A position is open in the Mass Spectrometry Unit (MSU) at Department of Experimental Oncology (DEO) a leading cancer research institution located in the south area of Milan (https://www.research.ieo.it, https://www.ieo.it/).

The Unit provide MS-based proteomics analysis for DEO scientists, including protein identification, protein expression profile either in Label-Free or label-Based methods (SILAC, TMT), interaction proteomics (AP-MS, proximity labelling), mass mapping and PTMs characterisation. The unit is equipped with state-of-art of Orbitrap-Hybrid mass spectrometers. The instruments are operating in bottom-up LC-MS workflows (DDA, DIA) and are coupled to a variety of nano-flow chromatography systems (nLC-1200, Neo Vanquish and Evosep-one). The unit also makes use of an 1680 HPLC (Agilent) for offline peptide fractionation (RP-HpH, SCX). Recently, we implemented Quantitative Proteomics Made Simple (QProMS), a user-friendly, search engine-agnostic data analysis and visualisation pipeline. QProMS guides the user through data analysis and statistical testing in a graphical interface. Statistical tests rely on established R functions and are compatible with all types of label-free quantification experiments (https://bioserver.ieo.it/shiny/app/qproms).

We are looking for a motivated, enthusiastic candidate with strong interest in computational science to work on dedicated bioinformatics suite aimed to quantitative proteomics data processing.

Key responsibilities are:

- Interact closely with DEO scientists to understand their data analysis needs and provide answers to technical questions through custom analyses, 1-on-1 communication, presentations, and written documents.
- Maintain and continue to develop in-house proteomics algorithms and software tools.
- Explore and deploy external algorithms, software, and tools as needed to complement in-house software.
- Develop data analysis strategies, write algorithms, and help with the analysis of proteomics data.

Requirements

Masters degree or Ph.D. in a quantitative discipline such as statistics, biostatistics, computer science, bioinformatics, or computational biology. Experience working with proteomics data and proteomics software (e.g. MaxQuant, Perseus, PD, Skyline, DEP etc). Expertise in statistical data analysis. Good coding skills in one or more programming languages (preferably R and/or python). A proactive approach to collaborations and a demonstrated ability to work in a team environment it is strongly preferable.

Contract and salary conditions will be discussed based on candidate profile.

Potential applicants are encouraged to contact Dr. Alessandro Cuomo (Head of the Unit) a CV with a CV with at list one referee to alessandro.cumo@ieo.it

IEO
Mass Spectrometry Unit
European Institute of Oncology