

# Stanford

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## Hayan Lee

Postdoctoral Research Fellow, Genetics

### Bio

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#### BIO

I am a postdoctoral scholar at Genetics Department, Stanford University. Before I moved to Stanford, I served as a Simons postdoctoral fellow at Joint Genome Institute (JGI). I have earned my Ph.D. in Computer Science Department at Stony Brook University. My dissertation is about “Algorithms and applications in genome assembly using long read sequencing technology”, advised by Prof. Michael Schatz, Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory (CSHL). I received my Master’s degree from Carnegie Mellon University. The master thesis was published at 70th IEEE Vehicular Technology Conference. My undergraduate degree with Cum Laude was received at Seoul National University in Korea and worked for 4 years at AhnLab, Inc., where I programmed Windows kernel-level file system filter driver for V3 anti-virus program.

I am interested in developing methods (tools/software) using statistical machine learning and deep learning using clinical data and/or long reads produced by 3rd generation sequencing technology such as PacBio, Moleculo, Oxford Nanopore, etc. This includes de novo genome assembly, single cell, cancer data analysis, time series data analysis and population structure to analyze big data, infer critical factors, predict the future and discover biological importance.

#### HONORS AND AWARDS

- Simons postdoctoral fellowship, Lawrence Berkeley National Laboratory (2015-2016)
- Fellowship, Stony Brook University (2009-2010)
- Scholarship from CyLab, Carnegie Mellon University, (2006-2007)

#### BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Program Committee, Pacific Symposium on Biocomputing (PSB) (2015 - 2015)
- Program Committee, Pacific Symposium on Biocomputing (PSB) (2014 - 2014)

#### PROFESSIONAL EDUCATION

- Doctor of Philosophy, S.U.N.Y. State University at Stony Brook (2015)
- Master of Science, Carnegie Mellon University (2008)

#### STANFORD ADVISORS

- Michael Snyder, Postdoctoral Faculty Sponsor

#### LINKS

- Webpage: <https://hayanlee.wordpress.com/>

### Research & Scholarship

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#### LAB AFFILIATIONS

- Michael Snyder, Snyder Lab (9/1/2016)

## Publications

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### PUBLICATIONS

- **Piercing the dark matter: bioinformatics of long-range sequencing and mapping** *NATURE REVIEWS GENETICS*  
Sedlazeck, F. J., Lee, H., Darby, C. A., Schatz, M. C.  
2018; 19 (6): 329–46
- **Hybrid assembly with long and short reads improves discovery of gene family expansions** *BMC GENOMICS*  
Miller, J. R., Zhou, P., Mudge, J., Gurtowski, J., Lee, H., Ramaraj, T., Walenz, B. P., Liu, J., Stupar, R. M., Denny, R., Song, L., Singh, N., Maron, et al  
2017; 18
- **The pineapple genome and the evolution of CAM photosynthesis** *NATURE GENETICS*  
Ming, R., VanBuren, R., Wai, C., Tang, H., Schatz, M. C., Bowers, J. E., Lyons, E., Wang, M., Chen, J., Biggers, E., Zhang, J., Huang, L., Zhang, et al  
2015; 47 (12): 1435–+
- **SplitMEM: a graphical algorithm for pan-genome analysis with suffix skips** *BIOINFORMATICS*  
Marcus, S., Lee, H., Schatz, M. C.  
2014; 30 (24): 3476–83
- **Whole genome de novo assemblies of three divergent strains of rice, *Oryza sativa*, document novel gene space of aus and indica** *GENOME BIOLOGY*  
Schatz, M. C., Maron, L. G., Stein, J. C., Hernandez Wences, A., Gurtowski, J., Biggers, E., Lee, H., Kramer, M., Antoniou, E., Ghiban, E., Wright, M. H., Chia, J., Ware, et al  
2014; 15 (11): 506
- **Virmid: accurate detection of somatic mutations with sample impurity inference** *GENOME BIOLOGY*  
Kim, S., Jeong, K., Bhutani, K., Lee, J., Patel, A., Scott, E., Nam, H., Lee, H., Gleeson, J. G., Bafna, V.  
2013; 14 (8): R90
- **Genomic dark matter: the reliability of short read mapping illustrated by the genome mappability score** *BIOINFORMATICS*  
Lee, H., Schatz, M. C.  
2012; 28 (16): 2097–2105
- **On the Security of Intra-Car Wireless Sensor Networks**  
Lee, H., Tsai, H., Tonguz, O. K., IEEE  
IEEE.2009: 663–+