```
eration == "MIRROR_X":
irror_mod.use_x = True
irror_mod.use_y = False
irror_mod.use_z = False
operation == "MIRROR_Y":
irror_mod.use_x = False
irror_mod.use_y = True
irror_mod.use_z = False
operation == "MIRROR_Z":
irror_mod.use_x = False
irror_mod.use_y = False
irror_mod.use_z = True

election at the end -add
_ob.select= 1
er_ob.select=1
ntext.scene.objects.active
("Selected" + str(modifier
irror_ob.select = 0
bpy.context.selected_obj
ata.objects[one.name].se

int("please select exactly

OPERATOR CLASSES ----

types.Operator):
X mirror to the selected
ject.mirror_mirror_x"
ror X"
```

Python Modules

Using libraries to do sophisticated calculations easily

What is a module?

Modules organize **libraries of functions** (and more) **providing new capabilities**.

- Python itself comes with over 200 modules.
- Many installations (e.g. on Google Colab, or via Anaconda) include lots more, enabling natural language processing, machine learning, bioinformatics, and more.
- Over 236,000 modules are available via PyPi and pip.

For a list of all modules in Python, see: https://docs.python.org/3/py-modindex.html

Informatics modules used in this course

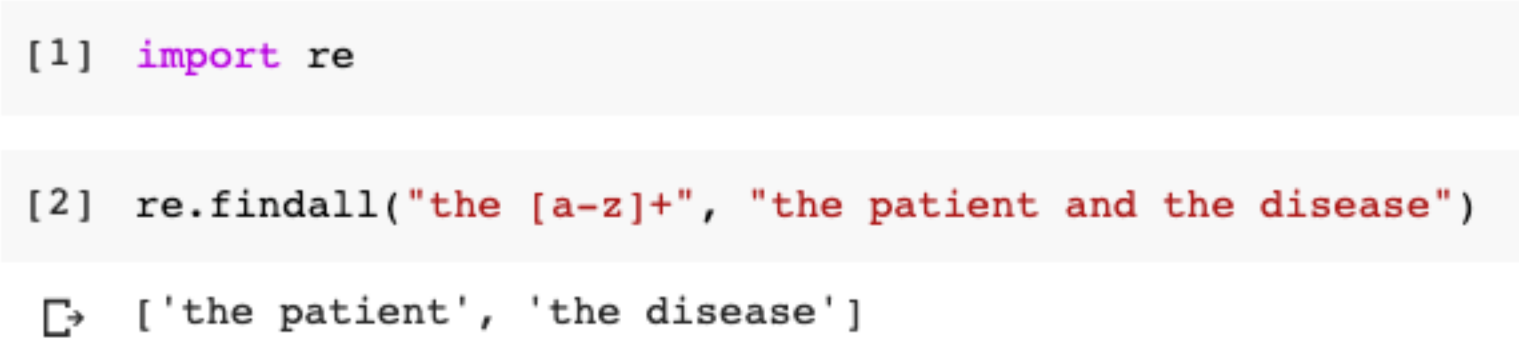
Generic data tools

- pandas
  - Data access, manipulation, and analysis.
- plotnine
  - Grammar of graphics plotting (ggplot).
- sqlite3
  - Basic relational database.

Specialized tools

- nltk
  - Natural language processing.
- re
  - Regular expressions (text pattern matching).
- sklearn
  - Machine learning.

import

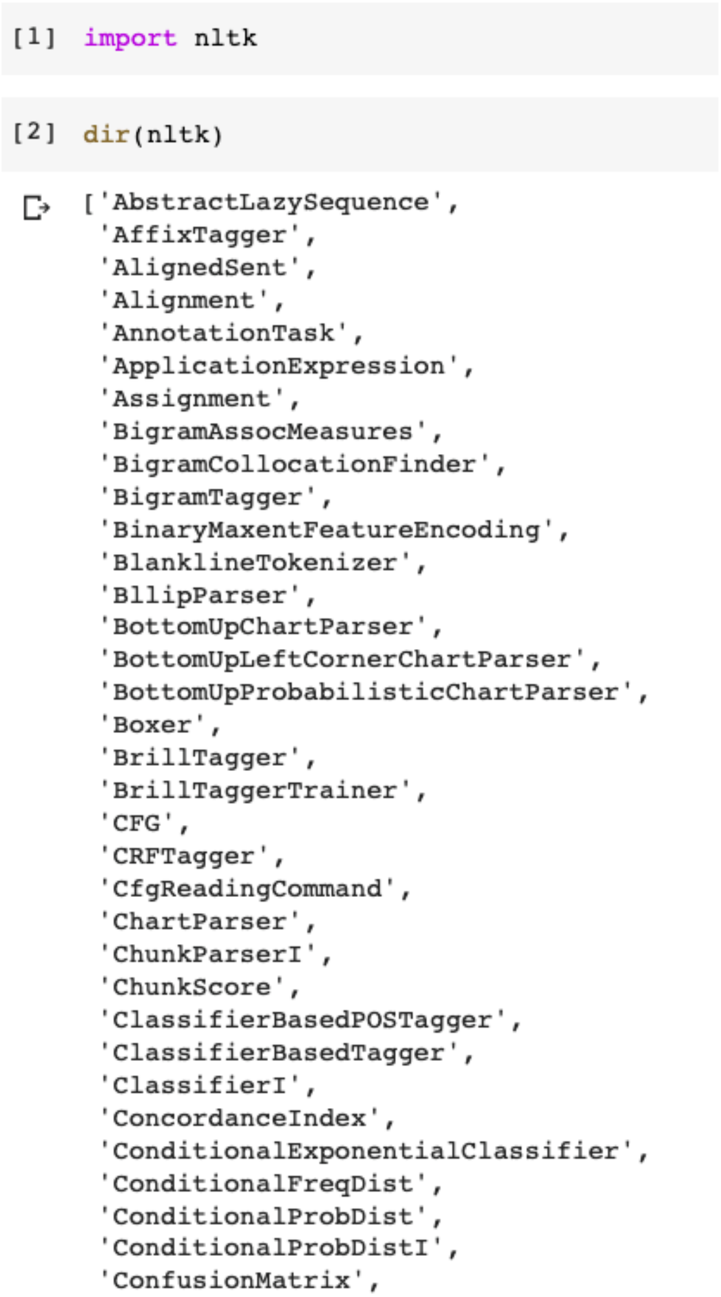


```
[1]  import re

[2]  re.findall("the [a-z]+", "the patient and the disease")

     ['the patient', 'the disease']
```

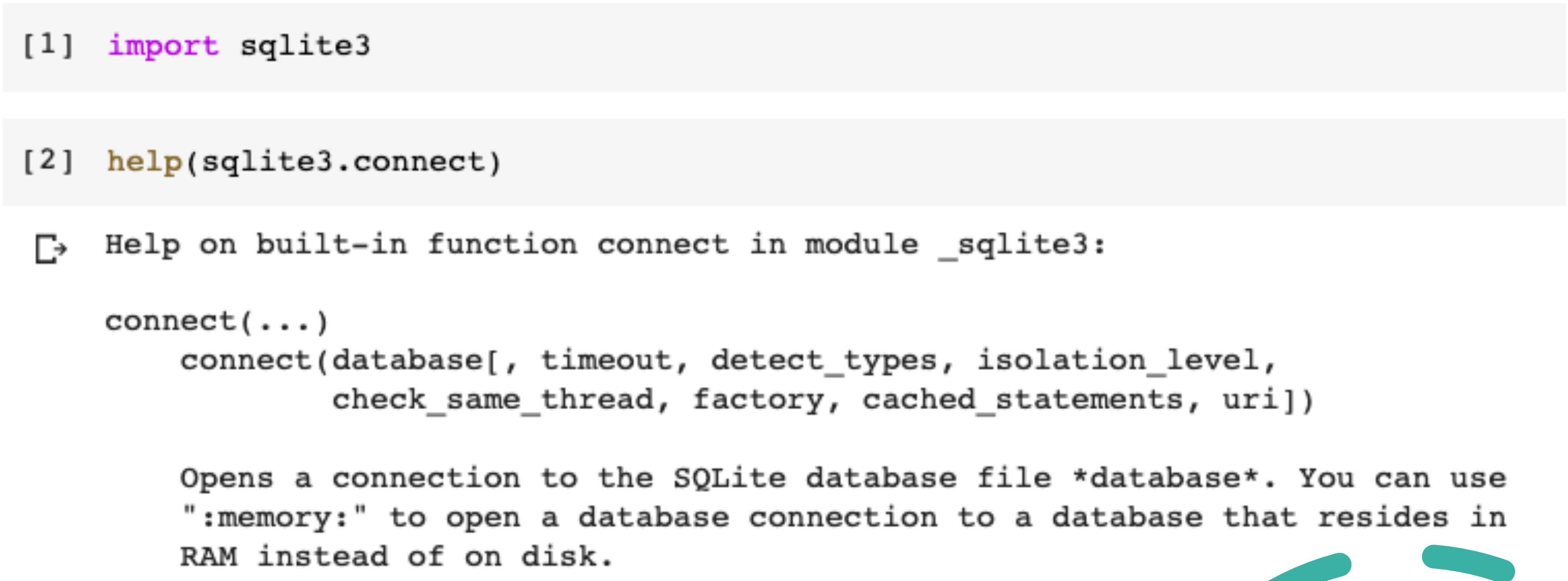
seeing what functions are available: dir



```
[1] import nltk
```

```
[2] dir(nltk)
```

```
['AbstractLazySequence',
 'AffixTagger',
 'AlignedSent',
 'Alignment',
 'AnnotationTask',
 'ApplicationExpression',
 'Assignment',
 'BigramAssocMeasures',
 'BigramCollocationFinder',
 'BigramTagger',
 'BinaryMaxentFeatureEncoding',
 'BlanklineTokenizer',
 'BllipParser',
 'BottomUpChartParser',
 'BottomUpLeftCornerChartParser',
 'BottomUpProbabilisticChartParser',
 'Boxer',
 'BrillTagger',
 'BrillTaggerTrainer',
 'CFG',
 'CRFTagger',
 'CfgReadingCommand',
 'ChartParser',
 'ChunkParserI',
 'ChunkScore',
 'ClassifierBasedPOSTagger',
 'ClassifierBasedTagger',
 'ClassifierI',
 'ConcordanceIndex',
 'ConditionalExponentialClassifier',
 'ConditionalFreqDist',
 'ConditionalProbDist',
 'ConditionalProbDistI',
 'ConfusionMatrix',
```



```
[1] import sqlite3
```

```
[2] help(sqlite3.connect)
```

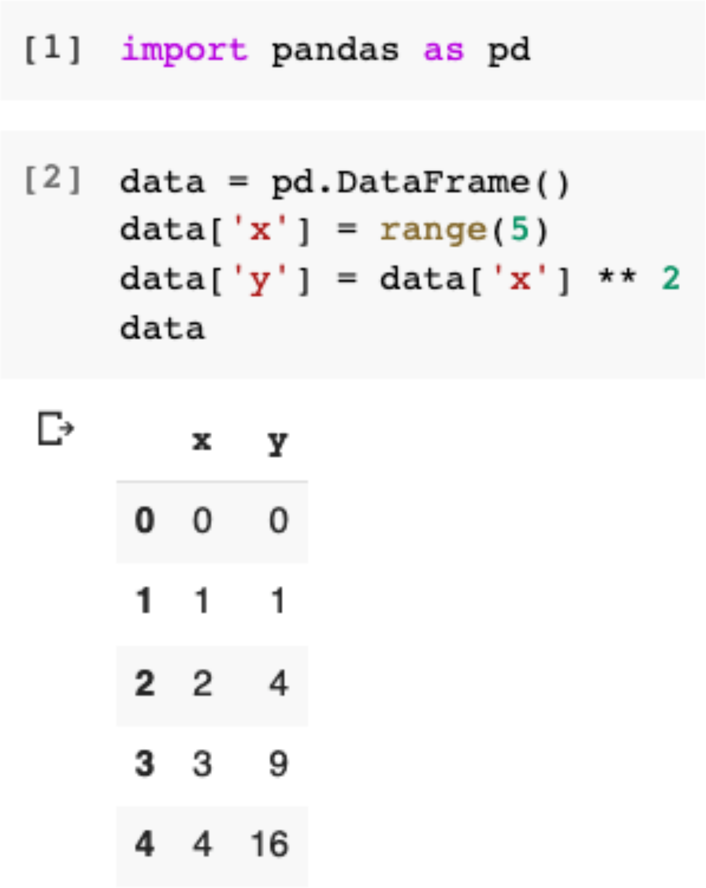
```
Help on built-in function connect in module _sqlite3:

connect(...)
    connect(database[, timeout, detect_types, isolation_level,
            check_same_thread, factory, cached_statements, uri])

    Opens a connection to the SQLite database file *database*. You can use
    ":memory:" to open a database connection to a database that resides in
    RAM instead of on disk.
```

getting help

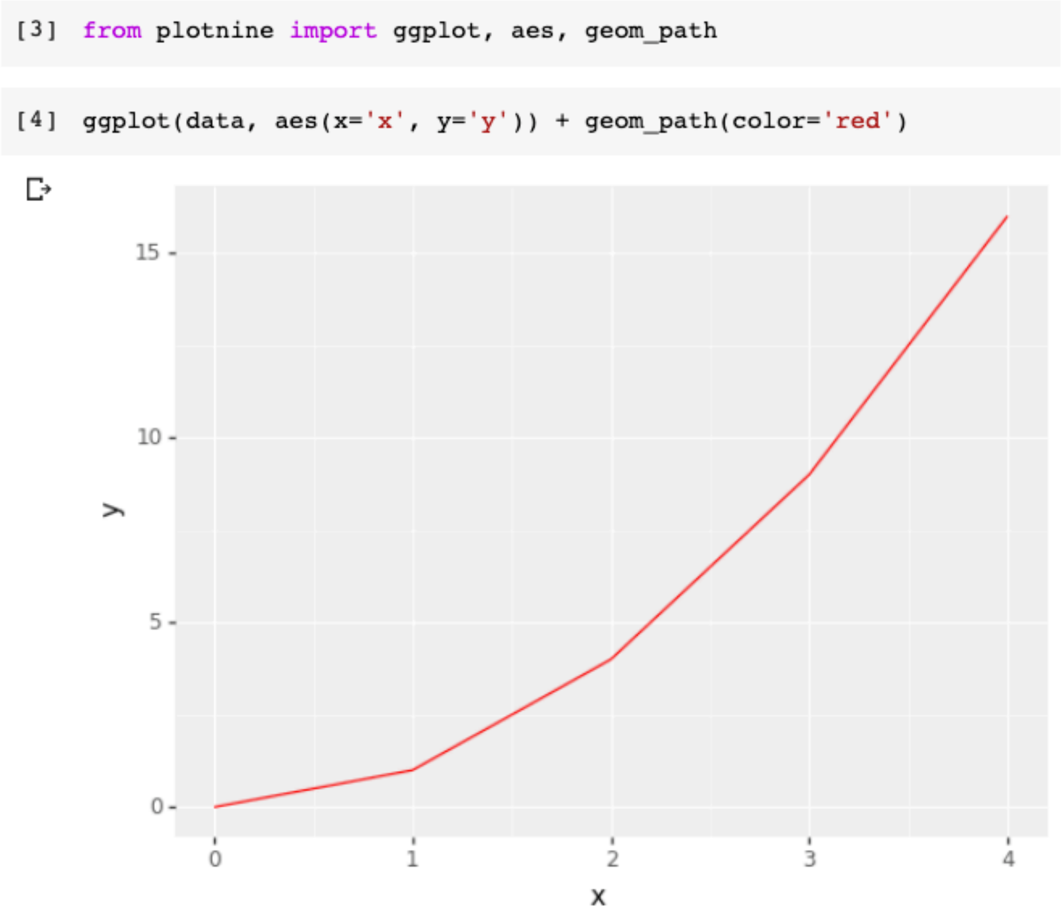
variations on import



```
[1] import pandas as pd
```

```
[2] data = pd.DataFrame()
    data['x'] = range(5)
    data['y'] = data['x'] ** 2
    data
```

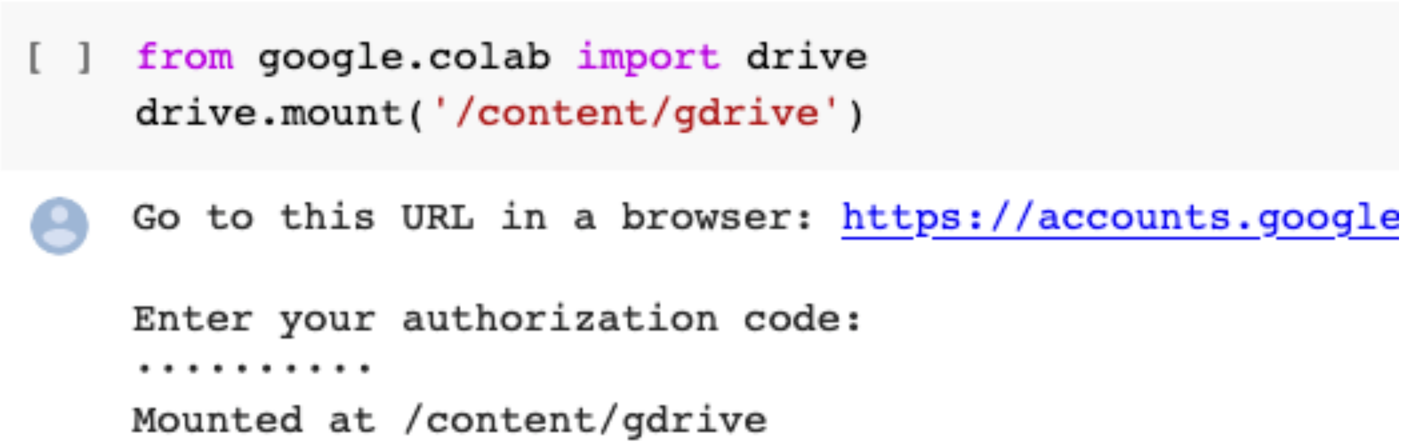
	x	y
0	0	0
1	1	1
2	2	4
3	3	9
4	4	16



```
[3] from plotnine import ggplot, aes, geom_path
```

```
[4] ggplot(data, aes(x='x', y='y')) + geom_path(color='red')
```

variations on import

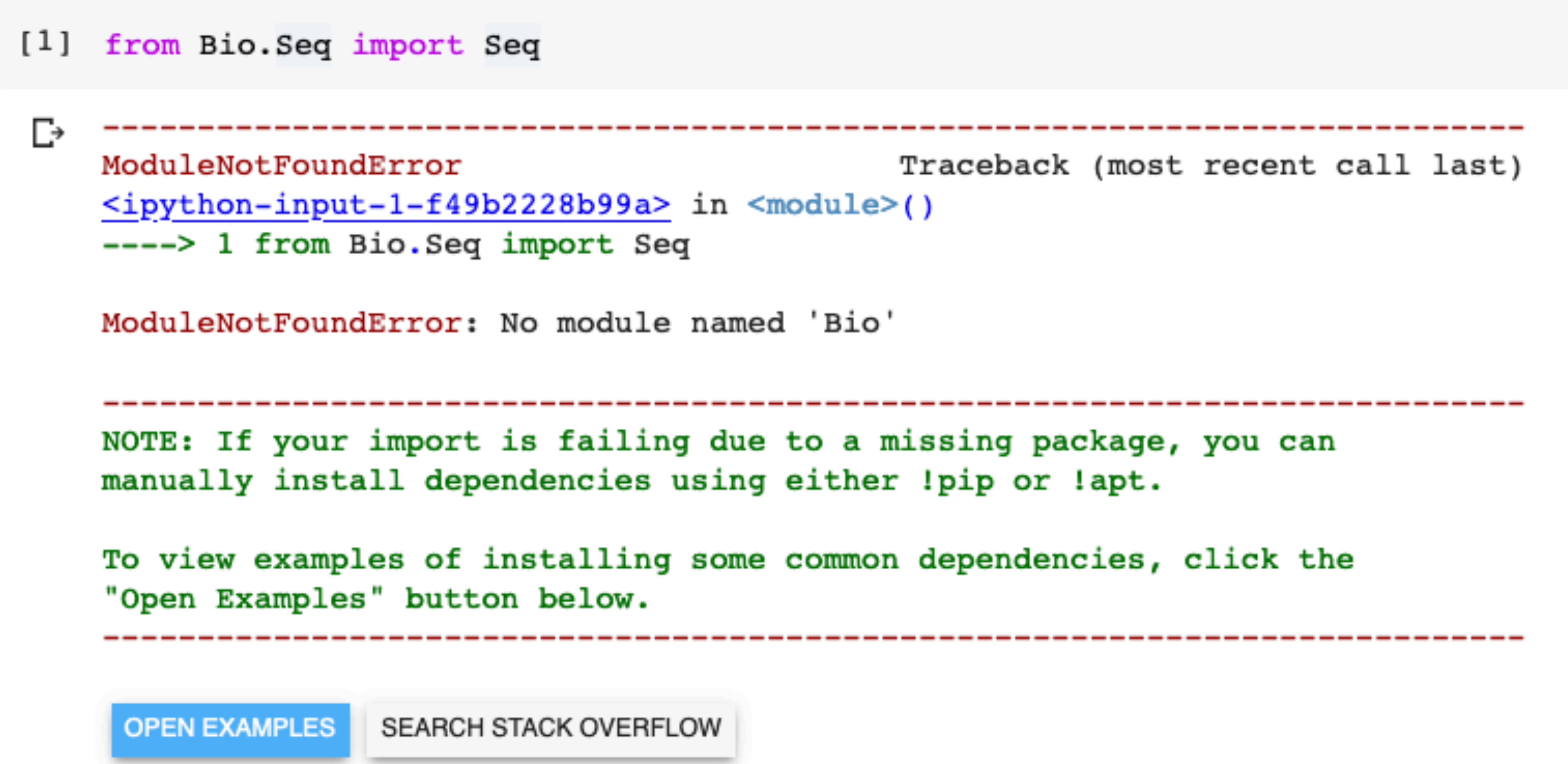


```
[ ]  from google.colab import drive
     drive.mount('/content/gdrive')
```

```
Go to this URL in a browser: https://accounts.google

Enter your authorization code:
··········
Mounted at /content/gdrive
```

how do we add more libraries?



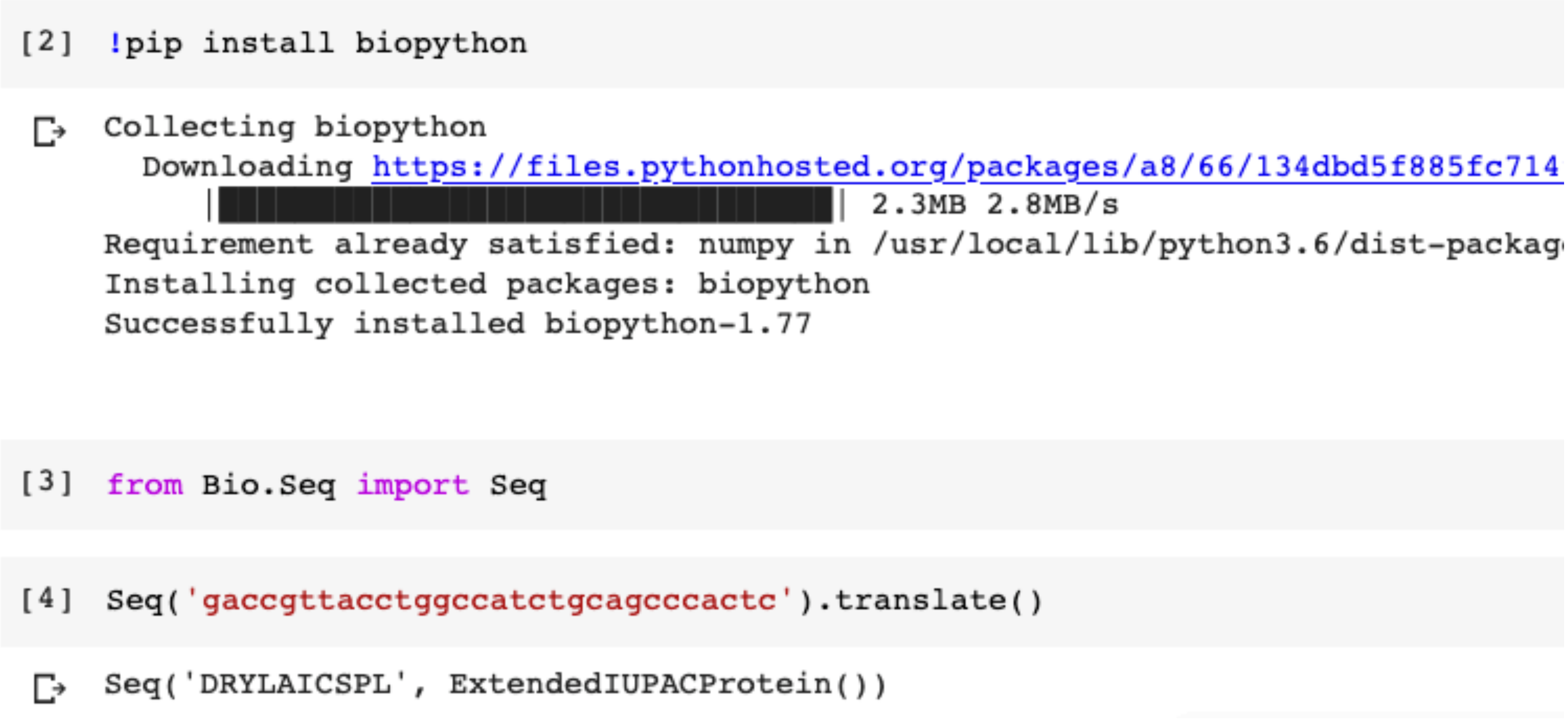
```
[1] from Bio.Seq import Seq
```

```
---------------------------------------------------------------------------
ModuleNotFoundError                       Traceback (most recent call last)
<ipython-input-1-f49b2228b99a> in <module>()
----> 1 from Bio.Seq import Seq

ModuleNotFoundError: No module named 'Bio'

---------------------------------------------------------------------------
NOTE: If your import is failing due to a missing package, you can
manually install dependencies using either !pip or !apt.

To view examples of installing some common dependencies, click the
"Open Examples" button below.
---------------------------------------------------------------------------
```



```
[2] !pip install biopython
```

```
Collecting biopython
  Downloading https://files.pythonhosted.org/packages/a8/66/134dbd5f885fc714
     |████████████████████████████████| 2.3MB 2.8MB/s
Requirement already satisfied: numpy in /usr/local/lib/python3.6/dist-packag
Installing collected packages: biopython
Successfully installed biopython-1.77
```

```
[3] from Bio.Seq import Seq
```

```
[4] Seq('gaccgttacctggccatctgcagcccactc').translate()
```

```
Seq('DRYLAICSPL', ExtendedIUPACProtein())
```

Excerpt of the gene described here: https://www.ncbi.nlm.nih.gov/nuccore/AB065646