

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
- C# (.NET Framework)
- C, C++

SOFTWARE

- Git
- 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.

UNDERGRADUATE RESEARCHER | PACHTER LAB

Oct 2019 – Jun 2020 | Pasadena, CA

Developed software tools to analyze scRNA-seq data. Most notably kb-python [4].

PROJECTS

LABYRINTH | SOFTWARE ENGINEER, GINKGO BIOWORKS

Jan 2024 – Present | Boston, MA

- Internal scientist-centric Python package for easy discovery and retrieval of data specific to a customer project.
- Developed by independently identifying gaps in core software, proposing and designing a solution, and driving implementation.

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.

KB-PYTHON 🌐 | UNDERGRADUATE RESEARCHER, PACHTER LAB [4]

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.