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Tae-Hyuk (Ted) Ahn  
ASSOCIATE PROF. OF COMPUTER SCIENCE, SAINT LOUIS UNIVERSITY

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

✉️ taehyuk.ahn@slu.edu  ☎️ 1-314-977-3633  🌐 cs.slu.edu/~ahn/
 minOccurs="false" xmlns="http://www.w3.org/2000/svg" xmlns:xlink="http://www.w3.org/1999/xlink" fill="#555" stroke="#555" stroke-width="1" stroke-linecap="round" stroke-linejoin="round" style="filter: brightness(1.1)"/>

Bioinformatics, biomedical informatics, high-performance computing, parallel programming, big data analytic, machine learning, deep learning, and open-source development.

| RESEARCH INTERESTS |
|---------------------|
| Bioinformatics, biomedical informatics, high-performance computing, parallel programming, big data analytic, machine learning, deep learning, and open-source development. |

| EDUCATION |
|-----------|
| **Virginia Tech**
PhD in Computer Science
Advisor: Dr. Adrian Sandu, Lab: Computational Science Lab (CSL)
Dissertation: Computational Techniques for the Analysis of Large Scale Biological Systems |

| **Northwestern University**
MS in Electrical and Computer Engineering |

| **Yonsei University**
BS in Electrical Engineering |

| ACADEMIC AND PROFESSIONAL APPOINTMENTS |
|---------------------------------------|
| **Associate Professor (tenured with a year advanced)**
Department of Computer Science, Saint Louis University
Graduate Program in Bioinformatics and Computational Biology
Secondary Appointment in Department of Mathematics and Statistics |

| Postdoctoral Research Associate
Computer Science and Mathematics Division, Oak Ridge National Laboratory |

| Research Intern
HPC Group, Business and Technology, Pfizer Inc. |

| Research Intern
Scalable Computing R&D Department, Sandia National Lab |

| Research/Teaching Assistant
Departments of Computer Science, Virginia Tech |

| Instructor & Lecturer
Private Mathematics Institute |

| Senior Software Engineer
Samsung SDS |

| Publications |
|---------------|
| **Journals** – bold: it’s me, *: corresponding, under-bar: I am the first or corresponding |

[25] iCAT: Diagnostic Assessment Tool of Immunological History using High-throughput T-cell Receptor Sequencing
A Rajeh, K Wolf, C Schiebout, N Sait, T Kosfeld, RJ DiPaolo* and TH Ahn*
F1000Research, 2021. (DOI)
[J24] MegaR: An Interactive R Package for Rapid Sample Classification and Pheno-type Prediction using Metagenome Profiles and Machine Learning
E Dhungel, Y Mreyoud, HJ Gwak, A Rajeh, M Rho, and TH Ahn*
_BMC Bioinformatics_ (IF=3.242), 22, 25, 2021. (DOI)

[J23] Diagnostic Differentiation of Zika and Dengue Virus Exposure by Analyzing T Cell Receptor Sequences from Peripheral Blood of Infected HLA-A2 Transgenic Mice
M Hassert, KJ. Wolf, A Rajeh, C Shiebout, SG Hoft, TH Ahn, RJ DiPaolo, JD Brien, and AK Pinto
_PLOS Neglected Tropical Disease_ (IF=4.487), 2020. (DOI)

[J22] Single Cell Transcriptional Analyses Identify Lineage-Specific Epithelial Responses to Inflammation and Metaplastic Development in the Gastric Corpus
K Bockerstett, S Lewis, C Noto, E Ford, N Saenz, N Jackson, TH Ahn, J Mills, and R DiPaolo
_Gastroenterology_ (IF=20.877), 159, 6, 2020. (DOI)

[J21] Single-cell Transcriptional Analyses of Spasmolytic Polypeptide-expressing Metaplasia Arising from Acute drug Injury and Chronic Inflammation in the Stomach
K Bockerstett, S Lewis, K Wolf, C Noto, N Jackson, E Ford, TH Ahn, R DiPaolo
_Gut_ (IF=17.943), 69, 6, 1027–1038, 2020. (DOI)

[J20] DNA Based Methods in Intelligence - Moving Towards Metagenomics
G Mason-Buck, A Graf, E Elhaik, J Robinson, E Pospiech, M Oliveira, J Moser, PKH Lee, D Githae, D Ballard, Y Bromberg, CS Casimiro-Soriguer, E Dhungel, TH Ahn, J Kawulok, C Loucera, F Ryan, AR Walker, C Zhu, CE Mason, A Amorim, D Syndercombe Court, W Branicki, P Labaj
_Preprints_, 2020. (DOI)

[J19] Rchimerism: An R-Package for Automated Chimerism Data Analysis
Z Siddiqui, J Maldonado, J Grojean, F Ye, D Zhang, J Longtine, TH Ahn*, and H Guo*
The Journal of Molecular Diagnostics (IF=4.426), 22, 1, 2020. (DOI)

[J18] Using Apache Spark on Genome Assembly for Scalable Overlap-graph Reduction
A Paul, D Lawrence, M Song, SH Lim, C Pan, and TH Ahn*
_Human Genomics_ (IF=3.526), 13, 1, 2019. (DOI)

[J17] Tool Support for Managing Repetitive Program Changes in Evolving Software
VK Epuri, S Sakala, TH Ahn, and M Song*
_IET Software_ (IF=1.070), 2019. (DOI)

[J16] Massive Metagenomic Data Analysis using Abundance-Based Machine Learning
Z Harris, E Dhungel, M Mosior, and TH Ahn*
_Biology Direct_ (IF=3.332), 14, 12, 2019. (DOI)

[J15] YeasTSS: An Integrative Web Database of Yeast Transcription Start Sites
J McMillan, Z Lu, J Rodriguez, TH Ahn*, and Z Lin*
_Database (Oxford)_ (IF=3.793), 2019, baz048, 2019. (DOI)

[J14] Identifying and Tracking Low Frequency Virus-Specific TCR Clonotypes Using High-Throughput Sequencing
K Wolf, T Hether, P Gilchuk, A Kumar, A Rajeh, C Schiebout, J Maybruck, RM Buller, TH Ahn, S Joyce, and RJ DiPaolo
_Cell Reports_ (IF=8.652), 25, 9, 2369–2378.E4, 2018. (DOI)
[J13] LONGO: An R Package for Interactive Gene Length Dependent Analysis for Neuronal Identity
M McCoy, A Paul, M Victor, M Richner, H Gabel, H Gong, A Yoo*, and TH Ahn*
Bioinformatics (IF=5.766), 34, 13, i422–428, 2018. (DOI)

[J12] Implicit Simulation Methods for Stochastic Chemical Kinetics
TH Ahn, X Han, and A Sandu
Journal of Applied Analysis and Computation (IF=1.116), 5, 3, 420–452, 2015. (DOI)

[J11] Insights from 20 Years of Bacterial Genome Sequencing
M Land, L Hauser, S Jun, I Nookaew, M Leuze, TH Ahn, T Karpinets, O Lund, G Kora, T Wassenaar, S Poudel, and D Ussery
Functional & Integrative Genomics (IF=2.745), 15, 2, 141–161, 2015. (DOI)

[J10] Sigma: Strain-level Inference of Genomes from Metagenomic Analysis for Bio-surveillance
TH Ahn, J Chai, and C Pan
Bioinformatics (IF=5.766), 31, 2, 170–177, 2015. (DOI)

[J9] A Framework to Analyze the Performance of Load Balancing Schemes for Ensembles of Stochastic Simulations
TH Ahn, A Sandu, LT Watson, CA Shaffer, Y Cao, and WT Baumann
International Journal of Parallel Programming (IJPP) (IF=1.258), 43, 4, 597–630, 2015. (DOI)

[J8] FunctionalPhylogenomics Analysis of Bacteria and Archaea using Consistent GenomeAnnotation with UniFam
J Chai, G Kora, TH Ahn, D Hyatt, and C Pan
BMC Evolutionary Biology (IF=3.559), 14, 1, 207, 2014. (DOI)

[J7] Omega: an Overlap-graph de novo Assembler for Metagenomics
B Haider, TH Ahn, B Bushnell, J Chai, A Copeland, and C Pan
Bioinformatics (IF=5.766), 30, 19, 2717–2722, 2014. (DOI)

[J6] Diverse and Divergent Post-translational Modification of Proteins of Closely Related Bacteria in Two Growth Stages of a Natural Microbial Community
Z Li, Y Wang, Q Yao, NB Justice, TH Ahn, D Xu, RL Hettich, JF Banfield, and C Pan
Nature Communication (IF=13.811), 5, 4405, 2014. (DOI)

[J5] Using SST/macro for Effective Analysis of MPI-based Applications: Evaluating Large-Scale Genomic Sequence Search
D Dechev and TH Ahn
IEEE Access (IF=3.745), 1, 428–435, 2013. (DOI)

[J4] Sipros/ProRata: a Versatile Informatics System for Quantitative Community Proteomics
Y Wang, TH Ahn, Z Li, and C Pan
Bioinformatics (IF=5.766), 29, 16, 2064–2065, 2013. (DOI)

[J3] Implicit Second Order Weak Taylor Tau-Leaping Methods for the Stochastic Simulations of Chemical Kinetics
TH Ahn and A Sandu
Procedia Computer Science (ICCS-2011), 4, 2297–2306, 2011. (DOI)

[J2] Stochastic Exit from Mitosis in Budding Yeast: Model Predictions and Experimental Observations
DA Ball, TH Ahn, P Wang, KC Chen, Y Cao, JJ Tyson, J Peccoud, and WT Baumann
*Cell Cycle* (IF=3.304), **10**, 6, 1-11, 2011. ([DOI](https://doi.org/)

**[J1]** Cell cycle modeling for budding yeast with stochastic simulation algorithms
TH Ahn, LT Watson, Y Cao, CA Shaffer, and WT Baumann
*Computer Modeling in Engineering and Sciences (CMES)* (IF=0.805), **51**, 1, 27–52, 2009. ([DOI](https://doi.org/)

**Peer-reviewed Conferences, Workshops, and Book Chapters**

**[P10]** Performance Evaluation of Viral Infection Diagnosis using T-Cell Receptor Sequence and Artificial Intelligence
T Kosfeld, J McMillan, R DiPaolo, J Hou*, and **TH Ahn**
In Proc. of the 11th ACM Int. Conf. on Bioinformatics, Computational Biology and Health Informatics (*ACM-BCB*) (AR=30%), Sep 21–24, 2020. ([DOI](https://doi.org/)

**[P9]** Deep Neural Network Modeling for Phenotypic Prediction of Metagenomic Samples
Y Mreyoud and **TH Ahn**
In Proc. of the 11th ACM Int. Conf. on Bioinformatics, Computational Biology and Health Informatics (*ACM-BCB*), Sep 21–24, 2020. ([DOI](https://doi.org/)

**[P8]** Practical Evaluation of Different Omics Data Integration Methods
T Kosfeld, J McMillan, R DiPaolo, J Hou*, and **TH Ahn**
In *Int. Workshop on Health Intelligence (W3PHAI 2019): Precision Health and Medicine* (Part of the Studies in Computational Intelligence book series, SCI, Vol 843), Aug 2019. ([DOI](https://doi.org/)

**[P7]** SORA: Scalable Overlap-graph Reduction Algorithms for Genome Assembly using Apache Spark in the Cloud
A Paul, D Lawrence, M Song, SH Lim, C Pan, and **TH Ahn**
In Proc. of the IEEE Int. Conf. on Bioinformatics and Biomedicine (*IEEE-BIBM*), Dec 2018. ([DOI](https://doi.org/)

**[P6]** Overlap Graph Reduction for Genome Assembly using Apache Spark
A Paul, D. Lawrence, and **TH Ahn**
In Proc. of the 8th ACM Int. Conf. on Bioinformatics, Computational Biology, and Health Informatics (*ACM-BCB*), Aug 2017. ([DOI](https://doi.org/)

**[P5]** Evaluating Performance Optimizations of Large-Scale Genomic Sequence Search Applications Using SST/macro
TH Ahn, D Dechev, H Lin, H Adalsteinsson and C Janssen
In Proc. of the Int. Conf. on Simulation and Modeling Methodologies, Technologies and Applications (*SIMULTECH*) (AR=17.7%), 2011. ([DOI](https://doi.org/)

**[P4]** Fully Implicit Tau-Leaping Methods for the Stochastic Simulation of Chemical Kinetics
TH Ahn and A Sandu
In Proc. of the 19th High Performance Computing Symposium, part of the Spring Simulation Multiconference (*HPC, SpringSim*), 2011. ([ACM](https://doi.org/)

**[P3]** Parallel Stochastic Simulations of Budding Yeast Cell Cycle: Load Balancing Strategies and Theoretical Analysis
TH. Ahn and A Sandu
In Proc. of the 1st ACM Int. Conf. on Bioinformatics, Computational Biology and Health Informatics (*ACM-BCB*) (AR=25%), Aug 2010. ([DOI](https://doi.org/)

**[P2]** Stochastic cell cycle modeling for budding yeast
TH Ahn, P Wang, LT Watson, Y Cao, CA Shaffer, and WT Baumann
In Proc. of the 17th High Performance Computing Symposium, part of the Spring Simulation Multiconference (HPC, SpringSim), 2009. (ACM)

[P1] Stochastic Simulation Algorithms for Chemical Reactions
TH Ahn, Y Cao, and LT Watson,
In Proc. of the 2008 Int. Conf. on Bioinformatics & Computational Biology (BIOCOMP), 2008.

Thesis

[T] Computational Techniques for the Analysis of Large Scale Biological Systems
TH Ahn
Ph.D. Thesis, Department of Computer Science, Virginia Tech, 2012.

### Awards and Grants

| Awards | Grants |
|--------|--------|
| CAMDA 2020 (Satellite Conf. of the ISMB 2020) Best Presentation Award | [Pending] 25 nm Xray Inspection System for Semiconductor Backend Process |
| Saint Louis University Scholarly Works Award | South Korean Ministry of Trade, Industry and Energy | May 2021 – Dec 2025 |
| NSF CISE CRII (Research Initiation Initiative) Award | Total $2.2M (My share: $300,000) |
| Postdoctoral Research, Oak Ridge National Laboratory | [Pending] A real-time genomic surveillance tool for nosocomial infections” |
| Upsilon Pi Epsilon (UPE), Virginia Tech | National Institutes of Health (NIH) | May 2021 – Apr 2023 |
| Travel and Research Awards, Virginia Tech | Total $200,000 (My share: $26,300) |
| Most Valuable Employee, Samsung SDS | [G8] [Active] Identifying and Tracking Low Frequency Virus-Specific TCR Clonotypes Using High-Throughput Sequencing |
| | Federal Bureau of Investigation (FBI) | May 2018 – May 2021 |
| | Total $1.2M (My share: $100,000) |
| | [G7] [Active] NSF S-STEM: Bioinformatics Training with Industry Support and Engagement (BITWISE) |
| | National Science Foundation (NSF) | May 2016 – Apr 2022 |
| | Total $649,681 (Award Abstract 1564894) |
| | [G6] 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 $26,513 (Sole-PI) |
| | [G5] SLU Big Ideas: Planning for the Development of a SLU Center for Systems Biology |
| | Saint Louis University (SLU) | Jan 2018 – Jan 2019 |
| | Total $50,000 |
| | [G4] SLU PRF: Deep Analysis of Human Virome using Machine Learning |
| | Saint Louis University (SLU) | Jan 2018 – Jan 2019 |
| | Total $15,608 (Sole-PI) |
[G3] Microsoft Research: Very Large Scale Metagenomics Analysis using Microsoft Azure Cloud Computing
Microsoft Research  
Jun 2016 – May 2017  
Total $20,000 to use Microsoft Azure computing equipment (Sole-PI)

[G2] Amazon AWS: Very Large Metagenomic Sequence Analysis using Apache Spark and Amazon Cloud
Amazon AWS  
May 2016 – Apr 2018  
Total $5,000 to use Amazon Web Service (AWS) computing equipment (Sole-PI)

[G1] NSF CRII: Accelerating Human Microbiome Analysis using Lightning-Fast Cloud Computing
National Science Foundation (NSF)  
Apr 2016 – Mar 2019  
Total $174,174 (Sole-PI) (Award 1566292 Abstract)

Selected Talks
- Xavies, Co. LTD., S. Korea – Invited 2020
  *The Convergence of AI, HPC, and Parallel Programming*
- University of Missouri St. Louis – Invited 2020
  *Advanced Computational Techniques for Genomics and Clinical Researches*
- Int. Conf. on Critical Assessment of Massive Data Analysis (CAMDA 2020) 2020
  *Improving Deep Learning Performance on Prediction of Drug-Induced Liver Injury*
- Int. Conf. on Critical Assessment of Massive Data Analysis (CAMDA 2020) 2020
  *Metagenomic Data Analysis with Probability-Based Reduced Dataset Representation*
- University of Nebraska Omaha (UNO) – Invited 2019
  *Metagenomic Data Analysis with Probability-Based Reduced Dataset Representation*
- Kyungpook National University, S. Korea – Invited 2019
  *Use Cases of Apache Spark and Machine/Deep Learning in Bioinformatics and Biomedical Researches*
- KOCSEA Technical Symposium – Invited 2018
  *Computer Science for Bioinformatics: Use case of Apache Spark and Machine Learning in Bioinformatics*
- Connections in Smart Health NSF PI Workshop 2018
  *Applying Bioinformatics and Cloud Techniques for Precision Medicine*
- Conference on Intelligence Systems for Molecular Biology (ISMB) 2018
  *LONGO: An R Package for Interactive Gene Length Dependent Analysis for Neuronal Identity*
- Nestle-Purina – Invited 2018, 2019
  *Bioinformatics, Big Data, and HPC*
- Korea Institute of Science and Technology Information (KISTI), S. Korea – Invited 2016
  *Accelerating Human Microbiome Analysis using Supercomputer and Cloud Computing*
- Gwangju Institute of Science and Technology (GIST) 2016
  *Accelerating Human Microbiome Analysis using Supercomputer and Cloud Computing*
- Korea Institute of Science and Technology Information (KISTI), S. Korea – Invited 2016
  *Challenges in Numerical Analysis and Parallel Computing for Computational Biology and Bioinformatics*

Teaching
- Saint Louis University, Associate Professor 2015 – Present
  *Department of Computer Science*
  - CSCI-2100: Data Structures  
    Fall 2017, 2018, 2019, 2020  
  *DESCRIPTION:* The design, implementation and use of data structures. Principles of abstraction, encapsulation and modularity to guide in the creation of robust, adaptable, reusable and efficient structures. Specific data types to include stacks, queues, lists, priority queues, dictionaries, trees and graphs.
  *Average student rating: 3.75/4.0*
Course Details

- **CSCI-4850/5850: High-Performance Computing**  
  **Spring 2016, 2017, 2018, 2019, 2020, 2021**  
  **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 system into clusters of computers, and the deployment of systems in large-scale grid and cloud computing environments with GPUs.  
  **Average student rating:** 3.71/4.0

**Graduate Program in Bioinformatics and Computational Biology**

- **BCB-5200/5250: Intro to Bioinformatics I, II**  
  **Fall 2015–2017, Spring 2016–2021**  
  **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-5300: Algorithms in Computational Biology**  
  **Fall 2019, 2020**  
  **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

- **BCB 5810 - Bioinformatics Colloquium**  
  **Fall 2016, 2018, 2020**  
  **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:** 3.77/4.0

**University of Tennessee Knoxville, Lecturer**  
**Graduate Program in Genome Science & Technology**  
**Fall 2015**

**Virginia Tech, Teaching Assistant**  
**Department of Computer Science**  
**Spring 2012**

**Saint Louis University, Associate Professor**  
**Graduate Program in Bioinformatics and Computational Biology**  
**2015 – Present**

**Research advisor for**

- Binita Febles, SLU BCB student  
  **Jan 2021 – Present**
- Yassin Mreyoudand, SLU BS/MS Bio/BCB student  
  **Aug 2019 – Present**
- Stephen Tahan, SLU BCB student  
  **Aug 2019 – Present**
- Sara Jain, SLU BS/MS CS/BCB student  
  **Aug 2018 – May 2019**
- Angela Wu, SLU BCB student  
  **Aug 2018 – May 2019**
- Keenan Berry, SLU BCB student  
  **Aug 2018 – May 2020**
- Scott Lewis, SLU BCB student  
  **Aug 2018 – May 2020**
- Ahmad Rajeh, SLU BS/MS CS/BCB student  
  **Aug 2017 – May 2019**
- Eliza Dhungel, SLU BCB student  
  **Aug 2017 – May 2019**
- Angela Wu, SLU BCB student  
  **Aug 2018 – May 2019**
- Pallavi Gupta, SLU BCB student  
  **Aug 2017 – May 2019**
- Courtney Schiebout, SLU BCB student  
  **Aug 2017 – Dec 2018**
- Matthew Mosior, SLU BCB student  
  **Aug 2017 – Dec 2018**
- Zekun Yu, Visiting MS student  
  **June 2017 – July 2017**
- Wenjia Feng, SLU BCB student  
  **Aug 2016 – May 2018**
• Alex Paul, SLU BS/MS Bio/CS/BCB student Aug 2015 – May 2018
• Dylan Lawrence, SLU BS/MS CS/BCB student Aug 2015 – May 2017
• James Gallien, SLU BCB student Aug 2015 – Dec 2016
• Barry Hykes, SLU BCB student Aug 2015 – Dec 2016

Department of Computer Science
Research advisor for
• Sadiya Ahmad, SLU CS MS student Aug 2019 – Present
• Tim Kosfeld, SLU CS student Aug 2019 – Present
• Nabeel Sait, SLU CS/CS BS/MS student Aug 2019 – Present
• Anh Nguyen, SLU CS student Aug 2019 – Present
• Zohair Siddiqui, SLU CS student Jan 2018 – May 2020
• Juan Maldonado, SLU CS student Jan 2018 – May 2020
• Kamran Madatov, John Mitton, and Bao Thai, SLU CS student Aug 2017 – May 2018
• Dustin Joosten, SLU CS student Aug 2015 – May 2016

PhD Committee Member for
• Yongjun Tan, Department of Biology, Saint Louis University Aug 2018 – Present
• Joel Swift, Department of Biology, Saint Louis University Aug 2017 – Present
• Zachary Harris, Department of Biology, Saint Louis University Aug 2017 – Present
• Zhaolian Lu, Department of Biology, Saint Louis University Aug 2015 – May 2020

Professional Activities
Grant and Panel Review
Swiss National Science Foundation 2019
National Science Foundation 2016

Technical Program Committee
IEEE Int. Conf. on Bioinformatics and Biomedicine (IEEE-BIBM) 2017, 2018, 2019, 2020, 2021
ACM Int. Conf. on Bioinformatics and Computational Biology (ACM-BCB) 2011
Int. Conf. on Bioinformatics Research and Applications (ICBRA) 2019, 2020, 2021

External Reviewer
Bioinformatics 2015, 2016, 2017, 2018, 2019, 2020
Briefings in Bioinformatics 2020
BMC Human Genomics 2019
Briefing in Bioinformatics 2015, 2018
Cluster Computing 2019, 2020
Communications Biology 2018
Giga Science 2018, 2021
IETE Technical Review 2014
International Journal of Data Mining and Bioinformatics 2018
Journal of Parallel and Distributed Computing 2015
Nature Communications Biology 2018
Nature Scientific Reports 2016, 2017, 2020
PLOS Computational Biology 2018
PLOS ONE 2014, 2016, 2017, 2018, 2019, 2020

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

Selected Services for Department, College, and University: Serve as a
Judge in Saint Louis University’s Annual Sigma Xi Research Symposium 2019, 2020
Judge in Saint Louis University’s Annual Graduate Research Symposium 2016, 2019
Computer Science Department Representative in College of A&S Faculty Council 2018, 2019
College of A&S Technology Committee Member 2018
BCB Program Grad Admission Committee member 2017, 2018, 2019, 2020, 2021
CS Department and Joint BCB Faculty Search Committee Chair 2019
CS Department Faculty Search Committee Member 2018
Bio Department and Joint BCB Faculty Search Committee Member 2016
CS Department Graduate Studies Committee Member 2016
CS Department Graduate Program Review Committee Member 2016
CS Department Undergraduate Capstone Project Committee Member 2016
CS Department Undergraduate Academic Mentor 2016

References Available upon a request.