



Post-doctoral position

"Application of DeepProt open mass search algorithms to bottom-up proteomics data"

- Location: Plateforme d'Analyse Protéomique de Paris Sud-Ouest (PAPPSO), Gif-sur-Yvette (France)
- Date: from autumn 2019 to spring 2021 (18 months)
- Salary: 27-30 K€ (gross salary)

Key words: proteomics, LC-MS/MS, mass spectra interpretation, open mass search, protein identification, protein modifications

Context:

Bottom-up proteomics generates tens of thousands of experimental spectra in a single LC-MS/MS injection. Software is essential to get information from so huge raw data, but at the moment on average 50 to 75% of the spectra remain uninterpreted after analysis. Modifications displayed by proteins are the most widespread hypothesis to explain this low rate. The ANR project DeepProt aims at developing new open mass search algorithms to more exhaustively interpret the set of experimental spectra generated by proteomics experiments - even those from complex metaproteomics studies - and next to deduce the list of proteins present in the analyzed mixture with detailed information about their post-translational modifications (PTM).

Objective:

The objective of this post-doctoral position is to define the fields of application in which the algorithms developed in the context of the DeepProt project are the most effective and to bring the proof of concept that these algorithms are highly effective to interpret protein mass modifications. To this end, several datasets are available at PAPPSO, including a metaproteomic dataset and datasets containing proteins with known modifications (either PTMs or amino-acid changes resulting from allelic modifications in the sequences of the encoding gene).

Environment:

PAPPSO (www.pappso.inra.fr) is a proteomic facility that aims to provide research teams with high skills and new-advanced equipments in the field of proteomics. It is more particularly specialized in high throughput proteomics (quantitative analysis of large cohorts of samples) and in the analysis of highly complex samples (metaproteomics). PAPPSO also develops bioinformatics tools that allow the processing of these experiments and provides assistance to users for data interpretation.

PAPPSO gathers two sites distant from 8 kms: one located at the Moulon (Gif-sur-Yvette) in the Quantitative Genetics and Evolution laboratory (GQE-Le Moulon, 98 people) and the other one in Jouy-en-Josas in the MICALIS Institute (Food and Gut Microbiology for Human Health, 350 people). Each site has developed specificities related with its home laboratory. The Moulon site, where the successful applicant will be based, has been specialized in plant proteomics for a long time.

Candidates:

Applicants should hold a PhD or a doctoral degree and show a sound expertise in comprehensive analysis of proteomics data and/or in bioinformatics and bioanalysis. Statistical skill would be much appreciated.

Interested candidates are encouraged to submit a cover letter, a CV with a list of publications and contact details of 2-3 referees by email to michel.zivy@inra.fr and melisande.blein-nicolas@inra.fr