KISUNG NAM

Postdoctoral Research Fellow

Massachusetts General Hospital, Harvard Medical School, Broad Institute of MIT and Harvard

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RESEARCH INTERESTS

Statistical Genetics | Computational Genomics | Rare Variant Analysis | Single-cell Genomics | AI for Genomics

EDUCATION

Seoul National University Mar 2020 – Aug 2025
Ph.D. in Data Science
Advisor: Dr. Seunggeun (Shawn) Lee

Korea Advanced Institute of Science and Technology (KAIST) Feb 2012 – Feb 2014
M.S. in Management Engineering (Finance track)
Advisors: Dr. Hoe Kyung Lee and Dr. Tong Suk Kim

Korea Advanced Institute of Science and Technology (KAIST) Mar 2006 – Feb 2012
B.S. in Mathematical Sciences
Summa Cum Laude

EXPERIENCE

Massachusetts General Hospital · Harvard Medical School · Broad Institute May 2026 – Present
Postdoctoral Research Fellow Boston, MA
Mentor: Dr. Wei Zhou

Graduate School of Data Science, Seoul National University Sep 2025 – May 2026
Postdoctoral Researcher Seoul, Korea
Mentor: Dr. Seunggeun (Shawn) Lee

Department of Biostatistics, University of Michigan Sep 2023 – Feb 2024
Visiting Research Scholar Ann Arbor, MI
Mentor: Dr. Bhramar Mukherjee

Financial Supervisory Service, Korea Jan 2014 – May 2025
Senior Manager Seoul, Korea

PUBLICATIONS

SELECTED PUBLICATIONS (* Equal contribution)

M. Choi*, **K. Nam***, S. Lee. Predicting human-gain curves under local proxy optimization from repeated ratings. ***NeurIPS***, 2026. *To appear; Spotlight (Top 1.3%).*

K. Nam, ..., S. Lee. Rare variant effect estimation and polygenic risk prediction. ***Nature Genetics***, 2026.

K. Nam*, B. Eom*, J. Kim*, ..., S. Kim. Integrative genomic analysis of 21 orofacial diseases identifies shared genetic architecture with systemic diseases. ***Nature Communications***, 2026.

E. Park*, **K. Nam***, S. Jeong*, ..., S. Lee. Scalable and accurate rare variant meta-analysis with Meta-SAIGE. ***Nature Genetics***, 2025.

K. Nam, J. Kim, S. Lee. Genome-wide study on 72,298 individuals in Korean biobank data for 76 traits. ***Cell Genomics***, 2022.

ADDITIONAL PUBLICATIONS AND PREPRINTS

Y. Liu, ..., **K. Nam**, ..., W. Zhou. Scalable context-dependent single-cell eQTL mapping reveals disease-relevant regulatory variation beyond static models. ***medRxiv***, 2026. *Preprint.*

J. T. Flanagan, **K. Nam**, S. Lee. ENCODE guided WGS analysis can identify trait associated regulatory regions driven by rare variants. ***BMC Genomics***, 2026.

N. Kim, J. Park, **K. Nam**, ..., H. Lee. Associations between polygenic risk score for blood pressure and risk of hypertension in Northeast Asian individuals. ***Journal of the American Heart Association***, 2025.

P. Nagarajan, ..., **K. Nam**, ..., H. Wang. A large-scale genome-wide study of gene-sleep duration interactions for blood pressure in 811,405 individuals from diverse populations. ***Molecular Psychiatry***, 2025.

L. Fritsche, **K. Nam**, ..., B. Mukherjee. Uncovering associations between pre-existing conditions and COVID-19 Severity: A polygenic risk score approach across three large biobanks. ***PLOS Genetics***, 2023.

A. Campos, ..., **K. Nam**, ..., L. Yengo. Boosting the power of GWAS within and across ancestries using polygenic scores. ***Nature Genetics***, 2023.

J. Kim, J. Lee, **K. Nam**, S. Lee. Investigation of genetic variants and causal biomarkers associated with brain aging. ***Scientific Reports***, 2023.

M. Kanai, ..., **K. Nam**, ..., H. Finucane. Meta-analysis fine-mapping is often miscalibrated at single-variant resolution. ***Cell Genomics***, 2022.

W. Zhou, ..., **K. Nam**, ..., B. Neale. Global Biobank Meta-analysis Initiative: Powering genetic discovery across human disease. ***Cell Genomics***, 2022.

Y. Zhuang, B. Wolford, **K. Nam**, ..., S. Lee. Incorporating family disease history and controlling case–control imbalance for population-based genetic association studies. ***Bioinformatics***, 2022.

K. Park, ..., **K. Nam**, ..., W. Li. Real-time mask detection on Google edge TPU. ***arXiv***, 2020. *Preprint.*

GRANTS AND AWARDS

Postdoctoral Research Fellowship (Domestic), National Research Foundation of Korea 2025–2026

- Topic: Advancing Disease Risk Prediction Models Using Multi-Omics Data

Research Fellowship for Ph.D. Candidates, National Research Foundation of Korea 2023–2025

- Topic: Advancing Disease Risk Prediction Models Using Large-scale Biobank and Data Science·AI

Youlchon AI Young Researcher Scholarship, Youlchon Foundation 2023

Reviewer's Choice Award, ASHG Annual Meeting, American Society of Human Genetics 2022

- Topic: Genome-wide study on 72,298 individuals in Korean biobank data for 76 traits