HYUN JUNG PARK

Assistant Professor of Human Genetics
School of Public Health
University of Pittsburgh
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Education and Training

2007~2012   **Ph.D., Computer Science**, Rice University, Houston, TX
Dissertation: Towards Accurate Reconstruction of Phylogenetic Networks
Thesis Advisor: Dr. Luay K. Nakhleh

2005~2007   **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

1997~2005   **B.S., Computer Science**, Yonsei University, Seoul, Korea

Appointments and Positions

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.

Publications

ˆ indicates first author. * indicates corresponding author. **bold** indicates group member.

Preprints

1. **Z. Fan**ˆ, K. F. Kernan, P. V. Benos, S. W. Canna, J. A. Carcillo, S. Kim, **H-J. Park***, "Causal inference using deep-learning variable selection identifies and incorporates direct and indirect causalities in complex biological systems." bioRxiv [Preprint] November 01, 2021, DOI:10.1101/2021.07.17.452800

Papers in Peer-reviewed Journals

1. Y. Qinˆ, K. F. Kernan, **Z. Fan**, **H-J. Park**, S. Kim, S. W. Canna, J. A. Kellum, R. A. Berg, D. Wessel, M. M. Pollack, K. Meert, M. Hall, C. Newth, J. C. Lin, A. Doctor, T. Shanley, T. Cornell, R. E. Harrison, A. F. Zuppa, R. Banks, R. W. Reeder, R. Holubkov, D. A. Notterman, J. M. Dean, J. A. Carcillo, on behalf of the Eunice Kennedy Shriver National Institute of Child Health and Human Development Collaborative Pediatric Critical Care Research Network, "Derivation of four computable 24-hour pediatric sepsis phenotypes to facilitate personalized enrollment in early precise anti-inflammatory clinical trials." Crit Care 26, 128, 2022, DOI:10.1186/s13054-022-03977-3

2. **Y. Bai**ˆ, **Y. Qin**, **Z. Fan**, **R. M. Morrison**, K. Nam, H. M. Zarour, R. Koldamova, Q. S. Padiath, S. Kim*, **H-J. Park***, "scMAPA: Identification of cell-type–specific alternative polyadenylation in complex tissues." GigaScience Volume 11, 2022, giac033, DOI:10.1093/gigascience/giac033

3. Kernan KFˆ, Ghaloul-Gonzalez L, Vockley J, Lamb J, Hollingshead D, Chandran U, Sethi R, **Park HJ**, Berg RA, Wessel D, Pollack MM, Meert KL, Hall MW, Newth CJL, Lin JC, Doctor A, Shanley T, Cornell T, Harrison RE, Zuppa AF, Banks R, Reeder RW, Holubkov R, Notterman DA, Dean JM, Carcillo JA* "Prevalence of Pathogenic and Potentially Pathogenic Inborn Error of Immunity Associated Variants in Children with Severe Sepsis." Journal of Clinical Immunology (2022), 42(2):350-364, DOI:10.1007/s10875-021-01183-4

4. P. Zieglerˆ, Y. Tian, **Y. Bai**, S. Abrahamsson, A. Bäckerholm, A. S. Reznik, A. Green, J. A. Moore, S. E. Lee, M. M. Myerburg, **H-J Park**, K-W, Tang, K. H. Shair, "A primary nasopharyngeal three-dimensional air-liquid interface cell culture model of the pseudostratified epithelium reveals differential donor- and cell type-specific susceptibility to Epstein-Barr virus infection." PLoS Pathogen (2021), 29;17(4):e1009041, DOI:10.1371/journal.ppat.1009041

5. **H-J. Park**ˆ, **Z. Fan**, **Y. Bai**, Q. Ren, Y. Rbaibi, K. R. Long, M. L. Gliozzi, N. Rittenhouse, J. D. Locker, A. C. Poholek, O. Q. Weisz* "Transcriptional Programs Driving Shear Stress-Induced Differentiation of Kidney Proximal Tubule Cells in Culture." Frontiers in Physiology (2020), DOI:10.3389/fphys.2020.587358

6. S. Kimˆ, E. Forno, R. Zhang, Z. Xu, **H-J. Park**, Q. Yan, N. Boutaoui, E. Acosta-Pérez, G. Canino, W. Chen, J. C. Celedón*, "Expression quantitative trait methylation analysis reveals methylomic associations with gene expression in childhood asthma." CHEST (2020), DOI:10.1016/j.chest.2020.05.601

7. S. Kimˆ, **Y. Bai**, B. Diergaarde, G. C. Tseng, **H-J. Park*** "The MicroRNA Target Site Landscape is a Novel Molecular Feature Associating Alternative Polyadenylation with Immune Evasion Activity in Breast Cancer." Briefings in Bioinformatics (2020), DOI:10.1093/bib/bbaa191

8. **F. Zhenjiang**ˆ, S. Kim, B. Diergaarde, **H-J. Park***, "3ʹ-UTR shortening disrupts ceRNA crosstalk of housekeeping genes resulting in subtype-specific breast cancer development." Frontiers in Bioengineering (2020), 8, 334, DOI:10.3389/fbioe.2020.00334

9. K. Guzmanˆ, L. Brink, , G. Rodriguez-Bey, R. Bodnar, L. Kuang, B. Xing, M. Sullivan, **H-J. Park**, **E. Koppes**, H. Zhu, Q. Padiath, F. Cambi, "Conditional depletion of Fus in oligodendrocytes leads to motor hyperactivity and increased myelin deposition associated with Akt and cholesterol activation." Glia (2020), DOI:10.1002/glia.23825

10. S. Kimˆ, E. Forno, R. Zhang, Z. Xu, **H. J. Park**, Q. Yan, N. Boutaoui, E. Acosta-Pérez, G. Canino, W. Chen, J. C. Celedón "Expression Quantitative Trait Methylation Analysis Reveals Methylomic Associations With Gene Expression in Childhood Asthma". CHEST (2020), DOI:10.1016/j.chest.2020.05.601

11. S. Kimˆ, **H-J. Park**, X. Cui, D. Zhi* "Collective effects of long-range DNA methylations predict gene expressions and estimate phenotypes in cancer." Scientific Reports 10(1):3920 (2020). e-print

12. A. Harold, Y. Amako, J. Hachisuka, **Y. Bai**, M. Li, Y. Meng, L. Kubat, J. Gravemeyer, J. Franks, J. R. Gibbs, **H-J. Park**, E. Ezhkova, J.C. Becker, M. Shuda*, "Conversion of Sox2-dependent Merkel cell carcinoma to a differentiated neuron-like phenotype by T antigen inhibition." PNAS, 116, 40 (2019). DOI:10.1073/pnas.1907154116

13. **H-J. Park**ˆ, P. Jiˆ, S. Kim, Z. Xia, B. Rodriguez, C-P. Masamha, A-B, Shyu, J. Neilson, E.J. Wagner*, W. Li*, "3ʹ UTR shortening Down-regulates Tumor Suppressors *in trans* by Disrupting the CeRNA Crosstalk." Nature Genetics, 50, 783-789, 2018. DOI:10.1038/s41588-018-0118-8

14. M. Jeongˆ, **H-J. Park**ˆ, 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*.", 23, 1(1-10), 2018. DOI:10.1016/j.celrep.2018.03.025

15. **H-J. Park^***, S. Kim, B. Rodriguez, W. Li*, "Model-based analysis of competing-endogenous pathways (MACPath) in human cancers." PLoS Computational Biology, 14(3): e1006074. DOI:10.1371/journal.pcbi.1006074

16. Y-h. Lee^, 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

17. L. Yang^, B. Rodriguez^, A Mayle^, **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, W. Li* and M. A. Goodell*, "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

18. X. Zhang^, J. Su^, M. Jeong, M. G. Ko, Y. Huang, **H. J. Park**, A. Guzman, Y. Lei, Y-H, Huang, A. Rao, W. Li* and M. A. Goodell*, "DNMT3A and TET2 compete and cooperate to repress differentialation lineage-specific factors in hematopoietic stem cells." Nature Genetics, 48(9), 1014-1023, 2016. DOI:10.1038/ng.3610

19. L. Min^, M. Jeong^, D. Sun^, **H-J. Park**^, B. Rodriguez^, Z. Xia, L. Yang, X. Zhang, GJ. Darlington, W. Li* and M.A. Goodell*, "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

20. D. Sun^, Y. Xi, B. Rodriguez, **H-J. Park**, T. Pan, M. Jeong, M.A. Goodell, W. Li*, "MOABS: model based analysis of bisulfite sequencing data." Genome Biology15: R38, 2014. DOI:10.1186/gb-2014-15-2-r38

21. L. Wang^, **H-J. Park**^, S. Wang, J-P Kocher, W. Li*, "CPAT: Coding-Potential Assessment Tool Using an Alignment-Free Logistic Regression Model." Nucleic Acid Research 41(6), 2013, DOI:10.1093/nar/gkt006

22. **H-J. Park**^ and L. Nakhleh*, "Inference of Reticulate Evolutionary Histories by Maximum Likelihood: The Performance of Information Criteria." BMC Bioinformatics, 13: S12, 2012. DOI:10.1186/1471-2105-13-S19-S12

23. **H-J. Park**^, G. Jin^, and L. Nakhleh^*, "Bootstrap-based Support of HGT Inferred by Maximum Parsimony." BMC Evolutionary Biology, 10: 131, 2010. DOI:10.1186/1471-2148-10-131

Papers in Peer-reviewed Conference Proceedings

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

1. **Y. Bai**^, **Y. Qin**, **Z. Fan**, **R. M. Morrison**, K. Nam, H. M. Zarour, R. Koldamova, Q. S. Padiath, S. Kim*, **H-J. Park***, "scMAPA: Identification of cell-type–specific alternative polyadenylation in complex tissues." International Society for Computational Biology, 2022, iRNA COSI: Integrative RNA Biology Track†

2. **H-J. Park**^ and L. Nakhleh*, "Inference of Reticulate Evolutionary Histories by Maximum Likelihood: The Performance of Information Criteria." RECOMB Comparative Genomics, 2012†

3. **H-J. Park**^ and L. Nakhleh*, "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

4. **H-J. Park**ˆ, G. Jin and L. Nakhleh*, "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

5. **H-J. Park**ˆ and T. L. Williams*, "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

Book Chapters

1. **H-J. Park**ˆ, S-J. Sul, and T. L. Williams*, "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

Technical Reports

1. **H-J. Park**ˆ, 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

Research Abstracts

1. C. Francis, **H-J. Park**, S. Manzi, F. Y. Demirci. "Circulating MicroRNA Profiling in Systemic Lupus Erythematosus, American Society of Human Genetics", American Society of Human Genetics, 2019

2. R. D. Nicholls, E. Koppes, M. A. Johnson, J. J. Moresco, J. K. Diedrich, D. Stolz, P. Luppi, S. M. Gollin, **H-J. Park**, J. R. Yates III, S. C. Watkins, and Peter Drain. "Hypoinsulinemia and neonatal hypoglycemia in Prader-Willi syndrome with β-cell developmental and functional deficits in insulin secretion highlights novel pathways and mechanisms for treatment of pancreatic endocrine disorders. Diagnosis and Management of Hyperinsulinism and Neonatal Hypoglycemia", Children's Hospital of Philadelphia, Phildelphia, Pennsylvania, 2019

3. X. Zhangˆ, 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

4. K. Jungˆ* and **H-J. Park**, "Multilevel Dynamic Generalized Structured Component Analysis." 8th International Conference on Partial Least Squares and Related Methods, 2014

5. M. Jeongˆ, D. Sunˆ, **H-J. Park**ˆ, 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

6. Y. Zhangˆ, 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.

7. M-K. Leeˆ, 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.

8. M-K. Leeˆ, 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.

9. M-K. Lee^, **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.

Teaching

Spring 2022	**Co-instructor** **(50% of coursework)**	Genomic Data Pipelines and Tools (HUGEN2072) Course audience: 11, Overall survey score: 4.18/5
Spring 2022	**Co-instructor** **(50% of coursework)**	Genomic Data Visualization and Integration (HUGEN2073) Course audience: 9, Overall score: 4.86/5
Spring 2021	**Co-instructor** **(50% of coursework)**	Genomic Data Pipelines and Tools (HUGEN2072) Course audience: 12, Overall survey score: 4.14/5
Spring 2021	**Co-instructor** **(50% of coursework)**	Genomic Data Visualization and Integration (HUGEN2073) Course audience: 9, Overall score: 4.33/5
Spring 2020	**Co-instructor** **(50% of coursework)**	Genomic Data Visualization, Pipelines, Tools and Integration (HUGEN2026) Course audience: 5, Overall survey score: 3.33/5
Fall 2018	**Co-instructor** **(50% of coursework)**	Bioinformatics resources for geneticists (HUGEN2010) Course audience: 31, Overall survey score: 3.06/5
Fall 2011	**Teaching Assistant**	Graduate Seminar on Computational Biology (Rice-Comp670)
Spring 2011	**Teaching Assistant**	Technology and Politics in the Information Age (Rice-Comp301)
Spring 2010	**Volunteer Instructor**	Adaptive Systems (Rice-Comp540)
Spring 2009 and 2010	**Teaching Assistant**	Applied Algorithms and Data Structures (Rice-Comp314)
Fall 2008 and 2009	**Teaching Assistant**	Intermediate Programming (Rice-Comp212)

Supervision of Post-Doctoral Students, Residents, and Fellows

07/2018 - present co-mentoring with Dr. Robert Nicholls	Erik Koppes, Ph.D, Department of Pediatrics, University of Pittsburgh
01/2019 - 08/2021 co-mentoring with Dr. David Whitcomb	Brandon Blobner, Ph.D, Department of Medicine, University of Pittsburgh
09/2019 - present	Kate Kernan, MD, MFA, Children's Hospital of Pittsburgh

Major Advisor for Graduate Student Essays, Theses, and Dissertations

09/2021~Present   Jie Sun, **Ph.D. program in Human Genetics**, University of Pittsburgh

03/2021~Present   Robert Morrison, **Ph.D. program in Computational Biology**, the Joint CMU-Pitt Program

11/2019~Present   Yidi Qin, **Ph.D. program in Human Genetics**, University of Pittsburgh

09/2018~Present   Yulong Bai, **Ph.D. program in Human Genetics** , University of Pittsburgh

06/2018~Present   Zhenjiang Fan, **Ph.D. program in Computer Science**, University of Pittsburgh

Service on Masters or Doctoral Committees

09/2020~05/2022   Dengxiaoyu Shi, **Biostatistics Masters**, University of Pittsburgh
(Advisor: Jenna Colavincenzo Carlson)

Title: *DNA Methylation Across Primary Motor Cortex at Single-cell Resolution*

02/2020~08/2020   Andrew-Jerome M. Charfauros, **Human Genetics Ph.D.**, University of Pittsburgh
(Advisor: Yesim Demirci)

Title: *Evaluation of Lupus Risk Variants for Their Potential Cis-Regulatory Effects on Long Non-coding RNA (LncRNA) Expression*

06/2019~04/2020   Jason Christopher Carson, **Human Genetics Ph.D.**, University of Pittsburgh
(Advisor: Cecilia Lo)

Title: *Enrichment for Rare Pathogenic and Highly Damaging Variants in Congenital Heart Disease Patients*

10/2018~06/2019   Tanbin Rahman, **Biostatistics Ph.D.**, University of Pittsburgh
(Advisor: George Tseng)

Title: *Clustering and Classification for RNA-Seq Data with Variable Selection*

07/2018~04/2019   Cynthia Francis, **Human Genetics M.S.**, University of Pittsburgh
(Advisor: Yesim Demirci)

Title: *Investigating Circulating MicroRNA Expression in Systemic Lupus Erythematosus*

03/2018~06/2018   Kexin Guo. **Biostatistics M.S.**, University of Pittsburgh
(Advisor: George Tseng)

Title: *Differentially Expressed Gene Detection with Covaraiate Selection under Small Sample Size Genomic Setting*

Service on Comprehensive or Qualifying Examination Committees

- Elynna Yum, Ph.D. Qualifying Exam (06/2022), **Human Genetics**, University of Pittsburgh (Advisor: Ora A. Weisz)

- Jie Sun, Ph.D. Qualifying Exam (05/2022), **Human Genetics**, University of Pittsburgh (Advisor: HJ Park)

- Anokhi Kashiparekh, Ph.D. Qualifying Exam (02/2022), **Human Genetics**, University of Pittsburgh (Advisor: Zsolt Urban)

- Yulong Bai, Ph.D. Comprehensive Exam (12/2021), **Human Genetics**, University of Pittsburgh (Advisor: HJ Park)

- Melissa Bulik, Ph.D. Comprehensive Exam (12/2021), **Human Genetics**, University of Pittsburgh (Advisor: Robert Lafyatis)

- Yidi Qin, Ph.D. Qualifying (03/2021), **Human Genetics**, University of Pittsburgh (Advisor: HJ Park)

- Yulong Bai, Ph.D. Qualifying (05/2020), **Human Genetics**, University of Pittsburgh (Advisor: HJ Park)

- Andrew-Jerome M. Charfauros, M.S. Comprehensive (05/2020), **Human Genetics**, University of Pittsburgh (Advisor: Yesim Demirci)

- Alexandra Schmidt, Ph.D. Qualifying (05/2020), **Human Genetics**, University of Pittsburgh (Advisor: Eric Goetzman)

- Yulong Bai, Ph.D. Qualifying (03/2020), **Human Genetics**, University of Pittsburgh (Advisor: Hyun Jung Park)

- Tianyu Zou, Ph.D. Qualifying(01/2020), **Human Genetics**, University of Pittsburgh (Advisor: John Shaffer)

- Zhenjiang Fan, Ph.D. Comprehensive (12/2019), **Computer Science**, University of Pittsburgh (Advisor: Hyun Jung Park)

- Jason Christopher Carson, Ph.D. Comprehensive (12/2019), **Human Genetics**, University of Pittsburgh (Advisor: Cecilia Wen Ya Lo)

- Qianqian Liang, Ph.D. Qualifying (08/2019), **Human Genetics**, University of Pittsburgh (Advisor: Dennis Kostka)

- Hallie Goldstein, M.S. Comprehensive (05/2019), **Human Genetics**, University of Pittsburgh (Advisor: Jerry Vockley)

- Dongjing Liu, Ph.D. Comprehensive and Qualifying (12/2019), **Human Genetics**, University of Pittsburgh (Advisor: John Shaffer)

- Yunqi Li, M.S. Comprehensive (03/2018), **Human Genetics**, University of Pittsburgh (Advisor: Daniel Weeks)

Presentations and Posters

Invited Talks

"Causal inference using deep-learning variable selection for direct and indirect causalities in complex biological systems" Department of Computer Science, University of Pittsburgh, Nov., 2021

"Novel transcriptomic analysis on scRNA-Seq data applicable to studying traumatic patients." Dr. Timothy Billiar's Lab, Department of Surgery, University of Pittsburgh and UPMC, Aug., 2020

"Alternative polyadenylation modifies microRNA target sites in cancer in association with viral infection." Cancer Virology Program Seminar, UPMC Hillman Cancer Center, Jan., 2020

"DNA signals contribute to post-transcriptional events in human brain and for brain disorders." Dr. Robert Sweet's Lab, Center for Neuroscience, University of Pittsburgh and UPMC, Dec., 2019

"Therapeutic RNA agents from Mechanism-based Computational Model." Cancer Biology Program Retreat, UPMC Hillman Cancer Center, Feb., 2019

"Therapeutic microRNA from 3'UTR shortening in human cancer." Core Monthly Meeting, University of Pittsburgh Clinical and Translational Science Institute (CTSI), Nov., 2018

"Insights into RNA Biology from Statistical Modeling for Cancer Therapeutics." Departmental Colloquium Series, University of Pittsburgh Department of Biomedical Informatics, Sep., 2018

"Insights into RNA Biology from Statistical Modeling for Cancer Therapeutics." Departmental Seminar Series, University of Pittsburgh Department of Biostatistics, Sep., 2018

"Insights into RNA Biology from Computational Modeling for Cancer Therapeutics." Special seminar, Seoul National University Hospital Department of Neurosurgery, June, 2018

"3′ UTR Shortening Down-regulates Tumor Suppressors *in trans* by Disrupting the ceRNA Crosstalk." Special seminar, Ewha Women's University Department of Biological Science, June, 2018

"Model-based analysis of competing-endogenous pathways (MACPath) in human cancers." Special seminar, Korea Advanced Institute of Science and Technology Department of Bio and Brain Engineering, June, 2018

"3′ UTR Shortening Down-regulates Tumor Suppressors *in trans* by Disrupting the ceRNA Crosstalk." Special seminar, UPMC and University of Pittsburgh Department of Pediatric Gastroenterology,Hepatology and Nutrition, June, 2018

"Computational modeling to make sense of big data for cancer therapeutics." Departmental Colloquim Series, University of Pittsburgh Department of Computer Science, Mar, 2018

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

"Insights into RNA Biology from Computational Modeling for Cancer Therapeutics." Special seminar, The Jackson Laboratory for Genomic Medicine and the University of Connecticut, School of Medicine, Sep,

2017

"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

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

"Computational Techniques to Accurately Reconstruct Phylogenetic Networks." Dr. Sun Kim's Lab, Seoul National University, May, 2013

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

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

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

"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

Contributed Talks

"Therapeutic MicroRNAs for Targeted Immunotherapy." The UPMC and University of Pittsburgh Inter-departmental Genetics Retreat, Sep, 2018

"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

"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, RECOMB 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

Posters

"Improving Clinical Care with Machine-learning Models." Research Recruitment Fair, University of Pittsburgh American Medical Student Association, Nov., 2021

"Machine-learning Based Understanding of Biological Problems." Research Recruitment Fair, University of Pittsburgh American Medical Student Association, Mar., 2021

"Quality Control Model for Next Generation Sequencing." The UPMC and University of Pittsburgh Interdepartmental Genetics Retreat, Sep, 2018

"Computational Models for Post-transcriptional Regulations in Cancer." The UPMC and University of Pittsburgh Interdepartmental Genetics Retreat, Sep, 2018

"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

Awards and Fellowships

Beckman Young Investigator Award, semi-finalist, 2022

Career Enhancement Program Award, the Melanoma and Skin Cancer SPORE at the University of Pittsburgh and UPMC Hillman Cancer Center, 2022

Silver Snapshot Awards, Society of Critical Care Medicine, Puerto Rico, 2022

Hillman Developmental Pilot Program Award, UPMC Hillman Cancer Center, 2021

Biomedical Modeling Pilot Award, Clinical and Translational Science Institute, University of Pittsburgh, 2019

Travel Fellowship, National Research Mentoring Network 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 Research in Computational Molecular Biology Satellite Workshop on Comparative Genomics, 2012

Graduate Scholarship, Rice University, 2007~2012

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

Graduate Scholarship, Texas A&M University, 2006~2007

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

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

Scientific Software

causalDeepVASE for learning causal structure in clinical or molecular data based on a deep neural network model, Z. Fan *et al.*, bioRxiv [Preprint] November 01, 2021, DOI:10.1101/2021.07.17.452800

scMAPA for detecting alternative polyadenylation signals in single-cell RNA-Seq data, Bai *et al.*, bioRxiv [Preprint] December 29, 2020, DOI:10.1101/2020.07.30.229096

PRIMATA-APA for characterizing a novel biological feature representing the number of microRNA binding sites in the transcriptome data, S. Kim *et al.*, Briefing in Bioinformatics (2020), bbaa191, DOI:10.1093/bib/bbaa191

geneEXPLORER for predict gene expression using long-range methylation for pan-cancer, S. Kim *et al.*, Scientific Reports 10(1):3920 (2020). e-print

MACPath for identifying competing-endogenous pathways from ceRNA crosstalk, Park *et al.*, PLoS Computational Biology (2018), 14(3): e1006074, DOI:10.1371/journal.pcbi.1006074

MAT3UTR for model-based analysis of the trans effect of 3'-UTR shortening, Park *et al.*, Nature Genetics (2018), 50, 783-789, 2018. DOI:10.1038/s41588-018-0118-8

MOABS for comparing DNA methylation analysis between experiments, Sun *et al.*, Genome Biology (2014), 15: R38, DOI:10.1186/gb-2014-15-2-r38

CPAT for estimating coding potential of transcripts, Wang *et al.*, Nucleic Acid Research (2013), 41(6), DOI:10.1093/nar/gkt006

MURPAR for inferring a phylogenetic network from a collection of gene trees, Park *et al.*, The 8th International Symposium on Bioinformatics Research and Applications (ISBRA 2011), LNBI 7292:213-224, DOI:10.1007/978-3-642-30191-9_20

NEPAL for phylogenetic network construction using the maximum parsimony and maximum likelihood criteria, Park *et al.*, BMC Evolutionary Biology (2010), 10: 131, DOI:10.1186/1471-2148-10-131 and Park *et al.*, BMC Bioinformatics (2011), 13:S12, DOI:10.1186/1471-2105-13-S19-S12

SLS for phylogenetic tree search under the maximum parsimony criterion, Park *et al.*, 1st Intl. Conference on Bioinformatics and Computational Biology (BiCoB 2009), Lecture Notes in Computer Science, vol. 5462, 331342, DOI:10.1007/978-3-642-00727-9_31 and Park *et al.*, Advances in Computational Biology, H.R. Arabnia, ed., Springer, vol. 680, pages 35-42, DOI:10.1007/978-1-4419-5913-3_5

Professional Service

Paper Reviewer

BMC Bioinformatics, International Conference on Genome Informatics, Cellular Physiology and Biochemistry, Nature Scientific Review, Molecular Psychiatry, Human Molecular Genetics, Frontiers in Cell and Developmental Biology, DNA and Cell Biology.

Internal Grant Reviewer

CTSI Exploring Existing Data Resources Pilot (11/2021)
CTSI Public Health Pilot (2/2022)

School-level Committees

Planning and Budget Policies Committee (PBPC), 2020~Present

Department-level Committees

Admission Committee, 2019~Present
Research Development Committee, 2019~Present
Teaching Faculty Search Committee, 2022

Science Mentor at Frontiers for Young Minds

Margaret E. Scollan and Christine T. Lauren, "What is Eczema?", 09/2021
Paolo Zucca, Alessandra Scagliarini, Yashwantrao Ramma, Ali S. Khan, "Zoonoses – diseases naturally transmitted from animal to humans", 01/2022

Memberships in Professional and Scientific Societies

The Society of Critical Care Medicine (2022)
American Society of Human Genetics (2020~Present)

American Statistical Association (2019~2020)

Professional Development

Teaching and Mentoring

- Attended Microaggression: Recognizing and Challenging a Subtle Form of Bias, led by the the University of Pittsburgh Center for Teaching and Learning, May 12th, 2022

- Attended Intercultural Competency, led by the the University of Pittsburgh Center for Teaching and Learning, May 3rd, 2022

- Attended Creating Equal Access: Getting Started with Digital Accessibility, led by the the University of Pittsburgh Center for Teaching and Learning, April 19th, 2022

- Attended Teaching with Equity, led by the the University of Pittsburgh Center for Teaching and Learning, March 24th, 2022

- Attended Designing Better Multiple Choice Questions, led by the University of Pittsburgh Center for Teaching and Learning, February 3rd, 2022

- Attended Better Grading and Feedback with Gradescope, led by the University of Pittsburgh Center for Teaching and Learning, January 12, 2022

Research Support

Ongoing

- 2/1/2022~1/31/2023   Career Enhancement Program (CEP) (Melanoma and Skin Cancer Program SPORE (MSCP) Hillman Cancer Center)

  PI: Park $ 50,000 (0%)
  Deep-learning approaches to identify predictors of outcome to immunotherapy in melanoma
  To identify response-associated bacteria in responder-derived fecal microbiota transplantation (FMT) followed by anti-PD-1 in a recent clinical trial (anti–PD-1/FMT), we will incorporate the host transcriptomics data with the gut bacteria data in novel AI-driven approaches under the hypothesis that the bacteria interact with host system to induce response.

- 9/1/2022~8/31/2023   Hillman Developmental Pilot Program (UPMC Hillman Cancer Center)

  PI: Park $ 50,000 (0%)
  Computational approaches to predict benefit and identify driver genes for the anti-PD-1 and fecal microbiota transplanation strategy for melanoma patients
  The objective of this study is to develop computational methods that can predict benefit of the anti-PD-1 and fecal microbiota transplanation strategy and identify gut bacterial species driving such benefit.

- 5/1/2021~4/30/2026   R01NS115815-01A1(NIH)   **co-I (PI: Jha)** $ 140,000 (0.5%)
  A translational evaluation of Sur1-Trpm4 imaging endophenotypes and genetics to direct precision medicine for cerebral edema after traumatic brain injury
  The objective of this translational R01 is to define the impact of Sur1-Trpm4 related genetic and

protein variability on different edema endophenotypes, contusion growth and response to inhibition in preclinical and human TBI.

- 1/1/2021∼5/31/2023   R01CA222203-01A1(NIH)   **sub (PI: Zarour)** $ 21,893 (15%)
Fecal Microbiota Transplant and PD-1 blockade in Melanoma
We will investigate whether resistance to anti-PD-1 can be overcome by changing the gut microbiota, and evaluate the safety and efficacy of this clinical trial.

- 8/1/2020∼7/31/2022   R21CA241840(NIH)   **co-I (PI: Demirci)** $ 285,994 (19%)
Metabolomic and miRNA profiling of vitreous humor in uveal melanoma
The objective of this study is to comprehensively examine the vitreous metabolites and miRNAs in UM patients in order to investigate their potential utility to distinguish UM prognostic subtypes, gain further insights into the UM biology, and unravel new potential biomarkers and/or therapeutic targets for future follow-up studies.

- 9/1/2019∼8/31/2024   R01GM108618 (NIH)   **co-I (PI: Carcillo)** $ 905,002 (38%)
Inflammation Phenotypes in Pediatric Sepsis Induced Multiple Organ Failure
We propose to use the clinical information and samples obtained in this previous study to take advantage of the wonderful advances made this milenia in computer technology, big data, bioinformatics, and human and virus genetics to attain our goals.

- 4/1/2019∼   University of Pittsburgh-Gollin Gaines Cancer Research Fund   **PI: Park** $ 10,000 (0%)
RNA interactions mined from big data of cancer patients: Personalized biomarkers for targeted immunotherapy The objective of this study is to computationally model RNA interactions through diverse types of RNA regulation.

- 8/1/2015∼7/31/2025   P30 CA047904(NIH)   **sub (PI: Ferris)** $ 25,648,270 (20%)
Cancer Center Support Grant (Biostatistics Facility)
The UPMC Hillman Cancer Center's Biostatistics Facility provides biostatistical and computer-related assistance to investigators in the design, planning, execution and reporting of cancer-related research studies.

Completed

- 4/1/2016∼7/31/2020   R01DK11872601A1(NIH)   **sub (PI: Weisz)** $ 410,677 (7%)   *Proximal tubule endocytosis in normal and nephrotic kidneys*
We will use proximal tubule (PT) cells under fluid shear stress in conjunction with studies in mouse models to study about how PT cells respond to normal and pathologic variations in flow and filtered protein load.

- 9/1/2019∼3/31/2020   Biomedical Modeling Pilot Awards (Clinical and Translational Science Institute)
PI: Park $ 25,000 (0%)
Therapeutic MicroRNAs Enhancing Immune Response
The objective of this study is to develop computational approaches to identify the role of broad 3'UTR shortening in diverse types of tumors.