LABORATORY REPORT #3

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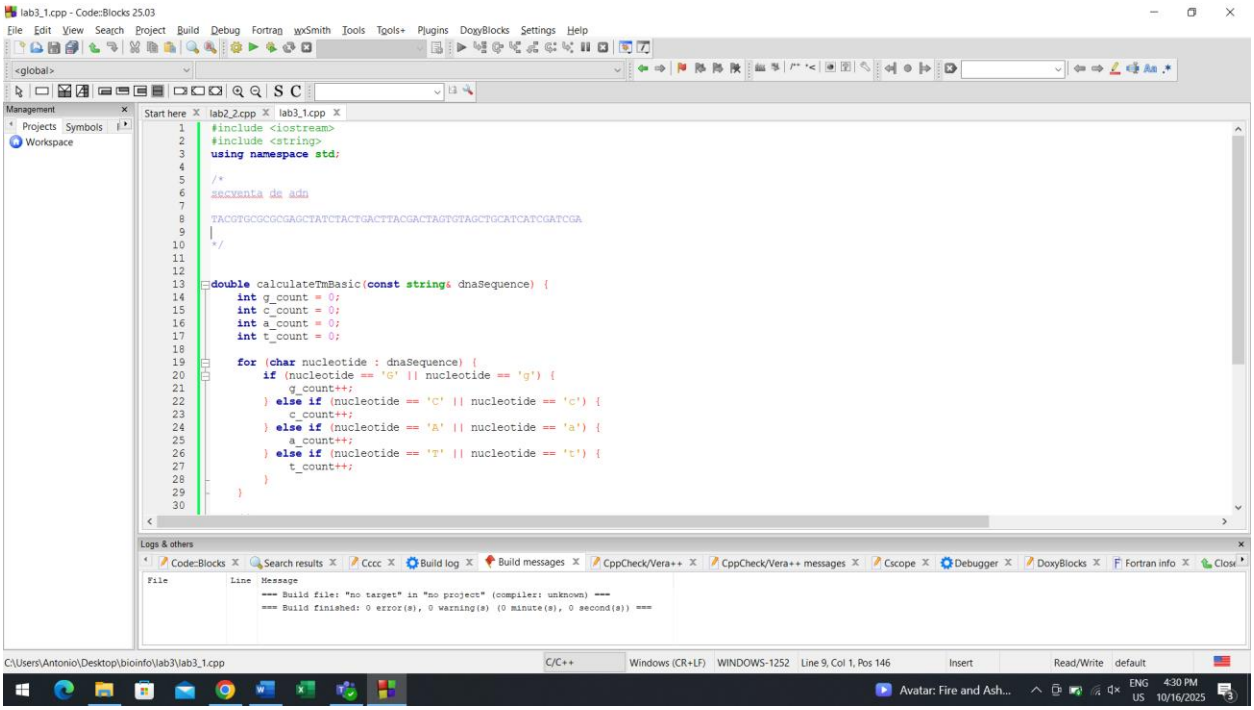
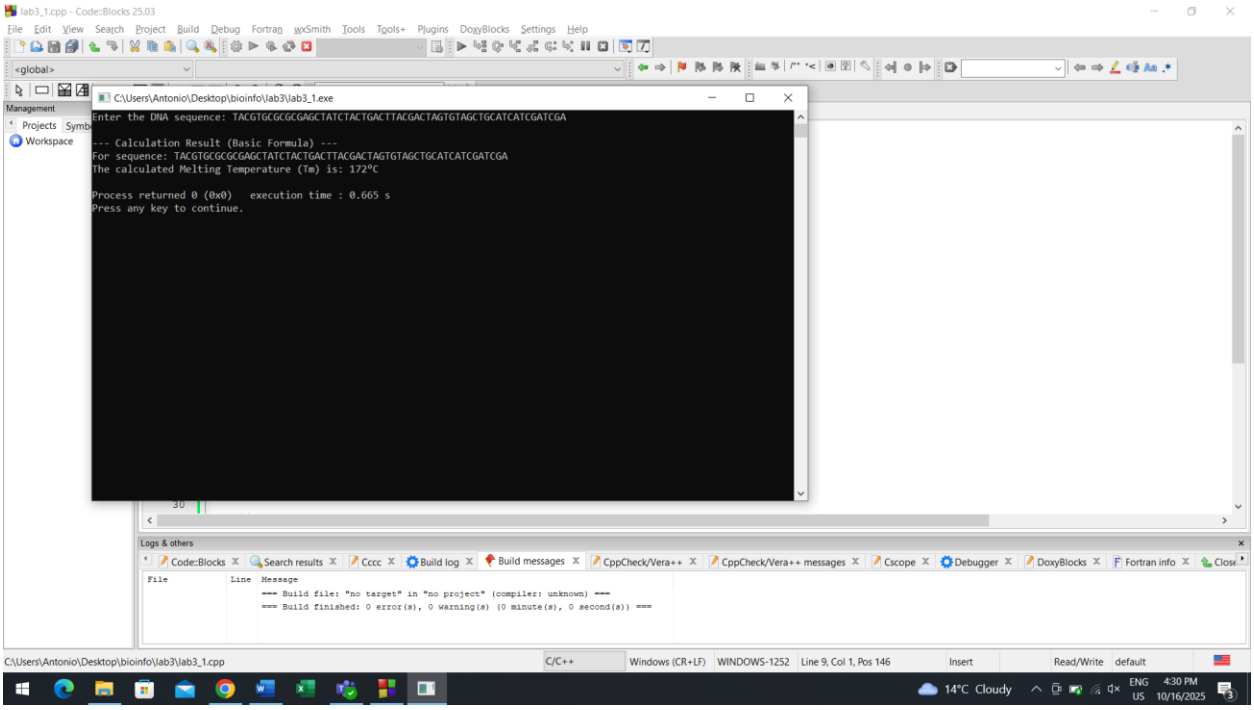
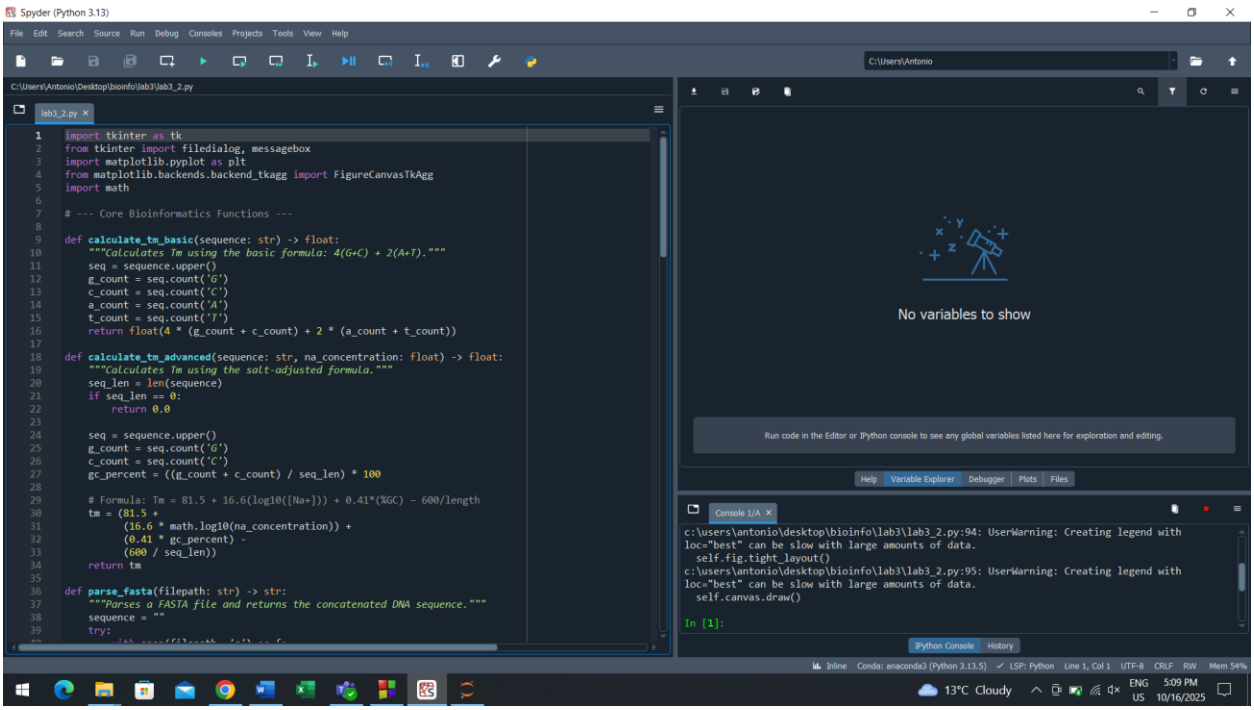
Bioinformatics, 4th year 1st semester, 2025-2026

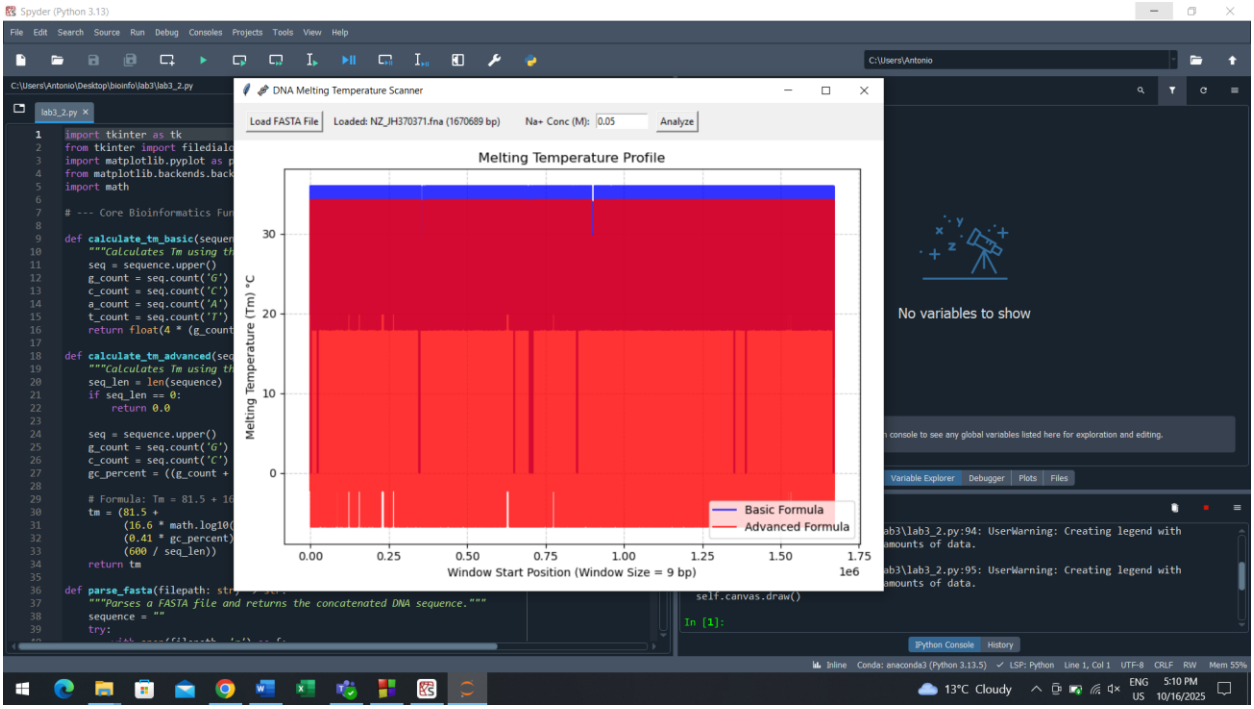
lab3_1.cpp



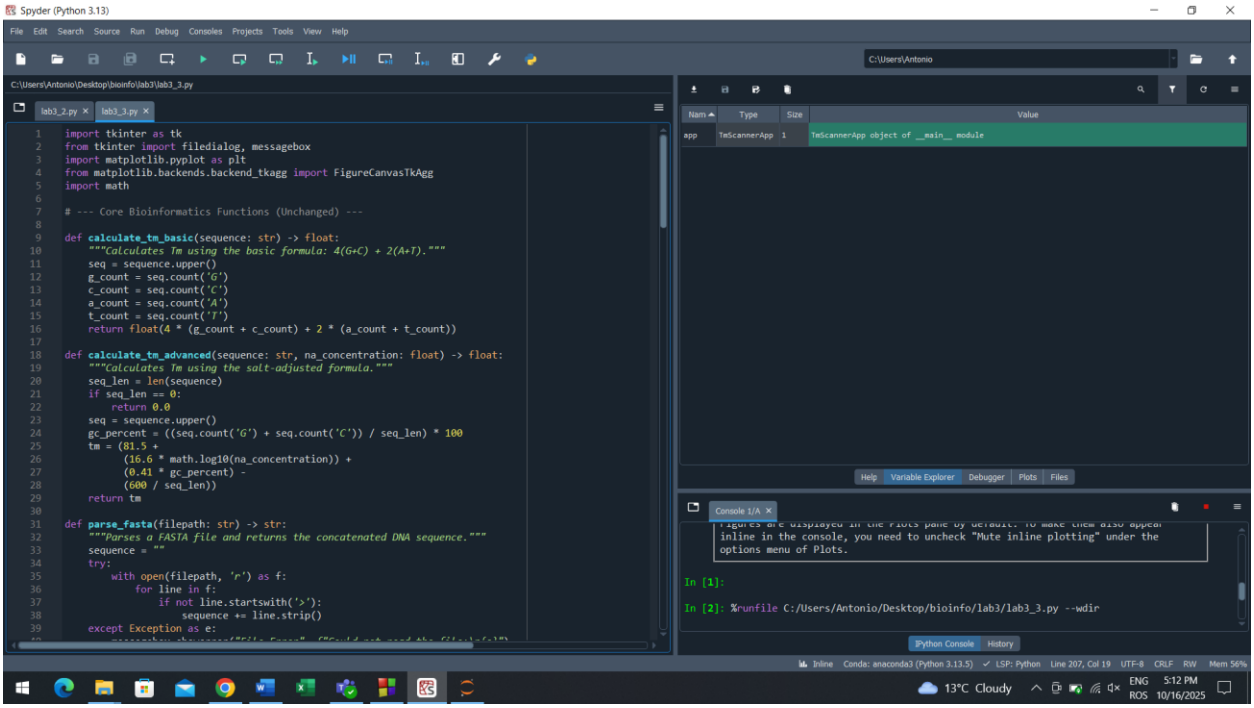

lab3_1.cpp - Code::Blocks 25.03
C:\Users\Antonio\Desktop\bioinfo\lab3\lab3_1.exe
Enter the DNA sequence: TACGTGCGCGCGAGCTATCTACTGACTTACGACTAGTGTAGCTGCATCATCGATCGA
--- Calculation Result (Basic Formula) ---
For sequence: TACGTGCGCGCGAGCTATCTACTGACTTACGACTAGTGTAGCTGCATCATCGATCGA
The calculated Melting Temperature (Tm) is: 172°C
Process returned 0 (0x0) execution time : 0.665 s
Press any key to continue.
Logs & others
Code::Blocks
Search results
Cccc
Build log
Build messages
CppCheck/Vera++
CppCheck/Vera++ messages
Cscope
Debugger
DoxyBlocks
Fortran info
File
Line
Message
=== Build file: "no target" in "no project" (compiler: unknown) ===
=== Build finished: 0 error(s), 0 warning(s) (0 minute(s), 0 second(s)) ===
C:\Users\Antonio\Desktop\bioinfo\lab3\lab3_1.cpp
C/C++
Windows (CR+LF)
WINDOWS-1252
Line 9, Col 1, Pos 146
Insert
Read/Write
default
14°C Cloudy
ENG
US
4:30 PM
10/16/2025

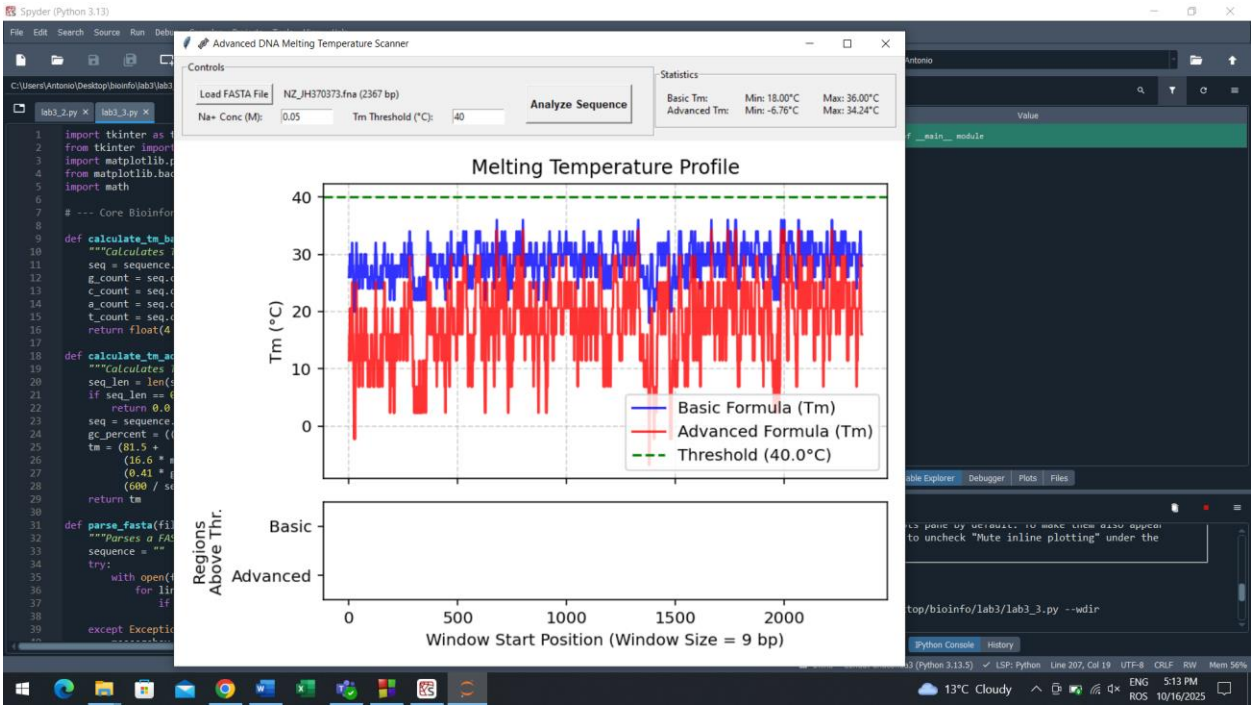
lab3_2.py


Spyder (Python 3.13)
C:\Users\Antonio\Desktop\bioinfo\lab3\lab3_2.py
import tkinter as tk
from tkinter import filedialog, messagebox
import matplotlib.pyplot as plt
from matplotlib.backends.backend_tkagg import FigureCanvasTkAgg
import math
# --- Core Bioinformatics Functions ---
def calculate_tm_basic(sequence: str) -> float:
"""Calculates Tm using the basic formula: 4(G+C) + 2(A+T)."""
seq = sequence.upper()
g_count = seq.count('G')
c_count = seq.count('C')
a_count = seq.count('A')
t_count = seq.count('T')
return float(4 * (g_count + c_count) + 2 * (a_count + t_count))
def calculate_tm_advanced(sequence: str, na_concentration: float) -> float:
"""Calculates Tm using the salt-adjusted formula."""
seq_len = len(sequence)
if seq_len == 0:
return 0.0
seq = sequence.upper()
g_count = seq.count('G')
c_count = seq.count('C')
gc_percent = ((g_count + c_count) / seq_len) * 100
# Formula: Tm = 81.5 + 16.6(log10([Na+])) + 0.41*(%GC) - 600/length
tm = (81.5 +
(16.6 * math.log10(na_concentration)) +
(0.41 * gc_percent) -
(600 / seq_len))
return tm
def parse_fasta(filepath: str) -> str:
"""Parses a FASTA file and returns the concatenated DNA sequence."""
sequence = ""
try:
C:\Users\Antonio
No variables to show
Run code in the Editor or IPython console to see any global variables listed here for exploration and editing.
Help
Variable Explorer
Debugger
Plots
Files
Console 1/A
c:\users\antonio\desktop\bioinfo\lab3\lab3_2.py:94: UserWarning: Creating legend with loc="best" can be slow with large amounts of data.
self.fig.tight_layout()
c:\users\antonio\desktop\bioinfo\lab3\lab3_2.py:95: UserWarning: Creating legend with loc="best" can be slow with large amounts of data.
self.canvas.draw()
In [1]:
IPython Console
History
13°C Cloudy
ENG
US
5:09 PM
10/16/2025


DNA Melting Temperature Scanner
Load FASTA File
Loaded: NZ_JH370371.fna (1670689 bp)
Na+ Conc (M):
0.05
Analyze
Melting Temperature Profile
Melting Temperature (Tm) °C
Window Start Position (Window Size = 9 bp)
1e6
Basic Formula
Advanced Formula
No variables to show

lab3_3.py




Advanced DNA Melting Temperature Scanner
Controls
Load FASTA File
NZ_JH370373.fna (2367 bp)
Na+ Conc (M):
0.05
Tm Threshold (°C):
40
Analyze Sequence
Statistics
Basic Tm:
Min: 18.00°C
Max: 36.00°C
Advanced Tm:
Min: -6.76°C
Max: 34.24°C
Melting Temperature Profile
Tm (°C)
Basic Formula (Tm)
Advanced Formula (Tm)
Threshold (40.0°C)
Regions Above Thr.
Basic
Advanced
Window Start Position (Window Size = 9 bp)