Aditya D. Sriram

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Education

2022 - 2026 Ph.D. **Human Genetics**
University of Pittsburgh, Dept. of Human Genetics, School of Public Health

2020 - 2022 M.S. **Genetic Epidemiology**
University of Washington, School of Public Health, Seattle, WA
Thesis: Genetic Risk Factors Associated with SARS-CoV-2 Susceptibility in Multiethnic Populations
Co-mentors: Kathleen F. Kerr and Bruce Weir

2016 - 2020 B.S. **Genetics & Genomics**
Minor **Statistics**
University of California, Davis, School of Biological Sciences, Davis, CA

A. Research and Career Aims

I currently work as a member of Dr. Hyun Jung Park's lab, where I am focusing on using machine learning and statistical modeling techniques to develop causal inference methods to better understand complex genetic diseases. I am currently implementing these tools in large-scale databases (i.e., UK Biobank, All of Us) to better identify risk factors for complex disease. My dissertation research aims focus on 1) developing a knockoff variable framework with polygenic risk score-based biological context for better exposome risk factor identification in complex disease models, 2) using SHAP to perform differential causal inference and identify subgroup-specific differences in larger population groups, and 3) implementing transfer learning in large databases for better clinical insights and hypothesis validation. I believe that understanding and harnessing bioinformatics and machine learning techniques will ultimately improve complex disease treatment and prevention strategies. My goal is to continue tackling challenging problems in causal inference and developing software to address these problems, with the primary focus being the implementation of advanced machine learning and statistical packages to create foundational models to better understand disease architecture.

I am passionate about teaching, instruction, and tutoring to give back to the science community while I pursue my own research as part of my PhD program. Concepts are initially tricky and abstract, especially in the domain of computational biology and machine learning. A strong foundation leads to a lifetime of positive experiences and a willingness to grow in the field, and I hope to provide that for the next generation of students and scientists.

B. Publications

1. **Sriram A**, Kim S, Carcillo J. A., Park H. J. (in press). DeepDiff-SHAP: Interpretable deep learning for subgroup-specific causal hypothesis generation using conditional SHAP. *Pac Symp Biocomput. 2026.*
2. **Sriram A**, Kernan K. F., Qin Y, et al. Epstein-Barr Virus Seropositivity, Immune Dysregulation, and Mortality in Pediatric Sepsis. *JAMA Netw Open.* 2025;8(8):e2527487. doi:10.1001/jamanetworkopen.2025.27487
3. **Sriram, A,** Bohn R. C., Kernan K. F., Di Y. P., Hsu D. J., Habibzadeh P, Carcillo J. A., Kim S, Park H. J. (in press). DeepEXPOKE: A Deep Learning Framework with Polygenic Risk Scores as

Knockoffs for Deconvoluting Genetic and Non-Genetic Exposure Risks in Sepsis and Coronary Heart Disease. *Genome Medicine*.

4. Sun, J., Fan, Z., **Sriram, A.** & Park, H. J. Unveiling the Gut Microbiome Network Fingerprint: A Deep Learning Approach to Predict Immunotherapy Response in Melanoma Patients. *bioRxiv*, 2024.2010.2021.619471 (2024). https://doi.org:10.1101/2024.10.21.619471
5. Frias-Anaya, E., Gallego-Gutierrez, H., Gongol, B., Weinsheimer, S., Lai, C. C., Orecchioni, M., **Sriram, A.**, Bui, C. M., Nelsen, B., Hale, P., Pham, A., Shenkar, R., DeBiasse, D., Lightle, R., Girard, R., Li, Y., Srinath, A., Daneman, R., Nudleman, E., Sun, H., … Lopez-Ramirez, M. A. (2024). Mild Hypoxia Accelerates Cerebral Cavernous Malformation Disease Through CX3CR1-CX3CL1 Signaling. Arteriosclerosis, thrombosis, and vascular biology, 10.1161/ATVBAHA.123.320367.
6. Qin, Y., Caldino Bohn, R. I., **Sriram, A.**, Kernan, K. F., Carcillo, J. A., Kim, S., & Park, H. J. (2023). Refining empiric subgroups of pediatric sepsis using machine-learning techniques on observational data. Frontiers in pediatrics, 11, 1035576.
7. Fan, Z., Kernan, K. F., **Sriram, A.**, Benos, P. V., Canna, S. W., Carcillo, J. A., Kim, S., & Park, H. J. (2022). Deep neural networks with knockoff features identify nonlinear causal relations and estimate effect sizes in complex biological systems. GigaScience, 12, giad044.
8. **Sriram, A.D.**, Kerr K. F. Genetic Risk Factors Associated with SARS-CoV-2 Susceptibility in Multiethnic Populations. J Biol Today's World, 2022, 11(4), 001-004.
9. Colón-Rodríguez, A., Uribe-Salazar, J. M., Weyenberg, K. B., **Sriram, A.**, Quezada, A., Kaya, G., Jao, E., Radke, B., Lein, P. J., Dennis, M. Y., (2020). Assessment of Autism Zebrafish Mutant Models Using a High-Throughput Larval Phenotyping Platform. Frontiers in Cell and Developmental Biology, 8.

C. Positions, Scientific Appointments and Honors

2025 – Present	SPH Dean's Scholarship Endowment, Travel Award
2025	Pacific Symposium on Biocomputing, Travel Award
2025 – Present	Member, International Society of Computational Biology
2024	Outstanding Public Health Impact, STATGEN 2024 Conference (speaker)
2023 – Present	Member, American Society of Human Genetics
2023 – Present	Member, American Statistical Association
2022 – 2024	Pitt Public Health – Doctoral Student Organization, Board Member
2020 – 2022	Consultant at StatCom, University of Washington

D. Contributions to Scientific Research

August 2022 – Present **Park Lab**
University of Pittsburgh, Department of Human Genetics
School of Public Health, Pittsburgh, PA
Principal Investigator: Dr. HJ Park
Project Mentors: Dr. HJ Park, Dr. Soyeon Kim, Dr. Joseph A. Carcillo, Dr. Jenna Carlson, Dr. John Shaffer, Dr. Kate Kernan

DeepEXPOKE: Identifying Exposure Risk Factors with Genetic and Non-genetic Effect in Sepsis and Coronary Heart Disease using a Deep Learning Framework with Polygenic Risk Scores as Knockoffs
- research concepts: *causal inference, network biology, neural networks, use of polygenic risk scores as instrumental variables, knockoff variables, nonlinear interactions*
- represents a transformative deep learning approach for exposome research, uniquely capable of disentangling genetic and non-genetic portions of exposure risk

DeepDiff-SHAP: Interpretable deep learning for subgroup-specific causal hypothesis generation using conditional SHAP
- research topics: *differential causal inference, deep learning, precision medicine, Shapley Additive exPlanations (SHAP)*
- DeepDiff-SHAP integrates conditional Shapley Additive exPlanations (SHAP) to estimate conditional dependencies and perform nonlinear differential causal inference in a principled, interpretable manner

Epstein-Barr Virus Seropositivity, Immune Dysregulation, and Mortality in Pediatric Sepsis
- research topics: *loop-erased random walks; causal association subnetwork identification; network biology; directed acyclic graphs; Markov conditions; structural equation modeling*
- evaluated the role of Epstein-Barr virus (EBV) in sepsis-related immune dysregulation; identified potential pathways through which EBV positivity may influence mortality

The eQTM Atlas (https://shiny.crc.pitt.edu/eqtm_browser/)
- research topics: *epigenetics, association studies, database development, CpG site analysis*
- the expression quantitative trait methylation (eQTM) Atlas provides information on eQTM genes that are significantly associated with various CpGs, some of which may have regulatory effects on gene expression; database is also linked to the EWAS Atlas to enable cross-referencing across two powerful resources for methylation data

Deep neural networks with knockoff features identify nonlinear causal relations and estimate effect sizes in complex biological systems
- research topics: *nonlinear interactions, deep learning, neural networks, causal inference*
- to our knowledge, the first computational method that explicitly learns nonlinear causal relations and estimates the effect size using a deep neural network approach coupled with the knockoff framework, named causal directed acyclic graphs using deep learning variable selection (DAG-deepVASE)
- can help identify driver genes/therapeutic agents in biomedical studies and clinical trials

Sept 2020 – June 2022 **University of Washington**
Institute for Public Health Genetics and Fred Hutch Cancer Center, Seattle, WA
Project Mentors: Dr. Kathleen Kerr, Dr. Bruce Weir, Dr. Gavin Ha

Master's Thesis Research
Thesis Committee Chair: Dr. Kathleen Kerr
Thesis Committee Member: Dr. Bruce Weir
- investigated genetic components contributing to SARS-CoV-2 susceptibility in multiethnic populations; UK Biobank-based GWAS

Ha Lab – Fred Hutchinson Cancer Center
Graduate Rotation Student January 2021 - December 2021
Principal Investigator: Dr. Gavin Ha
Project Mentor: Dr. Gavin Ha

- Gene expression analysis of circulating tumor DNA from pediatric neuroblastoma Identified target transcription factor binding sites of interest in Neuroblastoma genetic pathways

June 2021 – March 2022 **UCSF – Visiting Summer Scholar**
Center for Cerebrovascular Research & Weill Institute for Neurosciences, San Francisco, CA
Project Mentors: Dr. Helen Kim, Dr. Lauren Weiss

Center for Cerebrovascular Research – UCSF Parnassus Campus
June 2021 - March 2022
Principal Investigator: Dr. Helen Kim
Project Mentors: Dr. Shantel Weinsheimer and Dr. Helen Kim

- Studied the genetic basis for familial cerebral cavernous malformation (CCM) progression
- Did functional enrichment and over-representation analysis using GWAS results for enriched biological pathways in CCM progression

Weiss Lab – UCSF Weill Institute for Neurosciences
June 2021 - September 2021
Principal Investigator: Dr. Lauren Weiss
Project Mentor: Dr. Michela Traglia

- Investigated hypothesis that maternal asthma can be a predictor of autism in children
- Worked on developing polygenic risk scores and using risk scores as a metric for disease prediction

June 2018 – July 2020 **Dennis Lab**
UC Davis Genome Center, Davis, CA
Project Mentors: Dr. Megan Dennis, Dr. Alexandra Cólon-Rodriguez

Dennis Lab - Human Genomics, Evolution, and Disease Genetics at UC Davis

- Investigated molecular and behavioral characteristics of autism spectrum disorder and studied epilepsy target genes using zebrafish models
- Tasks included: Zebrafish genotyping, PAGE-gel preparation and characterization of Zebrafish variants, qPCR and Melt Curve data analysis, primer design for both standard PCR and qPCR assays, microinjections of Zebrafish with fluorescent markers to study gene function and developmental processes.

E. Invited Talks and Panels

- Pacific Symposium on Biocomputing: Precision Medicine Panel, January 2026
  Affiliation: University of Pittsburgh
- Human Genetics Department Seminar, University of Pittsburgh, September 2025
  Affiliation: University of Pittsburgh
- PittGene 2024, University of Pittsburgh, October 2024
  Affiliation: University of Pittsburgh
- STATGEN 2024, hosted by the American Statistical Association (ASA), May 2024
  Affiliation: University of Pittsburgh
- International Stroke Conference 2022, February 2022 at New Orleans, LA
  Session Title: *Aneurysms and Vascular Malformations*
  Affiliation: UCSF; **Transcript**
- Angioma Alliance 2021 International CCM Scientific Meeting, November 2021
  Session Title: *Session 1 – Basic Science panel*
  Affiliation: UCSF

F. Teaching and Volunteering

- Guest lectures, **HUGEN 2078** - Genomic Data & Advanced Topics in Bioinformatics [September 2023, September 2024, September 2025]
- Guest lecture, **HUGEN 2080** - Statistical Genetics [April 2024]
- StatCom @UW [Volunteer, January 2021 - June 2022]
- Teaching Assistant for Dr. Alison Fohner @UW [March 2021 - June 2021]
- **PHG401/BIOST401** - Computational and Applied Genetic Epidemiology
  - average rating: 4.92/5
- Tutor @UW School of Public Health [September 2021 - June 2022]

G. References

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