

Day 3: Control flow Practicals

Let's get down to business and start typing some real code. In order to solve the proposed exercises you are required to use the provided examples.

```
In [35]: from data import cytb, translations, IUPAC_codes, Species_list
```

In the imported module you will find 4 things:

- . a dictionary with *cytb* sequences
- . a dictionary with the nucleotide to AA translations
- . a list with the IUPAC valid letters
- . A list of species

Just print() any of them to see what's *inside*.

Don't worry if you can't solve the *Hard* and *Very Hard* problems yet. These are based on real world problems, and are here for later, or if you think the others are too easy for you.

Problem 1: (Easy)

Print every species in *Species_list* in a new line.

```
In []:
```

Problem 2: (Easy)

Print every sequence in *cytb* and the respective name so that it looks like this:

```
Seq1_name - SEQUENCE
Seq2_name - SEQUENCE
```

```
In []:
```

Problem 3: (Medium)

Verify that there are no illegal characters in the sequence "lb8" in *cytb*.

####Tip: Use the *IUPAC_codes* list that was imported from the *data* module to check if the sequence's nucleotides are legal.

```
In []:
```

Problem 4: (Medium)

####Tip: Use a nested loop to solve this problem.

<http://nbviewer.ipython.org/gist/ODiogoSilva/8...>

In []:

Problem 5: (Medium)

Reverse and complement the sequence "lb8" in *cytb*.

####Tips: Use slicing to reverse the sequence.

You can either use `replace()` or `maketrans()` to "complement" the sequence.

In []:

Problem 6: (Hard - real world problem)

Reverse and complement all the sequences in *cytb*.

####Tip: You guessed it - use a nested loop to solve this one.

In []:

Problem 7: (Hard)

Translate the sequence "lb8" in *cytb* from nucleotides into aminoacids.

####Tips: Use the translations dictionary from the data module (*translations*);

Translating the sequences into a list of aminoacids rather than a string will save you work in the next exercises.

In []:

Problem 8: (Very Hard - real world problem)

Translate all the sequences in *cytb* from nucleotides into aminoacids.

####Tip: Use another nested loop to solve this problem just like you did for problem 2.

In []:

Problem 9: (Very hard - real world problem)

Find all the equal sequences in *cytb* and "collapse" them into a single sequence (with the name of all the collapsed sequences).

In []:

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