Postdoctoral Position in Computational Neurobiology/Bioinformatics/Data mining

The Computational Neurobiology Data Scientist is a post-doctoral position available at the University of California, Los Angeles (within the Department of Human Genetics or the Semel Institute for Neuroscience and Behaviour). This position is an integral part of a collaboration between UCLA and CHDI, a non-profit virtual pharma dedicated to hastening the advance of therapeutics to delay the onset and progress of Huntington’s disease (HD).

The Computational Neurobiology Data Scientist will lead the integration and interpretation of Computational Models that represent the molecular networks and disease mechanisms underlying Huntington’s disease (HD) and in potential responses to treatment. Working both independently, and in tandem with both UCLA and CHDI colleagues, s/he will interrogate these models to help define the underlying molecular cascades causing HD pathology as well as, drug mechanisms of action, mechanisms of toxicity, and biomarkers that can be used clinically to follow these mechanisms in patients.

The Computational Neurobiology Data Scientist will work closely with the laboratory of PI: Steve Horvath to align the use of statistical correlative and causative networks developed from transcriptomics, proteomics and epigenetic profiling data to reflect underlying biology and HD pathophysiology, and will perform integrated data mining over networks/modules/models developed by the Horvath lab. S/he will work closely with the laboratory of Giovanni Coppola to lead the integration of diverse HD-related datasets generated both within and without UCLA, in service of integrated data mining. S/he will also drive requirements for tool development and data dissemination within the Coppola lab. S/he will work closely with the lab of William Yang to understand, develop, test, refine biological hypotheses to identify Mechanism(s) of Actions relevant to HD pathophysiology, and to develop insight into therapeutic strategies to intervene in the disease process.

**Job Responsibilities**

- Lead the integration and analysis of preclinical and clinical ‘omics data within the biological and disease context to enable the development of systems models for HD.
- Analyze, interpret and leverage of computational network models of biology (logical, causal, etc.) that describe aspects or the entirety of HD disease mechanisms
- Evaluate computational models to define potential therapeutic interventions for HD.
- Participate as a member of the UCLA-CHDI collaboration, providing direct support for the key objectives of the collaboration.
- Contribute as a member of the UCLA team to the development and testing of therapeutic strategies that will drive experimental interventions to support and advance HD drug discovery
- Identify appropriate models for testing therapeutic strategies, through comparative modeling
- Publish scientific results in peer-reviewed journals.

**Qualifications**

- Strong scientific problem solving skills, an advanced degree in bioinformatics, computational biology, molecular biology, neuroscience, biostatistics, computer science, genetics (PhD, MD or Master's level with several years of work experience). An affinity for modeling and hypothesis development and testing in a collaborative research environment, and a strong desire to learn new areas and skills.
- Demonstrated ability to work collaboratively in a technical, interdisciplinary team oriented environment, including other scientists, statisticians, software engineers, and knowledge modelers as well as with external partners.
- Familiar with network modeling, with experience with one or more systems biology modeling methods/platforms.
- Good computational biology skills, with significant experience analyzing and interpreting high-throughput, genome-scale data.
- Good biological skills, with experience extracting biological hypotheses from computational results. Neurobiology background preferred, but not required.
- Knowledge of basic statistics, proficiency in scripting in R, fluency in Linux and intermediate SQL skills.
- Good understanding of core gene expression profiling techniques and algorithms.
- Familiarity with core Bioinformatics data and data types.
- Good awareness of Bioinformatics community resources.
- Excellent written and oral communication skills, and effective interpersonal skills.
- Evidence of being highly self-motivated and a demonstrated ability to work independently.

**Additional Skills**
- Experience in modeling Huntington's disease or other neurodegenerative disorders.
- Experience with causal modeling and/or Bayesian network modeling.
- Experience in Network modeling to an applied drug discovery environment.
- Experience supervising external collaborators and contracts.

**Application Procedure**
If interested, please email a resume, cover letter, and the names of 2 references to

Prof. Steve Horvath (shorvath@mednet.ucla.edu)
Please cc Margaret Chu on the email (mchu@mednet.ucla.edu).

Subject heading of the email: HD Position

This announcement expires March 15, 2016