Karim Itani
PA05 - report

In order to find the longest gene sequence (and its length), I used a recursive approach. The recursive function checks for all possible sequences and returns the array that contains the longest sequence. The function works similar to an adjacency matrix. It checks the numbers that can be accessed by a particular node, attempts to find them in the following sequences, and if it cannot be found, it returns back to the function that called it. While doing so it makes appropriate updates to the maximum length and the array that contains the longest sequence. In order to make sure that the recursive function takes into account the order of the numbers, an array that contains the position of the previous number that was 'found' is passed into it as an input. While searching for the next number in the sequence, it searches from this position, to the end of the array. This ensures that for any given sequence, it only checks each value once.

As there are m arrays with n sequences each, and each of the n positions are traversed in the worst case n times, the time complexity of the code is **O(m * n^2).**