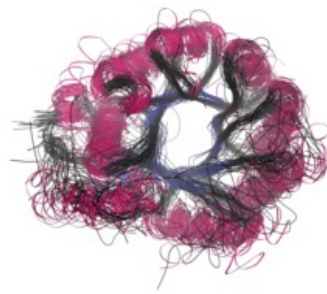Structural superimposition & sequence alignments from agglomerative clustering
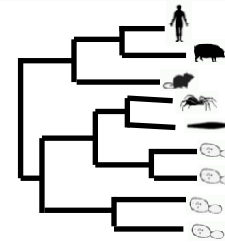
FunFam 1
FunFam 2
FunFam 3

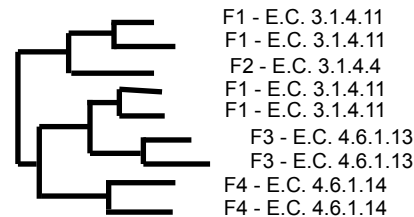Structurally informed multipule sequence alignment

Filtered alignment maintaining UniProt reviewed entries with function annotation

Generate phylogenetic tree using TreeBest, combining ML and taxonomic lineage tree

Add functional information i.e. E.C. numbers

F1 - E.C. 3.1.4.11
F1 - E.C. 3.1.4.11
F2 - E.C. 3.1.4.4
F1 - E.C. 3.1.4.11
F1 - E.C. 3.1.4.11
F3 - E.C. 4.6.1.13
F3 - E.C. 4.6.1.13
F4 - E.C. 4.6.1.14
F4 - E.C. 4.6.1.14

Calculate ancestral character estimations for each node in the tree. Using max likelihood at each node, count changes from root to branch.

F1
F1
F1
F1
F1
F3
F1
F4

F1 - E.C. 3.1.4.11
F1 - E.C. 3.1.4.11
F2 - E.C. 3.1.4.4
F1 - E.C. 3.1.4.11
F1 - E.C. 3.1.4.11
F3 - E.C. 4.6.1.13
F3 - E.C. 4.6.1.13
F4 - E.C. 4.6.1.14
F4 - E.C. 4.6.1.14