



JOB OPENING AT UPF BARCELONA

Researcher/technical support position at structural bioinformatics group.

The Structural Bioinformatics Laboratory (SBI) is integrated in the Research Program on Biomedical Informatics (GRIB), which is affiliated with the Pompeu Fabra University (UPF) and the Municipal Institute for Medical Research (Parc de Salut Mar/Hospital del Mar), and it is located at the Barcelona Biomedical Research Park (PRBB) in Barcelona (Spain).

Research Outline of SBI group

Protein-protein interactions play a relevant role among the different functions of a cell. Identifying the protein-protein interaction network of a given organism (interactome) is useful to shed light on the key molecular mechanisms within a biological system. A paradox in protein-protein binding is to explain how the unbound proteins of a binary complex recognize each other among a large population within a cell and how they find their best docking interface in a short time-scale. We interrogate protein structure to unveil its function, generate the network of interactions and to relate genes/proteins with diseases by means of exploiting the topology of the network.

For more information, visit our web at http://sbi.imim.es

We are seeking for a researcher/bioinformatician with capacity to offer technical support for the improvement of programmes generated in the group and the development of new ideas and services within the scientific subject of this announcement (see further).

Note: interest in developing new approaches and research advances in the scientific topics of our group, with potential achievement of a PhD, may also be considered.

DUTIES

✓ The successful candidate will be involved in the improvement, development, update and webplatform service development of the programs of the SBI. The work will be focused in the development and improvement of the tools of the group for the analysis of proteininteractions and network rewiring, implying new aspects of research.

SKILLS AND EXPERIENCE

- ✓ Knowledge of structural bioinformatics techniques (docking, template-based homology modelling, sequence and structure alignment, etc.)
- ✓ Oral and written communication skills.
- ✓ Fluent spoken and written English.
- ✓ Excellent programming/scripting skills in:
 - o Script/Programming languages: Python
 - Specificities: BioPython, Numpy, Tkinter.
 - Programming languages: C or C++ or Java.
 - Web programming knowledge:
 - Angular JS, JavaScript or PHP.
 - Django or Bottle.
 - CGI.
 - o Database programmer: SQL/MySQL or SQLite or MongoDB
- ✓ Graduate/engineer in one of the following areas: mathematics, physics, chemistry, biochemistry, informatics, human biology, biomedical engineering.

✓ Master or equivalent in bioinformatics or computational biology, or in the process of obtaining it.

WORK CONDITIONS

- ✓ One-year contract with possible extension for one more year under the same funding.
- ✓ Salary will depend on the experience and qualifications of the applicant and the possibility of industry collaborations.

SUPPORT

The work is supported by grant: BIO2014-57518 from the Spanish Ministry of Economy (MINECO) and FEDER sources.

SCIENTIFIC TOPIC

Summary: The structural characterization of PPIs helps us to understand the mechanistic causes of the rewiring in a healthy network motivating a disorder or pathologic phenotype. However, network rewiring is also a normal mechanism of regulation of a healthy cell. The modification of the sequence and/or conformation of a protein can affect an interaction either by direct changes in the binding region or through allosteric sites. Post-transcriptional modifications (PTMs) play a key role on the regulation of cell signalling by transiently changing protein interactions with mechanisms of switch-on and switch-off. Nowadays, that the first draft of the human proteome has been obtained by means of proteomic methods, the role of PTMs has become crucial to understand the mechanisms of regulation of interactions. The combined study of the dynamics of PPIs and PTMs has begun to reveal conditional rewiring of molecular networks through PTM-mediated recognition events. These studies highlight the utility of protein interaction networks (PINs) to functionally prioritize certain PTMs mapped in human cells, whereas the activity of some of them can cause a wide variety of human diseases. In our project we plan to study the mechanisms involved in the disruption and formation of PPIs and use it to analyze the rewiring of protein interaction networks (PIN) caused by PTMs, mutations or splicing, specifically affecting human health. Our study is based in: 1) the analysis of the interface of known and modelled structures of PPIs to predict the strength of the interaction; and 2) the analysis of changes in regions outside the interface of a PPI that modify its prediction. In previous works we demonstrated the role of loop conformations to decide whether two proteins could interact or not. We plan to study the role of residues outside the interface to improve the prediction of the association between two proteins and use it to predict if changes in sequence (or conformation) can disrupt an interaction and modify the network.

HOW TO APPLY

Applications for this opening should include a CV, a motivation letter and the names of two potential referees. Send them by **e-mail** to sbi+candidates@upf.edu

Reference: SBI494.2

For more information, contact Dr. Baldo Oliva (<u>baldo.oliva@upf.edu</u>) or visit our web site at http://sbi.imim.es