HARVARD MEDICAL SCHOOL

BRIGHAM AND WOMEN'S HOSPITAL

77 Avenue Louis Pasteur • Boston, MA 02115 • tel: 617 525-4451 • fax: 617 525-4488 • rplenge@partners.org

Robert M. Plenge, M.D., Ph.D.
Assistant Professor of Medicine
Harvard Medical School

Director, Genetics & Genomics
Division of Rheumatology, Immunology and Allergy
Brigham and Women's Hospital

BIOINFORMATIC ANALYST: *Computational scientist to study genetic predictors of rheumatoid arthritis (RA) and other autoimmune diseases*

A research position as a computational scientist and bioinformatics analyst is available in the *Plenge Lab* at Brigham and Women's Hospital (BWH), Harvard Medical School. The position entails analyzing large-scale genetic datasets generated by genome-wide association studies (GWAS) and next-generation sequencing technology to investigate the genetic basis of autoimmunity (and RA in particular). **In particular, the position is to conduct a multi-ethnic GWAS of >50,000 case-control samples, followed by replication in an additional >30,000 case-control samples.** The person will work closely with geneticists and computational scientists at BWH, Harvard Medical School, Broad Institute, and Harvard School of Public Health.

The position is for either a PhD-trained post-doctoral research fellow or someone with equivalent experience. The applicant must have more than 5 years of experience with a scripting language (e.g., perl, python) and expertise with a statistical or mathematical language (e.g., R, MatLab). Experience with more advanced object oriented languages (C++ or Java) is helpful but not required. Experience working in a biomedical research setting and a basic understanding of statistics is strongly preferred.

The focus of the *Plenge Lab* is to translate genetic discoveries to care of patients with common diseases, including autoimmune diseases such as RA. This ambitious goal requires a multidisciplinary team of motivated individuals willing to work together to address critical scientific questions. Together with close collaborators, the *Plenge Lab* has identified >35 gene variants that contribute to risk of RA. We anticipate that this project will more than double the number of RA risk loci. During the course of the project, opportunities will develop, allowing independent lines of investigation.

Sample tasks required:

(1) *Manage and organize large GWAS and sequence data sets*: requires ability to format and manipulate the content of large genetic datasets using perl scripts or similar scripting languages.
(2) *Use of established software to filter, analyze and process GWAS and next-generation sequence data*: requires the ability to run jobs on cluster servers, use basic Unix commands or similar methods to extract data from large genetic datasets and to map sequences to the human genome.
(3) *Develop, implement, and operate statistical tools to analyze GWAS and next-generation sequence data:* requires an understanding of basic concepts pertaining to human genetics
(4) *Use genotype calling algorithms to identify genetic variants from next-generation sequence data:* requires ability to use perl scripts and basic Unix commands (or similar tools) to identify which DNA base pairs are variant in next-generation sequencing data.

The Plenge Lab Home Page and relevant links:

www.brighamandwomens.org/research/depts/medicine/rheumatology/Labs/Plenge/

Please contact Robert Plenge (rplenge@partners.org or 617.525.4451)