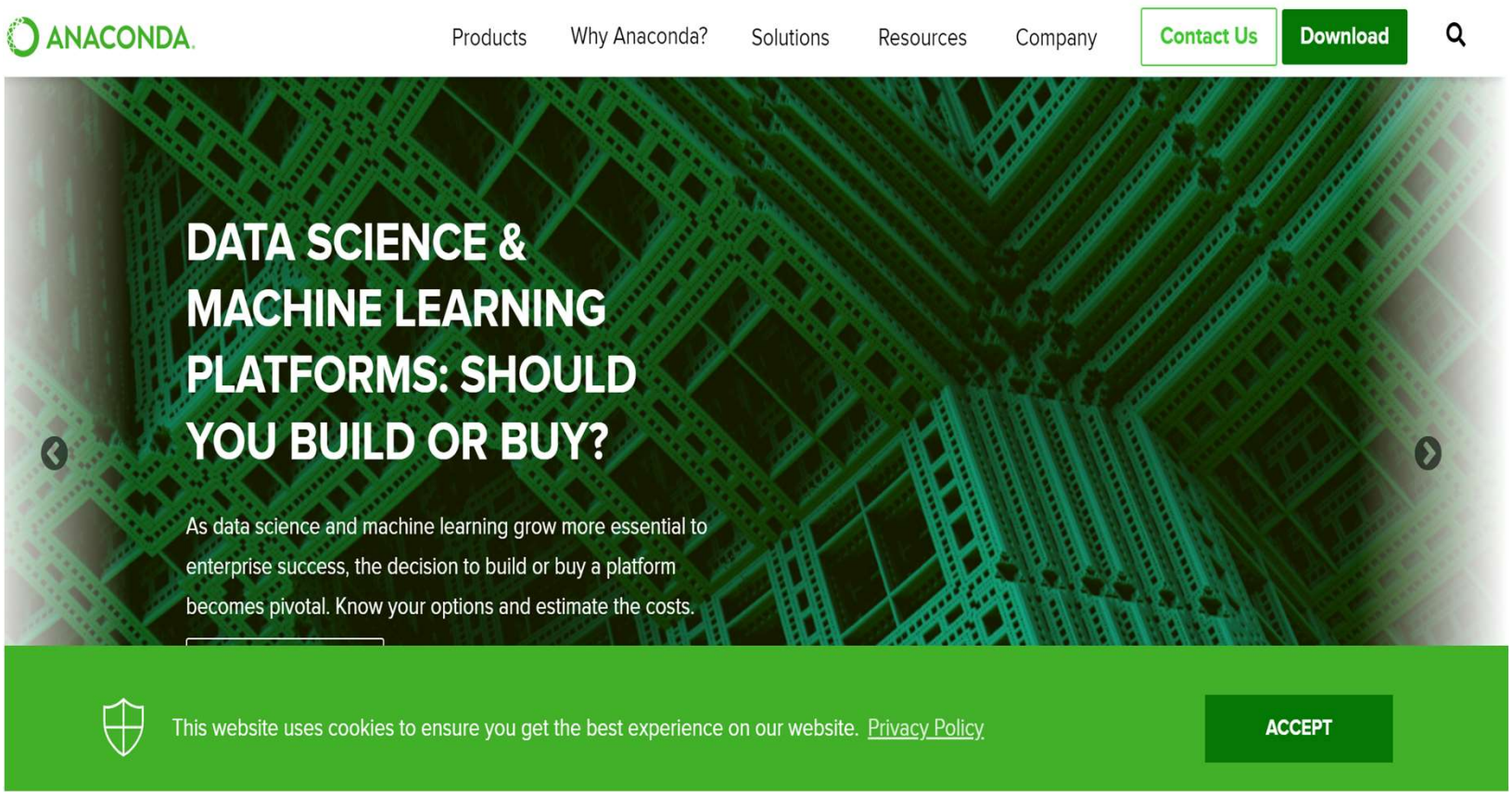
Python and Jupyter Notebook Setup

Anaconda: https://www.anaconda.com/

- Anaconda is a distribution of Python.
- It includes python and also lots of libraries, tools and its own virtual environments that we use in this course.
- It is an “all in one” install that's extremely popular in data science and machine learning.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As data science and machine learning grow more essential to enterprise success, the decision to build or buy a platform becomes pivotal. Know your options and estimate the costs.
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The open-source Anaconda Distribution is the easiest way to perform Python/R data science and machine learning on Linux, Windows, and Mac OS X. With over 15 million users worldwide, it is the industry standard for developing, testing, and training on a single machine, enabling *individual data scientists* to:

- Quickly download 1,500+ Python/R data science packages
- Manage libraries, dependencies, and environments with Conda
- Develop and train machine learning and deep learning models with scikit-learn, TensorFlow, and Theano
- Analyze data with scalability and performance with Dask, NumPy, pandas, and Numba
- Visualize results with Matplotlib, Bokeh, Datashader, and Holoviews

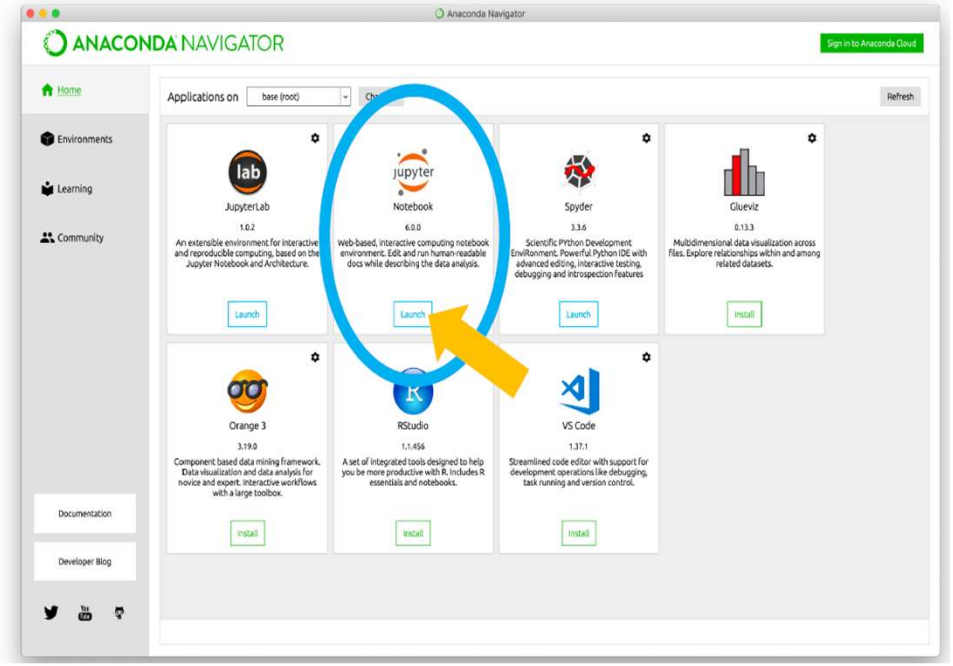
Windows | macOS | Linux

How to launch Jupyter Notebook

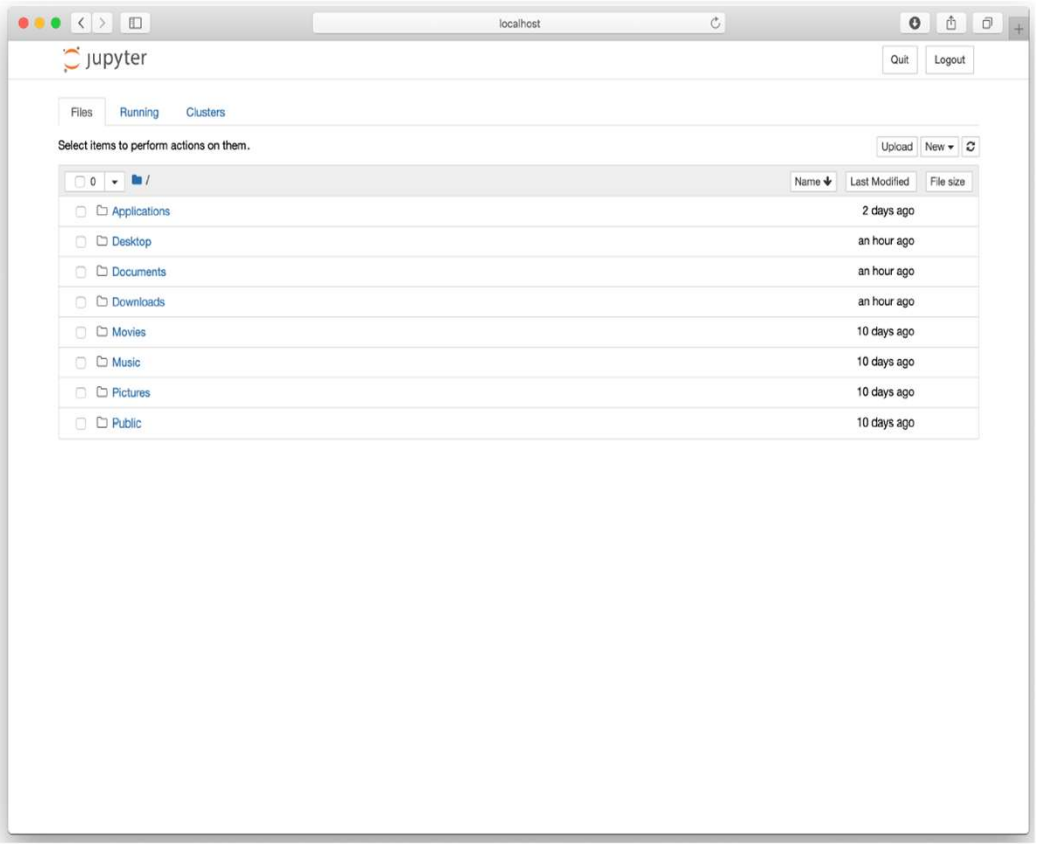
Using Anaconda Navigator

a) Open the application called Anaconda Navigator (this may take a couple of minutes)

b) Click on “Launch” in the Jupyter Notebook box

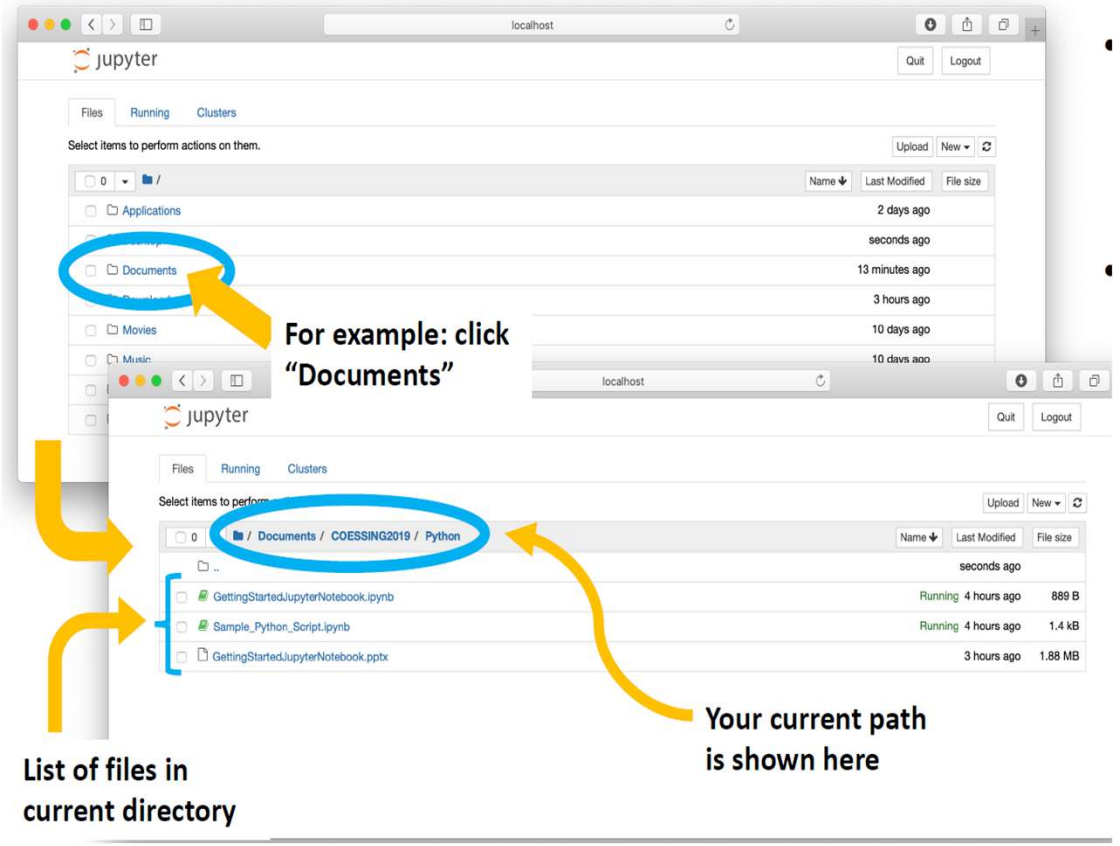


You will know that Jupyter Notebook opened correctly if you see a page similar to this one open in your browser!

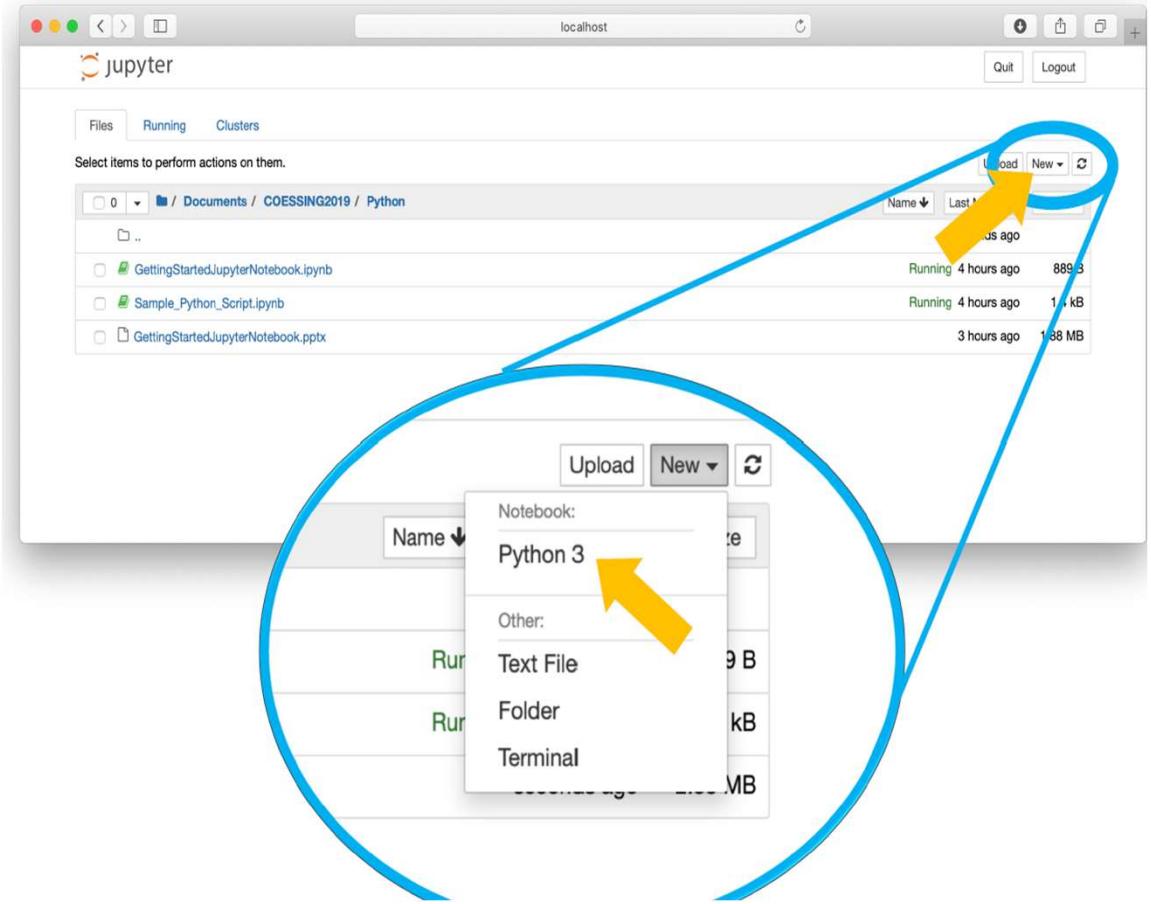


How to open a Notebook file?

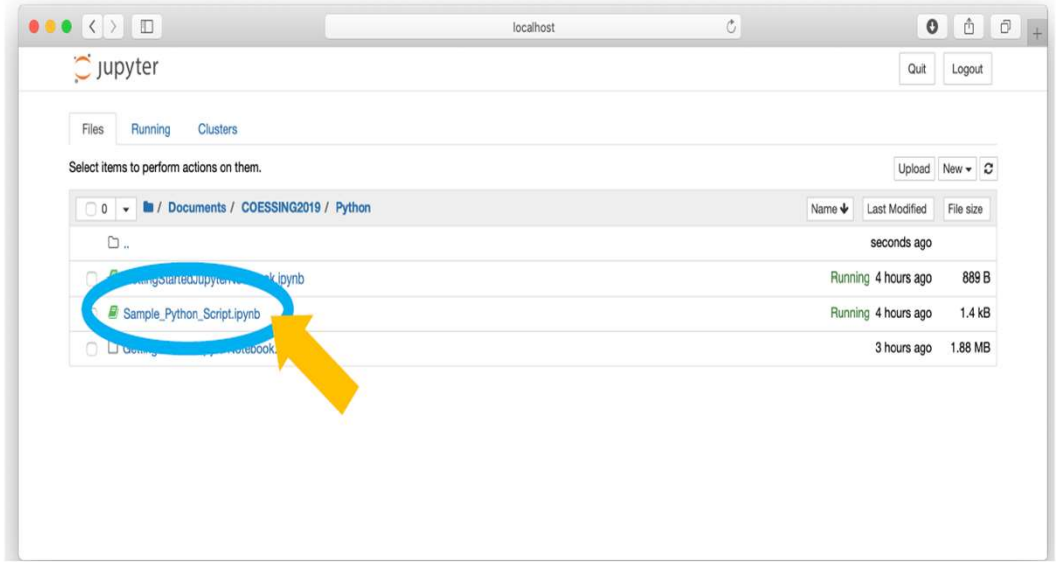
- Navigate through your folders until you get to the directory you want to save your scripts in.
- You can navigate through by clicking on the name of the Folder.



- Open a new Notebook file by clicking on the "New" menu on the upper right

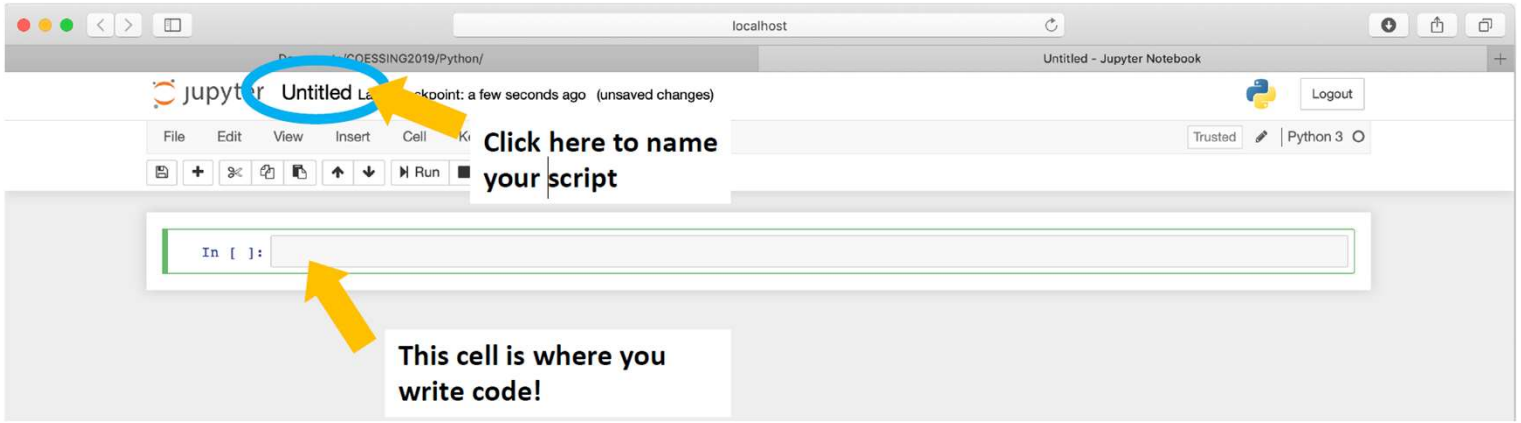


- **Open a previously saved Notebook file** by clicking on the name of the file The extension for a Jupyter Notebook file is ".ipynb", which is short for "interactive python notebook"



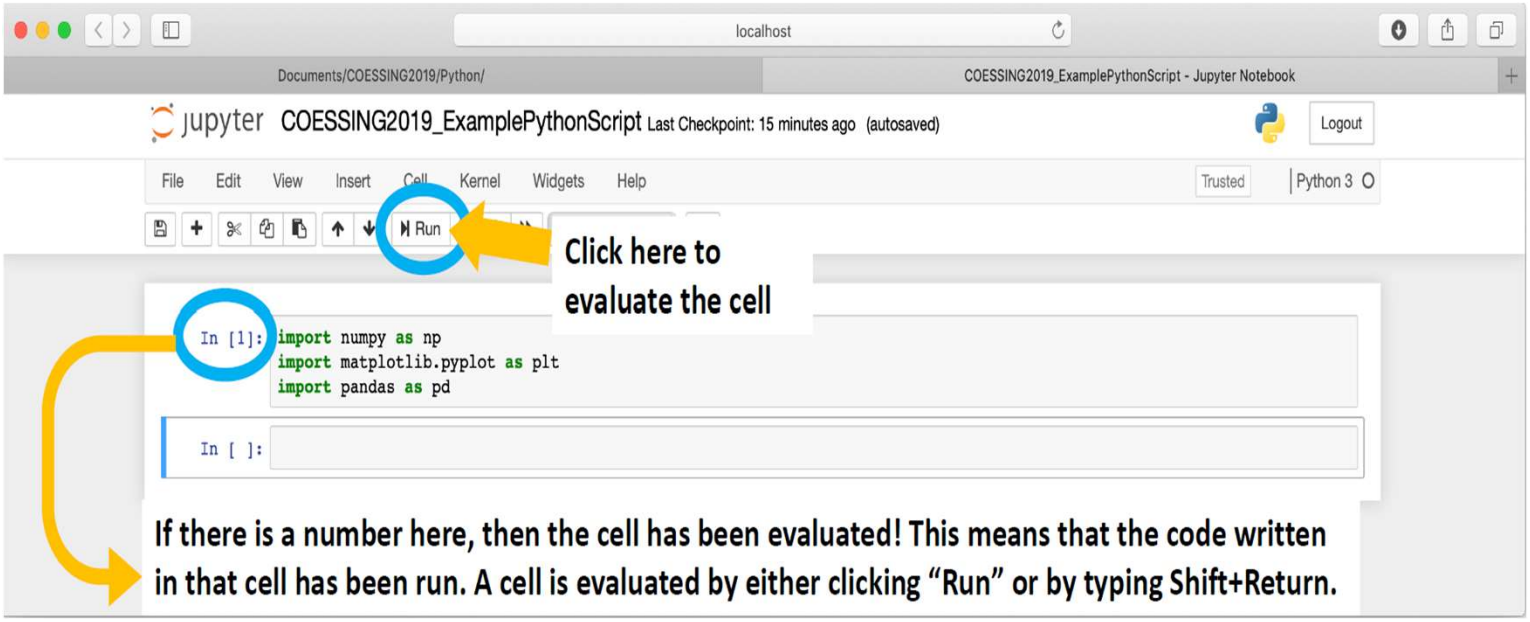
How to start writing a Jupyter Notebook

- A new Notebook looks like this:



First, click on “Untitled” to name your script.

- It's good practice to start your script by importing libraries you will need.

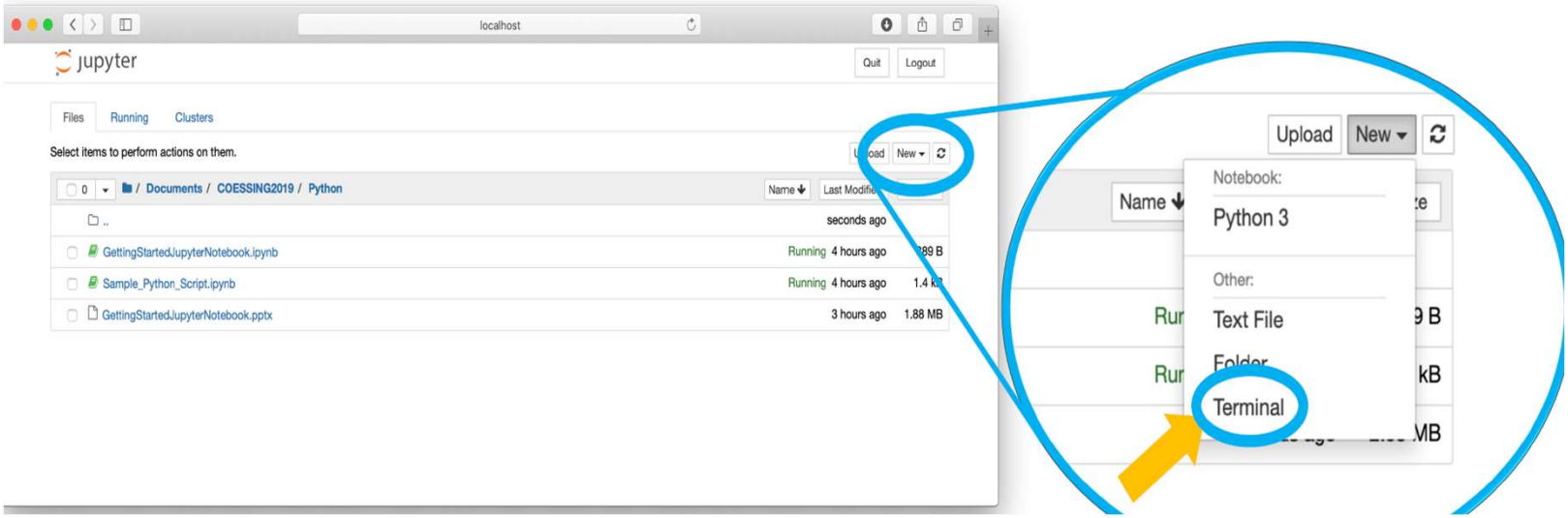


How to install other libraries to Anaconda

- There are some libraries that my be useful that do not come with Anaconda. But, we can install them directly to our conda library!
- There are two methods to install these libraries:

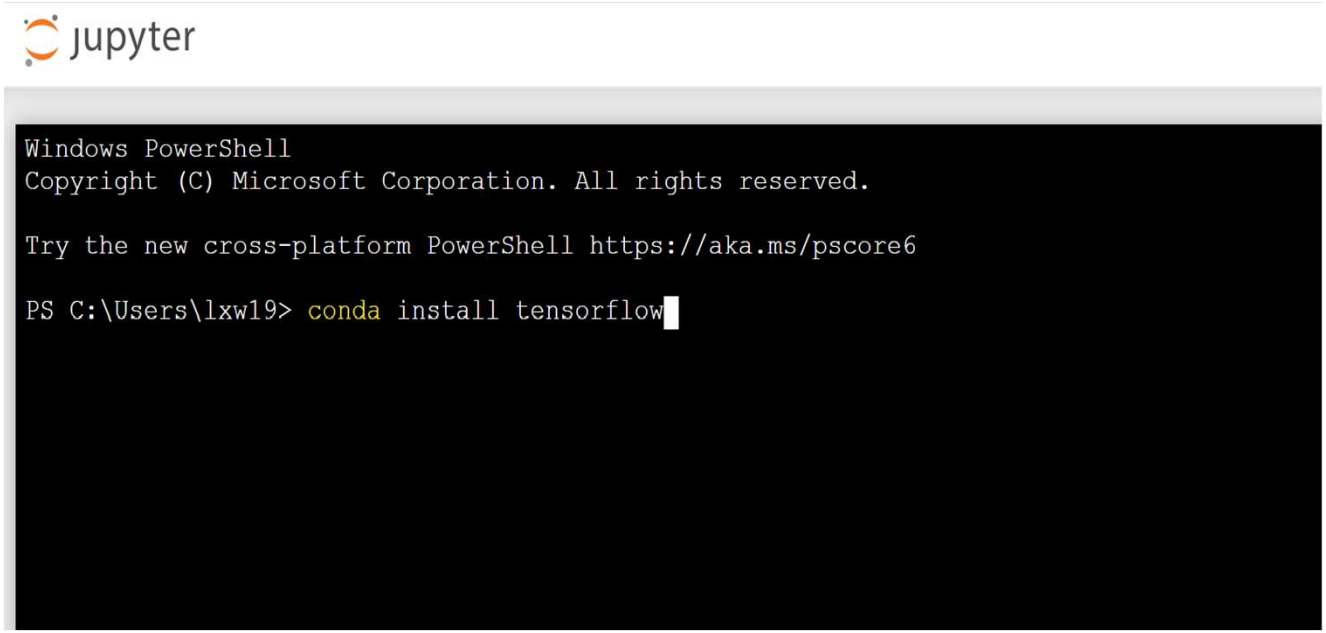
1. Open Anaconda Prompt

2. Open a “Terminal” instance from Jupyter Notebook (see below image for instructions!)



Install Tensorflow

With either method, you will see something like this:



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NATURE GENETICS | ANALYSIS

日本語要約

Multi-tiered genomic analysis of head and neck cancer ties *TP53* mutation to 3p loss

Andrew M Gross, Ryan K Orosco, John P Shen, Ann Marie Egloff, Hannah Carter, Matan Hofree, Michel Choueiri, Charles S Coffey, Scott M Lippman, D Neil Hayes, Ezra E Cohen, Jennifer R Grandis, Quyen T Nguyen & Trey Ideker

Affiliations | Contributions | Corresponding author

Nature Genetics **46**, 939–943 (2014) | doi:10.1038/ng.3051

Received 20 March 2014 | Accepted 10 July 2014 | Published online 03 August 2014

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Abstract

Abstract • Introduction • Results • Discussion • Methods • References • Acknowledgments • Author information • Supplementary information

Head and neck squamous cell carcinoma (HNSCC) is characterized by aggressive behavior with a propensity for metastasis and recurrence. Here we report a comprehensive analysis of the molecular and clinical features of HNSCC that govern patient survival. We find that *TP53* mutation is frequently accompanied by loss of chromosome 3p and that the combination of these events is associated with a surprising decrease in survival time (1.9 years versus >5 years for *TP53* mutation alone). The *TP53*-3p interaction is specific to chromosome 3p and validates in HNSCC and pan-cancer cohorts. In human papillomavirus (HPV)-positive tumors, in which HPV inactivates *TP53*, 3p deletion is also common and is associated with poor outcomes. The *TP53*-3p event is modified by mir-548k expression, which decreases survival further, and is mutually exclusive with mutations affecting RAS signaling. Together, the identified markers underscore the molecular heterogeneity of HNSCC and enable a new multi-tiered classification of this disease.

Editors' pick

Focus on TCGA Pan-Cancer Analysis ▸

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Center for Quantitative Biology and Peking-Tsinghua Center for Life Sciences, Peking University

Assistant Professor in Human Genetics
UT Southwestern Medical Center at Dallas, TX

Faculty Positions Available in Southwest University
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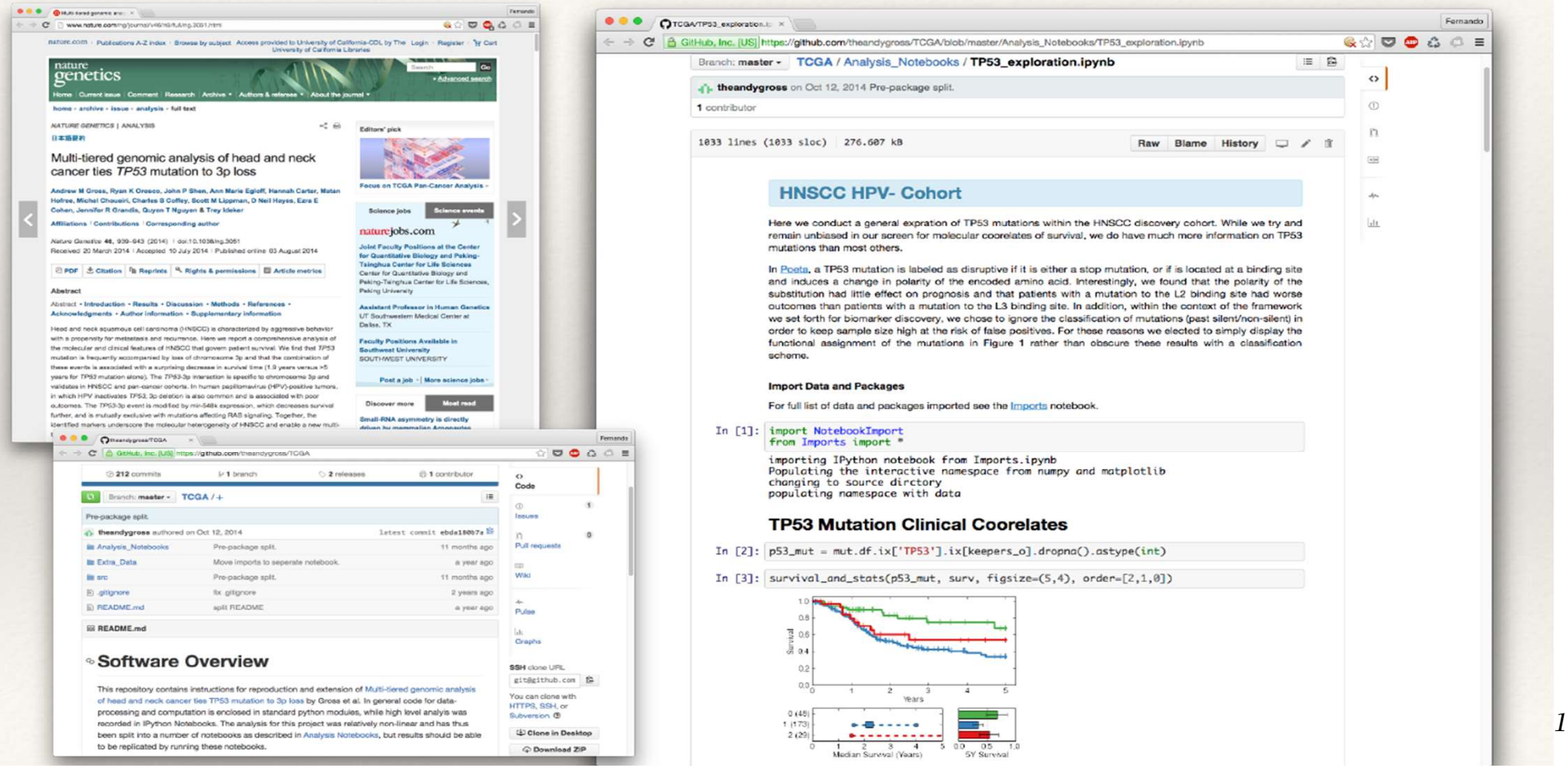
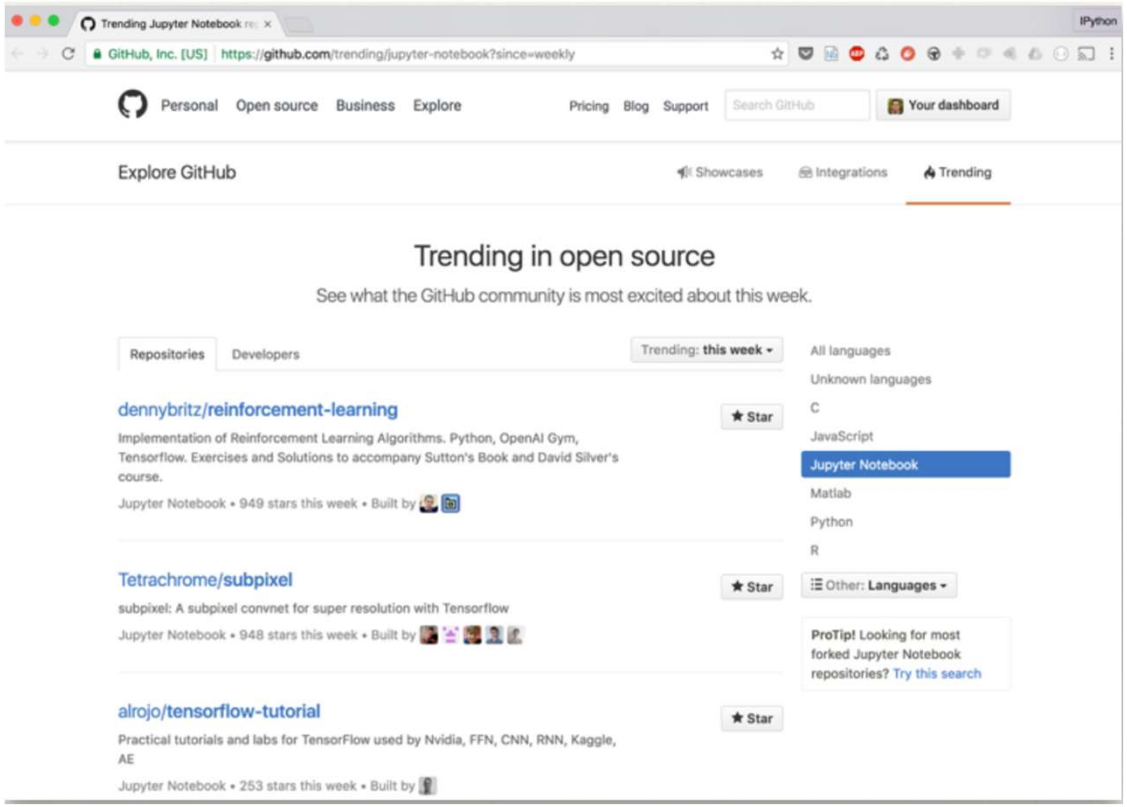
Small-RNA asymmetry is directly driven by mammalian Argonautes
Nature Structural & Molecular Biology | 22

Notebooks on Github: the "actual scolarship"



Changing the scientific culture

Over 500,000 notebooks on Github



Python Libraries for Data Science

- Many popular Python toolboxes/libraries:
  - NumPy
  - SciPy
  - Pandas
  - SciKit-Learn

- Visualization libraries
  - matplotlib
  - Seaborn

- and many more …

Python Libraries for Data Science

NumPy:

- introduces objects for multidimensional arrays and matrices, as well as functions that allow to easily perform advanced mathematical and statistical operations on those objects
- provides vectorization of mathematical operations on arrays and matrices which significantly improves the performance
- many other python libraries are built on NumPy

Link: http://www.numpy.org/

Python Libraries for Data Science

SciPy:

- collection of algorithms for linear algebra, differential equations, numerical integration, optimization, statistics and more
- part of SciPy Stack
- built on NumPy

Link: https://www.scipy.org/scipylib/

Python Libraries for Data Science

Pandas:

- adds data structures and tools designed to work with table-like data (similar to Series and Data Frames in R)
- provides tools for data manipulation: reshaping, merging, sorting, slicing, aggregation etc.
- allows handling missing data

Link: http://pandas.pydata.org/

Python Libraries for Data Science

SciKit-Learn:

- provides machine learning algorithms: classification, regression, clustering, model validation etc.

- built on NumPy, SciPy and matplotlib

Link: http://scikit-learn.org/

Python Libraries for Data Science

matplotlib:

- python 2D plotting library which produces publication quality figures in a variety of hardcopy formats
- a set of functionalities similar to those of MATLAB
- line plots, scatter plots, barcharts, histograms, pie charts etc.
- relatively low-level; some effort needed to create advanced visualization

Link: https://matplotlib.org/

Python Libraries for Data Science

Seaborn:

- based on matplotlib
- provides high level interface for drawing attractive statistical graphics
- Similar (in style) to the popular ggplot2 library in R

Link: https://seaborn.pydata.org/

Loading Python Libraries

In [ ]:
```
#Import Python Libraries
import numpy as np
import scipy as sp
import pandas as pd
import matplotlib as mpl
import seaborn as sns
```

Press `Shift+Enter` to execute the *jupyter* cell

Reading data using pandas

```
# Import pandas
import pandas as pd

# reading csv file
pd.read_csv("filename.csv")
```

Note: The above command has many optional arguments to fine-tune the data import process.

```
#Read csv file
df = pd.read_csv("http://rcs.bu.edu/examples/python/data_analysis/Salaries.csv")
```

Exploring data frames

In [3]:
```
#List first 5 records
df.head()
```

Out[3]:

	rank	discipline	phd	service	sex	salary
0	Prof	B	56	49	Male	186960
1	Prof	A	12	6	Male	93000
2	Prof	A	23	20	Male	110515
3	Prof	A	40	31	Male	131205
4	Prof	B	20	18	Male	104800

Data Frame data types

Pandas Type	Native Python Type	Description
object	string	The most general dtype. Will be assigned to your column if column has mixed types (numbers and strings).
int64	int	Numeric characters. 64 refers to the memory allocated to hold this character.
float64	float	Numeric characters with decimals. If a column contains numbers and NaNs(see below), pandas will default to float64, in case your missing value has a decimal.
datetime64, timedelta[ns]	N/A (but see the datetime module in Python's standard library)	Values meant to hold time data. Look into these for time series experiments.

Data Frame data types

```
In [4]:#Check a particular column type
       df['salary'].dtype
```

```
Out[4]: dtype('int64')
```

```
In [5]:#Check types for all the columns
       df.dtypes
```

```
Out[4]:rank          object
       discipline    object
       phd           int64
       service       int64
       sex           object
       salary        int64
       dtype: object
```

Data Frames attributes

Python objects have *attributes* and *methods*.

df.attribute	description
dtypes	list the types of the columns
columns	list the column names
axes	list the row labels and column names
ndim	number of dimensions
size	number of elements
shape	return a tuple representing the dimensionality
values	numpy representation of the data

Data Frames methods

Unlike attributes, python methods have *parenthesis.*
All attributes and methods can be listed with a *dir()* function:

```
dir(df)
```

df.method()	description
head([n]), tail([n])	first/last n rows
describe()	generate descriptive statistics (for numeric columns only)
max(), min()	return max/min values for all numeric columns
mean(), median()	return mean/median values for all numeric columns
std()	standard deviation
sample([n])	returns a random sample of the data frame
dropna()	drop all the records with missing values

Selecting a column in a Data Frame

Method 1: Subset the data frame using column name:

```
df['sex']
```

Method 2: Use the column name as an attribute:

```
df.sex
```

Note: there is an attribute *rank* for pandas data frames, so to select a column with a name "rank" we should use method 1.

Data Frames groupby method

Using "group by" method we can:

- Split the data into groups based on some criteria
- Calculate statistics (or apply a function) to each group
- Similar to dplyr() function in R

In [ ]:
```
#Group data using rank
df_rank = df.groupby(['rank'])
```

In [ ]:
```
#Calculate mean value for each numeric column per each group
df_rank.mean()
```

rank	phd	service	salary
AssocProf	15.076923	11.307692	91786.230769
AsstProf	5.052632	2.210526	81362.789474
Prof	27.065217	21.413043	123624.804348

Data Frames groupby method

Once groupby object is created we can calculate various statistics for

each group:

```
In [ ]:#Calculate mean salary for each professor rank:
       df.groupby('rank')[['salary']].mean()
```

rank	salary
AssocProf	91786.230769
AsstProf	81362.789474
Prof	123624.804348

Note: If single brackets are used to specify the column (e.g. salary), then the output is Pandas Series object. When double brackets are used the output is a Data Frame

Data Frame: filtering

To subset the data we can apply Boolean indexing. This indexing is commonly known as a filter. For example if we want to subset the rows in which the salary value is greater than $120K:

```
In [ ]:#Calculate mean salary for each professor rank:
       df_sub = df[ df['salary'] > 120000 ]
```

Any Boolean operator can be used to subset the data:

> greater; >= greater or equal;

< less; <= less or equal;

== equal; != not equal;

```
In [ ]:#Select only those rows that contain female professors:
       df_f = df[ df['sex'] == 'Female' ]
```

Data Frames: Slicing

There are a number of ways to subset the Data Frame:

- one or more columns
- one or more rows
- a subset of rows and columns

Rows and columns can be selected by their position or label

Data Frames: Slicing

When selecting one column, it is possible to use single set of brackets, but the resulting object will be a Series (not a DataFrame):

In [ ]:
```
#Select column salary:
df['salary']
```

When we need to select more than one column and/or make the output to be a DataFrame, we should use double brackets:

In [ ]:
```
#Select column salary:
df[['rank','salary']]
```

Data Frames: Selecting rows

If we need to select a range of rows, we can specify the range using ":"

```
In [ ]:#Select rows by their position:
       df[10:20]
```

Notice that the first row has a position 0, and the last value in the range is omitted:
So for 0:10 range the first 10 rows are returned with the positions starting with 0 and ending with 9

Data Frames: method loc

If we need to select a range of rows, using their labels we can use method loc:

In [ ]:
```
#Select rows by their labels:
df_sub.loc[10:15,['rank','sex','salary']]
```

Out[ ]:

	rank	sex	salary
10	Prof	Male	128250
11	Prof	Male	134778
12	AsstProf	Male	88000
13	Prof	Male	162200
14	Prof	Male	153750
15	Prof	Male	150480

Data Frames: method iloc

If we need to select a range of rows and/or columns, using their positions we can use method iloc:

In [ ]:
```
#Select rows by their labels:
df_sub.iloc[10:20,[0, 3, 4, 5]]
```

Out[ ]:

	rank	service	sex	salary
26	Prof	19	Male	148750
27	Prof	43	Male	155865
29	Prof	20	Male	123683
31	Prof	21	Male	155750
35	Prof	23	Male	126933
36	Prof	45	Male	146856
39	Prof	18	Female	129000
40	Prof	36	Female	137000
44	Prof	19	Female	151768
45	Prof	25	Female	140096

Data Frames: method iloc (summary)

```
df.iloc[0]  # First row of a data frame
df.iloc[i]  #(i+1)th row
df.iloc[-1] # Last row
```

```
df.iloc[:, 0]  # First column
df.iloc[:, -1] # Last column
```

```
df.iloc[0:7]        #First 7 rows
df.iloc[:, 0:2]     #First 2 columns
df.iloc[1:3, 0:2]   #Second through third rows and first 2 columns
df.iloc[[0,5], [1,3]]  #1st and 6th rows and 2nd and 4th columns
```

Data Frames: Sorting

We can sort the data by a value in the column. By default the sorting will occur in ascending order and a new data frame is return.

In [ ]:
```
# Create a new data frame from the original sorted by the column Salary
df_sorted = df.sort_values( by ='service')
df_sorted.head()
```

Out[ ]:

	rank	discipline	phd	service	sex	salary
55	AsstProf	A	2	0	Female	72500
23	AsstProf	A	2	0	Male	85000
43	AsstProf	B	5	0	Female	77000
17	AsstProf	B	4	0	Male	92000
12	AsstProf	B	1	0	Male	88000

Data Frames: Sorting

We can sort the data using 2 or more columns:

In [ ]:
```
df_sorted = df.sort_values( by =['service', 'salary'], ascending = [True, False])
df_sorted.head(10)
```

Out[ ]:

	rank	discipline	phd	service	sex	salary
52	Prof	A	12	0	Female	105000
17	AsstProf	B	4	0	Male	92000
12	AsstProf	B	1	0	Male	88000
23	AsstProf	A	2	0	Male	85000
43	AsstProf	B	5	0	Female	77000
55	AsstProf	A	2	0	Female	72500
57	AsstProf	A	3	1	Female	72500
28	AsstProf	B	7	2	Male	91300
42	AsstProf	B	4	2	Female	80225
68	AsstProf	A	4	2	Female	77500

Missing Values

Missing values are marked as NaN

In [ ]:
```
# Read a dataset with missing values
flights = pd.read_csv("http://rcs.bu.edu/examples/python/data_analysis/flights.csv")
```

In [ ]:
```
# Select the rows that have at least one missing value
flights[flights.isnull().any(axis=1)].head()
```

Out[ ]

	year	month	day	dep_time	dep_delay	arr_time	arr_delay	carrier	tailnum	flight	origin	dest	air_time	distance	hour	minute
330	2013	1	1	1807.0	29.0	2251.0	NaN	UA	N31412	1228	EWR	SAN	NaN	2425	18.0	7.0
403	2013	1	1	NaN	NaN	NaN	NaN	AA	N3EHAA	791	LGA	DFW	NaN	1389	NaN	NaN
404	2013	1	1	NaN	NaN	NaN	NaN	AA	N3EVAA	1925	LGA	MIA	NaN	1096	NaN	NaN
855	2013	1	2	2145.0	16.0	NaN	NaN	UA	N12221	1299	EWR	RSW	NaN	1068	21.0	45.0
858	2013	1	2	NaN	NaN	NaN	NaN	AA	NaN	133	JFK	LAX	NaN	2475	NaN	NaN

Missing Values

There are a number of methods to deal with missing values in the data frame:

df.method()	description
dropna()	Drop missing observations
dropna(how='all')	Drop observations where all cells is NA
dropna(axis=1, how='all')	Drop column if all the values are missing
dropna(thresh = 5)	Drop rows that contain less than 5 non-missing values
fillna(0)	Replace missing values with zeros
isnull()	returns True if the value is missing
notnull()	Returns True for non-missing values

Missing Values

- When summing the data, missing values will be treated as zero
- If all values are missing, the sum will be equal to NaN
- cumsum() and cumprod() methods ignore missing values but preserve them in the resulting arrays
- Missing values in GroupBy method are excluded (just like in R)
- Many descriptive statistics methods have *skipna* option to control if missing data should be excluded . This value is set to *True* by default (unlike R)

Aggregation Functions in Pandas

Aggregation - computing a summary statistic about each group, i.e.

- compute group sums or means
- compute group sizes/counts

Common aggregation functions:

min, max
count, sum, prod
mean, median, mode, mad
std, var

Aggregation Functions in Pandas

agg() method are useful when multiple statistics are computed per column:

In [ ]:
```
flights[['dep_delay','arr_delay']].agg(['min','mean','max'])
```

Out[ ]:

	dep_delay	arr_delay
min	-16.000000	-62.000000
mean	9.384302	2.298675
max	351.000000	389.000000

Basic Descriptive Statistics

df.method()	description
describe	Basic statistics (count, mean, std, min, quantiles, max)
min, max	Minimum and maximum values
mean, median, mode	Arithmetic average, median and mode
var, std	Variance and standard deviation
sem	Standard error of mean
skew	Sample skewness
kurt	kurtosis

Graphics to explore the data

Seaborn package is built on matplotlib but provides high level interface for drawing attractive statistical graphics, similar to ggplot2 library in R. It specifically targets statistical data visualization

To show graphs within Python notebook include inline directive:

```
In [ ]:%matplotlib inline
```

Graphics

	description
distplot	histogram
barplot	estimate of central tendency for a numeric variable
violinplot	similar to boxplot, also shows the probability density of the data
jointplot	Scatterplot
regplot	Regression plot
pairplot	Pairplot
boxplot	boxplot
swarmplot	categorical scatterplot
factorplot	General categorical plot

Basic statistical Analysis

statsmodel and scikit-learn - both have a number of function for statistical analysis

The first one is mostly used for regular analysis using R style formulas, while scikit-learn is more tailored for Machine Learning.

statsmodels:

- linear regressions
- ANOVA tests
- hypothesis testings
- many more ...

scikit-learn:

- kmeans
- support vector machines
- random forests
- many more ...

See examples in the Tutorial Notebook