Overview

day one

0. introduction
1. text output and manipulation
2. reading and writing files

today

3. lists and loops
4. writing functions

day three

5. conditional statements
6. dictionaries

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7. files, programs and user input
8. biopython

day five

hands on training

feedback and discussion

Etherpad for today:
http://python-from-scratch.pad.spline.de/2

This course (apart from chapter 8) is based on the book "**Python for Biologists**":

http://pythonforbiologists.com/

python™ from scratch

A primer for scientists working with Next-Generation-Sequencing data

CHAPTER 3

lists and loops

Chapter 3: lists and loops

lists and loops help us deal with these issues:

- performing tasks repeatedly for multiple, similar objects
- usually not possible to know the number of data items
- necessary for dealing with large datasets

Dealing with repetitive tasks

often the **same task** needs to be performed **repeatedly** for a **set of similar objects** with only slight variation for each object

lists can hold a variable number of elements

loops enable running the same commands multiple times

Creating lists and retrieving elements

- creating lists:

```
apes = ["Homo","Pan","Gorilla"]
conserved_sites = [24,56,132]
```

- each list now has 3 elements
- to get an element from a list, use its index like this:

```
print(apes[0])
site = conserved_sites[2]
```

- to get the index of an element use the index method:

```
chimp_index = apes.index("Pan")
# chimp_index is now 1
```

Splitting a string into a list

If a string is structured by separators, we can use the **split** method to create a list from it:

```
>>> data_text = "comma,separated,values"
>>> data_list = data_text.split(",")
>>> data_list
["comma","separated","values"]
```

The separator is not important, though:

```
>>> sentence = "This is a sentence"
>>> sentence.split(" ")
["This","is","a","sentence"]
```

Use the split method when dealing with **CSV files**

Accessing list elements

- directly access the last element of a list by index -1:

```
last_ape = apes[-1]
```

- retrieve a sequence of elements by start and end index:

```
ranks = ["kingdom","phylum","class","order","family"]
lower_ranks = ranks[2:5]
# lower ranks are class, order and family
```

(start is inclusive, end is exclusive)

- remember this from strings?
that's right – **strings behave a lot like lists**!

Modifying lists

- add **one** element to a list with the append method:

```
apes = ["Homo","Pan","Gorilla"]
apes.append("Pongo")
```

- add **more than one** element with the extend method:

```
apes = ["Homo","Pan","Gorilla"]
apes.extend(["Pongo","Gibbon"])
```

- concatenate two lists:

```
apes = ["Homo","Pan","Gorilla"]
monkeys = ["Papio","Macaca"]
primates = apes + monkeys
```

Modifying lists (pt. 2)

- invert the order of a list with the reverse method:

```
ranks = ["kingdom","phylum","class","order","family"]
ranks.reverse()
# ranks are now in reverse order
```

- sort a list (alphabetically) with the sort method

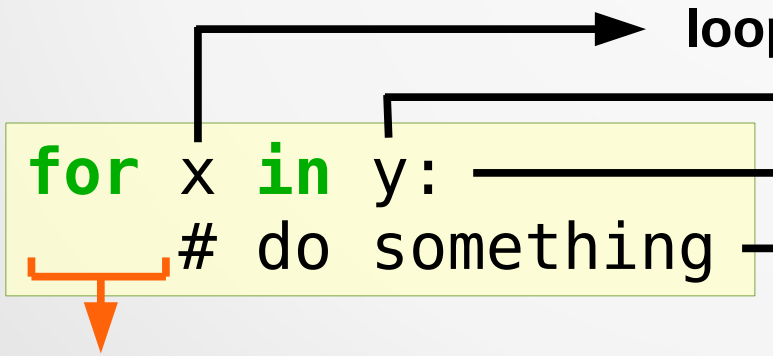
```
ranks.sort()
# new order: class, family, kingdom, ...
```

Introducing loops

- loop over elements in a list using a **for** loop:

```
apes = ["Homo","Pan","Gorilla"]
for ape in apes:
    print(ape + " is an ape")
```

- physiology of a **for** loop:



loop variable: changes with every iteration

list of elements: does not change

loop header (always ended by a **colon**)

loop body: here the loop variable x can be used (with a different value in each iteration)

mind the gap!
the *indentation* is used to distinguish the **loop body** from the **loop header**

blocks and scopes

- In python (and most other programming languages) a variables live in a context, called a scope
- scopes are also called blocks of code
- code blocks are denoted by indentations (spaces or tabs)
- indentations are flexible, but every line in a scope must have exactly the same indentation!
- examples for scopes are
  - the global scope, actually called module scope
  - functions and methods
  - loops

indentation matters – a lot!

- using different kinds of indentation (a mix of spaces and TABs) **will** result in `IndentationErrors`
  → **never mix spaces and TABs**
- it is best practice to use four spaces for indentation
- make sure that you configure your editor to use consistent indentation (often called "tab emulation")
- take care when exchanging scripts with other people

Looping over a string

- strings behave like lists in a lot of ways.
- we can also loop over the characters of a string:

```
for letter in "ACGT":
    print("one letter is " + letter)
```

iterating over lines in a file

- a file can be read line by line using a **for** loop

```
file = open("some_input.txt")
for line in file:
    print(line)
```

- advantageous when dealing with *structured* files or *very large* files (only one line is read into memory in each iteration)

looping with ranges

- run some commands a certain number of times

```
for number in range(6):
    print(number)
```

```
protein = "vlspadktnv"
for end_pos in range(3,8):
    print(protein[0:end_pos])
```

- note: end number given to `range` is exclusive

Recap

In this unit you have learned

- how to loop over a list of elements using a for loop
- the importance of indentations to denote blocks of code
- the notion of a loop variable and variable scopes
- reading files line by line
- iterating over number ranges

splitting a string into a list

- essential when working with structured files (like CSV)
- splitting a string is done with the `split` function

```
names = "mus,rattus,cricetus,cavia"
rodents = names.split(",")
print(str(rodents))
```

- a delimiting character or string must be specified (here: `","`)

Exercise 3-1: Processing DNA in a file

- file `ex3-1_input.txt` contains a number of DNA sequences
- the **first 14 positions** are identical and represent a **sequencing adapter** which is supposed to be removed

  a) **trim** the adapter sequence off, write the trimmed sequences to a (single) new file

  b) print out the **length** of each sequence to the screen

Exercise 3-1: Processing DNA in a file

expected output:
If your scripts works as intended you should get printed **output in the terminal** like this:

```
processed sequence with length 43
processed sequence with length 38
processed sequence with length 49
processed sequence with length 34
processed sequence with length 48
```

Additionally a **file** should have been **created** like this one:

trimmed.txt

```
TCGATCGATCGATCGATCGATCGATCGATCGATCGATC
ACTGATCGATCGATCGATCGATCGATGCTATCGTCGT
ATCGATCACGATCTATCGTACGTATGCATATCGATATCGATCGTAGTC
ACTATCGATGATCTAGCTACGATCGTAGCTGTA
ACTAGCTAGTCTCGATGCATGATCAGCTTAGCTGATGATGCTATGCA
```

Exercise 3-2: Exons from genomic DNA

- file `genomic_dna.txt` contains a section of genomic DNA
- file `exons.txt` contains a list of start/stop positions of exons (one line each, start/stop separated by a comma)
- Write a program that will
  - **extract** the exon segments
  - **concatenate** them, and
  - **write** them to a new file.

Exercise 3-2: Exons from genomic DNA

expected output:
If your scripts works as intended a **file** should have been **created** like this one:

coding_sequence.txt

```
CGTACCGTCGACGATGCTACGATCGTCGATCGTAGTCGATCATCGATCG
ATCGCGATCGATCGATATCGATCGATATCATCGATGCATCGATCATCGA
TCGATCGATCGATCGACGATCGATCGATCGTAGCTAGCTAGCTAGATCG
ATCATCATCGTAGCTAGCTCGACTAGCTACGTACGATCGATGCATCGAT
CGTACGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGTAG
CTAGCTACGATCG
```

Getting help

- Python interactive help