

# Dohoon Lee

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## EDUCATION

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Apr. 2022 ~ Present	<b>BK21 Four Intelligence Computing, Seoul National University</b> <i>Postdoctoral Fellow</i>	Seoul, Korea
Sep. 2021 ~ Present	<b>Bioinformatics Institute, Seoul National University</b> <i>Postdoctoral Fellow</i>	Seoul, Korea
Sep. 2017 ~ Aug. 2021	<b>Seoul National University</b> 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	<b>Seoul National University</b> 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

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- **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

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1. **D. Lee**, J. Yang, S. Kim (2022). Learning the histone codes with large genomic windows and three-dimensional chromatin interactions using transformer. *Nature Communications*.
2. 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*.
3. **D. Lee**, B. Koo, J. Yang, S. Kim (2022). Metheor: Ultrafast DNA methylation heterogeneity calculation from bisulfite read alignments. *bioRxiv*.
4. 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*.

5. 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*.
6. 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, J. Park, T. Roh, S. Kim, J. Kim (2022). Targeted erasure of DNA methylation by TET3 drives adipogenic reprogramming and differentiation. *Nature Metabolism*.
7. **D. Lee**, J. Yang, S. Kim (2021). Learning the histone codes of gene regulation with large genomic windows and three-dimensional chromatin interactions using transformer. *bioRxiv*.
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

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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 – *Poster presentation*.

## RESEARCH EXPERIENCES

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- **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 <sup>th</sup> 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 <sup>th</sup> Annual Meeting of Korean Cancer Association and 5 <sup>th</sup> 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