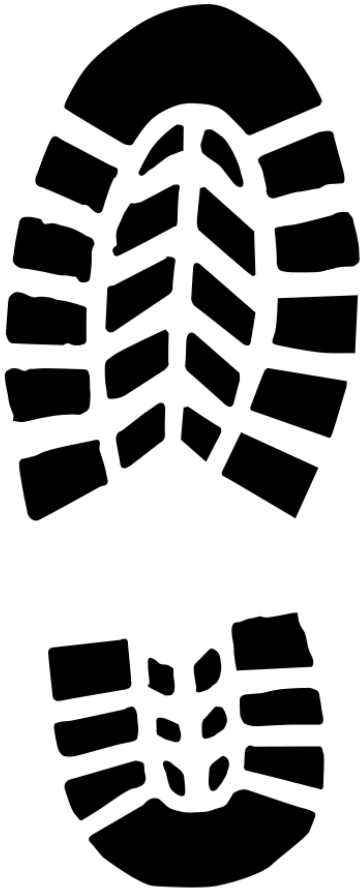


Welcome to

Python 2

Session #3

Michael Purcaro & The GSBS Bootstrappers

February 2014

michael.purcaro@umassmed.edu

Building Blocks: Classes

- Strings, dictionary, defaultdict, set are all examples of classes
- In an ideal world, a class contains
  - data (numbers, strings, lists, other classes, etc.)
  - the functions allowed to manipulate the data
- Provides further mechanisms to give code structure
  - Allows data and concepts to be encapsulated (i.e. hidden or only occur in one place)

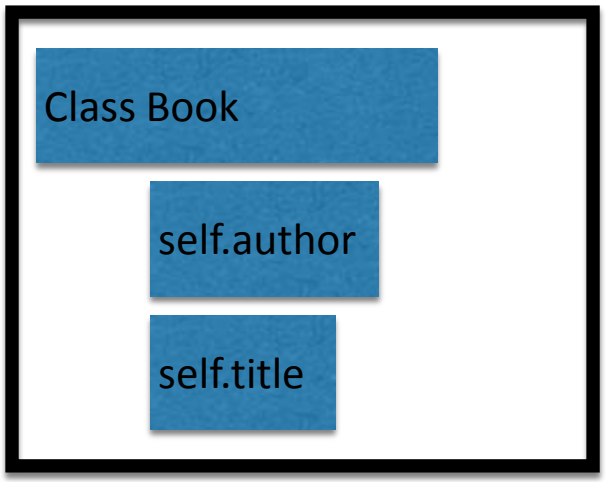
Classes and Objects

- In object-oriented programming, a “class” is the code that defines
  - the class variables
  - the functions allowed to operate on those class variables
  - No memory taken up
  - *Like the abstract concept of a book*
- An “object” is an instance of a class
  - Memory will be allocated for the variables in the object
  - *Like an actual book*

Simple Book Class

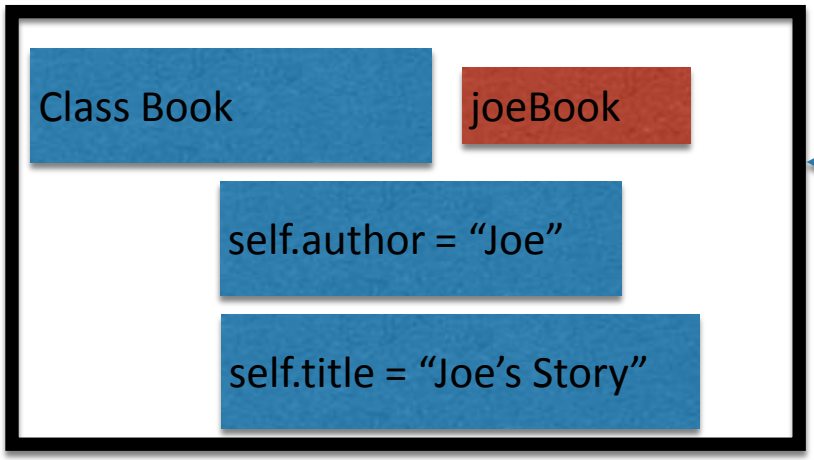
```
class Book():
        def __init__(self, title, author):
            self.title = title
            self.author = author

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

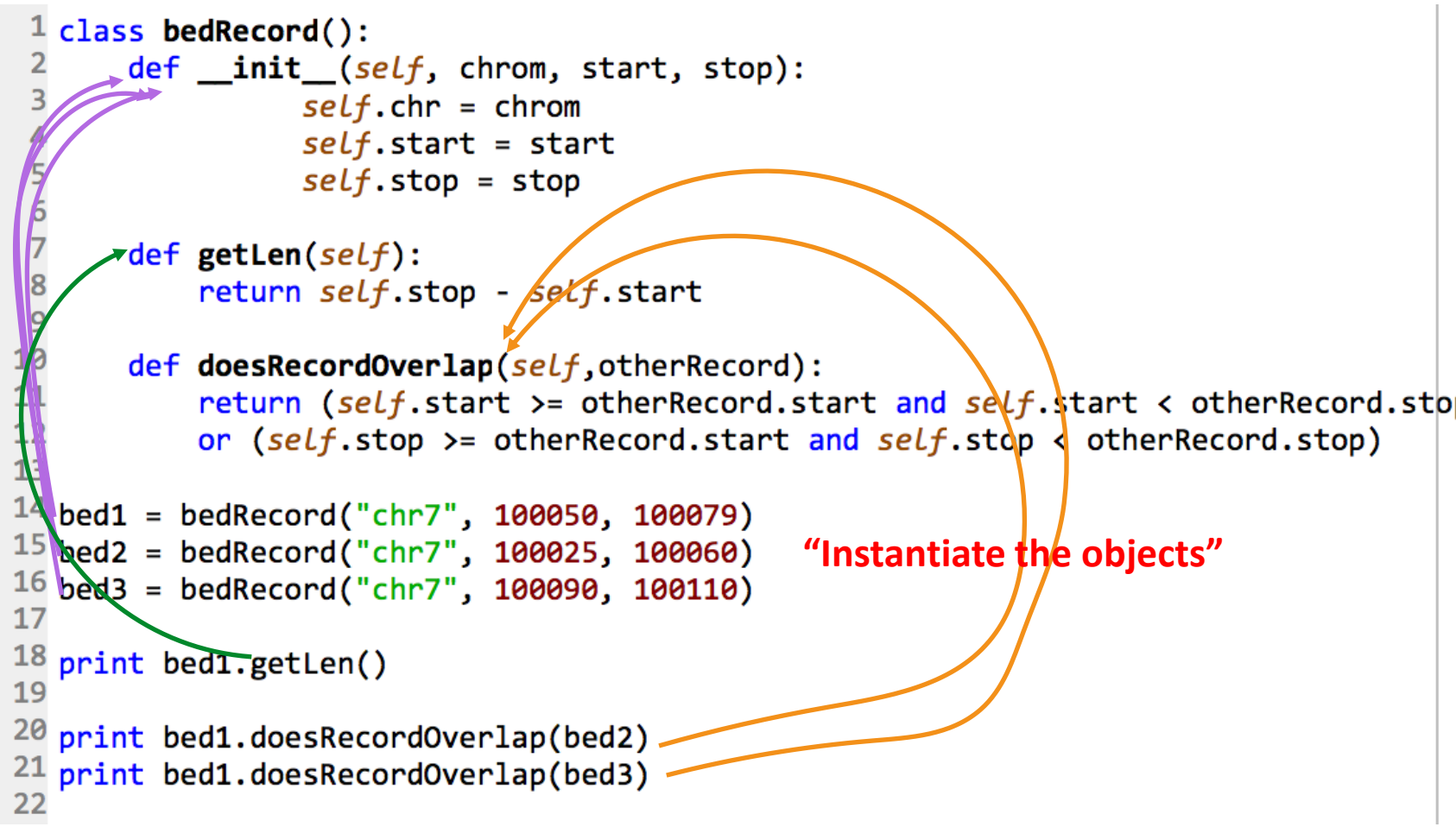
```
1  class bedRecord():
2      def __init__(self, chrom, start, stop):
3              self.chr = chrom
4              self.start = start
5              self.stop = stop
6
7      def getLen(self):
8          return self.stop - self.start
9
10     def doesRecordOverlap(self,otherRecord):
11         return (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
```

“Instantiate the objects”

By Nick

Bed Record Class

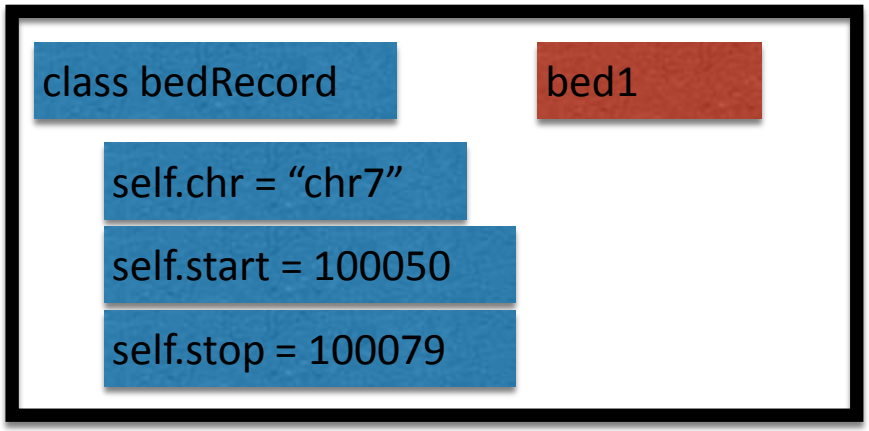
```
1  class bedRecord():
2      def __init__(self, chrom, start, stop):
3              self.chr = chrom
4              self.start = start
5              self.stop = stop
6
7      def getLen(self):
8          return self.stop - self.start
9
10     def doesRecordOverlap(self,otherRecord):
11         return (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
```



“Instantiate the objects”

By Nick

Instance Methods




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

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

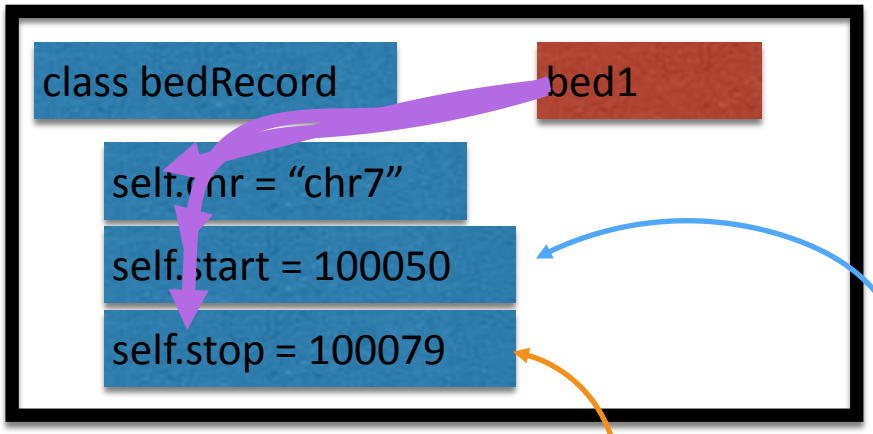
Definition

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

usage

By Nick

Instance Methods




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

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

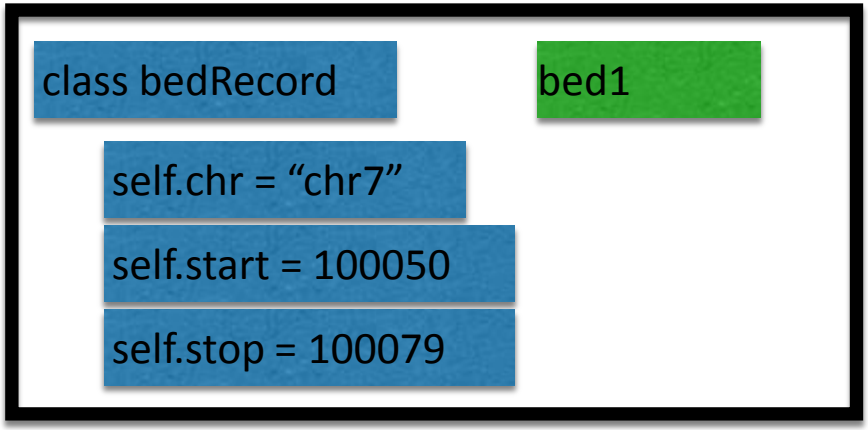
Definition

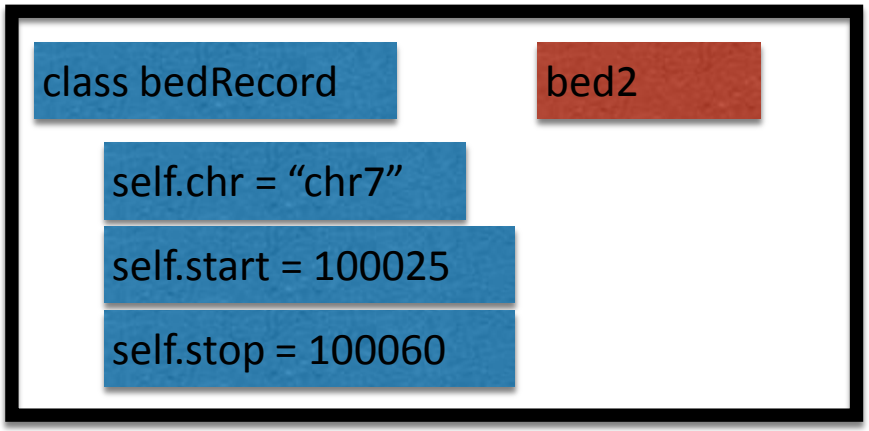
```
18 print bed1.getLen()
19
```

usage

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

By Nick

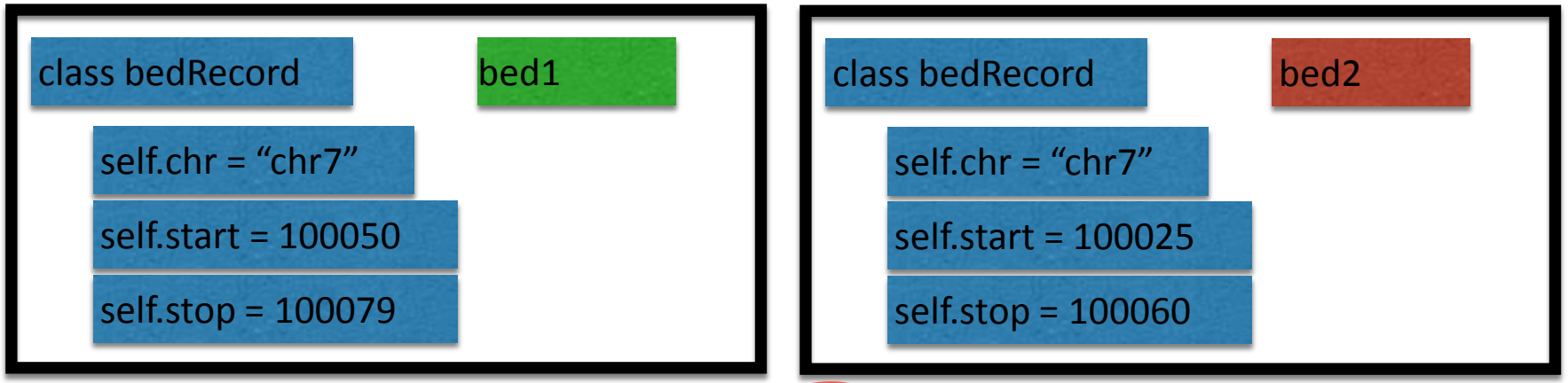





```
10      def doesRecordOverlap(self,otherRecord):
11          return (self.start >= otherRecord.start and self.start < otherRecord.stop)\
12          or (self.stop >= otherRecord.start and self.stop < otherRecord.stop)
13
```

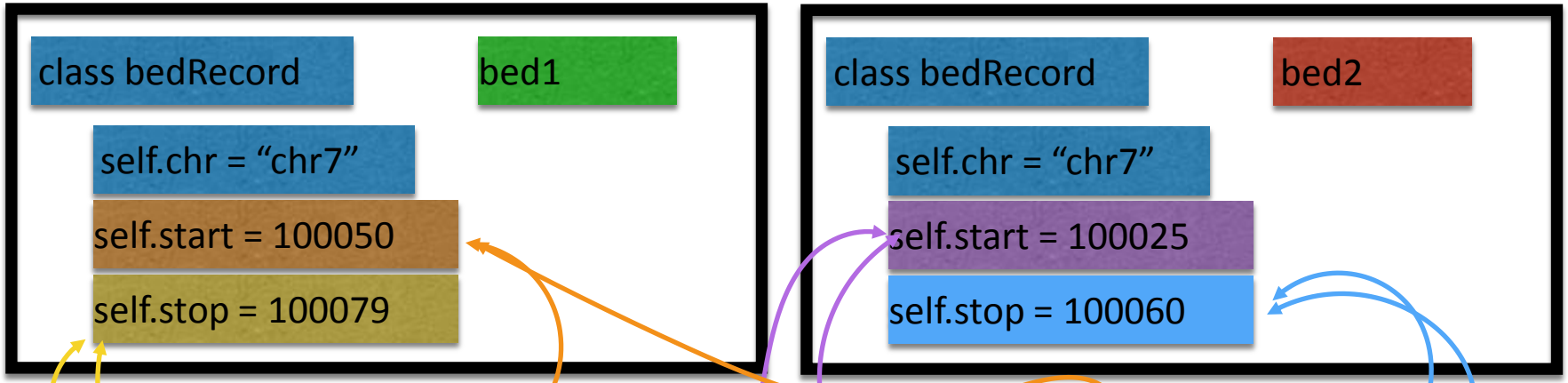
```
20 print bed1.doesRecordOverlap(bed2)
```

By Nick




```
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




```
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 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)

    def makeRawDataPath(self, fn):...

    def makePreprocessDataPath(self, fn):...

    def makeOutputPath(self, 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 length file url:

`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 dictionary:

    ```
    numPeaks = {}
    numPeaks["chr1"] = …
    ```

  - Store the `computePercentageChromosomeCovered()` output in another dictionary:

    ```
    percChromCovered = {}
    ```

```
chrLengths = HG19chrSize(paths)

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]
```

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