The BIO3 group at the Systems and Modeling Unit of the Montefiore Institute (University of Liège - ULg/ Interdisciplinary Cluster for Applied Genoproteomics - GIGA) is offering one post-doctoral research position (for 2 years) and one position for a programmer (for 2 years).

These are two positions in the context of a WELBIO project, DESTinCT, for the development of analytic tools in the research area of large-scale omics integrated gene-gene interaction analyses. Buzz words include population stratification and admixture, data integration, meta-epistasis and precision medicine via applications to whole exome/genome sequence data.

Requirements

Short term Postdoctoral Fellow:

We are looking for enthusiastic applicants with a strong interest and motivation for fundamental research, eager to learn and to develop novel techniques. To be eligible, you have a PhD degree in Statistical Genetics, Biostatistics, Genetic Epidemiology, Bioinformatics, or a related relevant field in life sciences. You have a record of high quality publications and (co-)authored at least three internationally published, peer-reviewed papers. Ideally, you have experience in bioinformatics or genomics research and have successfully followed some courses in statistics. These experiences will be a distinct advantage. As a creative thinker, yet with a critical mind, you are able to work both autonomously and as a collaborative team player, willing to work with interdisciplinary teams. Excellent English communication skills, both oral and written, are necessary. Ability to meet deadlines and efficiently multitask is a must.

Programmer:

We are looking for an exceptional team player who has a passion for open-source software development with a strong interest in contributing to biomedical research. To be eligible, you have a Bachelor’s Degree in Computer Science, Bioinformatics, Computational Biology or a related field, and have an excellent knowledge of C++. As a programmer / software developer in DESTinCT you are able to translate basic code (primarily written in a high level language such as R, Python, MATLAB) into a functional software tool, set up testing frameworks to detect bugs and remove errors, and to create a user interface. Experience in modern software development technologies, including distributed versioning systems and continuous integration, as well as experience in fast computing (parallel computing, cloud computing) are an advantage. Good English communication skills, both oral and written, are necessary, as well as being able to meet deadlines and efficiently multitask.

Terms of employment

Due to mobility requirements for the post-doctoral position, only post-docs who have not been resident in the host country (Belgium) or have carried out their main activity (job, studies, ...) for more than 24 months during the last 3 years directly before the first stay as a post-doctoral fellow dedicated to DESTinCT, may apply. No such requirements apply for the programmer position. The 2-year positions will be funded according to the regulations of the Fund for Strategic Fundamental Research (FRFS) and in particular FRFS-WELBIO.
How to apply?

Applications should be sent as a single PDF file by e-mail to kvansteen.applications@gmail.com by December 15, 2015. These should include a cover letter explaining your qualifications for this position, a motivation, and the names and contact information of 2 academic referees, as well as a scientific CV with detailed information on education, diplomas, grades, past research positions, and publications. Informal inquiries can also be made to kvansteen.applications@gmail.com.

About our group

BIO3 is part of the Systems Biology and Chemical Biology thematic research unit of GIGA-R and of the Systems and Modeling Unit of the Montefiore Institute, within the University of Liège (Belgium). The areas of expertise of BIO3 are biostatistics, biomedicine and bioinformatics. BIO3’s mission is to help biomedical researchers carry out their investigations and analyze their data, as well as designing new statistical and bioinformatics methods whenever they are needed. Methods development cover the areas of data mining and machine learning (including supervised, semi- and unsupervised learning techniques), parametric, semi- and non-parametric methods and variable selection methods, for the inference of gene networks, for patient subphenotyping, for the assessment of (the determinants) of population strata, and for purposes of investigating association, prediction and causal relationships. Furthermore, algorithm optimization and computations methods are developed in the context of “Big Data” analyses.


More details about the Montefiore Institute: http://www.montefiore.ulg.ac.be/