

28. Bioinformatic sequence identification from sequence family databases

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We have developed a tool in order to identify sequences in relation to a sequence family database. This tool combines several algorithms: BLAST, multiple sequence alignment and phylogenetic tree building. After identification of the most similar gene family to the query sequence, this query sequence is added to the whole family alignment and the phylogenetic tree of the family is rebuilt including the query sequence. Thus, the query sequence can be easily located in its gene family.