

**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

## **STATISTICAL GENETICIST: *biomedical scientist to study polygenetic predictors of treatment response and other complex traits***

A research position as a statistical geneticist and bioinformatics analyst is available in the *Plenge Lab* at Brigham and Women's Hospital, 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 polygenetic basis response to treatment with a variety of drugs in different complex traits. **More specifically, genetic models of "polygenic inheritance" will be tested in available GWAS datasets.** Computer simulations will be performed to help interpret empirical data. The person hired for this position will work closely with a team of scientists brought together from multiple institutions as part of an NIH-funded U01 grant from the Pharmacogenomics Research Network (PGRN; see link below). The person will work closely with statistical geneticists at Harvard Medical School, the 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 3 years of experience with statistical analysis (e.g., multivariate regression analysis). While the project entails application to human genetics, previous experience in non-human genetics (e.g., model organisms, animal breeding) is acceptable. Experience with a scripting language (e.g., perl, python) and expertise with a mathematical language (e.g., R, MatLab) is strongly preferred. Experience working in a biomedical research setting and a basic understanding of statistics is also 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 rheumatoid arthritis (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.

### **Sample tasks required:**

- (1) *Manage and organize large GWAS and sequence data sets*
- (2) *Perform statistical modeling of thousands of SNPs in aggregate for association with response to therapy; methods include multivariate regression analysis, mixed linear model analysis, Bayesian computation, maximum likelihood estimation*
- (3) *Perform simulations to help interpret empirical GWAS data*
- (4) *Work closely with a multi-disciplinary team of researchers*

### **The Plenge Lab Home Page and relevant links:**

[www.brighamandwomens.org/research/depts/medicine/rheumatology/Labs/Plenge/](http://www.brighamandwomens.org/research/depts/medicine/rheumatology/Labs/Plenge/)

Please contact Robert Plenge ([rplenge@partners.org](mailto:rplenge@partners.org) or 617.525.4451)