ReF No SU-XXXX

Projekttitel: Prediction and studies of membrane protein interactions.

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Membrane proteins are the gateways to the cells and as such they are of great importance for the development of drugs. In addition membrane proteins are quite difficult to handle experimentally, therefore prediction methods are important to gain information about these protein. We have developed many of the leading methods for prediction of membrane protein structures. For a full list of publication see http://bioinfo.se/papers/ .

The primarily aim of this project is to obtain detailed structural information about large biological complexes and networks, such as membrane protein translocases, by integrating different types of genomic sequence data. The information from a sufficient number of homologous sequences is often sufficient to predict the fold of soluble globular proteins or membrane proteins.

Two types of information will primarily be used. First, the identification of co-evolving residues can be used to predict interacting residue pairs. Secondly the use of structural homology combined with analysis of interaction surfaces can be used to identify potentially interacting proteins. These purely computational methods will then, if needed, be combined with experimental data from Cryo-EM and other techniques.

A general interest in protein, programming and machine learning methods and a solid background in bioinformatics, physics or computer science is suitable for this position. This position is a part of a European Union Marie Skłodowska Curie Initial Training Network named “protein factory”. The overall aim of this network is to develop new protein production systems that can deliver secreted enzymes and membrane proteins in greater yields, with higher quality and at lower costs. The network consists of 11 partners from 7 different European countries and in total 15 PhD students will be recruited. All these students will participate in several workshops, meetings and courses. This provides a unique possibility to form a network of fewllow scientists with a common research interest. The position is funded by a European Union Marie Skłodowska Curie Initial Training Network. Therefore, potential candidates must not have resided or carried out their main activity (work, studies, etc.) in Sweden for more than 12 months in the 3 years immediately prior to the recruitment, and have no more than 4 years of research experience.

Include a short motivation, a CV (plus diplomas and certificates/date when you expect to finish your studies), an example of computer code you have written and the contact details of at least 2 references in your application.

References:

1) Bernsel, A., Viklund, H., Falk, J., Lindahl, E., von Heijne, G. and Elofsson, A. (2008) Prediction of membrane-protein topology from first principles. Proc Natl Acad Sci U S A 105 (20) : 7177-718
2) Bendz, M., Skwark, M., Nilsson, D., Granholm, V., Cristobal, S., Kall, L. and Elofsson, A. (2013) Membrane protein shaving with thermolysin can be used to evaluate topology predictors. Proteomics 13 (9) : 1467-1480.
3) Peters, C. and Elofsson, A. (2014) Why is the biological hydrophobicity scale more accurate than earlier experimental hydrophobicity scales? Proteins 82 (9) : 2190-2198.
4) Skwark, M.J., Raimondi, D., Michel, M. and Elofsson, A. (2014) Improved contact predictions using the recognition of protein like contact patterns. PLoS Comput Biol 10 (11) : e1003889.