Dan F. DeBlasio, PhD

dan@dandeblasio.com
http://dandeblasio.com

Education

Doctor of Philosophy, Computer Science   University of Arizona · Tucson, AZ · 2016
Advisor: John Kececioglu.
Dissertation: "Parameter Advising for Multiple Sequence Alignment"
Minor: Ecology and Evolutionary Biology

Master of Science, Computer Science   University of Central Florida · Orlando, FL · 2009
Advisor: Shaojie Zhang
Thesis: "New Computational Approaches to Multiple RNA Alignment and RNA Search"

Bachelor of Science, Computer Science   University of Central Florida · Orlando, FL · 2007

Professional Experience

Assistant Teaching Professor   Carnegie Mellon University · Pittsburgh, PA · 08/2023–present
Computational Biology Department, School of Computer Science

Assistant Professor   University of Texas at El Paso · El Paso, TX · 08/2019–07/2023
Department of Computer Science, College of Engineering

Lane Fellow   Carnegie Mellon University · Pittsburgh, PA · 9/2016–08/2019
Computational Biology Department, School of Computer Science
Advisor: Carl Kingsford

Graduate Research Assistant   University of Arizona · Tucson, AZ · 8/2010–6/2016
Fellow of the NSF IGERT in Comparative Genomics Grant DGE-0654435 (2010-2013)
Funded under NSF Grant IIS-1217886 (2013-2016)

Research Associate II   Sanford-Burnham Institute for Medical Research · Orlando, FL · 5/2010–8/2010

Graduate Research Assistant   University of Central Florida · Orlando, FL · 8/2007–8/2010
Department of Engineering Technology, College of Engineering and Computer Science

Developer   Cloudspace · Orlando, FL · 8/2005–8/2007

Mentorship

CMU

Fiyinfoluwa Gbosibo May–July 2017, Summer Intern at CMU
Best Student Paper Award, ACM-BCB 2019
Last known position: Senior Data Scientist at Visa
Kwanho Kim September 2017–May 2019, MSCB at CMU
Thesis: Analyzing the Influence of Assessment Metrics on Automated Transcript Assembly Parameter Selection
Last known position: Associate Computational Biologist at the Broad Institute

UTEP

Md. Easin Hasan December 2019–October 2021, MS Bioinformatics, PhD Data Science at UTEP
Hector Richart Ruiz November 2019–May 2022, BS Computer Science at UTEP
  Last known position: Programmer at Columbus Industries
Demetrius Hernandez August 2021–December 2022, BS Computer Science at UTEP
  Best Student Poster Presentation, UTEP COURI Symposium, Spring 2022
  Last known position: PhD student at Notre Dame
Marissa Stephens August 2021–December 2021, Googler in Residence at UTEP
Taposh Kumer Sarker June 2022–May 2023, PhD Computer Science at UTEP
Kevin Acosta January 2023–December 2023, BS Computer Science at UTEP
Luis Cedillo November 2021–Present, BS Computer Science at UTEP

Teaching Experience

Instructor   Carnegie Mellon University · Pittsburgh, PA
  Advanced Topics in Computational Genomics (02-715), Spring 2018.
  Essentials of Mathematics and Statistics (02-680), Fall 2023
  Professional Issues for Computational and Automated Sciences (02-602/03-604), Fall 2023
  Introduction to Computational Biology (02-250), Spring 2024
  Algorithms and Advanced Data Structures (02-613/15-351/15-650), Spring 2024

Instructor   University of Texas at El Paso, El Paso, TX
  Discrete Structures 1/2 (CS 2101/2202), Spring 2023.
  Machine Learning (CS 4361/5361/6361), Fall 2022.
  Elementary Data Structures (CS 2401), Spring, Fall 2020, Fall 2021, Fall 2022 (with Googler in Residence F21).
  Algorithmic Foundations of Computational Biology (CS 4390/5390), Fall 2019.
  Algorithms for Computational Biology (CS 4364/5364), Spring 2021, 2022.

Instructor   University of Arizona · Tucson, AZ
  Evolutionary and Functional Genomics Lab (ECOL 553L), Fall 2012.

Teaching Assistant   University of Arizona · Tucson, AZ
  Evolutionary and Functional Genomics (ECOL 553), Fall 2012.

Teaching Assistant   University of Central Florida · Orlando, FL
  Burnett Honors College Summer Institute (high school programming summer camp), Summer 2008.
  Burnett Honors College Summer Institute (high school programming summer camp), Summer 2007.
  Introduction to C Programming, Fall 2006

Grants and Funding

Department of Defense though the Universities Space Research Association — *Innovative Analysis of Spectro-Temporal Signatures using Machine Learning for Ground-Based Remote Sensing of Unresolved Space Objects* — Role: Co-I (Velez-Reyes, PI) — Amount awarded: $350,000 (May 2022-September 2024)

Georgia Tech Research Institute   — *Classification of Unresolved Space Objects from Spectro Temporal Signatures* — Role: Co-I (Velez-Reyes, PI) — Amount awarded: $50,000 (August 2022-January 2023)

Notable Training

  Autism & Mental Health Series — Fall 2023
  Teaching as Research (TAR) Institute: Generative AI — October 2023
  Disability Resources 101 – September 2023

Adapting to Generative AI in the Classroom — August 2023
ACUE Inclusive Teaching for Equitable Learning Mircrocredential — Spring 2022
UTEP Center for Instructional Design's Teaching Online Academy — July 2020

Book

[1] **Parameter advising for multiple sequence alignment**. Dan DeBlasio and John Kececioglu. Springer International Publishing, 2018, (cited ≥28 times).

Theses

[1] **Parameter advising for multiple sequence alignment**. Daniel F DeBlasio. PhD Thesis. University of Arizona, Tucson, Arizona, 2016.

[2] **New Computational Approaches For Multiple RNA Alignment And RNA Search**. Daniel F DeBlasio. Masters Thesis. University of Central Florida, Orlando, Florida, 2009.

Preprints/In Progress

[1] **Identifying Cislunar Orbital Families via Machine Learning on Light Curves**. Gregory P. Badura, Dan DeBlasio, Aryzbe Najera, Ana C. Chavez-Lopez, Miguel Velez-Reyes, Nathan Un, Yuri Shimane, and Koki Ho. *Journal of the Astronautical Sciences (in review)*, 2024.

[2] **Exploiting Large Datasets Improves Accuracy Estimation for Multiple Sequence Alignment**. Luis Cedillo, Hector Richart, and Dan DeBlasio. *bioRxiv*, 2022.

Publications

[1] **Using Neural Networks to Classify Hyperspectral Signatures of Unresolved Resident Space Objects**. Luis Cedillo, Kevin Acosta, Miguel Velez-Reyes, and Dan DeBlasio. *Proceedings of Algorithms, Technologies, and Applications for Multispectral and Hyperspectral Imaging XXX at SPIE Defense + Commercial Sensing*, 2024.

[2] **Sketching methods with small window guarantee using minimum decycling sets**. Guillaume Marçais, Dan DeBlasio, and Carl Kingsford. *Journal of Computational Biology (in press)*, 2024.

[3] **Simulating ground-based measurements of spectral signatures of resident space objects**. Aryzbe Najera, Miguel Velez-Reyes, Hector Erives-Contreras, and Dan DeBlasio. *Proceedings of Algorithms, Technologies, and Applications for Multispectral and Hyperspectral Imaging XXIX at SPIE Defense + Commercial Sensing*, 2023.

[4] **How much data is sufficient to learn high-performing algorithms? Generalization guarantees for data-driven algorithm design**. Maria-Florina Balcan, Dan DeBlasio, Travis Dick, Carl Kingsford, Tuomas Sandholm, and Ellen Vitercik. *Proc. of the 53nd ACM SIGACT Symp. on Theory of Computing (STOC)*, 2021.

[5] **More Accurate Transcript Assembly via Parameter Advising**. Dan DeBlasio, Kwanho Kim, and Carl Kingsford. *The Journal of Computational Biology*, August 2020,

> originally appeared as **Towards building an automated bioinformatician: more accurate transcript assembly via parameter advising** Dan DeBlasio, Kwanho Kim, and Carl Kingsford, *Proceedings of the Workshop on Computational Biology at The International Conference on Machine Learning (WCB@ICML), June 2019.*

[6] **Practical universal k-mer sets for minimizer schemes**. Dan DeBlasio, Fiyinfoluwa Gbosibo, Carl Kingsford, and Guillaume Marçais. *Proceedings of the 10th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, September 2019. ***Best Student Paper Award***.

[7] **Locality sensitive hashing for the edit distance**. Guillaume Marçais, Dan DeBlasio, Prashant Pandey, and Carl Kingsford. *The joint proceedings of the 26th International Conference on Intelligent Systems for Molecular Biology (ISMB) and the 18th European Conference on Computational Biology (ECCB)*, July 2019, (cited ≥42 times).

[8] **Boosting Alignment Accuracy by Adaptive Local Realignment**. <u>Dan DeBlasio</u> and John Kececioglu. *accepted to Journal of Computational Biology*, 25(7), July 2018,

originally appeared as **Boosting Alignment Accuracy by Adaptive Local Realignment.** <u>Dan DeBlasio</u> and John Kececioglu. *Proceedings of the 21st Conference on Research in Computational Molecular Biology (RECOMB), April 2017.*

[9] **Asymptotically optimal minimizers schemes**. Guillaume Marçais, <u>Dan DeBlasio</u>, and Carl Kingsford. *Proceedings of the 26th International Conference on Intelligent Systems for Molecular Biology (ISMB)*, July 2018.

[10] **Core column prediction for protein multiple sequence alignments**. <u>Dan DeBlasio</u> and John Kececioglu. *Algorithms for Molecular Biology*, 12(1), April 2017,

originally appeared as **Predicting Core Columns of Protein Multiple Sequence Alignments for Improved Parameter Advising.** <u>Dan DeBlasio</u> and John Kececioglu. *Proceedings of the 16th International Workshop on Algorithms in Bioinformatics (WABI), August 2016.*

[11] **Genome Sequence of Ophidiomyces ophiodiicola, an Emerging Fungal Pathogen of Snakes**. Mana Ohkura, Robert R. Fitak, Jennifer H. Wisecaver, <u>Dan DeBlasio</u>, Faheem Niazi, Michael Egholm, Steven D. Rounsley, Chinnappa D. Kodira, and Marc J. Orbach. *Genome Announcements*, 5(30), July 2017.

[12] `SICLE`**: a high-throughput tool for extracting evolutionary relationships from phylogenetic trees**. <u>Dan F. DeBlasio</u> and Jennifer H. Wisecaver. *PeerJ*, 4, August 2016.

[13] **Ensemble Multiple Sequence Alignment via Advising**. <u>Dan DeBlasio</u> and John Kececioglu. *Proceedings of the 6th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, September 2015.

[14] **Learning Parameter-Advising Sets for Multiple Sequence Alignment**. <u>Dan DeBlasio</u> and John Kececioglu. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(9), May 2017,

originally appeared as **Learning Parameter Sets for Alignment Advising.** <u>Dan DeBlasio</u> and John Kececioglu. *Proceedings of the 5th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB), September 2014.*

[15] **Accuracy estimation and parameter advising for protein multiple sequence alignment**. John Kececioglu and <u>Dan DeBlasio</u>. *Journal of Computational Biology*, 20(4), April 2013, (cited $\geq$64 times combined),

originally appeared as **Estimating the accuracy of multiple alignments and its use in parameter advising.** Dan DeBlasio, Travis Wheeler, and John Kececioglu, *Proceedings of the 16th Conference on Research in Computational Molecular Biology (RECOMB), April 2012.*

[16] **A Memory Efficient Method for Structure-Based RNA Multiple Alignment**. <u>Daniel DeBlasio</u>, Jocelyne Bruand, and Shaojie Zhang. *IEEE/ACM Trans. on Comp. Biology and Bioinf.*, 9(1), January 2012,

originally appeared as `PMFastR`**: A New Approach to Multiple RNA Structure Alignment.** <u>Dan DeBlasio</u>, Jocelyne Bruand, and Shaojie Zhang. *Proceedings of the 9th International Workshop on Algorithms in Bioinformatics (WABI), September 2009.*

[17] **Epigenetic regulation of microRNA genes and the role of miR-34b in cell invasion and motility in human melanoma.** Joseph Mazar, Divya Khaitan, <u>Dan DeBlasio</u>, Cuncong Zhong, Subramaniam S Govindarajan, Sharmila Kopanathi, Shaojie Zhang, Animesh Ray, and Ranjan J Perera. *PlOS ONE*, 6(9), September 2011. (cited $\geq$92 times).

[18] **Epigenetic regulation of microRNA-375 and its role in melanoma development in humans.** Joseph Mazar, <u>Dan DeBlasio</u>, Subramaniam S Govindarajan, Shaojie Zhang, and Ranjan J Perera. *FEBS Letters*, 585(15), August 2011. (cited $\geq$117 times).

Service Related Publication

[1] **Closing the computational biology "knowledge gap": Spanish Wikipedia as a case study**. Nelly Sélem-Mojica, Tölay Karakulak, Audra Anjum, Antón Pashkov, Rafael Pérez Estrada, Karina Enriquez-Guillén, <u>Dan DeBlasio</u>, Sofia Ferreira-Gonzalez, Alejandra Medina-Rivera, Daniel Rodrigo-Torres, Alastair M. Kilpatrick, Farzana Rahman, and Lonnie R. Welch. *Proceedings of Intelligent Systems for Molecular Biology (ISMB) [conditional accept]*, 2024.

[2] **Global network of computational biology communities: ISCB's Regional Student Groups breaking barriers**. Sayane Shome, ... 39 others ..., <u>Dan DeBlasio</u>, and Farzana Rahman. *F1000Research*, 8(1574), August 2019 (editorial without peer-review).

[3] **Nurturing tomorrow's leaders: The ISCB Student Council Symposia in 2018**. Daniele Parisi*, Gabriel J. Olguin-Orellana*, Eli J. Draizen*, Nilson Da Rocha Coimbra, Nikolaos Papadopoulos, Susanne Kirchen, Yvonne Saara Gladbach, Numrah Fadra, Nazeefa Fatima, Aishwarya Alex Namasivayam, Sayane Shome, <u>Dan DeBlasio</u>, Alexander M. Monzon, Farzana Rahman, and R. Gonzalo Parra. *F1000Research*, 8(ISCB Community Journal), January 2019 (editorial without peer-review).

[4] **Reflections on a journey: a retrospective of the ISCB Student Council symposium series**. Mehedi Hassan, Aishwarya Alex Namasivayam*, <u>Dan DeBlasio</u>*, Nazeefa Fatima*, Benjamin Siranosian, R. Gonzalo Parra, Bart Cuypers, Sayane Shome, Alexander Miguel Monzon, Julien Fumey, and Farzana Rahman. *BMC Bioinformatics*, 19(12):347, October 2018.

[5] **The ISCB Student Council Internship Program: Expanding computational biology capacity worldwide**. Jigisha Anupama, Margherita Francescatto, Farzana Rahman, Nazeefa Fatima, Al berto Santos, Pandurang Kolekar, Avinash Kumar Shanmugam, Venkata Satagopam, <u>Dan DeBlasio</u>, Magali Michaut, and Emre Guney. *PLOS Computational Biology*, 14(1), January 2018.

[6] **Highlights of the second ISCB Student Council Symposium in Africa, 2017**. Candice N. Rafael, Efejiro Ashano, Yumna Moosa, Sayane Shome, and <u>Dan DeBlasio</u>. *F1000Research*, 6(ISCB Community Journal), December 2017 (editorial without peer-review).

[7] **Highlights from the 11th ISCB Student Council Symposium 2015**. Katie Wilkins, Mehedi Hassan, Margherita Francescatto, Jakob Jespersen, R. Gonzalo Parra, Bart Cuypers, <u>Dan DeBlasio</u>, Alexander Junge, Anupama Jigisha, and Farzana Rahman. *BMC Bioinformatics*, 17(3), February 2016 (editorial without peer-review).

[8] **Highlights from the tenth ISCB Student Council Symposium 2014**. Farzana Rahman, Katie Wilkins, Annika Jacobsen, Alexander Junge, Esmeralda Vicedo, <u>Dan DeBlasio</u>, Anupama Jigisha, and Tomás Di Domenico. *BMC Bioinformatics*, 16(Suppl 2):A1, January 2015 (editorial without peer-review).

[9] **Parameter advising for multiple sequence alignment**. <u>Dan DeBlasio</u> and John Kececioglu. *BMC Bioinformatics*, 16(Suppl 2):A10, January 2015 (editorial without peer-review).

Posters

[1] **Practical universal k-mer sets for minimizer schemes**. <u>Dan DeBlasio</u>, Fiyinfoluwa Gbosibo, Carl Kingsford, and Guillaume Marçais. ISMB/ECCB 2019.

[2] **The Bioinformatics Internship Program: An Initiative of The ISCB Student Council**. Emre Guney, Farzana Rahman, Nazeefa Fatima, Jigisha Anupama, and <u>Dan DeBlasio</u>. ISMB 2018. ***F1000 Poster Award***.

[3] **Automatically eliminating errors induced by suboptimal parameter choices in transcript assembly**. <u>Dan DeBlasio</u>, Kwanho Kim, and Carl Kingsford. ISMB 2018, ECCB 2018, WCB@ICML 2019.

[4] **Adaptive local realignment via parameter advising**. <u>Dan DeBlasio</u> and John Kececioglu. ISMB 2016, WABI 2016, ACM-BCB 2016.

[5] **Ensemble multiple sequence alignment using advising**. <u>Dan DeBlasio</u> and John Kececioglu. ISMB/ECCB 2015.

[6] **Learning parameter sets for alignment advising**. <u>Dan DeBlasio</u> and John Kececioglu. ACM-BCB 2014.

[7] **Learning advisors for multiple sequence alignment**. <u>Dan DeBlasio</u> and John Kececioglu. ISMB 2014.

[8] **FACET: a feature-based accuracy-estimation tool for protein multiple sequence alignments**. <u>Dan DeBlasio</u> and John Kececioglu. ISMB/ECCB 2013, MAGE 2013, IGERT Symposium on Deep Genomics.

[9] **Improving the Quality of Protein Sequence Alignments**. <u>Dan DeBlasio</u> and John Kececioglu. IGERT online poster competition, 2013, video: http://posterhall.org/igert2013/posters/350.

[10] **Estimating the Accuracy of Protein Multiple Alignments Without a Reference**. <u>Dan DeBlasio</u>, Travis Wheeler, Vladamir Filkov, and John Kececioglu. ISMB/ECCB 2011.

[11] **A New Approach to Multiple RNA Structure Alignment**. <u>Dan DeBlasio</u>, Jocelyn Bruand, Vineet Bafna, and Shaojie Zhang. RECOMB 2009.

Invited Talks

New Mexico Tech, Computer Science Symposium · **Socorro, NM** · *September 2022* · "Toward building an automated bioinformatician"

University of Texas at El Paso, Interdisciplinary Research Event · **El Paso, TX** · *March 2022* · "Who needs a manual? Automating scientific tools to accelerate innovation"

University of Texas at El Paso, Biology Department Seminar · **El Paso, TX** · *October 2019* · "Toward building an automated bioinformatician: more accurate transcript assembly via parameter advising"

Workshop on Automated Algorithm Design at the Toyota Technical Institute · **Chicago, IL** · *August 2019* · "Toward building an automated bioinformatician: more accurate transcript assembly via parameter advising"

Rutgers University, Camden · **Camden, NJ** · *April 2019* · "Toward building an automated bioinformatician: parameter advising for improved scientific discovery"

University of Texas at El Paso · **El Paso, TX** · *February 2019* · "Toward building an automated bioinformatician: parameter advising for improved scientific discovery"

Biological Data Science · **Cold Spring Harbor, NY** · *November 2018* · "Building an automated bioinformatician—More accurate, large-scale genomic discovery using parameter advising"

StringBio 2018 · **Orlando, FL** · *October 2018* · "Multiple sequence alignment accuracy estimation and its role in creating an automated bioinformatician"

ESCS 2018 · **Athens, Greece** · *September 2018* · "Building an automated bioinformatician: More accurate, large-scale genomic discovery using parameter advising"

ISMB 2018 · **Chicago, IL** · *July 2018* · "Building an automated bioinformatician: More accurate, large-scale genomic discovery using parameter advising"

ISMB 2016 · **Orlando, FL** · *July 2016* · "Adaptive local realignment via parameter advising"

Carnegie Mellon University · **Pittsburgh, PA** · *May 2016* · "Parameter advising for multiple sequence alignment"

Reed College · **Portland, OR** · *March 2016* · "Parameter advising for multiple sequence alignment"

ISCB Student Council Symposium 2014 · **Boston, MA** · *July 2014* · "Advising multiple sequence alignments"

Released Software

Scallop Parameter Advising   github.com/Kingsford-Group/scallopadvising

Feature-based Accuracy Estimator (Facet)   facet.cs.arizona.edu

Opal v3.0   opal.cs.arizona.edu

Sister Clade Extractor (SiClE)   eebweb.arizona.edu/sicle/

Profile based Multiple Fast RNA alignment (PMFastR)   genome.ucf.edu/PMFastR

Honors and Awards

Best Student Poster Presentation, UTEP COURI Symposium, Spring 2022 (to advisee Demetrius Hernandez)
Best Student Paper Award, ACM-BCB 2019 (to advisee Fiyin Gbosibo)
Outstanding Poster Presentation, ISMB 2018 (presenting author for the EIC poster)
Lane Fellowship, CMU CBD, 2016-2019
UA Department Fellowship, 2013,2014,2015
UA Department Service award, 2013
UA Department Scholarship award, 2016
NSF IGERT Fellow, 2010-2013
NSF REU in Computer Vision, 2006
Travel Fellowships
        {Event} — {Location} — {Funding Agency}

ECCB 2018 — Athens, Greece — ISCB Student Council
ISMB 2018 — Chicago, IL — ISCB
ISMB/ECCB 2017 — Prague, Czech Republic — ISCB Student Council
ISMB 2016 — Orlando, FL — ISCB Student Council
ISMB/ECCB 2015 — Dublin, Ireland — ISCB Student Council
ACM-BCB 2014 — Newport Beach, CA — NSF
ISMB 2014 — Boston, MA — ISCB Student Council
ISMB/ECCB 2013 — Berlin, Germany — NSF
RECOMB 2012 — Barcelona, Spain — UA GPSC
RECOMB 2012 — Barcelona, Spain — NSF
ISMB/ECCB 2011 — Vienna, Austria — UA GPSC
WABI 2009 — Philadelphia, PA — UCF Graduate Council
RECOMB 2009 — Tucson, AZ — RECOMB
RECOMB 2009 — Tucson, AZ — UCF Graduate Council

Service and Leadership Activities

Member   Professional organizations
International Society for Computational Biology (ISCB)
Association for Computing Machinery (ACM), ACM SIGBio, ACM SIGAct
Upsilon Pi Epsilon

Editor
Social Media Editor & Editorial Board
Journal of Computational Biology

Committee Member   International conferences and workshops.
Program Committee
IEEE ICCABS 2017; RECOMB-SEQ 2020, 2021, 2022, 2024; ISMB(/ECCB) 2020, 2021, 2022, 2024;
ACM-BCB 2022
Outreach Coordinator
ACM-BCB 2020
Organizing Committee
Workshop on the Future of Algorithms in Biology (FAB) 2018; ISCB SCS 2014, 2015, 2017;
ISCB SCS-Africa 2017; ISCB SCS-Latin America 2018;
Student Activities Co-Chair
ACM-BCB 2016
Publicity Chair
ACM-BCB 2020
Travel Fellowships Co-Chair
GLBIO 2024

Reviewer
Research Grants
NSF (including BIO, CISE, MPS Directorates; 2019, 2021 [x2], 2022, 2024), U.S.-Israel Binational Science
Foundation (2021), Antwerp University Association (2021)
Books
CRC Press
Journals
Bioinformatics, BMC Bioinformatics, Journal of Computational Biology, AI (MDPI), PLOS One, PeerJ,
Nucleic Acids Research, Journal of Health Informatics Research, Current Bioinformatics.
Conferences
ISCB SCS (2014-19), ISCB SCS-LA (2014), ISCB ESCS (2016), RECOMB (2017-20), WABI (2017,22),
ISMB/ECCB (2017,19,21), IEEE ICCABS (2017), ISMB (2018,20,22), ACM-BCB (2018-22), Grace Hopper (2019), ESA (2019).
Competitions
ISMB Posters (2017-18), RECOMB Posters (2019), ISCB Wikipedia Competition (2017-20)

Other
ISCB SCS Travel Grants (2016-18), UA GPSC Travel Grants (various 2011-2014)

Board of Directors   International Society for Computational Biology · 2017–2019
Student Council representative
advocate for students needs within the society
help make decisions on the societal operations

Executive Team   International Society for Computational Biology Student Council · 2017–2019
oversee and advise on committee actions and conference planning
help make decisions on the council operations

Web Committee Co-chair   International Society for Computational Biology Student Council · 2012-2017
managed a group of student volunteers to maintain the ISCB-SC website
oversaw the development and maintenance of the conference submission system

AGCCS Computer Science Representative   University of Arizona · 7/2012–5/2013
Associate Graduate Council for the College of Science at the University of Arizona
advocate for students in the Computer Science department in affairs to the deans and college administration

Chair, Graduate Student Council   University of Arizona · 7/2011–5/2012
organized events for graduate students and prospective students in the Computer Science Department
coordinate discussions with the department administration

Volunteer Coordinator, Graduate Student Council   University of Arizona · 7/2010–5/2011
find volunteers to organize department seminar setup and tear down
coordinate responsibilities for department events planned by the council

Co-chair, Science Salon   University of Arizona · 7/2011–5/2013
organized discussions about interdisciplinary science
vetted topic ideas and assisted in their presentation
guided discussion at events

Conference Volunteer
ISMB 2012, RECOMB Satellites 2019

Conference Attendance
ACM-BCB 2014, 15, 16, 19, 20
Cold Spring Harbor Laboratory: Biological Data Sciences 2018
ECCB 2018
ESCS 2018
FoCS 2009
ICML 2019
IGERT Symposium on Deep Genomics 2013
International Workshop on String Algorithms in Bioinformatics (StringBio) 2018
ISMB/ECCB 2011,13, 15, 17, 19, 21, 23
ISMB 2012, 14, 16, 18, 20, 22
MAGE 2013
NSF-NIH Joint Workshop in Emerging AI in Biology 2023
RECOMB 2009, 12, 17, 19, 20, 21, 22
ISCB-SCS 2012, 13, 14, 15, 16
WABI 2009, 15, 16, 20, 21
Workshop on Automated Algorithm Design at the Toyota Technical Institute 2019
Workshop on Learning-Based Algorithms at the Toyota Technical Institute 2019
Workshop on Emerging Technologies for Sequence Analysis 2018
Workshop on the Future of Algorithms in Biology 2018