Ancestral sequence reconstruction using the FireProt [ASR] web server

Ancestral Sequence Reconstruction (ASR) is a technique used in the study of molecular evolution. In protein engineering, a field that seeks new proteins for use not only in medicine but also in biotechnology or other industrial applications, ASR is used to find unknown ancestral proteins from which the current ones have evolved.

Basically, it's molecular archeology at the gene level. While human development can be mapped based on the skeletal remains of our ancestors, ASR uses gene sequences. If we know of a particular protein, then related gene sequences can be selected that can be used to reconstruct the "ancestor" of an already known protein. Although the theoretical foundations of ASR are more than fifty years old, the true potential of this method did not develop until the last ten years, with the advent of powerful computers. One example of the use of this method is the reconstruction of thioredoxin from organisms four billion years old. While the chemical properties of this enzyme were almost indistinguishable from the current version, its resistance to heat and acids was far greater, which, according to some scientists, proves that life originated in oceans with much higher temperatures and higher acid content.

On the ASR method are working researchers in Loschmidt Laboratories of the Faculty of Science, Masaryk University and the International Clinical Research Center of St. Anne's University Hospital Brno (FNUSA-ICRC). In cooperation with the Institute of Information Systems FIT VUT Brno, they have even developed their own web application for the use of this method - FireProt [ASR].

The benefits of using this software were described by **Rayyan Tariq Khan**, a doctoral student at Masaryk University and a member of the FNUSA-ICRC Protein Engineering team, in the article "Fully Automated Ancestral Sequence Reconstruction Using FireProt [ASR]" published in Current Protocols in Bioinformatics. "One of the advantages, is that our program is the only one of its kind that allows us to use the technique of ancestral reconstruction using only a single protein sequence as a starting point for the calculation," said Rayyan Tariq Khan. FireProt [ASR] is also suitable for beginners and novices who are unable to build a phylogenetic tree or create a data set of related sequences and compare them, which is an important starting point for ASR. "FireProt [ASR] is fully automated and can do all these activities for the user. At the same time, it allows the use of your own data and the start of calculations from different parts of the computing environment," added Rayyan Tariq Khan, who is also involved in the European network ES-CAT (Evolution, Synthetic Biology and Biocatalysis) coordinated by the University of Cambridge.

You can use FireProt [ASR] here: http://loschmidt.chemi.muni.cz/fireprotasr

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