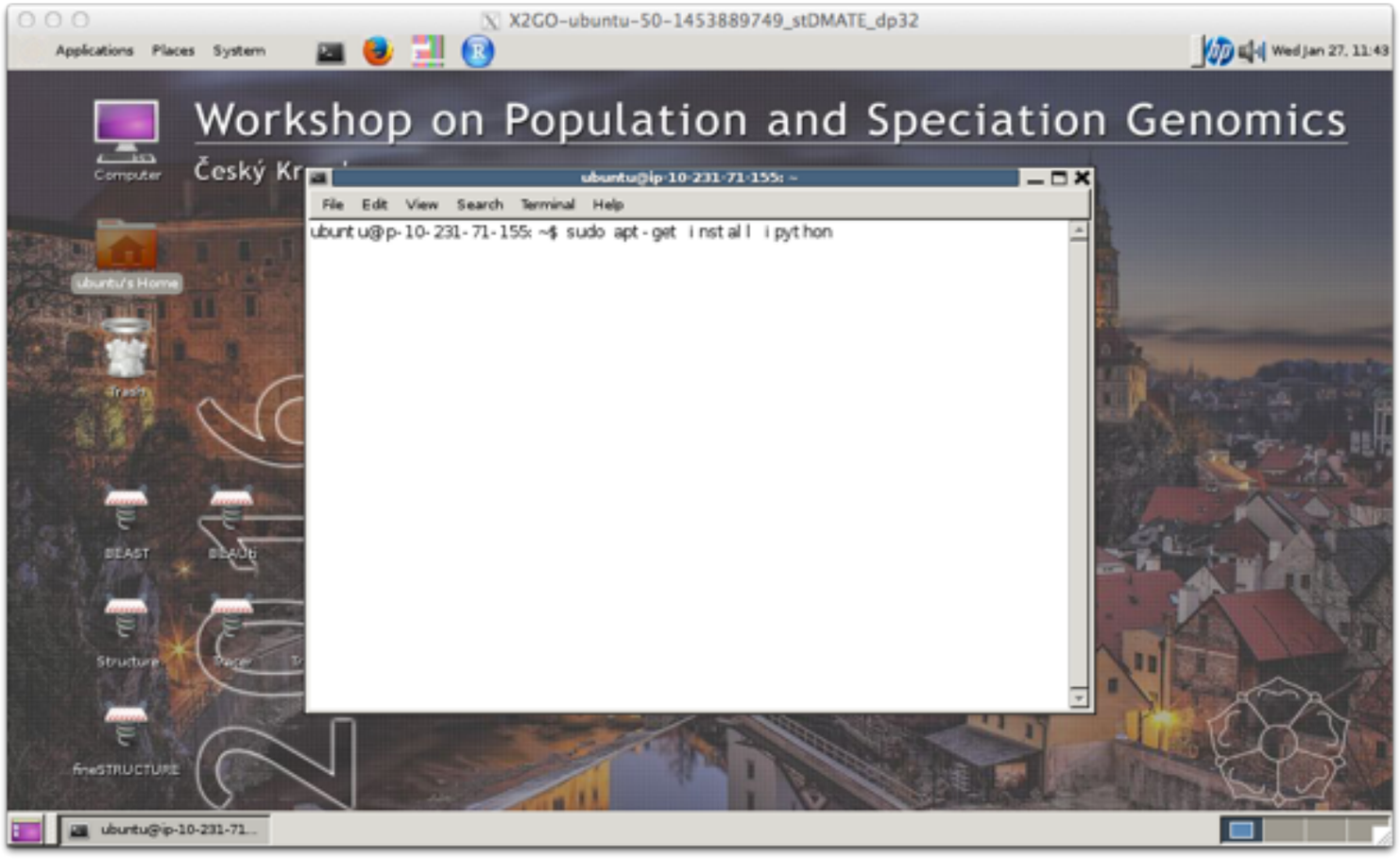
Introduction to Python

Ryan Gutenkunst
Molecular and Cellular Biology
University of Arizona

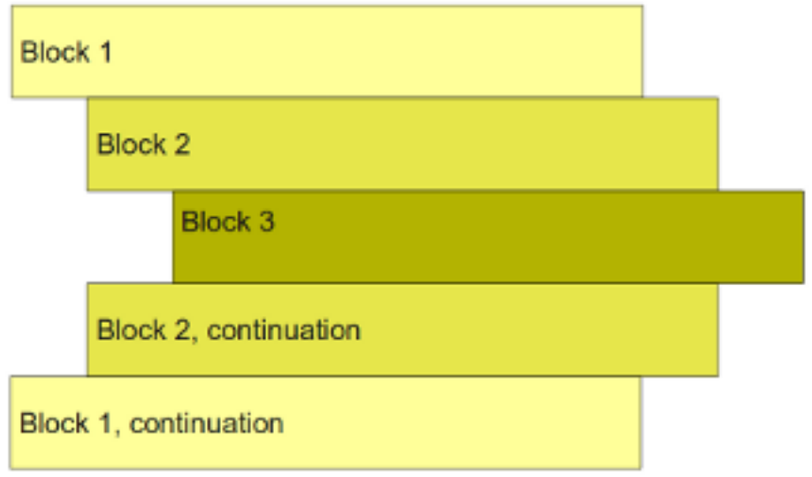
Before we start, fire up your Amazon instance, open a terminal, and enter the command

```
sudo apt-get install ipython
```



Why Python?

- Interpreted language
  Use interactively, for fast development
- Clean syntax
  Indentation matters
- Duck typing
  Easy to write general functions
- Open Source with a large community



Why Python?

- Numpy
  Efficient computation for arrays of data
- SciPy
  Grab bag of scientific algorithms

- Matplotlib
  Matlab-like plotting interface

- Biopython
  Bioinformatics tools

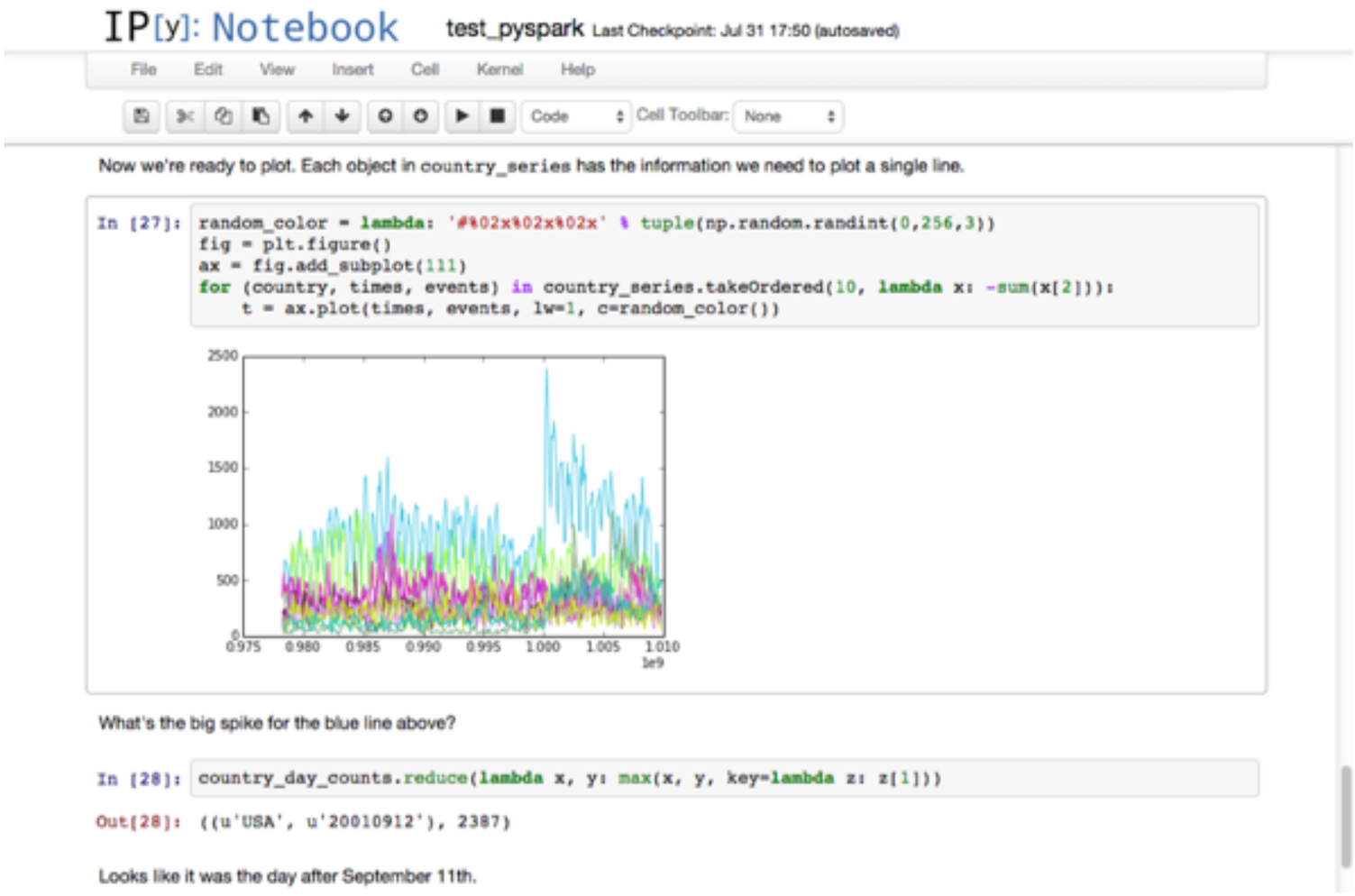
- cPickle
  Simple storage of arbitrary data to disk

Why not Python?

- Python is relatively slow (like R and Matlab)
  - But can speed up by interfacing directly with C
- Installation of libraries can be a headache

iPython

- For me (and you today): a better Python shell
- Start with `ipython --pylab`
  - Tab completion
    - `a = '1'`
    - `a.<tab>`
  - Interactive help
    - `a.upper?`
  - Command history



- The future: iPython notebooks

Python data structures

- Strings
- Lists for sequential data
- Dictionaries (hashes) for mapping keys to values

Strings

- For storing and manipulating textual data
- `a = 'b'`
- `'b'+'c'`
- `'c'.upper()`
- `'a_b_c'.split('_')`
- `'{0}_{1}'.format(1,'d')`
- `'\t'` - Tab character

Lists

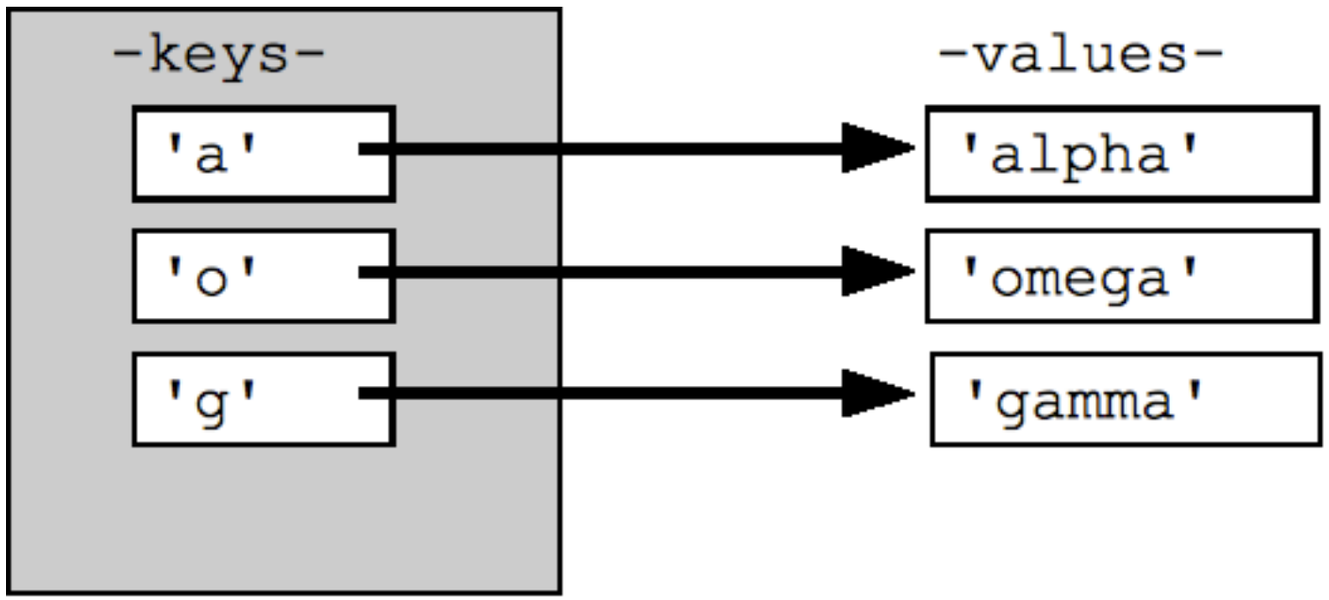
- Ordered sequences of potentially heterogeneous data
- `a = [1,'a']`
- `a`
- `a.append(9)`
- `a`
- `a.extend(['b',4])`
- `len(a)`

Indexing and Slicing Lists

- Accessing elements within lists
- `a`
- `a[0]`
- `a[2:4]`
- `a[:3]`
- `a[-1]`
- `a[1:]`

Dictionaries

- Key-value pairs of potentially heterogeneous data
- `b = {'a':4,'b':[1,2],62:'c'}`
- `b['a']`
- `b['a'] = 2`
- `b`
- `b.keys()`
- `b.values()`
- `b.items()`



Files

- Files read and written sequentially
- `fid = file('small.vcf', 'r')`
- `fid.readline()`

Using libraries

- `import numpy`
- `a = numpy.array([3,4,5])`
- `import numpy as np`
- `b = np.array([5,6,7])`

- `import this`

Plotting with Matplotlib

- `import matplotlib.pyplot as plt`
- `x = np.linspace(0,4*np.pi, 1000)`
- `plt.plot(x, np.sin(x), '-r')`
- `plt.show()`
  Not necessary in iPython, but needed in scripts.

My work style with iPython

- `%run <filename>`
  - Runs code in `filename`, with a clear namespace
- `%run -i <filename>`
  - Runs code in `filename`, with access to all currently defined variables
- So I have an editor window open with my script, which I'm continually re-running as I edit.
- If I have slow steps, I comment out the code that generates them and use `%run -i` to use live data.

nano

- Simple text editor available on most systems.
- Ctrl+o to save files
- Ctrl+x to exit
- If your favorite editor (vim, emacs, etc.) is available, feel free to use it.
- Start editing a new file
  `nano test.py`

Functions

- ```
  def adder(a, b):
          return a+b+2
  ```
- ```
  adder(2,3)
  ```
- ```
  adder(np.array([4,5,6]),
          np.array([-1,2,3]))
  ```
- ```
  adder(np.array([4,5,6]), 2)
  ```
- ```
  adder(np.array([4,5,6,]),
          np.array([-1,2]))
  ```
  ```

Conditionals

- ```
  if 5 < 10:
      print 'hello'
  ```
- ```
  if 5 < 10 and 10 < 7:
      print 'no'
  ```
- ```
  if 5 < 10 or 10 < 7:
      print 'hello'
  ```
  ```

For loop

- ```
  for ii in range(5):
      print ii
  ```
- ```
  for ii,val in enumerate('abcd'):
      print ii, val
  ```
- ```
  for val1,val2 in zip('abcd','wxyz'):
      print val1, val2
  ```
- ```
  for line in file('test.dat'):
      print line
  ```

While loop

- a = 0
- ```
  while a < 9:
      print a
      a = a + 4
  ```
  ```

Exercises

- Two sets of exercises available:
  - DataProcessing.pdf: Parse a frequency spectrum (crudely) from 1000 Genomes Data.
  - Simulation.pdf: Simulate the Wright-Fisher model
- Start with the one that seems most interesting to you.
- Work together!
- Make a new directory, and switch to it.
  ```
  mkdir dadiExercise; cd dadiExercise
  ```
- To get the data on your instance, run
  ```
  wget gutengroup.mcb.arizona.edu/temp/wspg2016.tgz
  tar -xzf wspg2016.tgz
  ```