

Postdoctoral positions in human population genomics and sequencing-based association studies at Cornell University

Two postdoctoral positions are available with Alon Keinan in the Department of Biological Statistics and Computational Biology at Cornell University to join a group of investigators tackling current problems in population genetic analysis of whole-genome data and in sequencing-based association studies. Research areas include (1) human population genetics and evolutionary history, method development for analysis of next-generation sequencing data sets, natural selection detection and characterization, and population genetics theory, and (2) method development for association studies, analysis of GWAS, and analysis of association studies based on whole-genome and whole-exome next-generation sequencing. Representative publications from the lab of related projects can be found below. Research projects will be closely aligned with the interests of the successful candidates.

The ideal candidate will have a strong track record in population genomics, quantitative genetics, or human genetics, as well as strong statistical and programming skills. The starting date is flexible and can be as early as Jan 2012. Applications will be accepted until the positions are filled. Competitive salaries commensurate with experience and skills, as well as a generous benefits package will be offered.

Relevant projects are in collaboration with the labs of Eric Boerwinkle (University of Texas), Carlos Bustamante (Stanford University), Andrew Clark (Cornell), and Adam Siepel (Cornell). The Keinan lab is part of the larger population genomics community at Cornell and is a member of the Cornell Center for Comparative and Population Genomics.

Interested applicants should send a PDF with CV, a brief description of research interests and experience, and contact information for three references to Ms. Shawna Carey (sls68@cornell.edu), indicating “position 204” in the subject line. Informal inquiries are welcome.

Representative publications:

Analyses of X-linked and autosomal genetic variation in population-scale whole genome sequencing. *Nature Genetics* (2011). (highlighted in [Science](#))

Integrating common and rare genetic variation in diverse human populations. *Nature* (2010).

Human population differentiation is strongly correlated with local recombination rate. *PLoS Genetics* (2010).

Accelerated genetic drift on chromosome X during the human dispersal out of Africa. *Nature Genetics* (2009). ([News and Views](#))