

LYDIA MOK

BIOINFORMATICIAN

(831) 854-3411 ■ lymok@ucsc.edu ■ Santa Cruz, CA 95064

PROFESSIONAL SUMMARY

Enthusiastic researcher specializing in immunogenomics and computational biology. Experienced in modeling and validating biological and therapeutic hypothesis using multiomics and clinical data. Skilled in the computational analysis of large scale, multi-modal omics data.

SKILLS

- Programming languages: Python, R, CLI, SQL
- Bioinformatics tools, Statistical Analysis, Model development and validation
- Multi-omics analysis (specialized in transcriptomics, single cell data)
- Machine Learning, Deep learning

EXPERIENCE

■ GRADUATE STUDENT RESEARCHER University of California, Santa cruz

Santa Cruz, CALIFORNIA

September 2021 - Present

- Developed a comprehensive pan-cancer, multi-omic single-cell T-cell atlas and antigen specificity database to advance cancer immunotherapy research.
- Investigated age-specific changes in megakaryopoiesis stem cells by identifying developmental intermediates between hematopoietic stem cells and megakaryocyte progenitor cells (MkPs) through single-cell RNA sequencing and CITE-seq data analysis.
- Constructed a computational pipeline for spatial transcriptomics analysis, specifically focusing on the metabolic system within TNBC tumors using 10x Visium data.
- Elucidated the lineage and dynamics of T stem-like cells in ovarian cancer by integrating single-cell RNA sequencing and TCR sequencing data.

■ RESEARCH SCIENTIST Seoul National University R&DB Foundation

Seoul

September 2019 - September 2020

- Engaged in a project at the Korea National Institutes of Health to develop a COVID-19 prognosis model and clinical platform, leading to the discovery of a key prognostic factor.
- Contributed to the 'Korea Post Genome Project,' focusing on multi-omics research and the development of statistical methodologies utilizing RNA-seq data.

■ RESEARCH SCIENTIST Korea National Institutes of Health (NIH)

Osong

April 2020 - September 2020

- Development of prognosis model and clinical application platform. Developed a key prognosis factor prediction model with significant implications for COVID-19 patients.

■ **RESEARCH ASSISTANT** Seoul National University
Seoul

March 2017 - August 2019

- Developed statistical prediction models and clinical application platforms for precision medicine by analyzing multi-omics data in collaboration with Seoul National Hospital
- GWAS single SNP analysis for Complex disease using Korea Association Resource (KARE) consortium data. Identified statistically significant common variants associated with Type 2 diabetes and high blood pressure.
- Developed the hierarchical structural component model (HisCoM-PAGE) for survival phenotype, which considers the correlation among pathways. Collaborative work with McGill University.
- Collaboration on genomic study for pathway analysis based on kernel learning.

■ **VISITING RESEARCHER** Virginia Poly Technic Institute State University
Blacksburg, VA

July 2019 - August 2019

- Collaboration on genomic study for pathway analysis method development based on kernel learning. Extends the Hierarchical structured Component model on survival phenotype using kernel algorithm.

■ **RESEARCH INTERN** Ewha Womans University
Seoul

August 2016 - December 2016

Anti-cancer drug sensitivity analysis project. Leveraged a public drug sensitivity databases to curate antibody specific drugs and develops a genomic database focused on drug resistance.

EDUCATION

■ **DOCTOR OF PHILOSOPHY (PH.D.) CANDIDATE IN BIOMOLECULAR ENGINEERING AND BIOINFORMATICS CANDIDATE**
University of California-Santa Cruz

Expected graduation June 2026

■ **MASTER OF SCIENCE (M.S.) IN BIOINFORMATICS**
Seoul National University , Seoul, Repulic of Korea

August 2019

■ **BACHELOR OF SCIENCE (B.S.) IN STATISTICS AND MOLECULAR BIOLOGY**
Ewha Womans University, Seoul, Repulic of Korea

February 2017

LANGUAGES

- **Korean**
Native
- **English**
Advanced

AWARDS

- Won Best Presentation awards at International Conference on Biological and Medical Sciences
- Won third prize for oral presentation in Graduate student presentation session at the Korean Statistical Society Conference
- Honors in Grade at Ewha Womans University

PUBLICATIONS

- Eiva, M. A., Brown, E. G., Mok, L., Rose, N., Golden, G. J., Pandey, V., ... & Powell, D. Jr. (Under submission). A non-canonical CD45RO⁺ stem cell memory T cell population with effector properties in human cancer.
- Poscablo, D. M., Jeong, H., Lee, S. Y., & Kim, H. J. (2024). An age-progressive platelet differentiation path from hematopoietic stem cells causes exacerbated thrombosis. *Cell*, 187(12), 3090–3107
- Kang, J. S., Mok, L., Heo, J. S., Han, I. W., Shin, S. H., Yoon, Y. S., ... & Park, T. (2021). Development and External Validation of Survival Prediction Model for Pancreatic Cancer Using Two Nationwide Databases: Surveillance, Epidemiology and End Results (SEER) and Korea Tumor Registry System-Biliary Pancreas (KOTUS-BP). *Gut and Liver*. (Co-first author)
- Mok, L., Kim, Y., Lee, S., Choi, S., Lee, S., Jang, J. Y., & Park, T. (2019). HisCoM-PAGE: Hierarchical structural component models for pathway analysis of gene expression data. *Genes*, 10(11), 931.
- Mok, L., & Park, T. (2019). HisCoM-PAGE: software for hierarchical structural component models for pathway analysis of gene expression data. *Genomics & Informatics*, 17(4).
- Jeong, H., Mok, L., & Park, T. (2018). Ovarian cancer prognostic prediction model using RNA sequencing data. *Genomics & Informatics*, 16(4), e32. (Co-first author)
- Jeong, H., Mok, L., & Park, T. (2018). Development of prediction models using high-dimensional RNA sequencing data for the prognosis of pancreatic ductal adenocarcinoma. *Journal of the Korean Data & Information Science Society*, 29(6), 1409–1419