HYUN JUNG PARK

Assistant Professor of Human Genetics
Graduate School of Public Health
Department of Biomedical Informatics
University of Pittsburgh
Pittsburgh, Pennsylvania 15216

Phone: (412) 383-0520
Email: hyp15@pitt.edu
Website: http://www.parklab.pitt.edu/
Office: 3122@130 De SoTo St. PA15216

EMPLOYMENT

1/16/2018 ~ 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

RESEARCH SUPPORTS

9/1/2019 – 8/31/2024 NIH (**PI: Carcillo**)	R01GM108618, "*Inflammation Phenotypes in Pediatric Sepsis Induced Multiple Organ Failure.*" $ 905,002
8/1/2015 – 7/31/2020 NIH (**PI: Ferris**)	P30 CA047904, "*Cancer Center Support Grant (Biostatistics Facility).*" $ 25,648,270
12/2018 - 05/2019 NIH (**PI: Park**)	UL1TR001857, "*Therapeutic MicroRNAs Enhancing Immune Response.*" $ 25,000
06/2019 - 08/2019 (**PI: Park**)	Gollin Gaines Cancer Research Fund, "*RNA interactions mined from big data of cancer patients.*" $ 10,000
08/2018 - 07/2019 NIH (**PI: Urban**)	UL1TR001857, "*Obesity Gene Regulation in Samoans.*" $50,000

PUBLICATIONS

Works in Progress

1. S. Kim^, Y. Bai, B. Diergaarde, G. C. Tseng, H. J. Park* "Alternative Polyadenylation Modifies Target Sites of MicroRNAs with Clinical Potential for Breast Cancer Progression". bioRxiv, p. 601518, Jan. 2019

2. H-c. E. Leungˆ*, **H-J Park**ˆ, L. M. Lui, W. Li, H. C. Adams III, Michael T. Lewis, "Towards deep protein sequencing: thermal hydroiodic acid disgestion of proteins."

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

Papers in Peer-reviewed Journals

1. **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", in press in Frontiers in Bioengineering

2. 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." in press in Glia (2020), 10.1002/glia.23825

3. S. Kimˆ, **H-J. Park**, X. Cui, D. Zhi* "Collective effects of long-range DNA methylations predict gene expressions and estimate phenotypes in cancer." Sci. Rep. 10(1):3920, 2020. 10.1038/s41598-020-60845-2

4. 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). 10.1073/pnas.1907154116

5. **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

6. 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. https://doi.org/10.1016/j.celrep.2018.03.025

7. **H-J. Park**ˆ*, 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

8. Y-h. Leeˆ, 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

9. L. Yangˆ, B. Rodriguezˆ, A Mayleˆ, **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

10. X. Zhangˆ, J. Suˆ, 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. nature.com/ng/journal/v48

11. L. Minˆ, M. Jeongˆ, D. Sunˆ, **H-J. Park**ˆ, B. Rodriguezˆ, 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

12. D. Sunˆ, 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

13. L. Wangˆ, **H-J. Park**ˆ, 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

14. **H-J. Park**ˆ and L. Nakhleh*, "Inference of Reticulate Evolutionary Histories by Maximum Likelihood: The Performance of Information Criteria." BMC Bioinformatics, 13: S12, 2012. bmcbioinformatics.biomedcentral.com/articles

15. **H-J. Park**ˆ, G. Jinˆ, and L. Nakhlehˆ*, "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 were published as a special issue of a journal; the paper is listed above as well.)

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

2. **H-J. Park**ˆ 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

3. **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

4. **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 Presented

1. 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, Sep. 5, 2019

2. C. Francis, **H-J. Park**, S. Manzi, F. Y. Demirci. "Circulating MicroRNA Profiling in Systemic Lupus Erythematosus, American Society of Human Genetics", Oct. 15, 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 GSA." 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. Leeˆ, **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. Leungˆ, H. C. Adams IIIˆ, and **H-J Park**ˆ, "Thermal Hydroiodic acid digestion of proteins.", ˆequally contributed.

TEACHING

Spring 2020, **Co-instructor**,Genomic Data Visualization, Pipelines, Tools and Integration (Pitt-HUGEN2026)

- Covered principles necessary for understanding and utilizing the current state of the art in data visualization

Fall 2018, **Co-instructor**, Bioinformatics resources for geneticists (Pitt-HUGEN2010)

- Covered webservers and databases to query diverse types of biological data and interpret the data therein

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

Current Ph.D. and Master's Committee Chair

06/2018 -   Zhenjiang Fan. Computer Science, University of Pittsburgh

09/2018 -   Yulong Bai. Human Genetics, University of Pittsburgh

11/2019 -   Yidi Qin. Human Genetics, University of Pittsburgh

Ph.D. and Master's Thesis Committee Member

- 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*

- 06/2019   Tanbin Rahman., Biostatistics Ph.D., University of Pittsburgh (Advisor: George Tseng)
Title: *Clustering and Classification for RNA-Seq Data with Variable Selection*

- 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   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*

Ph.D. and Master's Comprehensive or Qualifying Examination Committee Member

- 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)

MENTORING

0.1 Co-supervising postdoctoral researchers

- Brandon Blobner, Ph.D. at University of Pittsburgh Medical Center

- Erik Koppe, Ph.D. at Childrens' Hospital of Pittsburgh, University of Pittsburgh Medical Center

- Lei Li, Ph.D. at Baylor College of Medicine

- Benjamin Rodriguez, Ph.D. at Baylor College of Medicine

- Soyeon Kim, Ph.D. at Rice University

0.2 Co-supervising Ph.D. students

- Weijiang Zhou at Baylor College of Medicine

- Jianfeng Xu at Baylor College of Medicine

- Xuequi Lin at Baylor College of Medicine

PRESENTATIONS AND POSTERS

Presentations and Invited Talks

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

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

"Therapeutic microRNA from 3'UTR shortening in human cancer." CTSI Core Monthly Meeting, Nov, 2018

"Therapeutic MicroRNAs for Targeted Immunotherapy." Genetics Retreat Seminar, Sep, 2018

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

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

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

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

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

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

"Computational modeling to make sense of big data for cancer therapeutics." Special seminar in Computer Science Department, University of Pittsburgh, Mar, 2018

"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

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

MACPath for identifying competing-endogenous pathways from ceRNA crosstalk, PLoS Comp. Bio. 2018

MAT3UTR for model-based analysis of the trans effect of 3′-UTR shortening, Nature Genetics, 2018

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, Molecular Psychiatry

PROFESSIONAL MEMBERSHIPS

American Society of Human Genetics, American Statistical Association