

Dohoon Lee

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EDUCATION

Apr. 2022 ~ Present	BK21 Four Intelligence Computing, Seoul National University <i>Postdoctoral Fellow</i>	Seoul, Korea
Sep. 2021 ~ Present	Bioinformatics Institute, Seoul National University <i>Postdoctoral Fellow</i>	Seoul, Korea
Sep. 2017 ~ Aug. 2021	Seoul National University Interdisciplinary Program in Bioinformatics <i>PhD</i> <i>Advisor: Prof. Sun Kim</i> <i>Thesis: Multi-omics driven computational modeling of the intrinsic heterogeneity of DNA methylation and its clinical application</i>	Seoul, Korea
Mar. 2013 ~ Aug. 2017	Seoul National University School of Biological Sciences <i>B.S., Major: Biological Sciences, Minor: Computer Science and Engineering</i> <i>Honors: summa cum laude (GPA 4.21/4.3)</i>	Seoul, Korea

RESEARCH INTEREST

- **Artificial Intelligence in Bioinformatics**
 - ✓ Artificial Intelligence-based modeling of genomes and epigenomes
 - ✓ Interpretable artificial intelligence for predicting the effect of alterations in genomes and epigenomes
- **Computational Biology/Epigenomics**
 - ✓ Inferring subclonal structure of cancer using next-generation sequencing data
 - ✓ Multi-omics integrative and genome-wide computational analysis of epigenomes
- **Reproducibility in Bioinformatics Research**
 - ✓ Establishing reproducible and reusable bioinformatic pipelines

PUBLICATIONS

1. **D. Lee**, B. Koo, S. Kim, J. Byun, J. Hong, D. Shin, C. Sun, J. Song, J. Kim, S. Jaiswal, S. Yoon, S. Kim, Y. Koh (2023). AMLs harboring DNMT3A-destabilizing variants show increased intratumor DNA methylation heterogeneity at bivalent chromatin domains. bioRxiv.
2. **D. Lee**, J. Yang, S. Kim (2022). Learning the histone codes with large genomic windows and three-dimensional chromatin interactions using transformer. Nature Communications.
3. B. Choi, C. Kang, S. Park, **D. Lee**, A. Lee, Y. Ko, S. Kang, K. Kang, Y. Koh, I. Jung (2022). Single-cell transcriptome analyses reveal distinct gene expression signatures of severe COVID-19 in the presence of clonal hematopoiesis. Experimental & Molecular Medicine.
4. **D. Lee**, B. Koo, J. Yang, S. Kim (2022). Meteor: Ultrafast DNA methylation heterogeneity calculation from bisulfite

read alignments. bioRxiv.

5. B. Koo, **D. Lee**, S. Lee, I. Sung, S. Kim, S. Lee (2022). Risk stratification for breast cancer patient by simultaneous learning of molecular subtype and survival outcome using genetic algorithm-based gene set selection. *Cancers*.
6. S. Park*, **D. Lee***, Y. Kim, S. Lim, H. Chae, S. Kim (2022). BioVLAB-Cancer-Pharmacogenomics: tumor heterogeneity and pharmacogenomics analysis of multi-omics data from tumor on the cloud. *Bioinformatics*.
7. J. Park, **D. Lee**, S. Ham, J. Oh, J. Noh, Y. Lee, Y. Park, G. Lee, S. Han, J. Han, Y. Kim, Y. Jeon, H. Nahmgoong, K. Shin, S. Kim, S. Choi, C. Lee, I. Park, T. Roh, S. Kim, J. Kim (2022). Targeted erasure of DNA methylation by TET3 drives adipogenic reprogramming and differentiation. *Nature Metabolism*.
8. **D. Lee**, S. Kim (2021). Knowledge-guided artificial intelligence technologies for decoding complex multiomics interactions in cells. *Clinical and experimental pediatrics*.
9. K. Jo, I. Sung, **D. Lee**, H. Jang, S. Kim (2021). Inferring transcriptomic cell states and transitions only from time series transcriptome data. *Scientific reports*.
10. **D. Lee***, Y. Park*, S. Kim (2020). Towards multi-omics characterization of tumor heterogeneity: a comprehensive review of statistical and machine learning approaches, *Briefings in Bioinformatics*.
11. M. Kang, S. Lee, **D. Lee**, S. Kim (2020). Learning Cell-Type-Specific Gene Regulation Mechanisms by Multi-Attention Based Deep Learning with Regulatory Latent Space. *Frontiers in Genetics*.
12. M. Oh, S. Park, S. Lee, **D. Lee**, S. Lim, D. Jeong, K. Jo, I. Jung, S. Kim (2020). DRIM: A web-based system for investigating drug response at the molecular level by condition-specific multi-omics data integration. *Frontiers in Genetics*.
13. **D. Lee**, S. Lee, S. Kim (2019). PRISM: methylation pattern-based, reference-free inference of subclonal makeup, *Bioinformatics*.

CONFERENCES

1. **D. Lee**, S. Lee, S. Kim (2019), "PRISM: methylation pattern-based, reference-free inference of subclonal makeup", ISMB/ECCB 2019, Basel, Switzerland – *Oral presentation (Proceedings presentation)*.
2. **D. Lee**, S. Lee, S. Kim (2019), "PRISM: methylation pattern-based, reference-free inference of subclonal makeup", BIOINFO 2019, Seoul, Korea – *Oral presentation (Award lecture session)*.
3. **D. Lee**, S. Lee, S. Kim (2019), "PRISM: methylation pattern-based, reference-free inference of subclonal makeup", The Second Korea-Japan Machine Learning Workshop, Jeju, Korea – *Foster presentation*.

RESEARCH EXPERIENCES

- **Research Intern** at *School of Biological Sciences, Seoul National University* Sep. 2015 ~ Dec. 2016
 - ✓ Gut metagenome-based Type 2 diabetes prediction model using machine learning techniques

AWARDS AND HONORS

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| 2021 | Participation prize, 27 th SAMSUNG Humantech Paper Award
- for "Deep learning reveals the general rules shaping the potential energy landscape of DNA methylation patterns" |
| 2020 | Youlchon AI for All fellowship, Youlchon Foundation, Korea |
| 2019 | Outstanding Paper Award, BIOINFO 2019, Seoul, Korea
- for "PRISM: methylation pattern-based, reference-free inference of subclonal makeup" |
| 2019 | Merit Award: Bronze prize, 45 th Annual Meeting of Korean Cancer Association and 5 th International Cancer Conference, Seoul, Korea
- for "PRISM: methylation pattern-based, reference-free inference of subclonal makeup" |
| 2017 | Graduation with honors: <i>summa cum laude</i> , Seoul National University, Korea |

2015 ~ 2016

KEF Domestic Scholarship, Kwanjeong Educational Foundation, Korea