

FYS 102: Bioinformatics
Homework 5
Due Wednesday, October 24
(Start now!)

1. Consider the DNA sequences $v = \text{CCTAGTTC}$ and $w = \text{TCATCTCG}$. Answer each of the following questions by constructing the appropriate dynamic programming table. In your answers, give both the scores and the actual sequences.
 - (a) Find the longest common subsequence for v and w .
 - (b) Find the maximum global sequence alignment for v and w using indel penalty $\sigma = 2$ and mismatch penalty $\mu = 1$.
 - (c) Find the maximum local sequence alignment for v and w using the same penalties as above.
2. How many different paths are there from source to sink in a rectangular $m \times n$ grid?
3. Write a recursive function in Python that adds all the numbers in a list of numbers. The function cannot contain any loops or any built-in Python functions.
4. Implement in Python the Smith-Waterman local sequence alignment algorithm by modifying the global sequence alignment function that we discussed in class (and available on my web site). The modifications are described in section 6.8.

Start early and have fun!