Jessica Au

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EDUCATION

University of California, Davis, Davis, California, USA

- B.S. in Mathematics and Scientific Computation - Biology Emphasis Sep 2013 – Dec 2017
  - Minor: Quantitative Biology and Bioinformatics

RESEARCH EXPERIENCE

Stanford School of Medicine Stanford, California, USA

- Associate Data Wrangler, Department of Genetics Sep 2019- Present
  ENCODE Data Coordination Center, Main Principal Investigator: **J. Michael Cherry, Ph.D**
  - **Description:** The ENCODE Data Coordination Center (DCC) curates, uniformly processes, and validates the data generated and submitted by ENCODE Consortium members for release to the scientific community.
  - Reviewed complex, scientific submissions to the database for quality and relevancy
  - Extracted information from submissions in the required formats to fit ENCODEd data model
  - Actively participated in the development, code review, QA, and release cycle of ENCODEd code base
  - Involved in the process of preparing experimental data for uniform processing and running of various analysis pipelines
  - Presented and participated at various scientific meetings

UC Davis, School of Medicine, Davis, California, USA

- Student Researcher, Department of Pharmacology May 2016 – Present
  Theoretical Cardiology Lab, Main Principal Investigator: **Daisuke Sato, Ph.D**
  - **Description:** Investigation of therapies to improve preventative care for cardiovascular diseases through mathematical analysis and multi-scale modeling of the heart.
  - Engineered software-hardware integrated machines using Raspberry Pi & Arduino in Python
  - Studied various other mathematical models in C/C++ for better performance on lab computing cluster
  - Conducted source control and code review through Github with project collaborators and comfortable writing Bash scripts in Unix/Linux

Stanford School of Medicine Stanford, California, USA

- Life Science Research Technician, Department of Developmental Biology Apr 2018- Sep 2019
  Kingsley Lab, Main Principal Investigator: **David Kingsley, Ph.D**
  - **Description:** Applications using a combination of genetic and genomic approaches to identify the detailed molecular mechanisms that control evolutionary change in vertebrates
  - Responsible for the livelihood of stickleback fish to ensure survivability in order to identify the key chromosome regions, genes, and mutations that control evolutionary traits.
  - Assisted in laboratory procedures and use of molecular biology techniques such as DNA extraction & PCR in order to investigate genetic variation within different populations of four-spine stickleback, *Apeltes quadracus*.

University of California, Davis, Davis, California, USA

- Undergraduate Researcher, Department of Microbiology & Molecular Genetics Jan 2017 – Dec 2017
  Topological Molecular Biology Lab, Main Principal Investigator(s): **Javier Arsuaga, Ph.D. Mariel Vazquez, Ph.D**
  - **Description**: Applications of knot theory, statistics, & low-dimensional topology to structural biology to infer the 3D organization of the human genome
  - Debugged and refractored group software to improve efficiency and readability in C/C++ in the form of simple test cases
  - Simulated and conducted statistical data analysis using Knotplot, Python, and R scripts in order to investigate how confinement affected low-dimensional topology

University of California, Davis Davis, California, USA

- Student Assistant, Department of Environmental Science and Policy Oct 2016- Dec 2017
  Flour Beetle Lab, Main Principal Investigator: **Alan Hastings, Ph.D**
  - **Description**: Collaborative scientific research group operating between University of California in Davis, CA and the University of Colorado in Boulder, CO
  - Coordinated daily objectives with 10+ team members and completed experimental protocols to answer biological questions concerning the spatial population dynamics of flour beetle species, *T. casenaum, T. confusum, & T. madens*
  - Administrator of the team's task management platform to ensure efficient communication and workflow
  - Organized and recorded relevant quantitative data for analysis and validation

RESEARCH PROJECTS

- **RyR cluster heterogeneity and Ca^{2+} spark formation** May 2017 – Present
  - Association: *Theoretical Cardiology Lab*
  - Collaborators: **Daisuke Sato, Ph.D, Leighton T. Izu, Ph.D, Donald M. Bers, Ph.D, Alexsey V. Zima, Ph.D, Roman Nikolaienko, Ph.D & Elisa Bovo, Ph.D**
  - *Description:* Investigating intracellular Ca^{2+} dynamics. We modeled the Ca^{2+} Induced Ca^{2+} Release (CICR) process within cardiac myocytes using a stochastic fire-diffuse-fire model of calcium release units (CRUs), as well as, random walks to describe Ca^{2+} diffusion. Using our model, we were able to illustrate the structural & spatial implications of RyR size heterogeneity on Ca^{2+} spark formation and termination.
  - Implementation of stochastic processes and mathematical modeling of ventricular cardiac myocyte in C/C++
  - Structured programming in C/C++ to simplify algorithm for readability and reusability
  - Parallel programming in C/C++ to improve efficiency while dealing with large amounts of data points on lab cluster (SLURM).
  - Data analysis, visualization in Matlab/GNU Octave to quantify results and compare to proven experimental results

- **Association Mapping of 4-spine Stickleback** May 2019 – Aug 2019
  - Association: *Kingsley Lab*
  - Collaborators: **David Kingsley, Ph.D & Julia Wucherpfennig**
  - *Description:* Investigation regarding whether the genotypic HoxDb cluster contributed to phenotypic spine number of the four-spine stickleback, *Apeltes quadracus*.
  - Use of molecular biology techniques and procedures such as DNA extractions, & PCR to amplify our regions of interest, i.e microsatellites, for association mapping
  - Analyze microsatellite data and use of various genomic software such as Geneious Prime and stickleback genome browser in order to make inferences about these microsatellites

- **Synchronization of Mechanical Fireflies** May 2017 – Oct 2017
  - Association: *Theoretical Cardiology Lab*
  - Collaborators: **Daisuke Sato, Ph.D & Zana Coulibaly, Ph.D**
  - *Description:* As a team of undergraduates, we engineered mechanical fireflies using the Raspberry Pi 3 in order to mimic the synchronization and entrainment phenomena of live fireflies
  - Modeling of the nonlinear, Fitzhugh-Nagumo system to demonstrate coupling of multiple oscillators in Matlab
  - Integration of Software-Hardware in Python

- **Cardiac Arrhythmias in relation to Nonlinear Dynamics** May 2016 – Apr 2017
  - Association: *Theoretical Cardiology Lab*
  - Collaborator(s): **Daisuke Sato, Ph.D**
  - *Description:* Simulated a mathematical model of a rabbit ventricular myocyte. Explored the effects of changes in ion channel conductances and investigated how these changes corresponded to the slope of a 0D simulation in relation to the phenomena of spiral wave break-up and reentry in 2D tissue.
  - Simulation of 2D tissue scripted in C/C++ with 0D analysis done in Matlab/GNU Octave

- **The Effects of Confinement on Topological Transitions for Lower Crossing Topologies through Local Reconnection Moves** Jan 2017 – Dec 2017
  - Association: *DNA Topology Lab*
  - Collaborator(s): **Mariel Vazquez, Ph.D & Robert Stolz**
  - *Description:* Structure implies functionality. With emerging techniques such as chromatin conformation capture assays, we are able to make inferences regarding the structure of DNA. Further, the possibility of local knotting increases as a chain increases in length. By using the BFACF algorithm, we investigate how changes in different levels of confinement affect the transition probabilities of lower crossing topological knots through local reconnection moves.
  - Investigated how changes in certain parameters affected inherent properties of self-avoiding polygons in 3D space
  - Use of Python for string processing and subsequent knot type identification
  - Use of R for statistical analysis and data management for visualizing transition probabilities within a Markov Chain

- **Conducting DNA Sequence Analysis using Integer Linear Programming** December 2017
  - Association: *Special Topics Computer Science Course*
  - Utilized integer linear programming (ILP) in DNA sequence analysis, in comparison to dynamic programming methods. Used longest common subsequence (LCS) as a criteria for similarity between 2 or more DNA sequences.
  - ILP formulations generated using Python, solved using Gurobi Optimizer & dynamic programming comparison in Perl

- **Investigation of Differentially Expressed Genes & Clustering Methods** Sept 2017 - Dec 2017
  - Association: *Theory and Practice of Bioinformatics Course*
  - Use of Bioconductor Package in R
  - Executed complete RNA-seq analysis pipeline [Tophat, CuffLinks, CuffMerge, CuffDiff] on Illumina BodyMap 2.0 adrenal/brain tissue datasets.
  - Statistical analysis to find differentially expressed genes in R
  - Utilized clustering methods such as GENIE3 (Random Forests algorithm) on the regulatory network of *E. coli*

PUBLICATIONS

[1] **Jessica N. Au**, Roman Nikolaienko, Elisa Bovo, Leighton T. Izu, Donald M. Bers, Alexsey V. Zima, Daisuke Sato ”Ryanodine receptor density is critical for calcium spark formation in cardiac myocytes”
Nov 2020 *Submitted for publication*

ACADEMIC PRESENTATIONS

[1] ”Cardiac Arrhythmias and its relations to Nonlinear Dynamics” at *UC Davis: 28th Annual Undergraduate Research, Scholarship & Creative Activities Conference*, Davis, California, USA, Apr 2017.

[2] ”Topological Transitions for Lower Crossing Topologies through Local Reconnection Moves” at *BaMBA: Biology and Mathematics in the Bay Area*, San Francisco, California, USA, Nov 2017.

[3] ”Modeling Calcium Dynamics in the Dyadic Space using Random Walks” at 62^{nd} *Annual Biophysical Society Conference*, San Francisco, California, USA, Feb 2018.

[4] ”Delving into chromatin on the ENCODE portal” at *American Society of Human Genetics*, Houston, Texas, USA, Oct 2019.

[5] ”Dive into the ENCODE portal- Navigation with Epigenetics and Gene Regulation” at *ENCODE Consortium Meeting*, Asilomar, California, USA, Dec 2019.

[6] ”Query Building and REST-API” at *ENCODE Consortium Meeting*, Asilomar, California, USA, Dec 2019.

[7] ”Dive into Epigenetics and Gene Regulation- Navigation using the ENCODE portal” at *European Society of Human Genetics*, Berlin, Germany, Jun 2020.

[8] ”ENCODE Portal Content Overview” at *American Society of Human Genetics*, USA, Oct 2020.

AWARDS & SCHOLARSHIPS

- Gail and Ruth Scholarship, University of California, Davis 2013 – 2014
  Awarded to undergraduates pursuing careers in the College of Agriculture and Environmental Science.
- Research Scholar Certificate, University of California, Davis Apr 2017
  For outstanding academic achievement in the presentation of scholarly research at the 28th annual Undergraduate Research, Scholarship, & Creative Activities Conference.

SKILLS

General

- Detailed oriented work efficiency
- Ability to adapt to new, developing environments
- Able to work collaboratively as a team member, as well as independently without supervision
- Apt analytical skills along with ability to synthesize practical decisions

Software/Tools

Unix/Linux, Microsoft Office, LaTeX, Adobe Photoshop, Gurobi Optimizer, KnotPlot, Github

Programming & Scripting Languages

C/C++, Matlab/ GNU Octave, R, Bash, Python, JavaScript, HTML/CSS, Ruby on Rails

Molecular Biology Techniques

PCR, DNA extractions

COURSEWORK

Mathematics

Linear Algebra, Differential Equations, Advanced Calculus, Number Theory, Ordinary Differential Equations, Mathematical Biology, Real Analysis, Numerical Analysis, Modern Algebra, Mathematical Statistics and Probability Theory

Biology

Introduction to Biology, Structure and Function of Biomolecules, Gene and Gene Expression, Functional Genomics

Computer Science

Programming and Problem Solving, Software Development and Object-Oriented Programming, Data Abstractions and Structures, Structural Computational Bioinformatics, Theory and Practice of Bioinformatics, Integer Linear Programming for Computational Biologists

INTERESTS

Owner of a treat tracking, forever curious dog, reading current events & scientific articles, sketching & watercolor painting, dadminton, powerlifting, and gardening

RELATED

Github: https://github.com/jnau | **My Personal Website**: https://jnau.github.io/