Dan F. DeBlasio, PhD

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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 Professor   University of Texas at El Paso · El Paso, TX · 08/2019–present
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
Software development and data analysis of RNA-Seq and Chip-Seq experiments related to melanoma classification.

Graduate Research Assistant   University of Central Florida · Orlando, FL · 8/2007–8/2010
Department of Engineering Technology, College of Engineering and Computer Science
Project was to interface with local law enforcement to improve communication

Developer   Cloudspace · Orlando, FL · 8/2005–8/2007
Develop and maintain web-based applications
Worked on both server side and client facing development

Mentorship

Fiyinfoluwa Gbosibo   May–July 2017
iBRIC (Internship in Biomedical Research, Informatics and Computer Science) student
Currently a graduate student at Bentley University

Kwanho Kim   September 2017–May 2019
MSCB at CMU
Thesis title: "Analyzing the Influence of Assessment Metrics on Automated Transcript Assembly Parameter Selection"

Book

[1] **Parameter advising for multiple sequence alignment**. <u>Dan DeBlasio</u> and John Kececioglu. Springer International Publishing, 2018.

Theses

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

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

Publications

[1] **More Accurate Transcript Assembly via Parameter Advising**. <u>Dan DeBlasio</u>, 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.*

[2] **Practical universal k-mer sets for minimizer schemes**. <u>Dan DeBlasio</u>, 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***.

[3] **Locality sensitive hashing for the edit distance**. Guillaume Marçais, <u>Dan DeBlasio</u>, 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.

[4] **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.*

[5] **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.

[6] **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.*

[7] **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.

[8] `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.

[9] **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.

[10] **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.*

[11] **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,

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.*

[12] **A Memory Efficient Method for Structure-Based RNA Multiple Alignment**. <u>Daniel DeBlasio</u>, Jocelyne Bruand, and Shaojie Zhang. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 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.*

[13] **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$79 times).

[14] **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$100 times).

Service Related Publication

[1] **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).

[2] **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).

[3] **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.

[4] **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.

[5] **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).

[6] **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).

[7] **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).

[8] **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

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

Teaching Experience

Instructor   University of Texas at El Paso, El Paso, TX
Elementary Data Structures (CS 2401), Spring 2020, Fall 2020.
Algorithmic Foundations of Computational Biology (CS 4390/5390), Fall 2019.

Instructor   Carnegie Mellon University · Pittsburgh, PA
Advanced Topics in Computational Genomics (02-715), Spring 2018.

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

Honors and Awards

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

Committee Member   International conferences and workshops.
   Program Committee
      IEEE ICCABS 2017; RECOMB-SEQ 2020; ISMB 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

Reviewer
   Research Grants
      NSF BIO Directorate (2019)
   Books
      CRC Press
   Journals
      Bioinformatics, BMC Bioinformatics, 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 (2017-19), WABI (2017), ISMB/ECCB (2017,19), IEEE ICCABS (2017), ISMB (2018), ACM-BCB (2018), Grace Hopper (2019), ESA (2019).
   Competitions
      ISMB Posters (2017-18), RECOMB Posters (2019), ISCB Wikipedia Competition (2017-18)
   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, 2015, 2016, 2019
  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, 2013, 2015, 2017, 2019
  ISMB 2012, 2014, 2016, 2018
  MAGE 2013
  RECOMB 2009, 2012, 2017, 2019
  ISCB-SCS 2012, 2013, 2014, 2015, 2016
  WABI 2009, 2015, 2016
  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