Dana-Farber
Cancer Institute

Intro to Python

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using python since 2007-ish

good programmer != effective programmer

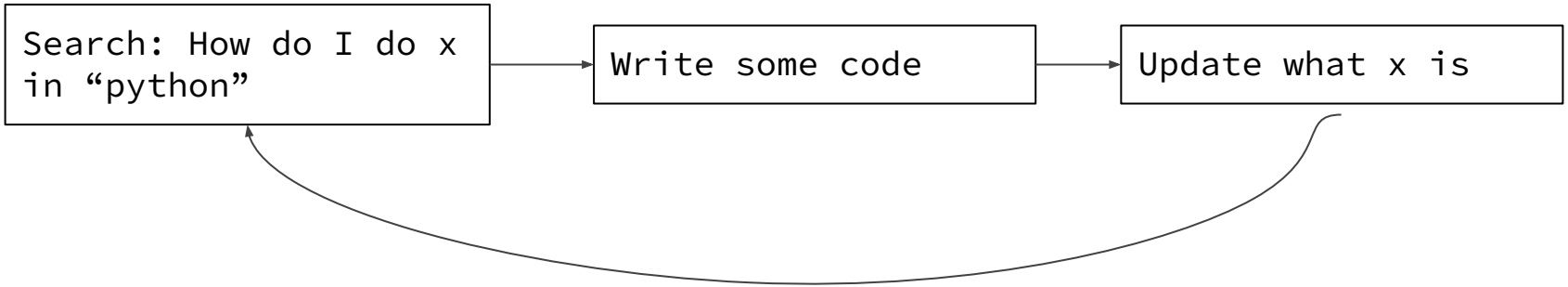
Assumptions and background

- You must have some exposure to programming concepts (variables, for-loops, print statements). If not: https://www.py4e.com/
- You can only learn so much in one sitting, you will need to use Python and find more courses to level up
- Get a copy of these slides and example programs here: {TODO}

Why python programming is great

You are almost never the first person to have done something so just ask Google / Stackoverflow your question

Anatomy of writing a python script



Tutorial overview

1. Hello world
2. Baby steps (python control flow)
3. CSV parsing (the hard way)
4. Libraries (pip/conda)
5. CSV parsing with pandas (the easy way)
6. Stretch goal: Jupyter notebooks

Project 0: Hello World

- Write a python script that prints “Hello World” to the command line
- Run the program like ```python project0.py```

Expected output

```
Hello World
```

Project 1: Baby steps (control flow)

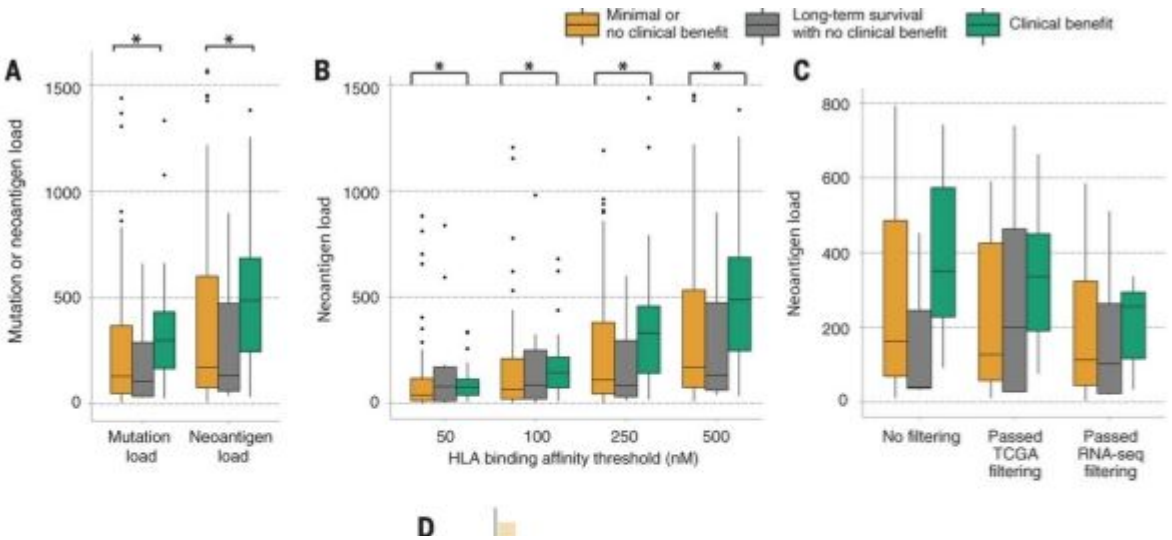
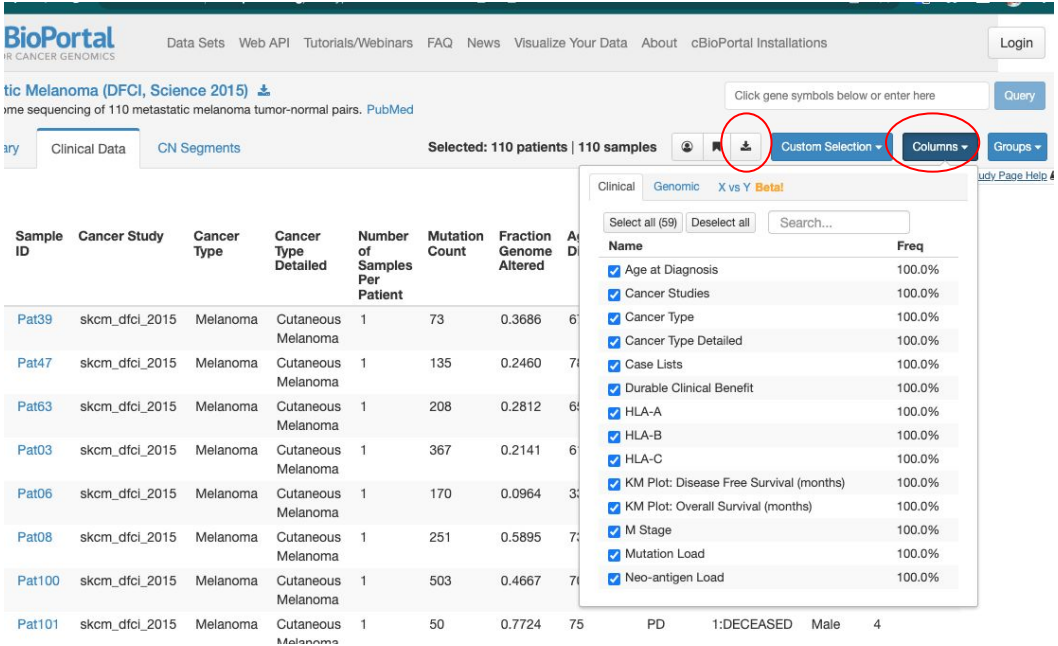
Write a program that:

- Uses the __name__ == “__main__” (*) entry point
- Calls a function called “load_data” which first sleeps for 3 seconds, then returns a string
- Print the value returned by “load_data” to stdout
- Include statements with unique outputs:
  - 0: at the very top of the script
  - 1: start of entrypoint
  - 2: start of “load_data”
  - 3: after sleep in “load_data”
  - 4: prints results of “load_data” to stdout

*__name__ is a built-in variable which evaluates to the name of the current module

Project 1: Baby steps (control flow)

Expected output

```
```python project1_babysteps.py```

0: Hello, I am here!
1: This is the second print statement
2: ... now I am here, going to sleep
3: ..waking up, loaded the data
4: here is your data:  Data loading
```
```

Project 2: CSV parsing

Problem statement

Calculate the mean mutational and neoantigen load for patients with clinical benefit (CB), no clinical benefit (NCB) or long-term survival (LTS-NCB)

PD=progressive disease
PR=partial response
CR=complete response
SD=stable disease



Fig. 2. Overall mutational load, overall neoantigen load, and expression-based neoantigen analysis as predictors of response to ipilimumab (A) Elevated nonsynonymous mutational load and neoantigen load are associated with response to ipilimumab (P = 0.0076 and 0.027, respectively). An additional 20 points are not shown because of outlying high neoantigen loads in a subset of patients.

https://pubmed.ncbi.nlm.nih.gov/26359337/

Project 2: CSV parsing

Fetch data

cbioportal.org, fetch the clinical data from “Metastatic Melanoma (DFCI, Science 2015)

- Click on study view
- Select all 59 columns
- Click the download (down arrow) to get a TSV



http://www.cbioportal.org/study/clinicalData?id=skcm_dfci_2015

Project 2: CSV parsing

Expected output

```
```python project2_csv.py```

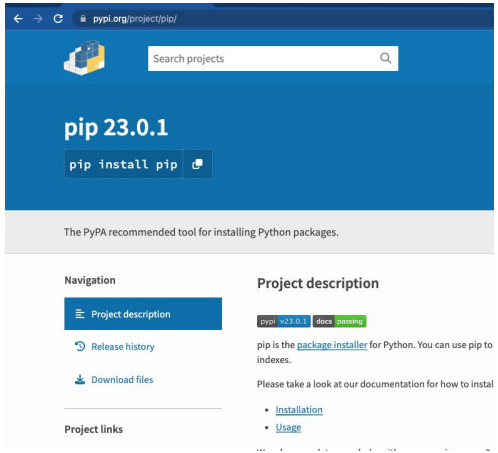
clinical_benefit: NCB, 74
NCB, Mutation Load mean: 396.81
NCB, Neo-antigen Load mean: 315.99

clinical_benefit: LTS-NCB, 10
LTS-NCB, Mutation Load mean: 571.50
LTS-NCB, Neo-antigen Load mean: 383.00

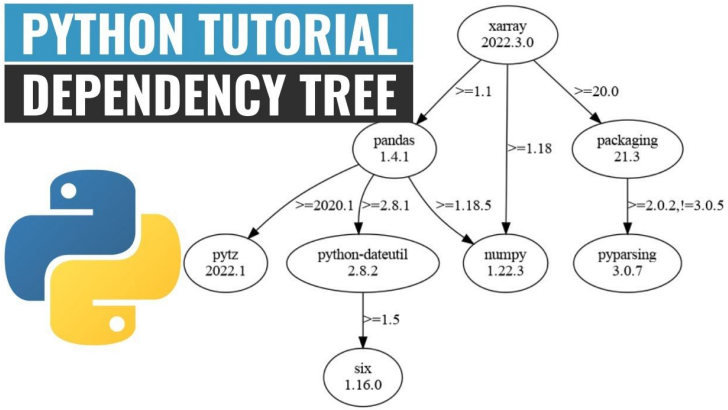
clinical_benefit: CB, 26
CB, Mutation Load mean: 737.15
CB, Neo-antigen Load mean: 467.69
```

Note: These results don’t seem to map up with the paper… oops? Bonus if someone can figure out why
```

Libraries, and virtual environments

- Best part of python is all the tools already built!
- There are two major repositories of libraries you can use:
  - pypi / pip —> the OG
  - Anaconda / conda —> packages with pre-built binaries



Libraries, and virtual environments

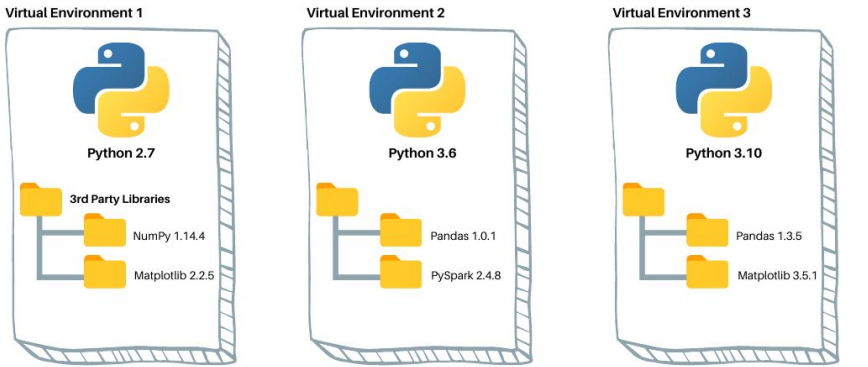


Python projects / libraries are a complicated mix of other python projects / libraries… we call these dependencies!

pip and conda, not only install the tool you want, but also its dependencies

However sometimes those dependencies can clash, hence virtual enviroments

Libraries, and virtual environments



Virtual environments are stand-alone copies of Python on your computer with (mostly) independent dependencies

Each project gets its own virtual environment

Conda is both a package and environment manager.

Pypi/pip use “virtualenv”

https://www.dataquest.io/blog/a-complete-guide-to-python-virtual-environments/

Libraries, and virtual environments

Try it (pip/virtualenv):

```
python3 -m pip install --user --upgrade pip
python3 -m pip --version
python3 -m pip install --user virtualenv
python3 -m venv .venv
source .venv/bin/activate
```

Try it (Anaconda/conda):

```
conda create --name myenv
conda activate myenv
```

Libraries, and virtual environments

Installing your dependencies

```
conda install --force-reinstall -y --name myenv -c conda-forge --file
requirements.txt
```

```
pip install -r requirements.txt
```

Project 3: CSV parsing with pandas

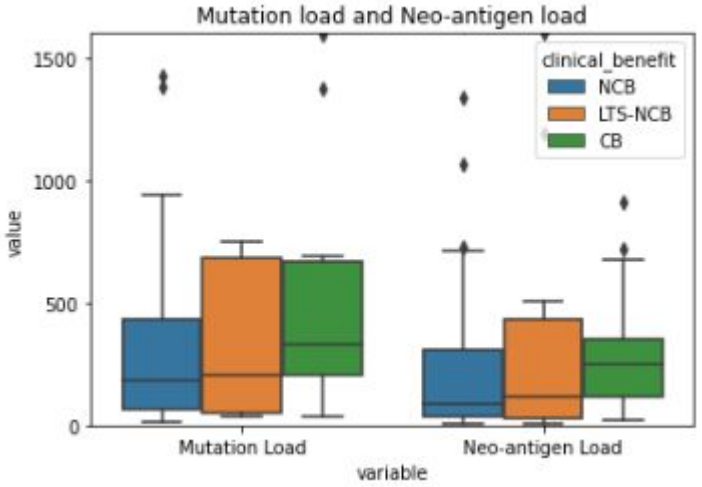
Do the following with way less code than before

1. Use the pandas library to load the CSV
2. Prepare the clinical_benefit derivative column
3. Calculate the summary stats as before
4. Make a plot like Figure 1A

Project 3: CSV parsing with pandas

Expected output

clinical_benefit	variable	value
CB	Mutation Load	737.153846
	Neo-antigen Load	467.692308
LTS-NCB	Mutation Load	571.500000
	Neo-antigen Load	383.000000
NCB	Mutation Load	396.810811
	Neo-antigen Load	315.986486



Project 4: Jupyter Notebook

Tasks:

- Install jupyter lab
- Modify notebook to point to the right file
- Run project4_jupyter.ipynb to generate the plots and stats from project 3.

Library

- https://docs.python-guide.org/writing/structure/
- https://stackoverflow.com/
- https://realpython.com/python-main-function/
- https://google.com
- https://chat.openai.com/chat