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Education

MIT Cambridge, MA

PhD. Student in EECS

Aug 2020 - Present

· Working as a research assistant in the Weissman Lab at the Whitehead Institute

Caltech Pasadena, CA

B.S. IN BIOLOGY AND COMPUTER SCIENCE

Sept 2016 - Jun 2020

- · Biology Courses: Regulation of Gene Expression, Cell Biology, Genetics, Bioinformatics
- CS Courses: Decidability and Tractability, Algorithms, Learning Systems

Experience _____

Research Assistant Cambridge, MA

Dec 2020 - Present WEISSMAN LAB

- Studying cancer evolution via synthetic lineage reconstruction using a CRISPR-enabled lineage tracer in a lung cancer mouse model.
- Developing a tool to preprocess single cell metabolic labeling data to quantify RNA splicing kinetics.

Software Solution Engineering Intern

Boston, MA

GINKGO BIOWORKS Jun 2020 - Aug 2020

- Worked on migrating Ginkgo's mass spectrometry data pipeline to AWS and Airflow.
- Was responsible for the full development cycle of the project—from conceptualization, making architectural and design decisions to implementation, validation, and release.

Undergraduate Researcher

Pasadena, CA

PACHTER LAB Sept 2019 - Jun 2020

- Worked with Sina Booeshaghi and Prof Lior Pachter on single-cell RNA-seg projects.
- Developed a friendly wrapper around a popular scRNA-seq pre-processing pipeline (kb-python).
- Developed a user interface for the open-source fraction collector (Colosseum) using PyQt5 and later as a web application with React.js.

Software Engineering Intern

Boston, MA

Jun. 2019 - Sept 2019

• Improved Ginkgo's in-house data analysis pipeline and various backend services.

· Worked with other software engineers in an Agile environment to deliver stable, scalable and tested products.

Undergraduate Researcher

Pasadena, CA Jan 2017 - Jun 2019

• Worked with **David Angeles PhD.** and **Prof Paul W. Sternberg** on projects involving the model organism C. elegans.

• Developed an automatic, complete RNA-seq pipeline for nematodes (Alaska).

Projects_____

STERNBERG LAB

GINKGO BIOWORKS

dynast

WEISSMAN LAB

aristoteleo/dynast-release

• Pipeline for complete splicing and labeling quantification from metabolic labeling scRNA-seq experiments.

Oct 2020 - Present

- Ability to perform estimation of labeled/unlabeled RNA using a Bayesian inference model.

Mass Spectrometry Pipeline

GINKGO BIOWORKS Jun 2020 - Aug 2020

- · Migrated mass spectrometry pipeline, which depended on an on-prem Windows machine, to Linux on AWS and Airflow.
- Implemented the ability to call Windows DLLs within Linux with Wine and IronPython.
- Retired an internal fork of ProteoWizard by contributing back to the project.

Colosseum pachterlab/colosseum

PACHTER LAB

• A low-cost, modular, open-source automated fluid sampling device for scalable microfluidic applications.

- Can be built for less than \$100 using off-the-shelf components in less than an hour.
- Developed its user interface using PyQt5 and installable from Pypi; later migrated to a fully-featured web application written with React.js.

kb-python pachterlab/kb_python

PACHTER LAB

- A Python wrapper around the kallisto | bustools pipeline for scRNA-seq pre-processing.
- Pre-processes scRNA-seq data into gene count matrices and RNA velocity matrices.
- Provides pre-built reference indices for pseudoalignment.

NGS Pipeline

GINKGO BIOWORKS Jun 2019 - Sept 2019

- Migrated in-house NGS pipeline to the cloud (AWS S3, Batch, DynamoDB).
- Implemented pipeline metrics collection with Elasticsearch and Grafana.
- Implemented contamination screening via taxonomy analysis with Centrifuge.

Alaska 🕠 lioscro/alaska-parse Jan 2017 - Aug 2019

STERNBERG LAB

- Developed a framework for automated, complete RNA-seq analysis.
- Parse Server backend. Frontend portal in Javascript, HTML/CSS. Containerization with Docker.
- Presented a poster at the 21st International C. elegans Conference.

Publications

Low-cost, scalable, and automated fluid sampling for fluidics applications, author 2021 Under review

Modular and efficient pre-processing of single-cell RNA-seq, author 2021

Published

Sept 2019 - Jun 2020

Oct 2019 - Jun 2020

Presentations

SURF Seminar Day Pasadena, CA

Presenter for <A Framework for Automated, Complete RNA-seq Analysis>

Oct 2018

• Presented work done on Alaska during summer fellowship.

21st International C. elegans Conference

Los Angeles, CA

POSTER PRESENTER FOR <A FRAMEWORK FOR AUTOMATED, COMPLETE RNA-SEQ ANALYSIS>

• Introduced Alaska, an RNA-seq analysis pipeline for nematodes.

Jun 2017

Awards & Honors _____

2018 Semi-finalist, Perpall Speaking Competition Pasadena, CA

2018 Fellow, Samuel P. and Frances Krown SURF Fellowship Pasadena, CA

2017 Fellow, SURF Fellowship Pasadena, CA

Skills

Programming Python, Javascript, C/C++, HTML/CSS

Software Docker, Django, Apache Airflow, AWS S3/Batch/DynamoDB, Elasticsearch, React.js, CI/CD, Numpy, Pandas

Data Analysis Bulk RNA-seq, Single-cell RNA-seq

Molecular Biology PCR, Cloning, Purification

Extracurriculars

The Big T Yearbook Pasadena, CA

Business Manager, Designer, Photographer; Editor-in-Chief Sept 2019 - Jun 2020

Sept 2016 - Jun 2020

- (Editor-in-Chief) Responsible for setting the theme, layout, content, and publishing of the 2019-2020 yearbook.
- Established a new advertisement system, shared cloud storage system, job organization and assignment system, and payment reimbursement system.
- Designed pages and took/edited photos with Adobe Creative Cloud software.

Caltech & American Red Cross

Pasadena, CA

HEALTH ADVOCATE & EMERGENCY MEDICAL RESPONDER

Sept 2017 - Jun 2020

- American Red Cross certified emergency medical responder and basic life support provider.
- Worked as the dormitory health advocate and provided first aid to students.

Student Government, Lloyd House

HISTORIAN

Pasadena, CA

Jun 2017 - May 2019

- Responsible for recording Lloyd House (dormitory) events by taking photos.
- Established a new shared cloud storage system to distribute these photos.