

Nelson Johansen

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| EDUCATION | University of California, Davis <i>Ph.D.</i> in Computer Science Advisor: Gerald Quon | 2020 |
| | Research Focus Development of unsupervised deep learning-based approaches to integrate biological data from multiple modalities (imaging, DNA sequence, electrophysiology) in order to bridge the gap between molecular biology events and human disease. Current research focuses on deep generative models to integrate imaging, DNA sequence and electrophysiological measurements, in order to better understand how changes in molecular phenotypes, reflected in high dimensional transcriptomic data, might fundamentally alter neuronal firing patterns. Previous works include the development of a novel neural network architecture and associated loss function, based on associative domain adaptation, to integrate high dimensional data collected across laboratories, conditions and species. | |
| | University of California, Davis <i>B.Sc.</i> in Computer Science | 2015 |
| PUBLICATIONS | Johansen, Nelson, and Gerald Quon. "scAlign: A Tool for Alignment, Integration, and Rare Cell Identification from ScRNA-Seq Data." <i>Genome Biology</i> , vol. 20, no. 1, Aug. 2019, p. 166, doi:10.1186/s13059-019-1766-4. | 2019 |
| | Hodge, Rebecca D., et al. "Conserved cell types with divergent features in human versus mouse cortex." <i>Nature</i> (2019): 1-8. | 2019 |
| INVITED TALKS | Characterizing cell type-specific responses to stimuli using single cell RNA sequencing. 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. Hierarchical and deep generative neural networks enable the deconvolution and purification of contaminated scRNA-seq data from multimodal assays. NCCB Symposium, UC Davis | 2019 |

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| | Characterizing cell type-specific responses to stimuli using single acell RNA sequencing. Lawrence Livermore National Laboratory | 2018 |
| | Characterizing cell type-specific responses to stimuli using single cell RNA sequencing. NASA's Ames Research Center | |
| | 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 | A deep deconvolution approach for combining the high-resolution of single cell atlases with the scale of bulk genomics. Nelson Johansen , Gerald Quon MLCB: Machine Learning for Computational Biology | 2019 |
| | Unsupervised Deep Neural Networks Harmonize Multiple Data Sources and Explain Inherent Biases. Nelson Johansen , Gerald Quon ML4H: Machine Learning for Health at NIPS 2018 | 2018 |
| | Characterizing cell type-specific responses to stimuli using single cell RNA sequencing. Nelson Johansen , Gerald Quon Beyond the Cell Atlas: Frontiers in Cell Biology Driven by New Technology. Chan Zuckerberg Initiative | |
| | Predicting combination therapies to target genetic vulnerabilities in cancer. Nelson Johansen , Gerald Quon UC Davis DEB Retreat. | 2017 |

Network based strategy for predicting combinations of compounds.
Nelson Johansen, Gerald Quon
22nd Annual Cancer Research Symposium, UC Davis Cancer Center &
3rd UC Davis Human Genomics Symposium

HONORS AND
ACTIVITIES
Top abstract: Inaugural AI & ML Symposium, UC Davis Medical Center
UC Davis Dean's Honor List
UC Davis Computer Science Tutor

TEACHING
Introduction to TensorFlow
2019

GRADUATE
COURSEWORK
Graph Theory
Machine Learning
Artificial Intelligence
2017
2017
2015