

# Hanbin Lee

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Curriculum Vitae

## About

Any statistical and computational methods operate under the constraints imposed by the data generating process. As such, I study how evolutionary processes shape statistical inference.

Current research topics:

- Evolutionary basis of statistical genetics
- Random dynamical systems on manifolds

## Education

### University of Michigan, Ann Arbor

- Doctor of Philosophy, Department of Statistics (2024.9 -)

### Seoul National University

- Bachelor of Mathematics, Department of Mathematical Sciences (2017.3 - 2023.8)
- Doctor of Medicine, Department of Medicine (2016.3 - 2023.8)

## Professional Service

### Peer Review

- International Journal of Epidemiology
- Nature Communications
- Genetics (GSA)
- HGG Advances
- BMC Medical Research Methodology
- NAR Genomics and Bioinformatics
- Bioinformatics Advances

## Publications

\* denotes equal contribution.

### Journals

- **Hanbin Lee, Jonathan Terhorst.** Parameterizing the genetic architecture under stabilizing selection. *Genetics*, *in press*, 2026. [link](#)
- **Hanbin Lee\***, **Nathaniel S. Pope\***, **Jerome Kelleher**, **Gregor Gorjanc**, and **Peter L. Ralph.** Genetic prediction with ARG-powered linear algebra. *Genetics*, 2026. [link](#)

- **Brieuc Lehmann, Hanbin Lee, Luke Anderson-Trocme, Jerome Kelleher, Gregor Gorjanc, and Peter L. Ralph.** On ARGs, pedigrees, and genetic relatedness matrices. *Genetics*, 2026. [link](#)
- **Hanbin Lee, Rosalind F. Craddock, Gregor Gorjanc, and Hannes Becher.** randPedPCA: Rapid approximation of principal components from large pedigrees. *Genetics Selection Evolution*, 2025. [link](#)
- **Hanbin Lee\***, **Moo Hyuk Lee\***, **Kangcheng Hou, Bogdan Pasaniuc, and Buhm Han.** Admixed and single-continental genome segments of the same ancestry have distinct linkage disequilibrium patterns. *Genome Biology*, 2025. [link](#)
- **Hanbin Lee, Buhm Han.** Pseudobulk with proper offsets has the same statistical properties as generalized linear mixed models in single-cell case-control studies. *Bioinformatics*, 2024. [link](#)
- **Hanbin Lee, Buhm Han.** FastRNA: an efficient exact solution for PCA of single-cell RNA sequencing data based on a batch-accounting count model. *American Journal of Human Genetics*, 2022. [link](#)
- **Hanbin Lee, Buhm Han.** A theory-based practical solution to correct for sex-differential participation bias. *Genome Biology*, 2022. [link](#)
- **Chanwoo Kim\***, **Hanbin Lee\***, **Juhee Jeong, Keehoon Jung and Buhm Han.** MarcoPolo: a clustering-free approach to the exploration of differentially expressed genes along with group information in single-cell RNA-seq data. *Nucleic Acids Research*, 2022. [link](#)