David H. Alexander

UCLA Department of Biomathematics
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Education

Ph.D. in Biomathematics, UCLA, 2011
Dissertation title: *Statistical and Computational Methods for Ancestry Estimation and Variable Selection in Genome-Scale Datasets*

Advisor: Professor Kenneth Lange.

M.S. in Biomathematics, UCLA, 2008

B.S. in Computer Science and Electrical Engineering, MIT, 2003

Research Interests

- Statistical and population genetics modeling and analysis

- Genomic sequencing and exploration of the role of rare sequence variants in disease

- Theoretical and computational statistics

- High-performance numerical computing

- Software engineering

Publications

H. Zhou, D. H. Alexander, and K. L. Lange. A quasi-Newton acceleration for high-dimensional optimization algorithms. *Statistics and Computing*, published online 12 December 2009.

D. H. Alexander, J. Novembre, and K. Lange. Fast model-based estimation of ancestry in unrelated individuals. *Genome Research*, 19:1655–1664, 2009.

H. Zhou, D. H. Alexander, M. E. Sehl, J. S. Sinsheimer, E. M. Sobel, and K. Lange. Penalized regression for genome-wide association screening of sequence data. In *Proceedings of the Pacific Symposium on Biocomputing*, 2011.

D. H. Alexander and K. Lange. Enhancements to the ADMIXTURE algorithm for individual ancestry estimation. *BMC Bioinformatics*, 12(1):246, 2011.

D. H. Alexander and K. Lange. Stability Selection for Variable Selection in Genome-Wide Association. *Genetic Epidemiology*, in press.

Publicly Available Software

- **ADMIXTURE:** http://www.genetics.ucla.edu/software/admixture
  A robust and fast package for ancestry estimation, usable as an alternative to the slower program STRUCTURE. I am the sole author.

- **MENDEL:** http://www.genetics.ucla.edu/software/mendel
  A software program that can perform a wide array of genetic analyses, from linkage analysis to association to haplotype phasing. I have made several contributions, including two new analysis modes.

Teaching experience

- UCLA Human Genetics 236B, 2010: one lecture

- UCLA Statistical Genetics Short Course 2010 (at UNC): four lectures

- UCLA Biomathematics 204 (Linear models in statistics): two lectures

Professional Affiliations

I am a member of the American Society of Human Genetics.

I have peer-reviewed articles for the journals *Bioinformatics*, *Genetic Epidemiology*, *Human Heredity*, and *BMC Medical Genetics*.

Employment (Software industry)

Software engineer, Azul Systems   *Summer 2003–Spring 2006*
Work on system tools and a Java Virtual Machine with novel features on a new hardware platform.

Software engineering intern, Apple Computer   *Summers 2001, 2002*
Work on the Java Virtual Machine for Mac OS X.

Research intern, Sun Microsystems Labs   *Summer 2000–Spring 2001*
Research on parallel garbage collection algorithms for Java Virtual Machines and exploration of the potential impact of a proposed change in the instruction set for SPARC processors.

Awards and Honors

- Recipient of NIH Systems & Integrative Biology Training Grant (2007–2009)

- National Merit Scholar (1999–2003)

- *New Jersey Star-Ledger* Scholar for Essex County, New Jersey (1999–2003)