1. **Suffix Trees for Finding MUMs:** Show how MUMmer would use a suffix tree to find the MUMs in the following two sequences. Be sure to show the MUMs returned.

   - Genome A: `ttacgc`
   - Genome B: `geatac`
2. **Threading:** Consider a simple threading problem in which we have a template with three segments \((i, j, k)\). We are given a sequence for which there are two possible starting positions for each segment.

(a) Given the following values for the scores of the individual segments and the scores for segment interactions, show how the branch-and-bound method would find the optimal threading.

\[
\begin{align*}
g_1(i, 2) &= 4 & g_1(j, 8) &= 2 & g_1(k, 13) &= 1 \\
g_1(i, 3) &= 3 & g_1(j, 9) &= 5 & g_1(k, 14) &= 10 \\
g_2(i, j, 2, 8) &= 6 & g_2(i, k, 2, 13) &= 1 & g_2(j, k, 8, 13) &= 3 \\
g_2(i, j, 2, 9) &= 0 & g_2(i, k, 2, 14) &= 0 & g_2(j, k, 8, 14) &= 12 \\
g_2(i, j, 3, 8) &= 1 & g_2(i, k, 3, 13) &= 9 & g_2(j, k, 9, 13) &= 5 \\
g_2(i, j, 3, 9) &= 0 & g_2(i, k, 3, 14) &= 0 & g_2(j, k, 9, 14) &= 11
\end{align*}
\]

Use the “simple lower bound” presented in class. When splitting a threading, split the segment having the minimal \(g_1\) value for some position (e.g. split on \(k\) first since \(g_1(k, 13) = 1\)). To split a selected segment, divide it into two intervals of length one.
3. RNA Secondary Structure Prediction: Show how the Nussinov algorithm would predict the secondary structure of the RNA sequence: \texttt{ccaccugg}.