

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

- Docker
- Django
- Apache Airflow
- AWS (S3, Batch, RDS, Lambda)
- React.js
- GraphQL
- Kubernetes
- Kafka
- Snowflake

DATA ANALYSIS

- scRNA-seq
- Spatial transcriptomics

PUBLICATIONS

- [1] Spateo: multidimensional spatiotemporal modeling of single-cell spatial transcriptomics. bioRxiv, 2022
- [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.

PROJECTS

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, PACTER 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.

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.

EXPERIENCE

SOFTWARE ENGINEER | GINKGO BIOWORKS

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

Worked as an individual contributor on the Solution Engineering team identifying gaps in core software, proposing and designing technical solutions, driving cross-team initiatives in an Agile environment, and unblocking high-impact projects.

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 a tool 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 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 | PACTER 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].

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.