

# Kyung Hoi (Joseph) Min

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## EDUCATION

### MIT

PHD. IN EECS

Present | Cambridge, MA

### CALTECH

BS IN BIOLOGY AND

COMPUTER SCIENCE

Jun 2020 | Pasadena, CA

## PUBLICATIONS

- [1] Low-cost, scalable, and automated fluid sampling for fluidics applications. Author, under review.
- [2] Modular and efficient pre-processing of single-cell RNA-seq. Author, published.

## 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

### MASS SPECTROMETRY PIPELINE | SOFTWARE SOLN. ENGINEERING

INTERN, GINKGO BIOWORKS

Jun 2020 – Aug 2020 | Boston, MA

- Migrated mass spectrometry pipeline, which depended on an on-prem Windows machine, to Linux on AWS and Airflow.
- Retired an internal fork of ProteoWizard by contributing back to the project.

### COLOSSEUM | UNDERGRADUATE RESEARCHER, PACHTER LAB

Sept 2019 - Jun 2020 | Pasadena, CA

- A low-cost, modular, open-source automated fluid sampling device for scalable microfluidic applications.
- Developed its user interface using PyQt5 and installable from Pypi; later migrated to a fully-featured web application written with React.js.

### KB-PYTHON | UNDERGRADUATE RESEARCHER, PACHTER LAB

Oct 2019 – Jun 2020 | 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.

## EXPERIENCE

### RESEARCH ASSISTANT | WEISSMAN LAB

Dec 2020 – Present | Cambridge, MA

Studying cancer evolution via synthetic lineage reconstruction using a CRISPR-enabled lineage tracer. Additionally, developing a tool to preprocess metabolic labeling data to quantify RNA splicing kinetics.

### SOFTWARE SOLN. ENGINEERING INTERN | GINKGO BIOWORKS

Jun 2020 – Aug 2020 | Boston, MA

Migrated company's mass spectrometry data pipeline to AWS and airflow. Took responsibility of the full development cycle of the project—from conceptualization, making architectural and design decisions to implementation, validation, and release.

### UNDERGRADUATE RESEARCHER | PACHTER LAB

Oct 2019 – Jun 2020 | Pasadena, CA

Worked with Sina Boeshaghi and Prof Lior Pachter on developing software tools to analyze scRNA-seq data. Most notably kb-python (above) and Colosseum (not listed).

### SOFTWARE ENGINEERING INTERN | GINKGO BIOWORKS

Jun 2019 – Sept 2019 | Boston, MA

Improved company's in-house data analysis pipeline and various backend services. Worked collaboratively with other software engineers in an Agile environment to deliver stable, scalable and tested products.