Algorithmic Approaches for Biological Data, Lecture #6

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Outline

Computing With Strings

- String variables

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- Simple string processing

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- Built-in string methods

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- Strings as Lists, Lists as Strings

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Computing With Strings

- String variables
- Simple string processing
- Built-in string methods
- Break
- Strings as Lists, Lists as Strings
- Using Files

String Variables

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- Concatenating ('adding') strings:
  ```
  print "message"+"message"
  print message+"message"
  print message+message
  ```
- Repetition operator:
  ```
  print 3*s
  ```

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- `s[start:stop]` gives the substring that begins at `start` and goes up to but not including the stop.

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- `s[start:stop]` gives the substring that begins at `start` and goes up to but not including the stop.
- Can also have a `step`: `s[start:stop:step]`.

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- `s[start:stop]` gives the substring that begins at `start` and goes up to but not including the stop.
- Can also have a `step`: `s[start:stop:step]`.
- `s[:x]` is the substring of `s` starting at 0 and going up to, but not including the element with index `x`.

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- Examples:
  - `s[-2]` is `"n"`
  - `s[0:-1]` is `"I love Python"`
  - `s[-3:]` is `"on!"`

Group Work

```
s = "I love Python!"
message = "Hello"
first = "Teddy"

last = "Roosevelt"
```

In pairs/triples, work out (and then try at the shell or pythonTutor):

1. ```
   lll = s[2:6]
   print lll*3
   print lll+first*5
   ```
2. ```
   for c in message:
       print c
   ```
3. ```
   for i in range(5):
       print message[i]
   ```
4. ```
   for i in range(4,-1,-1):
       print message[i]
   ```
5. ```
   print message[-1::-1]
   ```
6. ```
   for c in message[-1::-1]:
       print c
   ```
7. ```
   for i in range(60):
           print "-",
       print
   ```
9. ```
   repeat = ""
   for i in range(20):
       repeat = repeat + "TA"
   ```
10. ```
    prefix = "outputRun"
    suffix = ".nex"
    fileNames = []
    for i in range(10):
        fileNames.append(prefix + str(i) + suffix)
    ```
11. ```
    prefix = "http://rest.ensemblgenomes.org/homology/id/"
    suffix = "?compara=pan_homology&content-type=application/json"
    genes = ["AT3G52260","AT3G52240","AT3G52610", "AT3G52150"]
    fileNames = []
    for g in genes:
        fileNames.append(prefix + g + suffix)
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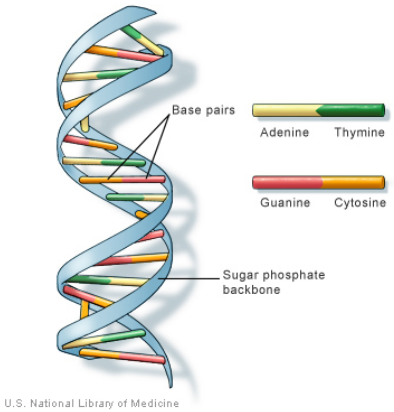
  - `s.replace(old, new)` returns string with all occurrences of `old` with `new`.
  - `s.strip()` returns string with leading and trailing whitespace removed.

Group Work



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- Using the string methods, write Python code that counts the number of 'A','C','G', and 'T' in a string.

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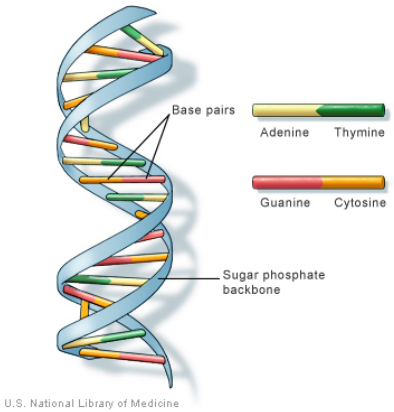

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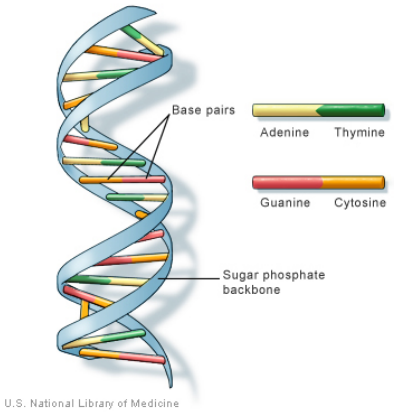

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Example:

```
>Rosalind_6404
CCTGCGGAAGATCGGCACTAGAATAGCCAGAACCGTTTCTCTGAGGCTTCCGGCCTTCCC
TCCCACTAATAATTCTGAGG
>Rosalind_5959
CCATCGGTAGCGCATCCTTAGTCCAATTAAGTCCCTATCCAGGCGCTCCGCCGAAGGTCT
ATATCCATTTGTCAGCAGACACGC
>Rosalind_0808
CCACCCTCGTGGTATGGCTAGGCATTCAGGAACCGGAGAACGCTTCAGACCAGCCCGGAC
TGGGAACCTGCGGGCAGTAGGTGGAAT
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Break

Strings as Lists, Lists as Strings

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  - Demo at shell.

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  specimen = "DOT 84 FLUID 11383, Ceyx lepidus collectoris, Solomon
  Islands, New Georgia Group, Vella Lavella Island, Oula River camp,
  , , 07 47 30 S, 156 37 30 E, Paul R. Sweet, 7-May-04,,PRS-2672,
  Tissue Fluid"

  fields = specimen.split(",")
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  fields = specimen.split('\t')
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- Converting comma-separated to tab-separated:
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- Converting comma-separated to tab-separated:
  ```
  fields = specimen.split(",")
  specTab = '\t'.join(fields)
  ```
  ```

Files

infile.txt
Hello! This is a test. 123

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- Write a program will double space a file.
- Write a program that asks the user for a input and output file. Your program should copy the contents of the input file to the output and number the lines.
- Write a program that takes as input a FASTA file and prints out the number of sequences in the file.

Recap

(Image by Ron Dunn)

- Lecture Wednesday at 1pm.

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