ADAM WEINER

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EDUCATION

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

University of California, Los Angeles *Sept 2015 - June 2019*
B.S. in Bioengineering, technical breadth in Computer Science
GPA: 3.67 overall / 3.86 junior-senior science

RESEARCH EXPERIENCE

Dr. Sohrab Shah, Memorial Sloan Kettering Cancer Center *Jan 2020 - Present*

- Developed computational methods for telomere length estimation and cell cycle classification in single-cell whole genome sequencing (scWGS) data.

- Built probabilistic graphical model for inferring single-cell replication timing profiles from scWGS data while robust to subclonal and cell-specific copy number aberrations.

- Studying connections between replication timing, replication stress, clonal fitness, and genomic instability.

Dr. Marcin Imielinski, Weill Cornell & New York Genome Center *Sept 2019 - Dec 2019*

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

Dr. Olivier Elemento, Weill Cornell *July 2019 - Sept 2019*

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

Dr. Aaron S. Meyer, UCLA *Sept 2017 - July 2019*

- Built model for common γ-chain cytokines to infer immeasurable receptor-ligand reaction rates and used tensor factorization to map how native and mutant cytokines preferentially activate specific immune cell populations.

- Built lineage tree hidden Markov model that used single-cell phenotypic measurements to quantify heterogeneity of resistance states that arose after combination cancer therapies.

Drs. Peter Reiher & Leonard Kleinrock, UCLA *Sept 2018 - May 2019*

- Used hemagglutinin sequencing data to predict flu vaccine efficacy against circulating strains. Awarded $7,500 and lab space by UCLA Internet Research Initiative (IRI).

Drs. Thomas Vallim & Elizabeth Tarling, UCLA *Summer 2017*

- Developed ChIP-seq analysis pipeline to quantify the dimerization patterns of Maf family transcription factors which play a role in bile acid and lipid metabolism disorders.

PUBLICATIONS

<u>A.C. Weiner</u>, M.J. Williams, H. Shi, S.P. Shah, A. McPherson "Modeling single cell DNA replication dynamics and aneuploidy in genomically unstable cancers", *bioRxiv.* 2023. doi: https://doi.org/10.1101/2023.04.10.536250.

H. Shi, M.J. Williams, G. Satas, <u>A.C. Weiner</u>, A. McPherson, S.P. Shah "Exploiting allele-specific transcriptional effects of subclonal copy number alterations for genotype-phenotype mapping in cancer cell populations", *bioRxiv*. 2023. doi: https://doi.org/10.1101/2023.01.10.523464.

T. Funnell, C.H. OFlanagan, M.J. Williams, ... <u>A.C. Weiner</u>, ... 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*, <u>A.C. Weiner</u>*, 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.

<u>A.C. Weiner</u>, 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.

<u>A.C. Weiner</u>, 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.

<u>A.C. Weiner</u>, 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.

<u>A.C. Weiner</u>, A. McPherson, S.P. Shah, "Single-cell replication dynamics in genomically unstable cancers", oral presentation at American Association of Cancer Research (AACR) Annual Meeeting, New Orleans, 2022.

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

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

<u>A.C. Weiner</u>, J.C. Link, E. Tarling, T.A. Vallim, "Integrating chromatin immunoprecipitation sequencing data to identify patterns of the small Maf family of transcription factors in HepG2 cells", poster at BIG Summer Poster Day, Los Angeles, 2017.

HONORS AND AWARDS

NIH F31 Predoctoral Fellowship   *March 2023 - present*
National Cancer Institute, F31-CA271673

AACR Scholar-in-Training Award   *April 2023*
Travel award for AACR Annual Meeting 2023

NIH T32 Training Award   *July 2020 - June 2022*
Awarded by Tri-I CBM Program Leadership, T32-GM132083

UCLA Bioengineering Symposium - Best Poster   *March 2019*
Awarded by UCLA Bioengineering and Medicine

UCLA Internet Research Initiative Prize Winner   *2018 - 2019*
Awarded by UCLA Computer Science

Stanley H. Black Memorial Scholarship *2017 - 2019*
Awarded by UCLA Engineering and JFLA

UCLA Deans Honor List (x5) *2016 - 2018*

EXTRA-CIRRUCULAR

Student Representative, CBM Directors Steering Committee *2022 - present*

Admissions Committee, MSK Comp Bio Summer Program (CBSP) *2021 - 2023*

Chair, CBM Annual Recruitment *2021 - 2022*

Chair, CBM Research in Progress Series *2020 - 2021*

Organizer, CBM Annual Retreat *2020 - 2022*

Member, Tri-I Science and Educational Policy Association (SEPA) *2019 - 2021*

Member, New York Academy of Sciences (NYAS) *2019 - 2022*

Mentor, UCLA Engineering (MentorSEAS) *2016 - 2017*

RELEVANT COURSEWORK

Foundations of Graphical Models
Dr. David Blei, Columbia (not for credit)

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

Biotransport and Bioreaction Processes
Dr. Daniel Kamei, UCLA