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

Personal Profile

Engineering background computer scientist for 20+ years in both industry and academia. My research focuses on developing new software tools to better analyze Big Data (principally, but not limited to, bio, health, and biomedical) using Artificial Intelligence (AI) and diverse computational techniques on High-Performance Computing (HPC) systems including supercomputers and cloud computing.

Education

Virginia Tech   *Blacksburg, VA, US*
PhD in Computer Science   *Aug 2007 - Jul 2012*
- Advisor: Dr. Adrian Sandu
- Dissertation: Computational Techniques for the Analysis of Large Scale Biological Systems

Northwestern University   *Evanston, IL, US*
MS in Computer Engineering   *Aug 2005 - Jun 2007*

Yonsei University   *Seoul, S. Korea*
BS in Electrical Engineering   *Mar 1994 - Feb 2000*

Professional Experience

2021-	**Adjunct Professor**, AI Graduate School, Gwangju Institute of Science and Technology (GIST)
2021-	**Interim Director of Computational Biology Core**, Institute for Vaccine Science and Policy, Saint Louis University School of Medicine
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

Journal Articles and Conference Proceedings

[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. 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. [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. Epuri, 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*, "YeasTSS: 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 Multi-conference, 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

ACTIVE GRANT AWARDS

[G11] [Active] **TCR Sequence Analysis of Human Cohorts from Zika Infection**
National Institutes of Health (NIH)   2022-2023
Total budget: $1M, My share: $25,000, Role: Key Personnel

[G10] [Active] **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] [Active] **25 nm Xray Inspection System for Semiconductor Backend Process**
South Korean Ministry of Trade, Industry and Energy   Apr 2021 – Dec 2024
Total budget: $2.2M, My share: $300,000, Role: co-PI

COMPLETED GRANT AWARDS

[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 Abstract: 1564894)

[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)

AWARDS AND FELLOWSHIPS

[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)

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

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. Lawrenc[+], 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

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* Fall 2017, 2018, 2019, 2020

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* Spring 2022

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. Spring 2023

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* Spring 2016, 2017, 2018, 2019, 2020, 2021

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: Spring 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023

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

GST: Development and biological applications of omics technologies DESCRIPTION: Graduate Program in Genome Science & Technology at University of Tennessee Knoxville Spring 2015

Mentorship & Supervision

PRIMARY ADVISOR – CURRENT GRADUATE STUDENTS

Cory Gardner, BCB M.S., CS Ph.D. [Saint Louis University] [Spring 2020 –] Computer vision using CUDA, Oxford Nanopore assembly, metagenomics

Tim Kosfeld, CS B.S., BCB M.S. [Saint Louis University] [Spring 2019 –] Deep learning for immune cell analysis Tool (with Dr. Richard DiPaolo, SLU Med School)

Reza Zakerian, CS M.S. [Saint Louis University] [Summer 2022 –] ML/HPC for autonomous driving simulator

Ethan Pang Kao, BCB M.S. [Saint Louis University] [Spring 2022 –] Large-scale analysis of massive blood metagenomics samples

William Schmitt, BCB M.S. [Saint Louis University] [Fall 2022 –] Immune cell sequencing analysis

RESEARCH SUPERVISOR – CURRENT UNDERGRADUATE AND HIGH-SCHOOL STUDENTS

Will Phoenix, CS B.S. [Saint Louis University] [Fall 2022 –] ML/HPC for autonomous driving simulator

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

Jihun Lim, High School Student [Saint Paul Preparatory Seoul, Korea] [Fall 2021 –] Metagenomics analysis

PRIMARY ADVISOR – FORMER GRADUATE AND UNDERGRAD STUDENTS

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

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 U 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, Washington University in St. Louis

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

Juan Maldonado, CS B.S. [Saint Louis University] [Spring 2018 – Spring 20220]

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] MD program, Saint Louis University School of Medicine

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

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

Eliza Dhungel, BCB M.S. [Saint Louis University] [Fall 2017 – Spring 2019] Staff scientist, 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, Washington University School of Medicine in St. Louis

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

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

Dylan Lawrence, CS BS, 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, McDonnell Genome Institute, Washington University

Advisory Committee

Seula Park, AI Graduate School M.S. [Gwangju Institute of Science and Technology (GIST)] [Spring 2022 – Spring 2023] M.S. Thesis: Prediction and analysis of Alzheimer's disease using blood microbiome

Junhao Chen, Bio Ph.D. [Saint Louis University] [Fall 2021 –]

Yongjun Tan, Bio Ph.D. [Saint Louis University] [Fall 2018 –]

Joel Swift, Bio Ph.D. [Saint Louis University] [Fall 2017 –] Ph.D. Thesis: THE ROOT OF IT ALL: THE ROLE OF GRAFTING IN SHAPING PLANT-ASSOCIATED MICROORGANISM COMMUNITIES IN VITIS

Zachary Harris, Bio Ph.D. [Saint Louis University] [Fall 2017 –] Ph.D. Thesis: PHENOMICS APPROACHES TO QUANTIFY THE EFFECTS OF GRAFTING ON GRAPEVINE PHENOTYPIC DIVERSITY

Zhaolian Lu, Bio Ph.D. [Saint Louis University] [Fall 2015 –] Ph.D. Thesis: THE REGULATION AND EVOLUTION OF TRANSCRIPTION INITIATION IN YEAST

Outreach & Professional Development

Service and Outreach

Remote Grant Proposal Reviewer for DOE-SBIR Phase II Reviewer 2022

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

NSF Grant Panel Review Reviewer 2016

Guest Editor and Technical Program Committee

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

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

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

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

Peer Review

Bioinformatics	2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022
BMC Human Genomics	2019
Briefing in Bioinformatics	2015, 2018, 2020
Cluster Computing	2019, 2020
Communications Biology	2018
Frontiers in Microbiome	2022
Giga Science	2018, 2021
IETE Technical Review	2014
International Journal of Data Mining and Bioinformatics	2018
Journal of Parallel and Distributed Computing	2015
Microbiology Spectrum	2021, 2022, 2023
Microbiome	2021, 2022
mSystems	2021, 2022
Nature Communications Biology	2018
Nature Scientific Reports	2016, 2017, 2020
PeerJ	2022
PLOS Computational Biology	2018
PLOS ONE	2014, 2016, 2017, 2018, 2019, 2020

Professional Memberships

International Society for Computational Biology (ISCB) Member
Association for Computing Machinery (ACM) Member
IEEE Computer Society (IEEE) Member