Abhishek Sarkar

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Research interests

Machine learning, single cell genomics, regulatory genomics, epigenomics, complex traits

Education

2017 Ph.D. Computer Science, Massachusetts Institute of Technology

2013 M.S. Computer Science, Massachusetts Institute of Technology

2011 B.S. Computer Science with Highest Honors, University of North Carolina at Chapel Hill

Research experience

2017– **University of Chicago**
Postdoctoral Scholar
Matthew Stephens (PI)
Human Genetics Department

2011–2017 **Massachusetts Institute of Technology**
Research Assistant
Computational Biology Group, Manolis Kellis (PI)
Computer Science and Artificial Intelligence Lab

Teaching experience

2014 Teaching assistant, "Computational Biology: Genomes, Networks, Evolution" (fall)

Pre-prints

1. **Abhishek Sarkar***, Po-Yuan Tung* et al. "Discovery and characterization of variance QTLs in human induced pluripotent stem cells." *BioRxiv* (2018) **Equal contribution*
2. Gao Wang, Abhishek Sarkar, Peter Carbonetto, and Matthew Stephens. "A simple new approach to variable selection in regression, with application to genetic fine-mapping." *BioRxiv* (2018).
3. Yongjin Park*, **Abhishek Sarkar***, et al. "A Bayesian approach to mediation analysis predicts 206 causal target genes in Alzheimer's disease." *BioRxiv* (2017) **Equal contribution*
4. Yongjin Park*, **Abhishek K. Sarkar***, et al. "Multi-tissue polygenic models for transcriptome-wide association studies." *BioRxiv*. (2017) **Equal contribution*

Peer-reviewed publications

1. Yaping Liu, **Abhishek Sarkar**, Pouya Kheradpour, Jason Ernst, and Manolis Kellis. "Evidence of reduced recombination rate in human regulatory domains." *Genome Biology*. (2017)
2. Felix Day, …, **Abhishek K. Sarkar**, et al. "Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility." *Nat Genet*. (2017) *Author 9/215*
3. Roadmap Epigenomics Consortium et al. "Integrative analysis of 111 reference human epigenomes." *Nature*, 518(7539), 317–330 (2015). *Integrative analysis lead (equal contributor)*.

Presentations

1. Yongjin Park*, **Abhishek Sarkar***, Liang He* and Manolis Kellis. "Variational Bayes inference algorithm for causal multivariate mediation with linkage disequilibrium." Workshop on Machine Learning in Computational Biology, Thirty-first Annual Conference on Neural Information Processing Systems, Los Angeles, California, USA. 2017. **Equal contribution*
2. Yongjin Park*, **Abhishek Sarkar***, Liang He* and Manolis Kellis. "Identification transcriptomic and epigenetic mediators in Alzheimer's disease: Bayesian inference and causal mediation analysis of regulatory programs in GWAS statistics." 69th meeting of the American Society of Human Genetics, Orlando, Florida, USA. 2017 **Equal contribution*
3. Yongjin Park*, **Abhishek Sarkar***, Kunal Bhutani, Manolis Kellis. "Multi-tissue polygenic models for transcriptome-wide association studies" (talk). Biology of Genomes, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 2017. **Equal contribution*
4. **Abhishek Sarkar**, Yongjin Park, Manolis Kellis. "Dissecting the non-infinitesimal architecture of complex traits using group spike-and-slab priors" (contributed talk). Workshop on Machine Learning in Computational Biology, Thirtieth Annual Conference on Neural Information Processing Systems, Barcelona, Spain. 2016.
5. **Abhishek Sarkar**, Yongjin Park, Manolis Kellis. "Dissecting the non-infinitesimal architecture of complex traits" (poster). 68th meeting of the American Society of Human Genetics, Vancouver, Canada. 2016.
6. **Abhishek Sarkar**, Luke Ward, Manolis Kellis. "Functional enrichments of disease variants across thousands of independent loci in eight diseases." (talk). Leena Peltonen School of Human Genomics, Wellcome Trust Sanger Institute, Hinxton, Cambridge, UK. 2016.
7. Yongjin Park, **Abhishek Sarkar**, Nick Mancuso, Alexander Gusev, Bogdan Pasaniuc, Manolis Kellis. "Computational discovery of epigenetic mediators in Alzheimer's disease from imputed methyomewide association statistics" (poster). The Biology of Genomes, Cold Spring Harbor, NY, USA. 2016.
8. Kunal Bhutani*, **Abhishek Sarkar***, Yongjin Park, Manolis Kellis, Nicholas Schork. "Propagating uncertainty of predicted expression in transcriptome-wide association studies" (poster). The Biology of Genomes, Cold Spring Harbor, NY, USA. 2016. **Equal contribution*
9. **Abhishek Sarkar**, Lucas D. Ward, Manolis Kellis. "Regulatory annotations implicate thousands of independent loci" (poster). 67th meeting of the American Society of Human Genetics, Baltimore, MD, USA. 2015.
10. **Abhishek K. Sarkar**, Lucas D. Ward, Manolis Kellis. "Genome-wide enrichments for regulatory regions across thousands of unlinked disease-associated variants" (poster). 65th meeting of the American Society of Human Genetics, Boston, MA, USA. 2013.
11. Vineeta Agarwala, **Abhishek Sarkar**, Kyle Gaulton. "Using the Epigenome Roadmap data to analyze genetic studies of Type 2 Diabetes" (workshop talk). 65th meeting of the American Society of Human Genetics, Boston, MA, USA. 2013.
12. **Abhishek K. Sarkar**, Lucas D. Ward, Manolis Kellis. "Systematically interpreting GWAS using regions from Roadmap" (poster). Epigenomics: A Roadmap to the Living Genome, Boston, MA, USA. 2013.

13. Lucas Ward, **Abhishek Sarkar**, Manolis Kellis. "Global contributions of regulatory elements to disease risk and evolutionary fitness in the human population" (poster). 5th annual RECOMB Conference on Regulatory and Systems Genomics, San Francisco, CA, USA. 2012.
14. **Abhishek Sarkar**. "Functional GWAS enrichments across tens of thousands of enhancer elements" (talk). Epigenomics Seminar Series, Broad Institute, Cambridge, MA, USA. 2011.

Technical reports

1. Kunal Bhutani, **Abhishek Sarkar**, et al. "Modeling prediction error improves power of transcriptome-wide association studies." *BioRxiv*. (2017) **Equal contribution*
2. **Abhishek K. Sarkar**, Lucas D. Ward, Manolis Kellis. "Functional enrichments of disease variants across thousands of independent loci in eight diseases." *BioRxiv*. (2016)

Honors

2016 Accepted to Leena Peltonen School of Human Genomics

2011 Awarded NSF Graduate Research Fellowship

2011 Inducted into Phi Beta Kappa honors fraternity