

Bioinformatique

Manipulations de séquences ADN, ARN, protéines,...



: à compléter (différents formats, bases de données ?)

Compter les nucléotides d'une séquence ADN

[Counting_DNA_Nucleotides-01.py](#)

```
#!/usr/bin/env python
# -*- coding: utf-8 -*-
"""
On dispose d'un exemple de chaîne ADN (constituée des symboles 'A',
'C', 'G', 'T')
Le programme utilise plusieurs techniques pour donner les nombres
d'occurrences respectifs des différentes bases
"""
adn =
"AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGC
"

# utilisation d'une liste et de la méthode .count()
bases = ["A", "C", "G", "T"]
for base in bases:
    print(adn.count(base),)
print()

# Variante :
for c in 'ACGT':
    print(adn.count(c),)
print()

# variante un peu moins lisible
out = []
for c in 'ACGT':
    out.append(str(adn.count(c)))
print(' '.join(out))

# utilisation de la technique "list comprehension"
count = [adn.count(c) for c in 'ACGT']
for val in count:
    print(val,)
print()

# autre "list comprehension", avec impression formatée → version "one
```

```
line"
print("%d %d %d %d" % tuple([adn.count(X) for X in "ACGT"]))

# count "à la main", sans utilisation de fonctions/librairie
ACGT = "ACGT"
count = [0,0,0,0]
for c in adn:
    for i in range(len(ACGT)):
        if c == ACGT[i]:
            count[i] +=1
for val in count:
    print(val,)
print()

# count "à la main", avec .index()
ACGT = "ACGT"
count = [0,0,0,0]
for c in adn:
    count[ACGT.index(c)] += 1
for val in count:
    print(val,)
print()

# utilisation de la librairie collections
from collections import defaultdict
ncount = defaultdict(int)
for c in adn:
    ncount[c] += 1
print(ncount['A'], ncount['C'], ncount['G'], ncount['T'])

# collections.Counter
from collections import Counter
for k,v in sorted(Counter(adn).items()):
    print(v,)
print()

# avec un dictionnaire
freq = {'A': 0, 'C': 0, 'G': 0, 'T': 0}
for c in adn:
    freq[c] += 1
print(freq['A'], freq['C'], freq['G'], freq['T'])

# avec un dictionnaire et count(), impression différente
dico={}
for base in bases:
    dico[base] = adn.count(base)
for key,val in dico.items():
    print("{} = {}".format(key, val))
```

Trouver un motif

+ lecture de fichier

[Finding_a_Protein_Motif-01.py](#)

```
#!/usr/bin/env python
# -*- coding: utf-8 -*-
"""
La description complète et les caractéristiques d'une protéine
particulière peuvent être obtenues via l'ID "uniprot_id" de la "UniProt
database", en insérant la référence dans ce lien :
http://www.uniprot.org/uniprot/uniprot\_id

On peut aussi obtenir la séquence peptidique au format FASTA via le
lien :
http://www.uniprot.org/uniprot/uniprot\_id.fasta
"""

from Bio import SeqIO
from Bio import ExpASy
from Bio import SeqIO

dic = {"UUU": "F", "UUC": "F", "UUA": "L", "UUG": "L",
      "UCU": "S", "UCC": "S", "UCA": "S", "UCG": "S",
      "UAU": "Y", "UAC": "Y", "UAA": "STOP", "UAG": "STOP",
      "UGU": "C", "UGC": "C", "UGA": "STOP", "UGG": "W",
      "CUU": "L", "CUC": "L", "CUA": "L", "CUG": "L",
      "CCU": "P", "CCC": "P", "CCA": "P", "CCG": "P",
      "CAU": "H", "CAC": "H", "CAA": "Q", "CAG": "Q",
      "CGU": "R", "CGC": "R", "CGA": "R", "CGG": "R",
      "AUU": "I", "AUC": "I", "AUA": "I", "AUG": "M",
      "ACU": "T", "ACC": "T", "ACA": "T", "ACG": "T",
      "AAU": "N", "AAC": "N", "AAA": "K", "AAG": "K",
      "AGU": "S", "AGC": "S", "AGA": "R", "AGG": "R",
      "GUU": "V", "GUC": "V", "GUA": "V", "GUG": "V",
      "GCU": "A", "GCC": "A", "GCA": "A", "GCG": "A",
      "GAU": "D", "GAC": "D", "GAA": "E", "GAG": "E",
      "GGU": "G", "GGC": "G", "GGA": "G", "GGG": "G",}

aminoacids = ''.join(sorted(list(set([v for k,v in dic.items() if v !=
"STOP"]))))
print(aminoacids)

# UniProt Protein Database access IDs
proteins = ['A2Z669', 'B5ZC00', 'P07204_TRBM_HUMAN',
            'P20840_SAG1_YEAST']

handle = ExpASy.get_sprot_raw(proteins[0])
seq_record = SeqIO.read(handle, "swiss")
```

```
handle.close()  
print()  
print(seq_record)
```

Références

- [Using biological databases to teach evolution and biochemistry](#)
- [Rosalind](#), plateforme d'apprentissage de la programmation en bioinformatique
- [GenBank](#)
- [Biopython](#)
- <https://en.wikipedia.org/wiki/Bioinformatics>
- https://en.wikipedia.org/wiki/Open_Bioinformatics_Foundation
- https://en.wikipedia.org/wiki/FASTA_format
- https://en.wikipedia.org/wiki/List_of_open-source_bioinformatics_software
- <http://www.amberbiology.com/>, "Python For The Life Sciences. A gentle introduction to Python for life scientists" (à paraître)
- références sur la lecture de fichiers :
 - http://www.uniprot.org/help/programmatic_access#id_mapping_python_example
 - <http://www.python-simple.com/python-biopython/Lecture-ecriture-sequences.php>
- Articles de la revue "Science in School" :
 - [Bioinformatics with pen and paper: building a phylogenetic tree](#) Cleopatra Kozlowski, 07/12/2010
 - [Using biological databases to teach evolution and biochemistry](#), Germán Tenorio, 02/06/2014
- documentation sur les arbres phylogénétiques : <https://biopython.org/wiki/Phylo>
- cours introductif sur biopython :
 - [Introduction to Biopython](#) VIB bioinformatics core, Kristian Rother

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