

# ADAM WEINER

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## EDUCATION

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

**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

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**Dr. Sohrab Shah - Memorial Sloan Kettering Computational Oncology** *Jan 2020 - Present*

- Building telomere length estimation tool for scDNA-seq data.
- Investigating replication timing in scDNA

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

- Investigated multi-way chromatin contacts in cancer genomes with Pore-C technology.

**Dr. Olivier Elemento - Weill Cornell Computational Biomedicine** *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 Bioengineering** *Sept 2017 - July 2019*

- Built an ODE model for common  $\gamma$ -chain cytokines and then used tensor factorization to map how native and mutant cytokines preferentially activate specific immune cell populations.
- Built a lineage tree hidden Markov model that uses phenotypic measurements to evaluate tumor heterogeneity within the context of single-cell response to cancer drug combinations and acquired resistance to therapy.

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

- Awarded \$7,500 and lab space by UCLA Computer Sciences Internet Research Initiative (IRI).
- Used hemagglutinin sequencing data to predict flu vaccine efficacy by finding the protein structure similarity between vaccine targets and circulating flu strains.

**Drs. Thomas Vallim & Elizabeth Tarling - UCLA Biological Chemistry** *Summer 2017*

- Developed analysis pipeline that used chromatin immunoprecipitation sequencing (ChIP-seq) data to quantify the dimerization patterns of transcription factors.
- Investigated transcription factors that play role in bile acid and lipid metabolic disorders.

## PUBLICATIONS, PRESENTATIONS, POSTERS, ETC.

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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”, bioRxiv, March 2020, doi: <https://doi.org/10.1101/778894>.

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, March 2019.

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

A.C. Weiner, 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, August 2017.

## HONORS AND AWARDS

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**UCLA Bioengineering Symposium - Best Poster in Devices and Diagnostics**     *March 2019*  
*Awarded by UCLA Bioengineering and Medicine Faculty*

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

**Stanley H. Black Memorial Scholarship (x2)**     *2017 - 2019*  
*Awarded by UCLA Engineering and Jewish Foundation of LA*

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

## EXTRA-CIRRICULAR

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Organizer, Tri-I CBM Annual Retreat     *2020*

Phonebank Volunteer, Florida Democratic Party     *2020*

Summer Outreach Coordinator, Hillel UCLA     *Summers 2016 - 2018*

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

## RELEVANT COURSEWORK

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### **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