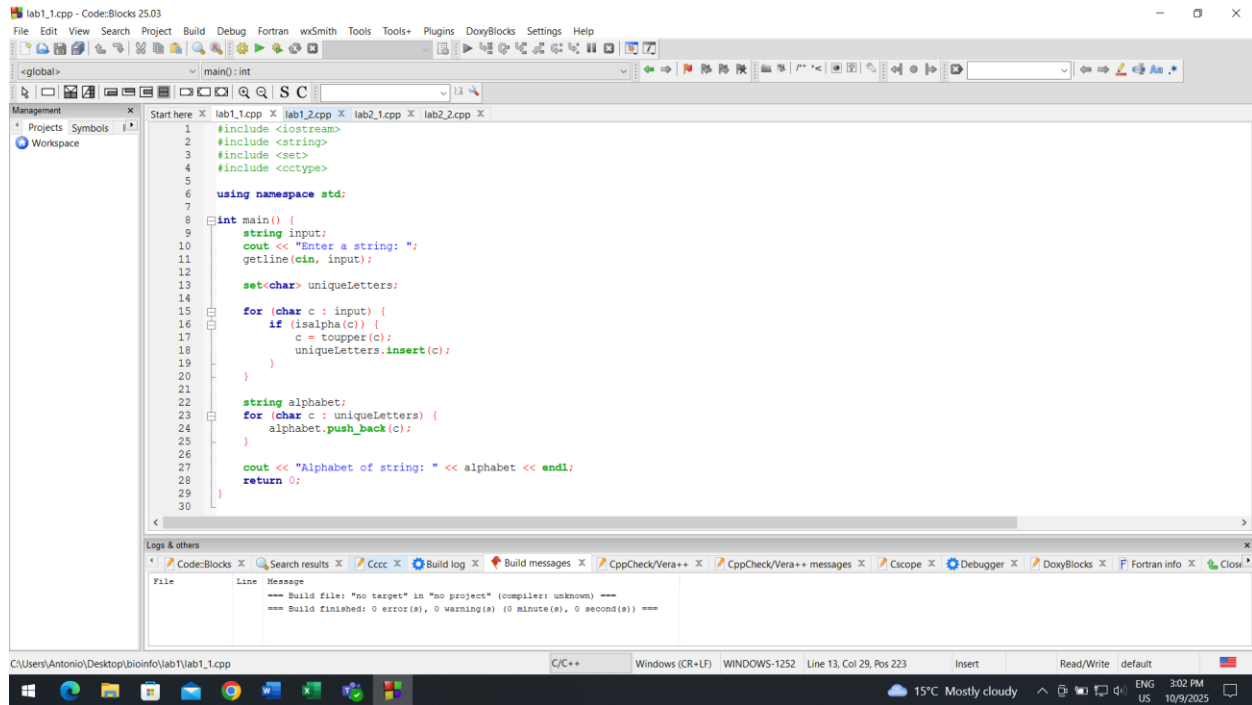


LABORATORY REPORT #1

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

lab1_1.cpp

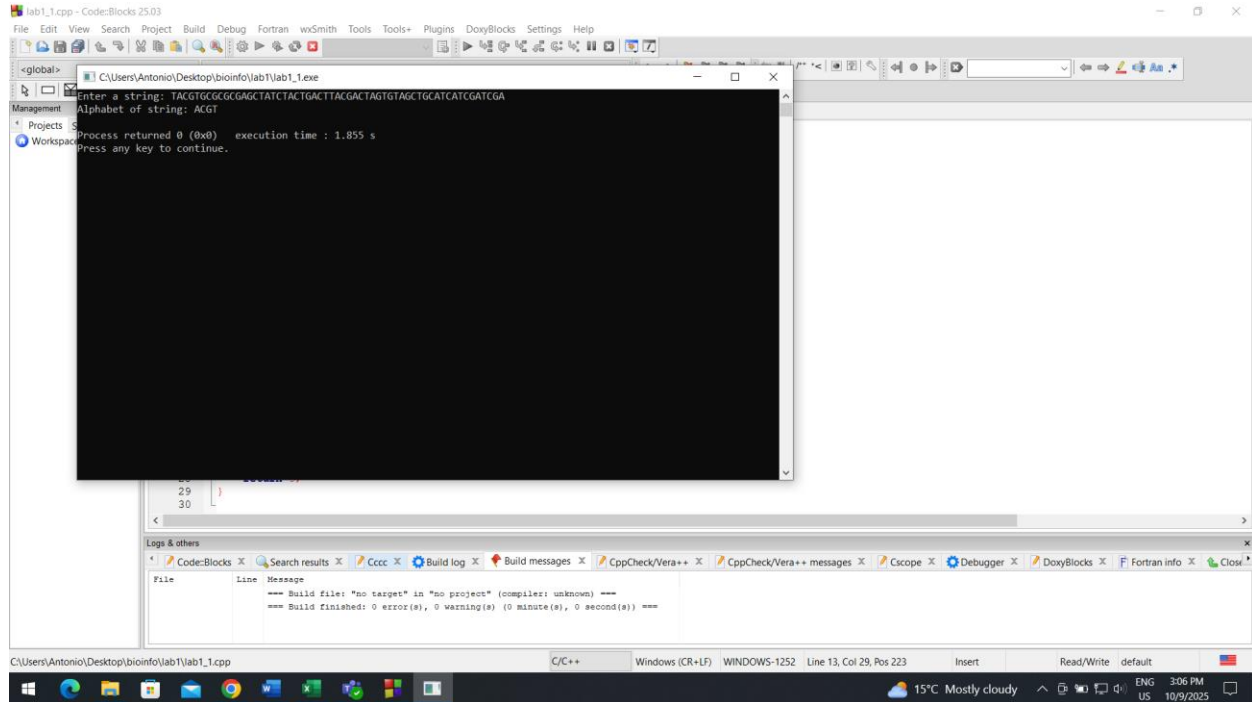


```
1 #include <iostream>
2 #include <string>
3 #include <set>
4 #include <ctype>
5
6 using namespace std;
7
8 int main() {
9     string input;
10    cout << "Enter a string: ";
11    getline(cin, input);
12
13    set<char> uniqueLetters;
14
15    for (char c : input) {
16        if (isalpha(c)) {
17            c = toupper(c);
18            uniqueLetters.insert(c);
19        }
20    }
21
22    string alphabet;
23    for (char c : uniqueLetters) {
24        alphabet.push_back(c);
25    }
26
27    cout << "Alphabet of string: " << alphabet << endl;
28    return 0;
29 }
```

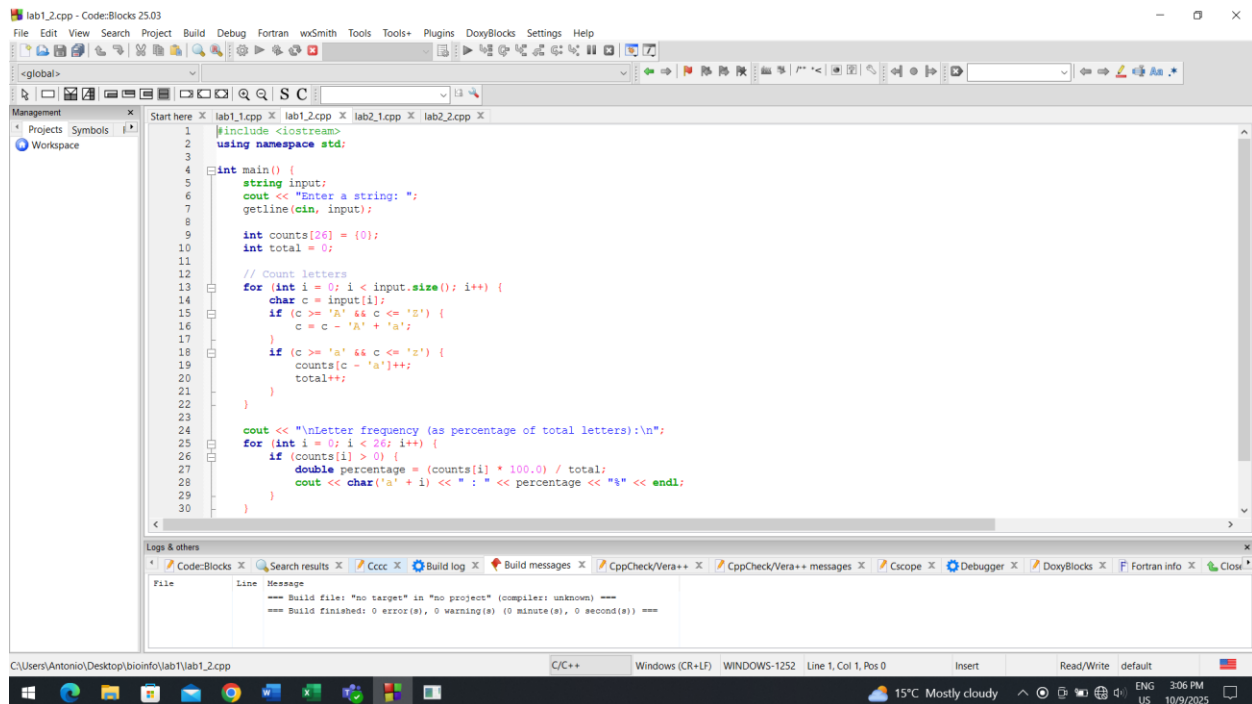
Build log:

```
==== Build file: "no target" in "no project" (compiler: unknown) ====
==== Build finished: 0 error(s), 0 warning(s) (0 minute(s), 0 second(s)) ====
```

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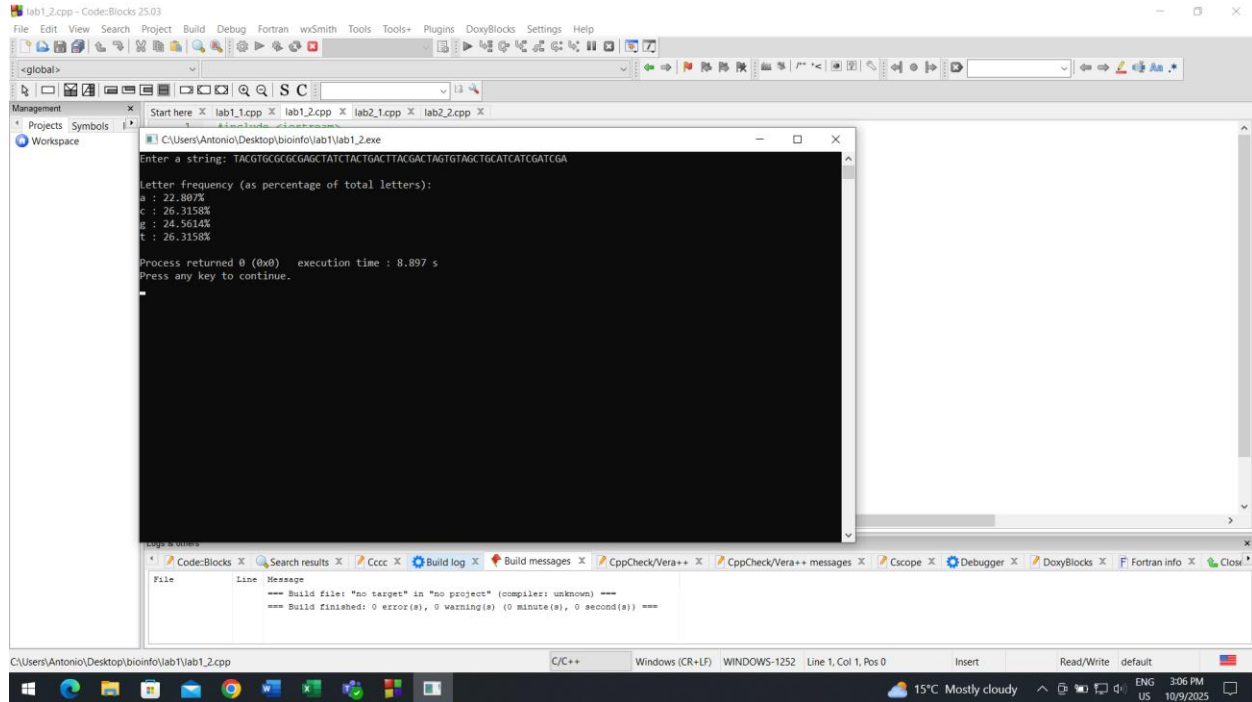


lab1_2.cpp



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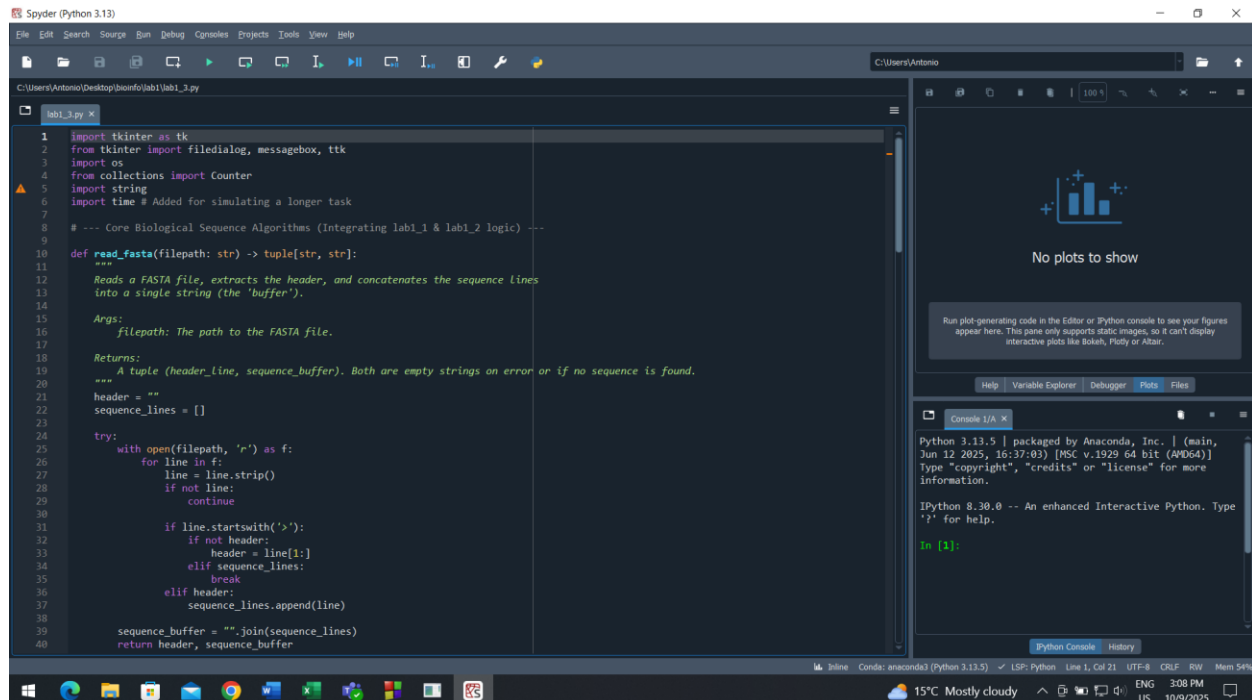


The screenshot shows the Code::Blocks IDE with a C++ project named 'lab1_2.cpp'. The program is running, and the output window displays the following text:

```
Enter a string: TACGTGCGCGAGCTATCTACTGACTTACGACTAGTGTAGCTGATCATCGATCGA
Letter frequency (as percentage of total letters):
a : 22.897%
c : 26.3158%
g : 24.5614%
t : 26.3158%
Process returned 0 (0x0)   execution time : 8.897 s
Press any key to continue.
```

The status bar at the bottom indicates the file is 'C:\Users\Antonio\Desktop\bioinfo\lab1\lab1_2.cpp' and the compiler is 'C/C++'.

lab1_3.py



The screenshot shows the Spyder Python IDE with a file named 'lab1_3.py'. The code is as follows:

```
1 import tkinter as tk
2 from tkinter import filedialog, messagebox, ttk
3 import os
4 from collections import Counter
5 import string
6 import time # Added for simulating a longer task
7
8 # --- Core Biological Sequence Algorithms (Integrating lab1_1 & lab1_2 logic) ---
9
10 def read_fasta(filepath: str) -> tuple[str, str]:
11     """
12     Reads a FASTA file, extracts the header, and concatenates the sequence lines
13     into a single string (the 'buffer').
14
15     Args:
16         filepath: The path to the FASTA file.
17
18     Returns:
19         A tuple (header_line, sequence_buffer). Both are empty strings on error or if no sequence is found.
20     """
21     header = ""
22     sequence_lines = []
23
24     try:
25         with open(filepath, 'r') as f:
26             for line in f:
27                 line = line.strip()
28                 if not line:
29                     continue
30
31                 if line.startswith('>'):
32                     if not header:
33                         header = line[1:]
34                     elif sequence_lines:
35                         break
36                 elif header:
37                     sequence_lines.append(line)
38
39     sequence_buffer = "".join(sequence_lines)
40     return header, sequence_buffer
```

The status bar at the bottom indicates the file is 'C:\Users\Antonio\Desktop\bioinfo\lab1\lab1_3.py' and the interpreter is 'Python 3.13.5'.

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