Practical 5. String and file operation

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Learning Objects

• Create and manipulate strings in Python
• Search and find regular expression patterns in strings in Python
• Read and write files in Python

You have learned how to use Github in previous practical. **Please create a directory Practical 8 in your Github repository IBI1_2019-20 and put all your Python scripts in this practical there.**

1. Reverse complementary sequence

In biological studies, we face a lot of sequence data (DNA, RNA and proteins). Under certain circumstances, we need to know the reverse complementary sequence of a DNA sequence. For example, the reverse complementary sequence of 'ATGCAC' is 'GTGCAT'.

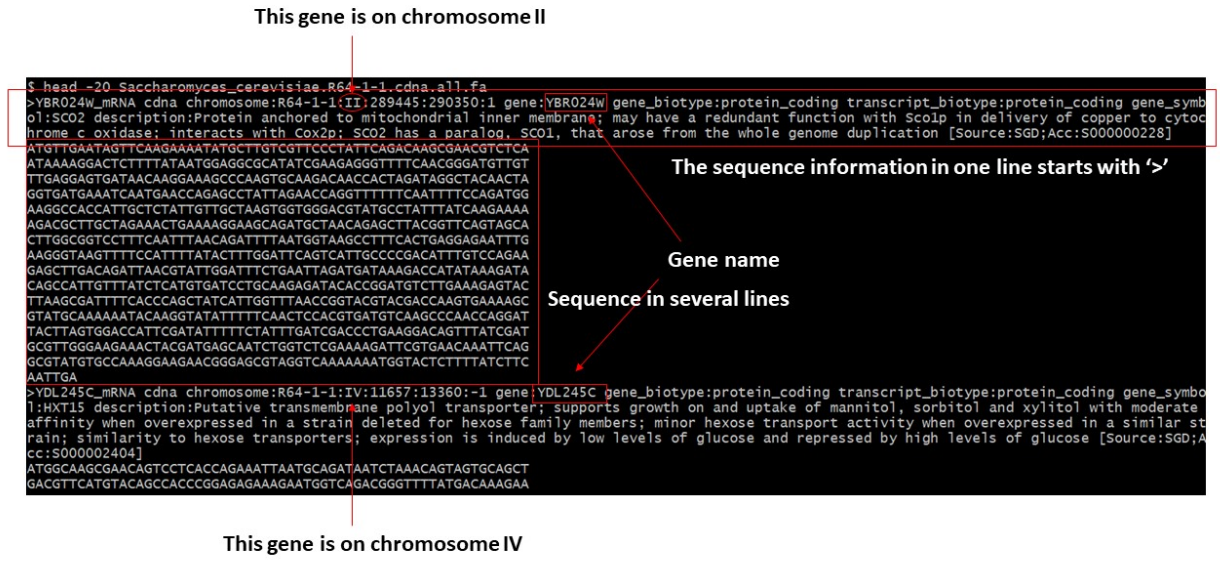
Please create a new Python script file **RC.py** in Spyder and create a string variable seq.

```
seq = 'ATGCGACTACGATCGAGGGCCAT'
```

then write codes to print out the reverse complementary sequence of it.

2. Get mitochondria gene sequence in fasta format

A common format to store the sequence data is FASTA. In a fasta/fa file, each sequence starts with a ">" symbol followed by the name of the sequence and the description of the sequence and the remaining line(s) contain the sequence itself. Here is a fasta file downloaded from ftp://ftp.ensemblgenomes.org/pub/fungi/release-46/fasta/saccharomyces_cerevisiae/cdna/. The file contains the cDNA sequences of all the genes in yeast *Saccharomyces Cerevisiae*. You can view the first lines of the file by using **head** command in your terminal (PC users can use Cypwin) as shown here. The name line has a list of gene information, such as the position in the chromosome, the gene name, the biotype, etc.,



Download the file Saccharomyces_cerevisiae.R64-1-1.cdna.all.fa from Learn. Starting from this file, now we want to extract all the genes on the mitochondria chromosome (There are 17 chromosomes in the species, named as I, II, III...XVI and Mito, among which the 'Mito' is the mitochondria chromosome). Create a new script file **get_mito_gene.py**. In it, write codes to read the file, extract the sequences of mitochondria genes and simplify the sequence name by only putting the gene name and the length of the sequence. Output the resulst in a new fasta file **mito_gene.fa**.

3. Reverse complementary sequences of mitochondria genes

Now let us combine your techniques above!

We are looking for a python script '**Mito_RC.py**' (use Spyder to write):

1) asks for the user to input a filename as the new fasta file;

2) stores the reverse complementary sequences of mitochondria genes in fasta format (do not put line breaks in the sequence as in the original file, so that the entire sequence is in one line);

3) the sequence name of each gene only has the gene name and sequence length.

The first lines in the file should be similar to this:

For your portfolio

The markers will look for and assess the following:

1. RC.py to see if it has the variable seq and prints out the reverse complementary sequence.
2. **get_mito_gene.py** to test if it can read the original fasta file and create a new file **mito_gene.fa** with mitochondria gene sequences in it.
3. **Mito_RC.py** to test if it can successfully finish the job in the instructions.