Steven M. Foltz, PhD

Children's Hospital of Philadelphia
Philadelphia, PA

Staff Scientist II, Tan Lab
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Research specialty: cancer bioinformatics, machine learning, single-cell multiomics data analysis

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Education and Training

Postdoctoral Fellow, University of Pennsylvania, Philadelphia, PA July 2020 – May 2023
NIH K12 IRACDA Postdoctoral Fellow (PennPORT)
Advisor: Casey Greene, PhD
Focus: Machine learning methods development in pediatric cancer genomics

PhD, Washington University in St. Louis, St. Louis, MO June 2014 – March 2020
Division of Biology and Biomedical Sciences (DBBS)
Human and Statistical Genetics Program
Precision Medicine Pathway
Advisor: Li Ding, PhD
Thesis: Multi-omics integration for gene fusion discovery and somatic mutation haplotyping in cancer

MS Biostatistics, University of Washington, Seattle, WA September 2011 – August 2013
Advisors: Brian Browning, PhD, and Sharon Browning, PhD
Thesis: Rare variant method for identity-by-descent detection in sequence data, and the time to most recent common ancestor given identity-by-descent segment length

BS Mathematics, Presbyterian College, Clinton, SC August 2006 – May 2010
Advisor: Doug Daniel, PhD
Thesis: Tiling 2-deficient Rectangles with Trominoes

Research Experience

Children's Hospital of Philadelphia, Philadelphia, PA May 2023 – present
Staff Scientist II, Laboratory of Kai Tan, PhD
Focus: Single-cell multiomics tool development and data analysis in pediatric oncology

- Analyzed tumor evolution and minimal residual disease using single-cell DNA-seq, ATAC-seq, and RNA-seq in high-risk pediatric B-ALL and sarcoma

- Led detection of chimeric antigen receptor (CAR) integration sites using longitudinal single-cell ATAC-seq in pediatric B-ALL patients receiving CAR T-cell therapy

University of Pennsylvania, Philadelphia, PA July 2020 – May 2023
Postdoctoral Fellow, Laboratory of Casey Greene, PhD, in partnership with the Childhood Cancer Data Lab at Alex's Lemonade Stand Foundation
Focus: Machine learning methods development in pediatric cancer genomics

- Evaluated methods for cross-platform normalization of gene expression data for machine learning

- Developed single-sample prediction models for cancer subtype prediction using gene expression data from multiple platforms, including single-cell data

Washington University in St. Louis, St. Louis, MO June 2014 – May 2020
Graduate Student, Laboratory of Li Ding, PhD
Thesis: Multi-omics integration for gene fusion discovery and somatic mutation haplotyping in cancer

- Led pan-cancer computational projects utilizing tumor and normal tissue sequencing data to understand patterns of germline and somatic variation

- Developed integrative data analysis tool and pipeline development, including variant calling and quality control using bulk DNA and RNA, single-cell RNA, and linked-read DNA sequencing

- Discovered gene fusions from The Cancer Genome Atlas (9,624 patients, 33 cancer types) and a large multiple myeloma cohort (742 patients), highlighting clinically-relevant events

- Analyzed linked-read whole genome sequencing data for phasing somatic mutations, understanding haplotype structures, and modeling tumor evolution

- Organized and delivered donor presentations to establish research funding through the Paula C. and Rodger O. Riney Blood Cancer Research Initiative Fund ($25 million since 2016)

Virginia Commonwealth University, Richmond, VA August 2013 – May 2014
Biostatistician, Laboratory of Nengliang Yao, PhD

- Led statistical aspects of cancer care research as part of a healthcare policy team

- Procured, cleaned, and analyzed data from national cancer databases, including SEER

- Developed geographically weighted regression and spatial panel data models

University of Washington, Seattle, WA September 2011 – August 2013
Graduate Research Assistant, Laboratory of Brian Browning, PhD, and Sharon Browning, PhD
Thesis: Rare variant method for identity-by-descent detection in sequence data, and the time to most recent common ancestor given identity-by-descent segment length

- Implemented novel algorithms to define identity-by-descent (IBD) between individuals using rare DNA variation and developed statistical models for shared ancestor inference

- Worked with data from the 1000 Genomes Project and simulated coalescent model data

- Assisted in methods development for missing data imputation and haplotype phasing

Presbyterian College, Clinton, SC Spring 2010
Undergraduate honors research in mathematics, advised by Doug Daniel, PhD
Thesis: Tiling 2-deficient Rectangles with Trominoes

- Developed analytical and computational approaches to answer an open question about tiling deficient rectangular fields with trominoes

Medical University of South Carolina, Charleston, SC   Summer 2009
Undergraduate Summer Research Fellow, Laboratory of Jim Zheng, PhD

- Created a weighted clustering coefficient model to detect regions of high interconnectivity in yeast gene networks based on synthetic lethal interactions

Presbyterian College, Clinton, SC   Fall 2008 – Spring 2009
Undergraduate Research Assistant, Laboratory of James Wanliss, PhD

- Analyzed space weather data to refine solar storm prediction models

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PUBLICATIONS
* co-first authors

17. **Foltz SM**, Li Y, Yao L, Terekhanova NV, Weerasinghe A, Gao Q, et al. Somatic mutation phasing and haplotype extension using linked-reads in multiple myeloma. *bioRxiv*. 2024. p. 2024.08.09.607342. (pre-print)

16. Hawkins AG, Shapiro JA, Spielman SJ, Mejia DS, Prasad DV, Ichihara N, et al. The Single-cell Pediatric Cancer Atlas: Data portal and open-source tools for single-cell transcriptomics of pediatric tumors. *bioRxiv*. 2024. p. 2024.04.19.590243. (pre-print)

15. Liang W-W, Lu RJ-H, Jayasinghe RG, **Foltz SM**, Porta-Pardo E, Geffen Y, et al. Integrative multi-omic cancer profiling reveals DNA methylation patterns associated with therapeutic vulnerability and cell-of-origin. *Cancer Cell*. 2023;41: 1567–1585.e7.

14. Li Y*, Dou Y*, Da Veiga Leprevost F*, Geffen Y*, Calinawan AP*, Aguet F, et al. Proteogenomic data and resources for pan-cancer analysis. *Cancer Cell*. 2023;41: 1397–1406.

13. Shapiro JA, Gaonkar KS, Spielman SJ, Savonen CL, Bethell CJ, Jin R, et al. OpenPBTA: The Open Pediatric Brain Tumor Atlas. *Cell Genom*. 2023;3: 100340.

12. Yao L*, Wang JT*, Jayasinghe RG*, O'Neal J, Tsai C-F, Rettig MP, et al. Single-Cell Discovery and Multiomic Characterization of Therapeutic Targets in Multiple Myeloma. *Cancer Res*. 2023;83: 1214–1233.

11. **Foltz SM**, Greene CS, Taroni JN. Cross-platform normalization enables machine learning model training on microarray and RNA-seq data simultaneously. *Commun Biol*. 2023;6: 222.

10. Liu R*, Gao Q*, **Foltz SM***, Fowles JS, Yao L, Wang JT, et al. Co-evolution of tumor and immune cells during progression of multiple myeloma. *Nat Commun*. 2021;12: 2559.

9. **Foltz SM**, Gao Q, Yoon CJ, Sun H, Yao L, Li Y, et al. Evolution and structure of clinically relevant gene fusions in multiple myeloma. *Nat Commun*. 2020;11: 2666.

8. McDermott JE, Arshad OA, Petyuk VA, Fu Y, Gritsenko MA, Clauss TR, et al. Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. *Cell Reports Medicine*. 2020;1: 100004.

7. Sanchez-Vega F, Mina M, Armenia J, Chatila WK, Luna A, La KC, et al. Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*. 2018;173: 321–337.e10.

6. Gao Q*, Liang WW*, **Foltz SM***, Mutharasu G, Jayasinghe RG, Cao S, et al. Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Rep*. 2018;23: 227–238.e3.

5. Dang HX, White BS, **Foltz SM**, Miller CA, Luo J, Fields RC, et al. ClonEvol: Clonal ordering and visualization in cancer sequencing. *Ann Oncol*. 2017;28: 3076–3082.

4. **Foltz SM**, Liang WW, Xie M, Ding L. MIRMMR: Binary classification of microsatellite instability using methylation and mutations. *Bioinformatics*. 2017;33: 3799–3801.

3. Olfson E, Saccone NL, Johnson EO, Chen LS, Culverhouse R, Doheny K, et al. Rare, low frequency and common coding variants in CHRNA5 and their contribution to nicotine dependence in European and African Americans. *Mol Psychiatry*. 2016;21: 601–607.

2. Ye K, Wang J, Jayasinghe R, Lameijer EW, McMichael JF, Ning J, et al. Systematic discovery of complex insertions and deletions in human cancers. *Nat Med*. 2016;22: 97–104.

1. Yao N, **Foltz SM**, Odisho AY, Wheeler DC. Geographic analysis of urologist density and prostate cancer mortality in the United States. *PLoS One*. 2015;10: e0131578.

Teaching Experience

Rutgers University – Camden, Camden, NJ

Adjunct Faculty, Cancer Data Science (BIO 393)   Spring 2022
Student profile: 20 undergraduate biology majors
Responsibilities: Designed and taught a special topics course around my research interests

Adjunct Faculty, Statistics for Biological Research (BIO 283)   Fall 2021
Student profile: 24 undergraduate biology majors
Responsibilities: Taught an existing course, with major overhauls to computer workshop materials

Washington University in St. Louis, St. Louis, MO

Instructor, Introduction to Python – Bioinformatics   Winter 2019
Student profile: 6 post-baccalaureate research fellows

Teaching Assistant, Genomics (Biol 5488)   Spring 2016
Student profile: 40 first-year biomedical graduate students

Tutor, Fundamentals of Biostatistics for Graduate Students (Biol 5075)   Fall 2015, Fall 2016
Student profile: 30 first-year biomedical graduate students

Presbyterian College, Clinton, SC

Tutor, Department of Mathematics   January 2007 – April 2010

Mentoring Experience
* undergraduate co-authors

Undergraduate mentoring at Children's Hospital of Philadelphia

- *Avi Loren (Summer 2023 – present)   UPenn 2025

Undergraduate mentoring with PennPORT Pals at Rutgers University – Camden

- John Crespo (Summer 2021 – Summer 2022)   RUC 2023

Undergraduate mentoring at Washington University in St. Louis

- *Moses Schindler (Summer – Fall 2019)   WashU 2023
  Tumor evolution modeling and graph-based methods using single cell RNA-seq

- Jessika Baral (Fall 2018)   WashU 2021
  Haplotype and variant data analysis from 1000 Genomes

- *Guanlan Dong (Fall 2018, Spring 2019)   WashU 2019
  Haplotype phase sets and genome assembly summarization

- Justin Chen (Summer 2018)   Columbia University 2022
  Multiple myeloma phased and unphased variant comparison

- Edwin Qiu (Spring 2018, Fall 2018)   WashU 2020
  Driver fusion prioritization methods development

High school mentoring with WashU Young Scientist Program

- Jada Reid (Fall 2014 – Spring 2018)   CSMB 2018

Presentations

Oral presentations

- "Multiomic single-cell tumor evolution models of minimal residual disesae in pediatric B-cell acute lymphoblastic leukemia." American Association for Cancer Research Annual Meeting. San Diego, CA. April 2024.

- "Cross-platform normalization enables machine learning in rare diseases." Rutgers University – Camden, Department of Biology Seminar Series. April 2022.

- "Multiple Myeloma: Groundbreaking DNA, RNA, and protein technologies at WashU." Washington University School of Medicine Paula C. and Rodger O. Riney Blood Cancer Research Initiative Advisory Board Meeting. February 2019.

- "RNA-Seq and fusion discovery pipeline for a large multiple myeloma cohort." WashU DBBS Precision Medicine Pathway Retreat. October 2017.

- "RNA and DNA methylation signatures for scoring tumor stemness." WashU DBBS Precision Medicine Pathway Retreat. September 2016.

Poster presentations

- "Medulloblastoma subtype single sample predictor built on multiple gene expression platforms." MidAtlantic Bioinformatics Conference. Philadelphia, PA. October 2022.

- "Cross-platform normalization enables machine learning model training on microarray and RNA-Seq data simultaneously." NIH IRACDA Conference. Albuquerque, NM. July 2022.

- "Fusion gene detection across a large cohort of multiple myeloma patients." International Myeloma Workshop. Boston, MA. September 2019.

- "Comprehensive Multi-Omics Analysis of Gene Fusions in a Large Multiple Myeloma Cohort." American Society of Hematology. San Diego, CA. December 2018.

- "Multiple Myeloma RNA-seq and Fusion Discovery Pipeline." WashU DBBS Computational and Systems Biology / Human and Statistical Genetics / Molecular Genetics and Genomics Joint Program Retreat. Potosi, MO. September 2017.

- "Genomic region and sample selection strategy for variant discovery and association analysis." Genome Informatics. Cold Spring Harbor, NY. October 2015.

- "Comprehensive Analysis of Germline Complex Insertions and Deletions." WashU DBBS Computational and Systems Biology / Molecular Genetics and Genomics Joint Program Retreat. New Haven, MO. September 2015.

- "Comprehensive Analysis of Germline Complex Insertions and Deletions." WashU DBBS Human and Statistical Genetics Program Retreat. St. Louis, MO. September 2015.

- "Identity-by-descent analysis of sequence data." International Genetic Epidemiology Society. Stevenson, WA. October 2012.

FUNDING

Rutgers Open and Affordable Textbooks Award ($1,000)   2022-2023
Co-PIs: Steven Foltz, PhD, and Nathan Fried, PhD
"Reimagining Statistics in Biology (SBR) with Open and Affordable Materials"

ASCB Promoting Active Learning and Mentoring (PALM) Fellowship ($2,000)   2021-2022
Mentor: Nathan Fried, PhD

ALSF Childhood Cancer Data Lab Postdoctoral Training Grant ($135,925)   2021-2023
PI: Steven Foltz, PhD

NIH K12 IRACDA Postdoctoral Fellow (PennPORT) (K12 GM081259)   2020-2023
PI: Janis Burkhardt, PhD

Professional Development

Genomics Education Partnership Training Workshop   January 4-6, 2023

Fundamentals of POGIL Virtual Workshop   May 16, 2022
Process Oriented Guided Inquiry Learning

The Teaching Center at Washington University in St. Louis   Fall 2014 – January 2020
Professional Development in Teaching Program

- Preparation in Pedagogy (PiP)

    Foundational and advanced level teaching workshops

    Qualifying teaching experience

    Teaching Philosophy Statement

- WU-CIRTL "Practitioner" level

    Completed PiP and Scholarship of Teaching and Learning course

Center for the Integration of Research, Teaching, and Learning (CIRTL)
National CIRTL Forum, Drexel University, Philadelphia, PA   October 13-15, 2019

Center for the Improvement of Mentored Experience in Research (CIMER)
Mentorship Training Program, WashU, St. Louis, MO   April 1-2, 2019

Science Education Partnership and Assessment Laboratory (SEPAL @SFSU)
Evidence-based Teaching for Researchers, WashU, St. Louis, MO   September 21, 2018

Midstates Consortium for Mathematics and Science   July 6-8, 2018
Early Career Workshop, Gustavus Adolphus College, St. Peter, MN

Honors and Awards

- "Best of *Cell Reports* 2018" – co-first author of a frequently cited publication (Driver Fusions and Their Implications in the Development and Treatment of Human Cancers).

- "Outstanding Mentor" – recognizing one mentor working with high schoolers through the Washington University Young Scientist Program (25th Anniversary Gala, October 22, 2016).

- "Outstanding Senior in Mathematics" – awarded to the top graduating senior in the department (Presbyterian College Honors Convocation, April 15, 2010).

Service and Outreach

Virtual Biology Day, Rutgers University – Camden, Camden, NJ
Scientific poster judge   Spring 2021, Fall 2021, Spring 2022

Young Scientist Program, Washington University in St. Louis, St. Louis, MO
Mentoring program cohort leader   Fall 2014 – Spring 2018

- Led 12 graduate students paired with high schoolers for four years

- Coordinated bi-weekly school visits and educational field trips

- Facilitated lesson planning and resources available for hands on science activities

St. Louis Science Center, St. Louis, MO   Summer 2015
Exhibit interpreter

- Smithsonian and NHGRI-sponsored exhibit Genome: Unlocking Life's Code

- Discussed the scientific, ethical, and societal importance of genomics with museum patrons

Other Work Experience

Across, Nairobi, Kenya   August 2010 – July 2011
Institutional and Organizational Development Volunteer
Promoted the organization and its mission (holistic transformation of South Sudan communities) to an international audience through the website and other publications. Key aspects of the organization's mission included: serving refugees and internally displaced people, promoting gender equity and sustainable agriculture, and training teachers and health care providers. Placement coordinated through the Presbyterian Church (U.S.A.) Young Adult Volunteers program.

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