

JESSICA CLAIRE

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Summary

A graduate student at the University of California, Irvine with a scientific background in computational biology and pharmaceutical science. Interested in computational approaches to pharmaceutical and therapeutics-based research, with expertise in computational multiomics, machine learning and drug design platforms.

Skills

- Programming Skills: R (Intermediate), Python (Basic), shell/bash scripting (Basic)
- OS platform: Linux, Window OS, Cluster distributed computing (HPC)
- NGS Data Processing: bulk RNA seq, ATAC-seq
- Database Experience: Gene Expression Omnibus (GEO), Sequence Read Archive (SRA), Single Cell Expression Atlas
- Sequencing Alignment: SRA toolkit, bedtools, bowtie2, STAR, picard tools, samtools
- Sequencing Quantification: macs2, featurecounts, Kallisto, TxImport, RNA-norm
- Differential Expression, Pathway Enrichment and Ontology Analysis: EdgeR, DEseq2, gprofiler2, HOMER, DAVID, Ingenuity Pathway Analysis (IPA)
- Multi-omic Data Integration: Paired Expression and Chromatin Accessibility (PECA), Multi-Omics Factor Analysis (MOFA)
- Network Biology: Transcription Factor-Target Gene Interaction network (Cytoscape, IPA), Centrality calculation (Cytohubba)
- Data Visualization: ChIPseeker(R), Cytoscape, Integrative Genomics Viewer (IGV), Adobe Illustrator
- Machine learning: Data curation, feature selection, model building and hyperparameter optimization
- Regression and classification models
- Neural network, Random Forest, XGBoost Models
- Python-sklearn, tensorflow, keras, pytorch

Experience

Data Science Intern, 01/2023 to Current

Covance – Baltimore, MD

- Development of machine learning models to predict the pharmacokinetic and quantum mechanical properties of molecules using Accelerating Therapeutics in Medicine Model Learning Pipeline (AMPL)
- Experience with generative molecular design model testing and validation

PhD Graduate, 09/2017 to Current

Cenergy – Freeport, NY

- Utilized machine learning analysis and multi-omic data integration to identify key regulatory network changes during stem cell reprogramming
- Gained expertise in transcriptional and epigenetic data processing and analysis methods
- Implemented network theory and centrality calculations to identify impediments to reprogramming efficiency
- Became proficient at using stem cell models for drug characterization and mechanistic understanding of the effects of pharmaceutical agents
- Communicated research results through conference presentations, departmental research presentations, and scientific publications
- Supported department faculty with administrative assistance, as well as curriculum and research support as a teaching assistant for the upper division course stem cell biology and regenerative medicine
- Served as mentor to high school and undergraduate students through Youth Research Summer Science Program, Women in STEM(WiSTEM) , Girls Engineering Change (GEC) Outreach Board Leader, R-ladies Irvine Chapter

Research Technician, 08/2016 to 06/2017

Children's Hospital Of Philadelphia – City, STATE

- Developed autoimmune disease models using CRISPR/Cas9 system
- Acquired computational skills with sequencing and genomic data

Education and Training

Ph.D.: Biological Chemistry, Computational Biology, 09/2023

University of California, Irvine - Irvine, CA

THESIS: Investigating the Mechanism of Cellular Reprogramming

Bachelor of Arts: Biology, 05/2016

Bryn Mawr College - Bryn Mawr, PA

Study Abroad Program: Chemistry With Medicine, 06/2015

King's College London - United Kingdom

Publications

1. *Jessica Claire, Trina Norden-Krichmar*, Network analysis across cellular reprogramming states, American Society of Human Genetics (ASHG) Conference, 2022.
2. *Richard C. Chang, Jessica S. Claire, Erika M. Joloya, Angela Kuo, Zhuorui Li, Bruce Blumberg*, Cannabidiol promotes adipogenesis of human and mouse mesenchymal stem cells via PPAR γ by inducing lipogenesis but not lipolysis, Biochemical Pharmacology, 2022.
3. *Jessica Claire, Trina Norden-Krichmar*, Investigating conservation of chromatin accessibility signatures during iPSC reprogramming across human and mouse ATAC-seq data, American Society of Human Genetics (ASHG) Conference, 2021.
4. *Jessica Claire, Trina Norden-Krichmar*, Meta-analysis of ATAC-seq data to explore chromatin accessibility during iPSC reprogramming, American Society of Human Genetics (ASHG) Conference, 2020.
5. *Jessica Claire, Gregory K Davis*, Patterns of torsolike and activated map kinase during oviparous development in the pea aphid, 18th Annual Undergraduate Research Symposium in the Chemical and Biological Sciences, 2015.

Awards

- National Science Foundation Graduate Research Fellowship Award September 2018-September 2022
- University of California Irvine Division of Teaching Excellence and Innovation Pedagogy Fellowship Summer Quarter 2022
- University of California Irvine Graduate Division Completion Fellowship Fall Quarter 2022
- National Science Foundation INTERN Supplemental Award January 2023-June 2023