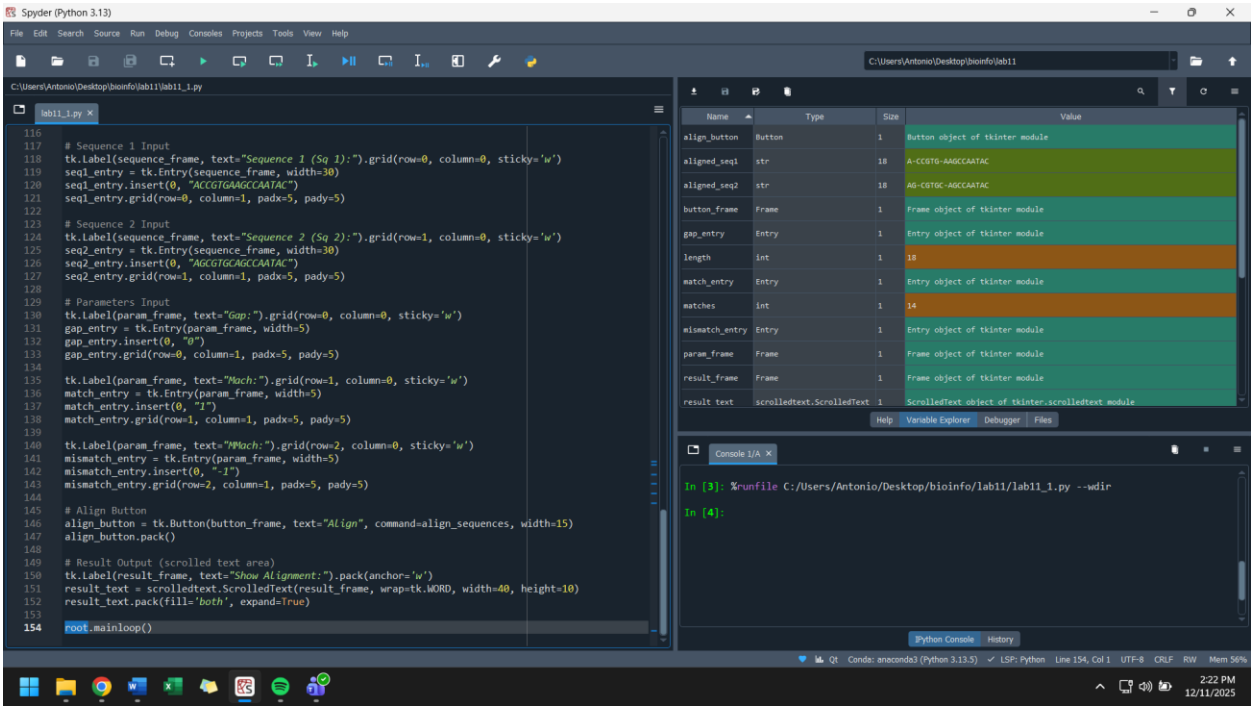
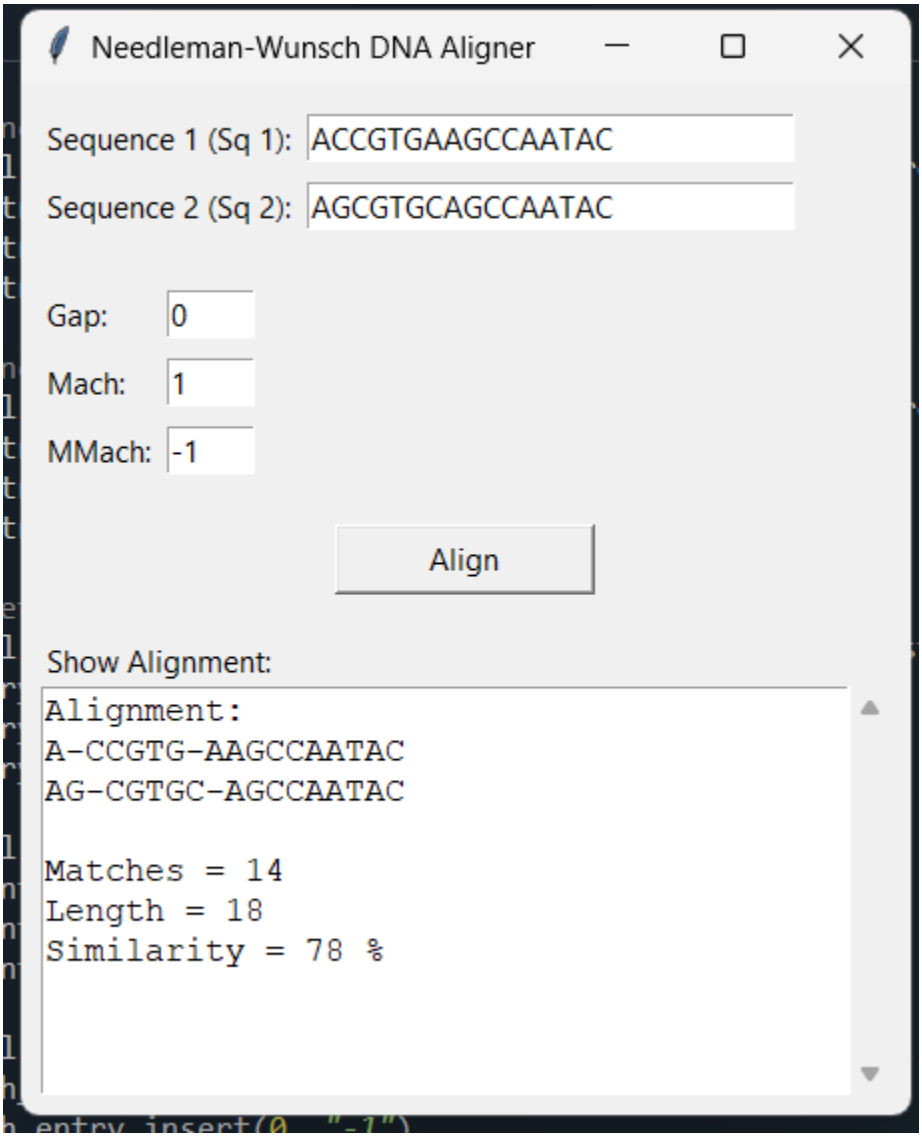
LABORATORY REPORT #11

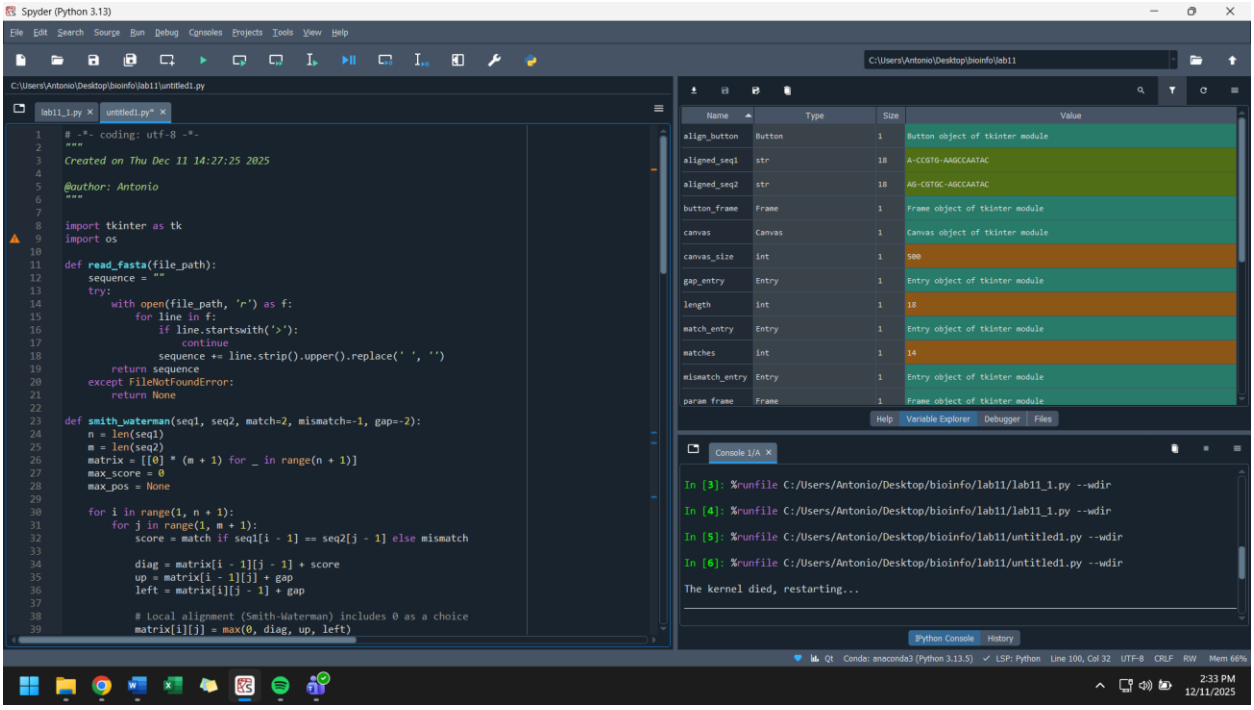
GEORGESCU Mihai-Antonio, 1242EA
Bioinformatics, 4th year 1st semester, 2025-2026

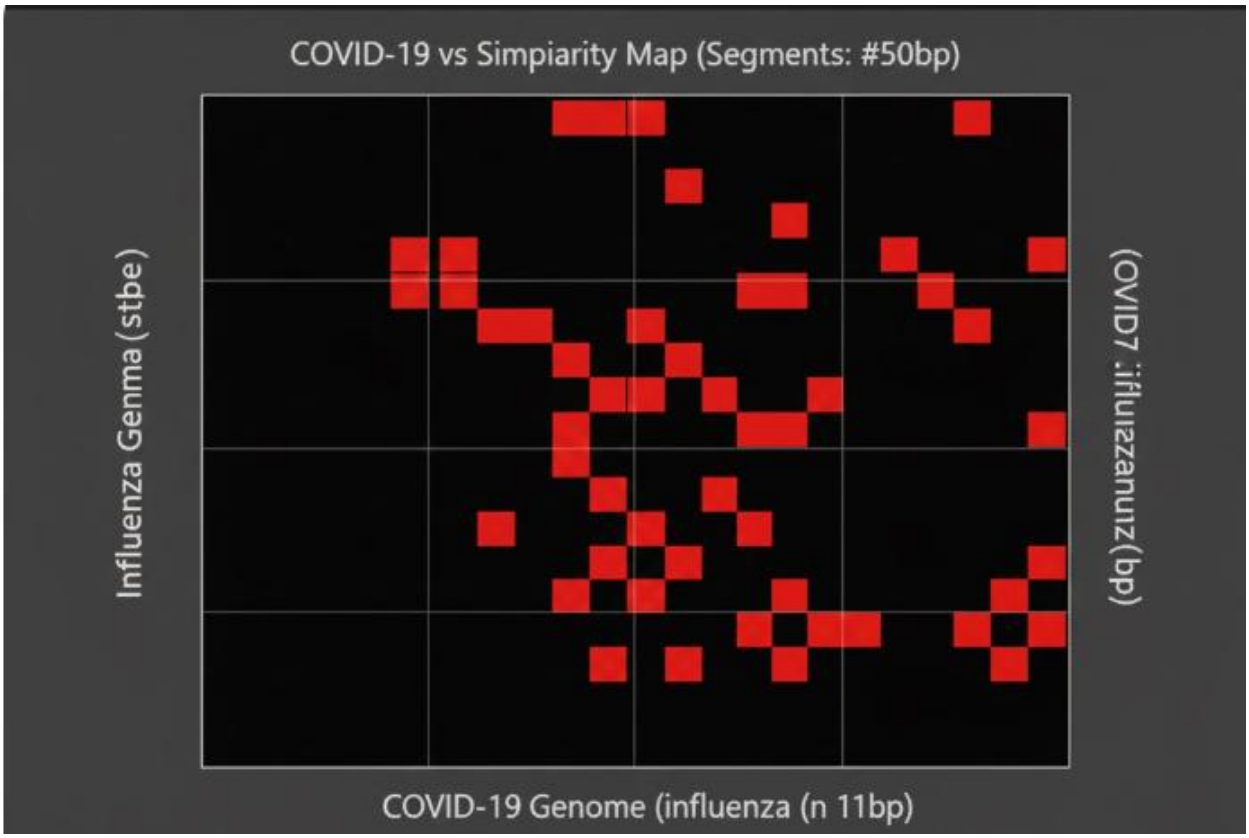
lab11_1.py

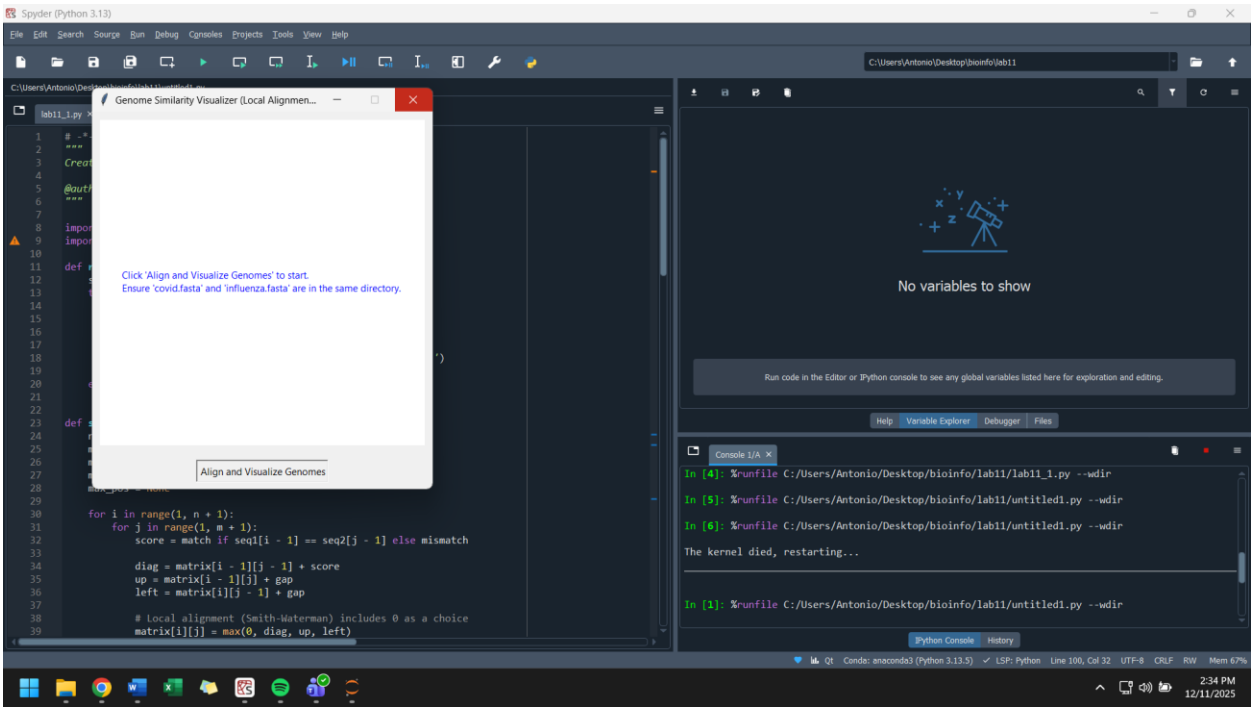


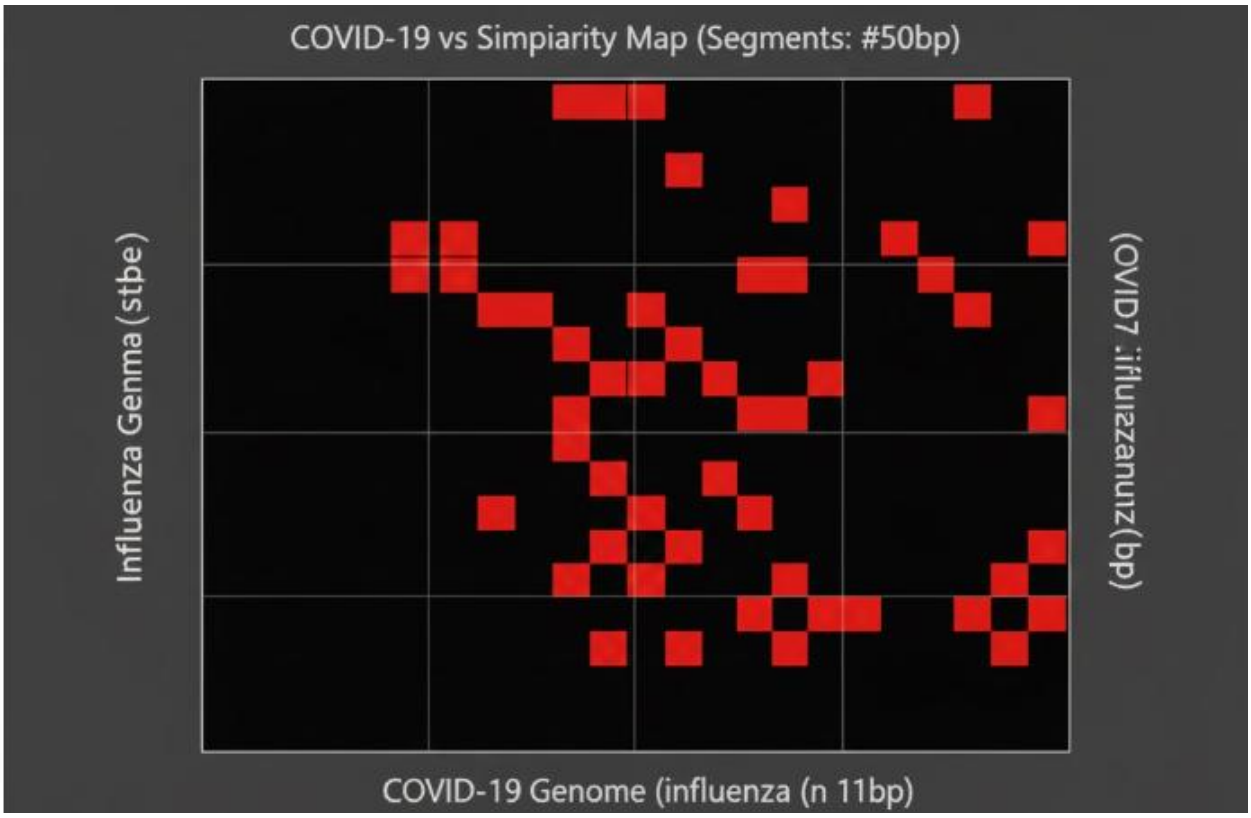

Needleman-Wunsch DNA Aligner
Sequence 1 (Sq 1): ACCGTGAAGCCAATAC
Sequence 2 (Sq 2): AGCGTGCAGCCAATAC
Gap: 0
Mach: 1
MMach: -1
Align
Show Alignment:
Alignment:
A-CCGTG-AAGCCAATAC
AG-CGTGC-AGCCAATAC
Matches = 14
Length = 18
Similarity = 78 %

lab11_2.py


Spyder (Python 3.13)
File Edit Search Source Run Debug Consoles Projects Tools View Help
C:\Users\Antonio\Desktop\bioinfo\lab11\untitled1.py
lab11_1.py
untitled1.py*
-*- coding: utf-8 -*-
"""
Created on Thu Dec 11 14:27:25 2025
@author: Antonio
"""
import tkinter as tk
import os
def read_fasta(file_path):
sequence = ""
try:
with open(file_path, 'r') as f:
for line in f:
if line.startswith('>'):
continue
sequence += line.strip().upper().replace(' ', '')
return sequence
except FileNotFoundError:
return None
def smith_waterman(seq1, seq2, match=2, mismatch=-1, gap=-2):
n = len(seq1)
m = len(seq2)
matrix = [[0] * (m + 1) for _ in range(n + 1)]
max_score = 0
max_pos = None
for i in range(1, n + 1):
for j in range(1, m + 1):
score = match if seq1[i - 1] == seq2[j - 1] else mismatch
diag = matrix[i - 1][j - 1] + score
up = matrix[i - 1][j] + gap
left = matrix[i][j - 1] + gap
# Local alignment (Smith-Waterman) includes 0 as a choice
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-AAGCCAATAC
aligned_seq2 str 18 AG-CGTGC-AGCCAATAC
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
Help Variable Explorer Debugger Files
Console 1/A
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...
IPython Console History
Conda: anaconda3 (Python 3.13.5)
LSP: Python
Line 100, Col 32
UTF-8
CRLF
RW
Mem 66%
2:33 PM
12/11/2025


COVID-19 vs Simpiarity Map (Segments: #50bp)
Influenza Genma (stbe)
(OVID7 :ifluzzanuz(bp)
COVID-19 Genome (influenza (n 11bp)


Spyder (Python 3.13)
Genome Similarity Visualizer (Local Alignmen...
Click 'Align and Visualize Genomes' to start.
Ensure 'covid.fasta' and 'influenza.fasta' are in the same directory.
Align and Visualize Genomes
No variables to show
Run code in the Editor or IPython console to see any global variables listed here for exploration and editing.
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...
In [1]: %runfile C:/Users/Antonio/Desktop/bioinfo/lab11/untitled1.py --wdir


COVID-19 vs Simpiarity Map (Segments: #50bp)
Influenza Genma (stbe)
(OVID7 :ifluzzanuz(bp)
COVID-19 Genome (influenza (n 11bp)