**PS4:** *Edit Distance*
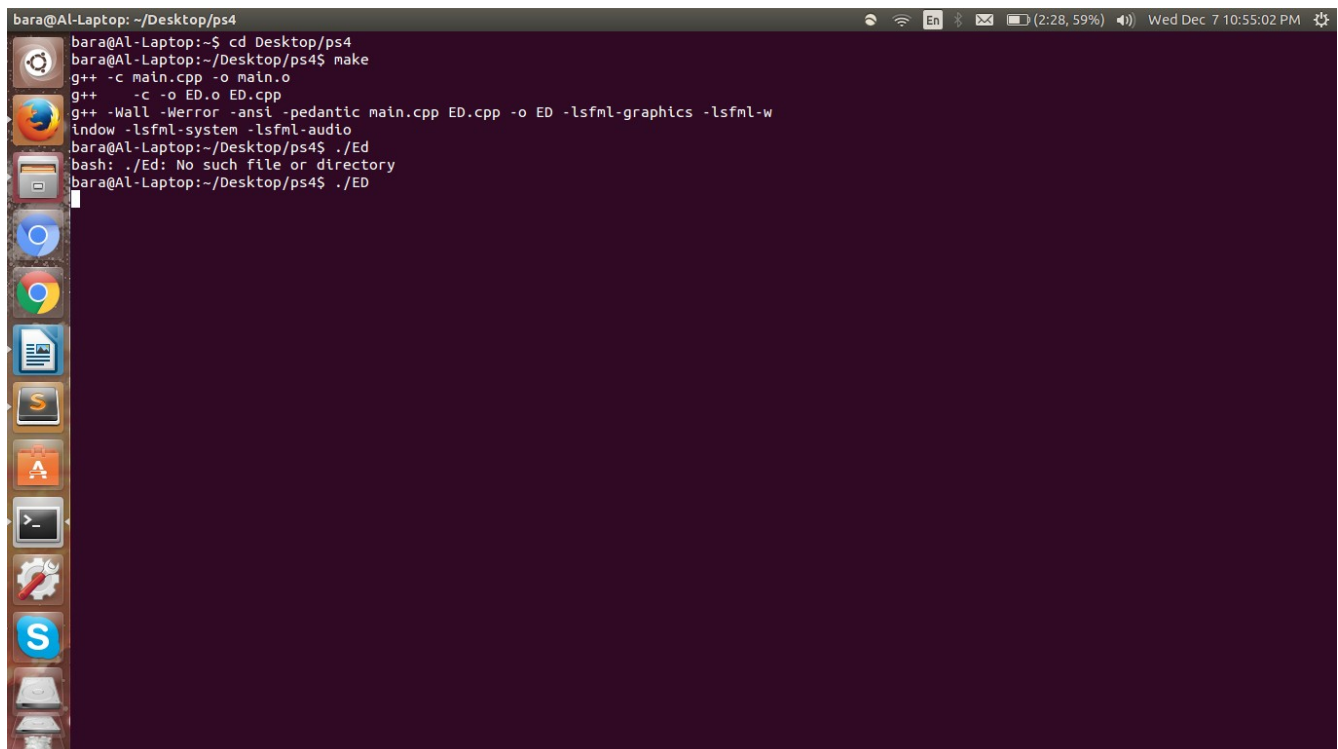
      In this assignment, this program is to create a optimal sequence alignment of two DNA strings. It will measure the similarity of two genetic sequences by the edit distance. It can be used for plagiarism detection, file revisioning. This is accomplished when two letters are aligned. If they are the same, it cost 0 bits. If they are different, it costs 1 bit. If their inset any at all, it will cost 2 bits.

      This assignment could be approached in many different ways. Recursion and dynamic programming were recommend choices for this assignment. I tried taking the dynamic approach using an NxM matrix. Creating a class called ED, the constructor took two string were set to the member variables.

      For the assignment, I didn't learn so much. However, I did learn the understand of edit distance. I learned what the necessary bits are needed, the alignment, and the total amount of distance needed for alignment.

      Sadly, I was not able to finish this assignment. I believe I was confused on how to approach this assignment and felt lost on what to do next. When I tried running the program, I had a continues loop and had to close the the program by killing it.