

Department of Pathology
Yale School of Medicine
Postdoctoral Associate Position (Computational Immunology)

Yale School of Medicine, Department of Pathology, is seeking a highly motivated postdoctoral associate to work on the development and application of computational methods for the analysis of large-scale B cell immunoglobulin (Ig) repertoire sequencing data.

Large-scale characterization of B cell receptor (BCR) and T cell receptor (TCR) repertoires is now feasible in humans. Driven by the dramatic improvements in high-throughput sequencing technologies, these repertoire sequencing (Rep-Seq) projects are opening up exciting avenues of inquiry. Features of the repertoire - including polymorphisms, biased segment usage, mutation profiles and diversity - can be correlated with clinically relevant outcomes, such as susceptibility to infection, vaccination or treatment responses and cancer prognosis. These data have broad applications not only for understanding the adaptive immune response to pathogens, but can also provide insights into the role of somatic hypermutation in autoimmunity and cancer. Achieving these goals requires effective frameworks to manage and analyze such “Big Data”.

The successful candidate will join the Kleinstein lab at Yale, which has developed many widely used computational methods for Rep-Seq analysis. These methods are currently made available to the wider scientific community as part of the Immcantation tool suite (<http://immcantation.readthedocs.io>). Potential research areas include: sequencing error correction and normalization, V(D)J segment assignment and novel allele detection, partitioning sequences into clones and constructing lineage trees, inferring cell differentiation and trafficking patterns from lineage trees, somatic hypermutation profiling and selection analysis, identification of recurrent motifs and convergent evolution, search and visualization of repertoire-scale data. Along with method development, the research will involve close collaboration with experimental and clinical research groups to apply these methods to gain immunological insights. Previous application areas have included: infection (Salmonella, West Nile Virus, HIV), vaccination (influenza), allergy (allergic rhinitis, atopic asthma) and autoimmune disease (Multiple Sclerosis, Myasthenia Gravis).

The ideal candidate will have strong quantitative and programming abilities, along with an interest in applying these skills to problems in biology. A Ph.D. in a quantitative discipline is desired (Bioinformatics, Computer Science, Statistics, Physics, Applied Mathematics, etc.).

Interested candidates should forward a CV and short description of research interests together with the names and addresses of three references to:

steven.kleinstein@yale.edu

-or-

Steven Kleinstein, Ph.D.
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Yale University is an affirmative Action/Equal Opportunity Employer and welcomes applications from women, persons with disabilities, protected veterans and member of minority groups.

Review of applications will begin immediately and will continue until the position is filled.