

P. Alexander Rolfe

34 Playstead Rd #2
Newton, MA 02458

(804) 513-9357
arolfe@mit.edu

Objective To combine statistics and machine learning skills, biology, and software engineering in a in biotechnology or pharmaceutical research career.

Experience COMPUTATIONAL GENOMICS RESEARCH GROUP, MIT June 2009-Present
Work as a Postdoctoral associate focused on pancreatic development. Applied ChIP-Seq, expression, and proteomic data to an in-vitro differentiation system to detect regulatory interactions in endoderm development. Developed computational infrastructure for high throughput sequencing and worked on algorithms for analysis of ChIP-Seq, DNase hypersensitivity, and proteomics data.

COMPUTATIONAL GENOMICS RESEARCH GROUP, MIT January 2003-May 2009
Research focused on ChIP-Chip data, microarray design, genetic regulatory network discovery, and computational tools for biology collaborators. Developed a novel method to identify transcription factor binding sites (Joint Binding Deconvolution). Expanded research group's computational infrastructure to include a compute cluster and Oracle databases for microarray and short-read sequencing data. Thesis project required experiment design and computational analysis to develop a novel technique to detect insertions, deletions, and inversions in nucleic acid samples.

WHITEHEAD INSTITUTE CENTER FOR GENOME RESEARCH January 1998-August 2002
Implemented a variety of laboratory information management and analysis systems for the Functional Genomics Group. Developed programming tools for rapid development of workflow systems as Master of Engineering thesis project. Other work involved database development to support SNP discovery project.

MIT LECTURE SERIES COMMITTEE 2000-Present
Chairman (2002) and Treasurer (2003) of MIT's on-campus cinema and lecture group. Negotiated film booking and supervised finances for \$100k annual budget. Managed operations for 3 weekly events and 90 student workers leading to over \$10k annual profit.

Selected Publications

Rolfe, Bernstein, *et al* **Ruler Arrays Reveal Haploid Genomic Structural Variation.** under revision.

Rolfe and Gifford **ReadDB Provides Efficient Storage for Mapped Short Reads.** under review.

Wu, Rolfe, Gifford, and Fink **Control of transcription by cell size.** PLoS Biology, Nov 2 2010.

Danford, Rolfe, and Gifford **GSE: a comprehensive database system for the representation, retrieval, and analysis of microarray data.** Pacific Symposium on Biocomputing, 2008.

Qi, Rolfe, Maclsaac, *et al* **High-resolution computational models of genome binding events.** Nature Biotechnology, August 2006.

Odom *et al* **Core transcriptional regulatory circuitry in human hepatocytes.** Molecular Systems Biology, May 2006.

Pokholok *et al* **Genome-wide map of nucleosome acetylation and methylation in yeast.** Cell, August 2005.

Education MASSACHUSETTS INSTITUTE OF TECHNOLOGY Department of Electrical Engineering and Computer Science
PhD completed in June 2009, GPA 4.7/5.0
Thesis project *Ruler Arrays Detect Insertions and Deletions between Genomes*
MEng completed in 2002, GPA 5.0/5.0
Thesis project *Code Versioning in a Workflow Management System*
SB completed in 2001, GPA 4.8/5.0

Skills

- Extensive Java, Perl, C, Scheme, shell scripting, and SQL experience
- Working knowledge of Matlab and R
- Over 13 years experience with biological and genomic datasets
- Extensive Linux and Oracle administration experience
- Familiar with numerous biology databases (Genbank, UCSC, SGD, JASPAR, SRA)