

Derek Cole Aguiar

Curriculum Vitae

May 2022

📍 Computer Science & Engineering Department, University of Connecticut, Storrs, CT 06269
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Research Interests

I am interested in advancing CS foundations of machine learning, Bayesian modelling, and applications including Bayesian nonparametrics and hierarchical latent variable models, probabilistic computing, variational inference, deep learning, graph theory and algorithms, population genomics, cancer genomics, transcriptomics, disease genetics, and medical informatics.

Academic Experience

UNIVERSITY OF CONNECTICUT, Computer Science and Engineering Department, Storrs, CT 2018-
Assistant Professor

PRINCETON UNIVERSITY, Department of Computer Science, Princeton, NJ 2014-2018
Postdoctoral Researcher, Advised by Barbara Engelhardt

BROWN UNIVERSITY, Department of Computer Science, Providence, RI 2008-2014
Ph.D., Computer Science, Advised by Sorin Istrail, 2014
Master of Science, Computer Science, 2010

UNIVERSITY OF RHODE ISLAND (URI), 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)

Teaching Experience

UNIVERSITY OF CONNECTICUT, Storrs, CT 2018-2019
Instructor, *Introduction to Computing for Engineers*: 2019, 2020

- 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, *Algorithms and Complexity*: 2019, 2021

- 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, *Bayesian Machine Learning*: 2018, 2019, 2021

- 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.

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.

Preprints and Unpublished Work

1. B. Alpay, P. Rodriguez, S. Santos, A. Kulkarni, J. Oviedo, M. Gosink, and **D. Aguiar**. A Unified Analysis of Methods for Predicting Adverse Drug Reactions (). In preparation.
2. R. De Vito, I. N. Grabski, **D. Aguiar**, L. M. Schneper, A. Verma, J. Castillo Fernandez, C. Mitchell, J. Bell, M. Sara, D. A. Notterman, and B. Engelhardt. Differentially methylated regions and methylation QTLs for depression and early puberty in the Fragile Families Child Wellbeing Study (). Submitted to Genome Biology.
3. C. Li, L. Qu, P. A. Murphy, Y. Liu, A. Manichaikul, **D. Aguiar**, S. S. Rich, D. M. Herrington, D. Vu, C. W. Johnson, J. I. Rotter, W. S. Post, A. T. Vella, A. Rodriguez, and B. Zhou. AtheroSpectrum reveals novel macrophage foam cell gene signatures associated with atherosclerotic cardiovascular disease risk (). Under revision for Circulation.
4. K. Udeh, D. W. Wanik, D. Cerrai, **D. Aguiar**, and E. Anagnostou. Modeling Utility Customer Outages with Deep Neural Networks (). In preparation.
5. **D. Aguiar**, G. Gliner, L. T. Elliott, Y. W. Teh, and B. E. Engelhardt. *The fragmentation coagulation process haplotype cluster graph model. (manuscript in final stages)*. 2020.
6. D. J. McConnell, B. Dumitrascu, B. E. Engelhardt, and **D. Aguiar**. *Robust and interpretable statistical genetic modelling. (manuscript in final stages)*. 2020.

Ph.D. Thesis

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

Refereed Papers

2. 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).
3. 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.
4. 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.
5. 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.
6. **D. Aguiar**, L.-F. Cheng, B. Dumitrascu, F. Mordélet, A. Pai, and B. Engelhardt. Bayesian nonparametric discovery of isoforms and individual specific quantification. *Nature Communications* **9**(1) (2018), 1681.
7. **D. Aguiar**, E. M. Morrow, and S. Istrail. Tractatus: An Exact and Subquadratic Algorithm for Inferring Identical-by-Descent Multi-shared Haplotype Tracts. In: *RECOMB*. Springer. 2014, pp.1–17.
8. **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.
9. 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.
10. **D. Aguiar** and S. Istrail. Haplotype assembly in polyploid genomes and identical by descent shared tracts. *Bioinformatics* **29**(13) (2013). *also in proceedings of ISMB 2013*, i352–i360.

11. 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.
12. **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). *also in proceedings of ISMB 2012*, i154–i162.
13. **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.
14. 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.
15. B. V. Halldórsson^{*}, **D. Aguiar**^{*}, R. Tarpine, and S. Istrail. The Clark Phaseable sample size problem: long-range phasing and loss of heterozygosity in GWAS. *Journal of Computational Biology* **18**(3) (2011). *also in proceedings of RECOMB 2010*, 323–333.

Book Chapters

16. 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.

Grant Activity

Ongoing.

Derek Aguiar (PI) 04/01/2022-03/01/2023

TBA

TBA

TBA

Role: Principal Investigator, \$250,000 total award

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

Our main objective in this grant is to support teacher learning of DS&AI to address societal problems with big data, an important aim in both math and science education. We develop and implement a framework for training math and science teachers to deliver carefully designed learning modules (1-3 day instructional tasks) that use DS&AI to engage and facilitate learning of core CS concepts among high school students. Our main hypothesis is that by making DS&AI accessible to students and teachers in secondary school, and foregrounding societal issues, we can make participation in CS more attractive and engaging, ultimately increasing enrollment, retention, and diversity in CS. We are well situated to meet our objective due to the team’s collective experience in math, science, and CS education, DS&AI, task design, and research and evaluation methods.

Role: Principal Investigator, \$80,000 total award

Completed.

Derek Aguiar (PI) 09/01/2019-06/01/2021

The Institute for Collaboration on Health, Intervention, and Policy (InCHIP)

^{*} denotes co-first authorship when ambiguous

Unifying clinical support methods for preventing and managing opioid use disorder

The declaration of the opioid crisis as a national epidemic by the U.S. government in 2017 was the culmination of an increasingly critical public health emergency that has worsened in recent years. In 2016, an average of 116 people died daily due to opioid related drug overdoses. At present, there is no comprehensive approach that integrates genetic, pharmacological and mobile health data to improve chronic pain treatment outcomes from before diagnosis to after treatment. The overall objective of this proposal is to develop statistical and machine learning methods that predict opioid use disorder (OUD) risk and suggest personalized behavioral interventions. Such a clinical support system will enable clinicians to make more informed and personalized treatment decisions and enable the exploration of alternative treatment strategies to improve patient outcomes.

Role: Principal Investigator, \$25,000 total award

Derek Aguiar (senior personnel) 08/01/20-02/01/22

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.

Prescription opioid misuse has significantly increased over the last decades and associated with adverse drug interactions, hospitalizations, and overdose deaths. Compared to non-pharmacologic treatments, medication-assisted treatments (MAT) is associated with lower rates of relapse, decreased healthcare utilization, and lower healthcare costs. There are four MAT currently available for chronic treatment of Opioid Use Disorder (OUD): methadone, buprenorphine, buprenorphine/naloxone, and naltrexone. Research has shown poor adherence rates (21-43%) to these medications and has identified age, gender, prior substance use history, polysubstance use, and structural barriers to be related to MAT non-adherence. There remains no known research on how facilitators and barriers differ across clinical sites per patient and provider perspectives and how differences relate to site MAT adherence rates. Connecticut (CT)-based research is needed to inform CT stakeholders about best practices to improve MAT adherence rates. In this project our goal is three-fold: (1) To identify the nature and extent of adherence to Medication-Assisted Treatments (MAT) for 3 diverse treatment locations in CT; (2) To describe patient factors affecting adherence to MAT for OUDs among patients receiving MAT from 3 diverse treatment locations in CT; and, (3) To describe organizational factors across 3 diverse treatment locations in CT that affect MAT adherence.

Role: Senior Personnel, \$25,000 total award

Invited Talks & Panels

1. ImmunoCardio Group Meeting, University of Connecticut, "Machine Learning, Genomics, Transcriptomics, Bash and R Tutorial." April 2022
2. Panelist, exploreCSR Workshop, University of Rhode Island, "Life after Grad School." April 2022
3. 35th Anniversary Lecture Series, University of Connecticut, "Bayesian machine learning and the isoform reconstruction problem." April 2022
4. Connecticut Computer Science Teachers Association Chapter Meeting, "An Update on our SMARTAI Education Module." February 2022
5. Computer Science Colloquium, University of Rhode Island, "Bayesian nonparametric modelling and scalable inference in genomics and transcriptomics data." November 2021
6. Panelist, [UConn STEM Seminar Series](#), Interdisciplinary Engineering Research, "An Interdisciplinary Tour of Machine Learning in Biology, Law, and More." September 2021

7. Bioinformatics Seminar Series, University of Connecticut, "Bayesian Networks and Nonparametric Haplotype Clustering." September 2021
8. Connecticut Computer Science Teachers Association Chapter Meeting, "Preparing Students for a Data-Centric Computer Science Curriculum." May 2021
9. Panelist, exploreCSR Workshop, University of Rhode Island, "Life after Grad School." April 2021
10. 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
11. Department of Statistics Colloquia, University of Connecticut, "Bayesian Nonparametric Modelling and Scalable Inference In Large-Scale Genomics Data." January 2020
12. New York Area Population Genomics Workshop, "Efficient construction of haplotype cluster graphs and estimating the age of mutations." January 2017
13. American Society of Human Genetics (ASHG) Annual Meeting, "Haplotype phasing using cluster graphs." October 2015
14. NIPS Workshop on Machine Learning in Computational Biology (MLCB) "A Bayesian nonparametric statistical framework for haplotype phasing." December 2014
15. 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
16. 19th Pacific Symposium on Biocomputing "Tumor Haplotype Assembly Algorithms for Cancer Genomics." January 2014
17. Brown University IPP Symposium: Putting Big Data to Work. "Ome sweet ome: the genome as a model for big data." April 25, 2013
18. 21st Annual International Conference on Intelligent Systems for Molecular Biology "Haplotype assembly in polyploid genomes and identical by descent shared tracts." July 2013
19. 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
20. 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
21. Brown Computational Biology Open House "SNPs and haplotypes and GWAS oh my!" Feb. 27, 2012
22. 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
23. Brown Computer Science - Research Exchange Seminars with Tea (REST) "Computational Challenges in Genome-wide Association Studies." Nov. 30, 2010
24. 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. 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.
2. 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.
3. 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.
4. 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.
5. 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.
6. 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.
7. 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.
8. 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.
9. 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)
10. 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)
11. 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.
12. 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.
13. 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

14. 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.
15. 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.
16. 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.

Scholarships & Honors

Excellence in Mentoring Award, Glastonbury High School Advanced Research Mentorship, 2022
Undergraduate Faculty Career Mentor of the Year Award Nominee from the UConn Center for Career Development, 2021

Graduate Faculty Career Mentor of the Year Award Nominee from the UConn Center for Career Development, 2021

2x Mentorship Excellence Award Nominee from the UConn Office of Undergraduate Research, 2020, 2021

Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research semifinalist, 2015

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) Academy Travel Award, 2013

IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS) Computational Advances for Next Generation Sequencing (CANGS) Workshop Student Travel Award, 2012

Outstanding Graduating Senior in Computer Engineering, URI, 2007

Outstanding Junior in Computer Engineering, URI, 2006

Software

1. **D. Aguiar**, L.-F. Cheng, B. Dumitrescu, 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.

Community Outreach

McNair Faculty Mentor, University of Connecticut 2021-
 University of Texas at El Paso BUILD Scholar Mentor, University of Connecticut Summer 2021
 Advanced Research Mentorship program, Glastonbury High School, Glastonbury, CT 2019-2020

- Responsibilities include assisting mentee students in developing an appropriate and feasible research project.

Explore Engineering Young Engineering Science Scholars Program, School of Engineering,
 UNIVERSITY OF CONNECTICUT, 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.

8th Annual 2022 SoE Poster Competition Judge, School of Engineering,
 UNIVERSITY OF CONNECTICUT, Storrs, CT 2022
 Senior Design Project Judge, School of Engineering, UNIVERSITY OF CONNECTICUT, Storrs, CT 2019-2020

- [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 2019-2021

- 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.

Academic Advising

Ph.D. Advising

Major Advisor, Marjan Hosseini, Computer Science;
 Major Advisor, Chandra Sekhar Dronavajjala, Computer Science;
 Major Advisor, Kingsley Udeh, Computer Science;
 Associate Advisor, Lina Kloub, Computer Science;
 Associate Advisor, Tianyu Wang, Computer Science;
 Associate Advisor, Fahad AlQahtani, Computer Science;

Masters Advising

Major Advisor, Sybille Legitime, 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;

Individualized Majors Advising

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

Honors Program Advising

Major Advisor, Berk Alpay, University Scholar, Computer Science and Engineering;

Other Advising

University of Texas at El Paso BUILD Scholar Mentor, Isaiah Perez
 Thesis Review Committee: Chao Shang, Timothy Becker
 Undergraduate Students Advising Total: 22
 Work Study, Christina Gorbenko, Computer Science and Engineering;
 Advanced Research Mentorship (ARM) program, Dhanush Kalangi, Glastonbury Highschool,
 received 2nd honors at Connecticut Science & Engineering Fair;

Academic Service

Grant Proposal Review

Reviewer, Natural Sciences and Engineering Research Council of Canada (NSERC) 2022

Committees

Program Committee, ISMB (2018), BNP Workshop at NIPS (2018), RECOMB (2019, 2020, 2021),
 BIBM (2019, 2020), AAI (2021,2022), IJCAI (2021,2022), ISBRA (2021)

Departmental, Faculty Search Open 2018-2019, Systems and ML 2018-2019;
 Session Chair, RECOMB (2020)

Editorial Boards

Journal of Computational Biology, 2021

Peer-Review

Nature Communications, 2017; *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 Bioinfor-*
matics, 2020; *Frontiers in Genetics* 2021; *Machine Learning* 2021, *IEEE CCWC* 2022; *AI4TS2022*
 (IJCAI Workshop) 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
- ▶ North Carolina Student Academy of Science State Competition Judge, 2016-2017

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