

PhD position: Inference of protein function from domain architecture and orthology

at the Stockholm Bioinformatics Center (http://www.sbc.su.se/), which is located at Science for Life Laboratory Stockholm (http://www.scilifelab.se/) and has excellent contacts with a number of life science and computer science departments at Stockholm University, KTH, and Karolinska Institutet. The research project will be supervised by Professor Erik Sonnhammer (http://sonnhammer.sbc.su.se/).

The function of a protein is very challenging to establish experimentally. A faster route is to predict the function based on the amino acid sequence. This project will employ several approaches that use sequence features to this end. A major goal is to understand the functional impact of the combination of domains in multidomain architectures by analysing the evolutionary history of both individual protein domains and domain architectures. This will be done by developing computational tools for studying domain architecture, and by applying orthology analysis to entire proteomes. Another area of study is "domain versatility", which indicates a domain's propensity to form functional partnerships with other domains.

The project includes both development of new algorithms and methods, as well as applications such as tools and workbenches to enable public access for database queries at http://Pfam.sbc.su.se/ and http://Pfam.sbc.su.se/ and http://InParanoid.sbc.su.se/. The methods include hidden Markov models, clustering methods, various statistical analyses, and own developed algorithms. The project involves programming, data analysis, benchmarking, as well as application of the developed methods to genes of particular interest in order to discover new protein functions.

The successful candidate should have an M.Sc. in bioinformatics or related field, and knowledge of molecular biology. Alternatively, an M.Sc. in molecular biology or related field and at least 1 year of practical experience in bioinformatics research. Familiarity with sequence analysis techniques is essential, as well as a high level of motivation. Computer programming (e.g. Perl, Python, R, C++, Java), UNIX skills, and knowledge of biological database systems are necessary merits.

The position is for 4 years of full-time study and will administratively belong to the Department of Biochemistry and Biophysics, Stockholm University. Applications are made on-line, see this file, the latest on November 20, 2013. For further information about the research project, contact Erik.Sonnhammer@scilifelab.se