

KISUNG NAM

Postdoctoral Research Fellow

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

<https://www.kisungnam.org/>

knam@broadinstitute.org / knam3@mgh.harvard.edu

RESEARCH INTERESTS

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

EDUCATION

Seoul National University Ph.D. in Data Science Advisor: Dr. Seunggeun (Shawn) Lee	Mar 2020 – Aug 2025
Korea Advanced Institute of Science and Technology (KAIST) M.S. in Management Engineering (Finance track) Advisors: Dr. Hoe Kyung Lee and Dr. Tong Suk Kim	Feb 2012 – Feb 2014
Korea Advanced Institute of Science and Technology (KAIST) B.S. in Mathematical Sciences Summa Cum Laude	Mar 2006 – Feb 2012

EXPERIENCE

Massachusetts General Hospital · Harvard Medical School · Broad Institute Postdoctoral Research Fellow Mentor: Dr. Wei Zhou	May 2026 – Present Boston, MA
Graduate School of Data Science, Seoul National University Postdoctoral Researcher Mentor: Dr. Seunggeun (Shawn) Lee	Sep 2025 – May 2026 Seoul, Korea
Department of Biostatistics, University of Michigan Visiting Research Scholar Mentor: Dr. Bhramar Mukherjee	Sep 2023 – Feb 2024 Ann Arbor, MI
Financial Supervisory Service, Korea Senior Manager	Jan 2014 – May 2025 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. Flanagan, **K. Nam**, S. Lee. ENCODE guided WGS analysis can identify trait-associated regulatory regions driven by rare variants. *BMC Genomics*, 2026. (*Accepted*).

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	