Nelson Johansen
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EDUCATION

University of California, Davis *2021*
Ph.D. in Computer Science
Advisor: Gerald Quon

Research Focus
- Unsupervised deep learning-based approaches to integrate biological data from multiple modalities to relate molecular events with disease.
- Deep generative models to integrate imaging, DNA sequence and electrophysiological measurements to relate neuronal modalities.
- scAlign: novel neural network utilizing domain adaptation to integrate high dimensional data across laboratories, conditions and species.

University of California, Davis 2015
B.Sc. in Computer Science

PUBLICATIONS

Johansen, N. & Quon, G. "scAlign: a tool for alignment, integration and rare cell identification from scRNA-seq data." Genome Biol. (2019) 2019

Hodge, Rebecca D., et al. "Conserved cell types with divergent features in human versus mouse cortex." Nature (2019): 1-8.

TEACHING

TA for BST 227: Machine Learning in Genomics 2019
[Introduction to TensorFlow]

INVITED TALKS (Selected)

Deep learning-based deconvolution of single cell resolution assays and spatial transcriptomes. 2020
CZI Seed Networks Virtual Meeting

Deconvolution in the single cell genomics era
Human Cell Atlas

Characterizing cell type-specific responses to stimuli using single cell RNA sequencing. 2019
RECOMB/ISCB Conference on Regulatory and Systems Genomics

Combining deep single cell atlases and case-control bulk RNA studies to identify cell type-specific signatures of disease using deep learning.
Human Genomics Symposium, UC Davis Med.

Deconvolution in the single cell genomics era
Beyond the Cell Atlas: Theory, Models, and Computation

	Characterizing cell type-specific responses to stimuli using single cell RNA sequencing. **NASA's Ames Research Center** **Lawrence Livermore National Laboratory**	2018
	Leveraging big data genomics for the inference of drug targets. **11th Annual Spotlight on Junior Investigators Cancer Research Symposium**, UC Davis Comprehensive Cancer Center.	2017
	The role of big data in genomics and medicine: predicting combination therapies to target genetic vulnerabilities in cancer. **38th Annual Institute on Research and Statistics** CSU Sacramento.	
PANEL MEMBER	Deep domain adaption networks identify and explain cell state changes after stimulus. **Artificial Intelligence & Machine Learning Symposium** UC Davis Medical Center	2018
POSTER PRESENTATIONS (Selected)	Deep learning-based deconvolution of multi-modal assays and spatial transcriptomes. **MLCB: Machine Learning for Computational Biology**	2020
	A deep deconvolution approach for combining the high-resolution of single cell atlases with the scale of bulk genomics. **MLCB: Machine Learning for Computational Biology**	2019
	Unsupervised deep neural networks harmonize multiple data sources and Explain Inherent Biases. **ML4H: Machine Learning for Health at NIPS 2018**	2018
	Characterizing cell type-specific responses to stimuli using single cell RNA sequencing. **Beyond the Cell Atlas: Frontiers in Cell Biology.** **Chan Zuckerberg Initiative**	
	Network based strategy for predicting combinations of compounds. **22nd Annual Cancer Research Symposium, UCD Cancer Center** **3rd UC Davis Human Genomics Symposium**	2017
CONFERENCE REVIEWER	MLCB ML4H: NeurIPS	2020 2019-2020
HONORS AND ACTIVITIES	Top abstract: Inaugural AI & ML Symposium, UC Davis Medical Center UC Davis Computer Science Tutor	