DOCTORAL INPhINIT FELLOWSHIPS PROGRAMME – INCOMING FRAME INFORMATION CALL 2021

PhD POSITION OFFER FORM

Position

1. Project Title/ Job Position title: **Bioinformatics for accurate genetic diagnosis and personalized medicine**

2. Area of Knowledge: LIFE SCIENCES

3. Group of disciplines: Biotechnology, Bioinformatics, Pharmacy, Food Technology

4. Research project/ Research Group description

Personalized Medicine is much needed because each of us carries a slightly different genetic information (with several million variations relative to the human reference DNA sequence) and because we keep accumulating fortuitous mutations all along our lives. While obtaining comprehensive genetic data from patients or healthy individuals is no longer difficult or expensive, understanding the phenotypic consequences of the variations found still is more a challenge than a reality. Even anticipating whether a single nucleotide variation (SNV) in a gen associated to a monogenic disease will be pathogenic or not poses significant difficulties. Existing predictive applications often provide conflicting forecasts for the same SNV and it is clear that they must improve before they can be used confidently to interpret variations. The fact is that they do not seem to have improved significantly in recent years.

Proteins are in most cases the performing biological molecules the functions of which are compromised by pathogenic variations. Therefore, a significant improvement of pathogenicity predictors is unlikely to take place if the variations' impact on protein stability and protein/protein interaction is not dealt with in fine detail.

We are a group of protein experts who study proteins in the laboratory, as protein engineers, **and in the computer**, as bioinformaticians. Our goals are:

1-To understand the phenotypic effect of mutations at the protein level in order to develop accurate bioinformatics tools to assist medical doctors in delivering accurate genetic diagnostic.

2-To develop new drugs to provide cure for people in need of personalized treatments (against resistant bacteria, rare inherited metabolic diseases or a variety of amyloidoses).

This project will focus in developing accurate bioinformatics tools for genetic diagnosis. A combined project including computational drug discovery work on selected diseases can be offered for students so inclined (see below).

5. Job position description

The successful candidate will get involved in:

-Developing and applying Bioinformatics tools for the accurate interpretation of human genetic variations.

-Evaluating novel SNVs found in neonatal screening programs run in Spain and France.

-Interpreting the deleterious "variomes" of selected genetic disorders.

-Improving new drugs discovered and developed in our group (if specific interest in this task is indicated).

We expect from the candidate some computational skills plus a strong interest in structural bioinformatics and in genetic interpretation, combined with personal initiative and ambition. We offer a friendly environment with plenty of computational resources available, several ongoing drug development programs, vast knowledge on the relationship between protein structure function and disease, and a proven record of knowledge dissemination through the implementation of publicly accessible biomedical web servers.

While the COVID19 pandemia continue being a concern, presencial work may be combined with work at home in active daily communication with the group leader and the other members of the team.

Group Leader

1. Title: Professor
2. Full name: Javier Sancho
3. Email: jsancho@unizar.es
4. Research project/ Research Group website (Url): https://www.bifi.es/biophysics/#0
5. Website description: Protein Folding and Molecular Design

Additional website

1. Url: http://webapps.bifi.es/prionscan
   Website description: **An online database of predicted prion domains in complete proteomes**. Made by us.
2. Url: http://webapps.bifi.es/protsa
   Website description: **Generation of unfolded ensembles of proteins and calculation of sequence-specific solvent accessibilities in folded and unfolded states**. Made by us.
3. Url: http://155.210.92.196/pirepred/pirepred.php
   Website description: **An interpretation tool designed for clinicians interested in the pathogenicity of clinical variants.** Made by us (**this is a beta version**).
4. Url: https://pirepred.com/
   Website description: Pirepred: From mutation to Patient; Project site.
5. Url: https://www.inpec.science/
   Website description: International Network of Protein Engineering Centers; Network site.