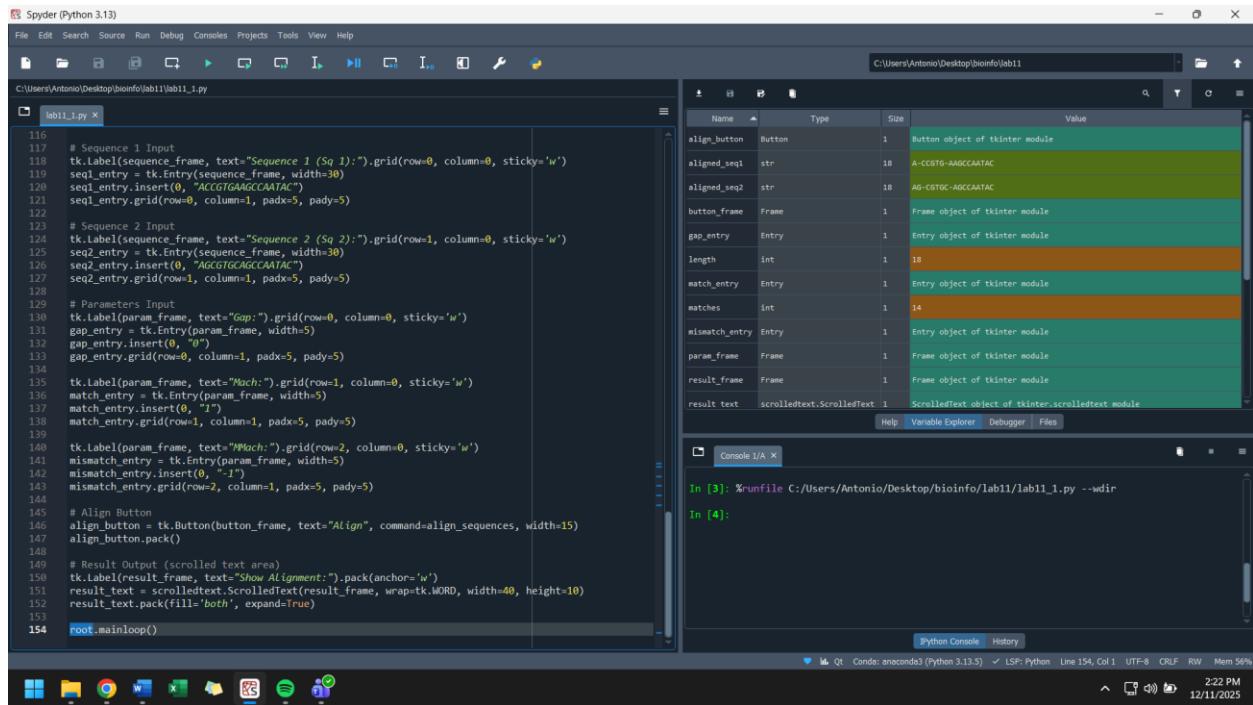


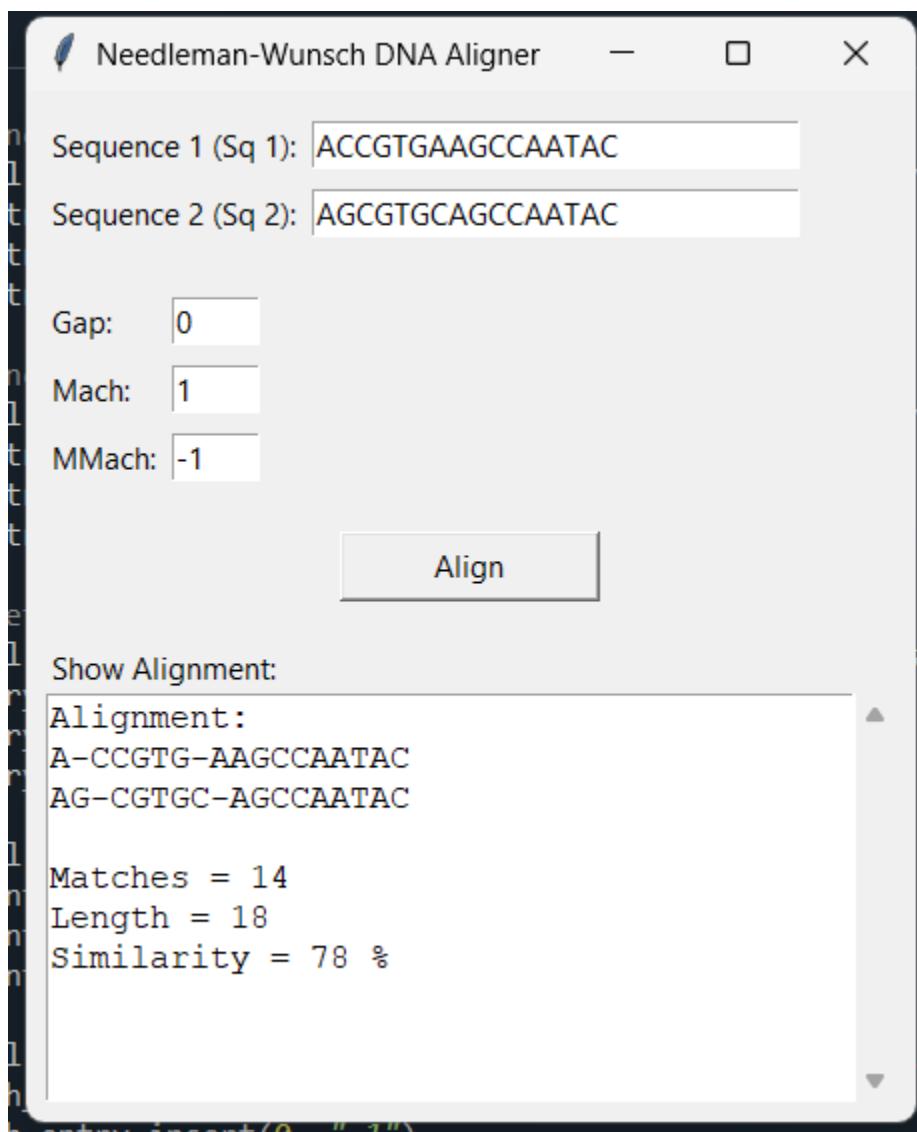
LABORATORY REPORT #11

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Bioinformatics, 4th year 1st semester, 2025-2026

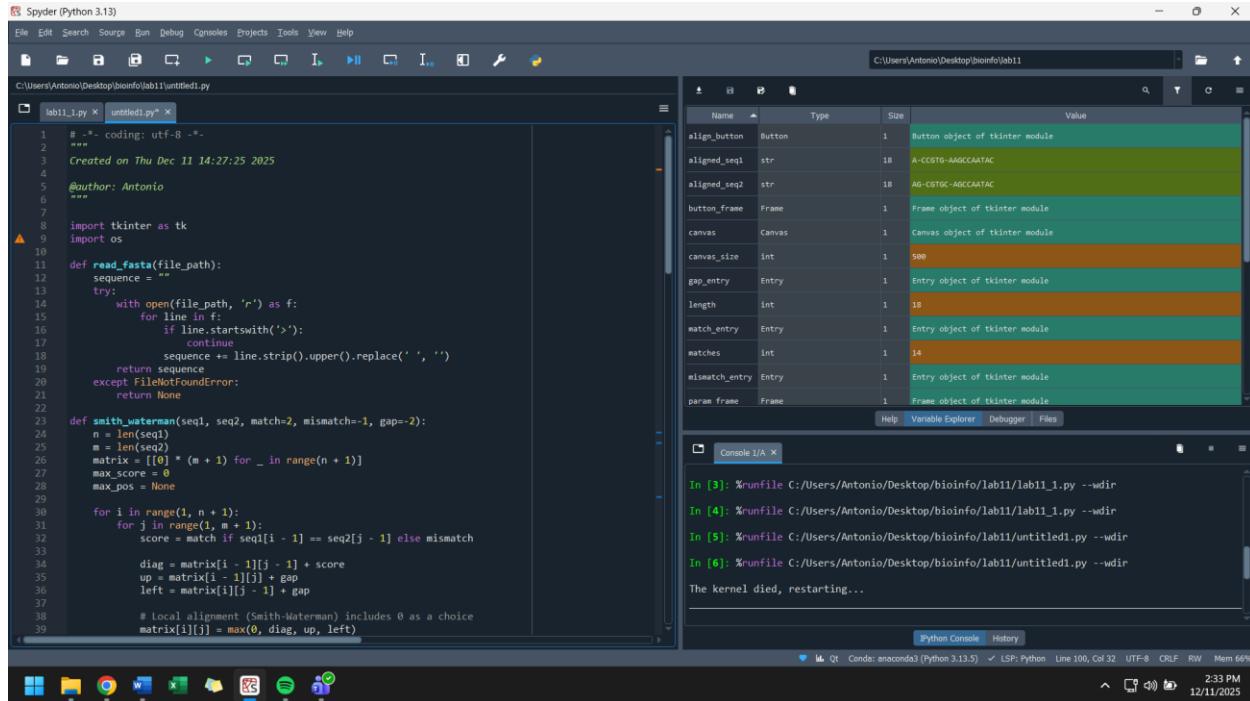
lab11_1.py



```
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, "ACCGTGAGCCAACT")
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, "AGCGTGAGCCAACT")
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()
```



lab11_2.py

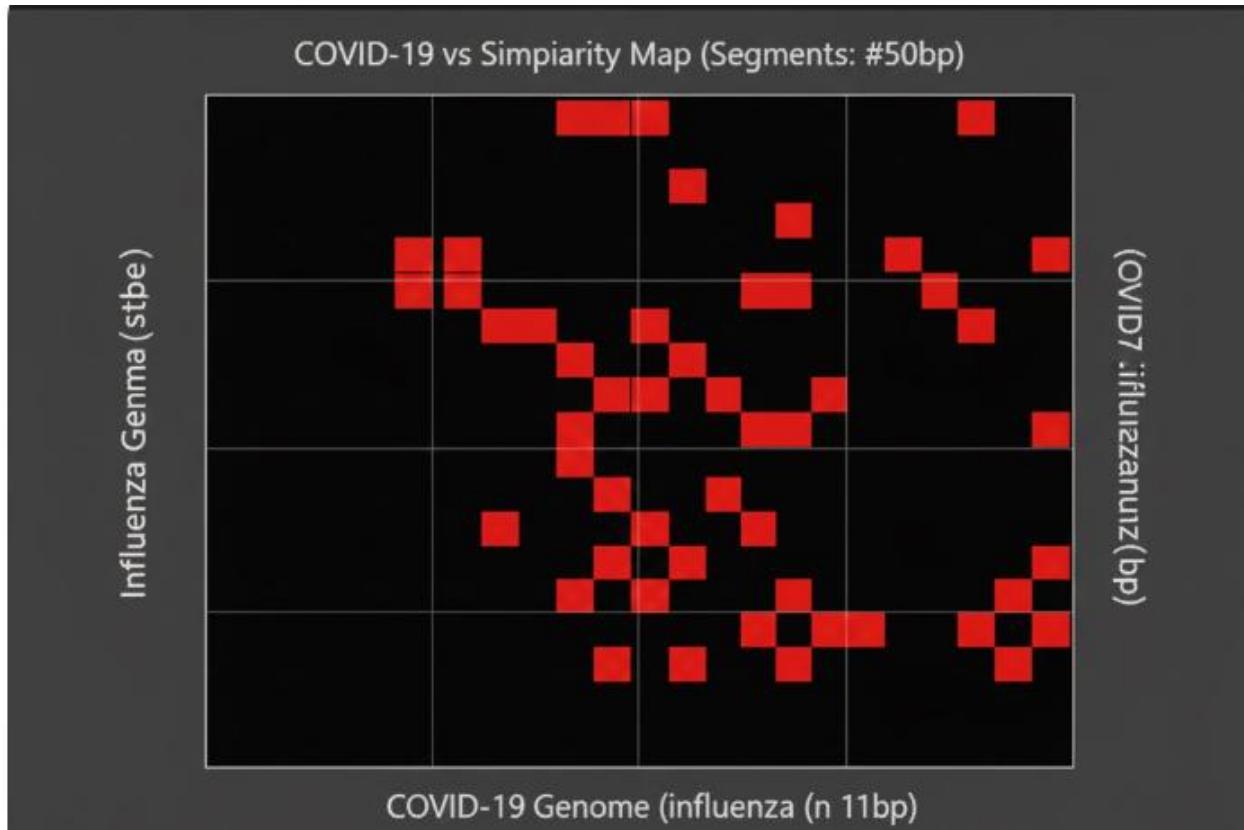


The screenshot shows the Spyder Python IDE interface. On the left, the code editor displays `lab11_1.py` containing Python code for reading FASTA files and performing Smith-Waterman local alignment. On the right, the Variable Explorer lists several objects: `align_button`, `aligned_seq1`, `aligned_seq2`, `button_frame`, `canvas`, `canvas_size`, `gap_entry`, `length`, `match_entry`, `matches`, `mismatch_entry`, and `param_frame`. The `aligned_seq1` and `aligned_seq2` variables are shown with their respective sequence values. Below the Variable Explorer is the Python Console, which shows the command `%runfile C:/Users/Antonio/Desktop/bioinfo/lab11/lab11_1.py --wdir` being run four times, resulting in the message "The kernel died, restarting...". The status bar at the bottom indicates the time as 2:33 PM and the date as 12/11/2025.

```

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     return sequence
20 except FileNotFoundError:
21     return None
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)

```



The screenshot shows the Spyder Python IDE interface. On the left, the code editor displays `lab11_1.py` with Python code for a local alignment. A tooltip window titled "Genome Similarity Visualizer (Local Alignmen..." is overlaid on the code, containing the instruction "Click 'Align and Visualize Genomes' to start. Ensure 'covid.fasta' and 'influenza.fasta' are in the same directory." On the right, the IPython console shows the command `%runfile C:/Users/Antonio/Desktop/bioinfo/lab11/lab11_1.py --wdir` being run, followed by the message "The kernel died, restarting...". Below the console is the "Python Console" tab. The status bar at the bottom indicates the time as 2:34 PM and the date as 12/11/2025.

