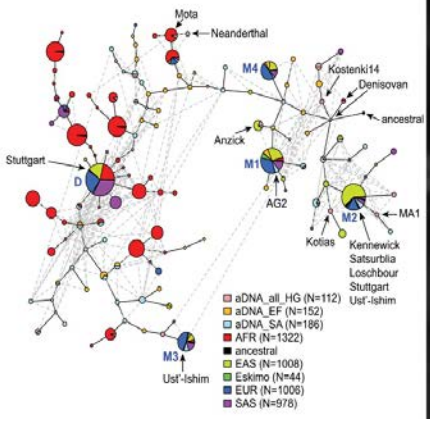
Alon Keinan, PhD
Associate Professor of Computational Biology
t. 607-254-1328|f. 607-255-2323
alon.keinan@cornell.edu
keinanlab.cb.bscb.cornell.edu
@AlonKeinan
Dept. of Biological Statistics & Computational Biology
Centers for Comparative and Population Genomics | Vertebrate Genomics | Enervating Neuroimmune Disease
Mailing: 102C Weill Hall, Cornell University, Ithaca, NY 14853

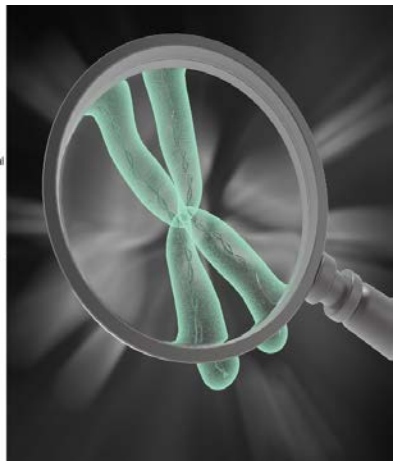
Postdoctoral positions in human population genomics, nutrigenomics, & association studies

Two postdoctoral positions and one programmer/analyst position are available in the group of Alon Keinan at Cornell University (keinanlab.cb.bscb.cornell.edu). Current and past lab members came from backgrounds in computer science, statistics, genetics, nutritional genomics, physics, mathematics, and genetic anthropology, which facilitates the **transdisciplinary development and genomics application of methodologies**, along with functional interpretation of discoveries. The following page lists a few representative publications from the lab of projects related to the fields of the new positions. The successful candidate can join one of the many ongoing projects in the group or start new projects, either from an array of planned projects or their own ideas. Thus, **projects will be aligned with the interests of the successful candidate** and her/his expertise, or expertise they desire to develop further. As the group also draws a large number of the strongest undergraduate students in computer science, computational biology, etc., postdoctoral fellows can aim to carry out a broader project or several projects by relying on their help, while potentially developing mentoring skills. Importantly, projects **do not necessarily have to be associated with any of the existing funding sources** of the PI.

The ideal candidate will have a strong track record in either population genomics, statistical genetics, nutritional genomics, or human genomics in general, as well as strong programming and statistical skills, with a Ph.D. in any of the fields mentioned above or a related field. **The starting date is flexible and can be as early as September 2017**. Applications will be accepted until the positions are filled. **Competitive salaries commensurate with experience and skills, as well as a very generous benefits package will be offered**. Funding will be guaranteed for at least 3 years, and the PI will also help the successful candidate secure fellowships/future funding. **Former postdocs in the group went on to** a tenure-track faculty position at University of Maryland College Park, a tenure-track faculty position at University of Minnesota Twin Cities, a Research Associate position at Cornell University, as well as research positions in industry: Associate Director of Think Team at Otsuka Pharmaceutical Companies (US), Investigator II at Novartis, Computational Biologist at NRGene, and Research Scientist at Embark.

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. The lab is situated at the gorgeous campus—often voted as most beautiful in the US—in Ithaca, NY, which is consistently ranked as one of the best towns to live in (e.g. AIER's top college towns, Best Places to Live 2016, USA Today's 10Best). As part of close ties with Weill Cornell Medical College, located in New York City's "science corridor," it is possible for members of the lab to also live and spend most of their time in the city.





Interested applicants should send one PDF with CV, a brief description of research interests and experience, and contact information for three references to keinan.lab.applicants@gmail.com, indicating "position 209" in the subject line for a postdoctoral position and "position 304" for a programmer/analyst position. Informal inquiries are also welcome.

Representative recent publications from the lab:

1. **Dietary adaptation of FADS genes in Europe varied across time and geography. *Nature Ecology & Evolution* (2017).**
2. Association between rs2294020 in X-linked CCDC22 and susceptibility to autoimmune diseases with focus on systemic lupus erythematosus. *Immunology Letters* (2017).
3. Positive selection on a regulatory insertion-deletion polymorphism in *FADS2* influences apparent endogenous synthesis of arachidonic acid. *Molecular Biology and Evolution* (2016).
4. **Clustered mutations in hominid genome evolution are consistent with *APOBEC3G* enzymatic activity. *Genome Research* (2016).**
5. Explosive genetic evidence for explosive human population growth. *Current Opinion in Genetics & Development* (2016).
6. Inference of super-exponential human population growth via efficient computation of the site frequency spectrum for generalized models. *Genetics* (2016).
7. Mitochondrial DNA variants correlate with symptoms in myalgic encephalomyelitis/chronic fatigue syndrome. Journal of Translational Medicine (2016).
8. **The genetic history of Cochin Jews from India. *Human Genetics* (2016).**
9. The genetics of Bene Israel from India reveals both substantial Jewish and Indian ancestry. *PLOS ONE* (2016).
10. Strong constraint on human genes escaping X-inactivation is modulated by their expression level and breadth in both sexes. *Molecular Biology and Evolution* (2016).
11. **XWAS: a software toolset for genetic data analysis and association studies of the X chromosome. *Journal of Heredity* (2015).**
12. X-inactivation informs variance-based testing for X-linked association of a quantitative trait. *BMC Genomics* (2015).
13. Host genetic variation impacts microbiome composition across human body sites. *Genome Biology* (2015).
14. Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. *Nature Medicine* (2015).
15. The utility of ancient human DNA for improving allele age estimates, with implications for demographic models and tests of natural selection. *Journal of Human Evolution* (2015).
16. Accounting for eXentricities: Analysis of the X Chromosome in GWAS reveals X-linked genes implicated in autoimmune diseases. *PLOS ONE* (2014)
17. **Contrasting X-linked and autosomal diversity across 14 human populations. *American Journal of Human Genetics* (2014).**
18. Neutral genomic regions refine models of recent rapid human population growth. *PNAS* (2014).
19. Principal component analysis characterizes shared pathogenetics from genome-wide association studies. *PLOS Computational Biology* (2014).
20. **Gene-based testing of interactions in association studies of quantitative traits. *PLOS Genetics* (2013).**
21. **Recent explosive human population growth has resulted in an excess of rare genetic variants. *Science* (2012).**