

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,
Department of Computational Medicine,
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

- NSF Career Award 2020
- Microsoft Investigator Fellowship 2019
- Northrop Grumman Excellence in Teaching Award 2019
- Okawa Foundation Research Grant 2017
- UCLA Hellman Fellow, 2017-2018
- Alfred P. Sloan Research Fellow, 2017
- Nominee, Second Leena Peltonen Prize for Excellence in Human Genetics Research, 2015 (one of ten).
- Semifinalist for Trainee Research Award, American Society of Human Genetics (ASHG), 2015.
- NIH K99/R00 Pathway to Independence Award, 2014 – present.
- 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, UC Berkeley, Fall 2006.
- The Berkeley fellowship (3 years), UC Berkeley, 2004.
- Visvesvaraya medal for the highest CGPA in the graduating class, IIT Madras, 2004.

PUBLICATIONS

†, * denote equal contributions

JOURNAL PAPERS

1. Ali Pazokitoroudi, Yue Wu, Kathryn S. Burch, Kangcheng Hou, Aaron Zhou, Bogdan Pasaniuc, and **Sriram Sankararaman**, Efficient variance components analysis across millions of genomes, *Nature Communications* (2020).
2. Ariel Wu, Eleazar Eskin[†], **Sriram Sankararaman[†]**, A unifying framework for imputing summary statistics in Genome-wide Association Studies, *Journal of Computational Biology* (2020).
3. Aman Agrawal*, Alec M. Chiu*, Minh Le, Eran Halperin, and **Sriram Sankararaman**. Scalable probabilistic PCA for large-scale genetic variation data. *PLoS Genetics* (2020).
4. Arun Durvasula, **Sriram Sankararaman**, Recovering signals of ghost archaic introgression in African populations, *Science Advances*, 2020.
5. Brian Hill*, Robert Brown*, Eilon Gabel, Christine Lee, Maxime Cannesson, Loes Olde Loohuis, Ruth Johnson, Brandon Jew, Uri Maoz, Aman Mahajan, Sriram Sankararaman[†], Ira Hofer[†], Eran Halperin[†], Preoperative predictions of in-hospital mortality using electronic medical record data, *British Journal of Anaesthesia*, (2019).
6. Kangcheng Hou*, Kathryn Burch*, Arunabha Majumdar, Huwenbo Shi, Nicholas Mancuso, Yue Wu, **Sriram Sankararaman**, and Bogdan Pasaniuc, Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture, *Nature Genetics*, (2019).
7. Elijah Rahmani, Regev Schweiger, Brooke Rhead, Lindsey A. Criswell, Lisa F. Barcellos, Eleazar Eskin, Saharon Rosset, **Sriram Sankararaman**, and Eran Halperin, Cell-type-specific resolution epigenetics without the need for cell sorting or single-cell biology, *Nature Communications*, (2019).
8. Arun Durvasula, **Sriram Sankararaman**, A statistical model for reference-free inference of archaic local ancestry, *PLoS Genetics*, (2019).
9. Charleston Chiang, Serghei Mangul, Christopher Robles, **Sriram Sankararaman**, A comprehensive map of genetic variation in the world's largest ethnic group - Han Chinese, *Molecular Biology and Evolution*, 2018.
10. Yue Wu, **Sriram Sankararaman**, A scalable estimator of SNP heritability for Biobank-scale data, *Bioinformatics*, 2018.
11. Ruth Johnson, Huwenbo Shi, Bogdan Pasaniuc[†], **Sriram Sankararaman[†]**, A unifying framework for joint trait analysis under a non-infinitesimal model, *Bioinformatics*, 2018.
12. Molly Schumer, Chenling Xu, Daniel Powell, Arun Durvasula, Laurits Skov, Chris Holland, John Balzier, **Sriram Sankararaman**, Peter Andolfatto, Gil Rosenthal, Molly Przeworski, Natural selection interacts with the local recombination rate to shape the evolution of hybrid genomes, *Science*, 2018.

13. Farhad Hormozdiari *et al.*, Widespread Allelic Heterogeneity in Complex Traits, *American Journal of Human Genetics*, (2017)
14. Bernard Jegou *et al.*, Meiotic genes are enriched in genes of reduced archaic ancestry, *Molecular Biology and Evolution*, (2017)
15. Hormozdiari *et al.*, Colocalization of GWAS and eQTL Signals Detects Target Genes, *American Journal of Human Genetics*, (2016)
16. Swapan Mallick *et al.*, The Simons Genome Diversity Project: 300 genomes from 142 diverse populations, *Nature*, (2016)
17. Priya Moorjani, **Sriram Sankararaman**, *et al.*, A genetic method for dating ancient genomes provides a direct estimate of human generation interval in the last 45,000 years, *Proceedings of the National Academy of Sciences*, (2016)
18. **Sriram Sankararaman**, Swapan Mallick, *et al.*, The landscape of Denisovan admixture in South Asians and Oceanians, *Current Biology*, (2016).
19. Mark Lipson, Po-Ru Loh, **Sriram Sankararaman**, *et al.*, Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes, *PLoS Genetics*, (2015).
20. Pier Francesco Palamara, *et al.*, Leveraging distant relatedness to quantify human mutation and gene conversion rates, *American Journal of Human Genetics*, (2015).
21. James Zou, Danny Park, Esteban Burchard, Dara Torgerson, Maria Pino-Yanes, Yun Song, **Sriram Sankararaman**[†], Eran Halperin[†], Noah Zaitlen[†], A genetic and socio-economic study of mate choice in Latinos reveals novel assortment patterns, *Proceedings of the National Academy of Sciences*, 112(44):13621-6 (2015).
22. James Zou, Eran Halperin, Esteban Burchard, **Sriram Sankararaman**, Inferring parental genomic ancestries using pooled semi-Markov processes, 31(12): i190–i196, *Bioinformatics*, (2015).
23. 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).
24. **Sriram Sankararaman**, Swapan Mallick, Michael Dannemann, *et al.*, The landscape of Neandertal ancestry in present-day humans, *Nature*, 507(7492): 354–357 (2014).
25. 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).
26. 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).
27. Gaurav Bhatia*, Nick Patterson*, **Sriram Sankararaman**, Alkes L. Price, Estimating and interpreting F_{ST} : The impact of rare variants, *Genome Research*, (2013).
28. 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).
29. **Sriram Sankararaman**, Nick Patterson, Heng Li, *et al.*, The date of interbreeding between Neandertals and modern humans, *PLoS Genetics*, 2012: e1002947.
30. 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).
31. 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).
32. Alexandre Bouchard-Côté, **Sriram Sankararaman**, Michael I. Jordan, Phylogenetic Inference using Sequential Monte Carlo, *Systematic Biology*, (2012).
33. **Sriram Sankararaman**, Fei Sha, Michael I. Jordan, Kimmen Sjölander, Active Site Prediction using Evolutionary and Structural Information, *Bioinformatics*, 26(5): 617–624, (2010).
34. 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).
35. **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.
36. Bogdan Pasaniuc*, **Sriram Sankararaman***, Gad Kimmel, Eran Halperin, Locus-specific Ancestry Inference in Closely-related populations, *Bioinformatics*, 25(12): i213–i221 (2009).

37. Ron Alterovitz, Aaron Arvey, **Sriram Sankararaman**, *et al.*, ResBoost: characterizing and predicting catalytic residues in enzymes, *BMC Bioinformatics*, 10: 197, (2009).
38. **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).
39. **Sriram Sankararaman***, Gad Kimmel*, Eran Halperin, Michael I. Jordan, On the inference of ancestries in admixed populations, *Genome Research* 18:668–675 (2008).
40. **Sriram Sankararaman**, Srinath Sridhar, Gad Kimmel, Eran Halperin, Estimating local ancestry in admixed populations, *American Journal of Human Genetics* 8:290–303 (2008).
41. **Sriram Sankararaman**, Kimmen Sjölander, INTREPID–INformation-theoretic TREE traversal for Protein functional site IDentification. *Bioinformatics*, 24(21):2445–2452 (2008).
42. 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).
43. **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).
44. **T. Bheemarjuna Reddy**, S. Sriram, B. S. Manoj, C. Siva Ram Murthy, MuSeQoR: Multi-path Failure-tolerant Security-aware QoS Routing in Ad hoc Wireless Networks, *Computer Networks*, 50(9):1349-1383, (2006).
45. 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 CONFERENCE PAPERS

46. Ruth Johnson, Kathryn S. Burch, Kangcheng Hou, Mario Paciuc, Bogdan Pasaniuc, and **Sriram Sankararaman**, A scalable method for estimating for regional polygenicity for complex traits, RECOMB (2020).
47. Gregory Plumb, Jonathan Terhorst, **Sriram Sankararaman**, and Ameet Talwalkar, Explaining Groups of Points in Low-Dimensional Representations, ICML (2020).
48. Yue Wu, Anna Yaschenko, Mohammadreza Hazy Heydary, **Sriram Sankararaman**, Fast estimation of genetic correlation for Biobank-scale data, RECOMB (2019).
49. 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).
50. **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).
51. **S. Sriram**, T. Bheemarjuna Reddy, B. S. Manoj, C. Siva Ram Murthy, MuSeQoR: 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).
52. **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

53. **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

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

INVITED REVIEWS

55. **Sriram Sankararaman**, Methods for detectign introgressed archaic sequences, *Current Opinions in Genetics and Development*, (2020).

REFEREED CONFERENCE PAPERS THAT ALSO APPEARED AS A JOURNAL PUBLICATION

1. Ali Pazokitoroudi, Yue Wu, Kathryn S. Burch, Kangcheng Hou, Bogdan Pasaniuc, and **Sriram Sankararaman**, Scalable multi-component linear mixed models with application to SNP heritability estimation, *23rd Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, RECOMB 2019.
2. Ruth Johnson, Huwenbo Shi, Bogdan Pasaniuc*, **Sriram Sankararaman***, A unifying framework for joint trait analysis under a non-infinitesimal model, *26th Conference on Intelligent Systems for Molecular Biology (ISMB)*, 2018.
3. Yue Wu, **Sriram Sankararaman**, A scalable estimator of SNP heritability for Biobank-scale data, *26th Conference on Intelligent Systems for Molecular Biology (ISMB)*, 2018.
4. Ariel Wu, Eleazar Eskin*, **Sriram Sankararaman***, A unified view of summary statistic imputation, *22nd Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, 2018.
5. Elinor Rahmani, Regev Schweiger, Saharon Rosset, **Sriram Sankararaman**, Eran Halperin, Tensor Composition Analysis Detects Cell-Type Specific Associations in Epigenetic Studies, *22nd Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, 2018.
6. 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.
7. 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.
8. **Sriram Sankararaman***, Gad Kimmel*, Eran Halperin, Michael I. Jordan, On the inference of ancestries in admixed populations, *12th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, 2008.

TECHNICAL REPORTS

9. **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
10. 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

FUNDING

- Microsoft AI for Health COVID-19 Award.
- UCLA Broad Stem Cell Research Center COVID-19 Research Award, 2020 – present (Co-PI: Sankararaman, PI: Ernst).
- NSF Career Award, 2020 – present.
- UCLA-AWS Medically relevant Machine Learning 2019.
- UCLA DGSOM Seed Grant: Machine Learning of Electronic Health Record Data and Genomic Data to predict Persistent Opioid Use following Surgery in Opioid Naive Patients, 2019–present (Co-PI: Sankararaman, PI: Rahman).
- UCLA DGSOM Seed Grant: Machine Learning Models for the Prediction of Adverse Outcomes after Surgery using EMR and Genetic Data, 2018–present (Co-PI: Sankararaman, PI: Halperin).
- NSF: A non-invasive and wearable molecular Diagnostic Platform for Remote and Passive Monitoring of Patients at Risk for Sepsis, 2017–present (Co-PI: Sankararaman, PI: Sam Emaminejad).
- NIH MIRA: R35GM125055 Statistical Models for Dissecting Human Population Admixture and its Role in Evolution and Disease. 2017–present (PI: Sankararaman)
- NIH K99/R00: 4R00GM111744 Statistical Methods to Infer Structure and Impact of Ancient Admixture, 2014–2018 (PI: Sankararaman).
- NSF: Scalable Machine Learning for Genome-wide Association Analyses, 2017–present (PI:Sankararaman)

TEACHING EXPERIENCE

At UCLA

- **Introduction to Machine Learning.** Winter 2017, 2019 – 2020, Fall 2017.
- **Machine Learning for Bioinformatics.** CM226. Fall 2016 – 2019.
- **Advanced Computational Genetics.** CM229. Spring 2017 – 2020.
- **Current topics in Bioinformatics: Machine Learning for Bioinformatics.** CM229. Spring 2016.
- **Advanced Human Genetics.** HG 236A. Fall 2019 (lectured for one week).

Prior to UCLA

- **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

- UCLA Computer Science Department Seminar, March 3, 2020.
- UCSD/Salk Center for Academic Research and Training in Anthropogeny, Symposium on Human Origins, February 21-22, 2020.
- Information Theory and Applications Workshop, February 7-10, 2020.
- Open Data Science West Conference, October 31, 2019.
- UCLA Bruin Family Weekend, October 25, 2019.
- UCLA Computational Medicine/AWS Symposium, February 1, 2019.
- UCLA Research Frontiers in Biomathematics, October 24, 2019.
- UCLA Health Data Day, May 9, 2019.
- Duke University Machine Learning/Algorithm Joint Seminar, December 12, 2018.

- Bertinoro Computational Biology, October 1–5, 2018.
- Society for Molecular Biology and Evolution, Yokohama, Japan, July 10, 2018.
- UCLA Statistics seminar, November 7, 2017.
- Simons Insitute, Berkeley. Data Privacy: Planning Workshop, May 24, 2017.
- Radcliffe Institute for Advanced Study, Advancing Genomic Biology Through Novel Method Development, June 05, 2017.
- CALTECH EE systems seminar, May 31, 2017.
- UCLA Electrical Engineering seminar, March 13, 2017
- UCLA Statistics seminar, January 31, 2017.
- UCSF Institute for Human Genetics seminar, January 05, 2017.
- UCLA Ecology and Evolutionary Biology seminar, October 12, 2016.
- World Congress on Probability and Statistics, Toronto, July 13, 2016.
- Bioinformatics Center, Copenhagen University, Copenhagen, Denmark, June 13 2016.
- Bioinformatics Seminar, Aarhus University, Aarhus, Denmark, June 10 2016.
- UCSD/Salk Center for Academic Research and Training in Anthropogeny, Symposium on Ancient DNA and Human Evolution, April 29-30, 2016.
- American Association of Anthropological Genetics (AAAG), Atlanta, April 2015.
- Stanford EVOLGENOME seminar, Stanford University, 4 Nov 2015.
- 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

ADVISING

Post-doctoral fellows

- Rob Brown
- Erin Molloy
- Richard Border (co-mentored with Prof. Noah Zaitlen)

Ph.D. students

- Christopher Robles, Genetics and Genomics
- Ariel (Yue) Wu, Computer Science (co-advised with Prof. Eleazar Eskin)
- Arun Durvasula, Genetics and Genomics (co-advised with Prof. Kirk Lohmueller)
- Ruth Johnson, Computer Science (co-advised with Prof. Bogdan Pasaniuc)
- Ali Pazokitoroudi, Computer Science
- Alec Chiu, Bioinformatics
- Ulzee An, Computer Science (co-advised with Prof. Eran Halperin)
- Boyang Fu, Computer Science

Visiting Ph.D. students

- Mukund Sudarshan, NYU

Ph.D. thesis committee

- Brandon Jew, Bioinformatics
- Tianyi Sun, Statistics
- Leah Briscoe, Bioinformatics
- Ha Vu, Bioinformatics

- Soo Bin Kwon, Bioinformatics
- Jennifer Zou, Computer Science
- Lisa Gai, Computer Science
- Brian Hill, Computer Science
- Sajad Darabi, Computer Science
- Elijah Rahmani, Computer Science
- Liat Shenav, Computer Science
- Dat Duong, Computer Science
- Peng Wei, Computer Science
- Sundara Rajan Srinivasavaradhan, Electrical Engineering
- Tevfik Dincer, Bioinformatics
- Kathryn Burch, Bioinformatics
- Tanya Phung, Bioinformatics
- Shan Sabri, Bioinformatics
- Artur Jaroszewicz, Bioinformatics
- Jazlyn Mooney, Genetics and Genomics
- Peng Wei, Computer Science
- Jiajin Li, Genetics and Genomics
- Tracey Chan, Bioinformatics
- Yidan Sun, Statistics
- Scott O'Donnell, Ecology and Evolutionary Biology

COMMITTEES

Organizer

- Co-organizer: RECOMB-Genetics Satellite Meeting 2020.
- Co-organizer: UCLA Computational Genomics Summer Institute 2019.
- Co-organizer: SoCal Machine Learning Symposium March 3, 2019.
- Co-organizer: IPAM workshop on Biomedical data privacy, Jan 10–12, 2018.
- Local co-organizer: Computational Genomics Winter Institute, UCLA, Feb 26–March 02, 2018.

Chair

- Area chair, ISMB 2018, 2019.
- Senior Program Committee Chair, IJCAI 2019, 2021
- Session chair, World Congress in Probability and Statistics, July 14, 2016.

Program Committee

- NeurIPS (2017, 2018, 2020)
- ICML (2017, 2018, 2019)
- ICLR (2018)
- AISTATS (2017, 2018)
- RECOMB (2016)
- RECOMB Satellite Meeting on Computational Methods in Genetics (2016, 2017)
- ISMB (2013, 2016)

Grant review

- Leakey Foundation (2019)
- NSF CISE (2017)

UCLA CS Department Committee

- Computer Science Department Faculty Hiring committee, 2017.
- Computer Science M.S. admission committee, 2017 – present.

- Chair, Publicity committee, 2017 – 2018.
- Member, Publicity committee, 2017 – present.
- Computer Science Ph.D. admission committee, 2015
- Adhoc committee for the merit increase of Dr. anonymous, 2016

UCLA Committee

- Co-director: UCLA Bioinformatics Minor, 2019–present.
- UCLA Bruins-In-Genomics (BIG) summer program steering committee, 2018–present.
- Director: UCLA Undergraduate Academy, 2018 – present.
- UCLA QCBio website committee, 2017.
- Chair, Bioinformatics Ph.D. admissions committee, 2017–present.
- Member, Bioinformatics Ph.D. admissions committee, 2016

REVIEWING ACTIVITIES

- 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, Science Advances, Cell.

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