

William Connell

RESEARCH SCIENTIST, MACHINE LEARNING · PH.D.

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Summary

As a consultant, I advise startups and investors on ML-driven drug discovery and platform strategy. At Vevo Therapeutics, I built the ML foundation for an scRNA-seq drug discovery platform, developing evaluation frameworks and scaling models, infrastructure, and teams from seed stage. My academic research in biological sequence-based representation learning guided our strategies for drug response prediction and interpretation. I thrive in collaborative environments and enjoy [communicating industry advancements](#).

Education

University of California, San Francisco

PHD IN PHARMACEUTICAL SCIENCES AND PHARMACOGENOMICS

San Francisco, CA

2018 - 2022

University of California, Los Angeles

BS IN MICROBIOLOGY, IMMUNOLOGY AND MOLECULAR GENETICS

Los Angeles, CA

2012 - 2016

Experience

BioxML, LLC

MACHINE LEARNING CONSULTANT

Berkeley, CA

Jun 2024 - Present

- Advised platform drug discovery startups on ML strategy, model selection, and infrastructure for high-throughput screening
- Developed experimental frameworks for benchmarking protein design models and virtual chemical screening approaches
- IGSC member; red-teamed oligomer sequence screening tools using protein design models to identify biosecurity risks
- Collaborated with venture capital firms to analyze AI/biotech market trends, distilling technical insights for stakeholder engagement

Vevo Therapeutics

RESEARCH SCIENTIST, MACHINE LEARNING

San Francisco, CA

Sep 2022 - Jan 2024

- Developed benchmarking suite for scRNA-seq foundation models (target retrieval, sensitivity prediction, biological recapitulation)
- Scaled models and data, expanding the pretraining corpus >50x and improving chemical retrieval top-k accuracy by 10x
- Led a proposal accepted into the AWS Gen AI Accelerator program (<1%), securing \$300k compute credits and industry recognition
- Managed contractors, recruited three FTEs, and mentored an intern, growing the ML team by 50%

Department of Pharmaceutical Chemistry, UCSF

GRADUATE RESEARCHER ADVISED BY MICHAEL KEISER

San Francisco, CA

Mar 2019 - Dec 2022

- Pioneered the application of self-supervised learning to scRNA-seq, advancing the transfer learning framework in the field [\[code\]](#)
- Developed an *in silico* chemical probing model (+10% baseline), discovering new indication responses and ferroptosis drug targets [\[code\]](#)
- Identified a genomic biomarker to stratify mAb ustekinumab response in psoriasis, advancing personalized treatment decisions

AI Research Group, Invitae

COMPUTATIONAL BIOLOGY RESEARCH INTERN

Remote

May 2021 - Aug 2021

- Assisted in developing a hierarchical Bayesian model that improved polygenic risk scoring accuracy by 5%
- Engineered efficient software pipelines for managing and analyzing large-scale genomic datasets using tools like Python, R, and AWS

Selected Publications

Learning chemical sensitivity reveals mechanisms of cellular response

William Connell, Kristle Garcia, Hani Goodarzi, Michael J Keiser; *Commun. Biol.* 7.1 (Sept. 2024) p. 1149. Springer, 2024 [DOI](#)

Genome-wide association study of ustekinumab response in psoriasis

William Connell, Julie Hong, Wilson Liao; *Frontiers in Immunology* 12 (Jan. 2022). 2022 [DOI](#)

A single-cell gene expression language model

William Connell, Umair Khan, Michael J. Keiser; *LMRL Workshop, NeurIPS* (Oct. 2022). 2022 [DOI](#)

Extracurricular Activity

Communication

[Behind BioML](#): thought leadership on AI in biology with 10k+ impressions, 175+ subscribers

Scientific community

[3rd place Bio x ML Hackathon](#), Evolved 2024; *Foundation Models for Bio*, SynBioBeta 2024 (panel moderator); *MLGenX Workshop*, ICLR 2024 (reviewer); *DNA Diffusion*, OpenBioML (contributing member)

Skills

programming

python [numpy, pandas, pytorch, scikit-learn, huggingface, wandb, lightning, pytorch-geometric, rdkit, hydra], AWS, R, bash, git, plink, snakemake

OS contributions

[OpenPlasmid](#), [enformer-finetune](#), [pytorch-metric-learning](#), [scikit-learn sprint \(WiMLDS\)](#)

model repos

[ChemProbe](#), [Exceiver](#)