

Harvard Medical School and Brigham & Women's Hospital Postdoctoral Position in Computational Neuroscience

Your qualifications: Applicants are expected to have (1) A previous publication as first author is desirable, (2) Ph. D. or equivalent doctoral degree with (3) proven research experience in bioinformatics and analyses of genome-wide data (for example, single cell RNA sequencing, GWAS, eQTL, AI methods, ATAC seq, whole genome sequencing, RNA-seq, epigenetics, eQTL). (4) Strong quantitative skills preferably in computer science, bioinformatics, or statistics are necessary. Programming background is desirable. Excellent written English is advantageous. Candidates working towards an academic career in computational neuroscience and PD are preferred.

How to apply: Please submit your application, including a statement of research interests, a biosketch, and one letter of reference to Clemens Scherzer at cscherzer@rics.bwh.harvard.edu.

A Postdoctoral Position in Computational Neurology is available at the Neurogenomics Laboratory (www.scherzerlaboratory.org) of Brigham & Women's Hospital and Harvard Medical School (Principal Investigator: Dr. Clemens Scherzer) with additional affiliations in the Precision Neurology Program and the Advanced Center for Parkinson's Disease Research (www.bwhparkinsoncenter.org). This fully funded position is available for an initial two-year appointment with the possibility of extension. The Neurogenomics Lab is interdisciplinary - located at the intersection of genomics, computing, and neurology.

The goal of the Neurogenomics Lab is to decipher how the human genome programs brain cells and to determine how the normal flow of genetic information is impaired in Parkinson's and other brain diseases. We are building a personalized medicine for neurologic disease that harnesses genomic information to diagnose and treat the right patient with the right drug at the right time. Two of the major ongoing projects are BRAINCODE (see Dong et al., *Nature Neuroscience*, 2018) for phase 1 results and the International Genetics of Parkinson Progression (IGPP) Consortium (see Liu et al., *Lancet Neurology*, 2017; Liu et al., *Annals of Neurology*, 2016)

Decoding human brain cells in health and disease: The BRAINcode project's goal is to chart the flow of information from the entire human genome into specific brain cells in health and brain disease. Genetic variation between hundreds of individuals is examined for correlation with differences in transcribed elements -- both protein-coding and non-coding --- to identify regions of the genome that influence whether, how, and how much a transcript is expressed in this specific cell type *in situ* in human brains. Transcriptomes of control and diseased brains are probed using single-cell RNAseq, as well as lcRNAseq (that is laser-capture microdissection plus ultra deep, total RNA sequencing), SNP arrays, expression Quantitative Trait Locus analysis, and epigenetics. BRAINCODE will provide a high-resolution encyclopedia of transcribed elements in prototype cell-types in human brains, help to understand inherited susceptibility to Parkinson's and other neuropsychiatric disease, and highlight targets for precision therapies.

Predicting the future of patients with Parkinson's disease: The progression of Parkinson's disease varies considerably between individual patients, ranging from a manageable functional decline to an aggressive course that leaves patients rapidly wheelchair bound or demented. This variation is a major source of noise and inefficiency in therapeutic trials. Predictors of progression are needed for tailored therapeutic trials and for precision medicine. In this project we are using next-generation genetics to delineate the genetic landscape of prognosis in patients with PD.

You will join our computational neuroscience team comprising bioinformatics engineers, Fellows, students, and a statistician, and benefit from our integrated wet lab and translational research in our program.

Your tasks: We are looking for enthusiastic, highly motivated, science-driven and experienced postdoctoral fellows to join our team to unravel how the genome functions in the human brain and in patients with Parkinson's using next generation genetics, transcriptomics, epigenetics, network analysis, and data science.

Moreover, you will participate in exome and whole genome sequencing studies designed to identify gene variants that predict prognosis in patients with Parkinson's.

Salary will be commensurate with experience.

Application deadline: August 31, 2019