

Scientific Computing with Python

Quick Introduction

Libraries and APIs

- A library is a collection of implementations of behavior (definitions)
- An Application Programming Interface (API) describes that behavior (declarations)

Declaration

```
int max(int a, int b);
```

Definition

```
int max(int a, int b) {  
    if (a > b) { return a; }  
    else { return b; }  
}
```

- Python only has declarations
- In Python, libraries are organized into packages, which are referenced using the `import` statement
- The same interfaces can be implemented by multiple libraries
 - Dill vs. Pickle
 - `pyFFTW` vs. `scipy.fftpack`
- Most Python libraries installed using `pip` command
- E.g. `$sudo pip install pandas`

When to use a library

- Programmer time (your time) is a nonrenewable resource
- Biology is hard – computing should FREE YOUR MIND for biological problems
- Use a library if you think the task has been done before (e.g. parsing most file types)
- Use a library if time spent looking for and learning a library is LESS THAN the time to reimplement
- Use a library for tasks which are NOT part of your scientific contribution
- Reimplement only when there is a tangible benefit
- “Premature optimization is the root of all evil”
 - Your time is more valuable than compute time
 - Profile code before optimizing
 - `python -m cProfile -s cumtime myprogram.py`
 - Or `%%prun` in a jupyter notebook

API Documentation

- Declarations + formatted comments can be automatically converted to documentation

scipy.stats.linregress ← Containing package

`scipy.stats.linregress(x, y=None)` ← Default values

[\[source\]](#) ← Link to source

Calculate a linear least-squares regression for two sets of measurements.

Parameters:	<code>x, y : array_like</code> Two sets of measurements. Both arrays should have the same length. If only x is given (and y=None), then it must be a two-dimensional array where one dimension has length 2. The two sets of measurements are then found by splitting the array along the length-2 dimension.
Returns:	<code>slope : float</code> slope of the regression line <code>intercept : float</code> intercept of the regression line <code>rvalue : float</code> correlation coefficient <code>pvalue : float</code> two-sided p-value for a hypothesis test whose null hypothesis is that the slope is zero. <code>stderr : float</code> Standard error of the estimated gradient.

Inputs

Outputs

numpy + scipy + matplotlib = PYLAB

- Three most important scientific libraries in Python, with functionality similar to MATLAB
 - Numpy is usually imported as `np` and `scipy` as `sp`
 - Matplotlib is usually used through the `pyplot` interface (`matplotlib.pyplot` as `plt`)
 - Numpy provides typed numerical arrays and array and matrix math
 - Create arrays with `np.array([])` or `np.zeros()`, `np.ones()`
 - Indexed and sliced like Python lists, element-wise arithmetic, broadcasting
 - Logical operations (`<` `>` `&` `|` `~`) on arrays produce binary masks that function as indices
- ```
>>> a = np.array([1, 3, 0])
>>> b = np.array([0, 3, 2])
>>> a > b
array([True, False, False], dtype=bool)
```
- Convert from logical index to numerical index using `where`
  - Numpy also provides many functions like `np.mean`, `np.std`, `np.max`, `np.argmax`, `np.sort`, `np.argsort`, `np.maximum`, etc.

# scipy

- Scipy contains packages with more advanced functionality built on numpy
- `sp.special`
- `sp.integrate`
- `sp.optimize`
- `sp.interpolate`
- `sp.linalg`
- `sp.spatial`
- `sp.stats`

# matplotlib

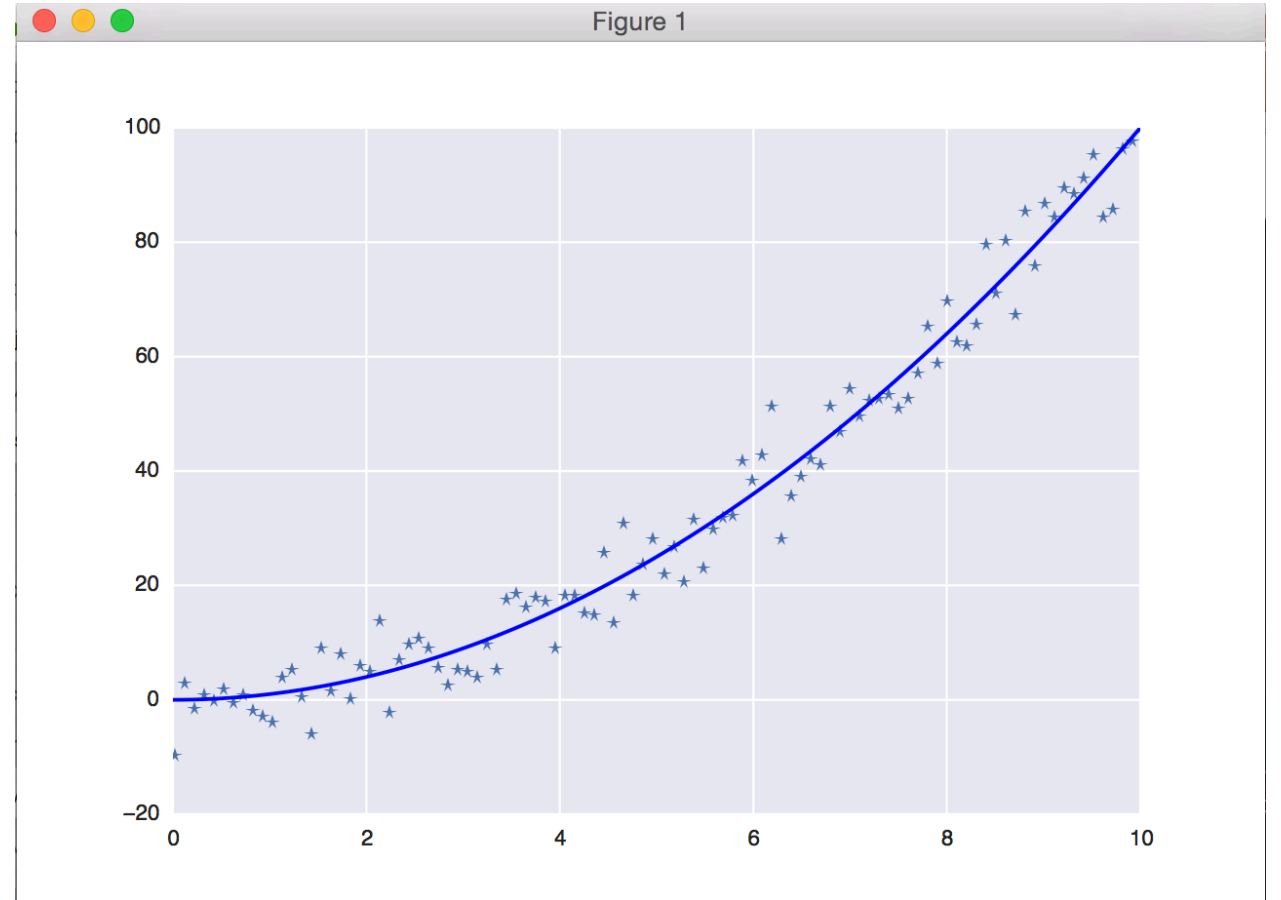
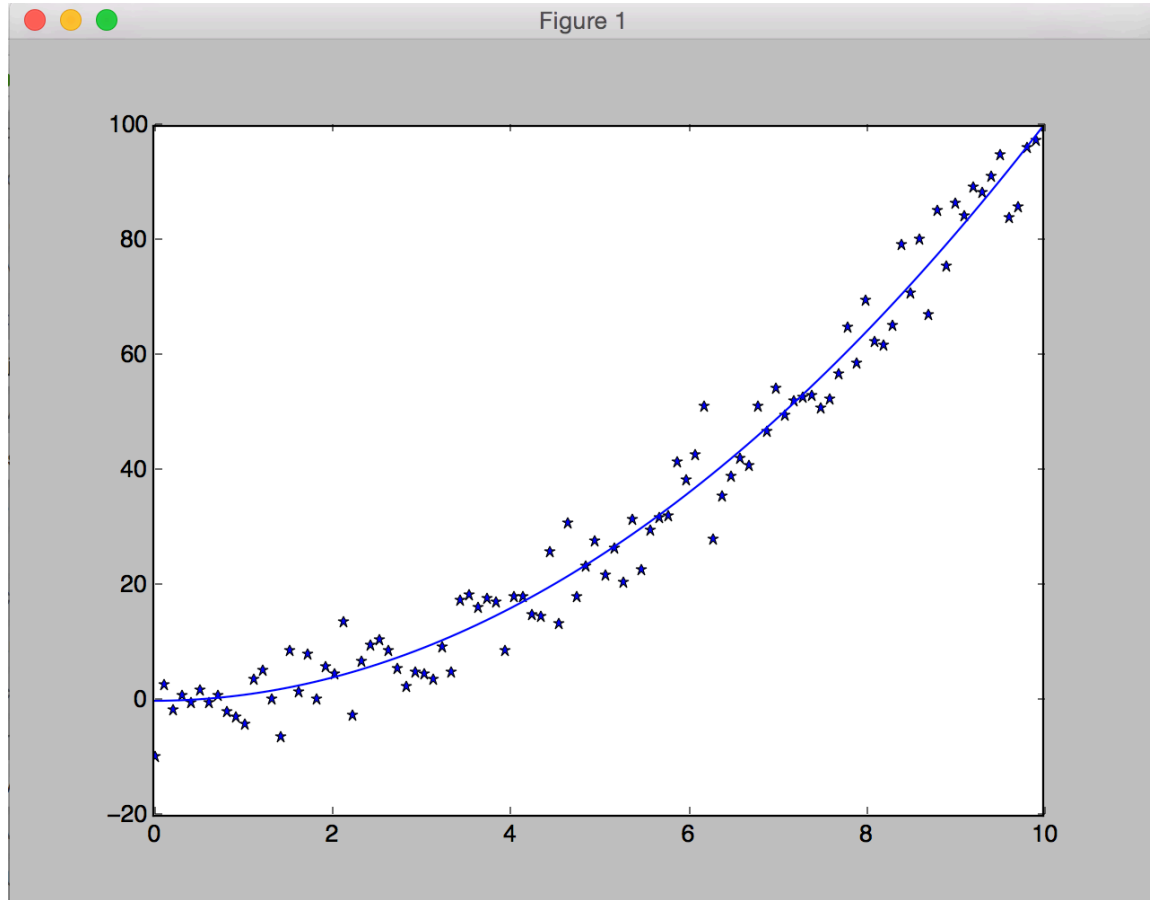
- The pyplot interface is highly similar to plotting in MATLAB
- The figure is the whole plotting window
- A figure can contain one or more axes
- The last used or selected figure is the current figure (same for axes)
- Functions like `plt.xlim`, `plt.xlabel`, `plt.set_xticklabels` modify current figure/axes
- Publication quality figures often require customization of figure size, DPI, axes labels and so forth
  - Parameters like size can be set on creation
  - Use `plt.gcf()` and `plt.gca()` to get handles to the current figure/axes

# seaborn

- Usually imported as `sns`
- Contains superior default fonts and styles for matplotlib
  - Activate with `sns.set()`
- Provides many short and sweet functions like `sns.regplot`, `sns.kdeplot`, `sns.heatmap`
- Good for producing example plots quickly
- Customization will usually require the same low-level matplotlib options
- Data analysis will usually require doing e.g. linear regression yourself in scipy (because seaborn doesn't return regression results)



# seaborn: before and after



# pandas

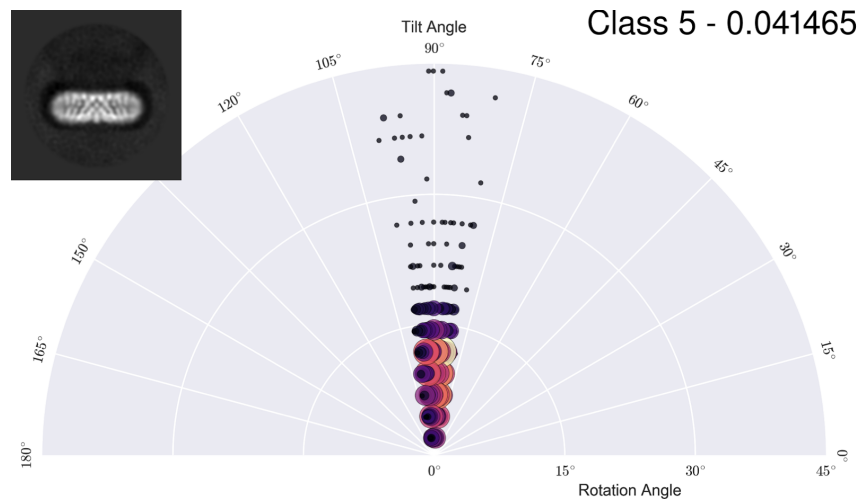
- Framework for “relational” or labelled data, import as `pd`
- Based on `pd.DataFrame` created from list of dict, dict of dict, dict of list, etc.
- Convenient parsing – `pd.read_csv()`, `pd.read_table()`
- Index using arbitrary labels (access a record based on the value of a field)
- Fast merging, `groupby`, aggregation
- Default plot labels in seaborn plots and `DataFrame.plot`, etc.
- Advanced multivariate visualization (Andrews plots and so forth)
- Real world example: `star.py` and `angdist.py`

# scikit & others

- Scipy toolkits (scikits) offer more specialized features from outside the main project
- `scikit-learn`, `scikit-image`
- Biopython has lots of useful functions for biology (`Bio.PDB`, `Bio.Seq`, etc.)
- Many others like `rdkit`, `opencv`, etc.

# Resources

- Documentation - <http://www.scipy.org/docs.html>
- Introduction to Numpy and Scipy (UCSB) - <http://www.engr.ucsb.edu/~shell/che210d/numpy.pdf>
- Pandas cheat sheet (U of Idaho) - <http://www.webpages.uidaho.edu/~stevel/504/Pandas%20DataFrame%20Notes.pdf>
- Really fancy plots – matplotlib & mpl\_toolkits



```
from matplotlib.projections.polar import PolarTransform
from matplotlib.transforms import Affine2D
from mpl_toolkits.axisartist import angle_helper
from mpl_toolkits.axisartist import floating_axes
```