

# Joseph Min

☎ 626.240.9851 | ✉ phoenixterg6@gmail.com | 🌐 lioscro | in lioscro | 🐦 @lioscro

## EDUCATION

### MIT

#### MS IN EECS

Jun 2022 | Cambridge, MA

### CALTECH

#### BS IN BIOLOGY AND

#### COMPUTER SCIENCE

Jun 2020 | Pasadena, CA

## PUBLICATIONS

- [1] Lineage tracing reveals the phylogenetics, plasticity, and paths of tumor evolution. *Cell*, 2022.
- [2] Mapping transcriptomic vector fields of single cells. *Cell*, 2022.
- [3] Low-cost, scalable, and automated fluid sampling for fluidics applications. *HardwareX*, 2021.
- [4] Modular and efficient pre-processing of single-cell RNA-seq. *Nature Biotechnology*, 2021.

## SKILLS

### PROGRAMMING

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

### SOFTWARE

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

### DATA ANALYSIS

- scRNA-seq
- Spatial transcriptomics

## PROJECTS

### SPATEO 🌐 | RESEARCH ASSISTANT, MIT

Dec 2021 - Jun 2022 | Cambridge, MA

- Python package for analysis of high-resolution spatial transcriptomics.
- Developed novel RNA-based cell segmentation approaches.

### DYNAST 🌐 | RESEARCH ASSISTANT, MIT

Dec 2020 - Jun 2022 | Cambridge, MA

- An inclusive and efficient preprocessing pipeline for quantifying metabolic labeling-enabled scRNA-seq.
- Simultaneous quantification of metabolically labeled and spliced transcripts.

### MASS SPECTROMETRY PIPELINE | SOFTWARE SOLN. ENGINEER INTERN, GINKGO BIOWORKS

Jun 2020 - Aug 2020 | Boston, MA

- Migrated mass spectrometry pipeline to Linux on AWS and Airflow.
- Retired an internal fork of ProteoWizard by merging back to upstream.

### 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.

### NGS PIPELINE | SOFTWARE ENGINEER 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.

## EXPERIENCE

### RESEARCH ASSISTANT | MIT

Dec 2020 - Jun 2022 | Cambridge, MA

Studied cancer evolution via synthetic lineage reconstruction using a CRISPR-enabled lineage tracer [1] at the Weissman lab. Developed a tool to preprocess metabolic labeling scRNA-seq data [2] and high-resolution spatial transcriptomics.

### SOFTWARE SOLN. ENGINEER 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 [4] (above) and Colosseum [3].

### SOFTWARE ENGINEERING INTERN | GINKGO BIOWORKS

Jun 2019 - Sept 2019 | Boston, MA

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