



**Cornell University**  
Department of Biological Statistics  
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## **Postdoctoral positions in human population genomics and association studies**

Two postdoctoral positions are available with Alon Keinan in the Department of Biological Statistics and Computational Biology at Cornell University. The Keinan lab studies how human genetic variation has arisen from evolutionary history and its role in common, complex disease risk. We develop computational and statistical methods in human population genomics, genome-wide association studies, and sequence-based association studies and apply them to large-scale sequencing data. Current lab members have backgrounds in computer science, genetics, nutrigenomics, statistics, and physics, which facilitates the collaborative development of methods and their genomic application. Below are representative publications from the lab of related projects, while specific projects will be aligned with the interests of the successful candidate.

The ideal candidate will have a strong track record in either statistical genetics, population genomics, or human genetics, as well as strong programming and statistical skills, with a Ph.D. in computational biology, computer science, statistics, mathematics, genetics, or a related field. The starting date is flexible and can be as early as April 2017. 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 can be as part of the lab's ongoing collaborations with Andrew Clark, Erez Levanon, John Novembre, Harry Ostrer, Yun Song, Haiyuan Yu and several consortia.

Interested applicants should send one PDF with CV, a brief description of research interests and experience, and contact information for three references to the attention of Ms. Sue Bishop, administrative assistant ([skp5@cornell.edu](mailto:skp5@cornell.edu)), indicating "position 207" in the subject line. Informal inquiries are also welcome.

### Representative recent publications from the lab:

- Clustered mutations in hominid genome evolution are consistent with *APOBEC3G* enzymatic activity. *Genome Research* (2016).
- Positive selection on a regulatory insertion-deletion polymorphism in *FADS2* influences apparent endogenous synthesis of arachidonic acid. *Molecular Biology and Evolution* (2016).
- Inference of super-exponential human population growth via efficient computation of the site frequency spectrum for generalized models. *Genetics* (2016).
- The genetic history of Cochin Jews from India. *Human Genetics* (2016).
- Strong constraint on human genes escaping X-inactivation is modulated by their expression level and breadth in both sexes. *Molecular Biology and Evolution* (2016).
- XWAS: a software toolset for genetic data analysis and association studies of the X chromosome. *Journal of Heredity* (2015).
- Contrasting X-linked and autosomal diversity across 14 human populations. *American Journal of Human Genetics* (2014).
- Neutral genomic regions refine models of recent rapid human population growth. *PNAS* (2014).
- Gene-based testing of interactions in association studies of quantitative traits. *PLOS Genetics* (2013).
- Recent explosive human population growth has resulted in an excess of rare genetic variants. *Science* (2012).