Homework for October 14, 2025

Directory `demo/` contains a simple program to perform the alignment of two sequences in FASTA file using the Needleman–Wunsch algorithm.

The main script (`main.py`) requires a custom package, in `newu2`, that contains three modules (`num.py`, `read.py`, and `write.py`).

Student's details

- **Name:** Add your name here
- **UNC Charlotte's ID (800 number):** Add your ID here
- **UNC Charlotte's email:** add your institutional email here

1. Answer these questions

1.1. Explain why `newu2` has an empty file called `__init__.py`

Add your response in here.

1.2. Explain the function `read_fa` from `read.py` in plain English

Add your response in here.

1.3. Explain the function `write_fa` from `write.py` in plain English

Add your response in here.

1.4. Explain the function `parse_fa` from `num.py` in plain English

Add your response in here.

1.5. Explain the function `fill_matrix` from `num.py` in plain English

Add your response in here.

1.6. Explain the function `trace_matrix` from `num.py` in plain English

Add your response in here.

1.7. Complete the table below

Match Cost	Mismatch Cost	InDel Cost	Expected Alignnment of Sequence 1	Expected Alignnment of Sequence 2
+1	-1	-1	GCA-TGCG	-GATTACA
+1	-1	-10	GCATGCG	GATTACA
+1	-2	-1		
+1	-2	-10		
+1	-10	-1		
-1	+1	+1		

2. Complete these programming challenges

Modify the Python3 project so that it completes the challenges below. Include a compressed version of your entire project, together with your responses above.

2.1. Report a consensus sequence representing the alignment of the two sequences

To resolve this challenge, create a new package, separate from `newu2` .

2.2. Report the cost of the alignment

To resolve this challenge, create a new package, separate from `newu2` .

2.3. Report the total number of possible alignments (OPTIONAL)

This challenge is optional.

To resolve this challenge, create a new package, separate from `newu2` .

Your goal is to count (and not cenessarily report) all the possible alignments of optimal equal cost for a given set of match, mismatch, and InDel costs. Your code should allow you to complete the table below:

Match	Mismatch	InDel	No. of Alignments
+1	-1	-1	
+1	-1	-2	
+1	-1	-10	