

Kyung Hoi (Joseph) Min

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EDUCATION

CALTECH

BS IN BIOLOGY AND

COMPUTER SCIENCE

Present | Pasadena, CA

Expected Graduation: Jun 2020

Cum. GPA: 4.0 / 4.3

COURSEWORK

UNDERGRADUATE

Biology

Regulation of Gene Expression

Cell Biology

Genetics

Bioinformatics (*Planned*)

Computer Science

Programming Methods

Decidability and Tractability

Communication Networks

Algorithms

Learning systems (*machine learning*)

SKILLS

PROGRAMMING

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

SOFTWARE

- Docker
- Django
- Apache Airflow
- AWS S3, Batch, DynamoDB
- Elasticsearch, Grafana
- React.js
- CI/CD
- Celery, RabbitMQ
- Numpy, Pandas

DATA ANALYSIS

- RNA-seq (QC, *Kallisto*, *Sleuth*)
- scRNA-seq (*Kallisto*, *Bustools*)

MOLECULAR BIOLOGY

- PCR
- Cloning
- Purification

PROJECTS

COMMONS CELL ATLAS | SOFTWARE DEVELOPER, CALTECH

Sept 2019 – Present | Pasadena, CA

- Repository for all the world's single-cell RNA-seq data.
- Arbitrary aggregation and comparison of data across multiple datasets.
- Web application written in React.js and Django.

KB-PYTHON | SOFTWARE DEVELOPER, CALTECH

Oct 2019 – Present | Pasadena, CA

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

NGS PIPELINE | SOFTWARE ENGINEERING INTERN, GINKGO BIOWORKS

Jun 2019 – Sept 2019 | Boston, MA

- 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 | FULL-STACK DEVELOPER, CALTECH

Jan 2017 – Aug 2019 | Pasadena, CA

- Developed a framework for automated, complete RNA-seq analysis.
- Presented a poster at the 21st International *C. elegans* Conference.
- Available at <http://alaska.caltech.edu/> and source code on Github.

RESEARCH

PACHTER LAB | UNDERGRADUATE RESEARCHER

Oct 2019 – Present | Pasadena, CA

Working with **Sina Booesaghhi** and **Prof Lior Pachter** on developing software tools to store, distribute, and analyze scRNA-seq data. Most notably kb-python and Commons Cell Atlas (both above).

STERNBERG LAB | UNDERGRADUATE RESEARCHER

Jan 2017 – Jun 2019 | Pasadena, CA

Worked with **David Angeles PhD.** and **Prof Paul W. Sternberg** on bioinformatics and molecular biology projects involving the model organism *C. elegans*, most notably Alaska (above).

AWARDS

- 2018 Peripall Speaking Competition Semi-finalist
- 2018 Samuel P. and Frances Krown SURF Fellowship
- 2017 SURF Fellowship

PUBLICATIONS

- [1] Feature demultiplexing for single-cell genomics assays. Co-first author, in preparation.
- [2] Modular and efficient pre-processing of single-cell RNA-seq. Author, in review.