

## NSF BIOGRAPHICAL SKETCH

NAME: DeBlasio, Daniel Frank

NSF ID: 000808206@nsf.gov

ORCID: 000-0003-4110-4431

POSITION TITLE & INSTITUTION: Assistant Professor, University of Texas at El Paso

### (a) PROFESSIONAL PREPARATION

INSTITUTION	LOCATION	MAJOR / AREA OF STUDY	DEGREE (if applicable)	YEAR YYYY
University of Central Florida	Orlando, FL	Computer Science	BS	2007
University of Central Florida	Orlando, FL	Computer Science	MS	2009
University of Arizona	Tucson, AZ	Computer Science	Ph.D.	2006
Carnegie Mellon University	Pittsburgh, PA	Lane Fellowship, Computational Biology Department	Fellow	2016-2019

### (b) APPOINTMENTS

2019 - present	Assistant Professor, University of Texas at El Paso, Department of Computer Science, El Paso, TX
2016–2019	Lane Fellow, Carnegie Mellon University, Computational Biology Department, Pittsburgh, PA
2014 - 2016	Graduate Research Assistant, University of Arizona, Department of Computer Science, Tucson, AZ
2010 - 2014	Fellow, University of Arizona, NSF IGERT in Genomics, Tucson, AZ
2010	Research Associate II, Sanford-Burnham Institute for Biomedical Research, Orlando, FL
2007 - 2010	Developer, University of Central Florida, Engineering Technology Department, Orlando, FL
2005 - 2007	Web Developer, cloudspace, Orlando, FL

### (c) PRODUCTS

#### Products Most Closely Related to the Proposed Project

1. DeBlasio D, Kececioglu J. Parameter advising for multiple sequence alignment. Cham, CH. Springer International Publishing. Computational Biology Series; 2017. 152p. DOI: 10.1007/978-3-319-64918-4
2. Hassan M, Namasivayam\* AA, DeBlasio\* D, Fatima\* N, Siranosian B, Parra RG, Cuyper B, Shome S, Monzon AM, Fumey J, Rahman F. Reflections on a journey: a retrospective of the iscb student council symposium series. BMC Bioinformatics. 2018; 19(12):347. PubMed PID: [30301451](#)
3. DeBlasio D, Kim K, Kingsford C. More accurate transcript assembly via parameter advising. Journal of Computational Biology. 2020. PubMed PID: [32315544](#)
4. Kececioglu J, DeBlasio D. Accuracy estimation and parameter advising for protein multiple sequence alignment. Journal of Computational Biology. 2013; 20(4):259–279. PubMed PID: [23489379](#)

5. Balcan MF, DeBlasio D, Dick T, Kingsford C, Sandholm T, Vitercik E. How much data is sufficient to learn high-performing algorithms? generalization guarantees for data-driven algorithm design. Proceedings of the 53rd Annual ACM SIGACT Symposium on Theory of Computing (STOC). 2021

#### **Other Significant Products, Whether or Not Related to the Proposed Project**

1. DeBlasio D, Bruand J, Zhang S. A memory efficient method for structure-based rna multiple alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics. 2011; 9(1):1–11. PubMed PID: [21576754](#)
2. Mazar J, DeBlasio D, Govindarajan SS, Zhang S, Perera RJ. Epigenetic regulation of microRNA-375 and its role in melanoma development in humans. FEBS Letters. 2011; 585(15):2467–2476. PubMed PID: [21723283](#)
3. Marçais G, DeBlasio D, Pandey P, Kingsford C. Locality sensitive hashing for the edit distance. Bioinformatics. 2019; i127–i135. PubMed PID: [21723283](#)
4. DeBlasio D, Gbosibo F, Kingsford C, Marçais G. Practical universal k-mer sets for minimizer schemes. Proceedings of the 10th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB). 2019; 167–176
5. DeBlasio DF, Wisecaver JH. SICLE: a high-throughput tool for extracting evolutionary relationships from phylogenetic trees. PeerJ. 2016; 4(e2359). PubMed PID: [27635331](#)

#### **(d) SYNERGISTIC ACTIVITIES**

1. **Efforts to broaden the community:** (i) Organizing committee for several Student Council Symposia 2014-2017, including in Africa and Latin America, (ii) Co-organized a student mentorship event at ACM-BCB 2020, (iii) Student Activities Co-Chair at ACM-BCB October 2016, (iv) Co-authored several papers related to building student lead computational biology groups and related issues,
2. **Community service:** (i) Member of the International Society for Computational Biology's (ISCB) board of directors, 2016-2019, (ii) Member of the internal organization of the ISCB Student Council, various positions incl. executive team member and web committee chair. (iii) Served as communications chair for ACM-BCB 2020.
3. **Efforts to increase community engagement:** (i) Organizing committee for the NSF sponsored “Workshop on the Future of Algorithms in Biology (FAB)”, September 2018, Carnegie Mellon University, Pittsburgh, PA, (ii) Co-moderated and co-organized a panel at RECOMB 2020 to discuss the changes in the ideas presented at FAB.
4. **Mentoring:** (i) Mentor of an undergraduate student in the University of Pittsburgh's Internship in Biomedical Research, Informatics and Computer Science (iBRIC) this work won best student paper at the 2019 ACM Conference on Bioinformatics, Computational Biology, and Health Informatics. (ii) Mentored a student through his masters thesis while a postdoc at Carnegie Mellon University. (iii) Currently mentoring one PhD student and one BS student at the University of Texas at El Paso.
5. **Teaching:** (i) Designed an undergraduate/graduate class on computational biology algorithms at the University of Texas at El Paso. (ii) Co-instructor for a graduate emerging topics course at Carnegie Mellon University. (iii) Instructor for a graduate class at the University of Arizona that taught algorithmic concepts to new interdisciplinary graduate students.