



Welcome to

Python 2

Session #6

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Problem 7: RNA Splicing

- After identifying the exons and introns of an RNA string, we only need to delete the introns and concatenate the exons to form a new string ready for translation.
- Given: A DNA string s and a collection
 of substrings of s acting as introns. (All strings are
 given in FASTA format.)
- Return: A protein string resulting from transcribing and translating the exons of s.
- Note: Only one solution will exist for the dataset provided.

Building Blocks: list comprehension

 Quick way to build lists under certain situations

```
v = []
for i in range(10):
    v.append(i)

v = [x for x in range(10)]
```

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 \text{ for } x \text{ in range}(10)]
print d
```

- 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
```

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

```
a = map(lambda x: x, range(10))
print a
                                         "anonymous" function!
                                         Function with no name
b = map(lambda x: x*x, range(10))
print b
c = map(str, range(10))
print c
                                      For examples on this slide, map
                                      assumes the function takes only
                                      1 argument
a = 5
d = map(lambda x: x+q, range(10))
print d
```

print chrs

 How would we extract 4-digit number from this sequence?

abcd1234dsfasdfa5643asdfasef

Try extracting the numbers; make sure the code also works for:

sadfaweqwe1235lkaf9843asdfaefaef

- An alternative way to extract the 4-digit number is to use regular expressions
 - We specify a <u>pattern</u> that we wish to match

To match a letter (a-z and A-Z)
 \D

- To match any two letters \D\D
- To match a digit (0-9)\d
- To match any 1 letter and any 1 digit (0-9)
 \D\d

To match any character

•

To match 0 or more times, add

*

To match 1 or more times, add

+

 Example: to match any number of characters, then a digit

*\d

To find out if a string matches a pattern, you can do:

```
import re
if re.search(r"<your pattern", variableName):
        # Successful match
else:
        # Match attempt failed</pre>
```

For example, to see if the string has two letters, two digits, and then two letters:

```
if re.search(r"\D\D\d\d\D\D", "aa22aa"):
    print "matched 2 letters, 2 digits, 2 letters"
else:
    print "could not match the pattern"
```

To denote what to copy out, surround with parenthesis

DD(dd)DD

Extract the number:

```
match = re.search(r"\D\D(\d\d)\D\D", "aa22aa")
if match:
    print "found number!", int(match.group(1))
else:
    print "no number found!"
```

import re

s = "abcd1234dsfasdfa5643asdfasef"

Write the code to extract two numbers from the above string

import re

```
s = "the1234next5643word"
```

Write the code to extract the words from the above string

- Many other patterns possible!
 - See https://docs.python.org/2/library/re.html

Other Exercises and Info

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):
```

```
Called without using an object!
Utils.mkdir_p(path)
Utils.get file if size diff(url, path)
```

@staticmethod
 def get_file_if_size_diff(url, path):

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)
```

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
```

```
fnp = paths.makeFilePath("ENCFF002CoQ.narrowPeak")
with open(fnp) as f:
    allPeaks = map(Peak, f)
print len(allPeaks)
```

```
fnp = paths.makeFilePath("ENCFF002COQ.narrowPeak")
with open (fnp) as f:
     allPeaks = map(Peak, f)
print len(allPeaks)
55551
```