

BYOUNGKOO LEE, Ph.D.

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Summary

- Expertise in Computational Biology, Bioinformatics, Data Science, and Computational Modeling & Simulation
- Recent 4 years working with NGS data analysis, pipeline development and visualization for 3D genomics ENCODE and 4DN research projects, funded by NIH.
- Strong background and experience in computational tools and statistical analysis (C/C++, Matlab, Shell Programming, Unix-based pipeline, R, Python)

Research projects in Jax:

- 1) ENCODE and 4DN consortium projects about 3D genomics
 - ChIA-PET (chromatin interaction analysis by paired-end tag sequencing)
Data processing pipeline (ChIA-PIPE) development, visualization and analysis of processed data files
 - Processing raw sequencing files, assessing data quality, and submitting datasets to ENCODE DCC
- 2) New method developments to reveal multiplex chromatin interactions
 - ChIA-Drop (droplet-based and barcode-linked sequencing)
 - ChIA-DropBox (data processing pipeline tool for ChIA-Drop)
- 3) 3D genome analysis of Acute Promyeloid Leukemia
 - Producing and analyzing whole genome wide interaction maps for various treatment conditions and control case
- 4) 3D chromatin folding super-resolution imaging projects
 - 3D-EMISH (electron microscopy with in situ hybridization), collaborated with Grzegorz M. Wilczyński's group
 - iPALM (interferometric photoactivated localization microscopy), collaborated with Dariusz Plewczynski's group

Research interests:

- 1) Genome Sciences based on multi-omics data (ChIP-seq, HiC, ChIA-PET, ATAC-Seq, RNA-Seq)
- 2) Long-read sequencing technology
- 3) 3D Genomics

Employments

2021 – present, Research Scientist, The Jackson Laboratory for Genomic Medicine, Farmington, CT.
2017 – 2021, Associate Research Scientist, The Jackson Laboratory for Genomic Medicine, Farmington, CT.
2016 – 2017, Postdoctoral research fellow, Center for Quantitative Medicine, UConn Health, Farmington, CT.
2011 – 2015, Postdoctoral research fellow, Mathematics and Statistics, Georgia State University, Atlanta, GA.
2009 – 2011, Postdoctoral research associate, Computational Biology, Carnegie Mellon University, Pittsburgh, PA.
2000 – 2004, Software engineer, Willtech, South Korea.
1998 – 2000, Research engineer, KNC, South Korea.

Educations

Ph.D., Joint Carnegie Mellon/University of Pittsburgh Computational Biology Program, Pittsburgh, PA, August 2009
M.S., Department of Electronic Engineering, Konkuk University, Seoul, Korea, August 1998
B.S., Department of Electronic Engineering, Konkuk University, Seoul, Korea, February 1996

Publications

1. **B. Lee**, J. Wang, L. Cai, M. Kim, S. Namburi, H. Tjong, Y. Feng, P. Wang, Z. Tang, A. Abbas, C. Wei, Y. Ruan, S. Li, ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization, *Science Advances*, 2020.
2. P. Trzaskoma, B. Ruszczycki, **B. Lee**, K. K. Pels, K. Krawczyk, G. Bokota, A. A. Szczepankiewicz, J. Aaron, A. Walczak, M. A. Śliwińska, A. Magalska, M. Kadlof, A. Wolny, Z. Parteka, S. Arabasz, M. Kiss-Arabasz, D. Plewczynski, Y. Ruan, G. M. Wilczyński, Ultrastructural visualization of 3D chromatin folding using volume electron microscopy and DNA in situ hybridization, *Nature Communications*, 2020. (**co-first author**)

3. P. Wang, Z. Tang, **B. Lee**, J. J. Zhu, L. Cai, P. Szalaj, S. Z. Tian, M. Zheng, D. Plewczynski, X. Ruan, E. T. Liu, C. Wei, Y. Ruan, Chromatin topology reorganization and transcription repression by PML-RAR α in acute promyeloid leukemia, *Genome Biology*, 2020.
4. M. Kim, M. Zheng, S. Z. Tian, **B. Lee**, J. H. Chuang, Y. Ruan, MIA-Sig: multiplex chromatin interaction analysis by signal processing and statistical algorithms, *Genome Biology*, 2019.
5. M. Zheng, S. Z. Tian, D. Capurso, M. Kim, R. Maurya, **B. Lee**, E. Piecuch, L. Gong, J. J. Zhu, Z. Li, C. H. Wong, C. Y. Ngan, P. Wang, X. Ruan, C. Wei, Y. Ruan, Multiplex chromatin interactions with single-molecule precision, *Nature*, 2019.
6. S. Z. Tian, D. Capurso, M. Kim, **B. Lee**, M. Zheng, Y. Ruan, ChIA-DropBox: a novel analysis and visualization pipeline for multiplex chromatin interaction, *BioRxiv*, 2019
7. J. J. Zhu, Z. Parteka, **B. Lee**, P. Szalaj, P. Wang, K. Jodkowska, J. Aaron, T. Chew, D. Plewczynski, Y. Ruan, Super resolution imaging of a distinct chromatin loop in human lymphoblastoid cells, *BioRxiv*, 2019.
8. L. Vian, A. Pekowska, S. S.P. Rao, K. Kieffer-Kwon, S. Jung, L. Baranello, S. Huang, L. El Khattabi, M. Dose, N. Pruett, A. L. Sanborn, A. Canela, Y. Maman, A. Oksanen, W. Resch, X. Li, **B. Lee**, A. L. Kovalchuk, Z. Tang, S. Nelson, M. Di Pierro, R. R. Cheng, I. Machol, B. G. St Hilaire, N. C. Durand, M. S. Shamim, E. K. Stamenova, J. N. Onuchic, Y. Ruan, A. Nussenzweig, D. Levens, E. L. Aiden, and R. Casellas, The energetics and physiological impact of cohesin extrusion, *Cell*, 2018.
9. **B. Lee**, J. Konen, S. Wilkinson, A. I. Marcus, Y. Jiang, Local alignment vectors reveal cancer cell-induced ECM fiber remodeling dynamics, *Scientific Reports*, 2017.
10. X. He, **B. Lee**, and Y. Jiang. Systems Biology of Tumor Microenvironment: Quantitative Modeling and Simulations, *Springer, Chapter IV*, 2016.
11. J. Konen, S. Wilkinson, **B. Lee**, H. Fu, W. Zhou, Y. Jiang, and A. I. Marcus. LKB1 kinase-dependent and – independent defects disrupt polarity and adhesion signaling to drive collagen remodeling during invasion, *Mol. Biol. Cell*, 2016.
12. **B. Lee**, X. Zhou, K. Riching, K. W. Eliceiri, P. J. Keely, S. A. Guelcher, A. Weaver, Y. Jiang, A three-dimensional computational model of collagen network mechanics, *PLoS ONE*, 2014.
13. G. R. Smith, L. Xie, **B. Lee**, R. Schwartz, Applying molecular crowding models to simulations of virus capsid assembly *in vitro*, *Biophysical Journal*, 2014.
14. **B. Lee**, P. R. LeDuc, and R. Schwartz, Three-dimensional stochastic off-lattice model of binding chemistry in crowded environments, *PLoS ONE*, 2012.
15. **B. Lee**, P. R. LeDuc, and R. Schwartz, Unified regression model of binding equilibria in crowded environments, *Scientific Reports*, 2011.
16. **B. Lee**, P. R. LeDuc, and R. Schwartz, Parameter effects on binding chemistry in crowded media using a two-dimensional stochastic off-lattice model, *Physical Review E*, 2009
17. **B. Lee**, P. R. LeDuc, and R. Schwartz, Stochastic off-lattice modeling of molecular self-assembly in crowded environments by Green's function reaction dynamics, *Physical Review E*, 2008

Under review:

1. Super-resolution imaging of chromatin loop structures in human cells
2. In situ chromatin interaction analysis using paired-end tag sequencing
3. Single-molecule mapping reveals the dynamics of chromatin folding in the human genome

Conference meeting and research symposiums

1. Poster Presentation, ENCODE annual meeting, 2019
B. Lee, M. Zheng, S. Z. Tian, M. Kim, Y. Ruan, ChIA-Drop and ChIA-DropBox to reveal multiplex chromatin interactions with single-molecule precision
2. Invited talk, Human Frontier Science Program, Mini-Symposium, Poland, 2018
3. Poster spotlight talk and poster presentation in Q-Bio Conference, Blacksburg, VA, August 7, 2015
B. Lee, J. Konen, S. Xu, A. I. Marcus, Y. Jiang, Cancer cell invasion analysis in ECM using *in vitro* models.
4. Research talk in Society for Mathematical Biology, Atlanta, GA, July 1, 2015
B. Lee, K. W. Eliceiri, P. J. Keely, A. Weaver, Y. Jiang, Three-dimensional computational model of collagen fiber network.
5. Two poster presentations in Scientific Research and Academic Development Symposium, Winship Cancer Institute Emory University, Atlanta, GA, October 23, 2014
B. Lee, S. Xu, J. Konen, A. I. Marcus, Y. Jiang, Invasion analysis from a cell and ECM perspective.
B. Lee, X. Zhou, K. Riching, K. W. Eliceiri, P. J. Keely, S. A. Guelcher, A. Weaver, Y. Jiang, Three-dimensional computational model of collagen network mechanics.
6. Poster presentation in Q-Bio Conference, Santa Fe, NM, August 14, 2014
B. Lee, S. Xu, J. Konen, A. I. Marcus, Y. Jiang, Invasive behavior analysis of glioblastoma spheroids in different mechanotransduction signaling molecules.
7. Research talk in Q-Bio Conference, Santa Fe, NM, August 8, 2013
B. Lee, K. W. Eliceiri, P. J. Keely, A. Weaver, Y. Jiang, Modeling extracellular matrix in breast cancer.
8. Poster presentation in Integrative Cancer Biology Program, Rockville, MD, May 7, 2013
B. Lee, K. W. Eliceiri, P. J. Keely, A. Weaver, Y. Jiang, Modeling extracellular matrix in breast cancer.
9. Research talk in Frontiers in Systems and Synthetic Biology, Atlanta, GA, March 22, 2013
B. Lee, K. W. Eliceiri, P. J. Keely, A. Weaver, Y. Jiang, Computational model of extracellular matrix interacting with growing and migrating cancer cells.
10. Poster presentation in Q-Bio Conference, Santa Fe, NM, August 9, 2012
B. Lee, K. W. Eliceiri, P. J. Keely, A. Weaver, Y. Jiang, Three dimensional mathematical model of extracellular matrix in breast cancer.
11. Poster presentation in Q-Bio Conference, Santa Fe, NM, August 12, 2011
B. Lee, P. R. LeDuc, and R. Schwartz, Multi-scale simulation method for self-assembly in crowded environments.
12. Research talk in Simulators Meeting, Carnegie Mellon University, Pittsburgh, PA, May 24, 2011
B. Lee, Multi-scale simulation method of virus assembly in crowded environments.
13. Poster presentation in Biophysical Society Meeting, Baltimore, MD, March 9, 2011
B. Lee, P. R. LeDuc, and R. Schwartz, Toward a unified model of molecular crowding: a regression approach to predict equilibria and kinetics of assembly systems in crowded environments.
14. Research talk in Simulators Meeting, Carnegie Mellon University, Pittsburgh, PA, June 15, 2010
B. Lee, Synergistic and non-synergistic parameter effects on binding equilibria in crowded conditions.
15. Poster presentation in Biophysical Society Meeting, San Francisco, CA, February 21, 2010
B. Lee, P. R. LeDuc, and R. Schwartz, Simulation study of binding chemistry in crowded conditions using two- and three-dimensional stochastic off-lattice models.
16. Research talk in Simulators' Meeting, Carnegie Mellon University, Pittsburgh, PA, June 9, 2009
B. Lee, Simulation study of parameter effects on binding chemistry in crowded media.
17. Research talk in Biomedical Engineering and Biotechnology Research Symposium (BEBRS), Carnegie Mellon University, Pittsburgh, PA, April 23, 2009
B. Lee, Parameter effects of crowding on binding chemistry using 2D stochastic off-lattice model.
18. Poster presentation in Biophysical Society Meeting, Boston, MA, March 1, 2009
B. Lee, P. R. LeDuc, and R. Schwartz, Parameter effects of crowding on binding chemistry using 2D stochastic off-lattice simulations.
19. Poster presentation in Biomedical Engineering and Biotechnology Research Symposium (BEBRS), Carnegie Mellon University, Pittsburgh, PA, April 25, 2008
B. Lee, P. R. LeDuc, and R. Schwartz, Stochastic off-lattice modeling of molecular self-assembly in crowded environments by Green's function reaction dynamics.

Teaching experience, seminar, and invitation

1. Lecture and tutorial session, ChIA-PET Workshop, The Jackson Laboratory, 2017
2. Guest lecture in “Science Perspective on Global Problems” course in Georgia State University, Fall 2015
3. Early stage investigators in Cancer Systems Biology steering committee meeting, Broad Institute, Boston, MA. 2014
4. Guest lectures in Systems Biology course in Georgia State University, Fall 2013 and Fall 2015
5. Mathematical biology seminar in Georgia State University, September 21, 2012
6. Guest lecture and teaching assistant in Computational Methods for Biological Modeling and Simulation course, Fall 2008

Article review

Mathematical Biosciences and Engineering, Briefings in Bioinformatics, Biomechanics and Modeling in Mechanobiology, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Workshop on Algorithms in Bioinformatics (WABI), Research in Computational Molecular Biology (RECOMB), International Mechanical Engineering Congress & Exposition - American Society of Mechanical Engineers (IMECE-ASME)

Professional organization memberships

Society for Mathematical Biology, 2015
Biophysical Society, 2009 - 2011
American Physical Society, 2009