
Lab 4

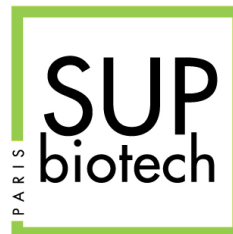
Sequences

Sup'Biotech 3

Python

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Preamble

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1 Introduction

In this fifth lab, we will manipulate strings, lists and dictionaries.

2 DNA Sequence Characteristics

2.1 Adenine Frequency

Write a function `freq_A(s: str) -> int` that returns the frequency of the adenine nucleotide in the DNA sequence `s`.

Example

```
>>> freq_A("AAATGT")
0.5
>>> freq_A("TGTGTCG")
0.0
```

2.2 Nucleotide Frequency

Write a function `freq_nuc(s: str) -> dict` that returns the frequency of each nucleotide on the DNA sequence `s`. The returned value is a dictionary of the form: `nucleotide:float`.

Example

```
>>> freq_nuc("ATGC")
{"A":0.25, "T":0.25, "G":0.25, "C":0.25}
>>> freq_nuc("AAAGCG")
{"A":0.5, "T":0.0, "G":0.33333, "C": 0.16666}
```

3 Modification Of Sequences

3.1 Complementary Strand

Write a function `complementary_DNA(s: str) -> str` that returns the complementary sequence corresponding to the DNA sequence `s`.

Example

```
>>> complementary_DNA("ATTTGC")
"TAAACG"
>>> complementary_DNA("CCGTA")
"GGCAT"
```

3.2 Reverse Complementary Sequence

Write a function `rev_complementary_DNA(s: str) -> str` that returns the reverse complementary sequence corresponding to the DNA sequence `s`.

Example

```
>>> rev_complementary_DNA("ATTTGC")
"GCAAAT"
>>> rev_complementary_DNA("CCGTA")
"TACGG"
```

3.3 Translation Of An Open Reading Frame

Write a function `translate(s: str) -> str` that returns the amino acid sequence corresponding to the RNA sequence `s`.

The following dictionary gives the mapping between codon and amino acid:

```
gencode = {
    "UUU": "Phe", "UCU": "Ser", "UAU": "Tyr", "UGU": "Cys",
    "UUC": "Phe", "UCC": "Ser", "UAC": "Tyr", "UGC": "Cys",
    "UUA": "Leu", "UCA": "Ser", "UAA": "STOP", "UGA": "STOP",
    "UUG": "Leu", "UCG": "Ser", "UAG": "STOP", "UGG": "Trp",
    "CUU": "Leu", "CCU": "Pro", "CAU": "His", "CGU": "Arg",
    "CUC": "Leu", "CCC": "Pro", "CAC": "His", "CGC": "Arg",
    "CUA": "Leu", "CCA": "Pro", "CAA": "Gln", "CGA": "Arg",
    "CUG": "Leu", "CCG": "Pro", "CAG": "Gln", "CGG": "Arg",
    "AUU": "Ile", "ACU": "Thr", "AAU": "Asn", "AGU": "Ser",
    "AUC": "Ile", "ACC": "Thr", "AAC": "Asn", "AGC": "Ser",
    "AUA": "Ile", "ACA": "Thr", "AAA": "Lys", "AGA": "Arg",
    "AUG": "Met", "ACG": "Thr", "AAG": "Lys", "AGG": "Arg",
    "GUU": "Val", "GCU": "Ala", "GAU": "Asp", "GGU": "Gly",
    "GUC": "Val", "GCC": "Ala", "GAC": "Asp", "GGC": "Gly",
    "GUA": "Val", "GCA": "Ala", "GAA": "Glu", "GGA": "Gly",
    "GUG": "Val", "GCG": "Ala", "GAG": "Glu", "GGG": "Gly",
}
```

Note: The file `gencode.py` on your intranet contains this dictionary.

Example

```
>>> translate("UUCUCACGU")
"PheSerArg"
>>> translate("UUCUCACGUUGAAGC")
"PheSerArg"
```

4 Distance Between DNA Sequences

4.1 Hamming Distance

The Hamming distance is the simplest method you can use to compare two sequences s_1 and s_2 . It works as follows: we compare s_1 and s_2 character by character if they are different we add +1 to the distance and 0 if they are identical. Mathematically, it gives the following formula:

$$\text{hamming}(s_1, s_2) = \sum_{i=0}^N \mathbb{1}_{s_1[i], s_2[j]}$$

where:

- N is the length of the sequences;
- $\mathbb{1}_{n_1, n_2} = \begin{cases} 1 & \text{if } n_1 \neq n_2 \\ 0 & \text{otherwise} \end{cases}$ is a function that evaluates to 1 if n_1 and n_2 are different and 0 otherwise.

Write a function `hamming(s1: str, s2: str) -> int` that returns the Hamming distance between the two DNA sequences `s1` and `s2`. We consider that `s1` and `s2` have the same size.

Example

```
>>> hamming("ATT", "TTA")
2
>>> hamming("AAA", "GGG")
3
```

4.2 Weighted Distance

The weighted distance is very similar to the Hamming distance except that we will now add different values to the distance depending of the type of mismatch. The new mathematical formula is the following:

$$d_{\text{weighted}}(s_1, s_2) = \sum_{i=0}^N w_{s_1[i], s_2[i]} * \mathbb{1}_{s_1[i], s_2[j]}$$

Where:

- N is the size of the sequences;
- $\mathbb{1}_{s_1[i], s_2[j]}$ is the same function as for the Hamming distance;
- $w_{s_1[i], s_2[j]}$ is the weight (or coefficient) associated to the mismatch between characters $s_1[i]$ and $s_2[j]$. We will represent it in Python using a dictionary.

This dictionary is used in the following way:

```
>>> w = {"A": {"A": 0, "T": 0.5, "G": -0.5, "C": 0.3},
         "T": {"A": 0.5, "T": 0, "G": 1.2, "C": -5},
         "G": {"A": -10, "T": 1.2, "G": 0, "C": 0.3},
         "C": {"A": 0.3, "T": -5, "G": 5.3, "C": 0}}
>>> w["A"]["T"]
0.5
>>> w["C"]["A"]
0.3
```

Write a function `weighted_dist(s1: str, s2: str, w: dict) -> float` that returns the weighted distance between the two DNA sequences `s1` and `s2` using the weights in `w`.

Example

```

>>> w = {"A":{"A":0,"T":0.5,"G":-0.5,"C":0.3}, \
        "T":{"A":0.5,"T":0,"G":1.2,"C":-5}, \
        "G":{"A":-10,"T":1.2,"G":0,"C":0.3}, \
        "C":{"A":0.3,"T":-5,"G":5.3,"C":0}}
>>> weighted_dist("ATT", "TTA", w)
1.0
>>> weighted_dist("AAAG", "GGGA", w)
-11.5
  
```