1. Find an optimal global alignment of $s = AACAG$ with $t = ATCCGA$ and scores 3 for match and $-2$ for mismatch but with the gap penalty function $\gamma(g) = -2 - g$.

2. Repeat the previous one for another pair, say $s = ACGA$ and $t = TATA$, keeping the same scores.

3. Show the following facts. Let $n$ be the length of one string, $m$ the length of another.
   
   • Time complexity of the global alignment algorithm with a linear gap penalty function is $\Theta(nm)$.
   • Time complexity of the global alignment algorithm with an affine gap penalty function is $\Theta(nm)$.
   • Time complexity of the global alignment algorithm with a "general" gap penalty function is $\Theta(nm(n + m))$.

4. Let $s = ACAGT$ and $t = AAACAGGTATATGCAT$ with scores 3 for match and $-2$ for mismatch and use the linear gap penalty with $\gamma(g) = -3g$. Find an optimal semi-global alignment of $s$ with $t$.

5. Assume the probability distribution for DNA characters is uniform, i.e. $p(A) = p(C) = p(G) = p(T) = 0.25$ and consider the local alignment problem. Check if given functions are proper scoring functions for the problem (Provide explanation):
   
   • 2 for match, $-1$ for mismatch, $\gamma(g) = -g$.
   • $-1$ for match, $-7$ for mismatch, $\gamma(g) = -2g$.
   • 11 for match, $-1.5$ for mismatch, $\gamma(g) = -g$. 