Vinay Swamy

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EDUCATION

University of California, Los Angeles: Biochemistry, BS June 2018

RESEARCH EXPERIENCE

Bioinformatics Group, Ophthalmic Genetics and Visual Function branch, National Eye Institute

Postbaccalaureate Fellow July 2018—Present

- Implemented parallel Snakemake pipeline for automated download, quality control, and analysis of >20TB of publicly available bulk short-read RNA-seq data from the Sequence Read Archive, routinely run to build the Eye in a Disk(EiaD), the underlying database of EyeIntegration, an R-Shiny webapp for visualizing gene expression in ocular tissues.
- Constructed *de novo* transcriptomes using the EiaD dataset to identify novel gene isoforms expressed in 6 ocular sub-tissues, incorporating PacBio long-read RNA sequencing to improve transcriptome construction accuracy. Designed R-Shiny web app for visualizing transcriptomes, displaying transcript models, gene and transcript expression, evolutionary conservation and associated SNPS.
- Developing pipeline for generating the single-cell Eye in a Disk(scEiaD), a database generated from aggregating publicly available single cell RNA-seq related to the retina. Pipeline integrates both well and droplet based scRNA-seq from 28 different studies across 3 species, performs deep-learning based batch correction, relabels cells types with a bespoke machine-learning classifier, and conducts down-stream analysis like clustering and trajectory calculation. Pipeline currently used to process 1.4 million cells worth of data.
- Design interactive, R-shiny webapp, PLAE , for visualizing data in the scEiaD. App efficiently plots UMAP reduced dimensions and gene expression, displays pseudobulk-based differential gene expression between cell clusters, allows for rapid subplotting by cell-type as well as other metadata and provides access to clean, pre-processed scEiaD data.

Coller Lab, Department of Molecular, Cellular, and Developmental Biology, UCLA

Student Lab Assistant August 2017—June 2018

- Analyzed 3' sequencing data and bulk RNA-seq to quantify usage of different alternative polyadenylation sites and analyzed polyadenylation factor binding motifs in RNA transcripts to study the role of polyadenylation in in regulating cellular quiescence

Aldave Lab, Stein Eye Institute, UCLA

Student Lab Assistant March 2017—June 2018

- Designed pipelines for analyzing and visualizing bulk RNA-seq data from corneal or corneal-like cells across multiple projects including validating a cell-line model of posterior polymorphous corneal dystrophy(PPCD) and examining the effect of culturing medium on passaging and expansion of primary human corneal endothelial cells.

TEACHING EXPERIENCE

Foundation for Advanced Education in Science, National Institutes of Health

Lead Instructor, Visualization in R (BIOF 079) September 2020—Present

- Designed a 5 day, 30 hour semi-annual workshop on making publication quality figures and interactive visualizations using the R programming language
- Created all lecture materials and workshop exercises and created a standalone computing environment using the bindr notebook hosting service for students to use for the course.

Co-instructor, Analysis of NGS Data (BIOF 045) September 2020—Present

- Instructor for 1 day of a semi-annual workshop on analyzing NGS data: taught students how to analyze bulk and single-cell RNA-seq data using bash and R. Designed lecture materials and student exercises for the day.

Teaching Assistant, Applied Machine Learning (BIOF 509) February 2019—June 2020

- Helped teach introductory machine learning concepts like data wrangling, classification, regression, clustering, dimensionality reduction, and project organization
- Lead lesson on methods for machine learning on imbalanced data sets and its application to biological data

Software Carpentry Workshop, National Eye Institute

Assistant June 2019

- Assisted in teaching a 2 day course on the basics of git, the bash command line, and programming and data visualization using R to scientists at the National Eye Institute

First Code Academy, San Francisco, CA

Remote Instructor May 2018—October 2019

- Taught students age 9-18 programming in Python, covering topics such as introductory programming, basic data structures, and object-oriented programming via a web-based platform
- Assisted in development of programming curriculum for beginner, experienced, and advanced students

PUBLICATIONS

- **Vinay S. Swamy**, Temesgen D. Fufa, Robert B. Hufnagel, David M. McGaughey "A short-read de novo transcriptome construction pipeline optimized by long reads reveals novel developmentally regulated gene isoforms and disease targets in hundreds of eye samples", *Bioarxiv*, August 23 2020 URL: https://www.biorxiv.org/content/10.1101/2020.08.21.261644v1
- Ricardo F. Frausto, **Vinay S. Swamy**, Gary S. L. Peh, Payton M. Boere, E. Maryam Hanser, Doug. D. Chung, Marco Morselli, Liyo Kao, Rustam Azimov, Matteo Pellegrini, Ira Kurtz, Jodhbir S. Mehta, Anthony J. Aldave "Phenotypic and functional characterization of corneal endothelial cells during in vitro expansion" *Scientific Reports,* May 04 2020 doi: https://doi.org/10.1038/s41598-020-64311-x
- Jorge L. Alió del Barrio MD, PhD*, Doug D. Chung PhD*, Olena Al-Shymali MD , Alice Barrington , Kavya Jatavallabhula , **Vinay S. Swamy** , Pilar Yébana OD , Maria Angélica Henríquez-Recine MD , Ana Boto-de-los-Bueis MD, PhD , Jorge L. Alió MD, PhD , Anthony J. Aldave MD "Punctiform and Polychromatic Pre-Descemet Corneal Dystrophy: Clinical Evaluation and Identification of the Genetic Basis" *American Journal of Ophthalmology,* Nov 19 2019. doi: https://doi.org/10.1016/j.ajo.2019.11.024
- **Vinay S. Swamy**, David McGaughey "Eye in a Disk: eyeIntegration human pan-eye and body transcriptome database version 1.0" *Investigative Ophthalmology and Vision Science*, July 1 2019. doi: https://doi.org/10.1167/iovs.19-27106
- Ricardo F Frausto, Doug D Chung, Payton M. Boere, **Vinay S. Swamy**, Huong N.V.Duong, Liyo Kao, Rustam Azimov, Wenlin Zhang, Liam Carrigan, Davey Wong, Marco Morselli, Marina Zakharevich, E. Maryam Hanser, Austin C. Kassels, Ira Kurtz, Matteo F Pellegrini, Anthony J. Aldave "ZEB1 insufficiency causes corneal endothelial cell state transition and altered cellular processing" *PLOS One*; June 13, 2019. doi: https://doi.org/10.1371/journal.pone.0218279
- Mithun Mitra, Elizabeth L Johnson, **Vinay S. Swamy**, Lois E Nersesian, David C Corney, David G Robinson, Daniel G Taylor, Aaron M Ambrus, David Jelinek, Wei Wang, Sandra L Batista and Hilary A Coller "Alternative polyadenylation factors link cell cycle to migration" *Genome Biology*. Oct 25, 2018 doi: https://doi.org/10.1186/s13059-018-1551-9

AWARDS

- MIT Hacking Medicine Grandhack in DC, 2019: 2nd place and Veteran Affairs Innovation Award
- Knight Templar Foundation ARVO Travel Grant, 2019
- Siemens National Merit Scholarship, 2014

PRESENTATIONS AND POSTERS

- "*De novo* Transcriptomes Built From Hundreds of Ocular Tissue Samples", *Biology of Genomes,* 2020 (virtual poster presentation)
- "*De novo* Transcriptomes Built From Hundreds of Ocular Tissue Samples", *Association for Research in Vision and Ophthalmology Annual Meeting,* 2019 (oral presentation)

- “Transcriptomic Profiling of *Slc4a11* Null Murine Corneal Endothelial Cells”, *Association for Research in Vision and Ophthalmology Annual Meeting,* 2018 (oral presentation)
- “Alternative Polyadenylation Links Cell Cycle to Migration”, *International Conference on Systems Biology of Human Disease,* 2018 (poster presentation)

SKILLS

Languages: R(advanced), python(intermediate), bash(intermediate), c++(beginner), sql(beginner)
Software/Libraries: Snakemake, docker, singularity, git, tidyverse, scikit-learn, TensorFlow, pandas, matplotlib
Other Skills: High Performance Computing, reproducible research, scientific writing.