# SRIRAM SANKARARAMAN

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## POSITIONS AND EMPLOYMENT

Professor *July 2023 – present*
Associate Professor *July 2021 – June 2023*
Assistant Professor *June 2018 – June 2021*
Department of Computer Science,
Department of Human Genetics,
Department of Computational Medicine,
University of California, Los Angeles

Assistant Professor *Nov 2015 – June 2018*
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

## 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

## 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

- Invited participant in the China-America Frontiers of Engineering Symposium, National Academy of Engineering, 2022.
- Invited participant in the Arab-American Frontiers of Science, Engineering, and Medicine symposium, U.S. National Academy of Sciences, 2021.
- NSF Career Award 2020
- Microsoft Investigator Fellowship 2019
- Northrop Grumman Excellence in Teaching Award 2019 (awarded annualy to one faculty across the UCLA School of Engineering)
- NIH Outstanding Investigator Award 2017
- 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 (highest PhD fellowship at UC Berkeley), 2004.
- Visvesvaraya medal for the Highest CGPA in the Graduating Class, IIT Madras, 2004.

## PUBLICATIONS

$^{\dagger}$, $^{*}$ denote equal contributions

### PREPRINTS

1. Angela Wei, *et al.*, The genetic underpinnings of variable penetrance and expressivity of pathogenic mutations in cardiometabolic traits, *medRxiv*, 2023.
2. Sajad Darabi, Shayan Fazeli, Ali Pazokitoroudi, **Sriram Sankararaman**, Majid Sarrafzadeh, Contrastive Mixup: Self- and Semi-Supervised learning for Tabular Domain, *arXiv*, 2021.
3. Robert Brown, **Sriram Sankararaman**, Bogdan Pasaniuc, Haplotype-based eQTL mapping finds evidence for complex gene regulatory regions poorly tagged by marginal SNPs, *bioRxiv*, 2018.

### JOURNAL PAPERS

1. Albert Xue, Jingyou Rao, Sriram Sankararaman$^{\dagger}$, Harold Pimentel$^{\dagger}$, dotears: Scalable, consistent DAG estimation using observational and interventional data, *iScience*, 2024.
2. Michal Sadowski, *et al.*, Characterizing the genetic architecture of drug response using gene-context interaction methods, *Cell Genomics*, 2024.
3. Varuni Sarwal$^{*}$, Seungmo Lee$^{*}$, *et al.*, VISTA: An integrated framework for structural variant discovery, *Briefings in Bioinformatics*, 2024.
4. Oren Avram$^{*}$, Berkin Durmus$^{*}$, *et al.*, Accurate prediction of disease-risk factors from volumetric medical scans by a deep vision model pre-trained with 2D scans, *Nature Biomedical Engineering*, (2024).
5. Ali Pazokitoroudi, *et al.*, A scalable and robust variance components method reveals insights into the architecture of gene-environment interactions underlying complex traits, *The American Journal of Human Genetics* (2024).
6. Boyang Fu$^{*}$, Prateek Anand$^{*}$, Aakarsh Anand$^{*}$, Joel Mefford, **Sriram Sankararaman**, A Scalable Adaptive Quadratic Kernel Method for Interpretable Epistasis Analysis in Complex Traits, *Genome Research*, (2024).

7. Moonseong Jeong, Ali Pazokitoroudi, Zhengtong Liu, **Sriram Sankararaman**, Scalable summary statistics-based heritability estimation method with individual genotype level accuracy, *Genome Research*, (2024).
8. Christophe Boetto, *et al.*, MANOCCA: A robust and computationally efficient test of covariance in high-dimension multivariate omics data, *Briefings in Bioinformatics*, (2024).
9. Brunilda Balliu, *et al.*, Personalized Mood Prediction from Patterns of Behavior Collected with Smartphones, *NPJ Digital Medicine*, (2024).
10. Ulzee An, Ali Pazokitoroudi, Marcus Alvarez, Lianyun Huang, Silviu Bacanu, Andrew J. Schork, Kenneth Kendler, Päivi Pajukanta, Jonathan Flint, Noah Zaitlen, Na Cai, Andy Dahl, **Sriram Sankararaman**, Deep Learning-based Phenotype Imputation on Population-scale Biobank Data Increases Genetic Discoveries, *Nature Genetics*, (2023).
11. Andrew Dahl, Michael Thompson, Ulzee An, Morten Krebs, Vivek Appadurai, Richard Border, Silviu-Alin Bacanu, Thomas Werge, Jonathan Flint, Andrew J. Schork, **Sriram Sankararaman**, Kenneth Kendler, Na Cai, Phenotype integration improves power and preserves specificity in biobank-based genetic studies of Major Depressive Disorder, *Nature Genetics*, (2023).
12. Boyang Fu, Ali Pazokitoroudi, Mukund Sudarshan, Lakshminarayanan Subramanian, **Sriram Sankararaman**, Fast Kernel-based Association Testing of non-linear genetic effects for Biobank-scale data, *Nature Communications*, (2023).
13. Nathan LaPierre*, Boyang Fu*, Steven Turnbull, Eleazar Eskin, **Sriram Sankararaman**, Leveraging family data to design Mendelian Randomization that is provably robust to population stratification, *Genome Research* (2023).
14. Xinzhu Wei*, Christopher Robles*, Ali Pazokitoroudi, Andrea Ganna, Alexander Gusev, Arun Durvasula, Steven Gazal, Po-Ru Loh, David Reich, **Sriram Sankararaman**, The lingering effects of Neanderthal introgression on human complex traits, *eLife* (2023).
15. Kangcheng Hou *et al.*, Causal effects on complex traits are similar across segments of different continental ancestries within admixed individuals, *Nature Genetics* (2023).
16. Xinjun Zhang, Bernard Kim, Armaan Singh, **Sriram Sankararaman**, Arun Durvasula, Kirk Lohmueller, MaLAdapt reveals novel targets of adaptive introgression from Neanderthals and Denisovans in worldwide human populations, *Molecular Biology and Evolution* (2023).
17. Richard Border, *et al.*, Cross-trait assortative mating is widespread and inflates genetic correlation estimates, *Science* (2022).
18. Haisong Lin, *et al.*, Autonomous wearable sweat rate monitoring based on digitized microbubble detection, *Lab on a Chip* (2022).
19. Oren Avram, *et al.*, Detecting risk factors for age-related macular degeneration from limited volumetric optical coherence tomography data by transfer learning and vision transformers, *ML4H* (2022).
20. Jeffrey Chiang *et al.*, Automated Identification of Incomplete and Complete Retinal Epithelial Pigment and Outer Retinal Atrophy Using Machine Learning, *Ophthalmology Retina* (2022).
21. Ruth Johnson *et al.*, Leveraging genomic diversity for discovery in an EHR-linked biobank: the UCLA ATLAS Community Health Initiative, *Genome Medicine* (2022).
22. Ulzee An*, Liat Shenav*, Christine Olson, Elaine Hsiao, Eran Halperin†, **Sriram Sankararaman†**, STENSL: microbial Source Tracking with ENvironment SeLection, *mSystems* (2022).
23. Jennifer Zou, Jinjing Zhou, Sarah Faller, Robert Brown, **Sriram Sankararaman**, Eleazar Eskin, Accurate modeling of replication rates in genome-wide association studies by accounting for Winner's Curse and study-specific heterogeneity, *G3: Genes, Genomes, and Genetics* (2022).
24. Hillary Coller, *et al.*, Bruins-in-Genomics: Evaluation of the Impact of a UCLA Undergraduate Summer Program in Computational Biology on Participating Students, *PLoS One*, 2022.
25. Mike Thompson*, Brian Hill*, *et al.*, Methylation risk scores are associated with a collection of phenotypes within electronic health record systems, *Nature Genomic Medicine*, 2022.
26. Alec Chiu, Erin Molloy, Zilong Tan, Ameet Talwalkar, **Sriram Sankararaman**, Inferring population structure in biobank-scale genomic data, *The American Journal of Human Genetics* (2022).
27. Carlos Cinelli, Nathan LaPierre, Brian Hill, **Sriram Sankararaman**, Eleazar Eskin, Robust Mendelian randomization in the presence of residual population stratification, batch effects and horizontal pleiotropy, *Nature Communications* (2022).
28. Leah Briscoe, Brunilda Balliu, **Sriram Sankararaman**, Eran Halperin†, Nandita Garud†, Correcting for Background Noise Improves Phenotype Prediction from Human Gut Microbiome Data, *PLoS Computational Biology*, 2022.
29. Yi Ding*, Kangcheng Hou*, Kathryn Burch, Sandra Lapinska, **Sriram Sankararaman**, Bogdan Pasaniuc, Large uncertainty in individual PRS estimation impacts PRS-based risk stratification, *Nature Genetics* (2021).

30. Yue Wu, Kathryn Burch, Andrea Ganna, Päivi Pajukanta, Bogdan Pasaniuc, **Sriram Sankararaman**, Fast estimation of genetic correlation for Biobank-scale data, *The American Journal of Human Genetics* (2021).
31. Evelyn Jagoda, James Xue, Steven Reilly, Michael Dannemann, Fernando Racimo, Emilia Huerta-Sanchez, **Sriram Sankararaman**, Janet Kelso, Luca Pagani, Pardis Sabeti, Terence D. Capellini, Detection of Neanderthal Adaptively Introgressed Genetic Variants that Modulate Reporter Gene Expression in Human Immune Cells, *Molecular Biology and Evolution* (2021).
32. Ruth Johnson, Kathryn Burch, Kangcheng Hou, Mario Paciuc, Bogdan Pasaniuc$^\dagger$, **Sriram Sankararaman**$^\dagger$, Estimation of regional polygenicity from GWAS provides insights into the genetic architecture of complex traits, *PLoS Computational Biology* (2021).
33. Anthony Findley *et al.*, Functional dynamic genetic effects on gene regulation are specific to particular cell types and environmental conditions, *eLife* (2021).
34. Erin Molloy, Arun Durvasula, **Sriram Sankararaman**, Advancing admixture graph estimation via maximum likelihood network orientation, *Bioinformatics (Special Issue for ISMB)* (2021).
35. Ali Pazokitoroudi, Alec Chiu, Kathryn Burch, Bogdan Pasaniuc, **Sriram Sankararaman**, Quantifying the contribution of dominance effects to complex trait variation in biobank-scale data, *The American Journal of Human Genetics* (2021).
36. Arunabha Majumdar, Kathryn Burch, **Sriram Sankararaman**, Bogdan Pasaniuc, James Gauderman, John Witte, A two-step approach to testing overall effect of gene-environment interaction for multiple phenotypes, *Bioinformatics* (2021).
37. Nadav Rakocz$^*$, Jeffrey Chiang$^*$, Muneeswar Nittala, Giulia Corradetti, Liran Tiosanoc, Swetha Velaga, Michael Thompson, Brian Hill, **Sriram Sankararaman**, Jonathan Haines, Margaret Pericak-Vance, Dwight Stambolian, Srinivas Sadda, Eran Halperin, Automated identification of clinical biomarkers from sparsely annotated 3-dimensional medical imaging, *NPJ Digital Medicine* (2021).
38. Ali Pazokitoroudi, Yue Wu, Kathryn Burch, Kangcheng Hou, Aaron Zhou, Bogdan Pasaniuc, **Sriram Sankararaman**, Efficient variance components analysis across millions of genomes, *Nature Communications* (2020).
39. Yue Wu, Eleazar Eskin$^\dagger$, **Sriram Sankararaman**$^\dagger$, A unifying framework for imputing summary statistics in Genome-wide Association Studies, *Journal of Computational Biology* (2020).
40. Aman Agrawal$^*$, Alec M. Chiu$^*$, Minh Le, Eran Halperin, **Sriram Sankararaman**. Scalable probabilistic PCA for large-scale genetic variation data. *PLoS Genetics* (2020).
41. Arun Durvasula, **Sriram Sankararaman**, Recovering signals of ghost archaic introgression in African populations, *Science Advances* (2020).
42. Brian Hill$^*$, Robert Brown$^*$, Eilon Gabel, Christine Lee, Maxime Cannesson, Loes Olde Loohuis, Ruth Johnson, Brandon Jew, Uri Maoz, Aman Mahajan, **Sriram Sankararaman**$^\dagger$, Ira Hofer$^\dagger$, Eran Halperin$^\dagger$, Preoperative predictions of in-hospital mortality using electronic medical record data, *British Journal of Anaesthesia* (2019).
43. Kangcheng Hou$^*$, Kathryn Burch$^*$, Arunabha Majumdar, Huwenbo Shi, Nicholas Mancuso, Yue Wu, **Sriram Sankararaman**, Bogdan Pasaniuc, Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture, *Nature Genetics* (2019).
44. Elior Rahmani, Regev Schweiger, Brooke Rhead, Lindsey A. Criswell, Lisa F. Barcellos, Eleazar Eskin, Saharon Rosset, **Sriram Sankararaman**, Eran Halperin , Cell-type-specific resolution epigenetics without the need for cell sorting or single-cell biology, *Nature Communications* (2019).
45. Arun Durvasula, **Sriram Sankararaman**, A statistical model for reference-free inference of archaic local ancestry, *PLoS Genetics* (2019).
46. 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).
47. Yue Wu, **Sriram Sankararaman**, A scalable estimator of SNP heritability for Biobank-scale data, *Bioinformatics (Special Issue for ISMB)* (2018).
48. Ruth Johnson, Huwenbo Shi, Bogdan Pasaniuc$^\dagger$, **Sriram Sankararaman**$^\dagger$, A unifying framework for joint trait analysis under a non-infinitesimal model, *Bioinformatics (Special Issue for ISMB)* (2018).
49. 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).
50. Farhad Hormozdiari *et al.*, Widespread Allelic Heterogeneity in Complex Traits, *American Journal of Human Genetics* (2017).
51. Bernard Jegou *et al.*, Meiotic genes are enriched in genes of reduced archaic ancestry, *Molecular Biology and Evolution* (2017).

52. Hormozdiari *et al.*, Colocalization of GWAS and eQTL Signals Detects Target Genes, *American Journal of Human Genetics* (2016).
53. Swapan Mallick *et al.*, The Simons Genome Diversity Project: 300 genomes from 142 diverse populations, *Nature* (2016).
54. 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).
55. **Sriram Sankararaman**, Swapan Mallick, *et al.*, The landscape of Denisovan admixture in South Asians and Oceanians, *Current Biology* (2016).
56. Mark Lipson, Po-Ru Loh, **Sriram Sankararaman**, *et al.*, Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes, *PLoS Genetics* (2015).
57. Pier Francesco Palamara, *et al.*, Leveraging distant relatedness to quantify human mutation and gene conversion rates, *American Journal of Human Genetics* (2015).
58. James Zou, Danny Park, Esteban Burchard, Dara Torgerson, Maria Pino-Yanes, Yun Song, **Sriram Sankararaman**$^\dagger$, Eran Halperin$^\dagger$, Noah Zaitlen$^\dagger$, A genetic and socio-economic study of mate choice in Latinos reveals novel assortment patterns, *Proceedings of the National Academy of Sciences* (2015).
59. James Zou, Eran Halperin, Esteban Burchard, **Sriram Sankararaman**, Inferring parental genomic ancestries using pooled semi-Markov processes, *Bioinformatics (Special Issue for ISMB)* (2015).
60. Noah Zaitlen, Bogdan Pasaniuc, **Sriram Sankararaman**, Gaurav Bhatia, Jianqi Zhang, *et al.*, Leveraging population admixture to characterize the heritability of complex traits, *Nature Genetics* (2014).
61. **Sriram Sankararaman**, Swapan Mallick, Michael Dannemann, *et al.*, The landscape of Neandertal ancestry in present-day humans, *Nature* (2014).
62. Kay Prüfer, Fernando Racimo, Nick Patterson, Flora Jay, **Sriram Sankararaman**, *et al.*, The complete genome sequence of a Neanderthal from the Altai Mountains, *Nature* (2014).
63. SIGMA Type 2 Diabetes Consortium, Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico, *Nature* (2014).
64. Gaurav Bhatia$^*$, Nick Patterson$^*$, **Sriram Sankararaman**, Alkes L. Price, Estimating and interpreting $F_{ST}$: The impact of rare variants, *Genome Research* (2013).
65. 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).
66. **Sriram Sankararaman**, Nick Patterson, Heng Li, *et al.*, The date of interbreeding between Neandertals and modern humans, *PLoS Genetics* (2012).
67. 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 Gonzàlez Burchard, Eran Halperin, Fast and accurate inference of local ancestry in Latino populations, *Bioinformatics* (2012).
68. 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* (2012).
69. Alexandre Bouchard-Côté, **Sriram Sankararaman**, Michael I. Jordan, Phylogenetic Inference using Sequential Monte Carlo, *Systematic Biology* (2012).
70. **Sriram Sankararaman**, Fei Sha, Michael I. Jordan, Kimmen Sjölander, Active Site Prediction using Evolutionary and Structural Information, *Bioinformatics* (2010).
71. 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* (2010).
72. **Sriram Sankararaman**$^*$, Guillaume Obozinski$^*$, Michael I. Jordan, Eran Halperin, Genomic Privacy and Limits of Individual Detection in a Pool, *Nature Genetics* (2009).
73. Bogdan Pasaniuc$^*$, **Sriram Sankaraman**$^*$, Gad Kimmel, Eran Halperin, Locus-specific Ancestry Inference in Closely-related populations, *Bioinformatics (Special Issue for ISMB)* (2009).
74. Ron Alterovitz, Aaron Arvey, **Sriram Sankararaman**, *et al.*, ResBoost: characterizing and predicting catalytic residues in enzymes, *BMC Bioinformatics* (2009).
75. **Sriram Sankararaman**, Bryan Kolaczkowski, Kimmen Sjölander, INTREPID: a web server for prediction of functionally important residues by evolutionary analysis, *Nucleic Acids Research* (2009).
76. **Sriram Sankararaman**$^*$, Gad Kimmel$^*$, Eran Halperin, Michael I. Jordan, On the inference of ancestries in admixed populations, *Genome Research* (2008).

77. **Sriram Sankararaman**, Srinath Sridhar, Gad Kimmel, Eran Halperin, Estimating local ancestry in admixed populations, *American Journal of Human Genetics* (2008).
78. **Sriram Sankararaman**, Kimmen Sjölander, INTREPID–INformation-theoretic TREe traversal for Protein functional site IDentification. *Bioinformatics* (2008).
79. 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* (2008).
80. **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).
81. **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* (2006).
82. Sougata Mukherjea, L. Venkata Subramaniam, Gaurav Chanda, **Sriram Sankararaman**, Ravi Kothari, Vishal Batra, Deo Bhardwaj, Biplav Srivastava, Enhancing a biomedical information extraction system with dictionary mining and context disambiguation. *IBM Journal of Research and Development* (2004).

## PEER-REVIEWED CONFERENCE PAPERS

83. Aditya Gorla, **Sriram Sankararaman**, Esteban Burchard, Jonathan Flint, Noah Zaitlen and Elior Rahmani, Phenotypic subtyping via contrastive learning, *RECOMB* (2023).
84. Meihua Dang, Anji Liu, Xinzhu Wei, **Sriram Sankararaman**†, Guy Van den Broeck†, Tractable and expressive generative models of genetic variation data, *RECOMB* (2022).
85. Brandon Jew*, Jiajin Li*, **Sriram Sankararaman**, Jae Hoon Sul, An efficient linear mixed model framework for meta-analytic association studies across multiple contexts, *Workshop on Algorithms in Bioinformatics (WABI)* (2021).
86. Amnon Catav, Boyang Fu, Jason Ernst, **Sriram Sankararaman**, Ran Gilad-Bachrach, Marginal Contribution Feature Importance – an Axiomatic Approach for The Natural Case, *ICML* (2021).
87. Ali Pazokitoroudi, Andrew Dahl, Noah Zaitlen, Saharon Rosset, and **Sriram Sankararaman**, Biobank-scale estimation of the proportion of trait variance explained by gene-environment interactions, *RECOMB* (2021).
88. Mukund Sudarshan, Aahlad Manas Puli, Lakshmi Subramanian, **Sriram Sankararaman**, and Rajesh Ranganath, CONTRA: Contrarian statistics for controlled variable selection, The 24th International Conference on Artificial Intelligence and Statistics (*AISTATS*) (2021).
89. Gregory Plumb, Jonathan Terhorst, **Sriram Sankararaman**, and Ameet Talwalkar, Explaining Groups of Points in Low-Dimensional Representations, *ICML* (2020).
90. 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).
91. **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*) (2005).
92. **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* (2004).
93. **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) (2004).

## INVITED PAPERS

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

## PEER-REVIEWED WORKSHOP PAPERS

95. Ulzee An, Simon Lee, Moonseong Jeong, Aditya Gorla, Jeff Chiang, **Sriram Sankararaman**, DK-BEHRT: Teaching Language Models International Classification of Disease (ICD) Codes using Known Disease Descriptions, AAAI 2025 Workshop on AI for Medicine and Healthcare (2025).
96. Nadav Rakocz, Boyang Fu, Eran Halperin†, **Sriram Sankararaman**†, A Statistical Model for Quantifying the Needed Duration of Social Distancing for the COVID-19 Pandemic, *KDD 2020 - AI For COVID-19* (2020).

## REVIEWS

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

## INVITED REVIEWS

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

## PEER-REVIEWED CONFERENCE PAPERS THAT ALSO APPEARED AS A JOURNAL PUBLICATION

1. Boyang Fu*, Prateek Anand*, Aakarsh Anand*, Joel Mefford, **Sriram Sankararaman**, A Scalable Adaptive Quadratic Kernel Method for Interpretable Epistasis Analysis in Complex Traits, *RECOMB*, (2024).
2. Moonseong Jeong, Ali Pazokitoroudi, Zhengtong Liu, **Sriram Sankararaman**, Scalable summary statistics-based heritability estimation method with individual genotype level accuracy, *RECOMB*, (2024).
3. Ulzee An, Na Cai, Andy Dahl, **Sriram Sankararaman**, AutoComplete: Deep Learning-based Phenotype Imputation for Large-scale Biomedical Data, *RECOMB* (2022).
4. Nathan LaPierre*, Boyang Fu*, Steven Turnbull, Eleazar Eskin, **Sriram Sankararaman**, Leveraging family data to design Mendelian Randomization that is provably robust to population stratification, *RECOMB* (2023).
5. Erin K. Molloy, Arun Durvasula, **Sriram Sankararaman**, Advancing admixture graph estimation via maximum likelihood network orientation, 29th *Conference on Intelligent Systems for Molecular Biology (ISMB)* (2021).
6. Ruth Johnson, Kathryn Burch, Kangcheng Hou, Mario Paciuc, Bogdan Pasaniuc, **Sriram Sankararaman**, A scalable method for estimating for regional polygenicity for complex traits, 24th *Annual International Conference on Research in Computational Molecular Biology (RECOMB)* (2020).
7. Yue Wu, Anna Yaschenko, Mohammadreza Hazy Heydary, **Sriram Sankararaman**, Fast estimation of genetic correlation for Biobank-scale data, 23rd *Annual International Conference on Research in Computational Molecular Biology (RECOMB)* (2019).
8. Ali Pazokitoroudi, Yue Wu, Kathryn 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)* (2019).
9. 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).
10. Yue Wu, **Sriram Sankararaman**, A scalable estimator of SNP heritability for Biobank-scale data, 26th *Conference on Intelligent Systems for Molecular Biology (ISMB)* (2018).
11. 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).
12. Elior 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).
13. 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).
14. Bogdan Pasaniuc*, **Sriram Sankaraman***, Gad Kimmel, Eran Halperin, Locus-specific Ancestry Inference in Closely-related populations, 17th *Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)* (2009).
15. **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

16. **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

17. 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

**Active**

1. NIH MIRA: Expressive and scalable statistical models for genomic and biomedical data, 2024–present (PI).
2. NIH R01: Multimodal Omics Approach to Identify Health to Cardiometabolic Disease Transitions, 2023 – 2027 (Co-I).
3. NIH R01: Improving the Interpretability of Genetic Studies of Major Depressive Disorder To Identify Risk Genes, 2022 – 2027 (Co-I).
4. NIH R01: Epigenetic Mechanisms Linking Psychosocial Stress with Coronary Heart Disease, 2022–2026 (subaward PI) ($197,128/$197,128).
5. NIH R01: Leveraging Functional Data to Predict Disease Risk in Multi-Ethnic Populations, 2021–2025 (Co-I) ($100,008/$152,308).
6. NIH U01: PRS Center for Admixed Populations and Health Equity (CAPE), 2021–2025 (Co-I) ($65,405/$4,149,193).
7. NIH R01: Combining Voice and Genetic Information to Detect Heterogeneity in Major Depressive Disorder, 2020 – 2025 (Co-I).
8. NSF Medium: Causal Inference in Biobanks: Leveraging Genetics to Infer Causal Relationships using Electronic Health Records, 2021–2025 (Co-PI) ($63,405/$839,735).
9. NIH R21: An Autonomous, Non-invasive, and Bioanalytics-enabled Wearable Platform for Precision Nutrition and Personalized Medicine, 2021–2025 (Co-PI) ($22,400/$303,234).
10. NSF EAGER: Understanding the Genomes and Strain Mutations of SARS-CoV-2 and other viruses using Comparative and Population Genetic Approaches, 2021–2023 (Co-PI), ($87,748/$216,758).
11. NSF Career Award, 2020 – 2025, ($473,142/$473,142).
12. NSF Medium: A Non-invasive and Wearable Molecular Diagnostic Platform for Remote and Passive Monitoring of Patients at Risk for Sepsis, 2017 – 2024 (Co-PI), ($54,322/$666,828).

**Completed**

13. UCLA-Amazon Science Hub for Humanity and AI, 2022–2023 (PI) ($53,000/$84,000).
14. NIH MIRA: Statistical Models for Dissecting Human Population Admixture and its Role in Evolution and Disease. 2017–2024 (PI), ($1,028,948/$1,028,948).
15. NSF Medium: Scalable Machine Learning for Genome-wide Association Analyses, 2017–2022 (PI), ($699,676/$699,676).
16. UCLA Broad Stem Cell Research Center COVID-19 Research Award, 2020 (Co-PI), ($15,525/$60,065).
17. UCLA-AWS Medically relevant Machine Learning 2019 (AWS credits).
18. 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, 2019–2020 (Co-PI), ($250,000/$250,000).
19. UCLA DGSOM Seed Grant: Machine Learning Models for the Prediction of Adverse Outcomes after Surgery using EMR and Genetic Data, 2018–2019 (Co-PI), ($250,000/$250,000).
20. NIH K99/R00: Statistical Methods to Infer Structure and Impact of Ancient Admixture, 2014–2018 (PI) ($508,659/$508,659).

# TEACHING EXPERIENCE

**At UCLA**

1. **Introduction to Machine Learning**. Winter 2017, 2019 – present, Fall 2017.
2. **Machine Learning Applications in Genetics**. CM124/224. Fall 2023.
3. **Machine Learning for Bioinformatics**. CM226. Fall 2016 – 2022.
4. **Advanced Computational Genetics**. CM229. Spring 2017 – present.
5. **Current topics in Bioinformatics: Machine Learning for Bioinformatics**. CM229. Spring 2016.
6. **Advanced Human Genetics**. HG 236A. Fall 2019 – present (lectured for one week).

**Prior to UCLA**

7. **Introduction to Protein Informatics**. Guest lecturer, UC Berkeley, Spring 2014.
8. **Practical Machine Learning**. Guest lecturer, UC Berkeley, Fall 2009.
9. **Computer Science self-paced**. Graduate Student Instructor, UC Berkeley, Fall 2009.
10. **Bayesian Inference and Modeling**. Graduate Student Instructor, UC Berkeley, Spring 2009.
11. **Practical Machine Learning**. Guest lecturer, UC Berkeley, Spring 2008.
12. **Genomics and Computational Biology**. Guest lecturer, UC Berkeley, Fall 2007.
13. **Introduction to Protein Informatics**. Guest lecturer, UC Berkeley, Fall 2007.
14. **Introduction to Protein Informatics**. Graduate Student Instructor, UC Berkeley, Fall 2006.

# TALKS

## INVITED TALKS

1. Gordon Research Conference on Quantitative Genetics and Genomics, Discussion Leader, 2025
2. AI Fairness in Genomics Panel, Biomedical AI symposium, UCLA, 2024
3. The Foundation des Treilles, 2024
4. UCLA Pediatrics Research Program, UCLA, 2024
5. MIT Bioinformatics Seminar, 2024
6. UCLA Computational Genomics Summer Institute, 2024
7. BIRS Workshop on Biobanks, Banff, Canada, 2024
8. SIAM Conference on Applied Linear Algebra, 2024
9. UC Riverside Department of Statistics Colloqium, 2024
10. USC Department of Quantitative and Computational Biology, 2024
11. Lange Symposium, 2024
12. Cedars-Sinai Computational Biomedicine, 2023
13. Yale Bioanthropology Colloqium, 2023
14. Weill Cornell Medicine Englander Institute for Precision Medicine Seminar Series, 2023
15. Princeton University Computer Science Colloqium, 2023
16. Joint Statistical Meetings (JSM), Invited Speaker, 2023
17. WNAR/IMS Invited Speaker, 2023
18. UCLA Computational Genomics Summer Institute, 2023
19. Columbia University Irving Institute for Cancer Dynamics Special Seminar, 2023.
20. Columbia University Department of Systems Biology Distinguished Speaker Series, 2023.
21. Cornell University Department of Computational Biology seminar, 2023
22. UCLA Brain, Evolution, and Culture seminar, 2023
23. NIH Bridge2AI Guest Lecturer, 2023
24. UCLA/Optum Labs AI in Healthcare Hub 2022
25. UCLA Computational Genomics Summer Institute, 2022
26. BIRS Workshop on Deep Learning in Genomics, Kelowna, Canada, 2022
27. Admixture: Inference and Evolutionary Consequences, Paris, 2022
28. **Plenary talk**: Information Theory and Applications Workshop, 2022
29. Caltech-UCLA NIH T32 mini-symposium, 2022
30. Google Genomics, 2022
31. Amazon Science Day, UCLA, 2021
32. Overseas Cloud Lecture Series, Zhejiang University, 2021
33. The Rockefeller University, 2021
34. RECOMB Computational Genomics Summer Institute, 2021
35. Institute for Mathematics and Statistics, University of Chicago, 2021
36. AI Robotics Ethics Society (AIRES) Conference, 2021
37. $20^{th}$ IEEE International Workshop on High Performance Computational Biology, 2021
38. McGill University Department of Human Genetics and McGill Genome Center Seminar, 2021
39. UCLA ACM AI in Medicine event, 2021
40. NHGRI Machine Learning in Genomics Workshop, 2021
41. UCSD Systems Biology and Genetics, 2021
42. Brown University, 2020
43. Open Data Science West Conference, 2020
44. UCLA Computer Science Department Seminar,2020

45. UCSD/Salk Center for Academic Research and Training in Anthropogeny, Symposium on Human Origins, 2020
46. Information Theory and Applications Workshop, 2020
47. Open Data Science West Conference, 2019
48. UCLA Bruin Family Weekend, 2019
49. UCLA Computational Medicine/AWS Symposium, 2019
50. UCLA Computational Genomics Summer Institute, 2019
51. UCLA Research Frontiers in Biomathematics, 2019
52. UCLA Health Data Day, 2019
53. Duke University Machine Learning/Algorithm Joint Seminar, 2018
54. Radcliffe Institute "Next in Evolution", 2018
55. Bertinoro Computational Biology, 2018
56. UCLA Computational Genomics Summer Institute, 2018
57. Society for Molecular Biology and Evolution, Yokohama, Japan, 2018
58. UCLA Statistics seminar, 2017
59. Simons Insitute, Berkeley. Data Privacy: Planning Workshop, 2017
60. Radcliffe Institute for Advanced Study, Advancing Genomic Biology Through Novel Method Development, 2017
61. CALTECH EE systems seminar, 2017
62. UCLA Computational Genomics Summer Institute, 2017
63. UCLA Electrical Engineering seminar, 2017
64. UCLA Statistics seminar, 2017
65. UCSF Institute for Human Genetics seminar, 2017
66. UCLA Ecology and Evolutionary Biology seminar, 2016
67. World Congress on Probability and Statistics, Toronto, 2016
68. UCLA Computational Genomics Summer Institute, 2016
69. Bioinformatics Center, Copenhagen University, Copenhagen, Denmark, 2016
70. Bioinformatics Seminar, Aarhus University, Aarhus, Denmark, 2016
71. UCSD/Salk Center for Academic Research and Training in Anthropogeny, Symposium on Ancient DNA and Human Evolution, 2016
72. American Association of Anthropological Genetics (AAAG), Atlanta, 2015
73. Stanford EVOLGENOME seminar, Stanford University, 2015
74. Sci Foo camp 2014 invitee, Google (declined due to scheduling)
75. Bioinformatics Seminar, UCLA, Los Angeles, CA, 2014
76. 23andme.com, Mountain View, CA, 2014
77. Evolutionary Biology Seminar, Simons Institute, Berkeley, 2014
78. Institute for Mathematics and its Applications workshop on "Group Testing Designs, Algorithms, and Applications to Biology", Minneapolis, 2012
79. WILLOW (Computer vision and Machine Learning Research Laboratory) at INRIA, Paris, France, 2011
80. Stanford Genome Technology Club seminar, Stanford University, CA, USA, 2009

## MENTORING

**Past trainees**

1. Nadav Rakocz (Ph.D. student graduated 2023; startup)
2. Ali Pazokitoroudi (Ph.D. student graduated 2023; postdoc at Harvard)
3. Ruth Johnson (Ph.D student graduated 2023; postdoc at Harvard)
4. Xinjun Zhang (postdoc ending 2023; Assistant Professor at Univeristy of Michigan)
5. April Wei (postdoc ending 2022; Assistant Professor at Cornell University)
6. Christopher Robles (Ph.D student graduated 2022; Research Scientist at Merck)

7. Alec Chiu (Ph.D student graduated 2022; Goldman Sachs)
8. Ariel (Yue) Wu (Ph.D student graduated 2022; postdoc at Astra Zeneca)
9. Shaan Mathur (Masters student graduated 2021; Google)
10. Rob Brown (postdoc ending 2021; Scientist at BioFire Diagnostics)
11. Arun Durvasula (Ph.D student graduated 2021; Assistant Professor at University of Southern California)
12. Erin Molloy (postdoc ending 2021; Assistant Professor at University of Maryland, College Park)
13. Misagh Kordi (postdoc ending 2020; Project Scientist at Natera)

**Post-doctoral fellows**

14. Prerit Terway
15. Richard Border

**Ph.D. students**

16. Berkin Durmus
17. Zeyuan (Johnson) Chen
18. Ulzee An
19. Boyang Fu
20. Albert Xue
21. Harold Wang
22. Aditya Gorla
23. Moon-Seong Jeong
24. Zhengtong Liu

**Ph.D. thesis committee**

25. Jingyou Rao, Computer Science
26. Chloe Hanson, Genetics and Genomics
27. Helena Winata, Bioinformatics
28. Chris Dong, Statistics
29. Alexander Pelletier, Computer Science
30. Jingyuan Fu, Computer Science
31. Rosemary He, Computer Science
32. Ella Petter, Computer Science
33. Jamie Matthews, Bioinformatics
34. Mariana Harris Heredia, Biomathematics
35. Kodi Taraska, Computer Science
36. Michal Sadowski, Bioinformatics
37. Kangcheng Hou, Bioinformatics
38. Patrick Chen, Computer Science
39. Jesse Garcia, Bioinformatics
40. Paheli Desai-Chowdhry, Biomathematics
41. Trent Kyono, Computer Science
42. Yi Ding, Bioinformatics
43. Dhaivat Joshi, Electrical Engineering
44. Brandon Jew, Bioinformatics
45. Tianyi Sun, Statistics
46. Leah Briscoe, Bioinformatics
47. Ha Vu, Bioinformatics
48. Soo Bin Kwon, Bioinformatics
49. Jennifer Zou, Computer Science
50. Lisa Gai, Computer Science

51. Brian Hill, Computer Science
52. Sajad Darabi, Computer Science
53. Elior Rahmani, Computer Science
54. Liat Shenhav, Computer Science
55. Dat Duong, Computer Science
56. Peng Wei, Computer Science
57. Sundara Rajan Srinivasavaradhan, Electrical Engineering
58. Tevfik Dincer, Bioinformatics
59. Kathryn Burch, Bioinformatics
60. Tanya Phung, Bioinformatics
61. Shan Sabri, Bioinformatics
62. Artur Jaroszewicz, Bioinformatics
63. Jazlyn Mooney, Genetics and Genomics
64. Peng Wei, Computer Science
65. Jiajin Li, Genetics and Genomics
66. Tracey Chan, Bioinformatics
67. Yidan Sun, Statistics
68. Scott O'Donnell, Ecology and Evolutionary Biology

**Master's thesis committee**

69. Amina Lazrak, Computer Science
70. Nicholas Darci-Maher, Bioinformatics

**Other**

71. Breanna Sparta, Post-doctoral Fellow, UCLA (consultant on F32 proposal)

## JOURNAL EDITORIAL SERVICE

1. Associate Editor, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2024 – present.
2. RECOMB-Genetics 2023 special issue of iScience. Editors: Sriram Sankararaman, Emilia Huerta-Sanchez, Nicholas Mancuso.
3. RECOMB-Genetics 2022 special issue of iScience. Editors: Sriram Sankararaman, Gillian Belbin.
4. *Journal of Computational Biology*, Editor, 2021 – present.
5. Guest editor, *PLoS Computational Biology*.

## COMMITTEES

Organizer

1. Co-organizer: RECOMB-Genetics Satellite Meeting 2020 – 2024.
2. Co-organizer: UCLA Computational Genomics Summer Institute 2019, 2022 – present.
3. Co-organizer: SoCal Machine Learning Symposium March 3, 2019.
4. Co-organizer: IPAM workshop on Biomedical data privacy, Jan 10–12, 2018.
5. Local co-organizer: Computational Genomics Winter Institute, UCLA, Feb 26–March 02, 2018.

Chair

6. Program Chair, RECOMB (2025).
7. All Satellite Chair, RECOMB (2022).
8. Chair, RECOMB-Genetics (2022–2023).
9. Session chair, RECOMB, 2021.
10. Area chair, Machine Learning in Computational Biology 2020.
11. Area chair, ISMB 2018, 2019.
12. Session chair Probabilistic Modeling in Genomics, Cold Spring Harbor, Nov 4–7, 2018.
13. Senior Program Committee Chair, IJCAI 2019, 2021
14. Session chair, World Congress in Probability and Statistics, July 14, 2016.

Program Committees

15. RECOMB highlights track 2022.
16. Steering committee, RECOMB-Genetics (2019 – 2021).
17. NeurIPS (2017, 2018, 2020)
18. ICML (2017, 2018, 2019)
19. ICLR (2018)
20. AISTATS (2017, 2018)
21. RECOMB (2016, 2021 – 2022)
22. RECOMB Satellite Meeting on Computational Methods in Genetics (2016, 2017)
23. ISMB (2013, 2016)

Grant review

24. NIH GVE study section (2024)
25. NHGRI R01 review panel (2024)
26. Leakey Foundation (2019)
27. NSF CISE (2017)
28. NSF BIO (2020, 2022)
29. Center for AI and data science, Tel Aviv University (2022)

UCLA CS Department Committees

30. Chair: Adhoc committee 2021, 2023.
31. Field Chair for Computational Systems Biology, 2022 – present.
32. Member: Computer Science Department Faculty Hiring committee, 2017, 2022.
33. Computer Science M.S. admission committee, 2017 – present.

34. Chair: Publicity committee, 2017 – 2018.
35. Member: Publicity committee, 2017 – present.
36. Computer Science Ph.D. admission committee, 2015
37. Member: Adhoc committee 2016, 2021

UCLA Committees

38. Director: Data Science in Biomedicine MS Program, 2023.
39. Member: Selection committee for the UCLA Society of Hellman Fellows Program, 2023 – 2024.
40. Member: UCLA/Optum Labs Steering Committee, 2022.
41. Chair, Computational Medicine Faculty Search Committee, 2021 – 2022.
42. Director: UCLA Bioinformatics Minor, 2021–present.
43. Co-director: UCLA Bioinformatics Minor, 2019–2021.
44. Co-chair: UCLA/AWS Medically relevant Machine Learning, 2019.
45. UCLA Bruins-In-Genomics (BIG) summer program steering committee, 2018 – 2022.
46. Director: UCLA Undergraduate Academy, 2018 – present.
47. UCLA QCBio website committee, 2017.
48. Chair: Bioinformatics Ph.D. admissions committee, 2017 – 2023.
49. Member: Bioinformatics Ph.D. admissions committee, 2016.

## REVIEWING ACTIVITIES

1. 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, Genome Biology, Nature Reviews Genetics, NPJ Genomic Medicine, Journal of Computational Biology.

## PROFESSIONAL ASSOCIATIONS

1. American Society for Human Genetics
2. International Society for Computational Biology
3. American Statistical Association
4. International Society for Bayesian Analysis
5. Association for Computing Machinery
6. Society for Molecular Biology and Evolution