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
Thesis: Advancing Methodological Foundations in Precision Medicine Through Novel Causal Inference, Machine Learning, and Artificial Intelligence Frameworks
Co-mentors: Kathleen F. Kerr and Bruce Weir

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 am a current postdoctoral fellow in neurology at Dr. Reza Abbasi-Asl's lab at UCSF. I work on causal inference method development in spatial transcriptomics data, primarily in neurological disease models. I recently obtained my PhD from the University of Pittsburgh Department of Human Genetics, and my research focused on advancing methodological foundations in precision medicine through novel causal inference, machine learning, and artificial intelligence frameworks. I worked as a member of Dr. Hyun Jung Park's lab, where I focused on using machine learning and statistical modeling techniques to develop causal inference methods to better understand complex genetic diseases. I implemented these tools in large-scale databases (i.e., UK Biobank, All of Us) to better identify risk factors for complex disease. My primary research centered around 1) implementing and developing a knockoff variable framework with polygenic risk score-based biological context for better exposome risk factor identification in complex disease models, 2) developing a differential causal inference method to identify subgroup-specific causal differences in heterogeneous population groups, and 3) improving interpretability for *in silico* gene perturbation prediction by benchmarking large single cell foundation models and creating biological context-aware measures to assess perturbation prediction quality. I believe that understanding and harnessing bioinformatics, machine learning, and artificial intelligence 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 artificial intelligence, machine learning and statistical packages to better understand disease architecture.

B. Publications

Recent projects that I would like to highlight include:

DeepDiff-SHAP: Interpretable deep learning for subgroup-specific causal hypothesis generation using conditional SHAP

This research was supported in part by the University of Pittsburgh Center for Research Computing, RRID:SCR_022735, through the resources provided. Specifically, this work used the HTC cluster, which is supported by NIH award number S10OD028483.

Epstein-Barr Virus Seropositivity, Immune Dysregulation, and Mortality in Pediatric Sepsis
This study was supported in part by grant RO1GM108618 from the National Institutes of General Medical Sciences (Drs Carcillo, Park, Storch, and Canna), grant 5U01HD049934-10S1 from the Eunice Kennedy Shriver National Institute of Child Health and Development (Dr Carcillo), and cooperative agreements U10HD049983, U10HD050096, U10HD049981, U10HD063108, U10HD63106, U10HD063114, U10HD050012, and U01HD049934 from the Eunice Kennedy Shriver National Institute of Child Health and Human Development.

eQTM Atlas: a comprehensive resource of over 11 million methylation–expression associations across 11 tissues and 4 diseases (ongoing)

This work was supported by grants HL079966, HL117191, MD011764 and HL168539 (to J.C.C.), and K01 HL153792 (to S.K.) from the U.S. National Institutes of Health (NIH). W.C. was supported by NIH grant HL150431 and NSF grant 2225775. H.J.P. was supported by the UPMC Hillman Cancer Center Biostatistics Shared Resource that is supported in part by award P30CA047904 and R01GM108618 at the NIH. H.J.P. is also supported by the Hillman Cancer Center Career Enhancement Program Award (P50 CA254865-01). This research was supported in part by the University of Pittsburgh Center for Research Computing, RRID:SCR_022735, through the resources provided. Specifically, this work used the HTC cluster, which is supported by NIH award number S10OD028483 and H2P cluster, which is supported by NSF award number OAC-2117681.

Citations:

1. **Sriram A,** Kim S, Carcillo JA, Park HJ. DeepDiff-SHAP: Interpretable deep learning for subgroup-specific causal hypothesis generation using conditional SHAP. Pac Symp Biocomput. 2026;31:722-737. doi: 10.1142/9789819824755_0052. PMID: 41758180.
2. **Sriram A, Kernan KF, 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, Kim S, Caldino Bohn R, Chen W, Liu T, Yue M, Jain N, Pierce BL, Joehanes R, Levy D, Patin E, Quintana-Murci L, Park HJ, Celedón JC. eQTM (expression quantitative trait methylation) Atlas: a comprehensive resource of over 11 million DNA methylation-gene expression associations through across 11 tissues and 4 diseases. bioRxiv [Preprint]. 2026 Jun 10:2026.06.07.730721. doi: 10.64898/2026.06.07.730721. PMID: 42327319; PMCID: PMC13278183.

B. Positions, Scientific Appointments, and Honors

2026	UCSF Bakar Aging Research Institute, Best Talk Honorable Mention
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

C. Contributions to Science

1) My early research focused on understanding the biological mechanisms underlying complex diseases using experimental model systems and classical genomic analysis tools. In work studying autism spectrum disorder, I contributed to the development and evaluation of zebrafish mutant models using

high-throughput larval phenotyping approaches, allowing for systematic characterization of behavioral and molecular phenotypes. I also participated in studies investigating cerebral cavernous malformations (CCMs), identifying biological pathways associated with lesion burden and demonstrating how environmental stressors such as hypoxia can accelerate disease progression through CX3CR1-CX3CL1 signaling pathways. Together, this body of work contributed to understanding how genetic variation and environmental context interact to influence neurological and vascular disease phenotypes.

a. Colón-Rodríguez, A., Uribe-Salazar, J. M., Weyenberg, K. B., **Sriram, A.**, et al. (2020). *Assessment of autism zebrafish mutant models using a high-throughput larval phenotyping platform.* **Frontiers in Cell and Developmental Biology**, 8, 586296.
b. Frias-Anaya, E., Gallego-Gutierrez, H., Gongol, B., Weinsheimer, S., Lai, C. C., Orecchioni, M., **Sriram, A.**, et al. (2024). *Mild hypoxia accelerates cerebral cavernous malformation disease through CX3CR1-CX3CL1 signaling.* **Arteriosclerosis, Thrombosis, and Vascular Biology**, 44(6), 1246–1264.
c. **Sriram, A.**, Weinsheimer, S., Nelson, J., et al. (2022). *Biological pathways enriched for genes associated with lesion burden in cerebral cavernous malformation.* **Stroke**, 53(Suppl_1), A109–A109.

2) Building on my background in genetics and computational biology, I contributed to studies applying machine learning and network-based approaches to identify clinically relevant biological patterns in complex diseases. In pediatric sepsis research, my research involved using observational clinical and molecular data to refine empiric disease subgroups and identify pathways associated with immune dysregulation and mortality. These studies demonstrated the value of causal inference approaches in revealing clinically meaningful heterogeneity in critical illness and in generating hypotheses about mechanisms linking infection, immune signaling, and patient outcomes.

a. 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.
b. **Sriram, A.,** Kernan, K. F., Qin, Y., et al. (2025). *Epstein-Barr virus seropositivity, immune dysregulation, and mortality in pediatric sepsis.* JAMA Network Open, 8(8), e2527487.

3) My recent research focuses on developing interpretable machine learning frameworks to identify causal relationships in high-dimensional biomedical data. I contributed to the development of deep neural network methods incorporating knockoff variables to detect nonlinear causal relationships and estimate effect sizes in complex biological systems. Building on this foundation, I developed DeepDiff-SHAP, a framework that helps perform differential causal inference and identify subgroup-specific causal relationships in population-scale datasets. In parallel, I introduced DeepEXPOKE, a deep learning approach that integrates polygenic risk scores within a knockoff framework to disentangle genetic and non-genetic exposure risks in diseases such as sepsis and coronary heart disease. Together, these methods advance interpretable machine learning approaches for precision medicine and causal hypothesis generation.

a. Fan, Z., Kernan, K. F., Sriram, A., Benos, P. V., Canna, S. W., Carcillo, J. A., Kim, S., & Park, H. J. (2023). *Deep neural networks with knockoff features identify nonlinear causal relations and estimate effect sizes in complex biological systems.* GigaScience, 12, giad044.b. Sriram, A., Kim, S., Carcillo, J. A., & Park, H. J. (2025). *DeepDiff-SHAP: Interpretable deep learning for subgroup-specific causal inference using conditional SHAP.* Pacific Symposium on Biocomputing.

c. Sun, J., Fan, Z., Sriram, A., & Park, H. J. (2024). *Unveiling the gut microbiome network fingerprint: A deep learning approach to predict immunotherapy response in melanoma patients.* bioRxiv.
d. Sriram, A., Bohn, R., Kernan, K., Carcillo, J., Kim, S., & Park, H. J. (2024). *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.* medRxiv.

D. Complete List of Published Work

1. **Sriram A**, Kim S, Carcillo J. A., Park H. J. 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.

Pending Manuscripts

1. Aditya Sriram, Hyun Jung Park, Wei Chen, Juan C. Celedón, Soyeon Kim. "Expression Quantitative Trait Methylation (eQTM) Atlas: connecting DNA methylation and gene expression"
2. Aditya Sriram, Hyun Jung Park, Kate F. Kernan, Joseph A. Carcillo. "Causal inference analysis identified viral DNA emia and cytokine therapeutic targets in pediatric hyperferritinemic sepsis"
3. Aditya Sriram, Hyun Jung Park, Tianze Luo. "scPerturbTrust predicts query-level reliability in single-cell perturbation foundation models"

E. Contributions to Scientific Research

August 2022 – June 2026 **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.

F. 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

G. 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]

H. References

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