Cue Hyunkyu Lee, Ph.D.

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Citizenship: South Korea | U.S. Permanent Resident

Academic Appointments

09/2021 – Present **Columbia University Mailman School of Public Health** New York, NY
Postdoctoral Research Scientist

- Expertise: statistical genetics, bioinformatics, genetic epidemiology; focused on disease architecture, risk quantification.
- Co-advised by I. Ionita-Laza (Biostat) and K. Kiryluk (Nephrology)
- Developed LTPI: EHR-based model for liability estimation and pleiotropy detection.
- CKD risk modeling via kidney function GWASs.
- EHR phenotype imputation using deep learning; collab. with H. Wu & N. Abiri (Lund/Halmstad).
- Local heritability and pleiotropy via Bayesian mixture model; collab. with S. Zoellner (UMich).

Work Experiences

09/2018 – 04/2021 **Genealogy** Seoul, S. Korea
Head of Research, establishing core R&D strategies and leading projects in IBD-based ancestry inference and PRS-based disease prediction, contributing to the company's research direction and product development.

Education

03/2019 – 08/2021 **Seoul National University College of Medicine** Seoul, S. Korea
PhD in Biomedical Science, focus on Biostatistics

03/2016 – 02/2018 **University of Ulsan College of Medicine** Seoul, S. Korea
PhD Candidate in Biomedical Science

01/2013 – 06/2014 **Carnegie Mellon University** Pittsburgh, PA
MS in Chemical Engineering

03/2003 – 02/2011 **Soongsil University** Seoul, S. Korea
BS in Chemical Engineering

Research and Training Experience

02/2018 – 02/2019 **Seoul National University College of Medicine** Seoul, S. Korea
Graduate Research Fellow

01/2015 – 02/2016 **Asan Medical Center** Seoul, S. Korea
Research Fellow

03/2011 – 02/2012 **Soongsil University** Seoul, S. Korea
Undergraduate Research Fellow

09/2005 – 01/2008 **S. Korea Military Service** Seoul, S. Korea

Honors and Awards

09/2025 **Neel Award finalist (IGES 2025)** Cologne, Germany
International Genetic Epidemiology Society (IGES)

08/2021 **Graduated with distinction (GPA:4.5/4.5)** Seoul, S. Korea
Seoul National University College of Medicine

09/2019 – 02/2021 **Lecture & Research Scholarship** Seoul, S. Korea
Seoul National University College of Medicine

09/2019 **Excellent Poster Award** Seoul, S. Korea
Korea Genome Organization

02/2018 **Best Presentation Award** Seoul, S. Korea
Korea Genome Organization

12/2017 **The Paper of the Year** Seoul, S. Korea
University of Ulsan College of Medicine

09/2017 **Presentation Award** Seoul, S. Korea
Korea Genome Organization

03/2016 – 02/2018 **Graduate Scholarship Recipient** Seoul, S. Korea
University of Ulsan College of Medicine

06/2016	**Graduate Student Scholarship** Korea Institute of Science and Technology Information	Seoul, S. Korea

Fellowship and Grant Support

(Current)

09/2024 – 09/2029	**NHGRI (K99/R00) 1K99HG013546**	New York, NY

(Past)

02/2019 – 02/2021	**Graduate School Scholarship in Biomedical Sciences** Asan Foundation ($20,000/yr)	Seoul, S. Korea

Peer-Reviewed Publications

First Author; Corresponding Author†; *Equal First Author

1. Wu, H*., **Lee, C. H*.,** Abiri, N., & Ionita-Laza, I. "Domain-aware matrix completion for phenotype prediction from Electronic Health Record data with applications to genomic analyses.", Ann. Appl. Stat, (Accepted).
2. **Lee, C. H.,** Khan, A., Wang, C., Weng, C., Buxbaum, J. D., Kiryluk, K., & Ionita-Laza, I. (2025). Liability threshold model-based disease risk prediction based on electronic health record phenotypes. Nat Genet (2025). https://doi.org/10.1038/s41588-025-02370-4
3. **Lee, C. H†.** (2025). "Pleiotropy in Multitrait Genome-Wide Association Studies: Approaches and Insights from Schizophrenia–Cognition Analyses." *Biological Psychiatry,* 98(9), 650–651. https://doi.org/10.1016/j.biopsych.2025.08.004
4. Luo, Y., Khan, A., Liu, L., **Lee, C. H.,** Perreault, G. J., Pomenti, S. F., Gourh, P., Kiryluk, K., Bernstein, E. J. (2025). "Cross-phenotype genome-wide association study of systemic sclerosis and primary biliary cholangitis." *Arthritis & Rheumatology.* 77(6): 727–739. https://doi.org/10.1002/art.43081
5. Jung, S*., **Lee, C. H*.,** Sul, J. H., & Han, B. (2023). "Building an optimal predictive model for imputing tissue-specific gene expression by combining genotype and whole-blood transcriptome data." *HGG Adv*, 4(4), 100223. https://doi.org/10.1016/j.xhgg.2023.100223
6. **Lee, C. H.,** Shi, H., Pasaniuc, B., Eskin, E., & Han, B. (2021). "PLEIO: a method to map and interpret pleiotropic loci with GWAS summary statistics." *American Journal of Human Genetics*, 108(1), 36-48. https://doi.org/10.1016/j.ajhg.2020.11.017
7. Kang, E. Y*., **Lee, C. H*.,** Furlotte, N. A., Joo, J. W. J., Kostem, E., Zaitlen, N., Eskin, E., & Han, B. (2018). "An Association Mapping Framework To Account for Potential Sex Difference in Genetic Architectures." *Genetics*, 209(3), 685-698. https://doi.org/10.1534/genetics.117.300501
8. Han, B., Akiyama, M., Kim, K. K., Oh, H., Choi, H., **Lee, C. H.,** Jung, S., Lee, H. S., Kim, E. E., Cook, S., Haritunians, T., Yamazaki, K., Park, S. H., Ye, B. D., McGovern, D. P. B., Esaki, M., Kawaguchi, T., Khor, S. S., Taylor, K. D., . . . Song, K. (2018). "Amino acid position 37 of HLA-DRbeta1 affects susceptibility to Crohn's disease in Asians." *Human Molecular Genetics*, 27(22), 3901-3910. https://doi.org/10.1093/hmg/ddy285
9. **Lee, C. H.,** Eskin, E., & Han, B. (2017). "Increasing the power of meta-analysis of genome-wide association studies to detect heterogeneous effects." *Bioinformatics*, 33(14), i379-i388. https://doi.org/10.1093/bioinformatics/btx242
10. Kim, E. E., Lee, S., **Lee, C. H.,** Oh, H., Song, K., & Han, B. (2017). "FOLD: a method to optimize power in meta-analysis of genetic association studies with overlapping subjects." *Bioinformatics*, 33(24), 3947-3954. https://doi.org/10.1093/bioinformatics/btx463
11. Yang, S. K., Hong, M., Oh, H., Low, H. Q., Jung, S., Ahn, S., Kim, Y., Baek, J., **Lee, C. H.,** Kim, E., Kim, K. M., Ye, B. D., Kim, K. J., Park, S. H., Lee, H. S., Lee, I., Shin, H. D., Han, B., McGovern, D. P. B., . . . Song, K. (2016). "Identification of Loci at 1q21 and 16q23 That Affect Susceptibility to Inflammatory Bowel Disease in Koreans." *Gastroenterology*, 151(6), 1096-+. https://doi.org/10.1053/j.gastro.2016.08.025
12. van 't Hof, F. N., Ruigrok, Y. M., **Lee, C. H.,** Ripke, S., Anderson, G., de Andrade, M., Baas, A. F., Blankensteijn, J. D., Bottinger, E. P., Bown, M. J., Broderick, J., Bijlenga, P., Carrell, D. S., Crawford, D. C., Crosslin, D. R., Ebeling, C., Eriksson, J. G., Fornage, M., Foroud, T., . . . de Bakker, P. I. (2016). "Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms." *J Am Heart Assoc*, 5(7). https://doi.org/10.1161/JAHA.115.002603

13. Network, N. S. G., & International Stroke Genetics, C. (2016). "Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study." *Lancet Neurology*, 15(2), 174-184. https://doi.org/10.1016/S1474-4422(15)00338-5
14. **Lee, C. H.,** Cook, S., Lee, J. S., & Han, B. (2016). "Comparison of Two Meta-Analysis Methods: Inverse-Variance-Weighted Average and Weighted Sum of Z-Scores." *Genomics Inform*, 14(4), 173-180. https://doi.org/10.5808/GI.2016.14.4.173
15. Jung, J*., **Lee, C. H*.,** Seol, H. S., Choi, Y. S., Kim, E., Lee, E. J., Rhee, J. K., Singh, S. R., Jun, E. S., Han, B., Hong, S. M., Kim, S. C., & Chang, S. (2016). "Generation and molecular characterization of pancreatic cancer patient-derived xenografts reveals their heterologous nature." *Oncotarget*, 7(38), 62533-62546. https://doi.org/10.18632/oncotarget.11530
16. Han, B., Pouget, J. G., Slowikowski, K., Stahl, E., **Lee, C. H.,** Diogo, D., Hu, X., Park, Y. R., Kim, E., Gregersen, P. K., Dahlqvist, S. R., Worthington, J., Martin, J., Eyre, S., Klareskog, L., Huizinga, T., Chen, W. M., Onengut-Gumuscu, S., Rich, S. S., . . . Raychaudhuri, S. (2016). "A method to decipher pleiotropy by detecting underlying heterogeneity driven by hidden subgroups applied to autoimmune and neuropsychiatric diseases." *Nat Genet*, 48(7), 803-810. https://doi.org/10.1038/ng.3572
17. Kwak, S. H., Kim, Y. J., Chae, J., **Lee, C. H.,** Han, B., Kim, J. I., Jung, H. S., Cho, Y. M., & Park, K. S. (2015). "Association of HLA Genotype and Fulminant Type 1 Diabetes in Koreans." *Genomics Inform*, 13(4), 126-131. https://doi.org/10.5808/GI.2015.13.4.126

Professional Organizations and Societies

01/2015 – Present	**American Society of Human Genetics**	International
01/2023 – Present	**International Genetic Epidemiology Society**	International

Educational and Service Contributions

01/2021 – 03/2021	**Graduate Internship Program Instructor** Genomics & Bioinformatics Lab, Seoul National University	Seoul, S. Korea
06/2018 – 10/2018	**Administrative Assistant** Genomics & Bioinformatics Lab, Seoul National University	Seoul, S. Korea
09/2013 – 06/2015	**Financial Chair** Graduate Student Organization, Carnegie Mellon University	Pittsburgh, PA

Conference Presentations – Peer-Selected (International)

- **Lee, C. H.,** Wu, H., Abiri, N., & Ionita-Laza, I. "covImpute: Leveraging Genetic Correlations to Impute Missing EHR Phenotypes". *International Genetic Epidemiology Society, Cologne, Germany*, September 2025
- **Lee, C. H.,** Eskin, E., & Han, B. "Increasing the Power of Meta-Analysis of Genome-Wide Association Studies to Detect Heterogeneous Effects". *In proceedings of the twenty-fifth conference on ISMB/ECCB,* Prague, Czech Republic, July 2017

Invited Presentations – Regional and National

- **Lee, C. H.** "Integrating Biobank-Scale EHR Data with Genome-Wide Analysis." *Oklahoma University Health Campus*, March 2026.
- **Lee, C. H.** "From Diagnosis to Liability: Quantitative Risk Stratification in Psychiatry Using Genomics and EHR Data." *Department of Psychiatry, University of Pittsburgh*, March 2026.
- **Lee, C. H.** "Integrating EHR Phenotypes and Genomics for Population-Scale Risk Estimation." *Graduate School of Medical Science and Engineering (GSMSE), KAIST*, February 2026.
- **Lee, C. H.** "Rethinking Germline Cancer Risk Modeling Using Population Genomics and Electronic Health Records". *Division of Molecular Medicine*, *University of New Mexico Comprehensive Cancer Center,* Jan 2026.
- **Lee, C. H.** "Medical Record-Based Disease Risk Prediction Model (LTPI)". *Academic Seminar hosted by Biological Research Information Center (BRIC), Pohang University of Science and Technology, South Korea*, January 2026.
- **Lee, C. H.** "From Phenotypic Correlation to Genetic Liability: Modeling Disease Risk with LTPI". *Division of Epidemiology, Vanderbilt University,* December 2025.
- **Lee, C. H.** "Multi-trait genetic inference using latent risk modeling." *Center for Disease Neurogenomics, Icahn School of Medicine at Mount Sinai,* December 2025.
- **Lee, C. H.** "My Journey to K99. Research Strategy and Innovation Social Lunch", *Office of the Vice Dean for Research Strategy, Columbia University, New York*, March 2025
- **Lee, C. H. "**Harnessing Pleiotropic Signals to Transform Precision Medicine". Cancer Control and Population Science Program Meeting, *Comprehensive Cancer Center, University of New Mexico*, New Mexico, February 2025