

Jason Laird

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Location: Baltimore, MD

Summary

Computational biologist specializing in multi-omics, single-cell and spatial methods, exposure-driven toxicology and disease modeling. Experienced in building end-to-end analytical pipelines that integrate omics data and exposure data to produce interpretable insights. Strong background in R and Python, with applied experience in statistical and machine-learning methods for high-dimensional data, scalable HPC workflows, and reproducible translational bioinformatics.

Skills

Software & Computing

- R / Shiny, Python
- Linux, Bash, High-performance computing (HPC), SLURM
- HTML/CSS
- Version control, Git, Docker

Data Analysis & Methods

- Single-cell, single-nucleus RNA-seq, spatial transcriptomics
- Bulk omics: RNA-seq, DNA methylation, proteomics, metabolomics
- Data quality control and exploratory data analysis
- Statistical modeling and applied machine-learning methods

Domain Expertise

- Bioinformatics
- Toxicology
- Exposomics
- Neuroimmunology
- Pharmacology

Education

Johns Hopkins University

PhD Toxicology, Physiology and Molecular Mechanisms

Expected 2027

Brandeis University*MS Bioinformatics*

June 2021

SUNY Binghamton*BA Biological Sciences*

May 2016

Professional Experience

Graduate Researcher

August 2023 - Present

Johns Hopkins University, Baltimore MD

- Conduct bioinformatics research on the effects of environmental exposures on neurodevelopment, utilizing transcriptomics, epigenomics, and other omics data.
- Collaborate with interdisciplinary teams, including toxicologists, neuroscientists, and epidemiologists.
- Assist in teaching environmental health courses, including grading, and mentoring students.
- Present research findings at conferences and contribute to manuscripts for publication.

Bioinformatics Scientist

January 2022 - August 2023

Tufts University, Medford MA

- Develop omics data workflows and curating reference data to support of bioinformatics research on the Tufts High Performance Compute Cluster (HPC) and Tufts Galaxy Server
- Consult on bioinformatics projects and provide input on workflow design and technical optimization
- Develop and lead omics data analysis and visualization seminars

Clinical Bioinformatics Analyst

January 2021 - December 2021

Foundation Medicine, Cambridge MA

- Lead team to develop R Shiny app to aid in data analysis/visualization.
- Analyze clinical oncology NGS data and annotate genomic aberrations in patient samples to inform oncologists of potentially actionable drug targets.
- Collaborate in cross disciplinary teams to complete research projects and implement process improvements.

Histology Systems Specialist

July 2020 - December 2020

Foundation Medicine, Cambridge MA

- Developed, captured, and analyzed performance metrics for the Histology team using R, Python and tools available through Microsoft Power BI.
- Tested technology products to accommodate changing workflows and the needs of the laboratory staff and updated SOPs accordingly.

Histotechnologist

October 2018 - July 2020

Foundation Medicine, Cambridge MA

- Operated under a CLIA/CAP environment with pathologists to assess tumor composition of cancer patient samples.
- Performed validation of new processes and revised SOPs.

Pathology Technician

May 2016 – August 2018

Covance, Madison WI

- Worked with pathologists in assessing the efficacy of new medical therapies by grossing and preparing tissue samples for microtomy.
- Identified and resolved issues in documentation, GLP/SOP compliance, and overall process improvements.

Publications

1. van der Molen T, Spaeth A, Chini M, Hernandez S, Kaurala GA, Schweiger HE, Duncan C, McKenna S, Geng J, Lim M, Bartram J, Ganswein T, Dendukuri A, Zhang Z, Gonzalez-Ferrer J, Bhaskaran-Nair K, Morson AL, Harder CRK, Petzold LR, Alam El Din D-M, **Laird J**, Schenke M, Smirnova L, Colquitt BM, Mostajo-Radji MA, Hansma PK, Teodorescu M, Hierlemann A, Hengen KB, Hanganu-Opatz IL, Kosik KS, Sharf T. Preconfigured neuronal firing sequences in human brain organoids. *Nat Neurosci* 2025. <https://doi.org/10.1038/s41593-025-02111-0>.
2. **Laird J**, Schenke M, Rittenhouse A, Kucheryavenko V, Neuhaus W, Chen O, Sabunciyan S, Maertens A, Smirnova L. Genetic background and sex modulate androgen responses in human brain microphysiological system. *bioRxiv* 2025. <https://doi.org/10.64898/2025.12.03.692130>.
3. Rittenhouse A, Krall C, Plotkin J, Alam El Din D-M, Kincaid B, **Laird J**, Smirnova L. Microglia-containing neural organoids as brain microphysiological systems for long-term culture. *Front Cell Neurosci* 2025;19:1616470. <https://doi.org/10.3389/fncel.2025.1616470>.
4. Alam El Din D-M, Moenkemoeller L, Loeffler A, Habibollahi F, Schenkman J, Mitra A,

- van der Molen T, Ding L, **Laird J**, Schenke M, Johnson EC, Kagan BJ, Hartung T, Smirnova L. Human neural organoid microphysiological systems show the building blocks necessary for basic learning and memory. *Commun Biol* 2025;8:1237. <https://doi.org/10.1038/s42003-025-08632-5>.
5. Ali SA, Perera G, **Laird J**, Batorsky R, Maron MS, Rivas VN, Stern JA, Harris S, Chin MT. Single cell transcriptomic profiling of MYBPC3-associated hypertrophic cardiomyopathy across species reveals conservation of biological process but not gene expression. *J Am Heart Assoc* 2025;14:e035780. <https://doi.org/10.1161/JAHA.124.035780>.
 6. Nagarajan A, **Laird J**, Ugochukwu O, Reppe S, Gautvik K, Ross RD, Bennett DA, Rosen C, Kiel DP, Higginbotham LA, Seyfried NT, Lary CW. Network analysis of brain and bone tissue transcripts reveals shared molecular mechanisms underlying Alzheimer's disease and related dementias and osteoporosis. *J Gerontol A Biol Sci Med Sci* 2024;79. <https://doi.org/10.1093/gerona/glae211>.
 7. **Laird J**, Perera G, Batorsky R, Wang H, Arkun K, Chin MT. Spatial transcriptomic analysis of focal and normal areas of myocyte disarray in human hypertrophic Cardiomyopathy. *Int J Mol Sci* 2023;24:12625. <https://doi.org/10.3390/ijms241612625>.
 8. Saad MK, Yuen JSK Jr, Joyce CM, Li X, Lim T, Wolfson TL, Wu J, **Laird J**, Vissapragada S, Calkins OP, Ali A, Kaplan DL. Continuous fish muscle cell line with capacity for myogenic and adipogenic-like phenotypes. *Sci Rep* 2023;13:5098. <https://doi.org/10.1038/s41598-023-31822-2>.
 9. Chin M, Codden C, Larson A, Perera G, **Laird J**, Batorsky R, Awata J. Altered intercellular communication in human hypertrophic cardiomyopathy inferred from single nuclei RNA-seq, Ligand-Receptor gene expression analysis and spatial transcriptomics. *J Mol Cell Cardiol* 2022;173:S45. <https://doi.org/10.1016/j.yjmcc.2022.08.090>.
 10. **Laird J**, Margolis M, Janovitz T, Mata DA, Montesion M, Lee JK, Madison RW, Schrock AB, Tukachinsky H, Allen JM, Erlich R, Hiemenz MC, Huang RSP, Elvin J, Vergilio J-A, Lin DI, Ross J, Oxnard G, Decker B. Activating IGF1R hotspot non-frameshift insertions define a novel, potentially targetable molecular subtype of adenoid cystic carcinoma. *Mod Pathol* 2022;35:1618–23. <https://doi.org/10.1038/s41379-022-01126-3>.
 11. **Laird J**, Maertens A. Personalized Perturbation Profiles Reveal Concordance between Autism Blood Transcriptome Datasets. *bioRxiv* 2021:2021.01.25.427953. <https://doi.org/10.1101/2021.01.25.427953>.

Podium and Poster Presentations

Laird J, Hartung T, Maertens A. Transcriptomic concordance among ASD in vitro and in vivo models. ASHG. October 2025.

Kopańska K, Hansell L, **Laird J**, Hartung T. The last mile challenge: Overcoming socio-technical barriers for AI implementation. HESI Global. June 2025.

Laird J. Transcriptomic concordance among ASD in vitro and in vivo models. JHSPH EHE Doctoral Student Seminar. October 2025.

Laird J. Revealing the Impact of Viral Exposure on Autism Through Transcriptomics. JHSPH EHE Doctoral Student Seminar. April 2025.

Laird J. Reducing Animal Research with Public Data Mining. MSU Animal and Natural Resource Law Review Symposium. March 2025.

Teaching Experience

Molecular Toxicology Teaching Assistant

Johns Hopkins University

2024/2025

- Assisted with lectures and grading of assignments.

Introduction To Risk Sciences Teaching Assistant

Johns Hopkins University

2024

- Assisted with lectures and grading of assignments.

Introduction to Bioinformatics - Recurring Guest Lecturer

Tufts University

2022/2023

- Lectured on the principles of RNA-seq, and led a live workshop on how to analyze RNA-seq data.

Protein Engineering Course - Recurring Guest Lecturer

Tufts University

2022/2023

- Lectured on the background and use of AlphaFold in protein engineering research and led a live workshop on how to use AlphaFold.

Introduction To 16S Metabarcoding

Tufts University

2022

- Lectured on 16S Metabarcoding data analysis to profile microbial communities and led a live workshop on how to analyze microbiome data.

Animal Histology Teaching Assistant

Binghamton University

2015

- Taught students about tissue composition, lesion formation, and tissue identification under microscope
- Proctored exams and supported laboratory preparation for classes

Awards and Honors

J Laird, A Maertens, J Smith, F Sille. Multiomics and Exposomics Integration Reveals Molecular Insights into Childhood Asthma. Best Toxicology Poster Award. JSPH research retreat. 2025.

Memberships

International Society for Computational Biology (ISCB)

2025 - Present

American Society for Human Genetics (ASHG)

2025 - Present

Carpentries Instructors

2022 - Present

Mentorship and Training Experience

Computational Toxicology Intern Program Mentor

Johns Hopkins University

Summer 2025

Bassant Said

Doctoral Students

Tufts University

2022-2023

Archana Nagarajan

Clinical Bioinformatics Interns

Foundation Medicine

Summer 2021

Clarissa May Babila and Victoria Gonzalez Canalle

Histotechnologist Trainer

Foundation Medicine

2019-2020

Pathology Technician Trainer

Covance

2017-2018