

LABORATORY REPORT #11

GEORGESCU Mihai-Antonio, 1242EA
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lab11_1.py

The screenshot displays the Spyder Python IDE interface. The main editor window shows the script `lab11_1.py` with the following code:

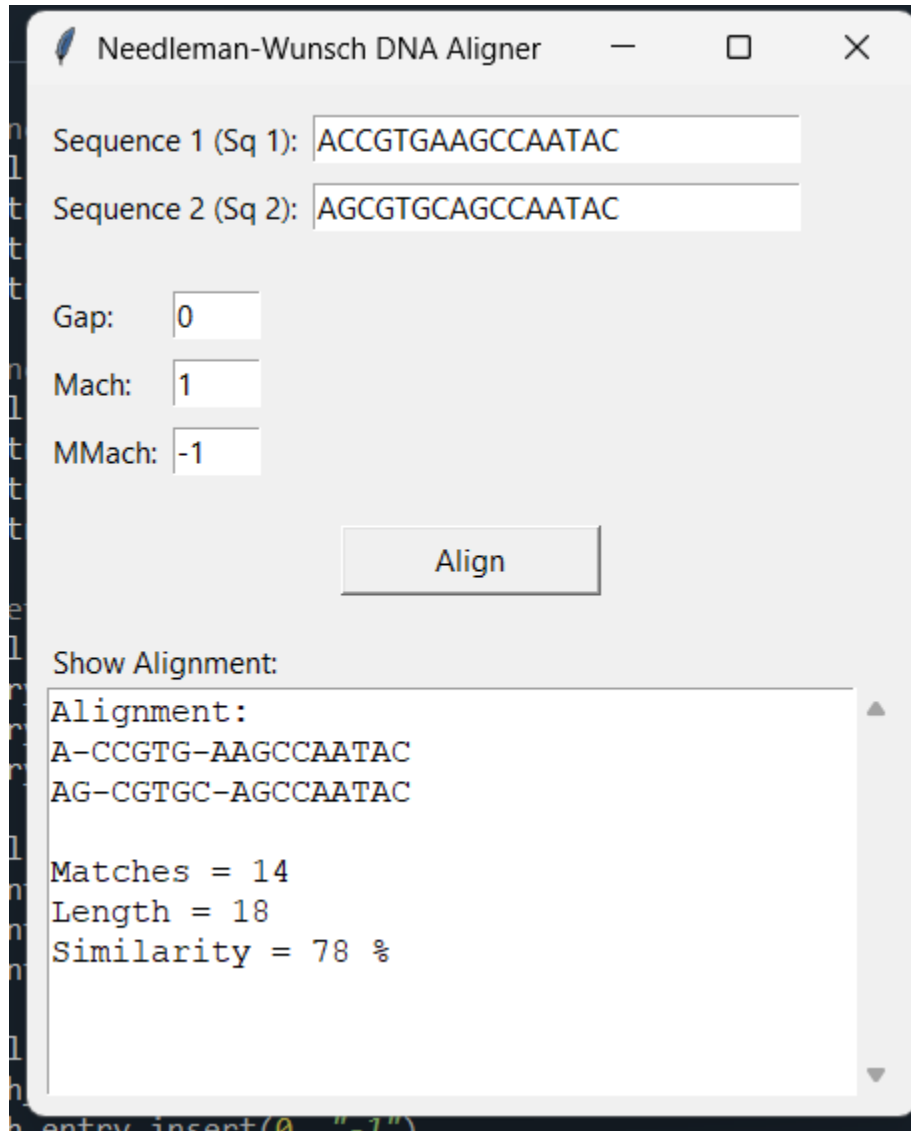
```
116 # Sequence 1 Input
117 tk.Label(sequence_frame, text="Sequence 1 (Sq 1):").grid(row=0, column=0, sticky='w')
118 seq1_entry = tk.Entry(sequence_frame, width=30)
119 seq1_entry.insert(0, "ACCGTGAGCCAATAC")
120 seq1_entry.grid(row=0, column=1, padx=5, pady=5)
121
122 # Sequence 2 Input
123 tk.Label(sequence_frame, text="Sequence 2 (Sq 2):").grid(row=1, column=0, sticky='w')
124 seq2_entry = tk.Entry(sequence_frame, width=30)
125 seq2_entry.insert(0, "AGCGTGAGCCAATAC")
126 seq2_entry.grid(row=1, column=1, padx=5, pady=5)
127
128 # Parameters Input
129 tk.Label(param_frame, text="Gap:").grid(row=0, column=0, sticky='w')
130 gap_entry = tk.Entry(param_frame, width=5)
131 gap_entry.insert(0, "0")
132 gap_entry.grid(row=0, column=1, padx=5, pady=5)
133
134 tk.Label(param_frame, text="Match:").grid(row=1, column=0, sticky='w')
135 match_entry = tk.Entry(param_frame, width=5)
136 match_entry.insert(0, "1")
137 match_entry.grid(row=1, column=1, padx=5, pady=5)
138
139 tk.Label(param_frame, text="Mismatch:").grid(row=2, column=0, sticky='w')
140 mismatch_entry = tk.Entry(param_frame, width=5)
141 mismatch_entry.insert(0, "-1")
142 mismatch_entry.grid(row=2, column=1, padx=5, pady=5)
143
144 # Align Button
145 align_button = tk.Button(button_frame, text="Align", command=align_sequences, width=15)
146 align_button.pack()
147
148 # Result Output (scrolled text area)
149 tk.Label(result_frame, text="Show Alignment:").pack(anchor='w')
150 result_text = scrolledtext.ScrolledText(result_frame, wrap=tk.WORD, width=40, height=10)
151 result_text.pack(fill='both', expand=True)
152
153 root.mainloop()
```

The right-hand pane shows the Variable Explorer with the following variables and their values:

Name	Type	Size	Value
align_button	Button	1	Button object of tkinter module
aligned_seq1	str	18	A-CCGTG-AGCCAATAC
aligned_seq2	str	18	AG-CGTG-AGCCAATAC
button_frame	Frame	1	Frame object of tkinter module
gap_entry	Entry	1	Entry object of tkinter module
length	int	1	18
match_entry	Entry	1	Entry object of tkinter module
mismatches	int	1	14
mismatch_entry	Entry	1	Entry object of tkinter module
param_frame	Frame	1	Frame object of tkinter module
result_frame	Frame	1	Frame object of tkinter module
result_text	scrolledtext.ScrolledText	1	ScrolledText object of tkinter.scrolledtext module

The bottom pane shows the Python Console with the following output:

```
In [3]: %runfile C:/Users/Antonio/Desktop/bioinfo/lab11/lab11_1.py --wdir
In [4]:
```



The screenshot shows a window titled "Needleman-Wunsch DNA Aligner". It contains two input fields for DNA sequences: "Sequence 1 (Sq 1):" with the value "ACCGTGAAGCCAATAC" and "Sequence 2 (Sq 2):" with the value "AGCGTGCAGCCAATAC". Below these are three input fields for alignment parameters: "Gap:" with "0", "Mach:" with "1", and "MMach:" with "-1". A central "Align" button is present. At the bottom, a section labeled "Show Alignment:" displays the following text:
Alignment:
A-CCGTG-AAGCCAATAC
AG-CGTGC-AGCCAATAC
Matches = 14
Length = 18
Similarity = 78 %

lab11_2.py

Spyder (Python 3.13)

```
1 # -*- coding: utf-8 -*-
2 """
3 Created on Thu Dec 11 14:27:25 2025
4
5 @author: Antonio
6 """
7
8 import tkinter as tk
9 import os
10
11 def read_fasta(file_path):
12     sequence = ""
13     try:
14         with open(file_path, 'r') as f:
15             for line in f:
16                 if line.startswith('>'):
17                     continue
18                 sequence += line.strip().upper().replace(' ', '')
19     except FileNotFoundError:
20         return None
21     return sequence
22
23 def smith_waterman(seq1, seq2, match=2, mismatch=-1, gap=-2):
24     n = len(seq1)
25     m = len(seq2)
26     matrix = [[0] * (m + 1) for _ in range(n + 1)]
27     max_score = 0
28     max_pos = None
29
30     for i in range(1, n + 1):
31         for j in range(1, m + 1):
32             score = match if seq1[i - 1] == seq2[j - 1] else mismatch
33
34             diag = matrix[i - 1][j - 1] + score
35             up = matrix[i - 1][j] + gap
36             left = matrix[i][j - 1] + gap
37
38             # local alignment (Smith-Waterman) includes 0 as a choice
39             matrix[i][j] = max(0, diag, up, left)
```

Name	Type	Size	Value
align_button	Button	1	Button object of tkinter module
aligned_seq1	str	18	A-CCGTG-AGCCCAATAC
aligned_seq2	str	18	AG-CGTGC-AGCCCAATAC
button_frame	Frame	1	Frame object of tkinter module
canvas	Canvas	1	Canvas object of tkinter module
canvas_size	int	1	500
gap_entry	Entry	1	Entry object of tkinter module
length	int	1	18
match_entry	Entry	1	Entry object of tkinter module
matches	int	1	14
mismatch_entry	Entry	1	Entry object of tkinter module
param_frame	Frame	1	Frame object of tkinter module

```
In [3]: %runfile C:/Users/Antonio/Desktop/bioinfo/lab11/lab11_1.py --wdir
In [4]: %runfile C:/Users/Antonio/Desktop/bioinfo/lab11/lab11_1.py --wdir
In [5]: %runfile C:/Users/Antonio/Desktop/bioinfo/lab11/untitled1.py --wdir
In [6]: %runfile C:/Users/Antonio/Desktop/bioinfo/lab11/untitled1.py --wdir
The kernel died, restarting...
```

Python Console History

