

# HYUN JUNG PARK

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## EMPLOYMENT

2018 ~ present **Assistant Professor**, Human Genetics, University of Pittsburgh  
2012 ~ 2017 **Postdoc Associate**, Duncan Cancer Center, Baylor College of Medicine  
2000 ~ 2003 **Lead, Security System Platform**, Department of R&D, SeNeX Technologies. Co. Ltd.

## EDUCATION

2012 **Ph.D., Computer Science**, Rice University, Houston, TX  
Dissertation: Towards Accurate Reconstruction of Phylogenetic Networks  
Thesis Advisor: Dr. Luay K. Nakhleh  
2007 **M.S., Computer Science**, Texas A&M University, College Station, TX  
Dissertation: Large-scale Analysis of Phylogenetic Tree Search Space  
Thesis Advisor: Dr. Tiffani L. Williams  
2005 **B.S., Computer Science**, Yonsei University, Seoul, Korea

## PUBLICATIONS

### *Works in Progress*

1. H-c. E. Leung<sup>^\*</sup>, **H-J Park<sup>^</sup>**, L. M. Lui, W. Li, H. C. Adams III, Michael T. Lewis, "Towards deep protein sequencing: thermal hydroiodic acid digestion of proteins." in revision in Nature Methods

<sup>^</sup> indicates first author. \* indicates corresponding author.

### *Papers in Peer-reviewed Journals*

1. **H-J. Park<sup>^</sup>**, P. Ji<sup>^</sup>, S. Kim, Z. Xia, B. Rodriguez, C-P. Masamha, A-B, Shyu, J. Neilson, E.J. Wagner\*, W. Li\*, "3' UTR shortening Down-regulates Tumor Suppressors *in trans* by Disrupting the CeRNA Crosstalk." accepted in principle in Nature Genetics
2. **H-J. Park<sup>^\*</sup>**, S. Kim, B. Rodriguez, W. Li\*, "Discovering Dysregulated Competing-endogenous Pathways in Cancer." accepted in principle in PLoS Computational Biology
3. M. Jeong<sup>^</sup>, **H-J. Park<sup>^</sup>**, M. Celik, E. L. Ostrander, J. M. Reyes, A. Guzman, B. Rodriguez, Y. Lee, L. Ding, W. Li, G. A. Challen\*, M. A. Goodell\*, "Loss of Dnmt3a Immortalizes Hematopoietic Stem Cell *in vivo*." accepted in principle in Cell Stem Cell
4. Y-h. Lee<sup>^</sup>, N. Martin-Orozco, P. Zheng, J. Li, P. Zheng, H. Tan, **H-J. Park**, M. Jeong, S. H. Chang, B. Kim, W. Xiong, W. Zang, L. Guo, Y. Liu, Z-j. Dong, W. Overwijk, P. Hwu, Q. Yi, L. Kwak, Z. Yang, T. W. Mak, W. Li, L. Radvanyi, L. Ni, D. Liu, C. Dong\*, "Inhibition of B7-H3 checkpoint limits tumor growth by enhancing cytotoxic lymphocyte function." Cell Research, 27(8), 1034-1045, 2017.  
[DOI:10.1038/cr.2017.90](https://doi.org/10.1038/cr.2017.90)

5. L. Yang<sup>^</sup>, B. Rodriguez<sup>^</sup>, A Mayle<sup>^</sup>, **H-J. Park**, X. Lin, M. Luo, M. Jeong, C. V. Curry, S. Kim, D. Ruau, X. Zhang, T. Zhou, M. Zhou, V. I. Rebel, G. A. Challen, B. Gottgens, J. Lee, R. Rau<sup>7</sup>, W. Li<sup>\*</sup> and M. A. Goodell<sup>\*</sup>, "DNMT3A loss drives enhancer hypomethylation in FLT3-ITD-associated leukemias." *Cancer Cell*, 29(6), 922-934, 2016. DOI:[10.1016/j.ccell.2016.05.003](https://doi.org/10.1016/j.ccell.2016.05.003)
6. X. Zhang<sup>^</sup>, J. Su<sup>^</sup>, M. Jeong, M. G. Ko, Y. Huang, **H. J. Park**, A. Guzman, Y. Lei, Y-H, Huang, A. Rao, W. Li<sup>\*</sup> and M. A. Goodell<sup>\*</sup>, "DNMT3A and TET2 compete and cooperate to repress differentiation lineage-specific factors in hematopoietic stem cells." *Nature Genetics*, 48(9), 1014-1023, 2016. [nature.com/ng/journal/v48](http://nature.com/ng/journal/v48)
7. L. Min<sup>^</sup>, M. Jeong<sup>^</sup>, D. Sun<sup>^</sup>, **H-J. Park**<sup>^</sup>, B. Rodriguez<sup>^</sup>, Z. Xia, L. Yang, X. Zhang, GJ. Darlington, W. Li<sup>\*</sup> and M.A. Goodell<sup>\*</sup>, "Long Non-coding RNAs Control Hematopoietic Stem Cell (HSC) Function." *Cell Stem Cell*, 16(4):426-38, 2015. DOI:[10.1016/j.stem.2015.02.002](https://doi.org/10.1016/j.stem.2015.02.002)
8. D. Sun<sup>^</sup>, Y. Xi, B. Rodriguez, **H-J. Park**, T. Pan, M. Jeong, M.A. Goodell, W. Li<sup>\*</sup>, "MOABS: model based analysis of bisulfite sequencing data." *Genome Biology*15: R38, 2014. DOI:[10.1186/gb-2014-15-2-r38](https://doi.org/10.1186/gb-2014-15-2-r38)
9. L. Wang<sup>^</sup>, **H-J. Park**<sup>^</sup>, S. Wang, J-P Kocher, W. Li<sup>\*</sup>, "CPAT: Coding-Potential Assessment Tool Using an Alignment-Free Logistic Regression Model." *Nucleic Acid Research* 41(6), 2013, DOI:[10.1093/nar/gkto06](https://doi.org/10.1093/nar/gkto06)
10. **H-J. Park**<sup>^</sup> and L. Nakhleh<sup>\*</sup>, "Inference of Reticulate Evolutionary Histories by Maximum Likelihood: The Performance of Information Criteria." *BMC Bioinformatics*, 13: S12, 2012. [bmcbioinformatics.biomedcentral.com/articles](http://bmcbioinformatics.biomedcentral.com/articles)
11. **H-J. Park**<sup>^</sup>, G. Jin<sup>^</sup>, and L. Nakhleh<sup>\*</sup>, "Bootstrap-based Support of HGT Inferred by Maximum Parsimony." *BMC Evolutionary Biology*, 10: 131, 2010. DOI:[10.1186/1471-2148-10-131](https://doi.org/10.1186/1471-2148-10-131)

### *Papers in Peer-reviewed Conference Proceedings*

(\* indicates the conference proceedings were published as a special issue of a journal; the paper is listed above as well.)

- \* 1. **H-J. Park**<sup>^</sup> and L. Nakhleh<sup>\*</sup>, "Inference of Reticulate Evolutionary Histories by Maximum Likelihood: The Performance of Information Criteria." *RECOMB Comparative Genomics*, 2012
2. **H-J. Park**<sup>^</sup> and L. Nakhleh<sup>\*</sup>, "MURPAR: A Fast Heuristic for Inferring Parsimonious Phylogenetic Networks from Multiple Gene Trees." *The 8th International Symposium on Bioinformatics Research and Applications (ISBRA). Lecture Notes in Bioinformatics (LNBI #7292)*, pp. 213-224, 2012. DOI:[10.1007/978-3-642-30191-9\\_20](https://doi.org/10.1007/978-3-642-30191-9_20)
3. **H-J. Park**<sup>^</sup>, G. Jin and L. Nakhleh<sup>\*</sup>, "Algorithmic strategies for estimating the amount of reticulation from a collection of gene trees." *Proceedings of the 9th Annual International Conference on Computational Systems Biology*, 114-123, 2010. [lifesciencessociety.org/CSB2010](http://lifesciencessociety.org/CSB2010)
4. **H-J. Park**<sup>^</sup> and T. L. Williams<sup>\*</sup>, "A Fitness Distance Correlation Measure for Evolutionary Trees." *1st International Conference on Bioinformatics and Computational Biology (BiCoB). Lecture Notes in Computer Science (LNCS #5462)*, pp. 331-342, 2009. DOI:[10.1007/978-3-642-00727-9\\_31](https://doi.org/10.1007/978-3-642-00727-9_31)

### *Book Chapters*

1. **H-J. Park**<sup>^</sup>, S-J. Sul, and T. L. Williams<sup>\*</sup>, "Large-Scale Analysis of Phylogenetic Search Behavior." *Advances in Computational Biology*, H.R. Arabnia, ed., Springer, vol. 680, pages 35-42, 2010, DOI:[10.1007/978-1-4419-5913-3\\_5](https://doi.org/10.1007/978-1-4419-5913-3_5)

*Technical Reports*

1. **H-J. Park**<sup>^</sup>, S-J. Sul, and T. L. Williams\*, "Large-Scale Analysis of Phylogenetic Search Behavior." Technical Report TR-2009-12-1, Department of Computer Science, Texas A&M University, 2009, [engineering.tamu.edu/media](http://engineering.tamu.edu/media)

*Research Abstracts Presented*

1. X. Zhang<sup>^</sup>, M. Jeong, J. Su, M. G. Ko, Y. Hunag, **H-J. Park**, A. Rao, W. Li, M. A. Goodell\*, "Dnmt3a and Tet2 interact to Repress differentiation lineage-specific transcriptional factors in Hematopoietic Stem Cells By the Regulation of Epigenome." *Blood*, 124, 21, 2014
2. K. Jung<sup>^\*</sup> and **H-J. Park**, "Multilevel Dynamic GSA." 8th International Conference on Partial Least Squares and Related Methods, 2014
3. M. Jeong<sup>^</sup>, D. Sun<sup>^</sup>, **H-J. Park**<sup>^</sup>, L. Yang, H. Wang, R. Chen, G. Darlington, W. Li, M. A. Goodell\*, "Long Non-Coding RNAs Control Hematopoietic Stem Cells (HSC) Function." *Blood*, 122, 21, 2013
4. Y. Zhang<sup>^</sup>, M-K. Lee, X. Zhang, B. Payne, **H-J. Park**, JJ. Dong, C. Scheuring, MP. Zhang, ME. Delany, JB. Dodgson, H-B. Zhang\*, "A BAC-based Integrated Physical, Genetic and Comparative Map of the Turkey, Chicken and Human Genomes." International Plant & Animal Genome Conference XIX, P470, 2011.
5. M-K. Lee<sup>^</sup>, X. Zhang, Y. Zhang, B. Payne, JJ. Dong, **H-J. Park**, C. Scheuring, ME. Delany, JB. Dodgson, H-B. Zhang\*, "Toward a robust BAC-based physical and comparative map of the turkey genome." International Plant & Animal Genome Conference XVII, P520, 2009.
6. M-K. Lee<sup>^</sup>, B. Payne, JJ. Dong, **H-J. Park**, X. Zhang, JB. Dodgson, H-B. Zhang\*, "First-generation physical and comparative map of the turkey genome constructed by BAC fingerprint analysis with capillary electrophoresis." International Plant & Animal Genome Conference XVI, P284. 2008.
7. M-K. Lee<sup>^</sup>, **H-J. Park**, JB. Dodgson, H-B. Zhang\*, "Toward A BAC-based physical and comparative map of the turkey genome." International Plant & Animal Genome Conference XV, P569, 2007.

## PATENT

*Pending*

H-c. E. Leung<sup>^</sup>, H. C. Adams III<sup>^</sup>, and **H-J Park**<sup>^</sup>, "Thermal Hydroiodic acid digestion of proteins.", <sup>^</sup>equally contributed.

## TEACHING

Fall 2011, **Teaching Assistant**, Graduate Seminar on Computational Biology (Rice-Comp670)

- Gave lectures on the coalescent theory and guided term collaborative projects to 30 students

Spring 2011, **Teaching Assistant**, Technology and Politics in the Information Age (Rice-Comp301)

- Designed over 4 homeworks for technical parts of the course

Spring 2010, **Volunteer Instructor**, Adaptive Systems (Rice-Comp540)

- Gave lectures on Bayesian network in analogy with phylogenetic networks

2009 Spring and 2010 Spring, **Teaching Assistant**, Applied Algorithms and Data Structures (Rice-Comp314)

- Reviewed project design of more than 10 term projects and guided students on the projects on a weekly basis

2008 Fall and 2009 Fall, **Teaching Assistant**, Intermediate Programming (Rice-Comp212)

- Gave lectures on the object-oriented programming in lab sessions and held discussion sessions for long-term projects

## MENTORING

- Weijiang Zhou, Ph.D. student at Baylor College of Medicine
- Jianfeng Xu, Ph.D. student at Baylor College of Medicine
- Dr. Xuequi Lin, former Ph.D. student at Baylor College of Medicine
- Dr. Lei Li, a junior postdoc at Baylor College of Medicine
- Dr. Benjamin Rodriguez, a junior postdoc at Baylor College of Medicine
- Dr. Soyeon Kim, former Ph.D. student at Rice University

## PRESENTATIONS AND POSTERS

### *Presentations and Invited Talks*

"Insights into RNA Biology from Computational Modeling for Cancer Therapeutics." Human Genetics seminar, University of Pittsburgh, Feb, 2018

"Insights into RNA Biology from Computational Modeling for Cancer Therapeutics." Special seminar, University of Pittsburgh, Department of Human Genetics, Sep, 2017

"Integrative Mechanisms of Post-transcriptional Regulation in Cancer." Special seminar, University of Texas, Health Science Center at Houston, Apr, 2017

"Integrative Mechanisms of Post-transcriptional Regulation in Cancer." Young Korean Scientist Trainee Meeting, Baylor College of Medicine, Feb, 2017

"3' UTR Shortening Down-regulates Tumor Suppressors *in trans* by Disrupting the ceRNA Crosstalk." RNA Group Meeting, Baylor College of Medicine, Feb, 2015

"CPAT: Coding-Potential Assessment Tool Using an Alignment-Free Logistic Regression Model." Bio and Health Informatics Lab, Seoul National University, May, 2013

"Long Non-coding RNAs Control Hematopoietic Stem Cell (HSC) Function." Ewha Research Center for System Biology, Ewha Women's University, May, 2013

"CPAT: Coding-Potential Assessment Tool Using an Alignment-Free Logistic Regression Model." The OMICS Lab, Korea Advanced Institution of Science and Technology, May, 2013

"Estimating coding potential and coding residue." RNA Group Meeting, Baylor College of Medicine, Mar, 2013

"Inference of Reticulate Evolutionary Histories by Maximum Likelihood: The Performance of Information Criteria." Research in Computational Molecular Biology, Comparative Genomics, Oct, 2012

"MURPAR: A Fast Heuristic for Inferring Parsimonious Phylogenetic Networks from Multiple Gene Trees." International Symposium on Bioinformatics Research and Applications, May, 2012

"Toward Accurate Reconstruction of Phylogenetic Networks." Dan L. Duncan Cancer Center and Department of Molecular and Cellular Biology, Baylor College of Medicine, Jan, 2012

"Computer Science Techniques in Computational Biology Studies." Computer Science Department, Yonsei University, Jun, 2010

"Horizontal Gene Transfer detection based on optimization criteria." Life Science Department, Ewha Women's University, Jun, 2010

"How to Use PKI System for Real-world Applications." Annual staff meeting in Mokwon University, Jan, 2003

### Posters

"3' UTR Shortening Down-regulates Tumor Suppressors *in trans* by Disrupting the ceRNA Crosstalk." 10th breast cancer retreat, Baylor College of Medicine, Oct, 2014

"Bootstrap-based Support of HGT Inferred by Maximum Parsimony." 8th Society for Molecular Biology and Evolution, Jun, 2010

"Gene interaction networks perspective enhance understanding enigmatic evolutionary phenomena." Rice University Centennial Poster Session, May, 2012

"The potential to predict linkage disequilibrium in the human haplotype map by gene-gene interaction network." Computational & Theoretical Biology Symposium, May, 2008

"8.63% functionally interacting genes co-locate on human haplotypes." 4th Annual Institute of Biosciences and Bioengineering Symposium, IBB Symposium, Mar, 2008

"How PKI System Works for Internet-banking." Security World Expo 2002, May, 2002

## SELECTED AWARDS AND FELLOWSHIPS

Travel Fellowship, NRMN Grant Writers Coaching Groups, Northwestern University, 2016

XLSTAT Best Paper Award, 8th International Conference on Partial Least Squares and Related Methods, 2014

Travel Fellowship, The 8th International Symposium on Bioinformatics Research and Applications, 2012

Travel Fellowship, The 10th Annual RECOMB Satellite Workshop on Comparative Genomics, 2012

The Korean Honor Scholarship, The Embassy of the Republic of Korea, 2011

Industry Affiliates Program scholarship, Texas A&M University, Fall 2005 and Spring 2006.

Yonsei Scholarip, Spring and Fall 1999, Spring 2000, Spring 2001, and Fall 2004

## SCIENTIFIC SOFTWARE

[MACPath](#) for identifying competing-endogenous pathways from ceRNA crosstalk, *submitted*

[MAT3UTR](#) for model-based analysis of the trans effect of 3'-UTR shortening, in minor revision in *Nature Genetics*

[MOABS](#) for comparing DNA methylation analysis between experiments, with D. Sun, Y. Xi, B. Rodriguez, T. Pan, M. Jeong, MA Goodell, W. Li, 2014

[CPAT](#) for estimating coding potential of transcripts, with L. Wang, S. Wang, J-P Kocher, W. Li, 2013

MURPAR for inferring a phylogenetic network from a collection of gene trees, with L. Nakhleh, 2012

[NEPAL](#) for phylogenetic network construction using the maximum parsimony and maximum likelihood criteria, with G. Jin and L. Nakhleh, 2010

SLS for phylogenetic tree search under the maximum parsimony criterion, with T. Williams, 2006

## PROFESSIONAL SERVICE

*Reviewer*

BMC Bioinformatics, GIW, Cellular Physiology and Biochemistry, Nature Scientific Review

## PROFESSIONAL MEMBERSHIPS

International Society for Matrix Biology