

ADAM WEINER

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EDUCATION

Weill Cornell Graduate School of Medical Sciences *July 2019 - June 2024*
Tri-Institutional Ph.D. Program in Computational Biology & Medicine (CBM)
Advised by Dr. Sohrab Shah

University of California, Los Angeles *Sept 2015 - June 2019*
B.S. in Bioengineering, technical breadth in Computer Science

RESEARCH EXPERIENCE

Barbara Engelhardt Lab, Gladstone Institutes *Jan 2025 - present*
Bioinformatics Postdoctoral Fellow

- Deep learning models for live-cell imaging and genomic data.

Sohrab Shah Lab, Memorial Sloan Kettering Cancer Center *Jan 2020 - Jan 2025*
PhD Student (Jan 2020 - July 2024), Postdoctoral Researcher (July 2024 - Jan 2025)

- Developed hierarchical Bayesian model to infer clone cell cycle distributions and replication timing profiles from unsorted single-cell whole genome sequencing (scWGS) data of genomically unstable cancers.
- Developed hierarchical Bayesian model to infer evolutionary timing of whole genome doubling events in ovarian cancer using scWGS.
- Graph attention autoencoder for analyzing single-cell resolution spatial transcriptomic, proteomic, and immunofluorescence data of the tumor microenvironment.

Marcin Imielinski Lab, Weill Cornell *Sept 2019 - Dec 2019*
PhD Rotation Student

- Investigated multi-way chromatin contacts in cancer genomes with Pore-C (ONT collaboration).

Olivier Elemento Lab, Weill Cornell *July 2019 - Sept 2019*
PhD Rotation Student

- Mined cancer drug combination therapy clinical trial results to build a machine learning pipeline for predicting specific adverse events.

Aaron S. Meyer Lab, UCLA *Sept 2017 - July 2019*
Undergraduate Researcher

- Built ODE model for common γ -chain cytokines to infer immeasurable receptor-ligand reaction rates.
- Used tensor factorization to map how native and mutant cytokines preferentially activate specific immune cell populations.
- Built lineage tree hidden Markov model that used live-cell imaging recordings to quantify heterogeneity of resistance states that arose after combination cancer therapies.

PUBLICATIONS

A.C. Weiner, M.J. Williams, H. Shi, I. Vazquez-Garcia, S. Salehi, N. Rusk, S. Aparicio, S.P. Shah, A. McPherson, “Inferring replication timing and proliferation dynamics from single-cell DNA sequencing data”, *Nature Communications*. 2024; **15**: 8512. doi: <https://doi.org/10.1038/s41467-024-52544-7>.

A. McPherson, I. Vazquez-Garcia, M. Myers, ..., A.C. Weiner, ..., S.P. Shah, “Ongoing genome doubling promotes evolvability and immune dysregulation in ovarian cancer”, *Nature* (in review). bioRxiv doi: <https://doi.org/10.1101/2024.07.11.602772>.

M.J. Williams, M.U.J. Oliphant, V. Au, ..., A.C. Weiner, ..., S.P. Shah, J.S. Brugge, S. Aparicio, “Luminal breast epithelial cells of wildtype and BRCA mutation carriers harbor copy number alterations commonly associated with breast cancer”, *Nature Genetics*. 2024. doi: <https://doi.org/10.1038/s41588-024-01988-0>.

M. Kim, A. Gorelick, ..., A.C. Weiner, ..., S.P. Shah, E. Reznik, “Single cell mtDNA dynamics in tumors is driven by ongoing co-regulation of nuclear and mitochondrial genomes”, *Nature Genetics*. 2024; **56**: 889-899. doi: <https://doi.org/10.1038/s41588-024-01724-8>.

H. Shi, M.J. Williams, G. Satas, A.C. Weiner, A. McPherson, S.P. Shah, “Allele-specific transcriptional effects of subclonal copy number alterations enable genotype-phenotype mapping in cancer cells”, *Nature Communications*. 2024; **15**: 2482. doi: <https://doi.org/10.1038/s41467-024-46710-0>.

K.N. Dinh , I. Vazquez-Garcia , A. Chan , R. Malhotra , A.C. Weiner, A. McPherson, S. Tavaré, “CINner: modeling and simulation of chromosomal instability in cancer at single-cell resolution”. *PLOS Comp Biol* (in review). bioRxiv doi: <https://doi.org/10.1101/2024.04.03.587939>.

T. Funnell, C.H. O’Flanagan, M.J. Williams, ..., A.C. Weiner, ... S.P. Shah, S. Aparicio, “Single-cell genomic variation induced by mutational processes in cancer”, *Nature*. 2022; **612**: 106115. doi: <https://doi.org/10.1038/s41586-022-05249-0>.

A.M. Farhat*, A.C. Weiner*, C. Posner, Z.S. Kim, B. Orcutt-Jahns, S.M. Carlson, A.S. Meyer, “Modeling cell-specific dynamics and regulation of the common gamma chain cytokines”, *Cell Reports*. 2021; **35**: 109044. doi: <https://doi.org/10.1016/j.celrep.2021.109044>.

PRESENTATIONS, POSTERS, ETC.

A.C. Weiner, M.J. Williams, H. Shi, I. Vazquez-Garcia, S. Salehi, N. Rusk, S.P. Shah, A. McPherson “Single-cell DNA replication dynamics in genomically unstable cancers”, poster presentation at American Association of Cancer Research (AACR) Annual Meeting, San Diego, 2024.

A.C. Weiner, M.J. Williams, H. Shi, A. McPherson, S.P. Shah, “Probabilistic modeling of single-cell DNA replication dynamics in genomically unstable cancer cells”, poster presentation at Keystone Symposium for Single Cell biology: From Development to Cancer, Keystone (CO), 2023.

A.C. Weiner, M.J. Williams, H. Shi, A. McPherson, S.P. Shah, “Probabilistic modeling of single-cell DNA replication dynamics in genomically unstable cancer cells”, poster presentation at Weill Cornell’s du Vigneaud Research Symposium, New York, 2023.

A.C. Weiner, M.J. Williams, H. Shi, A. McPherson, S.P. Shah, “Probabilistic modeling of single-cell DNA replication dynamics in genomically unstable cancer cells”, poster presentation at American Association of Cancer Research (AACR) Annual Meeting, Orlando, 2023.

A.C. Weiner, M.J. Williams, H. Shi, A. McPherson, S.P. Shah, “Probabilistic modeling of single-cell DNA replication dynamics in genomically unstable cancer cells”, poster presentation at Mathematical and Computational Methods in Cancer and Biology hosted by Columbia University Irving Institute of Cancer Dynamics, New York, 2023.

A.C. Weiner, A. McPherson, S.P. Shah, “Single-cell replication timing and stress in genomically unstable cancers”, poster presentation at Rockefeller University Anderson Cancer Symposium, New York,

2022.

A.C. Weiner, A. McPherson, S.P. Shah, “Single-cell replication timing and stress in genomically unstable cancers”, poster presentation at Cold Spring Harbor Laboratory 86th Quantitative Biology Symposium: Genome Stability & Integrity, Cold Spring Harbor, 2022.

A.C. Weiner, A. McPherson, S.P. Shah, “Single-cell replication dynamics in genomically unstable cancers”, oral presentation at American Association of Cancer Research (AACR) Annual Meeting, New Orleans, 2022.

A.M. Farhat*, A. Lim*, N.K. Namiri*, S. Visagan*, A.C. Weiner*, A.S. Meyer, “Lineage tree hidden Markov model quantifies intratumor heterogeneity in cancer therapy”, poster & presentation at UCLA Bioengineering Symposium, Los Angeles, 2019.

A.C. Weiner, A.M. Farhat, A.S. Meyer, “Building a Reaction Model for Common γ -chain Cytokines”, poster at Biomedical Engineering Society Annual Meeting, Atlanta, 2018.

HONORS AND AWARDS

NIH F31 Predoctoral Fellowship <i>National Cancer Institute, F31-CA271673</i>	<i>2023 - 2024</i>
AACR Scholar-in-Training Award <i>Travel award for AACR Annual Meeting 2023</i>	<i>April 2023</i>
NIH T32 Training Award <i>Awarded by Tri-I CBM Program Leadership, T32-GM132083</i>	<i>2020 - 2022</i>
UCLA Bioengineering Symposium - Best Poster <i>Awarded by UCLA Bioengineering and Medicine</i>	<i>March 2019</i>
UCLA Internet Research Initiative Prize Winner <i>Awarded by UCLA Computer Science</i>	<i>2018 - 2019</i>
Stanley H. Black Memorial Scholarship <i>Awarded by UCLA Engineering and JFLA</i>	<i>2017 - 2019</i>
UCLA Deans Honor List (x5)	<i>2016 - 2018</i>

PROGRAMMING

Languages: Python, R
ML Frameworks: Pyro, PyTorch, scikit-learn, JAX, TensorFlow, TensorLy
UNIX Clusters: Slurm, LSF
Miscellaneous: Git, Snakemake, Docker, scanpy, AnnData, pandas, numpy, SciPy

EXTRA-CURRICULAR

Student Representative, CBM Directors Steering Committee	<i>2022 - 2023</i>
Admissions Committee, MSK Comp Bio Summer Program (CBSP)	<i>2021 - 2023</i>
Chair, CBM Annual Recruitment	<i>2021 - 2022</i>
Chair, CBM Research in Progress Series	<i>2020 - 2021</i>
Organizer, CBM Annual Retreat	<i>2020 - 2022</i>
Member, Tri-I Start-Up Venture Group	<i>2020 - 2022</i>
Member, Tri-I Science and Educational Policy Association	<i>2019 - 2021</i>

Member, New York Academy of Sciences (NYAS)

2019 - 2022

Mentor, UCLA Engineering (MentorSEAS)

2016 - 2017

STUDENT SUPERVISION

BS project on chromosomal instability (CIN) signatures in HGSOc patients

Summer 2023

BS project to improve scWGS copy number calling using variational inference

Summer 2021

AREAS OF EXPERTISE

Biology: cancer genomics, clonal evolution, DNA copy number, cell cycle, mutational signatures, tumor microenvironment, innate immunity, cytokine signaling

Statistics: Bayesian probabilistic graphical models, autoencoders, graph neural networks, ODE models, variational inference, tensor factorization, causality, interpretability, regression, trees and forests, clustering, dimensionality reduction

Data modalities: bulk and single-cell DNA-, RNA-, and ATAC-seq, ChIP-seq, chromatin conformation capture (Hi-C), spatial multi-panel immunofluorescence (mpIF), spatial transcriptomics (10X Visium, Visium HD, Xenium), circulating tumor DNA-seq (ctDNA), nanopore, flow cytometry, clinical annotation

Data sources: Human patients, mice, cell lines, patient-derived xenografts, public repositories (i.e. TCGA, ENCODE)

THESIS COMMITTEE

Dr. Sohrab Shah (sponsor)

Dr. Christina Leslie (chair)

Dr. Wesley Tansey

Dr. John Maciejowski

Dr. Andrew McPherson (non-voting)

Dr. Elli Papaemmanuil (non-voting)

RELEVANT COURSEWORK

Foundations of Graphical Models

Dr. David Blei, Columbia

Applied Machine Learning

Dr. Nathan Kallus, Cornell Tech

Functional Interpretation of High-Throughput Data

Dr. Jan Krumsiek, Weill Cornell

Data Structures and Algorithms in Computational Biology

Dr. Iman Hajirasouliha, Weill Cornell

Algorithms in Bioinformatics

Dr. Eleazar Eskin, UCLA

Computational Genetics

Dr. Eran Halperin, UCLA

Machine Learning and Data-Driven Modeling in Bioengineering

Dr. Aaron Meyer, UCLA

Systems Biomodeling

Dr. Joe DiStefano III, UCLA