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Lab 4 Report

Report the difference in your results for 7LESS using Pfam_fs and Pfam_ls:
While the sequences returned for pfam_ls and pfam_fm were exactly the same, the acceptance thresholds were not. Pfram_fs can partially match to a family while pfam_ls must match the entire sequence. The returned sequences were close enough that the distinction between the two methods was insignificant.

Briefly summarize the advantages and disadvantages of HMMER vs. BLAST:
HMMER's HMM contains information about position specific gap penalties, make the process much more intelligent than BLAST, whose alignments depend largely on a user inputted gap penalty. They are similar in the amount of time needed to search. An advantage of BLAST is the nice user interface and sequence visualizations; all of HMMER's output was in plain text. Another disadvantage of HMMER is that it requires prebuilt libraries of protein families whose contents are decided by an expert. Consequently, HMMER results can mirror expert preconception rather than computationally driven conclusion.