

LAB 4 – Perl IV

This lab can be rather advanced, especially for beginners. If you feel that you still have some unfinished business related to Labs 2 or 3, and that getting help with this will teach you more Perl, then you should take care of that before moving to lab 4.

Task 1 - Motif finding

Use the pseudo-code from the lecture slides and write two programs that finds the best scoring 15mers in the sequences in *motifs.txt*:

- a) An exhaustive algorithm.
- b) A greedy algorithm.

Task 2 - Global sequence alignment

Use the pseudo-code from the lecture slides to implement a global sequence alignment. Start by filling in the dynamic programming matrix and then try to write a program that reconstruct the actual alignment. Test you program on Yeast paralogs from previous labs.

Optional: Extend you code with more advanced scoring schemes. Try implementing local alignment.

To get the lab approved, send your code to: [jenny.onskog \(at\)plantphys.umu.se](mailto:jenny.onskog@plantphys.umu.se)