

Strings

Genome 559: Introduction to Statistical
and Computational Genomics
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Strings

- A string is a sequence of characters.
- In Python, strings start and end with single or double quotes (they are equivalent but they have to match).

```
>>> s = "foo"
```

```
>>> print s
```

```
foo
```

```
>>> s = 'Foo'
```

```
>>> print s
```

```
Foo
```

```
>>> s = "foo'
```

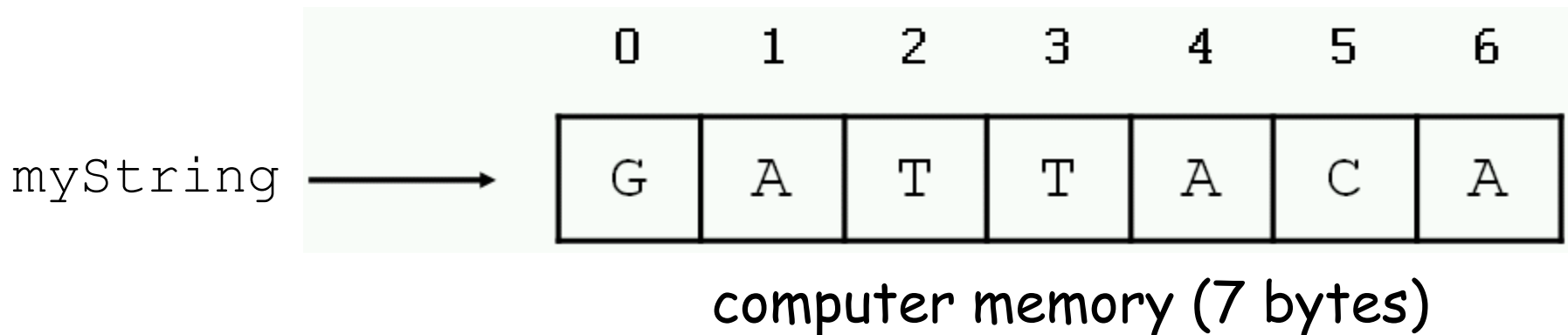
```
SyntaxError: EOL while scanning string literal
```

(EOL means end-of-line)

Defining strings

- Each string is stored in the computer's memory as a list (array) of characters.

```
>>> myString = "GATTACA"
```



How many bytes are needed to store the human genome? (3 billion nucleotides)

Accessing single characters

- You can access individual characters by using indices in square brackets.

```
>>> myString = "GATTACA"
```

```
>>> myString[0]
```

```
'G'
```

```
>>> myString[2]
```

```
'T'
```

```
>>> myString[-1]
```

```
'A'
```

```
>>> myString[-2]
```

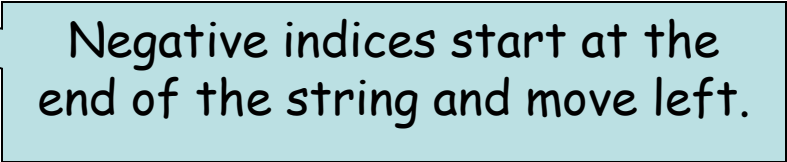
```
'C'
```

```
>>> myString[7]
```

```
Traceback (most recent call last):
```

```
  File "<stdin>", line 1, in ?
```

```
IndexError: string index out of range
```



Negative indices start at the end of the string and move left.

Accessing substrings

```
>>> myString = "GATTACA"
```

```
>>> myString[1:3]
```

```
'AT'
```

```
>>> myString[:3]
```

```
'GAT'
```

```
>>> myString[4:]
```

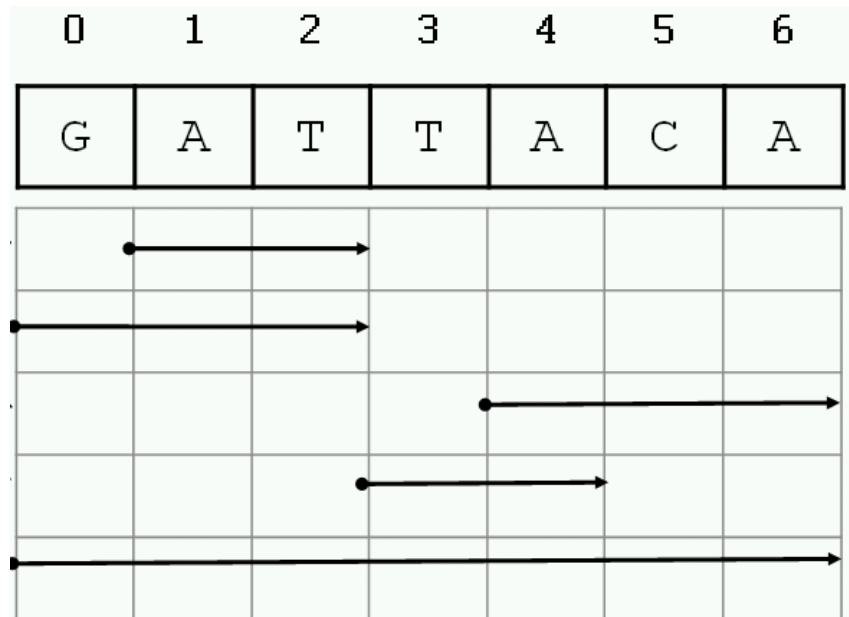
```
'ACA'
```

```
>>> myString[3:5]
```

```
'TA'
```

```
>>> myString[:]
```

```
'GATTACA'
```



notice that the length of the returned string [x:y] is $y - x$

Special characters

- The backslash is used to introduce a special character.

```
>>> print "He said "Wow!""
SyntaxError: invalid syntax
>>> print "He said, \"Wow!\""
He said "Wow!"
>>> print "He said:\nWow!"
He said:
Wow!
```

Escape sequence	Meaning
\\	Backslash
\'	Single quote
\"	Double quote
\n	Newline
\t	Tab

More string functionality

```
>>> len("GATTACA")
```

← Length

```
7
```

```
>>> print "GAT" + "TACA"
```

← Concatenation

```
GATTACA
```

```
>>> print "A" * 10
```

← Repeat

```
AAAAAAAAAAAA
```

```
>>> "GAT" in "GATTACA"
```

(you can read this as "is *GAT* in *GATTACA*")

```
True
```

```
>>> "AGT" in "GATTACA"
```

← Substring tests

```
False
```

String methods

- In Python, a method is a function that is defined with respect to a particular object.
- The syntax is:

object.method(arguments)

```
>>> dna = "ACGT"
```

```
>>> dna.find("T")
```

```
3 ←———— the first position where "T" appears
```


String methods

```
>>> s = "GATTACA"
>>> s.find("ATT")
1
>>> s.count("T")
2
>>> s.lower()
'gattaca'
>>> s.upper()
'GATTACA'
>>> s.replace("G", "U")
'UATTACA'
>>> s.replace("C", "U")
'GATTAUA'
>>> s.replace("AT", "**")
'G**TACA'
>>> s.startswith("G")
True
>>> s.startswith("g")
False
```

Function with no arguments

Function with two arguments

Strings are immutable

- Strings cannot be modified; instead, create a new string from the old one.

```
>>> s = "GATTACA"
```

```
>>> s[0] = "R"
```

```
Traceback (most recent call last):
```

```
  File "<stdin>", line 1, in ?
```

```
TypeError: 'str' object doesn't support item assignment
```

```
>>> s = "R" + s[1:]
```

```
>>> s
```

```
'RATTACA'
```

```
>>> s = s.replace("T", "B")
```

```
>>> s
```

```
'RABBACA'
```

```
>>> s = s.replace("ACA", "I")
```

```
>>> s
```

```
'RABBI'
```

Strings are immutable

- String methods do not modify the string; they return a new string.

```
>>> seq = "ACGT"  
>>> seq.replace("A", "G")  
'GCGT'  
>>> print seq  
ACGT
```

```
>>> seq = "ACGT"  
>>> new_seq = seq.replace("A", "G")  
>>> print new_seq  
GCGT
```

String summary

Basic string operations:

S = "AATTGG"

s1 + s2

s2 * 3

s2[i]

s2[x:y]

len(S)

int(S)

float(S)

assignment - or use single quotes ' '

concatenate

repeat string

get character at position 'i'

get a substring

get length of string

turn a string into an integer

turn a string into a floating point decimal number

Methods:

S.upper()

S.lower()

S.count(substring)

S.replace(old,new)

S.find(substring)

S.startswith(substring)

S.endswith(substring)

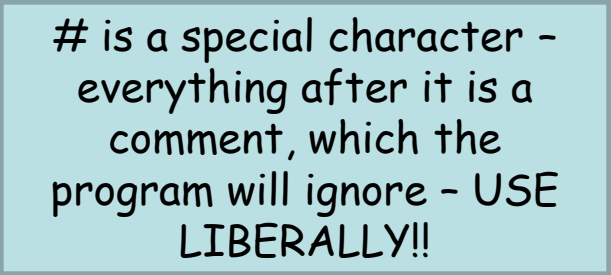
Printing:

print var1, var2, var3

print "text", var1, "text"

print multiple variables

print a combination of explicit text (strings) and variables



is a special character -
everything after it is a
comment, which the
program will ignore - USE
LIBERALLY!!

Sample problem #1

- Write a program called `dna2rna.py` that reads a DNA sequence from the first command line argument and prints it as an RNA sequence. Make sure it retains the case of the input.

```
> python dna2rna.py ACTCAGT
```

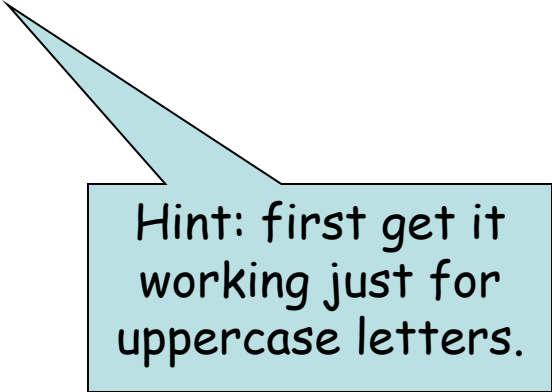
```
ACUCAGU
```

```
> python dna2rna.py actcagt
```

```
acucagu
```

```
> python dna2rna.py ACTCagt
```

```
ACUCagu
```



Hint: first get it working just for uppercase letters.

Two solutions

```
import sys
seq = sys.argv[1]
new_seq = seq.replace("T", "U")
newer_seq = new_seq.replace("t", "u")
print newer_seq
```

OR

```
import sys
print sys.argv[1]
```

(to be continued)

Two solutions

```
import sys
seq = sys.argv[1]
new_seq = seq.replace("T", "U")
newer_seq = new_seq.replace("t", "u")
print newer_seq
```

```
import sys
print sys.argv[1].replace("T", "U")
```

(to be continued)

Two solutions

```
import sys
seq = sys.argv[1]
new_seq = seq.replace("T", "U")
newer_seq = new_seq.replace("t", "u")
print newer_seq
```

```
import sys
print sys.argv[1].replace("T", "U").replace("t", "u")
```

- It is legal (but not always desirable) to chain together multiple methods on a single line.

Sample problem #2

- Write a program `get-codons.py` that reads the first command line argument as a DNA sequence and prints the first three codons, one per line, in uppercase letters.

```
> python get-codons.py TTGCAGTCG
```

```
TTG
```

```
CAG
```

```
TCG
```

```
> python get-codons.py TTGCAGTCGATC
```

```
TTG
```

```
CAG
```

```
TCG
```

```
> python get-codons.py tcgatcgac
```

```
TCG
```

```
ATC
```

```
GAC
```

(challenge - print the codons on one line separated by spaces)

Solution #2

```
# program to print the first 3 codons from a DNA
# sequence given as the first command-line argument
import sys
seq = sys.argv[1] # get first argument
up_seq = seq.upper() # convert to upper case
print up_seq[0:3] # print first 3 characters
print up_seq[3:6] # next 3
print up_seq[6:9] # next 3
```

These comments are simple, but when you write more complex programs good comments will make a huge difference in making your code understandable (both to you and others).

Sample problem #3 (optional)

- Write a program that reads a protein sequence as a command line argument and prints the location of the first cysteine residue (C).

```
> python find-cysteine.py
```

```
MNDLSGKTVIITGGARGLGAEAARQAVAAGARVVLADVLDEEGAATARELGDAARYQHLDVTI  
EEDWQRVCAYAREEFGSVDGL 70
```

```
> python find-cysteine.py
```

```
MNDLSGKTVIITGGARGLGAEAARQAVAAGARVVLADVLDEEGAATARELGDAARYQHLDVTI  
EEDWQRVVAYAREEFGSVDGL -1
```

Solution #3

```
import sys
protein = sys.argv[1]
upper_protein = protein.upper()
print upper_protein.find("C")
```

Challenge problem

- Write a program `get-codons2.py` that reads the first command-line argument as a DNA sequence and the second argument as the frame, then prints the first three codons on one line separated by spaces.

```
> python get-codons2.py TTGCAGTCGAG 0
```

```
TTG CAG TCG
```

```
> python get-codons2.py TTGCAGTCGAG 1
```

```
TGC AGT CGA
```

```
> python get-codons2.py TTGCAGTCGAG 2
```

```
GCA GTC GAG
```

Challenge solution

```
import sys
seq = sys.argv[1]
frame = int(sys.argv[2])
seq = seq.upper()
c1 = seq[frame:frame+3]
c2 = seq[frame+3:frame+6]
c2 = seq[frame+6:frame+9]
print c1, c2, c3
```

Reading

- Chapter 8 of *Python for Software Design* by Downey.

