

# Derek Cole Aguiar

## Curriculum Vitae

December 2025

📍 School of Computing, University of Connecticut (UConn), Storrs, CT 06269  
Institute for Systems Genomics, UConn, Storrs, CT 06269  
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### Research Interests

I am interested in advancing the foundations of computer science and machine learning and their applications including hierarchical and Bayesian nonparametric latent variable modelling, variational inference and graph theoretic algorithms, and the modelling of haplotypes, transcription, disease genetics, and population genomics.

### Academic Experience

UNIVERSITY OF CONNECTICUT, School of Computing, Storrs, CT 2024-  
*Associate Professor*  
Affiliated with the Institute for Systems Genomics and the Mathematics Department

UNIVERSITY OF CONNECTICUT, School of Computing, Storrs, CT 2018-2024  
*Assistant Professor*  
Affiliated with the Institute for Systems Genomics

PRINCETON UNIVERSITY, Department of Computer Science, Princeton, NJ 2014-2018  
*Postdoctoral Researcher*  
Advised by Barbara Engelhardt, performed research on probabilistic machine learning and Bayesian nonparametric methods for isoform reconstruction and haplotype modelling.

### Education

BROWN UNIVERSITY, Department of Computer Science, Providence, RI 2008-2014  
Ph.D. (2014) and M.S. (2010), Computer Science  
Dissertation Title: "Genome-wide algorithms for haplotype assembly, haplotype phasing, and IBD inference"  
Advisor: Sorin Istrail

UNIVERSITY OF RHODE ISLAND, Department of Computer Science, Kingston, RI 2003-2007  
Bachelor of Science, Computer Engineering, 2007  
Bachelor of Science, Computer Science, 2007  
summa cum laude, President's Awards for Excellence (CE & CS)

### Publications

Journal manuscripts are annotated with impact factors; conference manuscripts included in [CS rankings](#) conferences are indicated by a 🌟. All Impact Factors are reported according to Clarivate's Journal Citation Reports 5 Year Impact Factor collected on July 2023. Advised UConn or UCHC students are indicated by bolding.

### Preprints and Works Under Review

1. D. McErlean\*, D. Aguiar\*, and S. Istrail. A globally optimal algorithm for computing maximum likelihood haplotype phasings: graph homomorphic expo-posynomial optimization. *submitted to RECOMB 2026* (2026).
2. **M. Hosseini, E. Veiner, T. Bergendahl, T. Yassenpoor**, Z. Smith, M. Staton, and D. Aguiar. pHapCompass: Probabilistic Assembly and Uncertainty Quantification of Polyploid Haplotype Phase. *arXiv preprint arXiv:2512.04393* (2025).

3. **S. Légitime, K. Prabhu, D. McConnell**, B. Wang, D. K. Dey, and D. Aguiar. Improving Opioid Use Disorder Risk Modelling through Behavioral and Genetic Feature Integration. *arXiv preprint arXiv:2309.10837* (2023).
4. R. De Vito, I. N. Grabski, D. Aguiar, L. M. Schneper, A. Verma, J. C. Fernandez, C. Mitchell, J. Bell, S. McLanahan, D. A. Notterman, et al. Differentially methylated regions and methylation QTLs for teen depression and early puberty in the Fragile Families Child Wellbeing Study. *bioRxiv* (2021), 2021–05.

## Refereed Papers

1. **J. Deng, H. Hong, A. Palmer**, X. Zhou, J. Bi, K. Mahmood, Y. Hong, and D. Aguiar. Certifying Adapters: Enabling and Enhancing the Certification of Classifier Adversarial Robustness. *IJCNN* (2025).
2. **J. Deng, A. Palmer**, R. Mahmood, E. Rathbun, J. Bi, K. Mahmood, and D. Aguiar. Distilling adversarial robustness using heterogeneous teachers. *Procedia Computer Science* **264** (2025), 12–24.
3. **M. Hosseini, D. McConnell**, and D. Aguiar. Bayesian Reconstruction and Differential Testing of Excised Introns. *Bioinformatics* (2025), btaf646.
4. **L. R. Mercado-Diaz**, D. Aguiar, and H. F. Posada-Quintero. Graph-Based Multi-Modal MRI Analysis with Probabilistic Attention for Stroke Lesion Detection. *Neurocomputing* (2025), 131620.
5. **J. Deng**, X. Zhou, H. Tian, Z. Pan, and D. Aguiar. GBSD: Generative Bokeh with Stage Diffusion. *ICASSP* (2024).
6. **K. Udeh**, D. W. Wanik, D. Cerrai, E. N. Anagnostou, and D. Aguiar. Probabilistic Storm and Electric Utility Customer Outage Prediction. *IEEE Access* **12** (2024), 126285–126295.
7. **J. Deng**, X. Zhou, H. Tian, Z. Pan, and D. Aguiar. Smooth and Stepwise Self-Distillation for Object Detection. *IEEE International Conference on Image Processing (ICIP)* (2023).
8. **M. Hosseini, A. Palmer, W. Manka**, P. G. Grady, **V. Patchigolla**, J. Bi, R. O’Neill, Z. Chi, and D. Aguiar. Deep statistical modelling of nanopore sequencing translocation times reveals latent non-B DNA structures. *Bioinformatics* **39**(Supplement\_1) (2023), i242–i251. Also in *proceedings of ISMB 2023* (🌟).
9. **M. Hosseini**, A. J. Sabet, S. He, and D. Aguiar. Interpretable fake news detection with topic and deep variational models. *Online Social Networks and Media* **36** (2023), 100249. (IF: 7.61, journal-reported).
10. **M. Hutchison**, B. S. Russell, **A. Leander**, N. Rickles, D. Aguiar, X. S. Cong, O. Harel, and A. V. Hernandez. Trends and Barriers of Medication Treatment for Opioid Use Disorders: A Systematic Review and Meta-Analysis. *Journal of Drug Issues* (2023).
11. **A. Palmer**, Z. Chi, D. Aguiar, and J. Bi. Auto-Encoding Goodness of Fit. In: *The Eleventh International Conference on Learning Representations (ICLR)*. 2023. <https://openreview.net/forum?id=JjCAAdMULu9v>. (🌟).
12. **B. A. Alpay**, M. Gosink, and D. Aguiar. Evaluating molecular fingerprint-based models of drug side effects against a statistical control. *Drug Discovery Today* (2022), 103364. (IF: 8.1).
13. C. Li\*, L. Qu\*, **A. J. Matz\***, P. A. Murphy, Y. Liu, A. W. Manichaikul, D. Aguiar, S. S. Rich, D. M. Herrington, D. Vu, et al. AtheroSpectrum Reveals Novel Macrophage Foam Cell gene Signatures Associated with Atherosclerotic Cardiovascular Disease Risk. *Circulation* (2022). (IF: 33.2).
14. **K. Udeh**, D. W. Wanik, D. Cerrai, D. Aguiar, and E. Anagnostou. Autoregressive Modeling of Utility Customer Outages with Deep Neural Networks. In: *2022 IEEE 12th Annual Computing and Communication Workshop and Conference (CCWC)*. 2022, pp.0406–0414.
15. **D. J. McConnell, J. Zhu**, S. Pandya, and D. Aguiar. Case-level prediction of motion outcomes in civil litigation. In: *Proceedings of the Eighteenth International Conference on Artificial Intelligence and Law*. 2021, pp.99–108.
16. **B. A. Alpay**, P. Demetci, S. Istrail, and D. Aguiar. Combinatorial and statistical prediction of gene expression from haplotype sequence. *Bioinformatics* **36**(Supplement\_1) (2020), i194–i202. Also in *proceedings of ISMB 2020* (🌟).
17. D. Aguiar, L.-F. Cheng, B. Dumitrascu, F. Mordelet, A. Pai, and B. Engelhardt. Bayesian nonparametric discovery of isoforms and individual specific quantification. *Nature Communications* **9**(1) (2018), 1681. (IF: 17.0).

18. D. Aguiar, E. M. Morrow, and S. Istrail. Tractatus: An Exact and Subquadratic Algorithm for Inferring Identical-by-Descent Multi-shared Haplotype Tracts. In: *Annual International Conference on Research in Computational Molecular Biology (RECOMB)*. Springer. 2014, pp.1–17. (✳).
19. D. Aguiar, W. S. Wong, and S. Istrail. Tumor haplotype assembly algorithms for cancer genomics. In: *Pacific Symposium on Biocomputing*. NIH Public Access. 2014, pp.3.
20. I. C. McDowell, C. Nikapitiya, D. Aguiar, C. E. Lane, S. Istrail, and M. Gomez-Chiarri. Transcriptome of American oysters, *Crassostrea virginica*, in response to bacterial challenge: insights into potential mechanisms of disease resistance. *PLoS One* **9**(8) (2014), e105097. (IF: 3.8).
21. D. Aguiar and S. Istrail. Haplotype assembly in polyploid genomes and identical by descent shared tracts. *Bioinformatics* **29**(13) (2013), i352–i360. Also in *proceedings of ISMB 2013* (✳).
22. S. Tulin\*, D. Aguiar\*, S. Istrail, and J. Smith. A quantitative reference transcriptome for *Nematostella vectensis* earlyembryonic development: a pipeline for de novo assembly in emerging model systems. *EvoDevo* **4**(1) (2013), 16. (IF: 3.1).
23. D. Aguiar, B. V. Halldórsson, E. M. Morrow, and S. Istrail. DELISHUS: an efficient and exact algorithm for genome-wide detection of deletion polymorphism in autism. *Bioinformatics* **28**(12) (2012), i154–i162. Also in *proceedings of ISMB 2012* (✳).
24. D. Aguiar and S. Istrail. HapCompass: a fast cycle basis algorithm for accurate haplotype assembly of sequence data. *Journal of Computational Biology* **19**(6) (2012), 577–590. (IF: 1.6).
25. B. V. Halldórsson\*, D. Aguiar\*, and S. Istrail. “Haplotype phasing by multi-assembly of shared haplotypes: phase-dependent interactions between rare variants”. In: *Pacific Symposium on Biocomputing*. 2011, pp.88–99.
26. B. V. Halldórsson\*, D. Aguiar\*, R. Tarpine, and S. Istrail. The Clark phase-able sample size problem: long-range phasing and loss of heterozygosity in GWAS. In: *Annual International Conference on Research in Computational Molecular Biology (RECOMB)*. Springer. 2010, pp.158–173. Note: Journal version published in *Journal of Computational Biology*. (✳).

### Book Chapters

27. S. Istrail, R. Tarpine, K. Schutter, and D. Aguiar. “Practical Computational Methods for Regulatory Genomics: A cisGRN-Lexicon and cisGRN-Browser for Gene Regulatory Networks”. In: *Computational Biology of Transcription Factor Binding*. Totowa, NJ: Humana Press, 2010, pp. 369–399.

### Ph.D. Thesis

28. D. Aguiar. “Genome-wide algorithms for haplotype assembly, haplotype phasing, and IBD inference”. PhD thesis. Brown University, 2014.

### Works in Progress

29. D. Aguiar, G. Gliner, L. T. Elliott, **A. Palmer**, **M. Hosseini**, Y. W. Teh, and B. E. Engelhardt. *The fragmentation coagulation process haplotype cluster graph model*. 2025. (In preparation for *Genome Biology*).
30. D. McErlean\*, D. Aguiar\*, and S. Istrail. *A globally optimal algorithm for computing maximum likelihood haplotype phasings: expo-posynomial optimization by graph homomorphism*. 2025. (In preparation for *PNAS*).

### Funded Proposals

My share of funding is given in parenthesis when ambiguous.

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Derek Aguiar (PI) 11/01/2025–10/31/2026  
 The Bushnell Performing Arts Center  
 Bushnell Virtual Mentor Digital Learning Project and AI Course

\* denotes co-first authorship when ambiguous

Role: Principal Investigator, \$49,855.00 total award

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Derek Aguiar (PI) 09/20/2025-08/31/2029

NIH

*Non-B DNA structure discovery and function assessment using nanopore translocation times*

Role: Principal Investigator, \$805,000.00 total award

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Derek Aguiar (PI) 07/01/2024-06/30/2025

The Bushnell Performing Arts Center

*Bushnell Virtual Mentor Digital Learning Project: Development of Conversational AI and Assessment Systems*

Role: Principal Investigator, \$48,049.00 total award

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Derek Aguiar (PI of subaward) 12/01/2023-11/30/2027

NIH

*ASCVD risk assessment in T2DM facilitated by novel computational immunology programs*

Role: Principal Investigator of subaward, \$182,294.00 total award

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Derek Aguiar (PI) 10/01/2023-06/30/2024

DEFENSEWERX

*Develop AI/ML Tools*

Role: Principal Investigator, \$175,000 total award (my share: \$58,333.33)

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Derek Aguiar (PI) 08/15/2023-06/30/2024

The Bushnell Performing Arts Center

*Bushnell Virtual Mentor Digital Learning Project: Development of Conversational AI and Assessment Systems*

Role: Principal Investigator, \$43,880.00 total award

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Derek Aguiar (PI) 07/15/2023-06/30/2028

National Science Foundation

*CAREER: Practical algorithms and high dimensional statistical methods for multimodal haplotype modelling*

Role: Principal Investigator, \$548,346.00 total award

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Derek Aguiar (co-PI) 05/05/2023-07/31/2025

Travelers Companies, Inc.

*Creating insurance-specific Transformers for representation learning from large-scale unstructured claim text*

Role: co-Principal Investigator, \$584,528 total award (my share: \$184,865.33)

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Derek Aguiar (Collaborator) 01/01/2023-12/31/2024

American Heart Association

*miR-150 regulated adipose tissue B cells in obesity-induced health risk*

Role: Collaborator, \$65,106.00 total award (my share: \$0.00)

Note: Relinquished after the proposal was awarded F30 from NIH/NHLBI

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Derek Aguiar (Senior Personnel) 01/01/2023-5/31/2023

American Heart Association

*Assessing cardiovascular risk using diabetes-induced transcriptomic networks*

Role: Senior Personnel, \$65,106.00 total award (my share: \$6,510.60)

Note: Relinquished after the proposal was awarded F30 from NIH/NHLBI

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Derek Aguiar (PI) 09/01/2022-08/01/2023  
 UConn Research Excellence Program  
*Probabilistic Learning Algorithms for Haplotype Phasing and Haplotype Assembly Unification*  
 Role: Principal Investigator, \$24,974.38 total award

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Derek Aguiar (PI) 04/01/2022-03/01/2023  
 DEFENSEWERX  
*Artificial Intelligence / Machine Learning (AIML) Development*  
 Role: Principal Investigator, \$250,000 total award (my share: \$145,790.04)

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Derek Aguiar (PI) 03/01/2021-02/01/2023  
 Google  
*Supporting math and science teacher learning to address societal problems with data science and artificial intelligence*  
 Role: Principal Investigator, \$80,000 total award

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Derek Aguiar (senior personnel) 08/01/2020-02/01/2022  
 The Institute for Collaboration on Health, Intervention, and Policy (InCHIP)  
*A Pilot Investigation Understanding the Connecticut experience on what factors most affect patient adherence to Medication Assisted Treatments (MAT) for Opioid Use Disorder.*  
 Role: Senior Personnel, \$25,000 total award (my share: \$0.00)

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Derek Aguiar (PI) 09/01/2019-06/01/2021  
 The Institute for Collaboration on Health, Intervention, and Policy (InCHIP)  
*Unifying clinical support methods for preventing and managing opioid use disorder*  
 Role: Principal Investigator, \$25,000 total award (my share: \$10,000.00)

## Teaching Experience

UNIVERSITY OF CONNECTICUT, Storrs, CT

2018-

Instructor, Undergraduate Core Course with a Lab, *Introduction to Computing for Engineers*: 2019 (307 students), 2020 (1051 students)

- Designed and Taught CSE1010 – Introduction to Computing for Engineers. Complete re-design and development of CSE1010, Introduction to Computing for Engineering. Creation of course materials, lab assignments, homeworks, a group project and presentation, a COVID-19 data science tracking project, lecture videos for 14 weeks using the lightboard room, new exams, exam reviews, and lecture notes.
- Integrated data science as a 3 week unit into an introductory computer science class.

Instructor, Undergraduate Core Course, *Algorithms and Complexity*: 2019 (48 students), 2021 (80 students), 2022 (95 students), 2023 (54 students), 2024 (TBD – includes honors section)

- Median scores (out of 5) for the question “What is your overall rating of the instructor’s teaching?” were 4, 4, 5, and 4 for 2019, 2021, 2022, and 2023, respectively.
- Taught CSE3500 – Algorithms and Complexity, which entailed creating lesson plans, syllabus, problem sets, programming assignments, tests, in-class demonstrations (FFT, GPU programming, optimization algorithms), honors projects, and worksheets.
- Topics included: asymptotic notations, solving summations, recurrences, invariants, proof techniques, dynamic programming, divide-and-conquer, data structures, probabilistic algorithms, competitive

analysis, greedy algorithms, graph algorithms, intractability and NP-completeness, parallel computing, approximation algorithms, and optimization algorithms.

Instructor, Graduate Course, *Bayesian Machine Learning*: 2018 (7 students), 2019 (24 students), 2021 (18 students), 2022 (21 students), 2023 (28 students)

- Median scores (out of 5) for the question “What is your overall rating of the instructor’s teaching?” were 5’s for each of the five years.
- Developed the course CSE5095 – Bayesian Machine Learning, which entailed creating lesson plans, a syllabus, and project assignments.
- We covered the three fundamental components of Bayesian Machine Learning: probabilistic modeling, inference algorithms, and model checking.
- The course culminates in research-quality projects related to each student’s research interests that implements some probabilistic framework from problem specification to model checking.

Instructor, Undergraduate Core Course, *Senior Design Project*: 2021 (5 students)

- Median scores (out of 5) for the question “What is your overall rating of the instructor’s teaching?” was a 5.
- Led Senior Design Project team along with the sponsor Pfizer Inc. on a drug discovery machine learning project that culminated in a research manuscript (Alpay *et al.* 2022).

Instructor, Undergraduate Independent Study (NASA), *Seminar*: 2022 (5 students)

- Mentored 5 CSE students taking part in the NASA Big Idea Challenge team. Topics included algorithms and machine learning.

Instructor, Graduate Course, *Seminar*: 2023 (10 students), 2024 (10 students)

- Bioinformatics seminar covering research in bioinformatics, machine learning, and algorithms.

BROWN UNIVERSITY, Providence, RI

2009-2014

Head Teacher’s Assistant, *Algorithmic Foundations of Computational Biology*: 2011, 2013-2014

- Assisted teaching of *Algorithmic Foundations of Computational Biology* to classes of intellectually diverse undergraduate students from the Computer Science and Applied Mathematics departments.
- Developed and delivered a week of lectures on Haplotype Assembly. Administered online discussion platform to encourage student participation.
- Mentored students participating in interdisciplinary CYRENE project on cis-regulatory genomics.
- Co-developed the syllabus, created the course webpage, developed homework assignments and exams, curated lecture notes.

Head Teacher’s Assistant, *Medical Bioinformatics*: 2009-2010, 2012-2013

- Co-created the Medical Bioinformatics course designed for computational and life sciences graduate students.
- Created the Genomathica, a set of interactive genomics algorithms written in Mathematica, and used Genomathica in lectures and homeworks enabling life science students to tinker and develop data analysis software pipelines without the burden of learning a programming language.
- Prepared and presented a week of lectures on haplotype phasing and genomic deletion inference in genome-wide association study data.
- Co-developed the syllabus, created the course webpage, developed homework assignments and exams, constructed lecture notes, and graded homework and exams.

Teacher’s Assistant, *Algorithmic Foundations of Computational Biology*: 2010

- ▶ Taught Algorithmic Foundations of Computational Biology to an intellectually diverse class of undergraduate students from the Computer Science and Applied Mathematics departments.
- ▶ Maintained course webpage, graded homework assignments and exams, and curated lecture notes.

UNIVERSITY OF RHODE ISLAND, Kingston, RI

2007

Teacher's Assistant, *Computer Communications*: 2007

- ▶ Provided instruction for Computer Communications, a computer engineering and computer science senior undergraduate course.
- ▶ Independently researched the topics covered in the course with the objective of assisting in the redesign of the curriculum. The five lesson plans I created, including programming and homework assignments, incorporated: working at the frame level with Application, Transport, and Internet layer protocols (DNS, SMTP, TELNET, ARP, TCP/IP), and C Socket programming.

### Invited Talks & Panels

1. Joint Symposium - how to leverage AI, data science and computing to help healthcare and medicine. "Non-B DNA Detection from Oxford Nanopore Sequencing" May 2025
2. Panelist, mAI dAI, Center for Excellence in Teaching and Learning, University of Connecticut, "Faculty Panel: the AI future of higher ed?" May 2025
3. Center of Computational Molecular Biology Colloquia, Brown University, "[Deep statistical modelling of nanopore sequencing translocation times reveals latent non-B DNA structures.](#)" November 2024
4. Panelist, BEACON Workshop, Center for Excellence in Teaching and Learning, University of Connecticut, "Artificial Intelligence in Teaching and Learning." November 2024
5. The 31st Annual Intelligent Systems For Molecular Biology and the 22nd Annual European Conference on Computational Biology "Deep statistical modelling of nanopore sequencing translocation times reveals latent non-B DNA structures." July 2023
6. Nutrition Sciences Colloquium, University of Connecticut "Deep statistical modelling of nanopore sequencing reveals latent non-B DNA structures" February 2023
7. 12th John A. Speziale Symposium, Quinnipiac University "[Artificial Intelligence in Law](#)" November 2022
8. ImmunoCardio Group Meeting, University of Connecticut, "Machine Learning, Genomics, Transcriptomics, Bash and R Tutorial." May 2022
9. Panelist, exploreCSR Workshop, University of Rhode Island, "Life after Grad School." April 2022
10. Connecticut Computer Science Teachers Association Chapter Meeting, "An Update on our SMARTAI Education Module." February 2022
11. 35<sup>th</sup> Anniversary Lecture Series, University of Connecticut, "Bayesian machine learning and the isoform reconstruction problem." January 2022
12. Computer Science Colloquium, University of Rhode Island, "Bayesian nonparametric modelling and scalable inference in genomics and transcriptomics data." November 2021
13. Panelist, [UConn STEM Seminar Series](#), Interdisciplinary Engineering Research, "An Interdisciplinary Tour of Machine Learning in Biology, Law, and More." September 2021
14. Bioinformatics Seminar Series, University of Connecticut, "Bayesian Networks and Nonparametric Haplotype Clustering." September 2021
15. Connecticut Computer Science Teachers Association Chapter Meeting, "Preparing Students for a Data-Centric Computer Science Curriculum." May 2021
16. Panelist, exploreCSR Workshop, University of Rhode Island, "Life after Grad School." April 2021

17. Panelist, Computational Modeling Meet & Speak, CT Institute for the Brain and Cognitive Sciences, "Bayesian machine learning in large models with applications in genomics." May 2020
18. Department of Statistics Colloquia, University of Connecticut, "Bayesian Nonparametric Modelling and Scalable Inference In Large-Scale Genomics Data." January 2020
19. New York Area Population Genomics Workshop, "Efficient construction of haplotype cluster graphs and estimating the age of mutations." January 2017
20. American Society of Human Genetics (ASHG) Annual Meeting, "Haplotype phasing using cluster graphs." October 2015
21. NIPS Workshop on Machine Learning in Computational Biology (MLCB) "A Bayesian nonparametric statistical framework for haplotype phasing." December 2014
22. 18th Annual International Conference on Research in Computational Molecular Biology "Tractatus: an exact and subquadratic algorithm for inferring identical-by-descent multi-shared haplotype tracts." April 2014
23. 19th Pacific Symposium on Biocomputing "Tumor Haplotype Assembly Algorithms for Cancer Genomics." January 2014
24. Brown University IPP Symposium: Putting Big Data to Work. "Ome sweet ome: the genome as a model for big data." April 25, 2013
25. 21st Annual International Conference on Intelligent Systems for Molecular Biology "Haplotype assembly in polyploid genomes and identical by descent shared tracts." July 2013
26. HiT-Seq workshop in the 21st Annual International Conference on Intelligent Systems for Molecular Biology "Haplotype assembly in the presence of hemizyosity, haplotype sharing, polyploidy, and viral quasispecies." July 2013
27. 20th Annual International Conference on Intelligent Systems for Molecular Biology "DELISHUS: An efficient and exact algorithm for Genome-Wide detection of deletion polymorphism in autism." July 2012
28. Brown Computational Biology Open House "SNPs and haplotypes and GWAS oh my!" Feb. 27, 2012
29. Second Annual IEEE ICCABS CANGS Workshop "Robust algorithms for inferring haplotype phase and deletion polymorphism from high throughput whole genome sequence data." Feb. 24, 2012
30. Brown Computer Science - Research Exchange Seminars with Tea (REST) "Computational Challenges in Genome-wide Association Studies." Nov. 30, 2010
31. Fourteenth International Conference on Research in Computational Molecular Biology "The Clark Phase-able Sample Size Problem Long-range Phasing and Loss of Heterozygosity in GWAS." August 12, 2010

### Extended Abstracts and Posters

1. Karlinsey, K., Matz, A., Sanders, M. M., Liang, B., Aguiar, D., Vella, A., & Zhou, B. (2025). Transcriptomic signature network discovery of type 2 diabetes-increased cardiovascular risk through single-cell transcriptomic analysis. *Circulation*, 152(Suppl\_3), A4366909-A4366909.
2. Keaton Karlinsey, Alyssa J Matz\*, Anthony T. Vella, Derek Aguiar, Bruce T. Liang, Melinda Sanders, Beiyan Zhou, "Transcriptomic signature network discovery of type 2 diabetes-increased cardiovascular risk through single-cell transcriptomic analysis." American Heart Association's Scientific Sessions November 2025, New Orleans, Louisiana.
3. Tala Yasenpoor, Ella Veiner, Marjan Hosseini, Alyssa Matz, Keaton Karlinsey, Beiyan Zhou and Derek Aguiar "Supervised Poisson Factorization for Uncovering Latent Gene Expression Patterns and Predicting Disease Risk" 13th International Conference On Computational Advances In Bio And Medical Sciences. January 2025, Atlanta, Georgia, USA.

4. Marjan Hosseini, Thomas Bergendahl, Ella Veiner, Tala Yasenpoor and Derek Aguiar “Probabilistic Assembly and Uncertainty Quantification of Polyploid Haplotype Phase” 13th International Conference On Computational Advances In Bio And Medical Sciences. January 2025, Atlanta, Georgia, USA.
5. Hosseini, Marjan and Sabet, Alireza Javadian and He, Suining and Aguiar, Derek “LDAVAE: An Interpretable Approach for Fake News Detection.” 10th International Conference on Computational Social Science. July, 17-20, 2024, Philadelphia, PA, USA.
6. M. Hosseini\*, A. Palmer\*, W. Manka, P. GS Grady, V. Patchigolla, J. Bi, R. J O’Neill, Z. Chi, D. Aguiar “Deep statistical modelling of nanopore sequencing translocation times reveals latent non-B DNA structures.” 10th Annual College of Engineering Poster Competition. February 23, Storrs, CT.
7. Alyssa J Matz, Lili Qu, Keaton Karlinsey, Ivy Li, Anthony T Vella, Derek Aguiar and Beiyan Zhou “Novel Function Annotation Tool Revealed Obesity-Induced Inflammation is Exacerbated by miR-150 Regulated B Cell Receptor Signaling” CARDIAC DEVELOPMENT, STRUCTURE AND FUNCTION. November 6, 2023. [https://doi.org/10.1161/circ.148.suppl\\_1.15626](https://doi.org/10.1161/circ.148.suppl_1.15626)Circulation.2023;148:A15626
8. Bai, Y., Campbell, T., Legitime, S., Aguiar, D., Staples, M., Corricelli, J. “Curriculum Design and Improvement: Integrating AI Concepts and Societal Problems in a Secondary Science Module.” Paper for the 2024 National Association for Research in Science Teaching (NARST) International Convention. March 17-20, Denver, CO.
9. Alyssa J Matz\*, Keaton Karlinsey, Anthony T. Vella, Derek Aguiar, Laura Haynes, Beiyan Zhou, “Novel multi-omics strategies to examine the impact of aging on B cell responses to influenza vaccination.” CHARGE 2023, San Antonio, Texas.
10. Alyssa J Matz\*, Keaton Karlinsey, Anthony T. Vella, Derek Aguiar, Laura Haynes, Beiyan Zhou, “Novel Function Annotation Tool Revealed Obesity-Induced Inflammation is Exacerbated by miR-150 Regulated B Cell Receptor Signaling.” American Heart Association’s annual Scientific Sessions 2023, Philadelphia, Pennsylvania.
11. Chuan Li\*, Lili Qu\*, Alyssa J Matz\*, Patrick A. Murphy, Yongmei Liu, Ani Manichaikul, Derek Aguiar, Stephen S Rich, David M Herrington, David Vu, Craig W Johnson, Jerome I Rotter, Wendy S Post, Anthony T. Vella, Annabelle Rodriguez, Beiyan Zhou, “AtheroSpectrum reveals pathogenic foaming program and provides gene signatures for CVE prediction.” CHARGE 2022, Philadelphia, Pennsylvania.
12. Alyssa J Matz, Chuan Li, Lili Qu, Patrick A. Murphy, Yongmei Liu, Ani W Manichaikul, Derek Aguiar, Stephen S Rich, David M Herrington, David Vu, W. Craig Johnson, Jerome I. Rotter, Wendy S. Post, Anthony T. Vella, Annabelle Rodriguez-Oquendo and Beiyan Zhou. AtheroSpectrum reveals novel macrophage foam cell gene signatures associated with atherosclerotic cardiovascular disease risk. 18th Society of Chinese Bioscientists in America (SCBA) International Symposium. July 2022.
13. Alyssa J Matz, Chuan Li, Lili Qu, Patrick A. Murphy, Derek Aguiar, Anthony T. Vella, Annabelle Rodriguez, Beiyan Zhou. AtheroSpectrum reveals novel macrophage foaming programs. Virtual Event. Society for Leukocyte Biology 54th Annual Event. October 2021.
14. Marjan Hosseini\*, Devin McConnell\*, Derek Aguiar, “Hierarchical Bayesian Admixture Modelling of Intron Excision Structure.” Workshop on Missing Data Challenges in Computation, Statistics and Applications 2020, Institute for Advanced Study, Princeton, New Jersey.
15. Derek Aguiar, Li-Fang Cheng, Bianca Dumitrascu, Fantine Mordelet, Barbara E. Engelhardt, “BIISQ: Bayesian nonparametric discovery of Isoforms and Individual Specific Quantification from RNA-seq data.” RECOMB 2016, Santa Monica, CA.
16. Derek Aguiar, Li-Fang Cheng, Bianca Dumitrascu, Fantine Mordelet, Barbara E. Engelhardt, “BIISQ: Bayesian nonparametric discovery of Isoforms and Individual Specific Quantification from RNA-seq data.” Probabilistic Modeling in Genomics 2016, Oxford, UK.
17. Derek Aguiar, Li-Fang Cheng, Bianca Dumitrascu, Fantine Mordelet, Athma Pai, Barbara E. Engelhardt, “Bayesian nonparametric isoform discovery and quantification of many RNA-seq samples.” American Society of Human Genetics Annual Meeting 2016, Baltimore, MD.

18. Derek Aguiar, Lloyd T. Elliott, Yee Whye Teh, and Barbara E. Engelhardt, "Haplotype phasing using cluster graphs." American Society of Human Genetics Annual Meeting 2015, Baltimore, MD.
19. Derek Aguiar, Lloyd T. Elliott, Yee Whye Teh, and Barbara E. Engelhardt, "Tractable haplotype phasing and imputation with nonparametric fragmentation-coagulation processes." Probabilistic Modeling in Genomics 2015, Cold Spring Harbor Laboratory, NY.
20. Derek Aguiar, Lloyd T. Elliott, Yee Whye Teh, and Barbara E. Engelhardt, "A statistical framework for modeling genetic data as haplotype cluster graphs with application to haplotype phasing, association mapping, and whole-genome compression." The Biology of Genomes 2015, Cold Spring Harbor Laboratory, NY.
21. Derek Aguiar, Lloyd T. Elliott, Yee Whye Teh, and Barbara E. Engelhardt, "A Bayesian nonparametric statistical framework for haplotype phasing." Workshop: Machine Learning in Computational Biology in NIPS 2014, Montreal, Canada. (selected for oral presentation)
22. Derek Aguiar, Austin Huang, Rami Kantor, Eric Morrow and Sorin Istrail, "Haplotype assembly in the presence of hemizyosity, haplotype sharing, polyploidy, and viral quasispecies." HiT-Seq workshop in the 21st Annual International Conference on Intelligent Systems for Molecular Biology, July 2013, Berlin, Germany. (selected for oral presentation)
23. Sarah Tulin, Derek Aguiar, Sorin Istrail, and Joel Smith, "Nematostella reference transcriptome and high throughput gene regulatory network construction." SDB 71st Annual Meeting, July 2012, Montreal, Canada.
24. Derek Aguiar and Sorin Istrail, "HAPCOMPASS: A fast cycle basis algorithm for accurate haplotype assembly of next-generation sequence data." 20th Annual Intelligent Systems for Molecular Biology, July 2012, Long Beach, CA.
25. Derek Aguiar, Ryan Tarpine, Fumei Lam, Bjarni V. Halldorsson, Eric Morrow, and Sorin Istrail, "Long-Range Haplotype Phasing by Multi-Assembly of Shared Haplotypes: Phase-Dependent Interactions Between Rare Variants." Genomics of Common Disease, Wellcome Trust Sanger Genome Center, Cambridge UK, December 2011
26. Derek Aguiar, Ryan Tarpine, Fumei Lam, Bjarni V. Halldorsson, Eric Morrow, and Sorin Istrail, "Long-Range Haplotype Phasing by Multi-Assembly of Shared Haplotypes: Phase-Dependent Interactions Between Rare Variants." The Gordon Research Conference on Human Genetics and Genomics, July 17-22, 2011, Salve Regina University, Newport, RI.
27. Ryan Tarpine, James Hart, Timothy Johnstone, Derek Aguiar, Sorin Istrail, "Report on the Cyrene Project: A cis-Lexicon Containing the Regulatory Architecture of 557 Regulatory Genes Experimentally Validated Using the *Davidson Criteria*." The Developmental Biology of the Sea Urchin Meeting, April 27-30, 2011, Woods Hole, MA.
28. Derek Aguiar, Ryan Tarpine, Eric Ruggieri, Jessica Nadel, David Moskowitz, Sorin Istrail, "Beyond GWAS: Robust Computational Analysis of the Multiple Sclerosis Genetic Consortium Data." Fourth Annual Center for Computational Biology Poster Session, April 28, 2010, Brown University, RI.

## Software

1. D. Aguiar, L.-F. Cheng, B. Dumitrascu, and B. Engelhardt. *Bayesian nonparametric discovery of Isoforms and Individual Specific Quantification with BIISQ*. Version 1.0.0. [\[code\]](#). 2017.
2. D. Aguiar and S. Istrail. *HapCompass: fast cycle basis algorithms for accurate diploid and polyploid haplotype assembly*. Version 0.8.2. [\[code\]](#). 2016.
3. D. Aguiar and S. Istrail. *Tractatus: an exact and subquadratic algorithm for inferring identity-by-descent multi-shared haplotype tracts*. Version 0.0.1. [\[code\]](#). 2013.
4. D. Aguiar, S. Tulin, S. Istrail, and J. Smith. *A quantitative reference transcriptome for Nematostella vectensis earlyembryonic development: a pipeline for de novo assembly in emerging model systems*. Version 1.0.0. [\[code\]](#). 2013.

5. D. Aguiar and S. Istrail. *DELISHUS: an efficient and exact algorithm for genome-wide detection of deletion polymorphism in autism*. Version 0.1.0. [\[code\]](#). 2012.
6. R. Tarpine, D. Aguiar, and S. Istrail. *CYRENE cis-Regulatory Genome Browser*. Version 1.0.0. [\[code\]](#). 2012.

## Academic Advising

### Ph.D. Advising (current)

- Major Advisor, Marjan Hosseini (expected graduation in AY 2025-2026), Computer Science;
- Major Advisor, Chandra Sekhar Dronavajjala, Computer Science;
- Major Advisor, Qianying Ren, Computer Science;
- Major Advisor, Tala Yasenpoor, Mathematics;
- Associate Advisor, Yushan Jiang, Computer Science;
- Associate Advisor, Cynthia Webster, Ecology and Evolutionary Biology;
- Associate Advisor, Keaton Karlinsey, Immunology;
- Associate Advisor, Alyssa Matz, Immunology;

### Ph.D. Advising (alumni)

- Major Advisor, Jieren Deng, Computer Science; now at Microsoft
- Major Advisor, Kingsley Udeh, Computer Science; now a *Postdoctoral Research Associate*, Eversource Energy Center, University of Connecticut
- Associate Advisor, Qinqing Liu, Computer Science;
- Associate Advisor, Saurabh Goswami, Electrical and Computer Engineering;
- Associate Advisor, Huiqun Huang, Computer Science;
- Associate Advisor, Yinuo Huang, Electrical and Computer Engineering;
- Associate Advisor, Yiming Zhang, Computer Science;
- Associate Advisor, Rakesh Joshi, Computer Science;
- Associate Advisor, Piyush Shrivastav, Computer Science;
- Associate Advisor, Pariksheet Nanda, Molecular and Cell Biology;
- Associate Advisor, Lina Kloub, Computer Science;
- Associate Advisor, Tianyu Wang, Computer Science;
- Associate Advisor, Fahad AlQahtani, Computer Science;
- Associate Advisor, Md Abdullah Al Fahim, Computer Science;
- Associate Advisor, Abhijit Mondal, Computer Science;

### MS and MEng Masters Advising (current)

- Major Advisor (Thesis track), Ella Veiner, Computer Science;

### MS and MEng Masters Advising (alumni)

- Major Advisor (Thesis track), Thomas Bergendahl, Computer Science;
- Major Advisor (Thesis track), Sybille Legitime, Computer Science; now a PhD student at Brown University
- Major Advisor (Thesis track), William Manka, Computer Science;
- Major Advisor, Jackie Ramirez, Computer Science;
- Major Advisor, Dongping Zhu, Computer Science;
- Major Advisor, Devin McConnell, Computer Science;
- Major Advisor, Kaustubh Prabhu, Computer Science;
- Major Advisor, Shubhangi Shubhangi, Computer Science;
- Associate Advisor, Saurav Dhar, Computer Science;
- Associate Advisor, Mingwan Zhang, Computer Science;
- Associate Advisor, Nachiket Deo, Computer Science;

### Honors Program Advising

- Major Advisor, Berk Alpay, University Scholar, Computer Science and Engineering; now a *Postdoc* at Harvard University/Medical School
- Associate Advisor, Alexey Pozdnyakov, University Scholar, Computer Science and Engineering;

### MS Data Science Masters Advising

- Major Advisor, Jennifer Minh, Computer Science;
- Major Advisor, Madison Beebe, Computer Science;

**Individualized Majors Advising**

- Undergraduate Advisor, Matthew Jane, Computational Neuroscience;
- Undergraduate Advisor, Patrick Cummins, Samuel Hughes, Anthony Zeimbekakis, Michael Zheng, Shannon Yeung, Data Science;

**Other Advising**

- CAPS Research Apprentice AY 2024, Dennis Gega, UConn;
- Advanced Research Mentorship (ARM) program AY 2024, Arnav Kamineni Glastonbury Highschool;
- Advanced Research Mentorship (ARM) program AY 2023, Naavya Jain, Aarav Mehta, Jay Tummala Glastonbury Highschool;
- Advanced Research Mentorship (ARM) program AY 2022, Arya Patel and Heather Newandee, Glastonbury Highschool;
- Advanced Research Mentorship (ARM) program AY 2021, Rachel Ha, Glastonbury Highschool;
- Advanced Research Mentorship (ARM) program AY 2019, Dhanush Kalangi, Glastonbury Highschool, received 2nd honors at Connecticut Science & Engineering Fair;
- University of Texas at El Paso BUILD Scholar Mentor (Summer 2021), Isaiah Perez
- Thesis Review Committee: Chao Shang, Timothy Becker
- Undergraduate Students Advising Total:  $\approx 60$
- Work Study, Christina Gorbenko, Computer Science and Engineering;

**Academic Service****Conference and Workshop Organizing Committees**

Organizing Committee Member, [SorinFest: Phase Transitions in Computer Science and Computational Biology](#), Brown University (2023)

Organizing Committee Member, [Rise Against the Machines: Challenges and Opportunities for AI in Industry](#), CT Advanced Computing Center, Organizing Committee Member (2023)

Organizing Committee Member, [Computer Science Teachers Association New England Annual Meeting: Building CS Pathways](#), Organizing Committee Member (2023)

**Grant Proposal Review**

Panel Reviewer, National Institutes of Health, SBIR/STTR Program, Study Section ZMD1 JT (J1) (2023)  
Reviewer, Natural Sciences and Engineering Research Council of Canada (NSERC) (2022)

**International Committees**

Program Committee, ISMB (2018), BNP Workshop at NIPS (2018), RECOMB (2020, 2021, 2022, 2023, 2025, 2026), RECOMB Highlights (2023), BIBM (2019, 2020, 2024), AAI (2021, 2022, 2024, 2025), IJCAI (2021, 2022, 2024), ISBRA (2021, 2022, 2023), ICCABS (2023, 2025, 2026)

Session Chair, RECOMB (2020)

**Editorial Boards**

Journal of Computational Biology, 2021-

**University Committees**

Dean of Engineering Search 2023;

**Departmental Committees**

Merit Committee 2023-2024;

Graduate Fellowship Awards Committee 2023-2025;

Workload Committee 2022-2025;

Undergraduate C&C Committee 2021-2022, 2023-2024;

UG Life Committee 2021-2022, 2023-2024;

Search Committee, Data Science RAP, Stamford 2021-2022;

MS DS Concentration Advisors 2021-2024;

Professional Education Committee 2020-2021;

Grad Life Committee 2020-2022;

Graduate C&C Committee 2020-2021;

Web and Publicity 2019-2024;

Open House 2019-2021;

Faculty Search Open 2018-2019, Systems and ML 2018-2019, Open, Security-SYF 2019-2020;

### **Peer-Review**

*Nature Communications*, 2017, 2022; *Genome Research*, 2016, 2021; *Bioinformatics*, 2012-2019; *Proceedings of the National Academy of Sciences (PNAS)*, 2011; *Journal of Computational Biology (JCB)*, 2010-; *IEEE Transactions on Computational Biology and Bioinformatics*, 2020; *BMC Bioinformatics*, 2020; *Frontiers in Genetics* 2021; *Machine Learning* 2021-2022, *IEEE CCWC* 2022; *AI4TS2022 (IJCAI Workshop)* 2022, 2024; *BMC Supplements* 2023; *PLoS ONE* 2024; *Bioinformatics Advances* 2023, 2025; *Nucleic Acids Research* 2024, 2025; *Nature Communications Biology* 2025

### **Other Service**

*School of Engineering Mentoring Workshop Panelist*. August 2022, 2023

*University of Connecticut ENGR 1000 Talk*. "Painting with cats and other nonsense" December 2022

### *Academic Web Administration and Development*

- ▶ Built and maintained the [Princeton BEEHIVE](#), 2014-2018
- ▶ Built and maintained the [Istrail Lab Web](#); in 2012 rebuilt in PHP, 2009-2014
- ▶ Managed Brown University's Center for Computational Molecular Biology (CCMB) website, 2009-2011

### *Organizational Support*

- ▶ Produced presentations and brochures for Brown University's CCMB Symposium, 2010
- ▶ Developed presentations and movies using Google Earth, Google SketchUp, and KML to support creation of the Ph.D. program for the Brown University's CCMB; Ph.D. program was approved in 2009

### *Other professional activities*

- ▶ Senior Design Project Judge, UConn CSE, 2019, 2020, 2022, 2023
- ▶ North Carolina Student Academy of Science State Competition Judge, 2016-2017

### **Scholarships & Honors**

- ▶ Student Nominated Graduate Faculty Career Mentor of the Year Finalist from the UConn Center for Career Development, 2023
- ▶ University Teaching Innovation Award Finalist from the Center for Excellence in Teaching & Learning, UConn, 2023
- ▶ Excellence in Mentoring Award, Glastonbury High School Advanced Research Mentorship, 2022
- ▶ Undergraduate Faculty Career Mentor of the Year Award Finalist from the UConn Center for Career Development, 2021
- ▶ Graduate Faculty Career Mentor of the Year Award Finalist from the UConn Center for Career Development, 2021
- ▶ 2x Mentorship Excellence Award Finalist from the UConn Office of Undergraduate Research, 2020, 2021
- ▶ Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research semifinalist, 2015
- ▶ Travel Awards: Research in Computational Molecular Biology (RECOMB) Student Travel Fellowship, 2010, 2014; Intelligent Systems for Molecular Biology (ISMB) Student Travel Fellowship, 2012, 2013; National Science Foundation (NSF) Established Program to Stimulate Competitive Research (EPSCoR), 2013; IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS) Computational Advances for Next Generation Sequencing (CANGS) Workshop, 2012
- ▶ Outstanding Graduating Senior in Computer Engineering, URI, 2007
- ▶ Outstanding Junior in Computer Engineering, URI, 2006

## Community Outreach

S-STEM Mentor, University of Connecticut	2025-
McNair Faculty Mentor, University of Connecticut	2021-
CAPS Research Faculty Mentor, University of Connecticut	2024-
William J. Johnston Middle School Career Fair	2023
University of Texas at El Paso BUILD Scholar Mentor, University of Connecticut	Summer 2021
Advanced Research Mentorship program, Glastonbury High School, Glastonbury, CT	AYs 19, 21-24

- Responsibilities include assisting mentee students in developing an appropriate and feasible research project.
- Ran weekly 2 hour meetings over both Fall and Spring semesters.

Explore Engineering Young Engineering Science Scholars Program, School of Engineering, UConn, Storrs, CT 2019

- [Explore Engineering](#) is a one-week STEM summer camp for high school juniors and seniors where they are introduced to engineering fields.
- Students in my CS section were introduced to Programming, Data Science, Machine Learning and Artificial Intelligence through a series of lectures, activities, Jupyter notebooks, and programming exercises.
- On a scale of 1 (Unacceptable) to 5 (Outstanding), students rated the CS section an average score of 4.77.

Senior Design Project Judge, School of Engineering, UConn, Storrs, CT 2019-2020, 2022

- [Senior design projects](#) are the culmination of a two-semester course where students team up with faculty and industry sponsors to work collaboratively to solve a real-world problem.

Invention Convention Judge, Connecticut Invention Convention, Storrs, CT 2019-2022

- The [Connecticut Invention Convention](#) is an internationally recognized nonprofit educational program that encourages interest in STEM fields and develops critical thinking skills in children in grades K-12 through invention and innovation.

AI4All Postdoctoral Mentor, Fragile Families group, PRINCETON UNIVERSITY, Princeton, NJ 2018

- [AI4All](#) is a high school summer camp aimed at popularizing AI among groups underrepresented in the field.
- Responsibilities include mentoring the Fragile Families project team; development of curriculum and Jupyter notebooks detailing machine learning applications to the Fragile Families data.

Volunteer for Kids Run Durham, Bull City Running Company, Durham, NC 2015-2016

- [Kids Run Durham](#) is a program meant to encourage building healthy lifestyle habits, self-esteem, and character development, goal setting, and management in young children.
- Responsible for registration of children into their age-appropriate race-series and organizing the children into their respective groups at the race starting line.

## Industry Experience

RAYTHEON INTEGRATED DEFENSE SYSTEMS (IDS), Portsmouth, RI 2006-2008

Software Engineer, 2007-2008

- Developed and tested data control and management software for the Zumwalt Total Ship Computing Environment Infrastructure.

Software Engineer, Mission Innovation (MI) Group, 2006-2007

- ▶ Applied company technology and resources to address world-threatening issues.
- ▶ Used Google Earth, KML, SQL, and .NET to create web-based collaborative disaster planning tool (Joint Rapid Integrated Planning Service); listed as co-inventor on Raytheon patent.

### **Memberships & Activities**

International Society for Computational Biology (ISCB), 2012-

Institute of Electrical and Electronics Engineers (IEEE), 2006-

Association for Computing Machinery (ACM), 2006-

American Association for the Advancement of Science (AAAS), 2019-

Six Sigma Specialist, 2007

Phi Eta Sigma Honor Society, 2006

Tau Beta Pi Honor Society, 2006