
Homework

Python-1

Sup'Biotech 3

Python

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Preamble

Document Property

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1 Introduction

In this homework we will apply the basic programming skills that you have just acquired to crack some biology-related questions.

1.1 File Architecture

You must respect the following architecture for your work:

```
login_1
├── AUTHORS
├── src
│   └── files.py
```

You must have a folder named with your login, this folder must contain:

1. A **text file** named *AUTHORS* containing your first and last names.
2. A **folder** named *src* that contains your code files.

1.2 Submission

- Deadline: until **Thursday October 13, 23h42**;
- Submission: a **zip file** named: *login_1.zip* to upload on the bioinformatics [intranet](#).

A bad architecture of your submission may result in a 2 points penalty.

1.3 Cheating

Basically, **DO NOT CHEAT**. Your work will be automatically tested against cheating. If two people are detected as cheaters, they will receive the **grade 0** for the homework and the administration will be told of their attempt. All detected cheaters are treated equally, I do not care who wrote the code and who took it.

2 Example

Here is an example of how to answer an homework question.

2.1 Question

File: *toto.py*

Write the function called `my_sum(a: int, b:int) -> int` that returns the sum of **a** and **b**.

2.2 Answer

The content of the file *toto.py* is thus:

```
def my_sum(a, b):
    return a + b
```

2.3 Testing your code

Although not mandatory in this first homework, **I strongly advise you to test your code.** You can do that by calling your function with some values and checking that the answer is what you expect. For example, your file *toto.py* becomes:

```
def my_sum(a, b):
    return a + b

print(my_sum(5, 9) == 16)
print(my_sum(5, 0) == 5)
print(my_sum(5, -5) == 0)
```

And the Python output is:

```
True
True
True
```

You must remove all your tests before you submit your code. In your code files I want only function declarations and nothing else.

3 Computer-science Problems

3.1 Integer Sequence (2 point)

File: *seq.py*

Consider the following sequence defined as follows for all $n \in \mathbb{N}$:

$$u_n = \begin{cases} u_0 & \text{if } n = 0 \\ 2 \times u_{n-1} \% (u_0)^2 & \text{otherwise} \end{cases}$$

Write the function `seq1(n: int, u0: int) -> int` that returns the value of $u(n)$.

Example

```
>>> seq1(0, 5)
5
>>> seq1(1, 5)
10
>>> seq1(2, 5)
20
>>> seq1(3, 5)
15
>>> seq1(4, 2)
0
```

Correction:

```
def seq1(n, u0):
    toto = u0
```

```

i = 1
while i <= n:
    toto = 2*toto % u0 ** 2
    i = i + 1
return toto

```

3.2 Number Of Solutions Of A Second Order Polynome (4 points)

File: *poly.py*

A second order polynomial equation is an equation of the form:

$$a \times x^2 + b \times x + c = 0$$

As you know from highschool the number of solutions of this equation depend of the value of its discriminant Δ defined as:

$$\Delta = b^2 - 4 \times a \times c$$

If $\Delta < 0$ the equation has **no solution**, if $\Delta = 0$ the equation has **one** solution and if $\Delta > 0$ the equation has **two** solutions.

Write the function `number_of_sol(a: float, b: float, c: float) -> int` that returns the number of solution(s) of the corresponding second order equation.

Example

```

>>> number_of_sol(1, 5, 2)
2
>>> number_of_sol(3, 2, 1)
0
>>> number_of_sol(0.5, -3, 4.5)
1

```

Correction:

```

def number_of_sol(a, b, c):
    delta = b**2 - 4 * a * c
    if delta < 0:
        return 0
    elif delta == 0:
        return 1
    else:
        return 2

```

3.3 Solution Of A Second Order Polynome (4 points)

File: *solve_pol.py*

The solution of the second order equation:

$$a \times x^2 + b \times x + c = 0$$

depends on the value of $\Delta = b^2 - 4 \times a \times c$ as follows:

- If $\Delta < 0$ the equation has no solution;
- If $\Delta = 0$ the equation has the solution $x^* = \frac{-b}{2a}$;
- If $\Delta > 0$ the equation has two solutions: $x_1 = \frac{-b - \sqrt{\Delta}}{2a}$ and $x_2 = \frac{-b + \sqrt{\Delta}}{2a}$.

Write the function `solve(a: float, b: float, c: float) -> int` that returns:

- `None` if the equation has no solution;
- The unique solution x^* if the equation has only one solution;
- The solution x_2 (defined above) if the equation has two solutions.

Note: To be able to compute the square root in your code you must fetch the function `sqrt` (short hand for "square root"). To do so you must put the following line at **the beginning** of your file (not in the body of the function !):

```
from math import sqrt
```

Example

```
>>> solve(1, 5, 4)
-1
>>> solve(3, 2, 1)
None
>>> solve(0.5, -3, 4.5)
3
```

Correction:

```
from math import sqrt
def solve(a, b, c):
    delta = b * b - 4 * a * c

    if delta < 0:
        return None
    elif delta == 0:
        return - b / 2 / a
    else:
        return (-b + sqrt(delta)) / 2 / a
```

3.4 Division

File: *division.py*

The result of the integer division between two two numbers $a, b > 0$ can be obtained using the following simple procedure:

- while $a \geq 0$ subtract b from a .

The number of times q that a was subtracted from b is called the quotient. The last value of a is called the remainder (we will not use it here).

Write the function `my_division(a: float, b: float) -> int` that computes the quotient (q) in the integer division of a by b as defined above.

Warning YOU can only use the `-` operator in this function. (No `/` nor `//`).

Example

```
>>> my_division(36, 6)
6
>>> my_division(37, 6)
6
>>> my_division(15, 2)
7
```

Correction:

```
from math import sqrt
def my_division(a, b):
    q = 0
    while a - b >= 0:
        a = a - b
        q = q + 1
    return q
```

4 Biology-related Problems

4.1 Translation

File: *codon.py*

A codon is a triplet of nucleotide. Each codon is associated to a specific amino acid during the translation of a mRNA sequence. The following table associates to each codon its amino acid:

1 st	2 nd	3 rd	AA	1 st	2 nd	3 rd	AA	1 st	2 nd	3 rd	AA
A	A	A	Lys	U	U	C	Phe	C	G	A	Arg
A	A	U	Asn	U	U	G	Leu	C	G	U	Arg
A	A	C	Asn	U	C	A	Ser	C	G	C	Arg
A	A	G	Lys	U	C	U	Ser	C	G	G	Arg
A	U	A	Ile	U	C	C	Ser	G	A	A	Glu
A	U	U	Ile	U	C	G	Ser	G	A	U	Asp
A	U	C	Ile	U	G	A	STOP	G	A	C	Asp
A	U	G	Met	U	G	U	Cys	G	A	G	Glu
A	C	A	Thr	U	G	C	Cys	G	U	A	Val
A	C	U	Thr	U	G	G	Trp	G	U	U	Val
A	C	C	Thr	C	A	A	Gln	G	U	C	Val
A	C	G	Thr	C	A	U	His	G	U	G	Val
A	G	A	Arg	C	A	C	His	G	C	A	Ala
A	G	U	Ser	C	A	G	Gln	G	C	U	Ala
A	G	C	Ser	C	U	A	Leu	G	C	C	Ala
A	G	G	Arg	C	U	U	Leu	G	C	G	Ala
U	A	A	STOP	C	U	C	Leu	G	G	A	Gly
U	A	U	Tyr	C	U	G	Leu	G	G	U	Gly
U	A	C	Tyr	C	C	A	Pro	G	G	C	Gly
U	A	G	STOP	C	C	U	Pro	G	G	G	Gly
U	U	A	Leu	C	C	C	Pro				
U	U	U	Phe	C	C	G	Pro				

Write the function `codon_to_AA(nuc1: str, nuc2: str, nuc3: str) -> str` that returns the abbreviated name of the amino acid associated to the codon `nuc1nuc2nuc3`.

Warning: If any of the characters provided is not AUCG your function must return `None`.

Warning: You can only use what we have seen up to course 3 to solve this function. Advanced structures like dictionaries are **PROHIBITED**.

Note: There is an "intelligent" way to do this function.

Exemple

```
>>> codon_to_AA("A", "U", "C")
"Ile"
>>> codon_to_AA("A", "U", "E")
None
>>> codon_to_AA("G", "G", "U")
"Gly"
>>> codon_to_AA("U", "A", "A")
"STOP"
```

Correction:

```
def codon_to_AA(nuc1, nuc2, nuc3):
    if nuc1 == "A":
        if nuc2 == "A":
            if nuc3 == "A":
                return "Lys"
            elif nuc3 == "U":
```

```

        return "Asn"
    elif nuc3 == "C":
        return "Asn"
    elif nuc3 == "G":
        return "Lys"
    else:
        return None
elif nuc2 == "U":
    if nuc3 == "A":
        return "Ile"
    elif nuc3 == "U":
        return "Ile"
    elif nuc3 == "C":
        return "Ile"
    elif nuc3 == "G":
        return "Met"
    else:
        return None
elif nuc2 == "C":
    if nuc3 == "A":
        return "Thr"
    elif nuc3 == "U":
        return "Thr"
    elif nuc3 == "C":
        return "Thr"
    elif nuc3 == "G":
        return "Thr"
    else:
        return None
elif nuc2 == "G":
    if nuc3 == "A":
        return "Arg"
    elif nuc3 == "U":
        return "Ser"
    elif nuc3 == "C":
        return "Ser"
    elif nuc3 == "G":
        return "Arg"
    else:
        return None
else:
    return None
elif nuc1 == "U":
    if nuc2 == "A":
        if nuc3 == "A":
            return "STOP"
        elif nuc3 == "U":
            return "Tyr"
        elif nuc3 == "C":
            return "Tyr"
        elif nuc3 == "G":
            return "STOP"

```

```

    else:
        return None
elif nuc2 == "U":
    if nuc3 == "A":
        return "Leu"
    elif nuc3 == "U":
        return "Phe"
    elif nuc3 == "C":
        return "Phe"
    elif nuc3 == "G":
        return "Leu"
    else:
        return None
elif nuc2 == "C":
    if nuc3 == "A":
        return "Ser"
    elif nuc3 == "U":
        return "Ser"
    elif nuc3 == "C":
        return "Ser"
    elif nuc3 == "G":
        return "Ser"
    else:
        return None
elif nuc2 == "G":
    if nuc3 == "A":
        return "STOP"
    elif nuc3 == "U":
        return "Cys"
    elif nuc3 == "C":
        return "Cys"
    elif nuc3 == "G":
        return "Trp"
    else:
        return None
else:
    return None
elif nuc1 == "C":
    if nuc2 == "A":
        if nuc3 == "A":
            return "Gln"
        elif nuc3 == "U":
            return "His"
        elif nuc3 == "C":
            return "His"
        elif nuc3 == "G":
            return "Gln"
        else:
            return None
    elif nuc2 == "U":
        if nuc3 == "A":
            return "Leu"

```

```

elif nuc3 == "U":
    return "Leu"
elif nuc3 == "C":
    return "Leu"
elif nuc3 == "G":
    return "Leu"
else:
    return None
elif nuc2 == "C":
    if nuc3 == "A":
        return "Pro"
    elif nuc3 == "U":
        return "Pro"
    elif nuc3 == "C":
        return "Pro"
    elif nuc3 == "G":
        return "Pro"
    else:
        return None
elif nuc2 == "G":
    if nuc3 == "A":
        return "Arg"
    elif nuc3 == "U":
        return "Arg"
    elif nuc3 == "C":
        return "Arg"
    elif nuc3 == "G":
        return "Arg"
    else:
        return None
else:
    return None
elif nuc1 == "G":
    if nuc2 == "A":
        if nuc3 == "A":
            return "Glu"
        elif nuc3 == "U":
            return "Asp"
        elif nuc3 == "C":
            return "Asp"
        elif nuc3 == "G":
            return "Glu"
        else:
            return None
    elif nuc2 == "U":
        if nuc3 == "A":
            return "Val"
        elif nuc3 == "U":
            return "Val"
        elif nuc3 == "C":
            return "Val"
        elif nuc3 == "G":

```

```

        return "Val"
    else:
        return None
elif nuc2 == "C":
    if nuc3 == "A":
        return "Ala"
    elif nuc3 == "U":
        return "Ala"
    elif nuc3 == "C":
        return "Ala"
    elif nuc3 == "G":
        return "Ala"
    else:
        return None
elif nuc2 == "G":
    if nuc3 == "A":
        return "Gly"
    elif nuc3 == "U":
        return "Gly"
    elif nuc3 == "C":
        return "Gly"
    elif nuc3 == "G":
        return "Gly"
    else:
        return None
else:
    return None
else:
    return None

```

4.2 Simulating The Noyes-Whitney Equation

File: *noyes_whitney.py*

The Noyes-Whitney equation describes the rate of dissolution in mass unit / time (for example *kg/s*) of a solid in a liquid . It is very used in pharmacology where the solid is a pill and the liquid can be water or blood or any physiological fluid.

The equation is stated as follows:

$$\frac{dW(t)}{dt} = \frac{D \times A \times (C_s - \frac{W(t)}{V})}{L}$$

where:

- $t \geq 0$ is the time in time units (for example *s*);
- $W(t)$ is the quantity of dissolved solid molecules at time t in mass units (for example *kg*);
- D is the diffusion coefficient of the solid molecule in the liquid in surface units squared / time (for example $\mu m^2/s$);
- A is the surface area of the solid in surface units (for example μm^2);

- C_s is the saturation concentration of the solid molecule in the solution in mass / volume units (for example mg/L);
- V is the volume of the solution in volume units (for example ml). Note that $\frac{W(t)}{V}$ is the concentration of the solid molecule in the solution.
- L is the thickness of the diffusion layer in distance units (for example μm).

Write the function:

`simu_nw(W0: float, A: float, D: float, V: float, Cs: float, L: float, dt: float t: int) -> float`
 that returns the quantity $W(t)$ given all the parameters of the equation A, D, C, C_s, L , the initial mass of dissolved solid molecule W_0 , the timestep for the simulation dt and the time to stop t .

Note: To compute $W(t)$ from the equation, you will use the Euler approximation (see also exercise from Lab1) stated as follows:

Considering a function f depending of one parameter t and its derivative $\frac{df}{dt}$, the Euler scheme is:

$$f(t + dt) = f(t) + \frac{df(t)}{dt} \times dt$$

where dt is called the simulation timestep, the smallest it is the more precise the result will be.

To get the value of f at some time τ , you have to compute all values from the time $t = 0$, for which the value $f_0 = f(t_0)$ is known, until you reach $t = \tau$ using the Euler scheme. At each iteration the time increases by dt .

Example

```
>>> A = 2800
>>> Cs = 20
>>> L = 0.05
>>> D = 1.6e-6
>>> W0 = 0
>>> V = 5.1
>>> simu_nw(W0, A, D, V, Cs, L, 0.0001, 10)
16.43414
>>> simu_nw(W0, A, D, V, Cs, L, 0.0001, 30)
41.78548
>>> simu_nw(W0, A, D, V, Cs, L, 0.0001, 60)
66.45305
>>> A = 50000
>>> simu_nw(W0, A, D, V, Cs, L, 0.0001, 10)
97.57324
>>> simu_nw(W0, A, D, V, Cs, L, 1, 10)
99.63637
```

The Figure 1 presents results of the simulation with the previous parameters.

Correction:

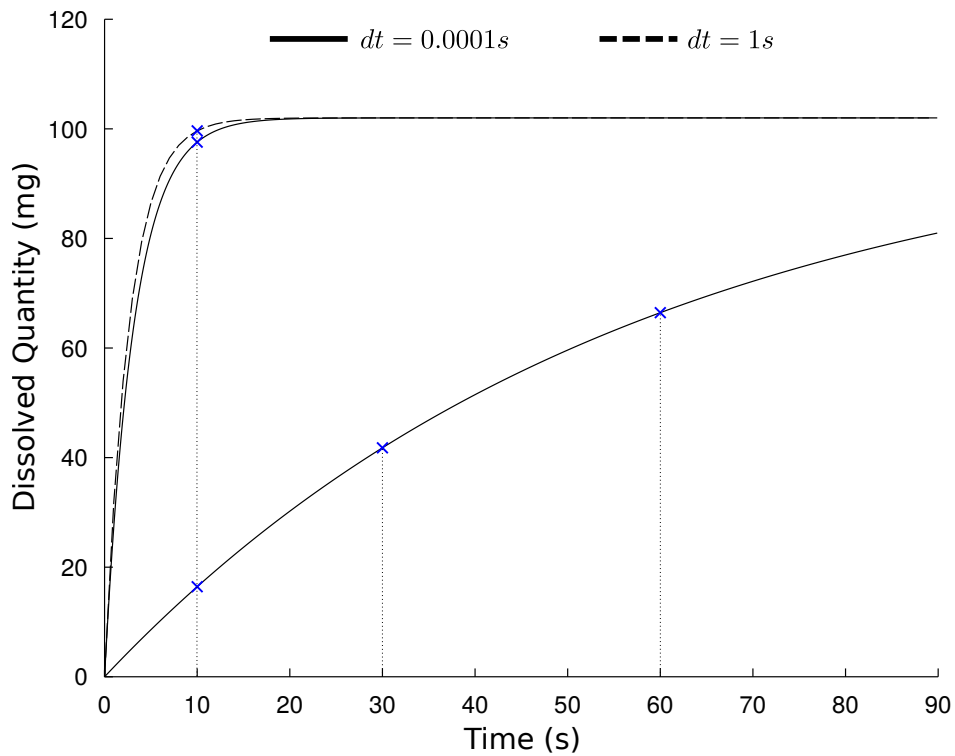


Figure 1: Simulation of the Noyes-Withney equation. Top lines corresponds to $A = 50000$ and the bottom solid line to $A = 2800$.

```
def simu_nw(W0, A, D, V, Cs, L, dt, t):
    cur_t = 0
    w = W0
    while cur_t < t:
        dw_dt = (A * D * (Cs - w/V)) / L
        w = w + dw_dt * dt
        cur_t = cur_t + dt
    return w
```