Jessica N. **Au**

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Experience

Stanford Medicine Center, Department of Developmental Biology — *Palo Alto, CA*

Life Science Research Technician <*Kingsley Lab*> — *June 2018 - Present*

- Responsible for the livelihood of Stickleback to ensure survivability in order to identify the key chromosome regions, genes, and mutations that control evolutionary traits.

UC Davis School of Medicine, Department of Pharmacology — *Davis, CA*

Student Researcher <*Sato Lab, Theoretical Cardiology*> — *May 2016 - Present*

- Aim to improve preventative care for cardiovascular diseases through mathematical analysis and multiscale modeling of the heart
- Use of Python in Software-Hardware integrated projects with Raspberry Pi & Arduino
- Use of C/C++ for better performance when simulating mathematical models and systems related to cardiac myocytes
- Use of Matlab/GNU Octave for visualization and specific mathematical toolboxes

UC Davis, Department of Microbiology and Molecular Genetics — *Davis, CA*

Student Researcher <*Arsuaga-Vazquez Lab, DNA Topology*> — *Jan. 2017 - Dec. 2017*

- 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
- Use of KnotPlot, Python, & R scripts as a pipeline in order to simulate, interpret, and analyze data

Projects/Presentations

The Modeling of Calcium Dynamics within the Dyadic Space using Random Walks — *Davis, CA*

Theoretical Cardiology Lab, Poster Presentation at <62nd Annual Biophysical Society Conference> — *May. 2017 - Present*

- Implementation of stochastic processes and mathematical modeling in C/C++ to study calcium dynamics in ventricular cardiac myocytes
- Structured programming in C/C++ to simplify algorithm for readability and reusability
- Parallel programming in C++ to improve efficiency while dealing with large amounts of data points and function calls
- Data analysis and visualization in Matlab/Octave GNU to quantify results and make accurate conclusions

Randomization and Confinement Effects Regarding the BFACF Algorithm — *Davis, CA*

DNA Topology Lab, Presented at <BaMBA 2017 Conference> — *Jan. 2017 - Aug. 2017*

- Investigated how changes in certain parameters affected inherent properties of self-avoiding polygons in three-dimensional 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 — *Davis, CA*

Special Topics Course in Computer Science, <Final Project> — *Dec. 2017*

- DNA sequence analysis using integer linear programming (ILP) in comparison to dynamic programming
- Formulated ILP for Gurobi Optimizer using integer linear programming in Python
- Implemented Needleman-Wunsch algorithm in Perl

Differentially Expressed Genes & Clustering Methods — *Davis, CA*

Theory and Practice of Bioinformatics Course, <Laboratory Project> — *Dec. 2017*

- Executed complete Galaxy RNA-seq analysis on Illumina BodyMap 2.0 adrenal/brain tissue datasets
- Statistical analysis to find differentially expressed genes in R using Bioconductor package
- Utilized clustering methods such as GENIE3 (Random Forests algorithm) on the regulatory network of *E. coli*

Skills

General
- Detailed oriented work efficiency and ability to adapt to new, developing environments.
- Able to work collaborately as a team member, as well as independently with minimal supervision
- Apt analytical skills along with ability to synthesize practical decisions

Programming Languages C/C++, Matlab/Octave, Python, Bash, R, Perl, Ruby on Rails

Software & Tools Unix/Linux, LaTeX, GitHub, Gurobi Optimizer, KnotPlot, Adobe Photoshop, Microsoft Office, HTML/CSS

Education

University of California-Davis — *Davis, CA*

B.S. in Mathematics and Scientific Computation- Biology Emphasis — *Graduated **December 2017***

- Minor: Bioinformatics and Quantitative Biology