FIREPROT ASR: AUTOMATED DESIGN OF ANCESTRAL PROTEINS

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Robust and stable proteins are one of the keystones of protein or metabolic engineering [1]. During evolution, nature generated diverse solutions to biomolecular functions by evolving natural proteins. While most of the ancestral proteins have not survived until today, we can statistically infer their sequences using Ancestral Sequence Reconstruction (ASR). ASR is a well-established method for deducing the evolutionary history of genes or whole genomes. Besides its ability to discover the most probable evolutionary ancestors of modern proteins, ASR can be used to infer robust proteins with high stability, broad specificity, and good yields. However, its broad applicability is restricted by the complicated nature of the method, which demands substantial knowledge of bioinformatics. Therefore, this study aims to remove the obstacle by constructing a fully automated pipeline to perform ASR. We developed a web server, FireProt[ASR], that enables us to perform all ASR steps, including searching protein homologous sequences, building a multiple sequence alignment, construction and rooting of the phylogenetic tree, and reconstruction of the ancestral sequences, including ancestral gaps [2,3]. The server is accompanied by an easy-to-use graphical interface and is freely available at: https://loschmidt.chemi.muni.cz/fireprotasr/.

References:
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