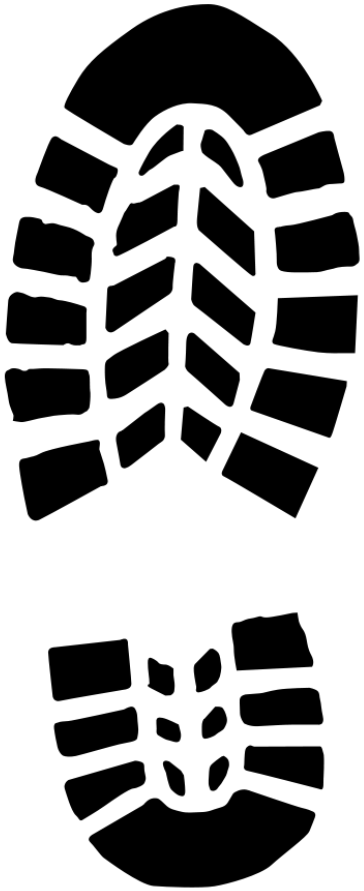

Welcome to

Python 2

Session #3

Michael Purcaro & The GSBS Bootstrappers

February 2014

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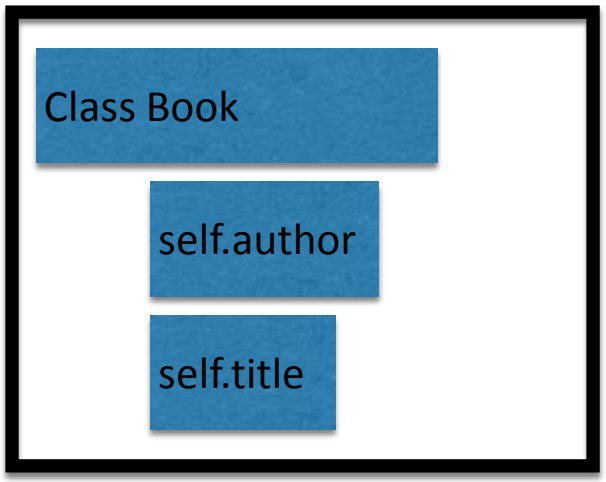
Simple Book Class

```
class Book():
        def __init__(self, title, author):
            self.title = title
            self.author = author

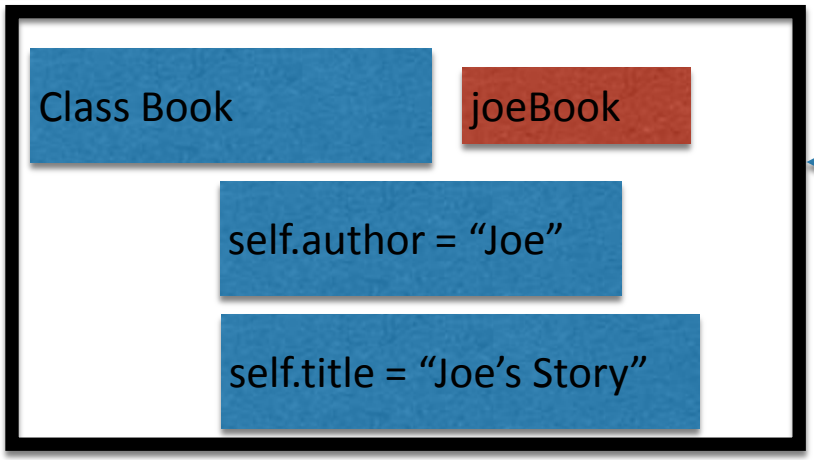
joeBook = Book("Joe", "Joe's Story")
daveBook = Book("Dave", "Dave's Tale")
```

By Nick



Definition

```
class Book():
        def __init__(self, title, author):
            self.title = title
            self.author = author
```



Usage 1

```
joeBook = Book("Joe", "Joe’s Story")
```

Usage 2

```
daveBook = Book("Dave", "Dave’s Tale")
```

By Nick

Bed Record Class

```
1  class bedRecord():
2      def __init__(self, chrom, start, stop):
3              self.chr = chrom
4              self.start = start
5              self.stop = stop
6
7      def getLen(self):
8          return self.stop - self.start
9
10     def doesRecordOverlap(self,otherRecord):
11         return (self.start >= otherRecord.start and self.start < otherRecord.stop)\
12         or (self.stop >= otherRecord.start and self.stop < otherRecord.stop)
13
14 bed1 = bedRecord("chr7", 100050, 100079)
15 bed2 = bedRecord("chr7", 100025, 100060)
16 bed3 = bedRecord("chr7", 100090, 100110)
17
18 print bed1.getLen()
19
20 print bed1.doesRecordOverlap(bed2)
21 print bed1.doesRecordOverlap(bed3)
22
```

By Nick

Bed Record Class

```
1  class bedRecord():
2      def __init__(self, chrom, start, stop):
3              self.chr = chrom
4              self.start = start
5              self.stop = stop
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12         or (self.stop >= otherRecord.start and self.stop < otherRecord.stop)
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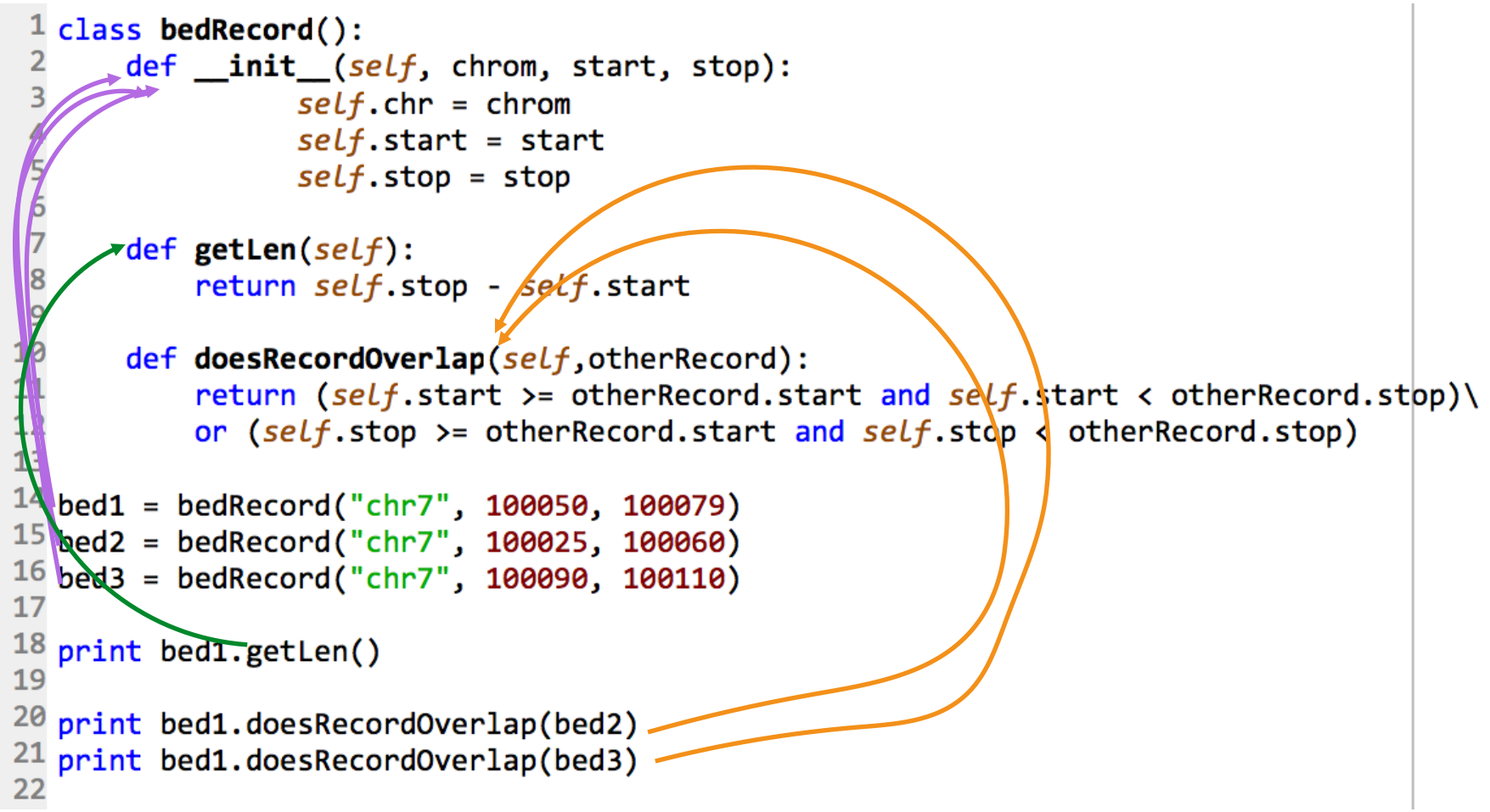
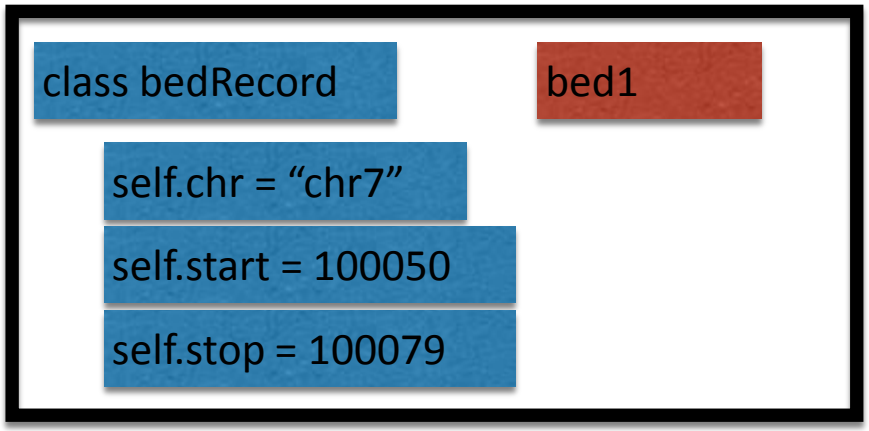
15 bed2 = bedRecord("chr7", 100025, 100060)
16 bed3 = bedRecord("chr7", 100090, 100110)
17
18 print bed1.getLen()
19
20 print bed1.doesRecordOverlap(bed2)
21 print bed1.doesRecordOverlap(bed3)
22
```



By Nick

Class Member Functions




```
14 bed1 = bedRecord("chr7", 100050, 100079)
```

```
7     def getLen(self):
8         return self.stop - self.start
```

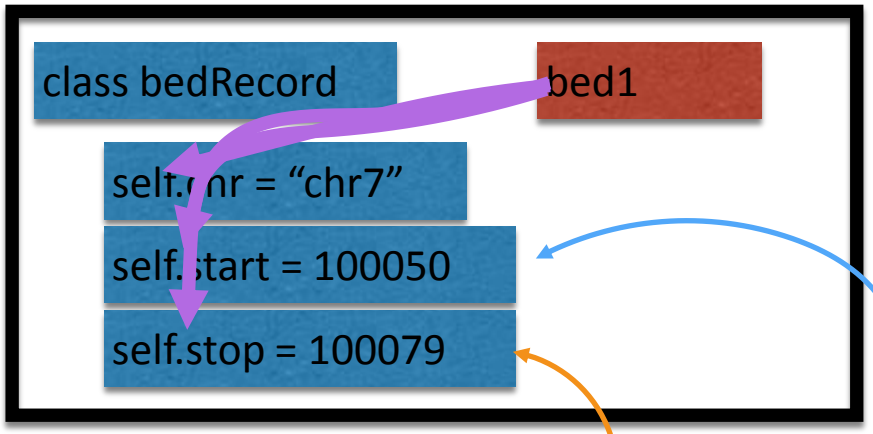
Definition

```
18 print bed1.getLen()
19
```

usage

By Nick

Class Member Functions




```
14 bed1 = bedRecord("chr7", 100050, 100079)
```

```
7     def getLen(self):
8         return self.stop - self.start
```

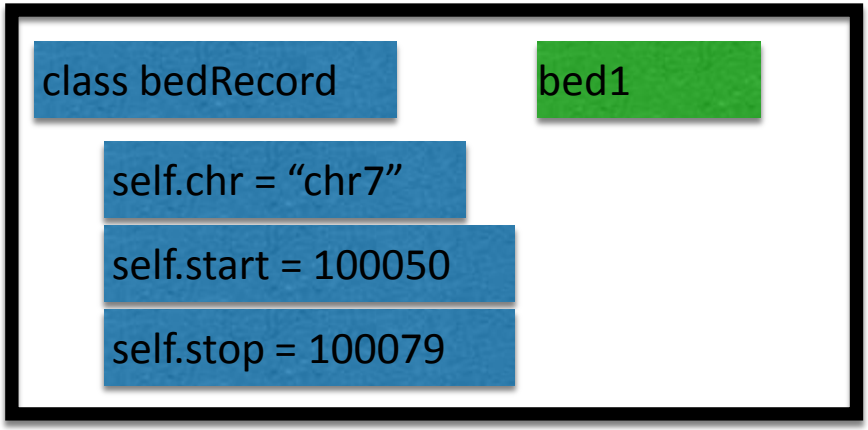
Definition

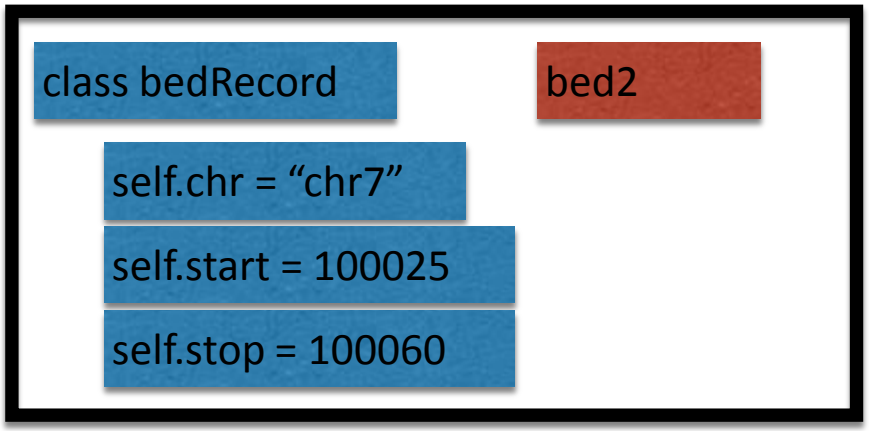
```
18 print bed1.getLen()
19
```

usage

Don’t need to use self when using the member function

By Nick

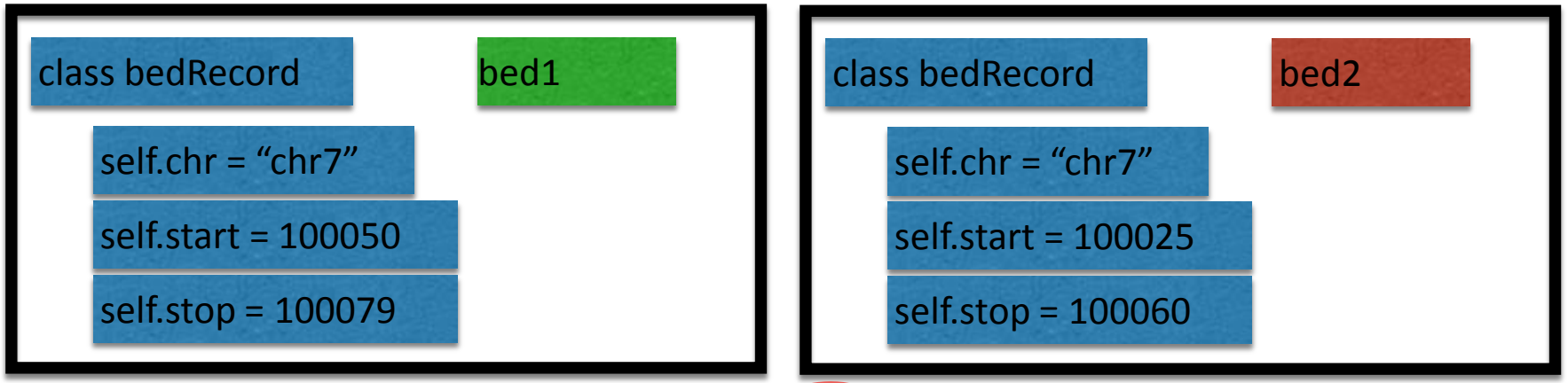





```
10      def doesRecordOverlap(self,otherRecord):
11          return (self.start >= otherRecord.start and self.start < otherRecord.stop)\
12          or (self.stop >= otherRecord.start and self.stop < otherRecord.stop)
13
```

```
20 print bed1.doesRecordOverlap(bed2)
```

By Nick

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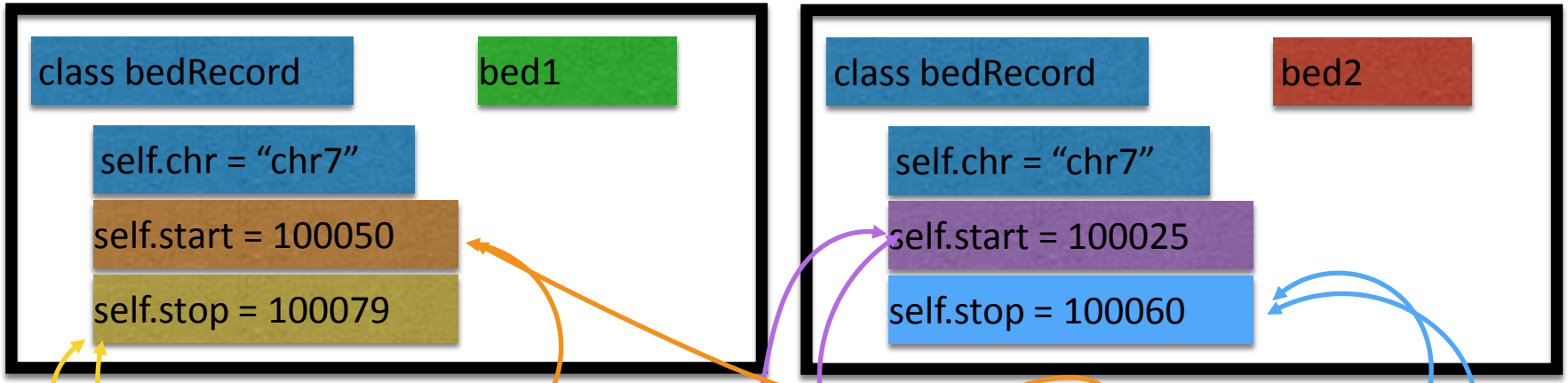
11          return (self.start >= otherRecord.start and self.start < otherRecord.stop)\
12          or (self.stop >= otherRecord.start and self.stop < otherRecord.stop)
13
20  print bed1.doesRecordOverlap(bed2)
```

By Nick




```
10    def doesRecordOverlap(self,otherRecord):
11        return (self.start >= otherRecord.start and self.start < otherRecord.stop)\
12        or (self.stop >= otherRecord.start and self.stop < otherRecord.stop)
13
```

```
20 print bed1.doesRecordOverlap(bed2)
```

By Nick

Extended Exercise 4

- Rework your code from the previous Extended Exercises into a ChipseqData class, similar to

```
class ChipseqData:
    def __init__(self, paths, url):
```

- The class initializer should only download the chipseq data if needed
  - What are the pros/cons of downloading the data during class initialization?
- The class should have a function to return the number of peaks found in a given chromosome
- The class should also have a function to compute the percentage of a given chromosome covered by peaks
- Would a Peak class (that understood how to parse each line of the narrow peak) be useful? Try it!

```
class Paths():
    def __init__(self, lectureNumber):
        self.homeFolder = os.path.abspath(os.path.expanduser("~"))
        self.desktopFolder = os.path.join(self.homeFolder, "Desktop")
        self.python2folder = os.path.join(self.desktopFolder, "python_2")
        lecture = "lecture_" + str(lectureNumber)
        self.lectureFolder = os.path.join(self.python2folder, lecture)
        print "today's lecture folder location will be:", self.lectureFolder
        Utils.mkdir_p(self.lectureFolder)

    def makeFilePath(self, fn):
        return os.path.join(self.lectureFolder, fn)
```

```
class ChipseqData:
    def __init__(self, paths, url):
        self.paths = paths
        self.url = url
        self.fnp = Utils.get_file_if_size_diff(self.url, paths.lectureFolder)

    def getPeaks(self, chr):
        peaks = []
        with open(self.fnp) as f:
            for line in f:
                toks = line.split()
                if chr != toks[0]:
                    continue
                peaks.append(toks)
        return peaks

    def numPeaks(self, chr):
        return len(self.getPeaks(chr))

    def computePercentageChromosomeCovered(self, chr, chromosomeLength):
        peaks = self.getPeaks(chr)
        numBases = 0
        for toks in peaks:
            numBases += int(toks[2]) - int(toks[1])
        return "{0:.2f}%".format(float(numBases) / chromosomeLength * 100)
```

http://bioinfo.umassmed.edu/bootstrappers/bootstrappers-courses/python2/lecture2/lecture2.txt

```
paths = Paths(3)

chipData = ChipseqData(paths,
"http://bib3.umassmed.edu/~purcarom/Python2/Lecture1/ENCFF002C
OQ.narrowPeak")

print "number of peaks on chromosome 7:",
      chipData.numPeaks("chr7")

print "% of chromosome 7 covered by peaks:",
      chipData.computePercentageChromosomeCovered("chr7",
                                                  159138663)
```

Extended Exercise 5

- Build a class “HG19chrSize” that holds chromosome lengths
  - Have its constructor download and parse the file
    - Store chromosome lengths in a dictionary
      - Key of “chromosome name” (i.e. “chr6” or “chrX”)
      - Value of integer
  - Have a class method “length(chrmosomeNum)” that returns the length of the chromosome requested
- Chromosome lengths in:

`http://bioinfo.umassmed.edu/bootstrappers/bootstrappers-courses/python2/lecture1/hg19.chrom.sizes`

```
class HG19chrSize():
    def __init__(self, paths):
        self.paths = paths
        self.url =
"http://bioinfo.umassmed.edu/bootstrappers/bootstrappers-
courses/python2/lecture1/hg19.chrom.sizes"
        fnp = Utils.get_file_if_size_diff(self.url,
paths.lectureFolder)
        self.chrsToLen = {}
        with open(fnp) as f:
            for line in f:
                toks = line.split()
                self.chrsToLen[toks[0]] = int(toks[1])

    def length(self, chr):
        if not chr in self.chrsToLen:
            raise Exception("unknown chromosome: " + chr)
        return self.chrsToLen[chr]
```

Extended Exercise 6

- Goal: Run `numPeak()` and `computePercentageChromosomeCovered()` for chromosomes 1 to 22
  - Store the `numPeak()` output into a dict:
    - `numPeaks = {}`
    - `numPeaks["chr1"] = …`
  - Store the `computePercentageChromosomeCovered()` output in
    - `percChromCovered = {}`

```
numPeaks = {}
percChromCovered = {}

for chrNum in range(1,23):
    chr = "chr" + str(chrNum)

    numPeaks[chr] = chipData.numPeaks(chr)

    percChromCovered[chr] =
chipData.computePercentageChromosomeCovered(chr,
chrLenths.length(chr))

    print chr, numPeaks[chr], percChromCovered[chr]
```

Extended Exercise 7

- Change the ChipseqData class to use Peak class:

```
class Peak:
    def __init__(self, line):
        toks = line.split()
        self.chr = toks[0]
        self.start = int(toks[1])
        self.end = int(toks[2])

    def length(self):
        return self.end - self.start
```

```
class ChipseqData:
    def __init__(self, paths, url):
        self.paths = paths
        self.url = url
        self.fnp =
Utils.get_file_if_size_diff(self.url,
paths.lectureFolder)

    def getPeaks(self, chr):
        peaks = []
        with open(self.fnp) as f:
            for line in f:
                peak = Peak(line)
                if chr != peak.chr:
                    continue
                peaks.append(peak)
        return peaks
```

```
def numPeaks(self, chr):
        return len(self.getPeaks(chr))

def computePercentageChromosomeCovered(self, chr,
                                       chromosomeLength):
        peaks = self.getPeaks(chr)
        numBases = 0
        for peak in peaks:
            numBases += peak.length()
        return "{0:.2f}%".format(float(numBases) /
                    chromosomeLength * 100)
```

Static Class Methods

- Methods that live in a class, but don't need any access to data (via `self`) in that class
- One use: organize miscellaneous functions together

```
class Utils:
    @staticmethod
    def mkdir_p(path):
...
@staticmethod
    def get_file_if_size_diff(url, path):
```

Called without using an object!

```
Utils.mkdir_p(path)
Utils.get_file_if_size_diff(url, path)
```

Building Blocks: list comprehension

- Quick way to build certain kinds of lists

```
a = [x for x in range(10)]
print a

b = [x*x for x in range(10)]
print b

c = [str(x) for x in range(10)]
print c

q = 5
d = [x+q for x in range(10)]
print d
```

Building Blocks: list comprehension

```
a = [x for x in range(10)]
print a
[0, 1, 2, 3, 4, 5, 6, 7, 8, 9]

b = [x*x for x in range(10)]
print b
[0, 1, 4, 9, 16, 25, 36, 49, 64, 81]

c = [str(x) for x in range(10)]
print c
['0', '1', '2', '3', '4', '5', '6', '7', '8', '9']

q = 5
d = [x+q for x in range(10)]
print d
[5, 6, 7, 8, 9, 10, 11, 12, 13, 14]
```

Building Blocks: list comprehension

```
fnp = paths.makeFilePath("ENCFF002COQ.narrowPeak")

with open(fnp) as f:
    allPeaks = [Peak(x) for x in f]

print len(allPeaks)
```

Building Blocks: list comprehension

```
fnp = paths.makeFilePath("ENCFF002COQ.narrowPeak")

with open(fnp) as f:
    allPeaks = [Peak(x) for x in f]

print len(allPeaks)
55551
```

Building Blocks: map

- Another way to build a list
- Applies a function to every element in a list

```
a = map(lambda x: x, range(10))
print a

b = map(lambda x: x*x, range(10))
print b

c = map(str, range(10))
print c

q = 5
d = map(lambda x: x+q, range(10))
print d
```

Building Blocks: map

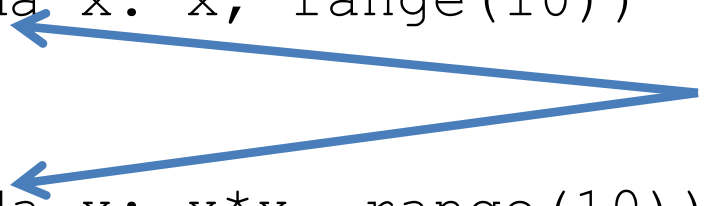
- Another way to build a list
- Applies a function to every element in a list

```
a = map(lambda x: x, range(10))
print a

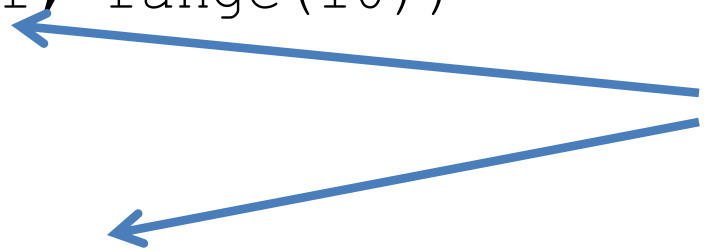
b = map(lambda x: x*x, range(10))
print b

c = map(str, range(10))
print c

q = 5
d = map(lambda x: x+q, range(10))
print d
```



"anonymous" function!
➔ Function with no name



For examples on this slide, map assumes the function takes only 1 argument

Building Blocks: map

```
a = map(lambda x: x, range(10))
print a
[0, 1, 2, 3, 4, 5, 6, 7, 8, 9]

b = map(lambda x: x*x, range(10))
print b
[0, 1, 4, 9, 16, 25, 36, 49, 64, 81]

c = map(str, range(10))
print c
['0', '1', '2', '3', '4', '5', '6', '7', '8', '9']

q = 5
d = map(lambda x: x+q, range(10))
print d
[5, 6, 7, 8, 9, 10, 11, 12, 13, 14]
```

Building Blocks: map

```
fnp = paths.makeFilePath("ENCFF002COQ.narrowPeak")

with open(fnp) as f:
    allPeaks = map(Peak, f)

print len(allPeaks)
```

Building Blocks: map

```
fnp = paths.makeFilePath("ENCFF002COQ.narrowPeak")


with open(fnp) as f:
    allPeaks = map(Peak, f)


print len(allPeaks)
55551
```

Homework #1

- Work through these problems from http://rosalind.info/problems/list-view/

- DNA Counting DNA Nucleotides
- RNA Transcribing DNA into RNA
- REVC Complementing a Strand of DNA
- GC Computing GC Content
- HAMM Counting Point Mutations
- SPLC RNA Splicing
- PROT Translating RNA into Protein
- SUBS Finding a Motif in DNA
- PRTM Calculating Protein Mass
- REVP Locating Restriction Sites

Review on February 12, 2015