William **Connell**

PHARMACEUTICAL SCIENCES · GRADUATE RESEARCHER

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Summary

I am a graduate student at UCSF applying my computational science expertise to understand, at a systems level, how gene network changes impact phenotype. To advance the state of precision medicine and answer questions regarding individual disease heterogeneity, I use statistical analyses and machine learning methods to bridge molecular genomics and chemoinformatics.

Education

University of California, San Francisco — *San Francisco, CA*

PHD IN PHARMACEUTICAL SCIENCES AND PHARMACOGENOMICS — *2018 - Expected 2022*

- Advisor: Dr. Michael Keiser
- Committee Members: Dr. Hani Goodarzi, Dr. Luke Gilbert

University of California, Los Angeles — *Los Angeles, CA*

BS IN MICROBIOLOGY, IMMUNOLOGY AND MOLECULAR GENETICS — *2012 - 2016*

Experience

Department of Pharmaceutical Chemistry, UCSF — *San Francisco, CA*

GRADUATE RESEARCHER, DR. MICHAEL KEISER, PHD — *March 2019 - Present*

- Developing machine learning methods for precision medicine and phenotype prediction: disease risk modeling, therapeutic response
- Applying language modeling to elucidate context-specific transcriptomic regulatory networks for transfer learning
- Developed a predictive model of individual tumor sensitivity to small molecules for precision oncology (+5.5% SOTA)
- Discovered a genomic biomarker for stratification of (non-)responders to mAb ustekinumab in psoriasis patients (2.5% global population)

AI Research Group, Invitae — *San Francisco, CA (Remote)*

COMPUTATIONAL BIOLOGY RESEARCH INTERN — *May 2021 - August 2021*

- Participated in the CAGI6 Polygenic Risk Score modeling competition
- Developed a hierarchical Bayesian model based on integrating population LD structure and functional genomic annotations
- Posterior SNP effect size prediction required parameter optimization through stochastic variational inference (SVI)
- Dataset scale required significant software and pipeline engineering

UCSF Innovation Ventures — *San Francisco, CA*

CATALYST AWARDS INTERNSHIP PROGRAM — *September 2018 - September 2019*

- Evaluated the potential scientific translation of academic discoveries alongside corporate strategy professionals
- Lead a team of 4 to develop a diagnostic discovery Target Product Profile (TPP) for a gene expression biomarker panel
- Collaborated with primary scientists to define minimal/optimal metrics of laboratory and clinical success
- Evaluated feasability of product development in consideration of commercialization routes and competitive landscape
- Compiled financial projections and market value estimations under consideration of IP challenges

Datacamp — *Remote*

SOFTWARE DEVELOPER & PROJECT DESIGNER — *November 2019 - January 2019*

- Created, designed, and implemented a data science project for a leading online education platform
- Developed software remotely for a data analysis course in R: *Data Science for Social Good: Crime Study*
- Engaged with >1000 learners resulting in an overall course rating of 4.7/5

Molecular Genetics Department, UCLA — *Los Angeles, CA*

RESEARCH ASSOCIATE, DR. DONALD KOHN, MD — *March 2017 - March 2018*

- Researched gene therapies for monogenic disorders
- Engineered lentiviral vectors for *ex vivo* transfer of anti-sickling β-globin gene for Sickle-cell disease

Publications

JOURNAL ARTICLES

Genome-Wide Association Study of Ustekinumab Response in Psoriasis

William T. Connell, Julie Hong, Wilson Liao

Frontiers in Immunology 12 (Jan. 2022). 2022. DOI: 10.3389/fimmu.2021.815121

Nurturing diversity and inclusion in AI in Biomedicine through a virtual summer program for high school students

Tomiko Oskotsky, Ruchika Bajaj, Jillian Burchard, Taylor Cavazos, Ina Chen, Will Connell, Stephanie Eaneff, Tianna Grant, Ishan Kanungo, Karla Lindquist, Douglas Myers-Turnbull, Zun Zar Chi Naing, Alice Tang, Bianca Vora, Jon Wang, Isha Karim, Claire Swadling, Janice Yang, AI4ALL Student Cohort, Marina Sirota

PLOS Computational Biology (Jan. 2022). 2022. DOI: `/10.1371/journal.pcbi.1009719`

Predicting Cellular Drug Sensitivity using Conditional Modulation of Gene Expression

William T Connell, Michael J Keiser

Learning Meaningful Representations of Life Workshop, NeurIPS 2020 (Dec. 2020). 2020. DOI: `10.1101/2021.03.15.435529`

Helical antimicrobial peptides assemble into protofibril scaffolds that present ordered dsDNA to TLR9

Ernest Y Lee, Changsheng Zhang, Jeremy Di Domizio, Fan Jin, Will Connell, Mandy Hung, Nicolas Malkoff, Veronica Veksler, Michel Gilliet, Pengyu Ren, Gerard C L Wong

Nat. Commun. 10.1 (Mar. 2019) p. 1012. 2019. DOI: `10.1038/s41467-019-08868-w`

A Single-Cell Transcriptomic Atlas of Human Neocortical Development during Mid-gestation

Damon Polioudakis, Luis Torre-Ubieta, Justin Langerman, Andrew G Elkins, Xu Shi, Jason L Stein, Celine K Vuong, Susanne Nichterwitz, Melinda Gevorgian, Carli K Opland, Daning Lu, William Connell, Elizabeth K Ruzzo, Jennifer K Lowe, Tarik Hadzic, Flora I Hinz, Shan Sabri, William E Lowry, Mark B Gerstein, Kathrin Plath, Daniel H Geschwind

Neuron 103.5 (Sept. 2019) 785–801.e8. 2019. DOI: `10.1016/j.neuron.2019.06.011`

PRESENTATIONS

Quantifying the Similarity of Transcriptomic States in Cancer

William Connell, Michael J Keiser

CZI Neurodegeneration Challenge Network 2020 Annual Meeting. Poster. 2020. Virtual.

Target Deconvolution Across Phenotypic Space

William Connell, Garrett Gaskins, Michael J Keiser

Quantitative Biology Consortium Retreat 2019. Poster. 2019. Santa Cruz, CA.

Target Deconvolution Across Phenotypic Space

William Connell, Garrett Gaskins, Michael J Keiser

Northern California Computational Biology Symposium. Oral. 2019. Davis, CA.

Program Committees

2020- **Outreach**, PSPG Diveristy, Equity and Inclusion Committee   *San Francisco, CA*

Skills

programming	python [numpy, pandas, pytorch, scikit-learn, pyro], R, SQL, bash, git, plink, snakemake
OS contributions	pytorch-metric-learning, scikit-learn sprint (WiMLDS)
featured blog posts	Blockchain: Tumber Network Analysis; Kanye West: Lyric Analysis