

Criterion A: Planning

Defining the Problem

The client is my IB Biology teacher, who regularly teaches lessons on DNA transcription, RNA translation, and protein synthesis. A common problem he encounters is the difficulty students face when trying to manually analyze DNA and RNA sequences. These sequences are often long strings of letters (e.g., ACGTCGTTA), making it easy to misread or misinterpret codons. Students frequently make mistakes while transcribing DNA to RNA, translating RNA into amino acids, or identifying structural protein features. Further, the lack of accessible tools to help view mutations in proteins makes it harder for students to develop a full understanding of how biological sequences function in real systems.

Rationale for the Proposed Solution

The client requested a software solution that could automate the transcription and translation processes while also offering advanced analysis of the resulting protein sequence. The goal is to reduce human error, improve learning comprehension, and speed up the process of analyzing genetic material. By entering a DNA or RNA strand, the user will be able to receive an accurate protein sequence, free from manual lookup errors or codon chart confusion.

The program will also highlight key features in the amino acid chain—such as start codons, hydrophobic stretches, and acidic patches—and offer predictions for simplified secondary structures. These features will be useful not only for classroom learning but also for future students engaged in biological data analysis or bioinformatics research.

Additionally, I suggested adding a mutation function where students can play around with different types to see how impactful each kind of mutation really is (point mutations, deletions, and insertions).

Java was chosen as the development language because it is supported on most platforms and aligns with the IB Computer Science curriculum. The project will also be built in Processing, allowing for the implementation of an interactive graphical interface suitable for student use.

Success Criteria

1. The application accepts both DNA and RNA sequences and validates input to prevent invalid characters.
2. The application transcribes DNA into RNA and translates RNA into the correct protein sequence using a codon chart.
3. The application identifies and displays key protein features such as motifs, hydrophobic regions, and acidic patches.
4. The application provides an interactive and user-friendly interface with clearly labeled input boxes and output areas.
5. The application allows users to save their results to a file for later reference or submission.