



Home assignment 2

Purpose: Explore your proteins with sequence alignment methods

1. Run BLAST over SwissProt databases looking for homologues to your study proteins (select two or three most significant). Get the accession numbers for the most relevant hits and retrieve the adequate GO annotations using ProteinON (<http://www.lasige.di.fc.ul.pt/webtools/proteinon/>) or other online resource.
2. Perform a PSI-BLAST over your proteins and repeat the same procedure for the GO annotations.
3. Separately perform multiple sequence alignments (MSA) with ClustalOmega for each of the BLAST results of your study proteins using the results from BLAST or PSI-BLAST
4. Construct the adequate Hidden Markov Models for each MSA using HMMER3
5. Use the HMMs produced to verify its adequacy in identifying conserved regions in all your study proteins.

Write a report detailing the most important conclusions of your work. Please detail and justify all the criteria used for each part of your work. On the last part your report give some suggestions about how this work could be automated if this type of analysis would be repeated a large number of times.

Each report must be identified on the first page with the name of the student, student ID and MSc program (**Maximum size:5 pages, but annexes are unlimited**)

Deadline: April 9, 2017

The submission will be online in a PDF file using FCUL's Moodle