

# Kyung Hoi (Joseph) Min

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## EDUCATION

### MIT

#### MS IN EECS

Jun 2022 | Cambridge, MA

### CALTECH

#### BS IN BIOLOGY AND

#### COMPUTER SCIENCE

Jun 2020 | Pasadena, CA

## SKILLS

### PROGRAMMING

- Python
- Javascript
- Ruby on Rails
- SQL
- C# (.NET Framework)
- C, C++

### SOFTWARE

- Git, CI/CD
- Docker
- Django
- Apache Airflow
- AWS (S3, Batch, RDS, Lambda)
- Nextflow
- React.js
- Snowflake
- Kubernetes
- Kafka

### OTHER

- Software design and architecture
- Technical communication
- Computational biology (NGS)

## PUBLICATIONS

- [1] Spateo: multidimensional spatiotemporal modeling of single-cell spatial transcriptomics. in press, 2024
- [2] Dynast: Inclusive and efficient quantification of metabolically labeled transcripts in single cells. MIT, 2022
- [3] Mapping transcriptomic vector fields of single cells. Cell, 2022.
- [4] Modular and efficient pre-processing of single-cell RNA-seq. Nature Biotechnology, 2021.

## EXPERIENCE

### SOFTWARE ENGINEER | GINKGO BIOWORKS

Aug 2022 – Present | Current title: Senior Software Engineer | Boston, MA

Individual contributor on the software team identifying gaps in core software, proposing and designing technical solutions, driving cross-team initiatives in an Agile environment, and unblocking high-impact projects. Technical lead in one customer project-specific team and mentored junior engineers.

### RESEARCH ASSISTANT | MIT

Dec 2020 – Jun 2022 | Cambridge, MA

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

### SOFTWARE SOLN. ENGINEER INTERN | GINKGO BIOWORKS

Jun 2020 – Aug 2020 | Boston, MA

Migrated in-house 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.

### 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.

## PROJECTS

### ANALYSIS PIPELINE | SOFTWARE ENGINEER, GINKGO BIOWORKS

Jan 2023 - Dec 2023 | Boston, MA

- Worked on a major initiative to refactor the company's automated analysis pipeline.
- Technical lead of the implementation of a new analysis registry. Mentored an intern.

### SPATEO | RESEARCH ASSISTANT, MIT [1]

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 [2]

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

### NGS PIPELINE | SOFTWARE ENGINEER INTERN, GINKGO BIOWORKS

Jun 2019 - Sept 2019 | Boston, MA

- Migrated in-house NGS pipeline to AWS and Apache Airflow.
- Implemented pipeline metrics collection with Elasticsearch and Grafana.