

SRIRAM SANKARARAMAN

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EDUCATION

Course in Advanced Bacterial Genetics *June 2010*
Cold Spring Harbor Laboratory

Ph.D. in Computer Science *Aug 2004 – May 2010*
with a Designated Emphasis in Computational and Genomic Biology
University of California, Berkeley

B. Tech. in Computer Science and Engineering *June 2000 – June 2004*
Indian Institute of Technology, Madras

POSITIONS AND EMPLOYMENT

Assistant Professor *Nov 2015 –*
Department of Computer Science,
Department of Human Genetics,
University of California, Los Angeles

Post-doctoral fellow *Sept 2010 – Nov 2015*
Department of Genetics,
Harvard Medical School
Mentor: David Reich

Fellow *January – May 2014*
Program in Evolutionary Biology and Theory of Computing
Simons Institute for the Theory of Computing, Berkeley

Intern *May–Aug 2006*
International Computer Science Institute, Berkeley
Mentor: Eran Halperin

Intern *May–Aug 2005*
International Computer Science Institute, Berkeley
Mentor: Scott Shenker

RESEARCH INTERESTS

Computational Biology, Computational/Statistical genomics, Statistical Machine Learning (Probabilistic Graphical Models, Bayesian Statistics).

My interests lie at the interface of computer science, statistics and biology. I am interested in developing statistical and computational tools to understand evolution as well as the genetic basis of complex phenotypes. I am also interested in the statistical and inferential challenges posed by the scale of genomic data.

DISSERTATION

Title: “Statistical Models for Analyzing Human Genetic Variation”
Advisors: Prof. Michael Jordan and Prof. Kimmen Sjölander

ACADEMIC HONORS AND FELLOWSHIPS

- Semifinalist for Trainee Research Award, American Society of Human Genetics (ASHG), 2015.
- NIH K99/R00 Pathway to Independence Award, 2014.

- Fellow at the Simons Institute for the Theory of Computing, UC Berkeley, Spring 2014.
- Stellar Abstract award, Program in Quantitative Genetics conference, Harvard School of Public Health, 2012.
- Harvard Science of the Human Past fellow, 2012.
- Semifinalist for Trainee Research Award, American Society of Human Genetics (ASHG), 2011.
- Post-doctoral Travel Award, Society for Molecular Biology and Evolution (SMBE) 2011.
- Outstanding Graduate Student Instructor award, U C Berkeley, Fall 2006.
- The Berkeley fellowship (3 years), U C Berkeley, 2004.
- Visvesvaraya medal for the highest CGPA in the graduating class, IIT Madras, 2004.

PUBLICATIONS

* denotes equal contributions

JOURNALS

1. James Zou, Eran Halperin, Esteban Burchard, **Sriram Sankararaman**, Inferring parental genomic ancestries using pooled semi-Markov processes, 31(12): i190–i196, *Bioinformatics*, (2015).
2. Noah Zaitlen, Bogdan Pasaniuc, **Sriram Sankararaman**, Gaurav Bhatia, Jianqi Zhang, *et al.*, Leveraging population admixture to characterize the heritability of complex traits, *Nature Genetics*, 46:1356–1362, (2014).
3. **Sriram Sankararaman**, Swapan Mallick, Michael Dannemann, *et al.*, The landscape of Neandertal ancestry in present-day humans, *Nature*, 507(7492): 354–357 (2014).
4. Kay Prüfer, Fernando Racimo, Nick Patterson, Flora Jay, **Sriram Sankararaman**, *et al.*, The complete genome sequence of a Neanderthal from the Altai Mountains, *Nature*, 505(7481): 43–49 (2014).
5. SIGMA Type 2 Diabetes Consortium, Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico, *Nature*, 506(7486): 97–101 (2014).
6. Gaurav Bhatia*, Nick Patterson*, **Sriram Sankararaman**, Alkes L. Price, Estimating and interpreting F_{ST} : The impact of rare variants, *Genome Research*, (2013).
7. Bogdan Pasaniuc*, **Sriram Sankararaman***, Dara G. Torgerson, *et al.*, Analysis of Latino populations from GALA and MEC studies reveals genomic loci with biased local ancestry estimation, *Bioinformatics*, (2013).
8. **Sriram Sankararaman**, Nick Patterson, Heng Li, *et al.*, The date of interbreeding between Neandertals and modern humans, *PLoS Genetics*, 2012: e1002947.
9. Yael Baran*, Bogdan Pasaniuc*, **Sriram Sankararaman***, Dara G. Torgerson, Christopher Gignoux, Celeste Eng, William Rodriguez-Cintron, Rocio Chapela, Jean G. Ford, Pedro C. Avila, Jose Rodriguez-Santana, Esteban González Burchard, Eran Halperin, Fast and accurate inference of local ancestry in Latino populations, *Bioinformatics*, 28(10): 1359–1367, (2012).
10. Michael C Turchin, Charleston WK Chiang, Cameron D Palmer, **Sriram Sankararaman**, *et al.*, Evidence of widespread selection on standing variation in Europe at height-associated SNPs, *Nature Genetics*, 44(9): 1015–1019, (2012).
11. Alexandre Bouchard-Côté, **Sriram Sankararaman**, Michael I. Jordan, Phylogenetic Inference using Sequential Monte Carlo, *Systematic Biology*, (2012).
12. **Sriram Sankararaman**, Fei Sha, Michael I. Jordan, Kimmen Sjölander, Active Site Prediction using Evolutionary and Structural Information, *Bioinformatics*, 26(5): 617–624, (2010).
13. Colin A. Hodgkinson, Mary-Anne Enoch, Vibhuti Srivastava, *et al.*, Genome-wide association identifies candidate genes that influence the human electroencephalogram, *Proceedings of the National Academy of Sciences*, 107(19):8695–8700, (2010).
14. **Sriram Sankararaman***, Guillaume Obozinski*, Michael I. Jordan, Eran Halperin, Genomic Privacy and Limits of Individual Detection in a Pool, *Nature Genetics*, 41:965–967, 2009.
15. Bogdan Pasaniuc*, **Sriram Sankararaman***, Gad Kimmel, Eran Halperin, Locus-specific Ancestry Inference in Closely-related populations, *Bioinformatics*, 25(12): i213–i221 (2009).
16. Ron Alterovitz, Aaron Arvey, **Sriram Sankararaman**, *et al.*, ResBoost: characterizing and predicting catalytic residues in enzymes, *BMC Bioinformatics*, 10: 197, (2009).
17. **Sriram Sankararaman**, Bryan Kolaczowski, Kimmen Sjölander, INTREPID: a web server for prediction of functionally important residues by evolutionary analysis, *Nucleic Acids Research*, 37(suppl 2):W390–W395, (2009).
18. **Sriram Sankararaman***, Gad Kimmel*, Eran Halperin, Michael I. Jordan, On the inference of ancestries in admixed populations, *Genome Research* 18:668–675 (2008).

19. **Sriram Sankararaman**, Srinath Sridhar, Gad Kimmel, Eran Halperin, Estimating local ancestry in admixed populations, *American Journal of Human Genetics* 8:290–303 (2008).
20. **Sriram Sankararaman**, Kimmen Sjölander, INTREPID–INformation-theoretic TREE traversal for Protein functional site IDentification. *Bioinformatics*, 24(21):2445–2452 (2008).
21. Christine F. Skibola, Paige M. Bracci, Eran Halperin, *et al.*, Polymorphisms in the Estrogen Receptor 1 and Vitamin C and Matrix Metalloproteinase Gene Families Are Associated with Susceptibility to Lymphoma, *PLoS ONE*, vol. 3(7), (2008).
22. **S. Sriram**, T. Bheemarjuna Reddy, C. Siva Ram Murthy, The Influence of QoS Routing on the Achievable Capacity in TDMA Based Adhoc Wireless Networks, *Wireless Networks Journal*, (2008).
23. **T. Bheemarjuna Reddy**, S. Sriram, B. S. Manoj, C. Siva Ram Murthy, MuSeQoS: Multi-path Failure-tolerant Security-aware QoS Routing in Ad hoc Wireless Networks, *Computer Networks*, 50(9):1349-1383, (2006).
24. Sougata Mukherjea, L. Venkata Subramaniam, Gaurav Chanda, **Sriram Sankararaman**, Ravi Kothari, Vishal S. Batra, Deo N. Bhardwaj, Biplav Srivastava, Enhancing a biomedical information extraction system with dictionary mining and context disambiguation. *IBM Journal of Research and Development*, 48(5-6): 693-702 (2004).

REFEREED CONFERENCES

25. James Zou, Eran Halperin, Esteban Burchard, **Sriram Sankararaman**, Inferring parental genomic ancestries using pooled semi-Markov processes, 23rd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), 2015 (journal version above).
26. Bogdan Pasaniuc*, **Sriram Sankararaman***, Gad Kimmel, Eran Halperin, Locus-specific Ancestry Inference in Closely-related populations, 17th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), 2009 (journal version above).
27. **Sriram Sankararaman***, Gad Kimmel*, Eran Halperin, Michael I. Jordan, On the inference of ancestries in admixed populations, in Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology (RECOMB), 2008 (journal version above).
28. Tyson Condie, Varun Kacholia, **Sriram Sankararaman**, Joseph M. Hellerstein, Petros Maniatis, Induced Churn as Shelter from Routing-Table Poisoning, In Proceedings of the 13th Annual Network and Distributed System Security Symposium (NDSS), 2006
29. **S. Sriram**, T. Bheemarjuna Reddy, B. S. Manoj, and C. Siva Ram Murthy, On the End-to-end Call Acceptance and the Possibility of Deterministic QoS Guarantees in Ad hoc Wireless Networks, in Proceedings of the Sixth ACM International Symposium on Mobile Ad Hoc Networking and Computing (MobiHoc), pp. 169-180, May 2005.
30. **S. Sriram**, T. Bheemarjuna Reddy, B. S. Manoj, C. Siva Ram Murthy, MuSeQoS: Multi-path Failure-tolerant Security-aware QoS Routing in Ad hoc Wireless Networks, in Proceedings of the 11th IEEE International Conference on High Performance Computing (HiPC), pp. 81-90, December 2004.
31. **S. Sriram**, T. Bheemarjuna Reddy, B. S. Manoj, C. Siva Ram Murthy, The Influence of QoS Routing on the Achievable Capacity in TDMA-based Ad hoc Wireless Networks, in Proceedings of the 47th annual IEEE Global Telecommunications Conference (GLOBECOM), vol. 5, pp. 2909-2913, 2004.

INVITED PAPERS

32. **Sriram Sankararaman**, Venugopalan Ramasubramanian and Lakshminarayanan Subramanian. TrickleDNS: A High Integrity Domain Name System, Fourth International Conference on Communication Systems and Networks (COMSNETS),2012

REVIEWS

33. Fernando Racimo, **Sriram Sankararaman**, Rasmus Nielsen, Emilia Huerta-Sánchez, Evidence for archaic adaptive introgression in humans, *Nature Reviews Genetics*, 16, 359–371 (2015).

IN SUBMISSION

34. James Zou, Danny S. Park, Esteban G. Burchard, Dara G. Torgerson, Maria Pino-Yanes, Yun S. Song, **Sriram Sankararaman***, Eran Halperin*, Noah Zaitlen*, A genetic and socio-economic study of mate choice in Latinos reveals novel assortment patterns.
35. Mark Lipson, Po-Ru Loh, **Sriram Sankararaman**, *et al.*, Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes.
36. Priya Moorjani, **Sriram Sankararaman**, *et al.*, Dating ancient human samples using the recombination clock.
37. Pier Francesco Palamara, *et al.*, Leveraging distant relatedness to quantify human mutation and gene conversion rates.

TECHNICAL REPORTS

38. **Sriram Sankararaman**, Byung-Gon Chun, Chawathe Yatin and Scott Shenker, Key Consistency in DHTs, EECS Department, University of California, Berkeley, Technical Report No. UCB/EECS-2005-21, November 29, 2005
39. Tyson Condie, Varun Kacholia, **Sriram Sankararaman**, Joseph M. Hellerstein, Petros Maniatis, Maelstrom: Churn as Shelter, EECS Department, University of California, Berkeley, Technical Report No. UCB/EECS-2005-11, November 10, 2005

TEACHING EXPERIENCE

- **Introduction to Protein Informatics**. Guest lecturer, U C Berkeley, Spring 2014.
- **Practical Machine Learning**. Guest lecturer, U C Berkeley, Fall 2009.
- **Computer Science self-paced**. Graduate Student Instructor, U C Berkeley, Fall 2009.
- **Bayesian Inference and Modeling**. Graduate Student Instructor, U C Berkeley, Spring 2009.
- **Practical Machine Learning**. Guest lecturer, U C Berkeley, Spring 2008.
- **Genomics and Computational Biology**. Guest lecturer, U C Berkeley, Fall 2007.
- **Introduction to Protein Informatics**. Guest lecturer, U C Berkeley, Fall 2007.
- **Introduction to Protein Informatics**. Graduate Student Instructor, U C Berkeley, Fall 2006.

TALKS

INVITED TALKS

- Bioinformatics Seminar, UCLA, Los Angeles, CA, 7 April 2014.
- 23andme.com, Mountain View, CA, 3 March, 2014.
- Evolutionary Biology Seminar, Simons Institute, Berkeley, 10 Feb, 2014.
- Institute for Mathematics and its Applications workshop on "Group Testing Designs, Algorithms, and Applications to Biology", Minneapolis, 15 Feb 2012.
- WILLOW (Computer vision and Machine Learning Research Laboratory) at INRIA, Paris, France, 9 July 2011
- Stanford Genome Technology Club seminar, Stanford University, CA, USA, 10 September 2009

SYNERGISTIC ACTIVITIES

- Author of the *LAMP* suite of programs for inferring local ancestries.
<http://lamp.icsi.berkeley.edu/lamp>.
- Author of the *SecureGenome* program for securely distributing pooled SNP data.
<http://securegenome.icsi.berkeley.edu/securegenome>.
- Author of the *INTREPID* and *Discern* programs for predicting functional residues in proteins.
<http://phylogenomics.berkeley.edu/INTREPID>.
- Reviewer for computational biology conferences – RECOMB, ISMB, ECCB.
- Ad-hoc reviewer for Nature, Nature Methods, Proceedings of the National Academy of Sciences, American Journal of Human Genetics, PLoS Biology, ACM Computing Surveys, PLoS Computational Biology, PLoS One, PLoS Genetics, Bioinformatics, Genetics, Genetic Epidemiology, Molecular Biology and Evolution, European Journal of Human Genetics, Genome Research, Entropy, PeerJ.
- Reviewer for computer science conferences such as Neural Information Processing Systems (NIPS) and IEEE International Conference on Communications.
- Reviewer for the France-Berkeley Fund project.
- Reviewer for the Leakey fund.
- Program Committee, 21st Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) 2013.

PROFESSIONAL ASSOCIATIONS

- American Society for Human Genetics
- International Society for Computational Biology
- American Statistical Association
- International Society for Bayesian Analysis
- Association for Computing Machinery
- Society for Molecular Biology and Evolution