JOB DESCRIPTION

JOB TITLE: Research Fellow in Statistical Bioinformatics

CONTRACT: 20 months full-time

APPLICATION DEADLINE: July 19th, 2017

DUTY STATION: Turin, Italy

ORGANIZATION UNIT: IIGM, Molecular and Genetic Epidemiology Unit

JOB DETAILS

1. The post

The Italian Institute for Genomic Medicine (IIGM) is a young non-profit research organisation in Torino (Italy) operating in the field of genetic and epigenetic research. The mission of IIGM is to promote basic and applied research and post-graduate training in scientific disciplines related to human genetics, genomics and post-genomics by using the most updated technological platforms in an integrated environment.


A research fellow position is available to work mainly within the recently started H2020 project LIFEPATH that investigates the determinants of diverging ageing pathways among individuals belonging to different socio-economic groups. The demographic data, and the majority of the biological one, are already available and come from European cohorts with intense phenotyping that provide information on healthy ageing at different stages of life and genome-wide methylation profiles (Illumina 850K array).

New data will be generated within the project and will consist of genome-wide methylation profiles, NGS data of miRNAs and gene expression, and inflammation-related proteins levels.

Dr. Silvia Polidoro and Professor Paolo Vineis at HuGeF will lead the project, in collaboration with Dr Marc Chadeau-Hyam at Imperial College London.

Analysis of such dataset requires computationally efficient algorithms and the anticipated weakness of the signals sought for requires a careful choice in the methodological choices to ensure an optimal statistical power at the cost of minimal loss in computational efficiency. To make the most of this unique resource, models to integrate these data and to elucidate potential mechanisms through which the effect of socioeconomic status is mediated, novel statistical approaches need to be developed. This includes unsupervised approaches (e.g. machine learning algorithms), and more parametric approaches (e.g. structural equation models).

2. Job description – Main duties

- Conducting in-depth computational and statistical analyses – these imply:
  a. Familiarity with the Linux ambient and programming skills (R, Mathlab, SAS) for the preparation of bespoken scripts to analyse huge omics datasets (hundreds of thousands of signals per subject for cohorts of thousands of subjects)
  b. Familiarity with OMICs data, including pre-processing algorithms, development of ad-hoc models accounting for technically –induced variation (e.g. laboratory artefacts)
c. Experience in analysing high-throughput data: correcting for multiple testing in the case of strong and complex correlation structures, interpretation of the results using publically available resources (e.g. gene enrichment analyses)
d. Capacity to develop novel approaches/strategies to investigate how data arising from several OMIC platforms interplay and ultimately mediate the effect of external exposures.
e. Application of knowledge-driven pathway analyses
f. Preferably experience with NGS data analysis pipelines

- Communicate with statisticians to identify the most appropriate methods, and with epidemiologists and biologists to identify the questions of interest and to interpret the findings.
- Make a contribution to reporting study results, including writing up for publication in peer-reviewed journals and presentations at seminars and conferences.
- Helping grant writing.

*Job descriptions cannot be exhaustive and so the post holder may be required to undertake other duties, which are broadly in line with the above key responsibilities.*

**PERSON SPECIFICATION**

**Qualifications/Knowledge**

*Essential:*
- Degree in Mathematics, Physics or related disciplines.
- PhD in Computational Biology, Biostatistics or Epidemiology (with experience in computational biology)
- Interested in pursuing a research career in epidemiology/public health

**Experience**

*Essential:*
- Experience in conducting statistical analyses in observational studies using high throughput data
- Extensive programming experience using common languages (R, C, C++)
- Experience in computational biology

*Desirable:*
- Publications in epidemiology or genetic epidemiology
- Experience/interest in molecular epidemiology
- Experience with pathways and transcription network analysis

**Skills/Abilities**

*Essential:*
- Ability to communicate well in writing, person to person, and in seminar or conference presentations
- Ability to solve problems using innovative and flexible thinking
- Ability to work autonomously and take responsibility
- Ability to work to tight deadlines
APPLICATION GUIDANCE

Please read the person specification carefully and describe, as part of your application, how much you feel you meet each of the criteria. If you need more space, please attach additional sheets to the application form.

A full curriculum vitae and a letter of intent should be sent by the closing date of July 19th, 2017

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and to: Dr. Silvia Polidoro
e.mail: silvia.polidoro@iigm.it

*The CV should include the following information:*

Applicant’s full name, private address and private telephone number
A confidential e-mail address, where possible
Degrees (including University and dates)
Past and present posts
List of publications
Brief description of future research plans

Short listed candidates will be contacted as soon as possible after the closing date.

We regret that we are unable to reply to each applicant; therefore, if you do not hear from us within eight weeks of the closing date for this post you should assume that you have been unsuccessful on this occasion.

If you have any further queries, please telephone +39 0116709538 or email silvia.polidoro@iigm.it

Thank you for your interest in this post.

We look forward to receiving your application.