Position in Computer Science and Statistics

- Recruitment grade: young researcher (i.e. Master, Engineer or Phd)
- Location: Anglet, France
- Duration: 12 to 24 months, starting March 2019
- Deadline: position open until filled
- Gross Salary Range: 2699 euros / month

Context and aims

Recently, several approaches were developed for completing the agnostic genome-wide association studies (GWAS) in the discovery of new genetic risk factors. One such approach is gene set analysis (GSA) that incorporates the available biological knowledge of genes in order to provide additional insights into the mechanisms involved in carcinogenesis. Another approach proposed to test variants for association for multiple phenotypes as over the years multiple loci have been found to be associated to several distinct traits revealing the existence of pleiotropic effects. Although a number of statistical approaches have been proposed in the literature for identifying the existence of pleiotropy at SNP-level, not a lot of work has been conducted for investigating pleiotropy at gene- and pathway-levels.

We aim to fill this gap by developing advanced statistical methods that test for pleiotropic effects at a pathway level. Also, we will extend these methods for the analysis of GxE interactions, as to the best of our knowledge, pleiotropy methods have not adapted for testing for GxE interactions.

Therefore, our first objective is to develop novel statistical methods that will identify shared pathways between different diseases. Our second aim is to extend these methods for testing GxE in general or in the context of pleiotropy. These methods will be applied to explore the genetic relationship between differentiated thyroid cancer (DTC) and breast cancer (BC) types. It has been shown that these two cancers are linked as women with a prior history of DTC are at an increased risk for BC and conversely. Both tumors have been shown to be associated to common hormonal risk factors and shared genetic susceptibility is suspected. We will use data from the CECILE study (1019 BC cases and 999 controls) and from EPITHYR (1345 DTC cases and 1399 controls). All subjects were genotyped using the OncoArray chip that includes more than 500 000 variants. Through the developments of novel statistical methods, we aim to elucidate the common mechanisms between BC and DTC.

This project will lead to the development of new statistical methods that will benefit both the epidemiology and statistical communities. These methods will permit to gain novel insights into the inherited genetic basis of BC and DTC by identifying the common biological elements that contribute to their aetiology.

Tasks

1) Methods development for GSA in GxE analyses.
2) Methods development for GSA for pleiotropy analyses
3) Simulation studies design and validation of methods. Performances of developed methods will be compared to those of most commonly used methods.
4) Application to real data: Standardization of environmental factors and genetic factors in datasets. Comparison of results while considering each cancer individually and while considering both cancers together.
5) Development of R packages.

Funding

This position is funded by the project CCGIP (Cross Cancer Genomic Investigation of Pleiotropy effect and GxE interactions at pathway level: application to breast and thyroid cancers) which is granted by “La Ligue contre le Cancer”.

Supervision and Contact

Supervisory team: Benoit Liquet (benoit.liquet@univ-pau.fr) at the LMA : Laboratory of Mathematics and its Applications, UMR CNRS 5142 (https://lma-umr5142.univ-pau.fr/fr/index.html) on the campus of Anglet (64600) France.

For additional information and proposal, please contact: Pr Benoit Liquet, Tel: + 33 6 95 46 10 61 Email: benoit.liquet@univ-pau.fr

Young Researcher skills required

- The applicants should have a Master, Engeneer diploma or a Phd in Computer Science or in Statistics, have strong experience with programming, good communication skills and interest in working in a cross-disciplinary team.
- A successful candidate might have experience in the development and application of Bayesian and Frequentist methods for computationally challenging problems.
- A successful candidate will also have experience in scientific computing. Prior experience in genetics is not necessary, but is counted as an advantage.

Salary

The salary of the successful candidate will be based on level chart for research personnel in the salary system of French universities. The salary will be 2699 euros/month (gross salary).

Applications

Please submit your application by email to benoit.liquet@univ-pau.fr. Please attach the following documents as a single pdf file: motivational letter (max 1 page), CV (max 2 pages) and publication list. Include also contact information of two persons who can provide a reference letter based on request.