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

PUBLICATIONS

[1] Lineage tracing reveals the phylodynamics, 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
- 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
- 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, 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.

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 at the Weissman lab. Developed a tool to preprocess metabolic labeling data to quantify RNA splicing kinetics.

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 Booeshaghi** 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.