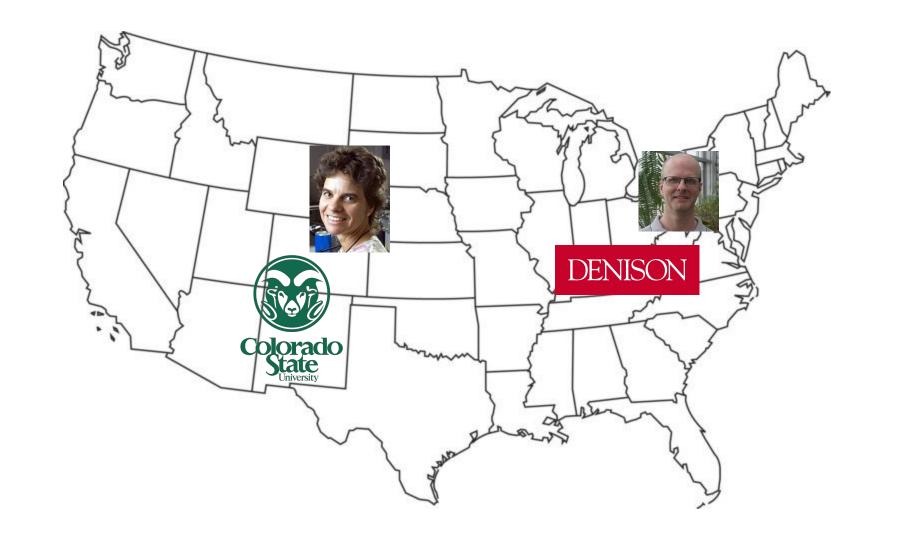
BD2K Summer Workshop 2018

Jacob Pfeil Graduate Student







Molecular Heterogeneity in Patient Population Leads to Differential Treatment Responses







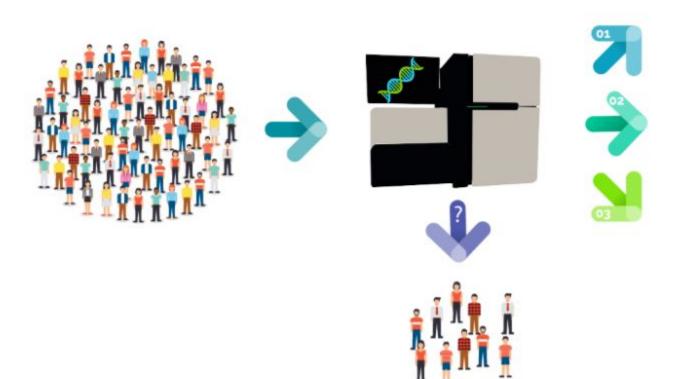




Drug is Not Toxic and Beneficial



DNA-Marker Approach to Stratify Patient Population

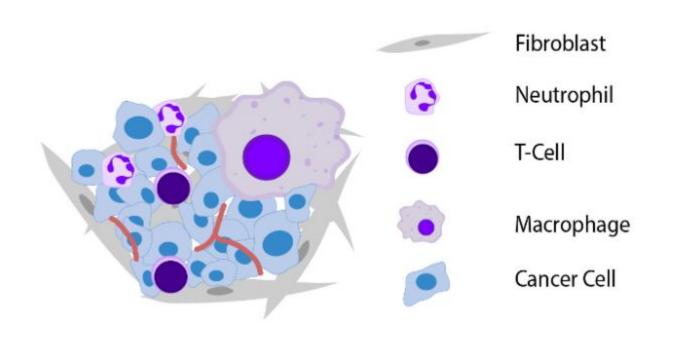




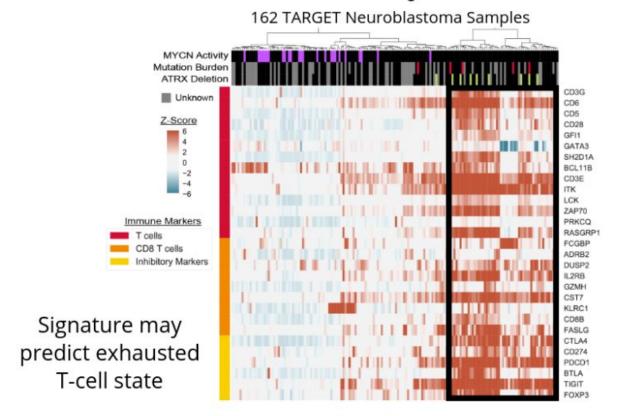




TME Influences Tumor Progression and Response to Therapies



Z-Score Heatmap for T-Cell Profiling Genes and Inhibitory Markers



Lyons, Y. A., Wu, S. Y., Overwijk, W. W., Baggerly, K. A., & Sood, A. K. (2017). Immune cell profiling in cancer: molecular approaches to cell-specific identification. npj Precision Oncology, 1(1), 26.

TREEHOUSE TEAM



Isabel Bjork Director

Ann Durbin Data Coordinator

Ellen Kephart Software Engineer

Sofie Salama Research Scientist

David Haussler Scientific Director



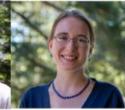
Katrina Learned Data Coordinator



Rob Currie CTO



Holly Beale Lead Computational Biologist



Lauren Sanders Graduate Student Researcher



Olena Morozova Scientific Lead

Basic Navigation

Basic Navigation

```
[Workshop-2018] ls
data images notebooks outline.md README.md rosalind
```

```
[Workshop-2018] cd notebooks
[notebooks] ls
matplotlib.ipynb numpy.ipynb pandas.ipynb seaborn.ipynb
```

Creating and Removing Directories

```
[Workshop-2018] mkdir tmp
[Workshop-2018] ls
data images no<u>t</u>ebooks outline.md README.md rosalind tmp
```

```
[Workshop-2018] rm -rf tmp
[Workshop-2018] ls
data images no<u>t</u>ebooks outline.md README.md rosalind
```



conda install <package>
conda update <package>
conda remove <package>

```
ls miniconda3
                           lib64
                                         mkspecs
                                                                   translations
                                                       aml
                  envs
compiler compat
                                          phrasebooks
                           libexec
                                                        resources
                                                                   var
conda-meta
                  include
                           LICENSE.txt
                                                                   x86 64-conda cos6-linux-gnu
                                          pkgs
                                                       share
                                          pluains
                                                       ssl
                           man
```

https://conda.io/miniconda.html

		Ć	A	
	Windows	Mac OS X	Linux	
Python 3.6	64-bit (exe installer) 32-bit (exe installer)	64-bit (bash installer)	64-bit (bash installer) 32-bit (bash installer)	
Python 2.7	64-bit (exe installer) 32-bit (exe installer)	64-bit (bash installer)	64-bit (bash installer) 32-bit (bash installer)	

Python REPL

```
[~] python
Python 3.6.5 |Anaconda, Inc.| (default, Mar 29 2018, 18:21:58)
[GCC 7.2.0] on linux
Type "help", "copyright", "credits" or "license" for more information.
>>>
```

ctrl-D to exit

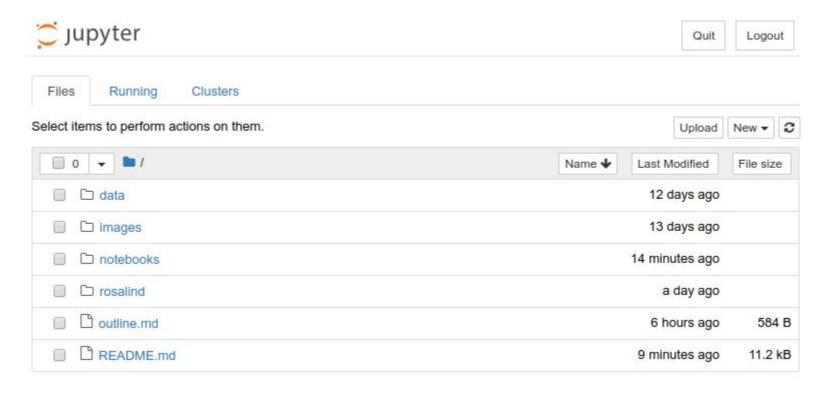
Interactive Python Basics

*i*Python

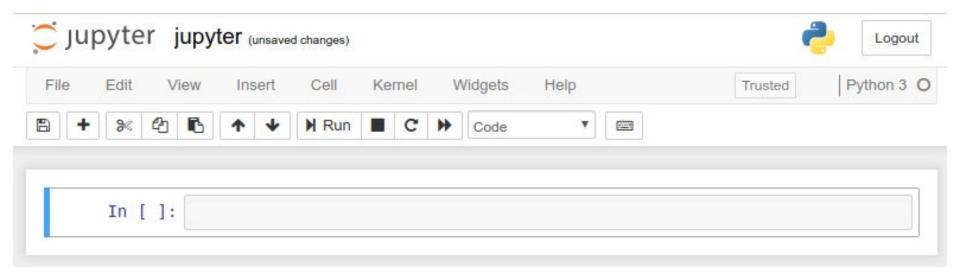
```
[Workshop-2018] ipython
Python 3.6.5 |Anaconda, Inc.| (default, Mar 29 2018, 18:21:58)
Type 'copyright', 'credits' or 'license' for more information
IPython 6.4.0 -- An enhanced Interactive Python. Type '?' for help.

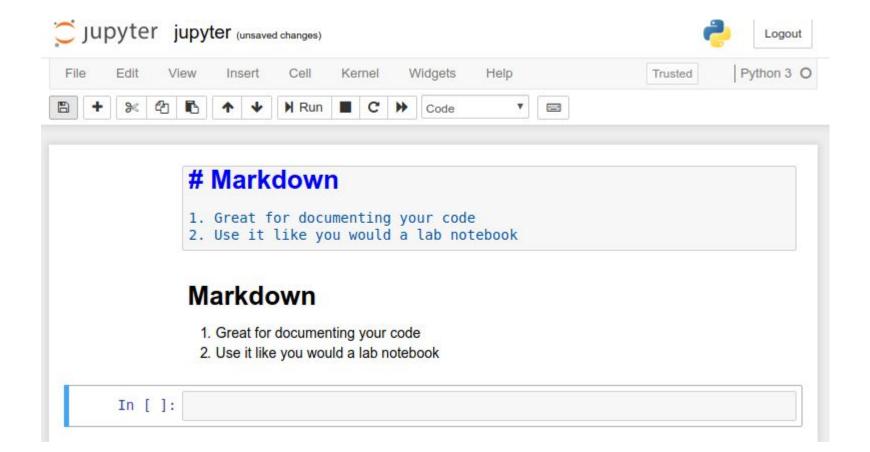
In [1]: ls
data/ images/ notebooks/ outline.md README.md rosalind/
```

\$ jupyter notebook



Jupyter Notebook

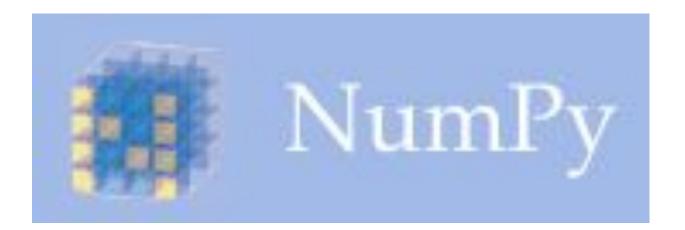




In [1]:	<pre>def hello_world(): print("hello, world!")</pre>
In [2]:	hello_world()
	hello, world!
In []:	

Computing Library

NumPy: The Scientific



Library for scientific computing

- N-dimensional array object
- linear algebra functions
- random number generator

Array Operations

```
>>> a = np.array(1,2,3,4) # WRONG
>>> a = np.array([1,2,3,4]) # RIGHT
>>> b = np.array([(1.5,2,3), (4,5,6)])
>>> b
array([[ 1.5, 2. , 3. ],
       [4., 5., 6.]])
```

```
v1 = np.array([1, 2, 3])
v2 = np.array([4, 5, 6])
v3 = np.array([7, 8, 9])
M = np.vstack([v1, v2, v3])
print M
>>> [[1 2 3]
     [4 \ 5 \ 6]
     [7 8 9]]
```

```
array([[ 0., 0., 0., 0.],
      [0., 0., 0., 0.],
      [0., 0., 0., 0.]
>>> np.ones( (2,3,4), dtype=np.int16 )
                                                   # dtype can also be specified
array([[[ 1, 1, 1, 1],
       [ 1, 1, 1, 1],
       [ 1, 1, 1, 1]],
      [[ 1, 1, 1, 1],
       [ 1, 1, 1, 1],
       [ 1, 1, 1, 1]]], dtype=int16)
>>> np.empty( (2,3) )
                                                   # uninitialized, output may vary
array([[ 3.73603959e-262, 6.02658058e-154,
                                             6.55490914e-260],
      [ 5.30498948e-313, 3.14673309e-307, 1.00000000e+000]])
```

>>> np.zeros((3,4))

Useful functions

```
>>> from numpy import pi

>>> np.linspace(0, 2, 9)  # 9 numbers from 0 to 2

array([0., 0.25, 0.5, 0.75, 1., 1.25, 1.5, 1.75, 2.])

>>> x = np.linspace(0, 2*pi, 100)  # useful to evaluate function at lots of points

>>> f = np.sin(x)
```

```
>>> B = np.arange(3)
>>> B
array([0, 1, 2])
>>> np.exp(B)
array([ 1. , 2.71828183, 7.3890561 ])
>>> np.sqrt(B)
            , 1. , 1.41421356])
array([ 0.
>>> C = np.array([2., -1., 4.])
>>> np.add(B, C)
```

array([2., 0., 6.])

Matrix Multiplication

$$A_{n \times m} = \begin{bmatrix} a_{11} & a_{12} & \dots & a_{1m} \\ a_{21} & a_{22} & \dots & a_{2m} \\ \vdots & \vdots & \vdots & \vdots \\ a_{n1} & a_{n2} & \dots & a_{nm} \end{bmatrix} \mathbf{a}_{\mathbf{i}}$$

$$B_{m \times p} = \begin{bmatrix} b_{11} & b_{12} & \dots & b_{1p} \\ b_{21} & b_{22} & \dots & b_{2p} \\ \vdots & \vdots & \vdots & \vdots \\ b_{m1} & b_{m2} & \dots & b_{mp} \end{bmatrix}$$

Product:

$$C_{n \times p} = A_{n \times m} B_{m \times p}$$

$$\mathbf{c}_{ij} = \mathbf{a}_i \cdot \mathbf{b}_j = \sum_{i=1}^{m} \mathbf{a}_{ik} \mathbf{b}_{kj}$$

 \mathbf{b}_{i}

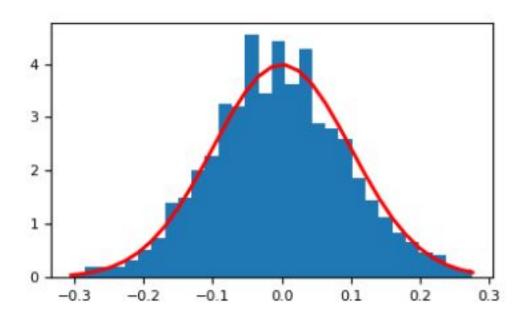
A and B must have compatible dimensions!

$$A_{n \times n} B_{n \times n} \neq B_{n \times n} A_{n \times n}$$

*Courtesy of last year's slides.

```
>>> A = np.array( [[1,1],
                 [0,1]])
. . .
>>> B = np.array( [[2,0],
                 [3,4]])
. . .
                                 # elementwise product
>>> A*B
array([[2, 0],
       [0, 4]])
                                 # matrix product
>>> A.dot(B)
array([[5, 4],
       [3, 4]])
                                 # another matrix product
>>> np.dot(A, B)
array([[5, 4],
       [3, 4]])
```

>>> mu, sigma = 0, 0.1 # mean and standard deviation >>> s = np.random.normal(mu, sigma, 1000)



$$\begin{array}{c|c}
\mathsf{pandas} \\
y_{it} = \beta' x_{it} + \mu_i + \epsilon_{it}
\end{array}$$







Implements a dataframe object

- similar to R dataframe
- commonly used for data analysis
- used in many other libraries (seaborn)

Examples were drawn from:

How to create a dataframe

Columns

Index

	Country	Rank
0	Russia	121
1	Colombia	40
2	Chile	100
3	Equador	130
4	Nigeria	11

How to create a dataframe

```
dates = pd.date_range('20130101',periods=6)

df = pd.DataFrame(np.random.randn(6,4),index=dates,columns=list('ABCD'))

df
```

	Α	В	С	D
2013-01-01	1.030816	-1.276989	0.837720	-1.490111
2013-01-02	-1.070215	-0.209129	0.604572	-1.743058
2013-01-03	1.524227	1.863575	1.291378	1.300696
2013-01-04	0.918203	-0.158800	-0.964063	-1.990779
2013-01-05	0.089731	0.114854	-0.585815	0.298772
2013-01-06	0.222260	0.435183	-0.045748	0.049898

How to access items

```
#slice based on date range df['20130101':'20130104']
```

	Α	В	С	D
2013-01-01	1.030816	-1.276989	0.837720	-1.490111
2013-01-02	-1.070215	-0.209129	0.604572	-1.743058
2013-01-03	1.524227	1.863575	1.291378	1.300696
2013-01-04	0.918203	-0.158800	-0.964063	-1.990779

How to access items

```
#slicing based on column names
df.loc[:,['A','B']]
```

	Α	В
2013-01-01	1.030816	-1.276989
2013-01-02	-1.070215	-0.209129
2013-01-03	1.524227	1.863575
2013-01-04	0.918203	-0.158800
2013-01-05	0.089731	0.114854
2013-01-06	0.222260	0.435183

How to access items by the index and columns

#slicing based on both row index labels and column names
df.loc['20130102':'20130103',['A','B']]

	Α	В
2013-01-02	-1.070215	-0.209129
2013-01-03	1.524227	1.863575

How to add a new row

```
df = pd.DataFrame(columns=['value'])

for _ in range(5):
    df.loc[len(df), :] = [np.random.normal(0, 1)]

df
```

value

- 0 -0.884526
- 1 0.304444
- 2 -0.288040
- 3 0.398078
- 4 1.006034

How to access items by numerical indices

```
#returns a specific range of rows
df.iloc[2:4, 0:2]
```

	Α	В
2013-01-03	1.524227	1.863575
2013-01-04	0.918203	-0.158800

How to access items using a boolean

df[df.A > 1]

	Α	В	С	D
2013-01-01	1.030816	-1.276989	0.837720	-1.490111
2013-01-03	1.524227	1.863575	1.291378	1.300696

How to assign values to a column or row

```
df2['E']=['one', 'one','two','three','four','three']
df2
```

	Α	В	С	D	E
2013-01-01	1.030816	-1.276989	0.837720	-1.490111	one
2013-01-02	-1.070215	-0.209129	0.604572	-1.743058	one
2013-01-03	1.524227	1.863575	1.291378	1.300696	two
2013-01-04	0.918203	-0.158800	-0.964063	-1.990779	three
2013-01-05	0.089731	0.114854	-0.585815	0.298772	four
2013-01-06	0.222260	0.435183	-0.045748	0.049898	three

How to subset df by overlap with a list

```
#select rows based on column values
df2[df2['E'].isin(['two','four'])]
```

	A	В	С	D	E
2013-01-03	1.524227	1.863575	1.291378	1.300696	two
2013-01-05	0.089731	0.114854	-0.585815	0.298772	four

How to access items using multiple booleans

```
titles[(titles.year < 1959) & (titles.year > 1955)].sort_values('year').head(2)
```

	title	year
225480	Tischlein, deck dich	1956
64366	Yield to the Night	1956

Wide versus Long Format

name	George	Lisa	Michael
date			
2000-01-03	500.0	450.0	200.0
2000-01-04	450.0	448.0	180.5
2000-01-05	420.0	447.0	177.0
2000-01-06	300.0	344.6	150.0

In	: df		
Out	:		
	date	person	dollars
0	2000-01-03	Michael	200
1	2000-01-03	George	500
2	2000-01-03	Lisa	450
3	2000-01-04	Michael	180.5
4	2000-01-04	George	450
5	2000-01-04	Lisa	448
6	2000-01-05	Michael	177
7	2000-01-05	George	420
8	2000-01-05	Lisa	447
9	2000-01-06	Michael	150
10	2000-01-06	George	300
11	2000-01-06	Lisa	344.6

```
In []: df2 = pd.DataFrame(columns=["ID", "Group", "Value"])
    for index, row in df.iterrows():
        value = row["Value"]  # May need the .item() method
        df2.loc[len(df2), :] = [index, group, value]
```

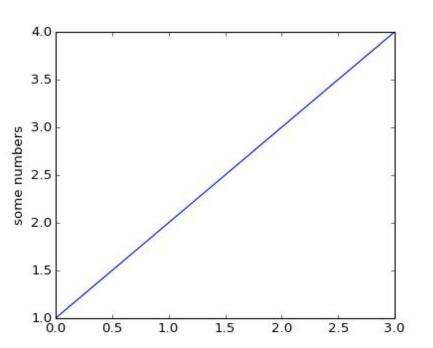


2D plotting library

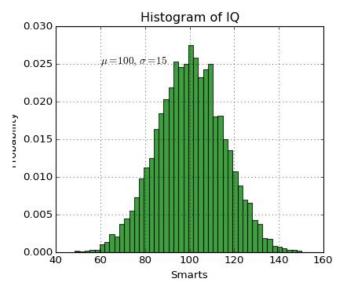
- similar to matlab plotting functions
- flexible environment for making figures
- creates publication quality figures

import matplotlib.pyplot as plt plt.plot([1,2,3,4]) plt.ylabel('some numbers') plt.show()

(Source code, png, hires.png, pdf)



```
import numpy as np
import matplotlib.pyplot as plt
mu, sigma = 100, 15
x = mu + sigma * np.random.randn(10000)
# the histogram of the data
n, bins, patches = plt.hist(x, 50, normed=1, facecolor='q', alpha=0.75)
plt.xlabel('Smarts')
plt.ylabel('Probability')
plt.title('Histogram of IQ')
plt.text(60, .025, r'$\mu=100, \ \sigma=15$')
plt.axis([40, 160, 0, 0.03])
plt.grid(True)
plt.show()
```



```
Simple plot
import matplotlib.pyplot as plt
                                                  1.00 -
import numpy as np
                                                  0.75 -
# Simple data to display in various forms
                                                  0.50 -
x = np.linspace(0, 2 * np.pi, 400)
                                                  0.25 -
y = np.sin(x ** 2)
                                                  0.00
plt.close('all')
                                                 -0.25 -
# Just a figure and one subplot
                                                 -0.50 -
f, ax = plt.subplots()
                                                 -0.75 -
ax.plot(x, y)
ax.set title('Simple plot')
                                                 -1.00 -
```

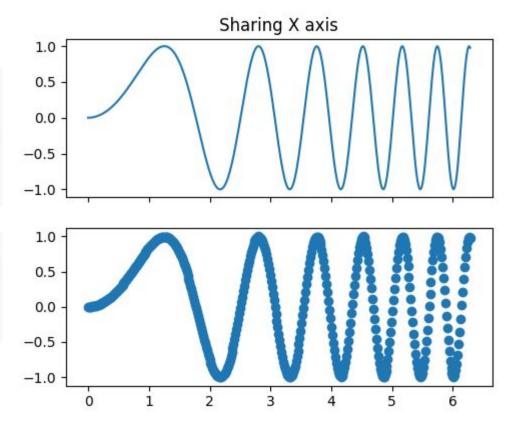
3

5

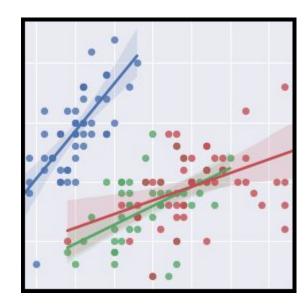
```
import matplotlib.pyplot as plt
import numpy as np

# Simple data to display in various forms
x = np.linspace(0, 2 * np.pi, 400)
y = np.sin(x ** 2)
```

```
# Two subplots, the axes array is 1-d
f, axarr = plt.subplots(2, sharex=True)
axarr[0].plot(x, y)
axarr[0].set_title('Sharing X axis')
axarr[1].scatter(x, y)
```



seaborn



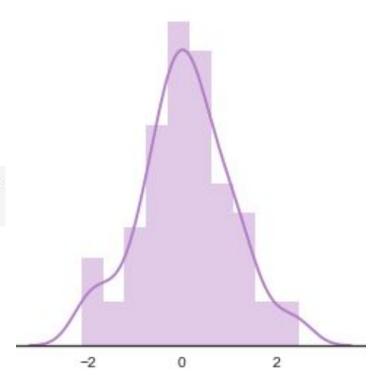
2D plotting library

- built on top of matplotlib
- figures look better with less work
- expanded set of plotting functions

distplot

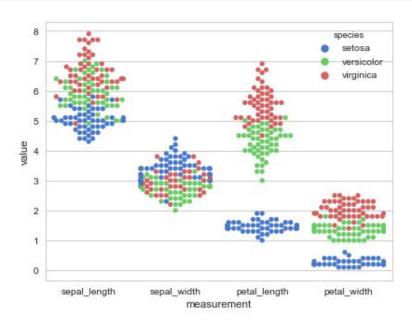
```
# Generate a random univariate dataset
d = rs.normal(size=100)
```

Plot a historgram and kernel density estimate
sns.distplot(d, color="m", ax=axes[1, 1])



swarmplot

```
# Draw a categorical scatterplot to show each observation sns.swarmplot(x="measurement", y="value", hue="species", data=iris)
```



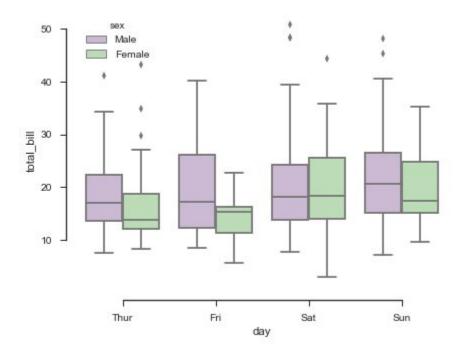
Wide versus Long Format

name	George	Lisa	Michael
date			
2000-01-03	500.0	450.0	200.0
2000-01-04	450.0	448.0	180.5
2000-01-05	420.0	447.0	177.0
2000-01-06	300.0	344.6	150.0

In	: df		
Out	:		
	date	person	dollars
0	2000-01-03	Michael	200
1	2000-01-03	George	500
2	2000-01-03	Lisa	450
3	2000-01-04	Michael	180.5
4	2000-01-04	George	450
5	2000-01-04	Lisa	448
6	2000-01-05	Michael	177
7	2000-01-05	George	420
8	2000-01-05	Lisa	447
9	2000-01-06	Michael	150
10	2000-01-06	George	300
11	2000-01-06	Lisa	344.6

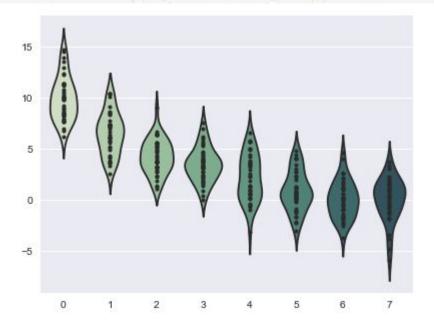
boxplot

```
# Draw a nested boxplot to show bills by day and sex
sns.boxplot(x="day", y="total_bill", hue="sex", data=tips, palette="PRGn")
sns.despine(offset=10, trim=True)
```



violinplot

```
# Show each distribution with both violins and points sns.violinplot(data=d, palette=pal, inner="points")
```

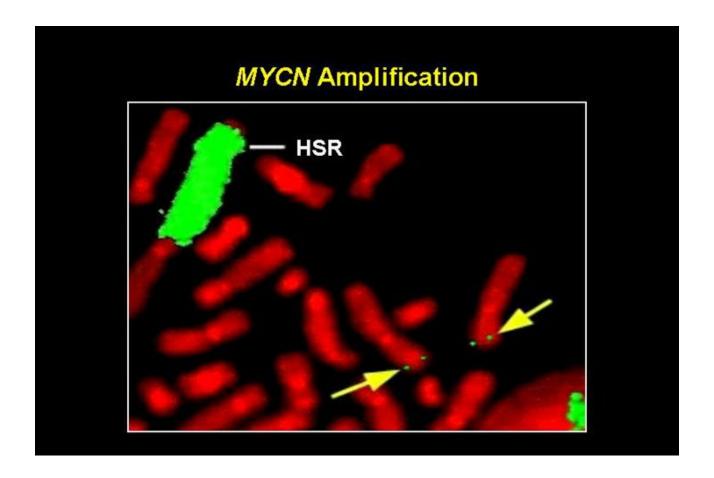


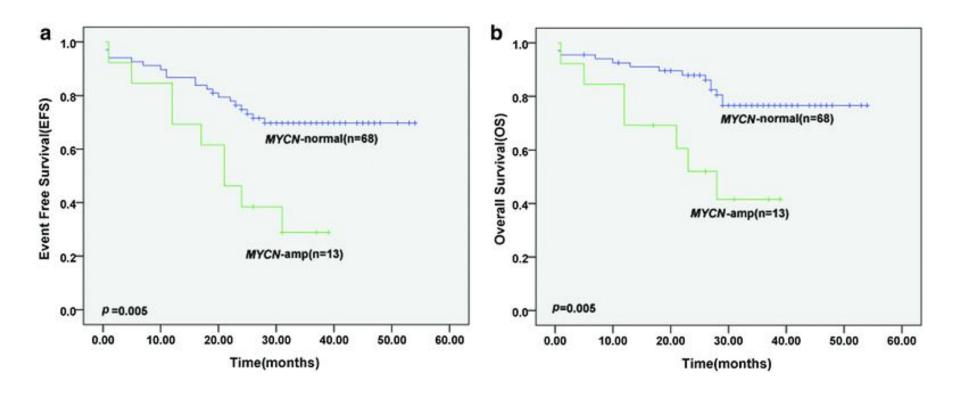
barplot

```
sns.barplot(x, y3, palette="Set3", ax=ax3)
ax3.set_ylabel("Qualitative")
```



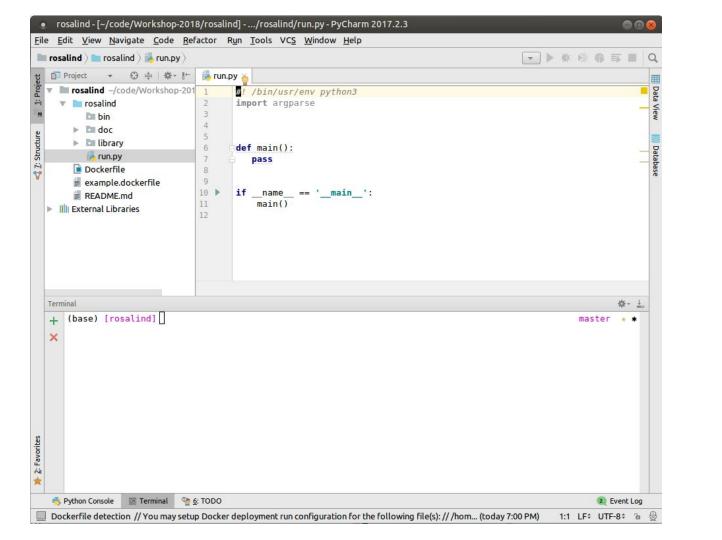
MYCN





https://cancerci.biomedcentral.com/articles/10.1186/s12935-017-0412-z

BD2K Summer Workshop 2018: Day 2

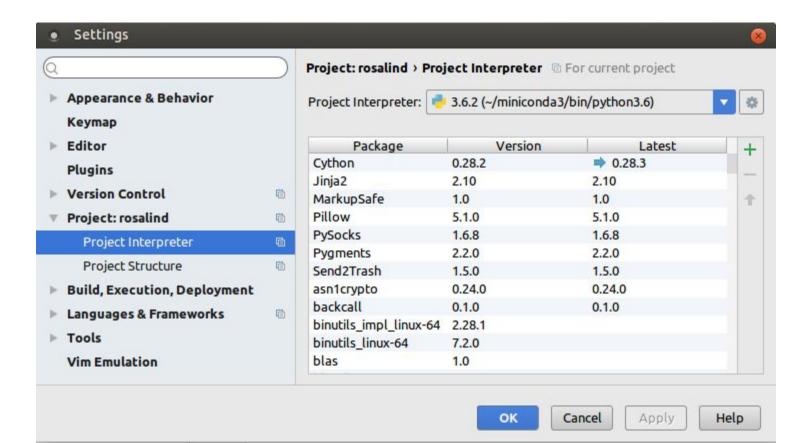


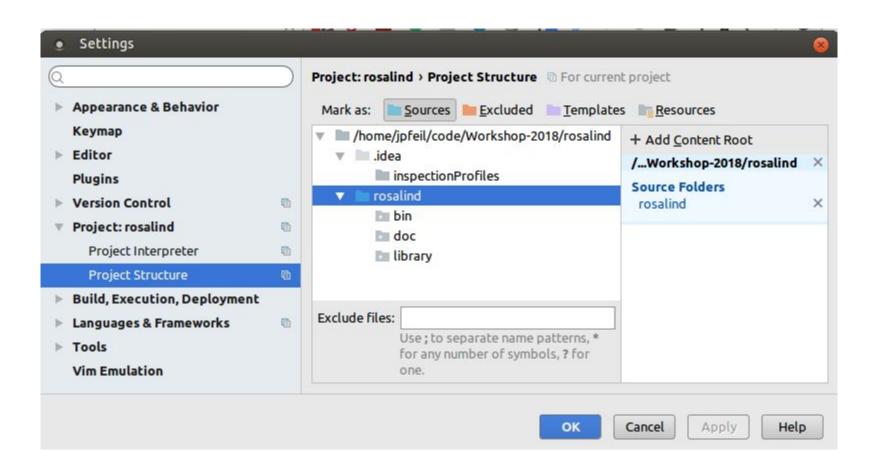
```
#! /bin/usr/env python3
import argparse
```

```
def main():
   pass
```

```
if __name__ == '__main__':
    main()
```

```
def example(arg):
    This is an example of how to structure a
    docstring for a function with a single argument.
    :param arg: The argument for the function
    :return: A transformation of the argument
    :rtype: int
    11 11 11
    value = code(arg)
   return value
```





```
#!/usr/bin/env python2.7
import argparse
import bnpy
import os
```

import logging import multiprocessing import numpy as np import pandas as pd

from collections import defaultdict

from library.utils import mkdir p, parallel fit

<pre>[rosalind] cd rosalind/library</pre>
[library] ls
initpy util.py [library]
[Library]

import argparse

```
parser = argparse.ArgumentParser(description='Description of your program')
parser.add_argument('-f','--foo', help='Description for foo argument', required=True)
parser.add_argument('-b','--bar', help='Description for bar argument', required=True)
args = vars(parser.parse_args())
```

```
if args['foo'] == 'Hello':
    # code here

if args['bar'] == 'World':
    # code here
```

```
© 6: TODO 9: Version Control Python Console Terminal

Dockerfile detection // You may setup Docker deployment run configuration for
```

[hydra] ./run.py --expression test/nbl-data.tsv --CPU 7

Terminal

+ [hydra] ls

[hydra] ls

[hydra] cd hydra

Dockerfile hydra README.md

gene-sets hydra-out library run.py test



Problems

Bioinformatics Stronghold ▼

List Tree

Rosalind is a platform for learning bioinformatics and programming through problem solving. Take a tour to get the hang of how Rosalind works.

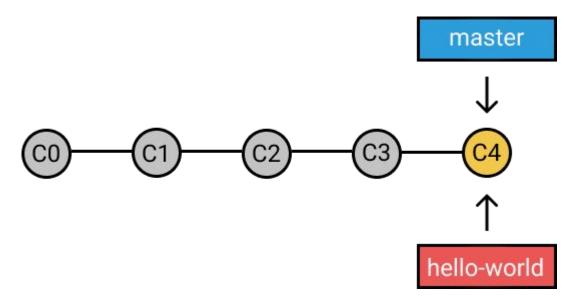
ID	Title	Solved By	Correct Ratio
DNA	Counting DNA Nucleotides	32486	
RNA	Transcribing DNA into RNA	29038	
REVC	Complementing a Strand of DNA	26301	
FIB	Rabbits and Recurrence Relations	14924	
GC	Computing GC Content	15520	
НАММ	Counting Point Mutations	17560	
IPRB	Mendel's First Law	9916	
PROT	Translating RNA into Protein	13595	
SUBS	Finding a Motif in DNA	13994	
CONS	Consensus and Profile	7841	
FIBD	Mortal Fibonacci Rabbits	6458	
GRPH	Overlap Graphs	6499	
IEV	Calculating Expected Offspring	5889	
LCSM	Finding a Shared Motif	5465	



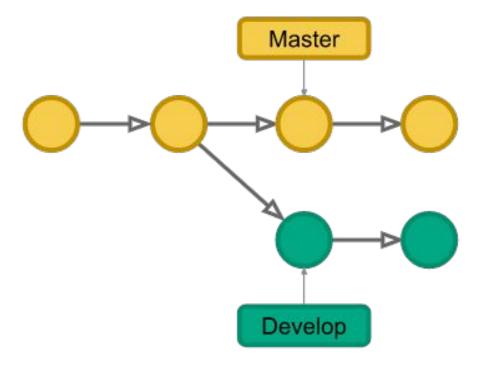
Version control system

- tracks code changes
- facilitates collaboration on projects
- supports distributed version control platforms like github

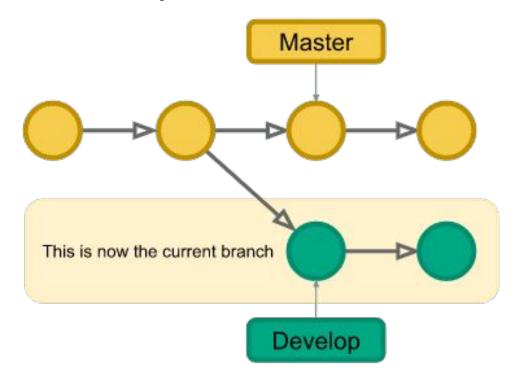
git add & git commit -m C4



git branch develop



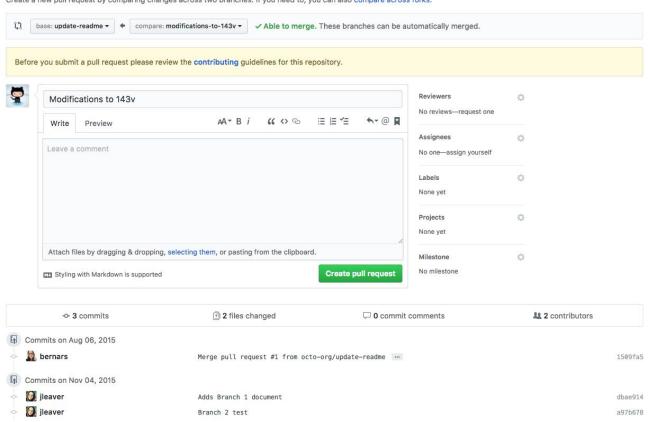
git checkout develop

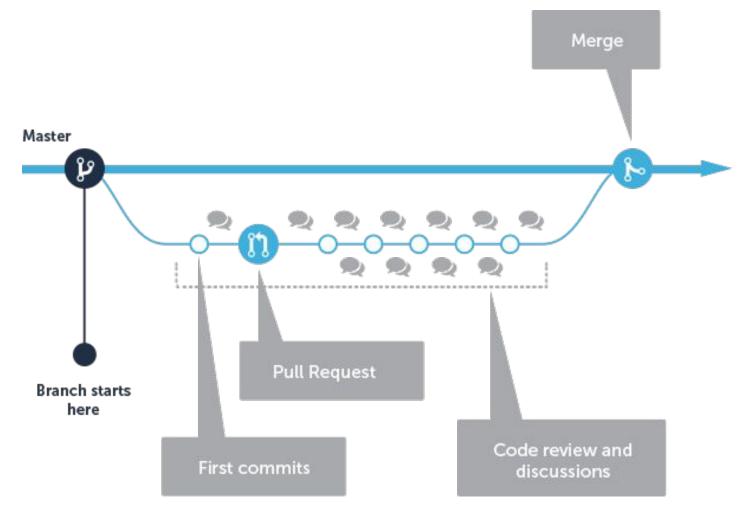




Open a pull request

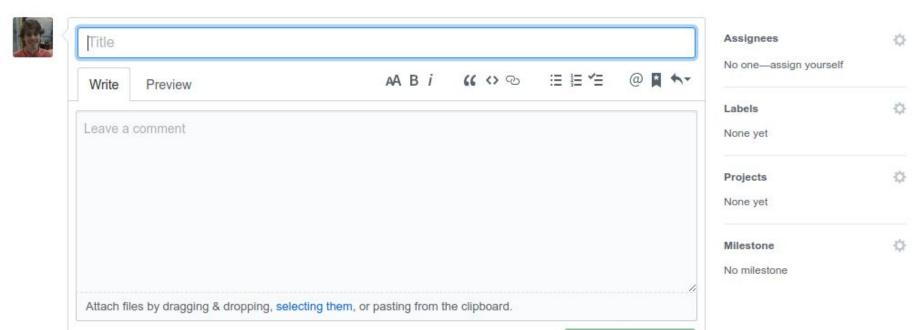
Create a new pull request by comparing changes across two branches. If you need to, you can also compare across forks.





https://www.gitcolony.com/features





Styling with Markdown is supported



Software Container Tool

- packages code and dependencies
- makes it easier to deploy
- kind of like a virtual machine

docker run

```
docker run hello-world
Unable to find image 'hello-world:latest' locally
latest: Pulling from library/hello-world
9bb5a5d4561a: Pull complete
Digest: sha256:f5233545e43561214ca4891fd1157e1c3c563316ed8e237750d59bde73361e77
Status: Downloaded newer image for hello-world:latest
Hello from Docker!
This message shows that your installation appears to be working correctly.
To generate this message, Docker took the following steps:

    The Docker client contacted the Docker daemon.

 The Docker daemon pulled the "hello-world" image from the Docker Hub.
    (amd64)
 3. The Docker daemon created a new container from that image which runs the
   executable that produces the output you are currently reading.
 4. The Docker daemon streamed that output to the Docker client, which sent it
    to your terminal.
To try something more ambitious, you can run an Ubuntu container with:
$ docker run -it ubuntu bash
Share images, automate workflows, and more with a free Docker ID:
https://hub.docker.com/
For more examples and ideas, visit:
https://docs.docker.com/engine/userguide/
```

docker images

<pre>[~] docker images</pre>				
REPOSITORY	TAG	IMAGE ID	CREATED	SIZE
jpfeil/mixture	0.3.3	10f4f835f845	4 weeks ago	4.11GB

```
ROM ubuntu:16.04
MAINTAINER Jacob Pfeil, jpfeil@ucsc.edu
RUN apt-get update --fix-missing \
   && apt-get install -y python python-matplotlib zlib1g-dev \
                          build-essential make wget libg[1-mesa-glx \
                          libboost-all-dev llvm autotools-dev libicu-dev \
                          g++ parallel \
   && apt-get clean \
   && rm -rf /var/lib/apt/lists/*
 RUN wget https://repo.continuum.io/miniconda/Miniconda3-latest-Linux-x86 64.sh -0 ~/miniconda.sh
RUN bash ~/miniconda.sh -b -p $HOME/miniconda
ENV PATH=/root/miniconda/bin:$PATH
RUN conda update -y conda
RUN conda install -y seaborn numpy pandas
RUN pip install pystan
COPY mixture /opt/mixture
ENV TH MIXTURE SRC=/opt/mixture
WORKDIR /opt
RUN wget https://github.com/stan-dev/cmdstan/releases/download/v2.17.0/cmdstan-2.17.0.tar.gz -0 /opt/cmd
stan-2.17.0.tar.gz
   && tar xvf /opt/cmdstan-2.17.0.tar.gz \
   && cd /opt/cmdstan-2.17.0 \
   && echo "CC=g++" > make/local \
&& make build -j 4
RUN cd /opt/cmdstan-2.17.0 && parallel make {.} ::: /opt/mixture/models/*.stan
ENV STAN SRC=/opt/cmdstan-2.17.0
WORKDIR /data
```

```
FROM ubuntu:16.04

MAINTAINER Jacob Pfeil, jpfeil@ucsc.edu
```

```
COPY mixture /opt/mixture

ENV TH_MIXTURE_SRC=/opt/mixture
```

```
# Data processing occurs at /data
WORKDIR /data
ENTRYPOINT ["python", "/opt/mlxture/rum.py"]
CMD ["-h"]
```

docker build . -t jpfeil/mixture:0.3.3

docker run -it -v \$(pwd):/data/ DockerhubName/rosalind:version