Data Science With Python

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Contents

Chapter 1

Prerequisites

This is a *sample* book written in **Markdown**. You can use anything that Pandoc's Markdown supports, e.g., a math equation $a^2 + b^2 = c^2$.

The **bookdown** package can be installed from CRAN or Github:

```
install.packages("bookdown")
# or the development version
# devtools::install_github("rstudio/bookdown")
```

Remember each Rmd file contains one and only one chapter, and a chapter is defined by the first-level heading `#`.

To compile this example to PDF, you need XeLaTeX. You are recommended to install TinyTeX (which includes XeLaTeX): https://yihui.name/tinytex/.

Chapter 2

Introduction

You can label chapter and section titles using `{#label}` after them, e.g., we can reference Chapter 2. If you do not manually label them, there will be automatic labels anyway, e.g., Chapter 4.

Figures and tables with captions will be placed in `figure` and `table` environments, respectively.

And this is some other random stuff.

```
par(mar = c(4, 4, .1, .1))
plot(pressure, type = 'b', pch = 19)
```

Reference a figure by its code chunk label with the `fig:` prefix, e.g., see Figure 2.1. Similarly, you can reference tables generated from `knitr::kable()`, e.g., see Table 2.1.

```
knitr::kable(
  head(iris, 20), caption = 'Here is a nice table!',
  booktabs = TRUE
)
```

```
knitr::include_graphics(rep("knit-logo.png", 3))
```

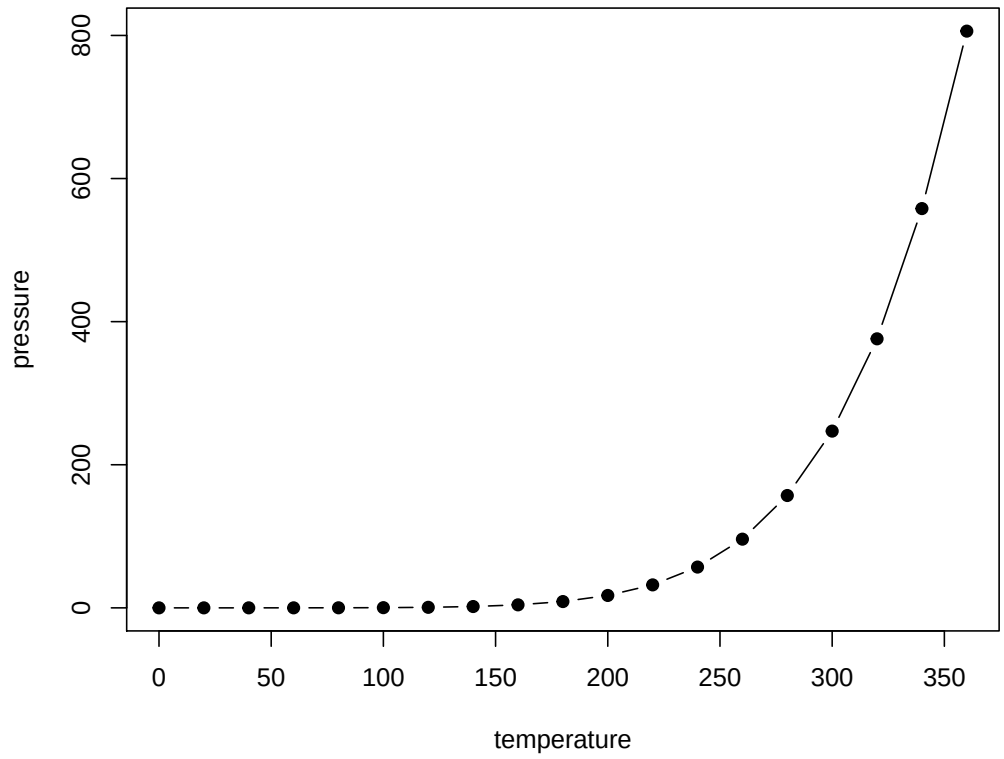
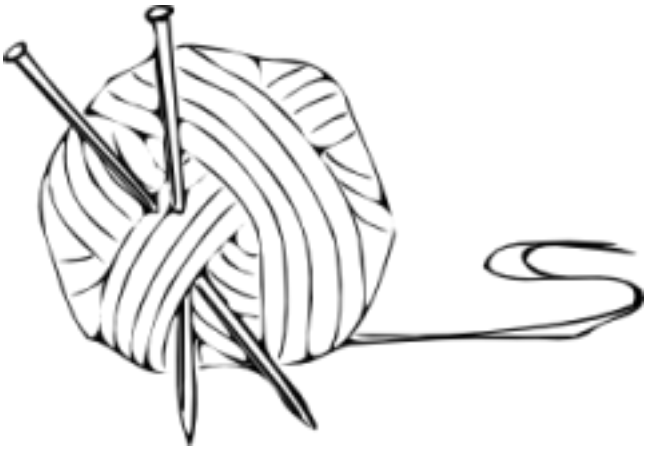


Figure 2.1: Here is a nice figure!



```
knitr::include_app("https://yihui.shinyapps.io/miniUI/",
                   height = "600px")
```

```
import pandas as pd
x = 'hello, python world!'
print(x.split(' '))
```

```
## ['hello,', 'python', 'world!']
```

You can write citations, too. For example, we are using the **bookdown** package (Xie, 2018) in this sample book, which was built on top of R Markdown and **knitr** (Xie, 2015).

Table 2.1: Here is a nice table!

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa
5.4	3.7	1.5	0.2	setosa
4.8	3.4	1.6	0.2	setosa
4.8	3.0	1.4	0.1	setosa
4.3	3.0	1.1	0.1	setosa
5.8	4.0	1.2	0.2	setosa
5.7	4.4	1.5	0.4	setosa
5.4	3.9	1.3	0.4	setosa
5.1	3.5	1.4	0.3	setosa
5.7	3.8	1.7	0.3	setosa
5.1	3.8	1.5	0.3	setosa

Chapter 3

JupyterLab

Here is a simple template that I use that controls a couple useful things when starting a new notebook.

```
import sys
sys.path.append('../util')

%reload_ext autoreload
%autoreload 2

from util import *
import numpy as np
import pandas as pd
from matplotlib import pyplot as plt
import seaborn as sns

sns.set_palette('pastel')
sns.set_style('ticks')
sns.set_context('paper', font_scale=1)
```

It is often convenient to have a notebook automatically refresh the imported libraries so that they can be modified while working on a JupyterLab notebook.

```
%reload_ext autoreload
%autoreload 2
```

To allow directory organization, dependcies can be separated into different directories and imported into a jupyter notebook using the following import statement.

```
import sys
sys.path.append('../util')
```

Chapter 4

Visualization

4.1 Colorschemes

Seaborn Themes Pastel: [Blue:‘#a3c6ff’, Orange:‘#f7ab60’, Green:‘#60f7a9’, Red:‘#fc9d94’, Purple:‘#bea3ff’, Brown:‘#d1b485’, Pink:‘#f7afdf’, Gray:‘#c4c4c4’, Yellow:‘#ffffaa’, LBlue:‘#baf6ff’] Deep: [Green:‘#5baf68’]

4.2 Matplotlib

Plotting a heatmap.

```
import matplotlib.pyplot as plt
import numpy as np
a = np.random.random((16, 16))
plt.imshow(a, cmap='RdBu'', interpolation='nearest')
plt.show()
```

Possible heatmap colors are:

```
Accent, Accent_r, Blues, Blues_r, BrBG, BrBG_r, BuGn, BuGn_r, BuPu, BuPu_r, CMRmap, CMRmap_r, Dark2, Da
Set1_r, Set2, Set2_r, Set3, Set3_r, Spectral, Spectral_r, Wistia, Wistia_r, YlGn, YlGnBu, YlGnBu_r, YlG
gist_stern, gist_stern_r, gist_yarg, gist_yarg_r, gnuplot, gnuplot2, gnuplot2_r, gnuplot_r, gray, gray_
twilight, twilight_r, twilight_shifted, twilight_shifted_r, viridis, viridis_r, vlag, vlag_r, winter, w
```

A simple venn diagram.

```
from matplotlib_venn import venn2
venn2(subsets = (3, 2, 1))
```

A more complicated venn diagram.

```
from matplotlib import pyplot as plt
import numpy as np
from matplotlib_venn import venn3, venn3_circles
plt.figure(figsize=(4,4))
```

```
v = venn3(subsets=(1, 1, 1, 1, 1, 1, 1), set_labels = ('A', 'B', 'C'))
v.get_patch_by_id('100').set_alpha(1.0)
v.get_patch_by_id('100').set_color('white')
v.get_label_by_id('100').set_text('Unknown')
v.get_label_by_id('A').set_text('Set "A"')
c = venn3_circles(subsets=(1, 1, 1, 1, 1, 1, 1), linestyle='dotted')
c[0].set_lw(1.0)
c[0].set_ls('dotted')
plt.title("Sample Venn diagram")
plt.annotate('Unknown set', xy=v.get_label_by_id('100').get_position() - np.array([0, 0.05]), xytext=(-
             ha='center', textcoords='offset points', bbox=dict(boxstyle='round,pad=0.5', fc='gray', al
                          arrowprops=dict(arrowstyle='->', connectionstyle='arc3,rad=0.5',color='gray'))
                          plt.show()
```

4.3 Seaborn

Here is a general bar plot that includes some commonly used parameters.

```
# fits my 22 inch monitor
plt.figure(figsize=(19.17,11.98))
# order controls the display order of the samples
sns.catplot(x="Sample", y="Somatic", kind="bar", data=var_counts, order=labels);
# keeps x-axis labels, but eliminates the tick mark
plt.tick_params(labelbottom=True, bottom=False)
# trim off the x-axis
sns.despine(offset=10, trim=True, bottom=True)
# labels
plt.title('')
plt.ylabel('')
plt.xlabel('')
# manual control of xlabels
labels = ['Indiv_1-a','Indiv_2','Indiv_3','Indiv_1-b']
# control xtick order
plt.xticks(range(len(labels)), labels, rotation=45)
# control the number of x-ticks
plt.locator_params(axis='x', nbins=10)
# legend positioning
plt.legend(loc='upper right')
# log scale
plt.gca().set_yscale('log')
# this is better if neg values are needed
plt.gca().set_yscale('symlog')
# fit plot to display
plt.tight_layout()
plt.show()
# save figure with tight_layout
plt.savefig("test.svg", format="svg", bbox_inches="tight")
```

Signifance information can be added by including p-values and label bars using the following code.

```
x1, x2 = 0, 1 # columns to annotate on the plot
y2, y1 = 20, 15 # placement of the line and how for down the vertical legs go
plt.plot([x1,x1, x2, x2], [y1, y2, y2, y1], linewidth=1, color='k') # stats line
plt.text((x1+x2)*.5, y2+2, "p=0.09", ha='center', va='bottom') # p-value or sig
```

Chapter 5

Biology

5.1 General

Some helpful commands for genetic sequence.

```
from string import ascii_uppercase # python 3
from string import upper, lower # python 2
upper('tcga')
lower('TCGA')
title('tcga') # capitalize the first letter
```

5.2 Biopython

Reverse complement of sequence

```
from Bio.Seq import Seq
str(Seq(i).reverse_complement())
```

5.3 UCSC Genome Browser

Get sequence from UCSC genome browser

```
from subprocess import check_output, STDOUT
temp = check_output('wget -qO- http://genome.ucsc.edu/cgi-bin/das/hg19/dna?segment=%s:%s,%s' % (vcfObj.
```

5.4 Ref Genome

Get sequence from reference genome

```
from subprocess import check_output, STDOUT
temp = check_output('samtools faidx %s %s:%s-%s' % (ref, vcfObj.chrom, low, high), stderr=STDOUT, shell=
```

```
finalSeq = ''
for line in temp.decode('UTF-8').split('\n'):
for line in temp.decode('UTF-8').split('\n'): # this is only necessary in python 3 to convert binary to
    if '>' not in line:
        finalSeq += line

finalSeq = finalSeq.upper()
```

5.5 Personal Information

```
# parse vcf file with parseline
if '#' not in line and 'chr' in line: # skip the info
# vcf handling
from parseline import VCFObj
# or
from util import VCFObj
vcfObj = VCFObj(vcfLine)
# available attributes: ao, dp, af, wt, var, chrom, location
```

Chapter 6

Data I/O

6.1 Reading Data Files

Opening .gz files

```
import gzip
for line in gzip.open('myFile.gz'):
    print line
```

6.2 Pickles

Writing data in pickle format

```
import pickle
p = open('principle.pkl', 'wb')
pickle.dump(principleData, p)
p.close()
```

Reading data in pickle format

```
import pickle
p = open('principle.pkl', 'rb')
principleData = pickle.load(p)
p.close()
```

Bibliography

Xie, Y. (2015). *Dynamic Documents with R and knitr*. Chapman and Hall/CRC, Boca Raton, Florida, 2nd edition. ISBN 978-1498716963.

Xie, Y. (2018). *bookdown: Authoring Books and Technical Documents with R Markdown*. R package version 0.9.