The Pfam database

The Pfam (protein family) data base is one of the main repositories for hosting information about evolutionarily conserved - and potentially functionally conserved - protein (sub)-sequences. Multiple sequence alignment of such (sub-)sequences - in common jargon they are typically referred to as Pfam domains - are used for training profile hidden Markov models (Pfam uses exclusively Plan7 pHMMs). Search algorithms, such as hmmscan or hmmsearch can then be used to identify instances of the modelled domains. Searches against the Pfam database can be performed online via the Pfam or the HMMER webpages. Alternatively, the HMMER package and the Pfam database can be downloaded for running the search locally on your computer.

Pfam provides an quick introductory tour that can be accessed via this LINK.

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Last update: **2019/01/21 20:24**