

Tae-Hyuk (Ted) Ahn

ASSOCIATE PROFESSOR · DEPARTMENT OF COMPUTER SCIENCE AT SAINT LOUIS UNIVERSITY

220 N. Grand Blvd., St. Louis, MO 63103, US

☎ +1 314-977-3633 | ✉ taehyuk.ahn@slu.edu | 🏠 cs.slu.edu/~ahn | 📺 BioHPC | 🌐 [taehyukahn](https://taehyukahn.com)

Personal Profile

Computer scientist with 20+ years of experience in industry and academia, specializing in bioinformatics and computational biology. My research focuses on developing innovative software tools to analyze big data using artificial intelligence (AI) and advanced computational techniques on high-performance computing (HPC) systems, including supercomputers and cloud platforms. I am committed to advancing computational methods for solving complex problems in biological, health, and biomedical sciences.

Education

Virginia Tech

PHD IN COMPUTER SCIENCE

- Advisor: Dr. Adrian Sandu
- Dissertation: Computational Techniques for the Analysis of Large Scale Biological Systems

Blacksburg, VA, US

Aug 2012

Northwestern University

MS IN COMPUTER ENGINEERING

Evanston, IL, US

Jun 2007

Yonsei University

BS IN ELECTRICAL ENGINEERING

Seoul, S. Korea

Feb 2000

Professional Experience

2021- **Adjunct Professor**, AI Graduate School, Gwangju Institute of Science and Technology (GIST)

2020- **(Tenured) Associate Professor**, Department of Computer Science, Saint Louis University

2015- **Same rank as the Department of Computer Science**, Secondary Appointment in Department of Mathematics and Statistics, Saint Louis University

2015- **Core Faculty Member**, Graduate Program in Bioinformatics and Computational Biology, Saint Louis University

2015-2020 **Assistant Professor**, Department of Computer Science, Saint Louis University

2014-2015 **Instructor**, The University of Tennessee and Oak Ridge National Laboratory

2012-2015 **Postdoctoral Research Associate**, Computer Science and Mathematics Division, Oak Ridge National Laboratory

2007-2012 **Research/Teaching Assistant**, Departments of Computer Science, Virginia Tech

2011 **Research Intern**, HPC Group, Business and Technology, Pfizer Inc., Groton, CT, US

2010 **Research Intern**, Scalable Computing R&D Department, Sandia National Lab, Livermore, CA, US

2005-2007 **MS Graduate Student**, Departments of Electrical and Computer Engineering, Northwestern University

2004-2005 **Instructor**, Private Mathematics Institute, Seoul, S. Korea

2000-2004 **Senior Software Engineer**, Samsung SDS, Seoul, S. Korea

Publications

[GOOGLE SCHOLAR LINK](#)

UNDER REVIEW

[U4] P. Kang*, **T.-H. Ahn**, "Interaction as Interference: A Quantum-Inspired Aggregation Approach for Classification", Under Review (*Mathematics*, Manuscript ID: mathematics-4455571), 2026. [DOI TBA]

- [U3] V. D Nguyen, C. Gao, C. Gardner, Z. Wang, A. J Margenot, L. Huang*, **T.-H. Ahn***, “First Metagenome-Assembled Genomes from the Historic Morrow Plots Reveal Management-Associated Dominance of Archaeal Ammonia Oxidizers”, Under Review (*Scientific Data* (IF=8.7) 1st round), 2026. [bioRxiv]
- [U2] K.-S. Kim, C. Gardner, A. Cullen, J. A. Stelzer, K. Cho, A. Sharma, M. T. Nemera, T. Law, H. Naz, G. Zhao, H. W. Gabel, G. J. Patti, E. S. Musiek, **T.-H. Ahn**, J. J. Yi*, “Persistent neuronal stress signaling underlies phenotypes in a mouse model of Angelman syndrome”, Under Review (*Nature* (IF=55) 2nd round), 2026. [DOI TBA]
- [U1] A. Cullen, A. Erickson, C. Gardner, J. R. Moore, A. Paneque, A. Gunelson, M. Mindt, **T.-H. Ahn**, H. W. Gabel, J. J. Yi*, “CTCF regulates the long gene expression program in neurons”, Under Review (*Molecular Psychiatry* (IF=10.1) 2nd round), 2026. [DOI TBA]

JOURNAL ARTICLES AND PEER-REVIEWED CONFERENCE PROCEEDINGS

- [J36] C. Gardner, A. Dhiren, B. Min* **T.-H. Ahn***, “Wavelet-Enhanced PaDiM for Industrial Anomaly Detection”, *IEEE Access* (IF=3.6) vol. 14, pp. 37702-37718, 2026. [DOI]
- [J35] G. Jung, **T.-H. Ahn**, and B. Min*, “Wildfire Smoke Detection with a Multi-Resolution Framework and Two-Stage Classification Pipeline”, *Fire* (IF=3.0) 9(2), 92, 2026. [DOI]
- [C16] C. Gardner, S. Jeong, O. Khatavkar, A. Moon, Q. Cao, **T.-H. Ahn***, “Evaluating Accuracy and Performance Tradeoffs in GPU Accelerated Single Cell RNA-seq Analysis”, in *Proceedings of the SC Workshops 25: International Conference for High Performance Computing, Networking, Storage, and Analysis (SC 25)*, pp. 349–358, 2025. [DOI] (**Best Paper Runner-Up Award**)
- [J34] Sojung Park, Eunhye Ahn, **Tae-Hyuk Ahn**, Sang Nam Ahn, Soobin Park, Eunsun Kwon, Seoyeon Ahn, Yuanyuan Yang, “Artificial Intelligence and Aging in Place: A Scoping Review of Current Applications and Future Directions,” *The Gerontologist* (IF=5.3), **65**, 6, gnaf130, 2025. [DOI]
- [C15] S. Maharjan, M. Xia, **T.-H. Ahn**, M. Song, “Intelligent Code Completion by a Unified Multi-task Learning with a Large Language Model”, in *Proceedings of the 2025 IEEE/ACIS 23rd International Conference on Software Engineering Research, Management and Applications (SERA)*, Las Vegas, NV, USA, pp. 134–142, 2025. [DOI]
- [J33] J. P. Sirasani, C. Gardner, G. Jung, H. Lee, **T.-H. Ahn***, “Bioinformatics approaches of blood and tissue microbiome analyses: challenges and perspectives,” *Briefings in Bioinformatics* (IF=7.7), **26**, 2, bbaf176, 2025. [DOI]
- [J32] C. Gardner, J. Chen, C. Hadfield, Z. Lu, D. Debruin, Y. Zhan, M. Donlin, **T.-H. Ahn***, Z. Lin*, “Chromosome-level subgenome-aware de novo assembly of *Saccharomyces bayanus* provides insight into genome divergence after hybridization”, *Genome Research* (IF=6.2), **34**, 11, 2133–2146, 2024.[DOI]
- [J31] T. Si, Y. Wang, L. Zhang, E. Richmond, **T.-H. Ahn**, H. Gong, “Multivariate Time Series Change-Point Detection with a Novel Pearson-like Scaled Bregman Divergence”, *Stats* (IF=1.3), **7**, 2, 462-480, 2024.[DOI]
- [J30] K. S. Cheng, P.-C. Huang, **T.-H. Ahn**, M. Song, “Tool Support for Improving Software Quality in Machine Learning Programs”, *Information* (IF=3.38), **14**, 1, 53, 2023. [DOI]
- [C14] P. Basia, **T.-H. Ahn**, M. Song, “An IDE Support for Validating Machine Learning Applications in Bioengineering Text Corpora”, in *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 2022. [DOI]
- [C13] K. S. Cheng, **T.-H. Ahn**, and M. Song, “Debugging Support for Machine Learning Applications in Bioengineering Text Corpora”, in *IEEE 46th Annual Computers, Software, and Applications Conference (COMPSAC)*, 2022. [DOI]
- [J29] Y. Mreyoud, M Song, J Lim, and **T.-H. Ahn***, “MegaD: Deep Learning for Rapid and Accurate Disease Status Prediction of Metagenomic Samples”, *Life* (IF=3.96), **12**, 5, 669, 2022. [DOI]
- [J28] Z. Lu, K. Berry, Z. Hu, Y. Zhan, **T.-H. Ahn***, and Zhenguo Lin*, “TSSr: an R Package for Comprehensive Analyses of TSS Sequencing Data”, *NAR Genomics and Bioinformatics*, **3**, 4, 2021. [DOI]
- [J27] Y. Yang, C. Gardner, P. Gupta, Y. Peng, C. Piasecki, R. J. Millwood, **T.-H. Ahn**, and C. N. Stewart Jr., “Novel Candidate Genes Differentially Expressed in Glyphosate-Treated Horseweed (*Conyza canadensis*)”, *Genes* (IF=3.96), **12**, 10, 2021. [DOI]
- [J26] S. Lewis, A. Nash, Q. Li, and **T.-H. Ahn***, “Comparison of 16S and Whole Genome Dog Microbiomes using Machine Learning”, *BioData Mining* (IF=4.078), **14**, 41, 2021. [DOI]
- [J25] A. Rajeh, K. Wolf, C. Schiebout, N. Sait, T. Kosfeld, R. J. DiPaolo* and **T.-H. Ahn***, “iCAT: Diagnostic Assessment Tool of Immunological History using High-throughput T-cell Receptor Sequencing”, *F1000Research* (IF=2.297), 2021. [DOI]

- [J24] E. Dhungel, Y. Mreyoud, H.-J. Gwak, A. Rajeh, M. Rho, and **T.-H. Ahn***, “MegaR: an Interactive R package for Rapid Sample Classification and Phenotype Prediction using Metagenome Profiles and Machine Learning”, *BMC Bioinformatics* (IF=3.169) **22**, 25, 2021. [DOI]
- [J23] M. Hassert, K. J. Wolf, A. Rajeh, C. Shiebout, S. G. Hoft, **T.-H. Ahn**, R. J. DiPaolo, J. D. Brien, A. K. Pinto, “Diagnostic Differentiation of Zika and Dengue Virus Exposure by Analyzing T Cell Receptor Sequences from Peripheral Blood of Infected HLA-A2 Transgenic Mice”, *PLOS Neglected Tropical Diseases* (IF=4.781), 2020. [DOI]
- [C12] Y. Mreyoud and **T.-H. Ahn***, “Deep Neural Network Modeling for Phenotypic Prediction of Metagenomic Samples”, in *Proceedings of the 11th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (BCB ’20)*, September 21–24, 2020, Virtual Event, USA 2020. [DOI]
- [C11] T. Kosfeld, J. McMillan, R. J. DiPaolo, J. Hou*, and **T.-H. Ahn***, “Performance Evaluation of Viral Infection Diagnosis using T-Cell Receptor Sequence and Artificial Intelligence”, in *Proceedings of the 11th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (BCB ’20)*, September 21–24, 2020, Virtual Event, USA (Acceptance Rate=30%), 2020. [DOI]
- [J22] K. Bockerstett, S. Lewis, C. Noto, E. Ford, J. Saenz, N. Jackson, **T.-H. Ahn**, J. Mills, R. DiPaolo, “Single Cell Transcriptional Analyses Identify Lineage-Specific Epithelial Responses to Inflammation and Metaplastic Development in the Gastric Corpus”, *Gastroenterology* (IF=22.682), **159**, 6, 2020. [DOI]
- [J21] K. Bockerstett, S. Lewis, K. Wolf, C. Noto, N. Jackson, E. Ford, **T.-H. Ahn**, R. DiPaolo “Single-cell Transcriptional Analyses of Spasmolytic Polypeptide-expressing Metaplasia Arising from Acute Drug Injury and Chronic Inflammation in the Stomach”, *Gut* (IF=17.943), **69** (6), 1027-1038, 2020. [DOI]
- [J20] Mason-Buck, G., Graf, A., Elhaik, E., Robinson, J., Pospiech, E., Oliveira, M., Moser, J., Lee, P.K.H., Githae, D., Ballard, D., Bromberg, Y., Casimiro-Soriguer, C.S., Dhungel, E., **Ahn, T.**, Kawulok, J., Loucera, C., Ryan, F., Walker, A.R., Zhu, C., Mason, C.E., Amorim, A., Syndercombe Court, D., Branicki, W., Labaj, P, “DNA Based Methods in Intelligence - Moving Towards Metagenomics”, *Preprints*, 2020. [DOI]
- [J19] Z. Siddiqui, J. Maldonado, J. Grojean, F. Ye, D. Zhang, J. Longtine, **T.-H. Ahn***, and H. Guo*, “Rchimerism: An R-Package for Automated Chimerism Data Analysis”, *The Journal of Molecular Diagnostics* (IF=5.568), **22** (1), 21-20, 2020. [DOI]
- [J18] A. Paul, D. Lawrence, M. Song, S.-H. Lim, C. Pan, and **T.-H. Ahn***, “Using Apache Spark on Genome Assembly for Scalable Overlap-graph Reduction”, *Human Genomics* (IF=5.88), Vol **13** Supplement 1, 2019. [DOI]
- [J17] V. K. Eपुरi, S. Sakala, **T.-H. Ahn**, and M. Song, “Tool Support for Managing RepetitiveProgram Changes in Evolving Software”, *IET Software* (IF=1.070), 2019. [DOI]
- [J16] Z. Harris, E. Dhungel, M. Mosior, and **T.-H. Ahn***, “Massive Metagenomic Data Analysis using Abundance-Based Machine Learning”, *Biology Direct* (IF=4.78), **14**, 12, 2019. [DOI]
- [J15] J. McMillan, Z. Lu, J. Rodriguez, **T.-H. Ahn***, and Z. Lin*, “YeastTSS: An Integrative Web Database of Yeast Transcription Start Sites”, *Database (Oxford)* (IF=4.462), Volume 2019, baz048, 2019. [DOI]
- [C10, B1] W. Feng, Z. Yu, M. Kang, H. Gong*, and **T.-H. Ahn***, “Practical Evaluation of Different Omics Data Integration Methods”, in *Precision Health and Medicine. W3PHAI 2019. Studies in Computational Intelligence*, vol **843**. Springer, Cham, 2019. [DOI]
- [C9] A. Paul, D. Lawrence, M. Song, S.-H. Lim, C. Pan, and **T.-H. Ahn***, “SORA: Scalable Overlap-graph Reduction Algorithms for Genome Assembly using Apache Spark in the Cloud”, in *proceedings of the 2018 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 2018. [DOI]
- [J14] K. Wolf, T. Hether, P. Gilchuk, A. Kumar, A. Rajeh, C. Schiebout, J. Maybruck, R. M. Buller, **T.-H. Ahn**, S. Joyce, R. DiPaolo, “Identifying and Tracking Low Frequency Virus-Specific TCR Clonotypes Using High-Throughput Sequencing”, *Cell Reports* (IF=9.423), **25**, 9, P2369-2378.E4, 2018. [DOI]
- [C8, J13] M. McCoy, A. Paul, M. Victor, M. Richner, H. Gabel, H. Gong, A. Yoo*, and **T.-H. Ahn***, “LONGO: An R Package for Interactive Gene Length Dependent Analysis for Neuronal Identity”, *Bioinformatics* (IF=6.937), vol. **34**, issue 13, pp. i422-428, *ISMB-2018*, 2018. [DOI]
- [C7] A. Paul, D. Lawrence, and **T.-H. Ahn***, “Overlap Graph Reduction for Genome Assembly using Apache Spark”, in *Proceedings of the 8th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics. ACM-BCB 2017*, ACM: Boston, Massachusetts, USA. poster, p. 613-613, 2017. [DOI]
- [J12] **T.-H. Ahn**, X. Han, and A. Sandu, “Implicit Simulation Methods for Stochastic Chemical Kinetics”, *Journal of Applied Analysis and Computation* (IF=1.116), **5** (3), pp. 420-452, 2015. [DOI]

- [J11] M. Land, L. Hauser, S. Jun, I. Nookaew, M. Leuze, **T.-H. Ahn**, T. Karpinets, O. Lund, G. Kora, T. Wassenaar, S. Poudel, and D. Ussery, “Insights from 20 Years of Bacterial Genome Sequencing”, *Functional & Integrative Genomics* (IF=3.889), **15** (2), pp141-161, 2015. [DOI]
- [J10] **T.-H. Ahn**, J. Chai, and C. Pan, “Sigma:Strain-level Inference of Genomes from Metagenomic Analysis for Biosurveillance”, *Bioinformatics* (IF=6.937), vol. 31, issue 2, pp. 170-177, 2015. [DOI]
- [J9] **T.-H. Ahn**, A. Sandu, L.T. Watson, C.A. Shaffer, Y. Cao, and W.T. Baumann, “A Framework to Analyze the Performance of Load Balancing Schemes for Ensembles of Stochastic Simulations”, *International Journal of Parallel Programming* (IF=1.258), Vol. **43** Issue 4, pp 597-630, 2015. [DOI]
- [J8] J. Chai, G. Kora, **T.-H. Ahn**, D. Hyatt, and C. Pan, “FunctionalPhylogenomics Analysis of Bacteria and Archaea using Consistent GenomeAnnotation with UniFam”, *BMC Evolutionary Biology* (IF=3.559), **14** (1):207, 2014. [DOI]
- [J7] B. Haider, **T.-H. Ahn**, B. Bushnell, J. Chai, A. Copeland, and C. Pan, “Omega: an Overlap-graph de novo Assembler for Metagenomics”, *Bioinformatics* (IF=6.937), vol. **30**, issue 19, pp. 2717-2722, 2014. [DOI]
- [J6] Z. Li, Y. Wang, Q. Yao, N.B. Justice, **T.-H. Ahn**, D. Xu, R.L. Hettich, J.F. Banfield, and C. Pan, “Diverse and Divergent Post-translational Modification of Proteins of Closely Related Bacteria in Two Growth Stages of a Natural Microbial Community”, *Nature Communication* (IF=13.811), **5**, article number 4405, 2014. [DOI]
- [J5] D. Dechev and **T.-H. Ahn**, “Using SST/macro for Effective Analysis of MPI-based Applications: Evaluating Large-Scale Genomic Sequence Search”, *IEEE Access* (IF=3.745), vol. **1**, pp. 428-435, 2013. [DOI]
- [J4] Y. Wang, **T.-H. Ahn**, Z. Li, and C. Pan, “Sipros/ProRata: a Versatile Informatics System for Quantitative Community Proteomics”, *Bioinformatics* (IF=6.937), vol. **29**, no. 16, pp. 2064-2065, 2013. [DOI]
- [C6, J3] **T.-H. Ahn** and A. Sandu, “Implicit Second Order Weak Taylor Tau-Leaping Methods for the Stochastic Simulations of Chemical Kinetics”, *Procedia Computer Science*, Volume **4**, pp 2297-2306, *International Conference on Computational Science, ICCS* (Acceptance rate = 24%), 2011. [DOI]
- [J2] D.A. Ball, **T.-H. Ahn**, P. Wang, K.C. Chen, Y. Cao, J.J. Tyson, J. Peccoud, and W.T. Baumann, “Stochastic Exit from Mitosis in Budding Yeast: Model Predictions and Experimental Observations”, *Cell Cycle* (IF=3.304), vol. **10**, issue 6, pp. 1-11, 2011. [DOI]
- [C5] **T.-H. Ahn**, D. Dechev, H. Lin, H. Adalsteinsson and C. Janssen, “Evaluating Performance Optimizations of Large-Scale Genomic Sequence Search Applications Using SST/macro”, in *Proceedings of International Conference on Simulation and Modeling Methodologies, Technologies and Applications (SIMULTECH 2011)*, Noordwijkerhout, Netherlands, (Acceptance rate: 25/141=17.7%), 2011. [DOI]
- [C4] **T.-H. Ahn** and A. Sandu, “Fully Implicit Tau-Leaping Methods for the Stochastic Simulation of Chemical Kinetics”, in *Proceedings of the 19th High Performance Computing Symposium (HPC 2011) part of the 2011 Spring Simulation Multiconference, ser. SpringSim '11*, Boston, MA, USA: Society for Computer Simulation International, 2011. [DOI]
- [C3] **T.-H. Ahn** and A. Sandu, “Parallel Stochastic Simulations of Budding Yeast Cell Cycle: Load Balancing Strategies and Theoretical Analysis”, in *Proceedings of the First ACM International Conference on Bioinformatics and Computational Biology, ser. BCB '10*, New York, NY, USA:ACM, pp. 237-246, (Acceptance rate: 76/307=25%), 2010. [DOI]
- [J1] **T.-H. Ahn**, L. T. Watson, Y. Cao, C. A. Shaffer, and W. T. Baumann, “Cell Cycle Modeling for Budding Yeast with Stochastic Simulation Algorithms”, *Computer Modeling in Engineering and Sciences* (IF=0.75), vol. **51**, no. 1, pp. 27-52, 2009. [DOI]
- [C2] **T.-H. Ahn**, P. Wang, L.T. Watson, Y. Cao, C.A. Shaffer, and W.T. Baumann, “Stochastic Cell Cycle Modeling for Budding Yeast”, in *Proceedings of the 2009 Spring Simulation Multiconference, ser. SpringSim '09*, San Diego, CA, USA: Society for Computer Simulation International, pp. 113:1-113:6, 2009. [DOI]
- [C1] **T.-H. Ahn**, Y. Cao, and L.T. Watson, “Stochastic Simulation Algorithms for Chemical Reactions”, in *Proceedings of the 2008 International Conference on Bioinformatics & Computational Biology, BIOCOMP'08*, Las Vegas, Nevada, USA, pp. 431-436, July 2008.

Awards, Fellowships, & Grants

Summary: I have been awarded a total of **over \$7 million** in funding through competitive grants, of which approximately **\$2.0 million** represents my share as a PI, co-PI, or SLU PI. These awards span federal agencies, international government programs, industry, and institutional funding, advancing research in bioinformatics, AI, computational biology, cybersecurity, and infrastructure development. Most recently, I received an international

research award from the Ministry of SMEs and Startups of the Republic of Korea to develop PUF–blockchain converged security technology robust against tampering attacks, serving as the SLU PI for approximately \$300,000 in institutional funding. I also led a university-level NSF CC* infrastructure award to modernize campus cyberinfrastructure for AI-enhanced research and education.

PENDING GRANT APPLICATIONS

- [P2] **Computational Discovery of Non-Invasive Salivary exRNA Biomarkers and Therapeutic Reversal Candidates for Immunologically Cold Head and Neck Cancer** NIH R03 Apr 2027 – Mar 2028 Total budget: \$305K, Dr. Ahn's budget: \$182K, Role: **multiple PI / lead PI**
- [P1] **A Genome-Resolved, Explainable AI Platform for Predicting Functional Soil Health Outcomes** USDA DSFAS SOHI Jul 2026 – Jun 2028 Total budget: 300K, Dr. Ahn's budget: 220K, Role: **PI**

ACTIVE GRANT AWARDS

- [G15] [Active] **Unveiling Security Risks to Scientific Integrity in AI-Driven Biological Discovery**
National Science Foundation (NSF) EAGER Sep 2026 – Aug 2028
Total budget: \$300,000; SLU budget: approximately \$180,000, Role: **SLU co-PI**
- [G14] [Active] **Development of Physically Unclonable Function (PUF)–Blockchain Converged Security Technology Robust Against Tampering Attacks**
Ministry of SMEs and Startups (MSS), Republic of Korea July 2026 – June 2029
Total budget: \$1,000,000; SLU budget: approximately \$300,000, Role: **SLU PI**
- [G13] [Active] **AI-Enhanced Spatial Transcriptomics for Gastric Cancer Risk Assessment**
Saint Louis University School of Medicine – School of Science and Engineering (SOM–SSE) Collaborative Seed Grant July 2025 – June 2026
Total budget: \$3,000, Role: **PI**
- [G12] [Active] **CC* Compute-Campus: Modernizing Campus Cyberinfrastructure for AI-Enhanced Research and Education (ModernCARE)**
National Science Foundation (NSF Award #2430236) Nov 2024 – Oct 2026
Total budget: \$630,000, Role: **PI**
([Award 2430236 Abstract Link](#))

COMPLETED GRANT AWARDS

- [G11] **TCR Sequence Analysis of Human Cohorts from Zika Infection**
National Institutes of Health (NIH) Sep 2022–Aug 2023
Total budget: \$1M, My share: \$25,000, Role: **Key Personnel**
- [G10] **Deep Immune Medicine: Unlocking Immune Cells using AI**
Saint Louis University Research Innovation Fund Apr 2021 – Dec 2023
Total budget: \$50,000, My share: \$25,000, Role: **PI**
- [G9] **25 nm Xray Inspection System for Semiconductor Backend Process**
South Korean Ministry of Trade, Industry and Energy Apr 2021 – Mar 2025
Total budget: \$2.2M, My share: \$300,000, Role: **co-PI**
- [G8] **Data-Driven Deep Analysis of Dietary Effects on Dog Gut Microbiomes using 16S rRNA Amplicon Sequencing and Shotgun Metagenomics**
Nestle-Purina May 2019 – Dec 2019
Total budget: \$26,513, My share: all, Role: **Sole-PI**
- [G7] **Identifying and Tracking Low Frequency Virus-Specific TCR Clonotypes Using High-Throughput Sequencing**
Federal Bureau of Investigation (FBI) May 2018 – May 2021
Total budget: \$1.2M, My share: \$100,000, Role: **Key Personnel**
- [G6] **SLU Big Ideas: Planning for the Development of a SLU Center for Systems Biology**
Saint Louis University (SLU) Jan 2018 – Jan 2019
Total budget: \$50,000, My share: all, Role: **Sole-PI**
- [G5] **SLU PRF: Deep Analysis of Human Virome using Machine Learning**
Saint Louis University (SLU) Jan 2018 – Jan 2019

Total budget: \$15,608, My share: all, Role: Sole-PI

- [G4] **NSF S-STEM: Bioinformatics Training with Industry Support and Engagement (BITWISE)**
National Science Foundation (NSF) May 2016 – Apr 2022
Total budget: \$649,681, Role: **co-PI**
([Award 1564894 Abstract Link](#))
- [G3] **Microsoft Research: Very Large Scale Metagenomics Analysis using Microsoft Azure Cloud Computing**
Microsoft Research Jun 2016 – May 2017
Total budget: \$20,000 to use Microsoft Azure computing equipment, My share: all, Role: **Sole-PI**
- [G2] **Amazon AWS: Very Large Metagenomic Sequence Analysis using Apache Spark and Amazon Cloud**
Amazon May 2016 – Apr 2018
Total budget: \$5,000 to use Amazon Web Service (AWS) computing equipment, My share: all, Role: **Sole-PI**
- [G1] **NSF CRII: Accelerating Human Microbiome Analysis using Lightning-Fast Cloud Computing**
National Science Foundation (NSF) Apr 2016 – Mar 2019
Total budget: \$174,174, My share: all, Role: **Sole-PI**
([Award 1566292 Abstract Link](#))

AWARDS AND FELLOWSHIPS

- [A7] **Best Paper Runner-Up Award**
[SC25 Workshop – DRBSD 2025](#) 2025
- [A6] **Best Presentation Award**
CAMDA 2020 (Satellite Conf. of the ISMB 2020) 2020
- [A5] **Saint Louis University Scholarly Works Award**
Saint Louis University 2018
- [A4] **Postdoctoral Research Fellowship**
Oak Ridge National Lab Tech 2012–2015
- [A3] **Graduate Student Travel Awards**
Virginia Tech 2008–2012
- [A2] **Graduate Research Assistantship**
Virginia Tech 2007–2012
- [A1] **Most Valuable Employee**
Samsung SDS, S. Korea 2003

Presentations

SELECTED INVITED TALKS (SINCE 2016)

- Jul 2025. *GPU-Enabled Parallel Computing & AI: From Signal Detection to Bioinformatics*, GIST Supercomputing Center HPC-AI Shared Infrastructure Training Program, Gwangju, South Korea.
- Jul 2024. *AI+HPC Revolution*, MarkAny, Seoul, S. Korea.
- Oct 2023. *Multimodal Biomedical Data, AI, and HPC* SLU Conference on AI for Medicine, Saint Louis University, MO, US.
- Apr 2023. *Advanced Computational Techniques for Real-Time Biological Sequence Analyses*, NEXUS Informatics Conference, Children's Mercy Research Institute, Kansas City, MO, US.
- Aug 2022. *Biomedical & Bioinformatics Research using AI and HPC*, Korea Institute of Science and Technology Information (KISTI), S. Korea.
- Aug 2022. *Programming for HPC and AI*, Gwangju Institute of Science and Technology (GIST), S. Korea.
- Aug 2021. *Advancing Bio and Medical Informatics using AI and HPC*, Gwangju Institute of Science and Technology (GIST), S. Korea.
- Jul 2021. *Single-cell RNA sequencing technologies and bioinformatics pipelines*, Saint Louis Univ School of Medicine, St. Louis, MO.
- Dec 2020. *The Convergence of AI, HPC, and Parallel Programming*, XAVIS, Co. LTD., S. Korea.

- Dec 2020. *Advanced Computational Techniques for Genomics and Clinical Researches*, University of Missouri St. Louis, St. Louis, MO.
- Nov 2019. *Advanced Computational Techniques for Real-Time Biological Sequence Analyses*, University Of Nebraska Omaha (UNO), Omaha, NE.
- Nov 2019. *Use Cases of Apache Spark and Machine/Deep Learning in Bioinformatics and Biomedical Researches*, Kyungpook National University (KNU), S. Korea.
- Feb 2019. *Metagenomic Sample Classification and Disease Prediction via Microbiota and Machine Learning*, Nestlé Purina PetCare Talk, St. Louis, MO.
- Nov 2018. *Computer Science for Bioinformatics: Use case of Apache Spark and Machine Learning in Bioinformatics*, KOCSEA 2018 symposium, Silicon Valley, CA.
- Sep 2018. *Applying Bioinformatics and Cloud Techniques for Precision Medicine*, NSF Smart and Connected Health Meeting, Arlington, VA.
- Jul 2017. *Bioinformatics, Big Data, and HPC*, Danforth Plant Science Research Center, St. Louis, MO
- Jun 2016. *Accelerating Human Microbiome Analysis using Supercomputer and Cloud Computing*, Korea Institute of Science and Technology Information (KISTI), S. Korea
- Jun 2016. *Accelerating Human Microbiome Analysis using Supercomputer and Cloud Computing*, Gwangju Institute of Science and Technology (GIST), S. Korea
- Jun 2016. *Accelerating Human Microbiome Analysis using Supercomputer and Cloud Computing*, Ajou University, S. Korea
- CONTRIBUTED PRESENTATIONS** *presenting author*; * mentored students
- C. Gardner⁺, S. Jeong⁺, O. Khatavkar⁺, A. Moon⁺, Q. Cao, **T.-H. Ahn**, “Evaluating Accuracy and Performance Tradeoffs in GPU Accelerated Single Cell RNA-seq Analysis”, in *SC25 DRBSD Workshop (Proceedings of the SC Workshops)*, 2025.
- C. Gardner⁺, **T.-H. Ahn**, “Efficient Anomaly Detection via Adaptive Wavelet Fusion”, Poster Presentation, *GCASR 2025 Workshop*, 2025.
- P. Basia, **T.-H. Ahn**, M. Song, “An IDE Support for Validating Machine Learning Applications in Bioengineering Text Corpora”, in *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 2022.
- K. S. Cheng, **T.-H. Ahn**, and M. Song, “Debugging Support for Machine Learning Applications in Bioengineering Text Corpora”, in *IEEE 46th Annual Computers, Software, and Applications Conference (COMPSAC)*, 2022.
- Y. Mreyoudand⁺ and **T.-H. Ahn**^{*}, “Deep Neural Network Modeling for Phenotypic Prediction of Metagenomic Samples”, in *Proceedings of the 11th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (BCB '20)*, September 21–24, 2020, Virtual Event, USA 2020.
- T. Kosfeld⁺, J. McMillan⁺, R. J. DiPaolo, J. Hou⁺, and **T.-H. Ahn**^{*}, “Performance Evaluation of Viral Infection Diagnosis using T-Cell Receptor Sequence and Artificial Intelligence”, in *Proceedings of the 11th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (BCB '20)*, September 21–24, 2020, Virtual Event, USA (Acceptance Rate=30%), 2020.
- W. Feng⁺, Z. Yu, M. Kang, H. Gong⁺, and **T.-H. Ahn**^{*}, “Practical Evaluation of Different Omics Data Integration Methods”, in *Precision Health and Medicine. W3PHAI 2019. Studies in Computational Intelligence*, vol **843**. Springer, Cham, 2019.
- A. Paul⁺, D. Lawrence⁺, M. Song, S.-H. Lim, C. Pan, and **T.-H. Ahn**^{*}, “SORA: Scalable Overlap-graph Reduction Algorithms for Genome Assembly using Apache Spark in the Cloud”, in *proceedings of the 2018 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 2018.
- M. McCoy, A. Paul⁺, M. Victor, M. Richner, H. Gabel, H. Gong, A. Yoo⁺, and **T.-H. Ahn**^{*}, “LONGO: An R Package for Interactive Gene Length Dependent Analysis for Neuronal Identity”, *Bioinformatics (IF=6.937)*, vol. **34**, issue 13, pp. i422-428, *ISMB-2018*, 2018.
- A. Paul⁺, D. Lawrence⁺, and **T.-H. Ahn**^{*}, “Overlap Graph Reduction for Genome Assembly using Apache Spark”, in *Proceedings of the 8th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics. ACM-BCB 2017*, ACM: Boston, Massachusetts, USA. poster, p. 613-613, 2017.
- T.-H. Ahn** and A. Sandu, “Implicit Second Order Weak Taylor Tau-Leaping Methods for the Stochastic Simulations of Chemical Kinetics”, *Procedia Computer Science*, Volume **4**, pp 2297-2306, *International Conference on Computational Science, ICCS* (Acceptance rate = 24%), 2011.

- T.-H. Ahn**, D. Dechev, H. Lin, H. Adalsteinsson and C. Janssen, “Evaluating Performance Optimizations of Large-Scale Genomic Sequence Search Applications Using SST/macro”, in *Proceedings of International Conference on Simulation and Modeling Methodologies, Technologies and Applications (SIMULTECH 2011)*, Noordwijkerhout, Netherlands, (Acceptance rate: 25/141=17.7%), 2011.
- T.-H. Ahn** and A. Sandu, “Fully Implicit Tau-Leaping Methods for the Stochastic Simulation of Chemical Kinetics”, in *Proceedings of the 19th High Performance Computing Symposium (HPC 2011) part of the 2011 Spring Simulation Multiconference*, ser. *SpringSim '11*, Boston, MA, USA: Society for Computer Simulation International, 2011.
- T.-H. Ahn** and A. Sandu, “Parallel Stochastic Simulations of Budding Yeast Cell Cycle: Load Balancing Strategies and Theoretical Analysis”, in *Proceedings of the First ACM International Conference on Bioinformatics and Computational Biology*, ser. *BCB '10*, New York, NY, USA:ACM, pp. 237-246, (Acceptance rate: 76/307=25%), 2010.
- T.-H. Ahn**, P. Wang, L.T. Watson, Y. Cao, C.A. Shaffer, and W.T. Baumann, “Stochastic Cell Cycle Modeling for Budding Yeast”, in *Proceedings of the 2009 Spring Simulation Multiconference*, ser. *SpringSim '09*, San Diego, CA, USA: Society for Computer Simulation International, pp. 113:1-113:6, 2009.
- T.-H. Ahn**, Y. Cao, and L.T. Watson, “Stochastic Simulation Algorithms for Chemical Reactions”, in *Proceedings of the 2008 International Conference on Bioinformatics & Computational Biology, BIOCOMP'08*, Las Vegas, Nevada, USA, pp. 431-436, July 2008.

Teaching Experience

Current (Spring 2026): CSCI-4610/5610 & BCB-5250

- CSCI-4610/5610: Concurrent and Parallel Programming** DESCRIPTION: The design and implementation of software that fully leverages a single computer's resources. Topics include profiling and optimization of codes, multi-threaded programming, parallelism using a graphical processor unit (GPU), and efficient use of memory cache. *Average student rating: 3.8/4.0* 2022S, 2023S, 2024S, 2024Summer, 2025S, 2026S
- BCB-5200/5250: Intro to Bioinformatics I, II** DESCRIPTION: Introduction to Bioinformatics I and II are designed to introduce senior/graduate students to the fundamental concepts, methods, and research topics in Bioinformatics for analyzing biological and even biomedical data. Intensive Omics data analyses (genomics, metagenomics, RNA-Seq, proteomics) with hands-on examples and projects are proposed to students. *Average student rating: 3.80/4.0* BCB-5200: Fall 2015–2017, BCB-5250: 2016S, 2017S, 2018S, 2019S, 2020S, 2021S, 2022S, 2023S, 2024S, 2025S, 2026S
- CSCI-2100: Data Structures** DESCRIPTION: The design, implementation, and use of data structures. Principles of abstraction, encapsulation, and modularity guide the creation of robust, adaptable, reusable, and efficient structures. Specific data types include stacks, queues, lists, priority queues, dictionaries, trees, and graphs. *Average student rating: 3.75/4.0* 2017F, 2018F, 2019F, 2020F, 2024F, 2025F
- GIST: GIST AI-HPC Tutorial Workshop** DESCRIPTION: GIST-AI-HPC-2024 tutorial: Deep Learning with HPC. 2024Summer
- CSCI-4620/5620: Distributed Computing** DESCRIPTION: The design and implementation of software solutions that rely upon the cooperation of multiple computing systems. Topics will include parallelization of computation and data storage across small clusters of computers, and the deployment of systems in large-scale grid and cloud computing environments. *Average student rating: 3.75/4.0* 2023S
- CSCI-4850/5850: High-Performance Computing** DESCRIPTION: The design and implementation of software solutions that rely upon the cooperation of shared and distributed computing systems. Topics will include parallelization of computation and data storage from shared memory systems into clusters of computers, and the deployment of systems in a large-scale grid and cloud computing environments with GPUs. *Average student rating: 3.71/4.0* 2016S, 2017S, 2018S, 2019S, 2020S, 2021S
- GIST AI School: High-Performance Computing** DESCRIPTION: The design and implementation of software solutions that rely upon the cooperation of shared and distributed computing systems. Topics will include parallelization of computation and data storage from shared memory systems into clusters of computers, and the deployment of systems in a large-scale grid and cloud computing environments with GPUs. *Average student rating: 4.0/4.0* Summer 2022, Summer 2023, Summer 2025
- BCB-5300: Algorithms in Computational Biology** DESCRIPTION: This course introduces the foundations of algorithmic techniques and analysis, as motivated by biological problems. Topics include dynamic programming, tree and graph algorithms, sequence analysis, clustering and hidden markov models. Motivations include sequence alignment, motif finding, genome assembly, gene prediction, and phylogeny. *Average student rating: 3.63/4.0* Fall 2019, 2020
- BCB 5810 - Bioinformatics Colloquium** DESCRIPTION: The course provides students with current information about studies in bioinformatics and computational biology through presentations given by faculty members, students, and invited speakers. Students who enroll for credit must present a 20-30 minute talk as part of the seminar, demonstrating their oral communication skills while presenting technical content. *Average student rating: 3.79/4.0* Fall 2016, 2018, 2020, 2022

Mentorship & Supervision

CURRENT GRADUATE (PH.D. AND M.S.) STUDENTS

Note: Computer Science (CS), Bioinformatics and Computational Biology Master Program (BCB)

Cory Gardner (CS Ph.D.) [Saint Louis University] [Jan 2022 – Current] Bioinformatics, high-performance computing (HPC), and multimodal AI

Franklin Lamin (BCB M.S.) [Saint Louis University] [Spring 2026 – Current] Monkeypox outbreak pan-genome analysis

Usha Rani Lankalapalli (BCB M.S.) [Saint Louis University] [Spring 2026 – Current] scRNA-seq analysis project

Seung Bum Jung (CS M.S.) [Saint Louis University] [Spring 2026 – Current] Dental data analysis using AI

Tanisha Londhe (BCB M.S.) [Saint Louis University] [Spring 2026 – Current] Vaginal microbiome analysis

Eric Nguyen (BCB M.S.) [Saint Louis University] [Spring 2025 – Current] Plant tissue microbiome analysis

Seyun Jeong (AI M.S.) [Saint Louis University] [Fall 2024 – Current] scRNA-seq analysis using GPU accelerators

Aendri Dhillon (AI M.S.) [Saint Louis University] [Fall 2024 – Current] Anomaly detection algorithms

Fnu Zaheer Khan (BCB M.S.) [Saint Louis University] [Fall 2024 – Current] Spatial transcriptomics data analysis

CURRENT UNDERGRADUATE STUDENTS

Yeeon Ryu (CS B.S.) [Saint Louis University] [Spring 2024 – Current] Biomedical informatics and T-cell receptor sequence analysis

CURRENT HIGH-SCHOOL STUDENTS

Aiden Moon (Parkway Central High School) [St. Louis, MO] [Spring 2024 – Current] scRNA-seq analysis using GPU accelerators; will attend Stanford University in Fall 2026

FORMER GRADUATE AND UNDERGRADUATE STUDENTS

Gihwan Jung (CS B.S.) [Saint Louis University] [Fall 2022 – Fall 2025] Large-scale analysis of massive blood metagenomics samples

Venkateswara Reddy Satti (AI M.S.) [Saint Louis University] [Fall 2024 – Fall 2025] Multimodal data membership inference attacks

Amy Chen (CS B.S.) [Saint Louis University] [Spring 2024 – Spring 2025] Medical image federated learning

Amina Ademovic (BCB M.S.) [Saint Louis University] [Fall 2024 – Spring 2025] Blood and tissue microbiome analysis

Kaarunya Nachimuthu (BCB M.S.) [Saint Louis University] [Graduated] scRNA-seq analysis (co-mentored with Dr. Richard DiPaolo)

Tim Kosfeld (CS B.S., BCB M.S.) [Saint Louis University] [Spring 2019 – Summer 2023] Ph.D. student at Princeton University

Jihun Lim (High School Student) [Saint Paul Preparatory Seoul, Korea] [Fall 2021 – Spring 2024] RPI student

Will Phoenix (CS B.S.) [Saint Louis University] [Fall 2022 – Spring 2023]

Reza Zakerian (CS M.S.) [Saint Louis University] [Summer 2022 – Summer 2023] Enterprise research

Ethan Pang Kao (BCB M.S.) [Saint Louis University] [Spring 2022 – Spring 2023] Bioinformatics Research Associate at Washington University

William Schmitt (BCB M.S.) [Saint Louis University] [Fall 2022 – Spring 2023] Bioinformatics Research Associate at Washington University

Wanxiang Liu (BCB M.S.) [Saint Louis University] [Fall 2021 – Spring 2022] Ph.D. student at Arizona State University

Binita Febles (BCB M.S.) [Saint Louis University] [Fall 2021 – Spring 2022] Bioinformatics Scientist at Washington University in St. Louis

Yassin Mreyoud (BCB M.S.) [Saint Louis University] [Fall 2020 – Spring 2022] MD/Ph.D. student at the University of Alabama

Stephen Tahan (BCB M.S.) [Saint Louis University] [Fall 2019 – Spring 2021]

Sadiya Ahmad (CS M.S.) [Saint Louis University] [Fall 2019 – Spring 2021]

Nabeel Sait (CS B.S., M.S.) [Saint Louis University] [Fall 2019 – Spring 2022] Software Engineer at Amazon

Scott Lewis (BCB M.S.) [Saint Louis University] [Fall 2018 – Spring 2020] Ph.D. student at Washington University in St. Louis

Jonathan McMillan (ECE B.S.) [Saint Louis University] [Fall 2020 – Spring 2022] Software Engineer at Watlow

Juan Maldonado (CS B.S.) [Saint Louis University] [Spring 2018 – Spring 2020]

Angela Wu (BCB M.S.) [Saint Louis University] [Fall 2018 – Spring 2019]

Keenan Berry (BCB M.S.) [Saint Louis University] [Fall 2018 – Spring 2020]

Zohair Siddiqui (CS B.S.) [Saint Louis University] [Spring 2018 – Spring 2020] M.D. program, Saint Louis University School of Medicine

Ahmad Rajeh (CS B.S., BCB M.S.) [Saint Louis University] [Fall 2017 – Spring 2019] M.D. program, University of Missouri School of Medicine (Columbia)

Pallavi Gupta (BCB M.S.) [Saint Louis University] [Fall 2017 – Spring 2019] Ph.D. program, University of Missouri (Columbia)

Eliza Dhungel (BCB M.S.) [Saint Louis University] [Fall 2017 – Spring 2019] Staff Scientist at Washington University in St. Louis

Courtney Schiebout (BCB M.S.) [Saint Louis University] [Fall 2017 – Spring 2019] Ph.D. program in Quantitative Biomedical Sciences, Dartmouth

Matthew Mosior (BCB M.S.) [Saint Louis University] [Fall 2017 – Spring 2019] Staff Bioinformatician at Washington University School of Medicine in St. Louis

Wenjia Feng (BCB M.S.) [Saint Louis University] [Fall 2016 – Spring 2018] Bioinformatics Scientist at Washington University School of Medicine in St. Louis

Alex Paul (BCB M.S.) [Saint Louis University] [Fall 2015 – Spring 2018] Bioinformatics Scientist at McDonnell Genome Institute, Washington University

Dylan Lawrence (CS B.S., BCB M.S.) [Saint Louis University] [Fall 2015 – Spring 2017] Ph.D. student at Washington University in St. Louis

James Gallien (BCB M.S.) [Saint Louis University] [Fall 2015 – Fall 2016]

Barry Hykes (BCB M.S.) [Saint Louis University] [Fall 2015 – Fall 2016] Bioinformatics Scientist at McDonnell Genome Institute, Washington University

THESIS COMMITTEE

Cory Gardner, Ph.D. in Computer Science [Saint Louis University] [Spring 2022 – Current] Committee Chair; Dissertation title: TBD

Seyun Jeong, M.S. in Computer Science [Saint Louis University] [Spring 2025 – Current] Committee Chair; Thesis title: TBD

Bohan Zhang, Ph.D. in Computer Science [Saint Louis University] [Spring 2024 – Fall 2025] Committee Member; Dissertation title: EXPERTLOOP: A Knowledge-Driven Framework for Community-Based Flight Log Analysis

Victor Onoja, M.S. in Computer Science [Saint Louis University] [Spring 2024 – Fall 2025] Committee Member; Thesis title: EXPERTLOOP: A Knowledge-Driven Framework for Community-Based Flight Log Analysis

Seula Park, M.S. in AI Graduate School [Gwangju Institute of Science and Technology (GIST)] [Spring 2022 – Spring 2023] Committee Member; Thesis title: Prediction and Analysis of Alzheimer's Disease Using Blood Microbiome

Xiao Niu, Ph.D. in Biology [Saint Louis University] [Fall 2021 – Current] Committee Member

Junhao Chen, Ph.D. in Biology [Saint Louis University] [Fall 2021 – Current] Committee Member

Yongjun Tan, Ph.D. in Biology [Saint Louis University] [Fall 2018 – Current] Committee Member

Joel Swift, Ph.D. in Biology [Saint Louis University] [Fall 2017 – Current] Committee Member; Dissertation title: The Root of It All: The Role of Grafting in Shaping Plant-Associated Microorganism Communities in Vitis

Zachary Harris, Ph.D. in Biology [Saint Louis University] [Fall 2017 – Current] Committee Member; Dissertation title: Phenomics Approaches to Quantify the Effects of Grafting on Grapevine Phenotypic Diversity

Zhaolian Lu, Ph.D. in Biology [Saint Louis University] [Fall 2015 – Current] Committee Member; Dissertation title: The Regulation and Evolution of Transcription Initiation in Yeast

Outreach & Professional Development

SELECTED SERVICE AND OUTREACH

Remote Grant Proposal Reviewer for DOE-SBIR Phase II Reviewer 2024

Computer Science Faculty Search Committee Member Saint Louis University 2016 (tenure track), 2018 (tenure track), 2025 (visiting faculty)

Computer Science Faculty Search Committee Chair Saint Louis University 2019, 2023

Rank and Tenure Structure Committee, School of Science and Engineering at Saint Louis University Member 2022

Remote Grant Proposal Reviewer for DOE-SBIR Phase I Reviewer 2021

Institute for Vaccine Science and Policy (IVSP) Computational Biology Core Interim Director 2020 –

Research Computing Group (RCG) Advisory Board Member 2020 –

Swiss National Science Foundation Grant Panel Review Reviewer 2019, 2020, 2024

NSF Grant Panel Review Reviewer 2016, 2023, 2025

JOURNAL EDITOR AND TECHNICAL PROGRAM COMMITTEE

Frontiers in Microbiomes (Omics and Bioinformatics for Microbiomes) Associate Editor 2025 –

Technical Program Committee for ACM Int. Conf. on Bioinformatics and Computational Biology (ACM-BCB) Committee Member 2021, 2024

Technical Program Committee for IEEE Int. Conf. on Bioinformatics and Biomedicine (IEEE-BIBM) Committee Member 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024

Guest Editor for *Plants* journal special session: Deep Learning in Plant Sciences Guest Editor 2022, 2023

Technical Program Committee for Int. Conf. on Bioinformatics Research and Applications (ICBRA) Committee Member 2019, 2020, 2021

PEER REVIEW

Bioinformatics	2015–2025
BMC Human Genomics	2019
Briefings in Bioinformatics	2015, 2018, 2020, 2025
Cluster Computing	2019, 2020
Communications Biology	2018
Environmental Microbiology	2026
Frontiers in Bioinformatics	2024, 2025
Frontiers in Microbiomes	2022, 2023, 2024, 2025
GigaScience	2018, 2021
IETE Technical Review	2014
International Journal of Data Mining and Bioinformatics	2018
Journal of Parallel and Distributed Computing	2015
Journal of Supercomputing	2025
Microbiology Spectrum	2021–2026
Microbiome	2021, 2022
mSystems	2021–2025
Nature Communications Biology	2018
Scientific Reports	2016, 2017, 2020
PeerJ	2022
PLOS Computational Biology	2018, 2025, 2026
PLOS ONE	2014, 2016–2020

PROFESSIONAL MEMBERSHIPS

International Society for Computational Biology (ISCB) Member

Association for Computing Machinery (ACM) Member

References

Available upon request.