.gov/Nchs/Nhanes/2017-2018/P\_DEMO.htm

<sup>159</sup> https://wwwn.cdc.gov/Nchs/Nhanes/2017-2018/P\_BMX.htm

<sup>160</sup> https://wwwn.cdc.gov/Nchs/Nhanes/2017-2018/AUX\_J.htm

<sup>161</sup> https://wwwn.cdc.gov/Nchs/Nhanes/continuousnhanes/default.aspx?BeginYear=2017

5. Name the basic set-theoretic operations on data frames.

# Observation Grouping

Consider a small subset of the urban\_forest<sup>162</sup> dataset which originally includes information on over 77,000 trees in Melbourne, VIC, Australia.

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
pd.set_option("display.notebook_repr_html", False) # disable "rich" output
plt.style.use("seaborn")
trees = pd.read_csv("https://raw.githubusercontent.com/gagolews/" +
 "teaching data/master/marek/urban forest subset2.csv",
 comment="#")
trees = trees.rename({
 "Common Name": "Species",
 "Diameter Breast Height": "Diameter",
 "Year Planted": "Year",
 "Located In": "Location",
 "Age Description": "Age",
}, axis=1).loc[:, ["Species", "Location", "Age", "Diameter", "Year"]]
trees.head()
##
 Species Location
 Aae Diameter Year
 London Plane Street
0
 Juvenile
 16 2009
 Japanese Zelkova Street Semi-Mature
 12 2008
1
2 Lemon Scented Gum Street
 Juvenile
 8 2009
 Japanese Zelkova Street Semi-Mature
3
 20 2008
 Japanese Zelkova Street Semi-Mature
 18 2006
4
```

These are heterogeneous data at their best – we have a mix of categorical (species, location, age) and numerical (diameter, year) variables. Unless we encoded qualitative variables as integers, this would not be possible with plain matrices.

<sup>&</sup>lt;sup>162</sup> https://data.melbourne.vic.gov.au/Environment/Trees-with-species-and-dimensions-Urban-Forest-/fp38-wiyy

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. This is like having many data frames stored in one object.

# 20.1 Manual Splitting Into Subgroups (\*\*)

As a low-level introduction to the current topic, let us demonstrate how easily the splitting can be done manually. 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 Location data:

```
trees_srt = trees.sort_values("Location", 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(trees_srt.loc[:, "Location"], return_index=True)
levels, where
(array(['Park', 'Street'], dtype=object), array([0, 27]))
```

This can now be used for dividing the sorted data frame into chunks:

```
trees_grp = np.split(trees_srt, where[1:])
```

We got 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(trees_grp[i].iloc[[0, -1], :])
 print("")
```

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```
level='Park'; preview:
 Species Location
 Aae Diameter
 Year
12 Peppercorn Tree
 Park Semi-Mature
 2009
99 Peppercorn Tree
 Park Semi-Mature
 40 2008
##
level='Street'; preview:
 Species Location
 Aae Diameter Year
##
 London Plane Street
0
 Juvenile
 16 2009
98 Japanese Zelkova Street Semi-Mature
 19 2008
```

We can apply any operation on each subgroup we have learned so far, our imagination is the only limiting factor, e.g., aggregate the two numeric columns:

```
trees_agg = [
 dict(
 level=t.loc[:, "Location"].iloc[0],
 diam_mean=np.mean(t.loc[:, "Diameter"]),
 year_mean=np.mean(t.loc[:, "Year"])
)
 for t in trees_grp
]
trees_agg
[{'level': 'Park', 'diam_mean': 22.62962962963, 'year_mean': 2008.
 -1851851851852}, {'level': 'Street', 'diam_mean': 15.465753424657533, 'year_mean': 2007.5753424657535}]
```

Finally, the results may be combined, e.g., to form a data frame:

```
pd.DataFrame(trees_agg)
level diam_mean year_mean
0 Park 22.629630 2008.185185
1 Street 15.465753 2007.575342
```

Manual splitting is very powerful but quite tedious in case we'd like to perform the basic operations such as the computing of aggregates. These scenarios are very common, no wonder why the *pandas* developers came up with an additional, convenience interface. The pandas.DataFrame.groupby and pandas.Series.groupby methods and the DataFrameGroupBy and SeriesGroupby class instances they yield, are discussed below.

(\*\*) Using numpy.split and matplotlib.pyplot.boxplot, draw a boxand-whisker plot of tree diameters grouped by species (four boxes side by side).

(\*\*) Using numpy.split, compute the z-scores of the Diameter column separately for each Location, e.g., standardise the park and street tree diameters separately.

(\*\*) 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 trees\_srt.Location + "\_\_\_" + trees\_srt.Species (assuming that trees\_srt is ordered with respect to these two criteria).

### 20.2 The groupby Methods

DataFrame and Series objects are equipped with groupby methods, which assist in performing a wide range of popular operations in data groups defined by one or more data frame columns.

They return objects of class DataFrameGroupBy and SeriesGroupby:

```
type(trees.groupby("Location"))
<class 'pandas.core.groupby.generic.DataFrameGroupBy'>
type(trees.groupby("Location")["Diameter"]) # or (...).Diameter
<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.** Skim through the documentation<sup>163</sup> of the said classes.

For example, the size method determines the number of observations in each group:

```
trees.groupby("Location").size()
Location
Park 27
Street 73
dtype: int64
```

This returns an object of type Series.

Another example, this time with the result converted to a neat data frame:

```
trees.groupby(["Species", "Location"]).size().rename("Counts").reset_index()
 Species Location Counts
 Japanese Zelkova
0
 Park
 2
 Japanese Zelkova
 Street
 26
1
2 Lemon Scented Gum
 Park
 11
3 Lemon Scented Gum
 Street
 14
 London Plane
 Park
 .3
4
 London Plane Street
 30
 Peppercorn Tree Park
 11
6
7
 Peppercorn Tree Street
 .3
```

<sup>163</sup> https://pandas.pydata.org/pandas-docs/stable/reference/groupby.html

**Exercise.** *Unstack* the above data frame (i.e., convert it from the *long* to the *wide* format).

(\*) **Exercise.** Note the difference between GroupBy.count and GroupBy.size methods.

### 20.2.1 Aggregating Data in Groups

The DataFrameGroupBy and SeriesGroupBy classes are equipped with a number of well-known aggregation functions, for example:

```
trees.groupby("Location").mean().reset_index()
Location Diameter Year
0 Park 22.629630 2008.185185
1 Street 15.465753 2007.575342
```

Note that the arithmetic mean was computed only on numeric columns.

A number of common aggregates is generated by describe:

```
trees.groupby("Location")["Diameter"].describe().reset_index()
Location count mean std min 25% 50% 75% max
0 Park 27.0 22.629630 26.029788 2.0 4.0 18.0 26.5 114.0
1 Street 73.0 15.465753 11.530253 1.0 8.0 13.0 20.0 70.0
```

But we can always apply a custom set of functions:

```
trees.groupby("Age").aggregate([np.mean, np.median]).reset_index()
Age Diameter Year
mean median mean median
0 Juvenile 9.428571 9.0 2007.464286 2008.0
1 Mature 75.600000 70.0 2007.600000 2008.0
```

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```
2 New 3.411765 3.0 2009.588235 2010.0

3 Semi-Mature 20.800000 20.0 2007.280000 2007.5

##

<string>:1: FutureWarning: ['Species', 'Location'] did not aggregate

-successfully. If any error is raised this will raise in a future version

-of pandas. Drop these columns/ops to avoid this warning.
```

Note that the result's columns slot is a hierarchical index.

(\*\*) Custom (anonymous) functions can be generated on the fly using the so-called lambda expressions:

```
(trees.loc[:, ["Age", "Diameter", "Year"]]
 .groupby("Age").aggregate(lambda x: (np.max(x)-np.min(x))/2)
 .reset index())
##
 Age Diameter Year
0
 Juvenile
 6.5
 2.0
 31.5
1
 Mature
 1.0
 2.5
2
 New
 1.0
 14.5
 1.5
3 Semi-Mature
```

(\*\*) Further, 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"
(trees.loc[:, ["Age", "Diameter", "Year"]]
 .groupby("Age").aggregate([np.mean, mr]).reset index())
 Age Diameter
##
 Year
##
 mean midrange
 mean midrange
0
 Juvenile
 9.428571
 6.5 2007.464286
 2.0
 Mature 75.600000
 31.5 2007.600000
 1.0
1
2
 New 3.411765
 2.5 2009.588235
 1.0
3 Semi-Mature 20.800000
 14.5 2007.280000
 1.5
```

# 20.2.2 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))/np.std(x)
trees["Diameter_Species_Std"] = (trees.loc[:, ["Species", "Diameter"]]
 .groupby("Species").transform(standardise))
(trees.loc[:, ["Species", "Diameter", "Diameter_Species_Std"]]
 .groupby("Species").aggregate([np.mean, np.std]))
/usr/local/lib/python3.9/dist-packages/numpy/core/fromnumeric.py:3472:
-FutureWarning: In a future version, DataFrame.mean(axis=None) will return□
-a scalar mean over the entire DataFrame. To retain the old behavior, use
→'frame.mean(axis=0)' or just 'frame.mean()'
 return mean(axis=axis, dtype=dtype, out=out, **kwargs)
 Diameter_Species_Std
##
##
 mean
 std
 mean
 std
Species
Japanese Zelkova
 11.214286 7.847421
 9.516197e-17 1.018350
Lemon Scented Gum 9.680000 6.606310
 3.663736e-17 1.020621
London Plane
 21.393939 16.813201
 -2.691450e-17 1.015505
 34.142857 26.935413
 -1.110223e-16 1.037749
Peppercorn Tree
```

The new column gives the *relative* z-scores: a London plane tree with relative z-score of o has the diameter at breast height of 21.4 cm, whereas a lemon scented gum tree with the same z-score has the true diameter of 9.7 cm.

**Exercise.** Create a data frame comprised of 5 trees of largest diameters located in a park, and 5 trees of largest diameters growing near a street.

## 20.3 Plotting Data in Groups with seaborn

The *seaborn* package is particularly convenient for plotting grouped data – it's highly interoperable with *pandas*.

For example: a boxplot with four boxes side by side:

sns.boxplot(x="Diameter", y="Species", data=trees)
plt.show()

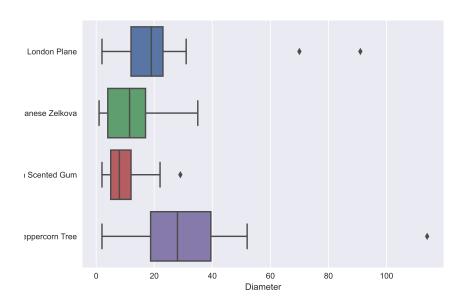


Figure 20.1: plot of chunk 440-group by-20

Let us contemplate for a while how easy it is now to compare the diameter distributions of each species.

**Exercise.** Create a similar series of violin plots.

**Exercise.** Add the average diameters in each group to the above boxplot.

And here is a bar plot with two grouping variables:

```
sns.barplot(
 y="Counts",
 x="Species",
 hue="Location",
 data=trees.groupby(["Species", "Location"]).size().rename("Counts").
 -reset_index()
)
plt.show()
```

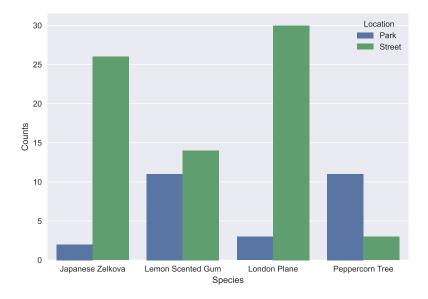


Figure 20.2: plot of chunk 440-group by-21

**Exercise.** Row-bind (concatenate rowwisely) the two datasets nhanes\_adult\_female\_bmx csv and nhanes\_adult\_male\_bmx\_2020.csv to a single data frame equipped

additionally with the sex column. Using seaborn.scatterplot, draw a scatterplot matrix (pairplot) for a few chosen columns, where a study participant's sex can be distinguished by the corresponding point's colour.

## 20.4 Further Reading

McKinney W. Python for Data Analysis: Data Wrangling with Pandas, NumPy, and IPython, O'Reilly, 2017.

Wickham H. The Split-Apply-Combine Strategy for Data Analysis. Journal of Statistical Software, 40 (1):1–29. 2011. https://doi.org/10.18637/jss.v040.i01.

# 20.5 Questions

- 1. Name the data type of an object that the DataFrame.groupby method returns.
- 2. What is the relationship between GroupBy, DataFrameGroupBy, and SeriesGroupBy?
- 3. What are relative z-scores and how can we compute them?

# Outliers, Missing, Censored, and Incorrect 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.

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
pd.set_option("display.notebook_repr_html", False) # disable "rich" output
plt.style.use("seaborn")
```

### 21.1 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)
 SEON BMDSTATS BMXWT BMIWT BMXRECUM
 WTINTPRP
 П
→WTMECPRP SDMVPSU SDMVSTRA
 INDFMPIR
0 109263
 NaN
 NaN
 NaN ...
 7891.762435
 8951.
 156
⊶815567
 4.66
1 109264
 1 42.2
 NaN
 NaN ... 11689.747264 12271.
157043
 1.5.5
 0.83
 1
```

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```
(continued from previous page)
```

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.

### 21.1.1 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
```

(continues on next page)

(continued from previous page)

```
BMXHEAD 13990.0 0.978322
BMIHIP 13924.0 0.973706
```

Looking at the column descriptions<sup>164</sup>, BMIHEAD stands for "Head Circumference Comment", whereas BMXHEAD is "Head Circumference (cm)", but it is only applicable for infants.

**Exercise.** 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.** Study the *pandas* manual to learn about the difference between the DataFrameGroupBy.size and DataFrameGroupBy.count methods.

## 21.1.2 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
```

<sup>164</sup> https://wwwn.cdc.gov/Nchs/Nhanes/2017-2018/P BMX.htm

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
 154.7
1
2
 89.3
3 160.2
4
 NaN
5 156.0
6
 182.3
Name: BMXHT, dtype: float64
y = (x > 40)
У
0
 False
1
 True
2
 True
3
 True
 False
4
 True
5
 True
Name: BMXHT, dtype: bool
```

(\*) 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
```

### 21.1.3 Missing at Random or Not?

At a general level (from the mathematical modelling perspective), we may distinguish between different missingness patterns (as per Rubin, 1976):

- 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.

## 21.1.4 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.** With the nhanes\_p\_demo\_bmx\_2020 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.

Hint: pandas.DataFrame.dropna might be useful in the simplest cases, and numpy.isnan or pandas.DataFrame.isna with.loc or.iloc otherwise.

## 21.1.5 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).

```
plt.subplot(131)
sns.histplot(x, binwidth=1, binrange=[130, 200], kde=True)
plt.ylim(0, 500)
plt.title("Original")
plt.subplot(132)
sns.histplot(xi, binwidth=1, binrange=[130, 200], kde=True)
plt.ylim(0, 500)
plt.title("Replace by mean")
plt.subplot(133)
sns.histplot(xg, binwidth=1, binrange=[130, 200], kde=True)
plt.vlim(0, 500)
plt.title("Replace by group mean")
plt.show()
(0.0, 500.0)
(0.0, 500.0)
(0.0, 500.0)
```

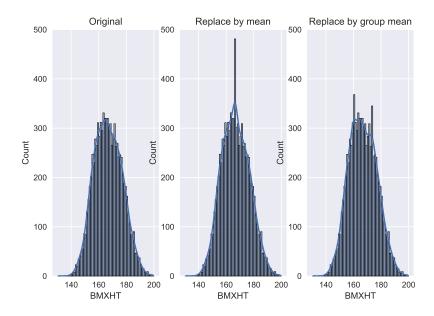


Figure 21.1: plot of chunk 450-missingness-14

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.** With the nhanes\_p\_demo\_bmx\_2020 dataset:

- 1. for each numerical column, replace all missing values with the column averages,
- 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.** sklearn.impute.KNNImputer implements missing value imputation based on averaging data from an observation's non-missing neighbours. 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 (1987, 1996) suggests the use of a procedure called *multiple imputation* (see also van Buuren, 2018), 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 algorithm's implementation is available in sklearn.impute.IterativeImputer.

### 21.1.6 Missing Values in Time Series

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.

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.

The classic air\_quality\_1973<sup>165</sup> 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:

<sup>165</sup> https://github.com/gagolews/teaching\_data/blob/master/r/air\_quality\_1973.csv

```
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,
 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
 313.000000
3
 313.0
 313.0
 313.0
4
 NaN
 313.0
 299.0
 308.333333
5
 NaN
 313.0
 299.0
 303.666667
6
 299.0
 299.000000
 299.0
 299.0
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
 194.0
 256.0
 225.000000
 NaN
11
 256.0
 256.0
 256.0
 256,000000
```

- (\*) **Exercise.** With the air\_quality\_2018<sup>166</sup> dataset:
- 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.

<sup>166</sup> https://github.com/gagolews/teaching\_data/blob/master/marek/air\_quality\_2018.csv.gz

- 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.

#### 21.2 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 errorneous observations, e.g., spell checkers such as *hunspell*<sup>167</sup>.

For smaller datasets, observations can also be manually inspected. However, sometimes we will have to develop our own algorithms for detecting "bugs" in data.

<sup>167</sup> https://hunspell.github.io/

**Exercise.** 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.
- 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 os and 1s only. It 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.

We will suggest more data validation exercises in the part on the processing of text data.

### 21.3 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.

#### 21.3.1 Unidimensional 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, one heuristic definition of an outlier that is particularly suited for data that are expected/suspected to come from a normal distribution, was to consider everything that does not fall into the interval  $[Q_1 - 1.5IQR, Q_3 + 1.5IQR]$ .

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.

That neither box plots themselves, nor the 1.5 IQR rule might not be ideal tools for multimodal data is exemplified below, 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")
plt.subplot(122)
sns.histplot(x, binwidth=1)
plt.show()
```

(\*) Note that for the normal distribution N(10,1), the probability of observing a value ≥ 15 is 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.

**Exercise.** For each column in nhanes\_p\_demo\_bmx\_2020, inspect a few smallest and largest observations and see if they make sense. Draw a histogram to verify if the data are perhaps multimodal.

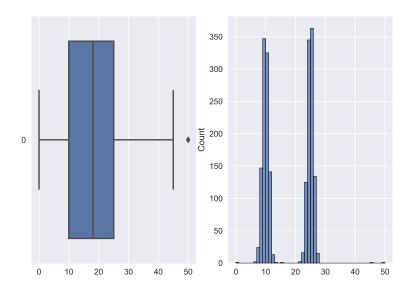


Figure 21.2: plot of chunk 450-missingness-16

**Exercise.** Perform the above separately for data in each group as defined by the RIAGENDR column.

## 21.3.2 Robust Aggregates

Some time ago 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.

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:  $median _{i=1}^{n}(|x_{i}-m|)$

### 21.3.3 Multidimensional Data (\*)

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:

```
x = np.loadtxt("https://raw.githubusercontent.com/gagolews/" +
 "teaching_data/master/marek/blobs1.txt", delimiter=",")
plt.subplot(221)
sns.boxplot(data=x[:, 0], orient="h")
plt.subplot(222)
sns.histplot(x[:, 0], bins=20)
plt.title("x[:, 0]")
plt.subplot(223)
sns.boxplot(data=x[:, 1], orient="h")
plt.subplot(224)
sns.histplot(x[:, 1], bins=20)
```

```
plt.title("x[:, 1]")
plt.show()
```

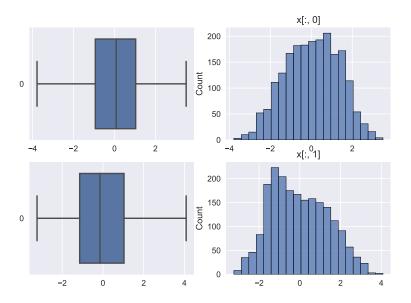


Figure21.3: plot of chunk 450-missingness-19

There is nothing suspicious here. Or is there?

Scatterplot already reveals that the data consist of two quite well-separable blobs:

```
plt.scatter(x[:, 0], x[:, 1])
plt.axis("equal")
plt.show()
(-4.1426233828018475, 3.863959941421967, -3.6005325979117258, 4.
-451040375538787)
```

Also, the are a few observations that we might consider outliers. Yours truly included 8 junk points at the very end of the dataset:

```
x[-8:,:]
```

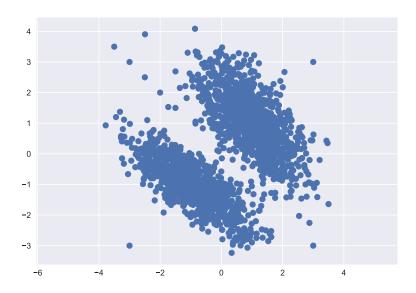


Figure 21.4: plot of chunk 450-missingness-20

```
array([[-3. , 3.],
[3. , 3.],
[-3. , -3.],
[-3.5, 3.5],
[-2.5, 2.5],
[-2.5, 2.5],
[-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  $\varepsilon > 0$ . If that is not the case, we may consider it an outlier.

## (\*\*) For example:

```
import scipy.spatial
```

```
t = scipy.spatial.KDTree(x)
n = t.query_ball_tree(t, 0.2) # epsilon=0.2 (radius)
c = np.array([len(e) for e in n])
c[[0, 1, -2, -1]] # preview
array([42, 30, 1, 1])
```

c[i] gives the number of points within x[i, :]'s  $\varepsilon$ -radius (with respect to the Euclidean distance), including the point itself. Therefore, c[i]==1 denotes a potential outlier.

```
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()
(-4.1426233828018475, 3.863959941421967, -3.6005325979117258, 4.
-451040375538787)
```

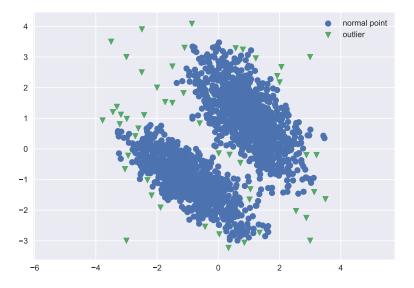


Figure 21.5: plot of chunk 450-missingness-23

(\*) **Exercise.** Use sklearn.neighbors.LocalOutlierFactor to detect some outliers in the above dataset.

(\*\*) **Exercise.** Use sklearn.svm.OneClassSVM for the same purpose.

(\*\*) **Exercise.** Play with sklearn.ensemble.IsolationForest.

## 21.4 Censored 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) in the course of the study. Our introductory course can't of course 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.

## 21.5 Further Reading

https://pandas.pydata.org/pandas-docs/stable/user\_guide/missing\_data.html
https://pandas.pydata.org/pandas-docs/stable/user\_guide/gotchas.html#gotchas-intna

- S. van Buuren, Flexible Imputation of Missing Data, CRC Press, 2018. https://stefvanbuuren.name
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- M. Modarres, M.P. Kaminskiy, V. Krivtsov, Reliability Engineering and Risk Analysis: A Practical Guide, CRC Press, 2016.
- D.B. Rubin, Inference and Missing Data, Biometrika 63(3), 1976, 581-590
- D.B. Rubin, Multiple Imputation for Nonresponse in Surveys, John Wiley & Sons, 1987
- D.B. Rubin, Multiple Imputation After 18+ Years, *Journal of the American Statistical Association* **91**(434), 1996, 473–89.

## 21.6 Questions

- 1. How can missing values be represented in *numpy* and *pandas*?
- 2. Explain some basic strategies for dealing with missing values in numeric vectors.
- 3. 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 don't like or otherwise deem inappropriate, controversial, dangerous, incompatible with our political views, etc.?
- 4. Is replacing missing values with the sample arithmetic mean for income data (as in, e.g., uk\_income\_simulated\_2020.txt) a sensible strategy?

- 5. What is the differences between data missing completely at random, missing at random, and missing not at random (according to Rubin's classification)?
- 6. List some basic strategies for dealing with data that might contain outliers.

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<sup>168</sup>, which is a lightweight, flat-file, and server-less database management system. Overall, SQLite is very good for working with 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).

import sqlite3

**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.

Other packages we use below:	
168 https://sqlite.org	

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
pd.set_option("display.notebook_repr_html", False) # disable "rich" output
plt.style.use("seaborn")
```

## 22.1 Example Database

In the course of this section, we will be working with a simplified data dump of the Q&A site http://travel.stackexchange.com which we have downloaded from https://archive.org/details/stackexchange on October 31, 2017. We have pre-processed the datasets and made them available at https://github.com/gagolews/teaching\_data/tree/master/travel\_stackexchange\_com\_2017.

**Exercise.** Before continuing, make yourself familiar with http://travel. stackexchange.com.

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
 2138.0 1 cruising
0
 104
 2137.0
1
 43
 357.0
 2 caribbean
 356.0
 43
 319.0 4 vacations
2
 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
 DisplayName
 →Location Reputation UpVotes Views
 -1.0 NaN 2011-06-21T15:16:44.253
 Community ... on the
⊶server farm
 1.0 2472.0 0.0
 2.0 40.0 2011-06-21T20:10:03.720 Geoff Dalaas
 П
⊶Corvallis, OR
 101.0 1.0 31.0
 7598.0 32.0 2011-06-21T20:11:02.490 Nick Craver ... Winston-
⇒Salem. NC
 101.0
 1.0 14.0
##
[3 rows x 11 columns]
```

Badges recall all rewards given to the users (User Id) 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
 3 2011-06-21T20:16:48.910 1 Autobiographer
0
 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 Parent Id 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 AnswerCount ...
 Title ViewCount
0
 393.0
 What are some Caribbean□
 4.0 ...
⇔cruises for October?
 419.0
1
 7.0 ... How can I find a guide that will \square
 NaN
⇒take me safel... 1399.0
 (continues on next page)
```

```
2 NaN NaN ...

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.

```
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
 NaN 2011-06-21T00:00:00.000 1
 1
0
 NaN
1
 NaN 2011-06-21T00:00:00.000 2
 1
 2
 NaN
 NaN 2011-06-21T00:00:00.000 3
2
 2
 NaN
 2
```

**Exercise.** See the README<sup>169</sup> file for the detailed description of each column.

### 22.2 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 (here, we use a temporary file):

```
import tempfile, os.path
dbfile = os.path.join(tempfile.mkdtemp(), "travel.db")
print(dbfile)
/tmp/tmpwu9wh_sg/travel.db
```

<sup>169</sup> https://github.com/gagolews/teaching\_data/blob/master/travel\_stackexchange\_com/README.md

And now:

```
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)
1743
44203
108812
72181
566062
```

- (\*) Note that 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 is of course possible without *pandas* as well, e.g., when data are to be imported from XML or JSON files 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 manual<sup>170</sup> of the sqlite3 package.

## 22.3 Example SQL Queries

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
##
 2138.0 1 cruising
 104
 2137.0
0
 357.0 2 caribbean
1
 43
 356.0
 319.0 4 vacations
2
 43
 318.0
```

Fetches all columns (SELECT \*) and the first 3 rows (LIMIT 3) from the Tags table.

**Exercise.** For the above and all the remaining 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.

For instance, here is the reference result:

Our example equivalent pandas implementation of the above operation might look like:

<sup>170</sup> https://docs.python.org/3/library/sqlite3.html

```
res1b = Tags.head(3)
```

To verify if the results are identical, we can call:

```
res1a.equals(res1b)
True
```

## 22.3.1 Filtering

Fetch all tag data for tags whose name contain "europe" as substring:

```
pd.read_sql_query("""
 SELECT * FROM Tags WHERE TagName LIKE '%europe%'
""", conn)
 Count ExcerptPostId
 Ιd
 TagName WikiPostId
##
0
 681
 286.0 30
 еигоре
 285.0
1
 27
 2384.0 174 eastern-europe
 2383.0
2
 12
 6403.0 512 southeast-europe
 6402.0
3
 4513.0 669 central-europe
 20
 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.

From Tags, select two columns TagName and Count and rows for which TagName is equal to one of the three choices provided.

Hint: use Tags. TagName. isin.

Select a number of columns from Posts whose rows fulfil given conditions:

```
pd.read_sql_query("""
```

```
SELECT Title, Score, ViewCount, FavoriteCount
 FROM Posts
 WHERE PostTypeId=1 AND
 ViewCount>=10000 AND
 FavoriteCount BETWEEN 35 AND 100
""", conn)
##
 Title Score ViewCount □
→ FavoriteCount
0 When traveling to a country with a different c...
 136
 16838.0
 35.0
 How can I do a "broad" search for flights?
1
 95
 33554.0
 49.0
 Tactics to avoid getting harassed by corrupt p...
 ## 2
 156
 13220.0
3 Flight tickets: buy two weeks before even duri...
 109
 49440.0
 OK we're all adults here, so really, how on ea...
 73808.0
4
 306
 How to intentionally get denied entry to the U...
 219
 63873.0
 ## 5
 53.0
 How do you know if Americans genuinely/literal...
 254
 30312.0
 П
 OK, we are all adults here, so what is a bidet...
 П
 140
 52265.0
 38.0
8
 How to cope with too slow Wi-Fi at hotel?
 82
 16380.0
 П
 41.0
```

Note that the SQL syntax is very readable, hence no explanations are needed.

## 22.3.2 Ordering

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):

```
pd.read_sql_query("""
 SELECT Title, Score
 FROM Posts
```

(continued from previous page)

```
WHERE ParentId IS NULL AND Title IS NOT NULL
 ORDER BY Score DESC
 LIMIT 5
""", conn)
 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
 Why prohibit engine braking?
 178
4
```

Hint: use Posts. sort\_values.

### 22.3.3 Removing Duplicates

Get all unique badge names for the user with Id=23.

```
pd.read_sql_query("""
 SELECT DISTINCT Name
 FROM Badges
 WHERE UserId=23
""", conn)
##
 Name
0
 Supporter
 Student
1
 Teacher
2
3
 Scholar
 Beta
4
 Nice Ouestion
5
 Editor
6
 Nice Answer
7
8
 Yearlina
 Popular Question
9
 Taxonomist
10
11 Notable Question
```

Hint: use Posts.drop\_duplicates.

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 are unique pairs (Name, Year).

```
pd.read_sql_query("""
 SELECT DISTINCT Name, strftime('%Y', Date) AS Year
 FROM Badges
 WHERE UserId=23
""", conn)
##
 Name Year
 Supporter 2011
0
1
 Student 2011
2
 Teacher 2011
3
 Scholar 2011
4
 Beta 2011
 Nice Ouestion 2011
5
6
 Editor 2012
7
 Nice Answer 2012
8
 Yearlina 2012
9
 Nice Question 2012
 Nice Question 2013
10
 Yearling 2013
11
12 Popular Question 2014
 Yearling 2014
13
14
 Taxonomist 2014
15 Notable Question 2015
 Nice Question 2017
16
```

Hint: use Badges.Date.astype("datetime64").dt.strftime("%Y").

## 22.3.4 Grouping and Aggregating

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).

```
pd.read_sql_query("""
 SELECT
 Name,
 COUNT(*) AS Count,
 MIN(strftime('%Y', Date)) AS MinYear,
 AVG(strftime('%Y', Date)) AS MeanYear,
 MAX(strftime('%Y', Date)) AS MaxYear
 FROM Badges
```

(continued from previous page)

```
WHERE UserId=23
 GROUP BY Name
 ORDER BY Count DESC
 LIMIT 4
""", conn)
 Name Count MinYear MeanYear MaxYear
##
 4
 2011 2013.25
0
 Nice Question
 2017
 3 2012 2013.00
1
 Yearlina
 2014
2 Popular Question
 3 2014 2014.00
 2014
3 Notable Ouestion
 2
 2015
 2015.00
 2015
```

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.

```
pd.read_sql_query("""
 SELECT
 Name,
 strftime('%Y', Date) AS Year,
 COUNT(*) AS Count
 FROM Badges
 WHERE UserId=23
 GROUP BY Name, Year
 HAVING Count > 1
 ORDER BY Count DESC
""", conn)
##
 Name Year Count
0 Popular Question 2014
 3
1 Notable Ouestion 2015
 2
```

Note that WHERE is performed before GROUP BY, and HAVING is applied thereafter.

## 22.3.5 Joining

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 5 records with respect to Tags.Count.

```
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 LIMIT 5
""", conn)
 П
##
 TagName Count OwnerUserId
 Age
 Location
→ DisplayName
 П
0
 canada
 802
 101.0 34.0
 Mumbai. India
∴hitec
1
 583.0 35.0 Philadelphia, PA
 Adam
 еигоре
 681
⊶ Tuttle
2 visa-refusals
 554
 1737.0
 34.0
 New York, NY Benjamin
-Pollack
3
 australia
 411
 101.0 34.0
 Mumbai, India
-hitec
4 new-york-city
 204
 101.0 34.0
 Mumbai, India
-hitec
```

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:

```
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)
 PostId UpVotes
##
 Title
 307 OK we're all adults here, so really, how on ea...
0
 3080
 (continues on next page)
```

#### (continued from previous page)

```
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?
```

### 22.4 Closing the Database Connection

We have said we should not forget about:

```
conn.close()
```

This gives some sense of closure. Such a relief.

## 22.5 Further Reading

```
sqlite3 package, https://docs.python.org/3/library/sqlite3.html
SQLite - SQL syntax, https://sqlite.org/lang.html
```

## 22.6 Questions

- 1. What are the benefits of using a SQL-supporting relational database management system in data science activities?
- 2. (\*\*) How to populate a database with gigabytes of data read from many CSV files?

# Part V

# **Text Data**

# Working with Text Data

In (Gagolewski, 2022) 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 (e.g., Dasu and Johnson, 2003; van der Loo and de Jonge 2018) 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*.

## 23.1 String Operations in Base Python

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] + "ecial"
'special'
```

It is worth knowing that all strings in Python (from version 3.0) use Unicode<sup>171</sup>, 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.** More precisely, Python strings are UTF-8<sup>172</sup>-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.

(\*\*) **Note.** Despite the wide support for Unicode, sometimes our own or other readers' display (e.g., web browsers when viewing a HTML version

<sup>171</sup> https://en.wikipedia.org/wiki/Unicode

<sup>172</sup> https://en.wikipedia.org/wiki/UTF-8

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.

#### 23.1.1 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  $ICU^{173}$  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"):

<sup>173</sup> https://icu.unicode.org/

```
(continued from previous page)
)
'chairete! gross gzegzolka - (C) la nina - koszonom - gagolewski'
```

Converting between different Unicode Normalisation Forms<sup>174</sup> (also available in the unicodedata package and via pd. Series.str.normalize) might be used for the removal of some formatting nuances:

```
icu.Transliterator.createInstance("NFKD; NFC").transliterate("¼ar²[") ## '¼qr2{'
```

## 23.1.2 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.

<sup>174</sup> https://www.unicode.org/faq/normalization.html

**Exercise.** 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 the next part, 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.

## 23.1.3 Locale-Aware Services (\*\*)

Recall that relational operators such as < and >= allow for the 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 codes<sup>175</sup> 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.

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 2nd argument is greater than the 1st). 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 greater than the 2nd one).

Also, with ICU, numeric collation is possible:

Which is the correct result (compare the above example using <).

<sup>175</sup> https://www.unicode.org/charts/

## 23.2 String Operations in pandas

String sequences in *pandas* Series are by default using the broadest possible object data type:

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.

Vectorised versions of base string operations are available via the pandas. Series.str accessor, which we usually refer to by calling x.str.method\_name(), for instance:

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:

#### Concatenating all items into a single string:

```
x.str.cat(sep="; ")
'spam; bacon; buckwheat; spam'
```

#### Vectorised string concatenation:

#### Conversion to numeric:

#### Selecting substrings:

## Replacing substrings:

```
4 tofuam
dtype: object
```

**Exercise.** Consider the nasaweather\_glaciers<sup>176</sup> 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.

## 23.3 Working with String Lists

Series can also consist of lists of strings of varying lengths. They can not only be input manually (via the pd. 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
```

 $<sup>^{176}\</sup> https://github.com/gagolews/teaching\_data/blob/master/other/nasaweather\_glaciers.csv$ 

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:

selecting, say, the first string in each list:

### or slicing:

(\*) **Exercise.** Using pandas.merge, join the following datasets: countries<sup>177</sup>, world\_factbook\_2020<sup>178</sup>, and ssi\_2016\_dimensions<sup>179</sup> based on the country names. Note that some manual data cleansing will be necessary.

- (\*\*) **Exercise.** Given a Series object featuring lists of strings:
- 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.

# 23.4 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:

```
import numpy as np
x = np.array(["spam", "bacon", "egg"])
x
array(['spam', 'bacon', 'egg'], dtype='<U5')</pre>
```

<sup>177</sup> https://github.com/gagolews/teaching\_data/blob/master/other/countries.csv

<sup>178</sup> https://github.com/gagolews/teaching\_data/blob/master/marek/world\_factbook\_2020.csv

<sup>179</sup> https://github.com/gagolews/teaching\_data/blob/master/marek/ssi\_2016\_dimensions.csv

Here, the data type "<US" (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')</pre>
```

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')</pre>
```

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')</pre>
```

The numpy.char 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"
])
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')
(continues on next page)</pre>
```

```
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])
```

# 23.5 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*<sup>180</sup>) it is important to be able to output nicely formatted content programmatically.

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 pt formatted as a float rounded to two places after the decimal separator. (\*\*) 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):

```
"n = \{:.2f\}".format(pi), "n = %.2f" % pi
('n = 3.14', 'n = 3.14')
```

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])
```

(continues on next page)

<sup>180</sup> https://pandoc.org/

```
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).

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.

Further, note that with IPython/Jupyter, we can output strings that will be directly interpreted as Markdown-formatted:

```
import IPython.display
x = 2+2
IPython.display.Markdown(f"""
Result: $2^2=2+2={x}$.
""")
<IPython.core.display.Markdown object>
```

Recall that Markdown<sup>181</sup> is a very flexible markup language, allowing us to insert itemised and numbered lists, mathematical formulae, tables, images, etc.

We can also generate Markdown code programmatically in form of standalone .md files:

<sup>181</sup> https://daringfireball.net/projects/markdown/syntax

```
50
7
8
7
7
46
12
12
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
##
And now for something completely different:
##
Rank | Food

##
 1 | maps
 2 | nocab
##
##
 3 | sgge
 4 | maps
##
```

We can run it through the  $pandoc^{182}$  tool to convert it to a number of formats, including HTML, PDF, EPUB, and ODT. We may also render it directly into our report:

<sup>182</sup> https://pandoc.org/

#### IPython.display.Markdown(out)

## <IPython.core.display.Markdown object>

**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.

# 23.6 Further Reading

M. Gagolewski, *stringi*: Fast and portable character string processing in R, *Journal of Statistical Software*, 2022, in press, https://stringi.gagolewski.com

T. Dasu, T. Johnson, Exploratory Data Mining and Data Cleaning. John Wiley & Sons, 2003.

M. van der Loo, E. de Jonge, Statistical Data Cleaning with Applications in R, John Wiley & Sons, 2018.

NumPy – String Operations, https://numpy.org/doc/stable/reference/routines.char.html

Pandas – Working with Text Data, https://pandas.pydata.org/pandas-docs/stable/user\_guide/t

string—Common string operations, https://docs.python.org/3/library/string.html

Built-in Types, https://docs.python.org/3/library/stdtypes.html

unicodedata — Unicode Database, https://docs.python.org/3/library/unicodedata.html

# 23.7 Questions

- 1. List some ways to normalise strings.
- 2. (\*\*) What are the challenges of processing non-English text?

# Regular Expressions (\*)

Note that this section contains large excerpts from yours truly's other work (Gagolewski, 2022).

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 (Kleene, 1951), see also (Rabin and Scott, 1959; Hopcroft and Ullman, 1979). 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 (Ritchie and Thompson, 1970; the predecessor of the well-known sed).

# 24.1 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! niiii! ni! niiiiii!"
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 "knights".

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, 'niiiiiiiii')
```

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", 'niiii', 'ni', 'niiiiii!']
```

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!"
```

(\*\*) 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!"
```

# 24.2 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:

Here are the most notable functions; their names are self-explanatory, so let's just get the picture instead of the words' abundance.

(continues on next page)

```
x.str.count(r"\bni+\b")
 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
1 nu, nu, nu!
 None
2
3 spam, bacon
4
 nu, nu!
dtype: object
x.str.findall(r"\bni+\b")
0
 [ni]
1
 [niiii, ni, nii]
2
 None
3
 Γ7
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! nininiii!")
['ni', 'ni', 'niiii']
```

# 24.3 Review of Regex Syntax

Most programming languages and text editors (including *Kate*<sup>183</sup>, *Eclipse*<sup>184</sup>, and *VSCode*<sup>185</sup>) support finding or replacing patters with regexes. Therefore, they should be amongst the instruments at every data scientist's disposal. One general introduction to regexes is (Friedl, 2006). The *re* module flavour is summarised in the official manual<sup>186</sup>. Below we review the most important elements of the regex syntax as we did in (Gagolewski, 2022).

# 24.3.1 Matching Individual Characters

We begin by discussing different ways to define character sets. In this part, determining the length of all matching substrings will be quite straightforward.

The following characters have special meaning to the regex engine:

Any regular expression that contains none of the above behaves like a fixed pattern:

<sup>183</sup> https://kate-editor.org/

<sup>184</sup> https://www.eclipse.org/ide/

<sup>185</sup> https://code.visualstudio.com/

<sup>186</sup> https://docs.python.org/3/library/re.html

```
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 "n".

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...")
['.', '.', '.']
```

#### **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).

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 "^" 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, ≤ 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', 'g', 'o', 'l', 'e', 'w', '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":

```
x = "aab&AAABD12DDD,.;'! \t-+=\n[]@DD",,"
re.findall(r"\w", x)
['a', 'a', 'b', '\b', '\b', '\A', '\A', '\B', '\D', '\1', '\2', '\D', '\0']

decimal digits:
re.findall(r"\d", x)
['1', '2', '\D', '\D', '\D']

and whitespaces:
re.findall(r"\s", x)
[' ', '\t', '\n']
```

Moreover, e.g., " $\W$ " is equivalent to " $[^\w]$ ", i.e., denotes its complement.

#### 24.3.2 Alternating and Grouping Subexpressions

#### **Alternation Operator**

The alternation operator, "|", 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']
```

"|" 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.

#### **Grouping Subexpressions**

Also, matching is always done left-to-right, on a first-come, first-served basis. So, 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
)
['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'
 "|" + # ... or ...
 "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']
```

# 24.3.3 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 o or 1 times:
- "\*" matches o 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, "ba+" captures "ba", "baa", "baaa", etc., but neither "b" alone nor "bababa" 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 = "spamamamnomnomnomammmmmmm"
re.findall("sp(?:am|nom)+", x)
['spamamamnomnomam']
re.findall("sp(?:am|nom)+?", x)
['spam']
And:
re.findall("sp(?:am|nom)+?m*", x)
['spam']
re.findall("sp(?:am|nom)+?m*", x)
['spamamamnomnomnomammmmmmmmmmm']
```

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.** Write a regex that extracts all #hashtags from a string #omg #SoEasy.

#### 24.3.4 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)
```

(continues on next page)

```
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:

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:

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
```

(continues on next page)

```
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 = "spam<code>eggs</code>"
re.findall(r"<[a-z]+>.*?</[a-z]+>", x)
['spam', '<code>eggs</code>']
re.findall(r"(<([a-z]+)>.*?</\2>)", x)
[('spam', '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)
[('spam', 'strong'), ('<code>eggs</code>', 'code
')]
```

#### 24.3.5 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
۰"])
rs = ["spam", "^spam", "spam$", "spam$|^spam", "^spam$"]
pd.concat([x.str.contains(r) for r in rs], axis=1, keys=rs)
 spam ^spam spam$ 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.** 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.** Write a regex that extract all standalone numbers accepted by Python, including 12.123, -53, +1e-9, -1.2423e10, 4. and .2.

**Exercise.** Write a regex that matches all email addresses.

**Exercise.** Write a regex that matches all URLs starting with http://or https://.

**Exercise.** Cleanse the warsaw\_weather<sup>187</sup> dataset so that it contains analysable numeric data.

# 24.4 Further Reading

- M. Gagolewski, *stringi*: Fast and portable character string processing in R, *Journal of Statistical Software*, 2022, in press, https://stringi.gagolewski.com
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- M. Rabin and D. Scott. Finite automata and their decision problems. IBM Journal of Research and Development, 3:114–125, 1959.
- re Regular Expression Operations, https://docs.python.org/3/library/re.html
- A.M. Kuchling, Regular Expression HOWTO, https://docs.python.org/3/howto/regex.html

# 24.5 Questions

- 1. What are the problems with the "[A-Za-z]" and "[A-z]" character sets?
- 2. Name the two ways to turn on case-insensitive regex matching.
- 3. What is a word boundary?
- 4. What is the difference between the "^" and "\$" anchors?

<sup>&</sup>lt;sup>187</sup> https://github.com/gagolews/teaching\_data/blob/master/marek/warsaw\_weather.csv

- 5. When we would prefer using "[0-9]" instead of "\d"?
- 6. What is the difference between the "?", "??", "\*", "\*?", "+", and "+?" quantifiers?
- 7. Does "." match all the characters?
- 8. What are named capture groups and how to refer to the matches thereto in re.sub?

# Fetching and Cleaning Text Data

#### 25.1 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.

It is recommended that the reader solves some of the following exercises to make sure they can fetch data in these formats. Warning: often, this will quite tedious labour, neither art nor science. Good luck.

**Exercise.** Consider the Web API for accessing the on-street parking bay sensor data in Melbourne, VIC, Australia, see https://data.melbourne.vic.gov.au/Transport/On-street-Parking-Bay-Sensors/vh2v-4nfs. Using, for example, the *json* package, convert the data in the JSON format fetched from https://data.melbourne.vic.gov.au/resource/vh2v-4nfs.json to a *pandas* data frame.

**Exercise.** Australian Radiation Protection and Nuclear Safety Agency publishes UV data for different Aussie cities. Using, for example, the *xml* package, convert the XML dataset fetched from <a href="https://www.arpansa.gov.au/our-package">https://www.arpansa.gov.au/our-package</a>, convert from <a href="https://www.arpansa.gov.au/our-package</a>, convert from <a href="https://www.arpansa.gov.au/our-package</a>,

	tion https://uvdata.arpa	tion-monitoring/ultraviolet insa.gov.au/xml/uvvalues.x	
20th-century		Tikipedia article featuring a Using pandas.read_html, c 1 to a data frame.	
converts each	bullet list featured in a g a.org/wiki/Category:Fr%	xml package, write a functic tiven Wikipedia article (e.g., 6C3%A9d%C3%A9ric_Chopi	https:
you find inter	resting and store it in an	ion of a Stack Exchange <sup>189</sup> si S <b>QLite database. You can fi</b> e.org/details/stackexchange	nd the
(**) Exercise.	. Download from https:/	//meta.wikimedia.org/wiki,	/Data_

<sup>188</sup> https://en.wikipedia.org/wiki/List\_of\_20th-century\_classical\_composers 189 https://stackexchange.com/

dumps and then import an archived version of one of the wikis hosted by the Wikimedia Foundation<sup>190</sup> (e.g., the whole English Wikipedia) so that it can be stored in an SOLite database.

## 25.2 Working with Many Files

For 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.

#### 25.2.1 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), therefore they should be input as, e.g., "c:\\users\\marek\\file.csv" or r"c:\users\\marek\\file.csv".

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("~", "file.csv") # we're on GNU/Linux
'~/file.csv'
```

Note that the tilde, ~, denotes the current user's home directory.

It is often also worth knowing what the working directory of the currently executed Python session is, as all non-absolute file names, e.g., "filetype.csv" or os.path.join("subdir", "filetype.csv") will be relative to it. This can be read by calling os.getcwd().

For creating temporary directory names, we can use tempfile.mkdtemp().

<sup>190</sup> https://wikimediafoundation.org/

#### 25.2.2 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.** Write a function that computes the total size of all the files in a given directory and all its subdirectories.

# 25.3 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.** Given an example data frame with text columns (manually invented, be creative), perform what follows.

- ${\tt 1.} \ \ {\tt Remove\ trailing\ and\ leading\ whitespaces\ from\ each\ string.}$
- 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 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 PESEL<sup>191</sup>, check if that PESEL is correct.
- 8. Determine if a string represents a correct International Bank Account Number (IBAN<sup>192</sup>) (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.
- Resolve all abbreviations by means of a custom dictionary, e.g., "Kat." → "Katherine", "Gr." → "Grzegorz".

# 25.4 Further Reading

Pandas - IO Tools, https://pandas.pydata.org/pandas-docs/stable/user\_guide/io.html

# 25.5 Questions

- 1. Find an example of an XML and JSON file. Which one is more human-readable? Do they differ in terms of capabilities?
- 2. What is wrong with constructing file paths like "~" + "\\" + "filename.csv"?

<sup>191</sup> https://en.wikipedia.org/wiki/PESEL

<sup>192</sup> https://en.wikipedia.org/wiki/International\_Bank\_Account\_Number

# Part VI

# **Appendix**

# Bibliography

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