



python™

Introduction to Python

BIO334

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courtesy of Sumner, Lyon, Tackmann, Dmitrijeva & Gable

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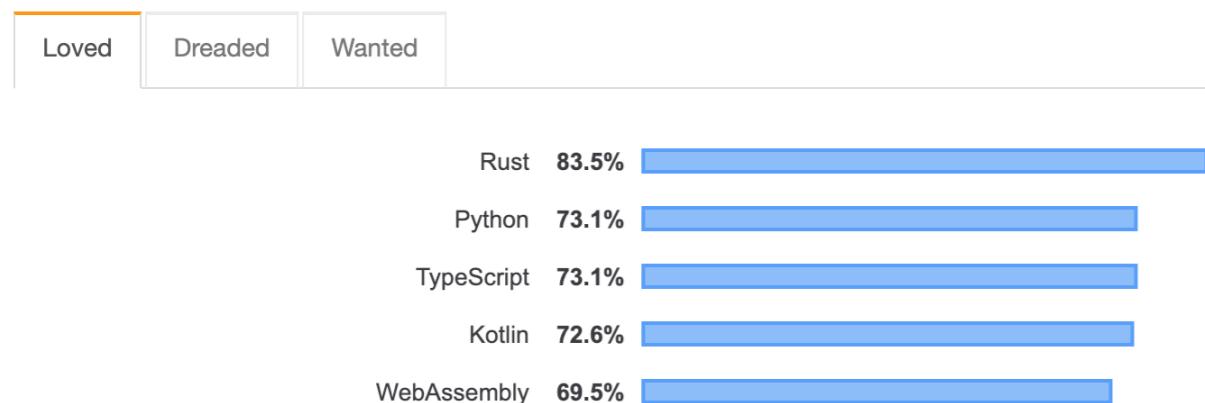
mihai-cosmin.danaila@uzh.ch

<https://github.com/meringlab/Bio334.git>

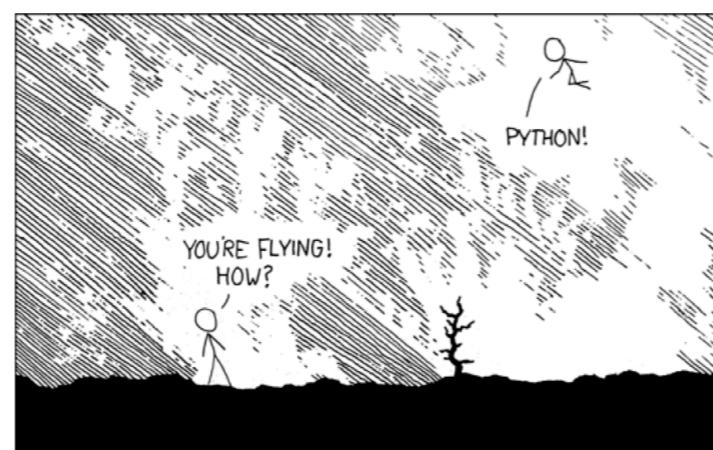
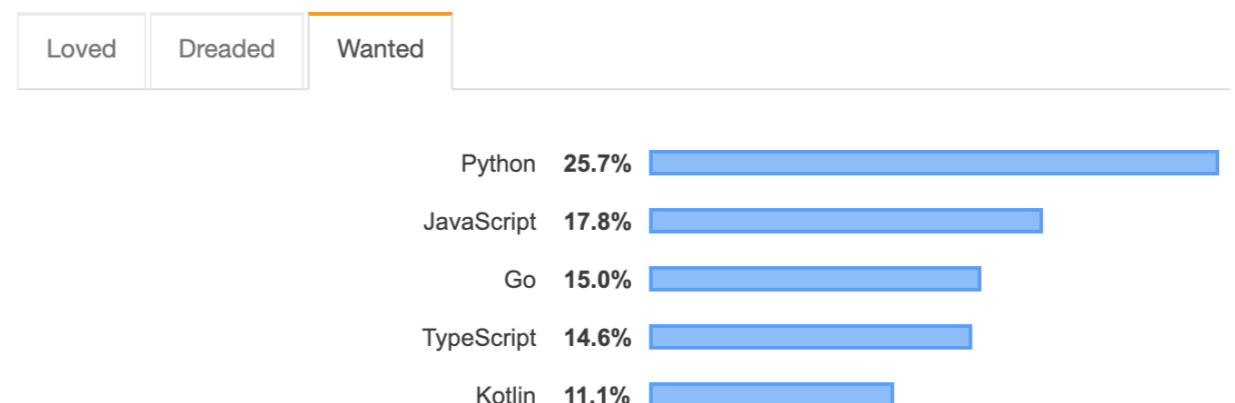
What is Python?

1. Dynamic, interpreted **programming language**
2. **Simple syntax** with fast learning curve

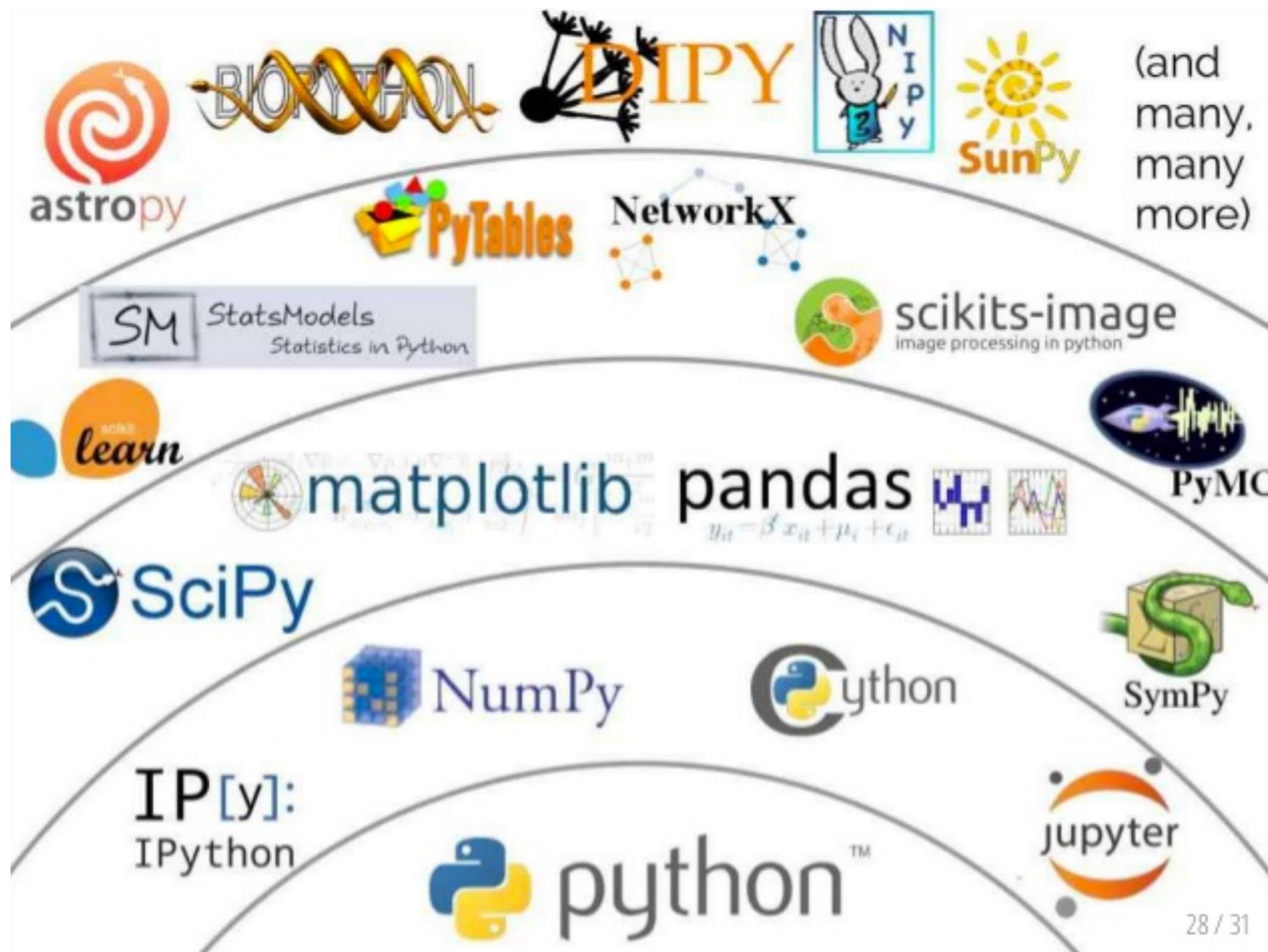
Most Loved, Dreaded, and Wanted Languages



Most Loved, Dreaded, and Wanted Languages



Scientific Python stack



Today's program

1. Introduction to programming
basic concepts with small hands-on sessions in
JupyterLab using iPython
2. Break
3. Writing Python code to solve Exercises 1 and 2
(and optional Exercises 3 and 4)
4. Optional: go through solutions of exercise 1 and 2
at 4.15pm

Part I:

Programming basics

Variables

- Store a piece of data and give it a specific name with the “=” (equal) operator

```
a = 4
```

```
pi = 3.14159
```

```
my_string = "hello"
```

```
# single and double ticks are equal
```

```
# (just stick to one) 'hello' or "hello"
```

```
my_protein_sequence = 'MRHIAHTQRCLSRLLTSLVALLLIVLP'
```

- Basic rules for variable names:
 - use descriptive names, NO spaces, don't start with numbers

Operators

I. Arithmetic operations

- addition + , subtraction -
- division /, multiplication *
- exponent **
- parenthesis ()

```
>>> 2 + 3  
5  
>>> 23 - 3  
20  
>>> 22.0 / 12  
1.833333333333333  
>>> (1 + 2) * 3
```

2. Boolean operations

- return **True** or **False**
- == , > , < ,
- & (AND) , | (OR)

```
>>> 1 < 2  
True  
>>> 3 > 34  
False  
>>> 23 == 45  
False  
>>> 34 != 323  
True
```

First live session

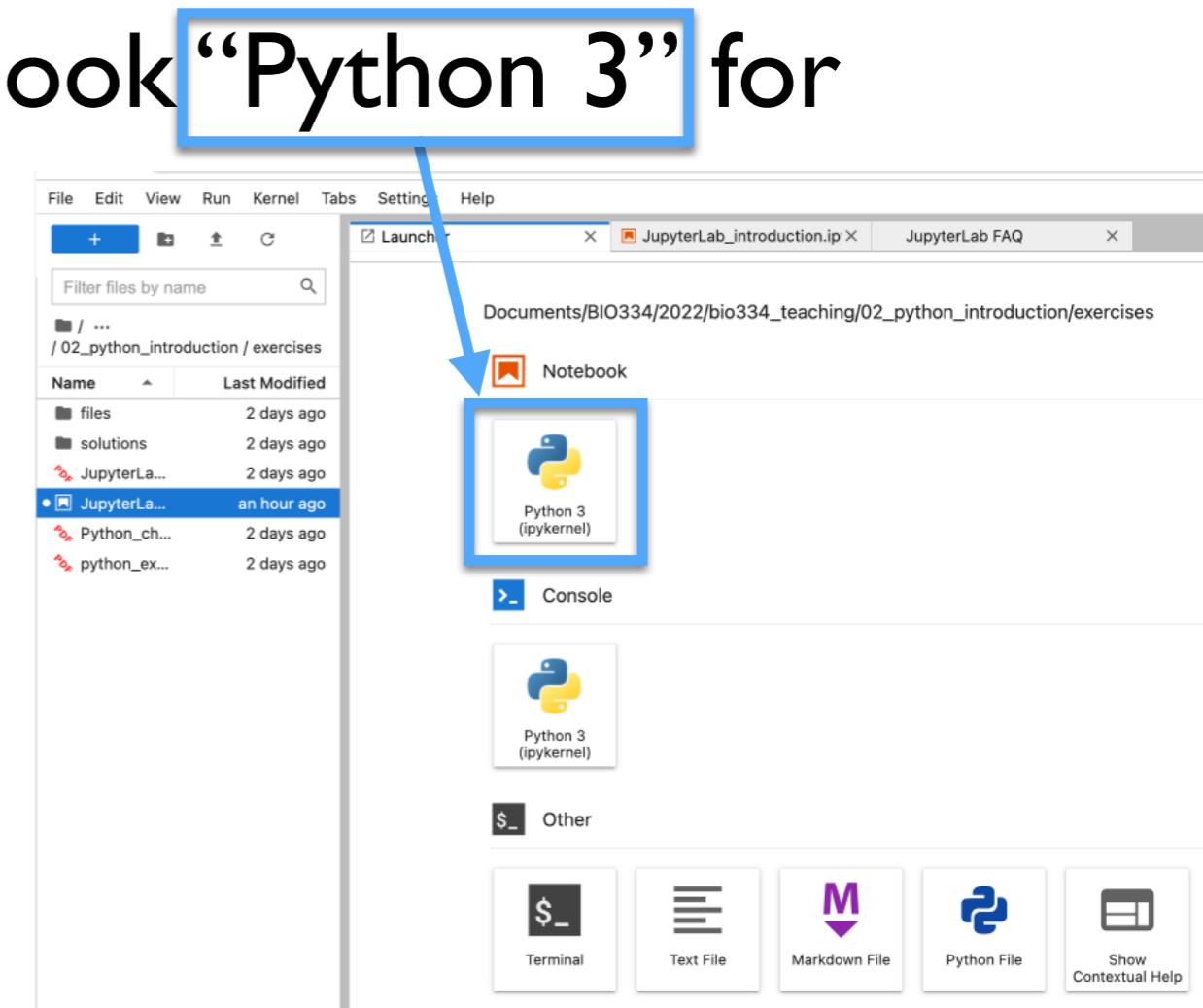
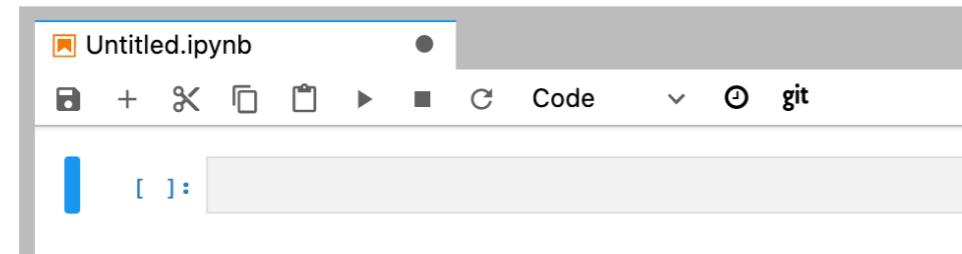
Show how to use **JupyterLab**
and
checkout **Cheat Sheets**

To access the files you need, enter the following command in a terminal window

```
git clone https://github.com/meringlab/Bio334.git
```

First live session

- Open the Anaconda Navigator from the Applications and launch Jupyter Lab
- Launch Jupyter Notebook “Python 3” for an interactive session



Session I:

Type a command and hit shift + enter

```
welcome_message = 'hello world!' # hit [shift + enter] after every line
welcome_message

# Arithmetics: use python as your advanced calculator
a = 4
b = a + 3
(a + b) * 4

a / 8

a**2

# Let's try with strings
welcome_message + welcome_message

a = '4'
a + 3 # anything strange?

# whats the difference?
a + str(3)
int(a) + 3
```

Arithmetics

```
>>> welcome_message = 'hello world!' # hit [shift + enter]
>>> welcome_message
'hello world!'

# Use python as your advanced calculator
>>> a = 4
>>> b = a + 3
>>> (a + b) * 4
44

# float division (caveat: Python 2 would return 0!)
>>> a / 8
0.5

>>> a**2
16
```

Concatenation

```
# Let's try with strings

# use + to add two strings
>>> welcome_message + welcome_message
'hello world!hello world!'

>>> a = '4'

# We need to have the same type to add elements
>>> a + 3      # anything strange?
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
TypeError: cannot concatenate 'str' and 'int' objects

# whats the difference?
>>> a + str(3)
'43'
>>> int(a) + 3
7
```

List data structure

- like a shopping list we have an object that can store multiple objects at once.

```
my_list = ['butter', 'milk', 'oranges']
```

- it can hold different objects as well

```
my_list = ['butter', 1, 1.5, 'milk']
```

- Every element has an index, starting from 0 which you can access with the square brackets []

- e.g. >>> my_list[0]
 'butter'

List data structure

- get subsets of a list (“slicing”)

```
>>> my_list[0:2]  
['butter', 'milk']
```

- assign new values to list elements

```
my_list[0] = 'bananas'
```

- powerful list operations

- e.g. sort, reverse, insert, search

Session II: Work with lists

```
# create your first list and try accessing it with indices
```

```
my_list = [1,2,3,4,5]
my_list[1]
my_list[5]
my_list[0:3]
my_list[-1]

len(my_list)
```

```
# mixed lists, put different variable types in your list
```

```
my_mixed_list = ['UZH','founded in',1834]
my_mixed_list[2] = 1834
del my_mixed_list[1]
my_mixed_list.append('A.D.')
```

```
my_mixed_list
```

```
# apply the arithmetic operators on lists
```

```
[1,2,3] + [3,4,6]
```

```
['Hello'] * 4
```

Accessing list elements

```
# create your first list and try accessing it with indices
>>> my_list = [1,2,3,4,5]
>>> my_list[1]
2
>>> my_list[5]
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
IndexError: list index out of range
```

```
# slice your list with index ranges
>>> my_list[0:3]
[1, 2, 3]
>>> my_list[-1]
5
```

```
# Check how many elements your list contains
>>> len(my_list)
5
```

List modifications

```
# mixed lists, put different variable types in your list
>>> my_mixed_list = ['UZH', 'founded in', 1834]
>>> my_mixed_list[2] = 1834

>>> my_mixed_list
['UZH', 'founded in', 1834]

# delete an element at a specified index
>>> del my_mixed_list[1]

>>> my_mixed_list
['UZH', 1834]

# add another element to the list with the append command
>>> my_mixed_list.append('A.D.')

>>> my_mixed_list
['UZH', 1834, 'A.D.']
```

List concatenation

```
# apply the arithmetic operators on lists

# use + to make a longer list out of two small ones

>>> [1,2,3] + [3,4,6]
[1, 2, 3, 3, 4, 6]

# Use * to form a new list by repeating the content of a list

>>> ['Hello'] * 4
['Hello', 'Hello', 'Hello', 'Hello']
```

Strings & Lists

- Strings can also be considered lists of characters and can be accessed by index
- To convert them to an actual list (and make them mutable) use `list`

```
>>> my_sequence = 'MRHIAHTQRCLSRL'  
>>> list(my_sequence)  
['M', 'R', 'H', 'I', 'A', 'H', 'T', 'Q', 'R', 'C', 'L', 'S', 'R', 'L']
```

- While this opens many possibilities, check the cheat-sheet for convenient built-in string operations
 - e.g. `split`, `join`, `replace`

Dictionaries

- Similar to lists but elements are accessed through a user defined ‘key’

```
my_proteins_seqs = {}  
my_proteins_seqs = dict() # same as above  
my_proteins_seqs[ 'DROME_HH_Q02936' ] = 'MRHIAHTQRCLSRSLTSLVA'  
my_proteins_seqs[ 'DROME_PATC_P18502' ] = 'MDRDSLPRVPDTHGDVVD'
```

- retrieve their **value** by using the **key**

```
>>> my_proteins_seqs[ 'DROME_HH_Q02936' ]  
'MRHIAHTQRCLSRSLTSLVA'
```

Session III: Strings and dictionaries

```
# Try accessing a string like a list
```

```
my_string = 'hello world!'
```

```
my_string[6]  
my_string[-1] = '?'
```

```
my_list = list(my_string)  
my_list[-1] = '?'  
my_modified_string = ''.join(my_list)
```

```
# create your first dictionary
```

```
dna_to_rna = {}  
dna_to_rna['A'] = 'A'  
dna_to_rna['T'] = 'U'  
dna_to_rna['C'] = 'C'  
dna_to_rna['G'] = 'G'
```

```
# or in one line
```

```
dna_to_rna = {'A': 'A', 'T': 'U', 'C': 'C', 'G': 'G'}
```

```
# dictionary operations
```

```
dna_to_rna['U']  
'U' in dna_to_rna  
dna_to_rna.keys()  
dna_to_rna + dna_to_rna
```

String lists

accessing a character by index

```
>>> my_string = 'hello world!'
>>> my_string[6]
'w'
```

Changes are not allowed

```
>>> my_string[-1] = '?'
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
TypeError: 'str' object does not support item assignment
```

Convert your string to a list to do that

```
>>> my_list = list(my_string)
>>> my_list[-1] = '?'
```

Combine your list into a string with the join method

```
>>> my_modified_string = ''.join(my_list)
>>> my_modified_string
'hello world?'
```

Dictionary definition

create your first dictionary

```
>>> dna_to_rna = {}  
>>> dna_to_rna[ 'A' ] = 'A'  
>>> dna_to_rna[ 'T' ] = 'U'  
>>> dna_to_rna[ 'C' ] = 'C'  
>>> dna_to_rna[ 'G' ] = 'G'  
  
>>> dna_to_rna  
{'A': 'A', 'C': 'C', 'T': 'U', 'G': 'G'}
```

#or in one line

```
>>> dna_to_rna = { 'A': 'A', 'T': 'U', 'C': 'C', 'G': 'G' }  
>>> dna_to_rna  
{'A': 'A', 'C': 'C', 'T': 'U', 'G': 'G'}
```

Dictionary usage

```
#access an element with its key
>>> dna_to_rna['U']
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
KeyError: 'U'

# Test if a key is in the dictionary
>>> 'U' in dna_to_rna
False

# See all keys in the dictionary
>>> list(dna_to_rna.keys())
['A', 'C', 'T', 'G']

# Dictionaries don't support concatenation
>>> dna_to_rna + dna_to_rna
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
TypeError: unsupported operand type(s) for +: 'dict' and 'dict'
```

Functions

- function: stores instructions (not values)
- basic use:
 - `function_name(arguments)`
- functions loaded by default in python, e.g.
 - `str()` - convert an object into a string
 - `int()` - convert an object into an integer
 - `float()` - convert a object into a floating point number
 - `type()` - tells you the type of an object
- see many other in the cheat-sheet and find them on
 - <https://docs.python.org/3/library/functions.html>

Functions

Let's create a function using "def" (for define)

```
[ ]: 1 def add_things(a, b):  
      2     result = a + b  
      3     return result
```

We need to have the same type to add elements

```
1 add_things(3, 5)
```

8

```
1 add_things("Hello ", "there")
```

'Hello there'

```
1 add_things("3", 5)
```

TypeError

Traceback (most recent call last)

```
<ipython-input-14-df373cddff49> in <module>
```

```
----> 1 add_things("3", 5)
```

```
<ipython-input-12-eb66cd937434> in add_things(a, b)
```

```
    1 def add_things(a, b):
```

```
----> 2     result = a + b
```

```
    3     return result
```

TypeError: can only concatenate str (not "int") to str

Methods

- functions of a specific object class
- access by `<variable_name>.<method>(arguments)`

```
>>> s = 'The quick brown fox jumps over the lazy dog'  
>>> s.split()  
['The', 'quick', 'brown', 'fox', 'jumps', 'over', 'the', 'lazy', 'dog']  
>>> s.split('fox')  
['The quick brown ', ' jumps over the lazy dog']
```

- in ipython: write `.` after a variable name and press `<tab>` to get an overview about available methods
- alternatively: `dir(object)`
- use `? / ??` (in ipython) or `help()` to get information about a method and its arguments e.g. `?str.split` or `help(str.split)`
- Alternatively: google!

Break

Part 2: Writing Python code

Why write a script?

- Organize your commands in a text file and build more complicated workflows that can be executed at once.
- save typing, make your work reproducible
- Use comments (#) to describe your code
- Run it at any point by executing your script

Scripting ingredients

- Use the **print** function to print the output

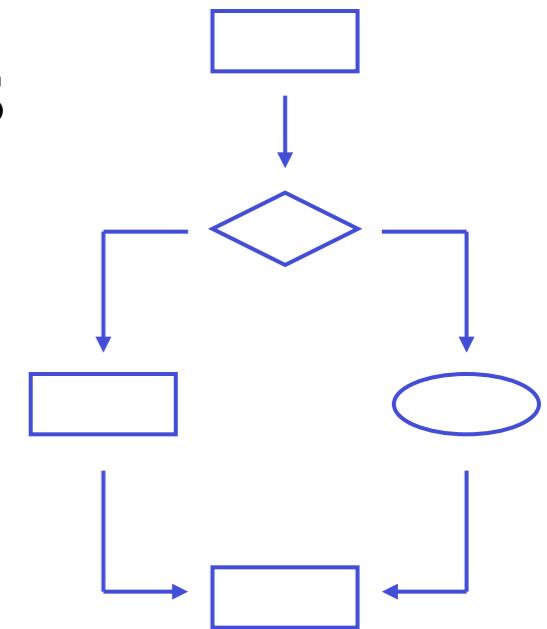
```
>>> print("Hello", "Python!")  
Hello Python!
```

```
print("Hello", "Python!") # use this (for Python 3)  
print 'hello world!' # not this (for Python 2)
```

Conditional statements

- Use if/else clauses to make decisions

```
if boolean_expression:  
    print("The statement is True")  
else:  
    print("The statement is False")
```



- Remember the indentation!

- While other programming languages use brackets or end statements, Python uses whitespace to structure code. Simply use tabulator to indent.



Loops

- Loops are essential for repeating an action several times
- The **for** loop executes the nested statements as many times as there are elements in the input list.

```
>>> input_list = [1,2,3,4,5]
>>> for my_number in input_list:
...     print(my_number)
...
1 2 3 4 5
```

- Note: Don't forget the colon (:) at the end.

for loop for reading

```
[1]: 1 for line in open("my_file.txt", "r"):  
2     print(line)
```

1st line

2nd line

3rd line

File:
my_file.txt

1st line

2nd line

3rd line

EOF

Conditional loop

- Use the **while** loop to continue an action until a condition is not satisfied anymore

```
>>> number_apples = 3
>>> while number_apples > 0:
...     number_apples -= 1
...     print("Ate an apple,",number_apples,'left')
...
Ate an apple, 2 left
Ate an apple, 1 left
Ate an apple, 0 left
```

Session IV: Loops and friends

1. try out this for loop

```
for my_number in range(6):  
    print(my_number)
```

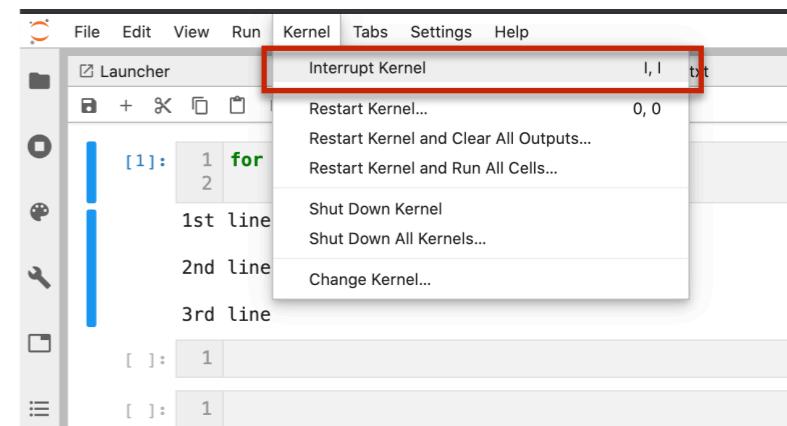
2. A new loop key-word: **continue**

```
for my_number in range(6):  
    if my_number == 5:  
        continue  
    print(my_number)
```

3. try using **break** instead of **continue**

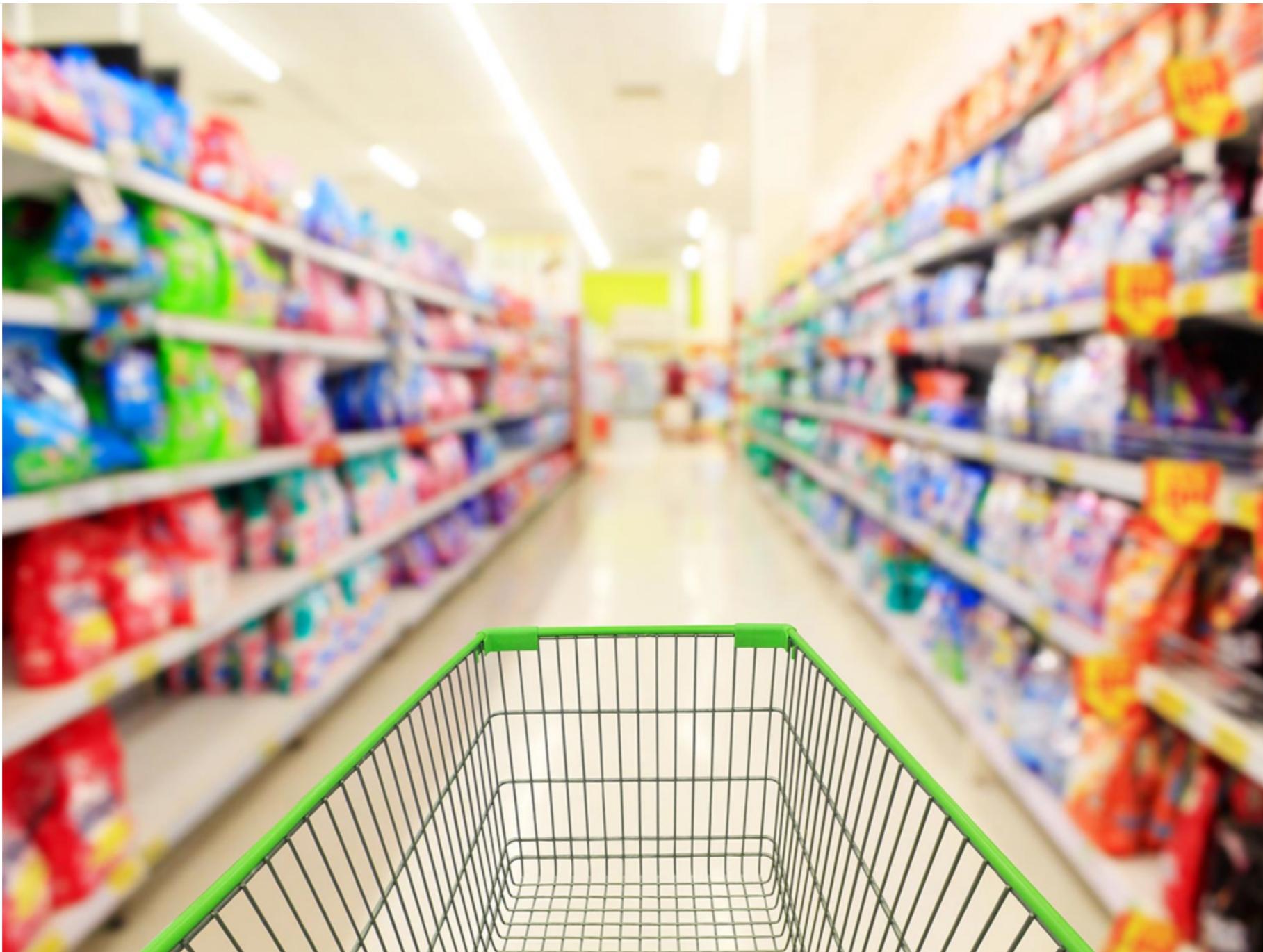
4. when will this while loop finish?

```
my_number = 1  
from time import sleep  
while my_number < 5:  
    print("hurray! my number is increasing:", my_number)  
    sleep(1)
```

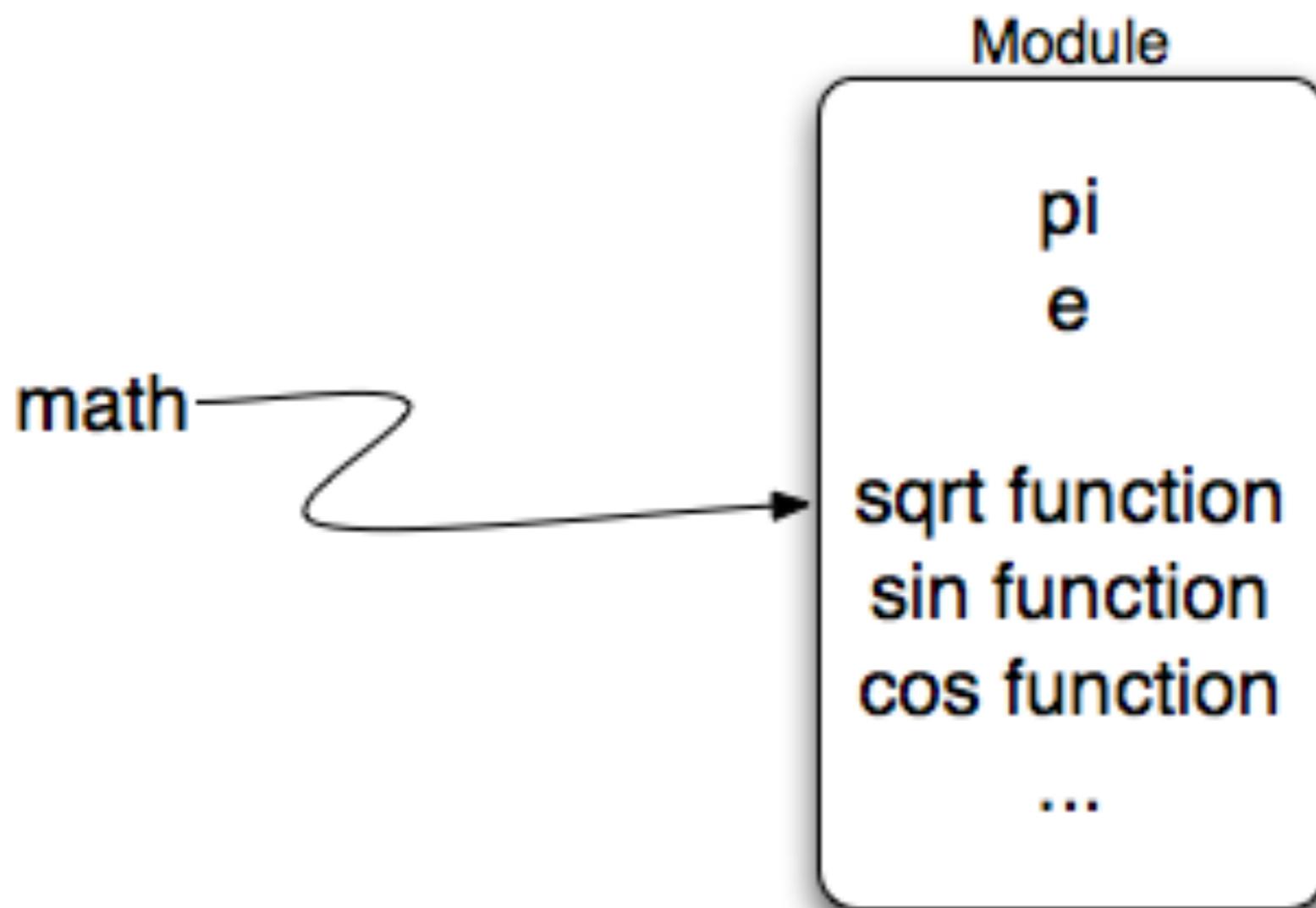


HINT: use Kernel —> Interrupt Kernel to stop the running program

python modules



math module



Import statement

- Use **import** to load additional modules for more functionalities
- For example the **math** module:

Script: print_pi.py

```
import math
print('Pi is equal to', math.pi)
print('or in degrees', math.degrees(math.pi))
```

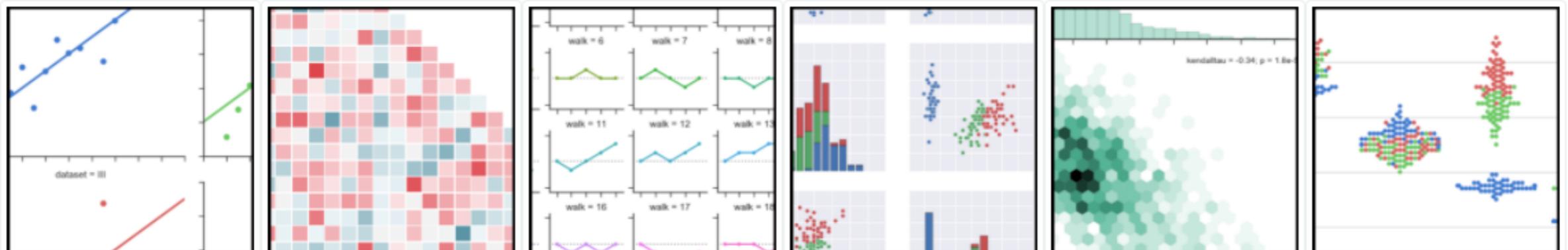
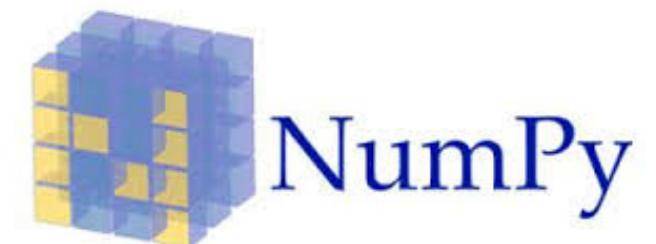
```
davide$ python print_pi.py
Pi is equal to 3.141592653589793 or in degrees 180.0
```

more details at: <https://docs.python.org/3/library/math.html>

Much more to discover

- ipython magics make your life a lot easier
 - time your code, debug it, call other languages
- make python lightning fast using numpy, scipy, and cython/pypy/numba
- visualize your data with seaborn, bokeh and matplotlib

IP[y]:
IPython



Further reading

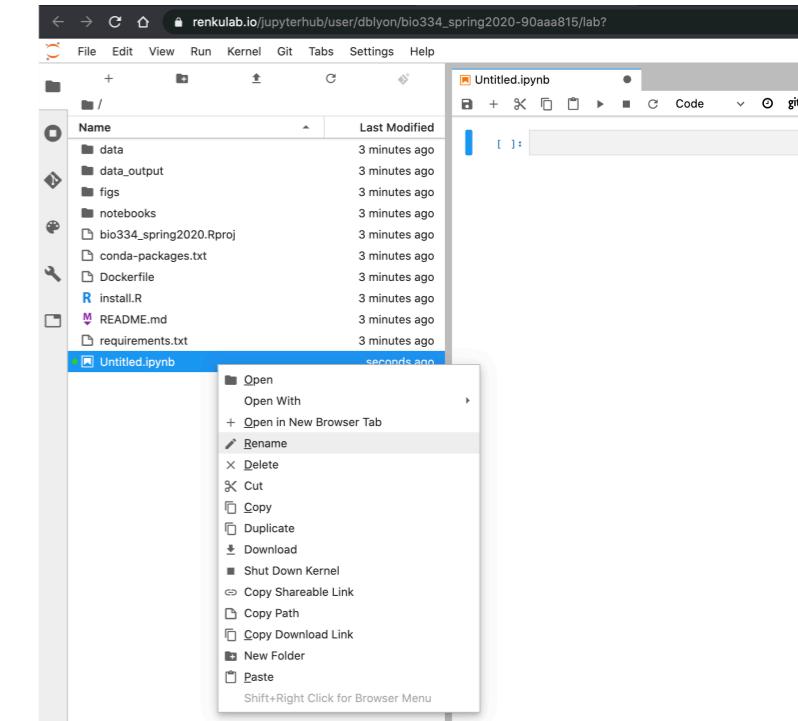
1. <https://snakify.org/> (interactive tutorial)
2. <http://www.diveintopython.net/> (comprehensive, general purpose)
3. <http://swcarpentry.github.io/python-novice-inflammation/> (scientific python by example)
4. <http://www.scipy-lectures.org/intro/intro.html> (intro by the scientific python consortium)
5. <https://github.com/dblyon/pandasintro> (extensive introduction to pandas)
6. <https://cs50.harvard.edu/college/2021/spring/weeks/0/>



Exercise session



1. Create a new Python3 Jupyter Notebook, save it to the folder `/Bio334/02_python_introduction/exercises` and start exploring
2. Change the name of your newly created file by right clicking on `Untitled.ipynb`
3. To execute a cell press Shift + Enter
4. To access the files you need enter the following command in a terminal window



```
git clone https://github.com/meringlab/Bio334.git
```

**optional exercise slides
follow**

Optional Exercise #3

Learn the basics of **Pandas**, a powerful python module for data analysis, including reading, writing, filtering, merging, arithmetic operations on and sorting of tabular data

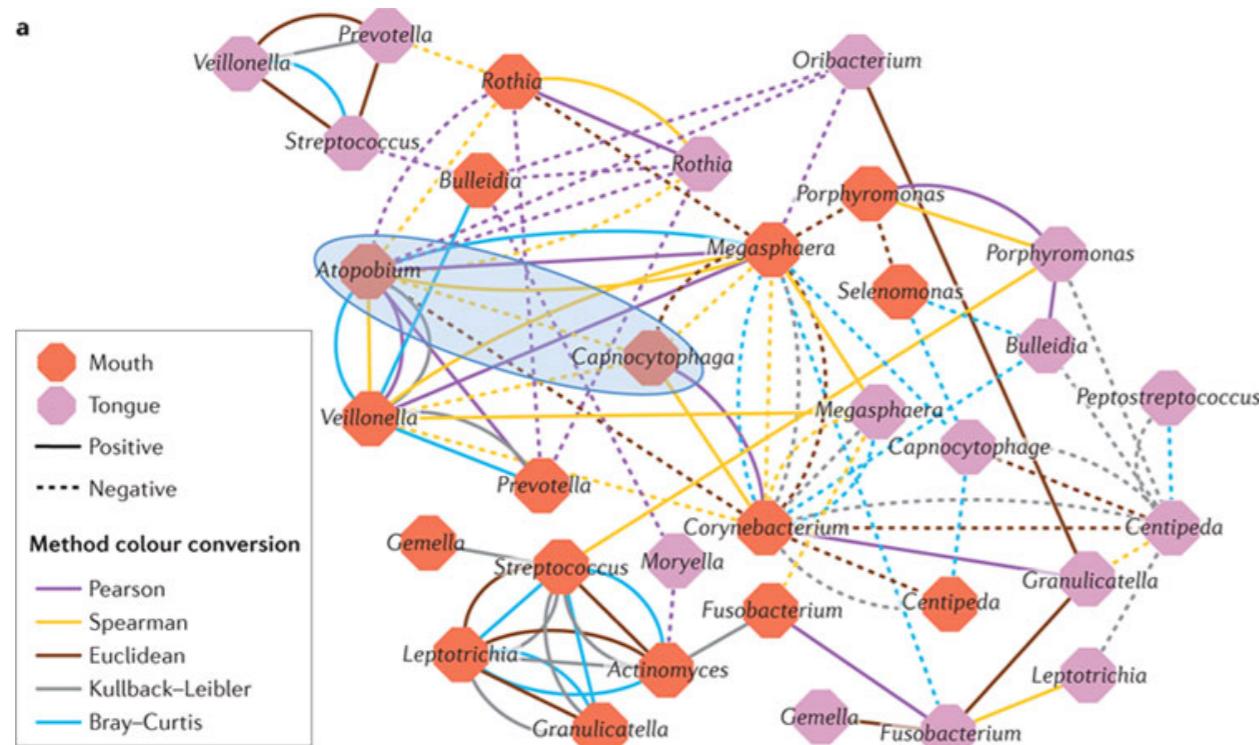
```
age animal priority visits
b   3.0 cat yes 3
d   NaN dog yes 3
f   2.0 cat no  3
```



	age	animal	priority	visits
b	3.0	cat	yes	3
d	NaN	dog	yes	3
f	2.0	cat	no	3

Optional Exercise #4

create a pipeline to infer simple ecological relationships in the Human Microbiome



Optional exercise

session

- Create a new text document and rename it, giving it a “.py” ending
- To execute, launch a terminal tab and enter
 - `ipython <script_name>.py`
- Good luck!

sys module

1. A built-in module that contains system-specific parameters and functions
2. For example we can use it to read arguments from the command line:

Script: say_hello.py

```
import sys
print('Hello there', sys.argv[1])
# Command line arguments are in sys.argv[1], sys.argv[2]...
# sys.argv[0] is the script name itself
```

```
davide$ python say_hello.py bio334_Students
Hello there bio334_Students
```

os module

1. Another built-in module that contains miscellaneous operating system interfaces
2. For example we can use it to obtain the name of the user currently logged in:

Script: check_directory.py

```
1 import os
2
3 dir_ = "Bio334"
4 if not os.path.exists(dir_):
5     print("It seems you haven't cloned the git repository yet. \
6           Please enter the following command in a terminal window.")
7     print("git clone https://github.com/meringlab/Bio334.git")
8 else:
9     print("Great! The 'Bio334' directory exists. You are good to go.")
```

Run the script in a terminal window

```
base > work > bio334_spring2020_dbl > master > 3? > $ > python check_directory.py
Great! The 'Bio334' directory exists. You are good to go._
```