



Bioinformatics position – Transcriptomic Imputation & Psychiatric Genomics

The Huckins Lab is looking for a motivated and enthusiastic bioinformatician to join our team. We focus on the development and application of Transcriptomic and multi-omic Imputation models.

Transcriptomic Imputation (TI) approaches leverage large, well-curated eQTL reference panels in order to predict gene expression from genotype. TI models can be applied to any large collection of genotypes (i.e., GWAS) to obtain predicted genetically regulated gene expression in cases and controls, and thereby identify associations between gene expression and disease. These higher-level genic associations may provide greater interpretability.

As part of the Huckins Lab, you will help to extend and improve these methods to incorporate new well-curated transcriptome, histone modification, and microbiome datasets, in order to build predictors of multi-omic data from genotypes. At every stage of our analysis, we will apply these predictors to schizophrenia, bipolar disorder and anorexia nervosa GWAS data in order to reveal more about multi-omic risk for these psychiatric disorders.

Your skills

A successful candidate will be motivated and enthusiastic about understanding the neurobiology of psychiatric disorders, and will show a wide interest in the work of the division. We hope that you will be highly motivated to complete your own bioinformatics projects, such as for example optimizing pipelines for eQTL or transcriptomic imputation analyses, as well as working collaboratively to support the needs of the lab. Ideally, you will enjoy communicating and explaining your work to peers and students, and in internal seminars.

Essential skills include working knowledge of genomic and GWAS-style analyses, and proficiency in programming in R/perl/python. Previous experience running software such as plink, LDSC, MAGMA (etc) will be of great benefit to this position.

Education: BS (/MS) in Bioinformatics, Computer Science, Statistics, Engineering, or similar.



Specific duties and responsibilities may include:

1. Write custom scripts, tools, and pipelines to run GWAS QC, association tests, and standard follow-up analyses
2. Write custom scripts, and optimize existing tools for EHR-based analyses
3. Optimize and run existing pipelines for eQTL analysis
4. Identify and resolve errors and bugs in existing pipelines and software
5. Work independently on bioinformatics projects
6. Collaborate with a range of PIs and postdocs in the division
7. Contributing to talks, posters, manuscripts, and software releases that describe our work

Environment

The Huckins Lab is part of the Pamela Sklar Division of Psychiatric Genomics, in the Icahn School of Medicine, New York. As a division, our focus is on understanding the causes, outcomes, and treatment of psychiatric disorders. Our researchers have diverse interests and backgrounds, including computational, wet-lab and clinical research teams, as well as post-doctoral fellows, grad students, and bioinformaticians. We hope that you will work collaboratively with this diverse groups of researchers, and will contribute to our goal of understanding psychiatric disease.

The Huckins Lab does not tolerate harassment of anybody, in any form. All members of the lab are required to abide by our code of conduct at all lab-related events.

(<https://github.com/laurahuckins/HuckinsLab/>)

How to apply

To apply for this position, email a cover letter and up-to-date CV to [laura.huckins @mssm.edu](mailto:laura.huckins@mssm.edu)

Please include the names & contact details for two references in your application.

We will consider all applicants without discrimination on grounds of disability, sexual orientation, pregnancy or maternity leave status, race or national or ethnic origin, age, religion or belief, gender identity and expression, marital status, protected veteran status (if applicable) or any other characteristic protected by law. We are open to a range of flexible working options including part-time or full-time employment as well as flexible hours due to caring or other commitments.