

# Dan F. DeBlasio, PhD

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

## Education

- University of Arizona** Tucson, AZ 2016  
Doctor of Philosophy, Computer Science, Ecology and Evolutionary Biology Minor  
Dissertation Title: *Parameter Advising for Multiple Sequence Alignment*  
Advisor: John Kececioglu
- University of Central Florida** Orlando, FL 2009  
Master of Science, Computer Science  
Thesis Title: *New Computational Approaches to Multiple RNA Alignment and RNA Search*  
Advisor: Shaojie Zhang
- University of Central Florida** Orlando, FL 2007  
Bachelor of Science, Computer Science

## Professional Experience

- Lane Fellow**, Carnegie Mellon University, Pittsburgh, PA September 2016-present  
Computational Biology Department, School of Computer Science

## Journal Publications

- Ensemble multiple sequence alignment using advising.** Dan DeBlasio and John Kececioglu. *in prep.*
- Genome sequence of *Ophidiomyces ophiodiicola*, an emerging fungal pathogen of snakes.** Mana Ohkura, Robert Fitak, Jennifer Wisecaver, Dan DeBlasio, Faheem Niazi, Michael Egholm, Steven Rounsley, Chinnappa Kodira, and Marc Orbach. *Genome Announcements*, July 2017.
- Core column prediction for protein multiple sequence alignments.** Dan DeBlasio and John Kececioglu. *BMC Algorithms for Molecular Biology (AMB)*. April 2017
- SICLE: a high-throughput tool for extracting evolutionary relationships from phylogenetic trees** Dan DeBlasio and Jennifer Weiscaver. *PeerJ*. August 2016
- Learning parameter-advising sets for multiple sequence alignment.** Dan DeBlasio and John Kececioglu. *ACM Trans. on Computational Biology and Bioinformatics (TCBB)*, *in press*.
- Accuracy estimation and parameter advising for protein multiple sequence alignment.** John Kececioglu and Dan DeBlasio. *Journal of Computational Biology (JCB)*. April 2013
- A Memory Efficient Method for Structure-Based RNA Multiple Alignment.** Dan DeBlasio, Jocelyne Bruand, Shaojie Zhang. *ACM Trans. on Comp. Bio. and Bioinfo. (TCBB)*. Jan. 2012
- Epigenetic Regulation of MicroRNA Genes and the Role of miR-34b in Cell Invasion and Motility in Human Melanoma.** Joseph Mazar, Divya Khaitan, Dan DeBlasio, Cuncong Zhong, Subramaniam Govindarajan, Sharmila Kopanathi, Shaojie Zhang, Animesh Ray, Ranjan Perera. *PLOS One*, Sept. 2011
- Epigenetic regulation of microRNA-375 and its role in melanoma development in humans.** J. Mazar, Dan DeBlasio, S. Govindarajan, S. Zhang and R. Perera. *FEBS Letters*, June 2011

## Conference Publications

- Boosting alignment accuracy by adaptive local realignment.** [Dan DeBlasio](#) and John Kececioglu. Proceedings of the 21<sup>st</sup> *International Conference on Research in Computational Molecular Biology (RECOMB)*, May 2017
- Predicting core columns of protein alignments improves parameter advising.** [Dan DeBlasio](#) and John Kececioglu. Proceedings of the 16<sup>th</sup> *Workshop on Algorithms in Bioinformatics (WABI)*, August 2016
- Ensemble multiple sequence alignment using advising.** [Dan DeBlasio](#) and John Kececioglu. Proceedings of the 6<sup>th</sup> *ACM Conference on Bioinformatics and Computational Biology (ACM-BCB)*, Sept 2015
- Learning parameter sets for alignment advising.** [Dan DeBlasio](#) and John Kececioglu. Proc. of the 5<sup>th</sup> *ACM Conf. on Bioinformatics and Comp. Biology (ACM-BCB)*, Sept 2014
- Estimating the accuracy of multiple alignments and its use in parameter advising.** [Dan DeBlasio](#), Travis Wheeler, and John Kececioglu. Proceedings of the 16<sup>th</sup> *International Conference on Research in Computational Molecular Biology (RECOMB)*, April 2012
- PMFastR: A New Approach to Multiple RNA Structure Alignment.** [Dan DeBlasio](#), J. Bruand, S. Zhang. Proc. of the 9<sup>th</sup> *Workshop on Algorithms in Bioinformatics (WABI)*, March 2009

## Conference Talks (not directly related to publications)

- Adaptive local realignment via parameter advising**, *ISMB 2016*, Orlando, FL
- Advising multiple sequence alignments**, *ISCB Student Council Symposium 2014*, Boston, MA

## Released Software

- Feature-based Accuracy Estimator (Facet)** [facet.cs.arizona.edu](http://facet.cs.arizona.edu)  
Developed in Perl and Java. This program learns a linear alignment accuracy estimation function based on easily computable feature values. Each of the values is computed independently. The coefficients of the estimation function are learned using a quadratic program solver based on structurally aligned references.
- Opal v3.0** [opal.cs.arizona.edu](http://opal.cs.arizona.edu)  
Developed in Java. The Opal alignment tool was originally published in 2007. Version 3.0 beta of the program, released Summer 2015, includes new functionality to allow the alignment step to be easily integrated with Facet and be seamlessly used for the task of parameter advising.
- Sister Clade Extractor (SiCIE)** [eebweb.arizona.edu/sicle/](http://eebweb.arizona.edu/sicle/)  
Developed in C++ this program is used for high throughput phylogeny analysis. Given an input tree in newick format, and a search term, SiCIE identifies if the tree is monophyletic for a the search prefix and returns the monophyletic sisters if they exist. Source code, examples and a detailed description are available online.
- Profile based Multiple Fast RNA alignment (PMFastR)** [genome.ucf.edu/PMFastR](http://genome.ucf.edu/PMFastR)  
Developed in C++ this program is based on FastR by S.H. Zhang *et al.* Utilizing the structural components of RNA to help builds a multiple alignment of these sequences. It also reduces the memory consumption of the original program from quadratic space to near linear. We also re-engineered it to run in a multi-processor environment.

## **Other Relevant Projects**

### **RNA-Seq and CHIP-Seq Analysis for MiR expression Differentiation**

Developed in Perl, a proprietary suite of software packages was developed at the Sanford-Burnham Institute in Orlando to extract Micro-RNA expression and methylation data as well as other genes from several runs of a SOLiD sequencer. The package enabled detection and verification of several novel interactions. The end goal of the project beyond my input is to find markers for the stage-3/4 transition in Melanoma. The results are published in several publications (above, first author Joseph Mazar)

## **Invited Talks**

**Reed College**, *March 2016*, Portland, OR

**Carnegie-Mellon University**, *May 2016*, Pittsburgh, PA

## **Un-refereed Publications**

**Highlights from the 11th ISCB Student Council Symposium 2015.** Katie Wilkins, Mehedi Hassan, Margherita Francescato, Jakob Jespersen, R. Gonzalo Parra, Bart Cuypers, Dan DeBlasio, Alexander Junge, Anupama Jigisha, Farzana Rahman. BMC Bioinformatics (conference supplement), February 2016

**Highlights from the tenth ISCB Student Council Symposium 2014.** Farzana Rahman, Katie Wilkins, Annika Jacobsen, Alexander Junge, Esmeralda Vicedo, Dan DeBlasio, Anupama Jigisha and Tomás Di Domenico. BMC Bioinformatics (conference supplement), January 2015

**Parameter advising for multiple sequence alignment.** Dan DeBlasio and John Kececioglu. BMC Bioinformatics (conference abstract), January 2015

## **Leadership and Service**

**Conference Program Committee**, IEEE ISCCABS 2017

**Journal Reviewer**, Bioinformatics, PLoS One, PeerJ, Nucleic Acids Research

**Conference Reviewer**, ISCB Student Council Symposium (2014-2016), ISCB Latin America SCS (2014), ISCB European SCS (2016), RECOMB 2017, WABI 2017, ISMB/ECCB 2017

### **International Society for Computational Biology (ISCB)**

Board of Directors (Student Council Representative)	2017-present
Student Council Web Committee, co-chair (chair in 2015)	2012-2017
Student Council Symposium, web chair	2014
organizing committee	2014, 15, 17
Intelligent Systems for Molecular Biology conference, volunteer	2012

### **ACM Conference on Bioinformatics, Comp. Biology and Health Info. (ACM-BCB)**

Student Activity co-chair	2016
---------------------------	------

### **Graduate Student Council**, Department of Computer Science, University of Arizona

AGCCS Representative	2012-2013
Council Chair	2011-2012
Volunteer Coordinator	2010-2011

<b>Science Salon</b> , University of Arizona, Steering Committee co-chair	2011-2013
---	-----------

## Mentorship

**Fiyinfoluwa Gbosibo** May-July 2017  
iBRIC (Internship in Biomedical Research, Informatics and Computer Science) student  
Currently an undergraduate student at Lincoln University

## Teaching Experience

**Evolutionary and Functional Genomics Lab, Primary Lecturer** Fall 2012  
University of Arizona  
Duties (hands on lab): course planning, lecturing, grading and office hours  
(main course): office hours

**Intermediate Computer Science, Teaching Assistant** 2008, 2007  
Burnett Honors College Summer Institute  
University of Central Florida high school summer camp  
Duties: lecturing, grading and office hours

**Introduction to C Programming, Teaching Assistant** Fall 2006  
University of Central Florida  
Duties: grading and office hours

## Selected Honors and Awards

**Lane Fellowship**, Computational Biology Dept., Carnegie Mellon University 2016-present

**Department Fellowship**, Dept. of Computer Science, University of Arizona 2013,14,16

**Service Award**, University of Arizona, Department of Computer Science 2013

Nominated for College of Science Graduate Service Award

**Scholarship Award**, Dept. of Computer Science, University of Arizona 2016

Nominated for College of Science Graduate Research Award

**NSF IGERT Fellowship**, University of Arizona 2010-2013

2-year incoming student fellowship, 1-year renewal

**NSF REU**, Computer Vision Internship, University of Central Florida Summer 2006

## Relevant Work Experience

**University of Arizona**, Graduate Research Assistant 2010-2016

- NSF IGERT Grant in Comparative Genomics DGE-0654435 (2010-2013)  
interdisciplinary research using genomic techniques
- NSF Grant IIS-1217886 (2013-2016),  
work related to multiple sequence alignment advising

**Sanford-Burnham Institute for Medical Research**, Research Associate II Summer 2010

- Wrote software to analyze melanoma derived NextGen sequence data
- Used ABI SOLiD sequence data to run RNA-Seq and Chip-Seq analysis

**University of Central Florida**, Graduate Research Assistant 2007- 2010

- Worked with the Engineering Technology Department at the College of Eng. and Comp. Sci.
- Developing a data sharing project between police agencies in the state of Florida
- Manage other programmer in completing tasks
- Developed interfaces from one database to another (often on multiple platforms)

**cloudspace**, Developer 2005-2007

- Maintaining live web sites and applications using PHP
- Develop new applications in PHP and JavaScript (AJAX/DOM) using XHTML and MySQL

## **Conference Posters**

- Adaptive local realignment via parameter advising.** *D. DeBlasio* and J. Kececioglu.  
ISMB 2016, WABI 2016, ACM-BCB 2016
- Ensemble multiple sequence alignment using advising.** *D. DeBlasio* and J. Kececioglu.  
ISMB 2015
- Learning parameter sets for alignment advising.** *D. DeBlasio* and J. Kececioglu.  
ACM-BCB 2014
- Learning advisors for multiple sequence alignment.** *D. DeBlasio* and J. Kececioglu.  
ISMB 2014
- FACET: a feature-based accuracy-estimation tool for protein multiple sequence alignments.**  
*D. DeBlasio* and J. Kececioglu  
ISMB 2013, MAGE 2013, IGERT Symposium on Deep Genomics
- Improving the Quality of Protein Sequence Alignments.** *D. DeBlasio* and J. Kececioglu.  
IGERT online poster competition, 2013, video: <http://posterhall.org/igert2013/posters/350>
- Estimating the Accuracy of Protein Multiple Alignments Without a Reference.** *D. DeBlasio*,  
T. Wheeler, V. Filkov and J. Kececioglu ISMB 2011
- A New Approach to Multiple RNA Structure Alignment.** *D. DeBlasio*, J. Bruand, V. Bafna, S.  
Zhang. RECOMB 2009

## **Conference Participation**

- IGERT Symposium on Deep Genomics.**
- Models and Algorithms for Genome Evolution.** MAGE 2013
- 50<sup>th</sup> Symposium on Foundations of Computer Science.** FoCS 2009
- Intl. Conf. on Intelligent Systems for Molecular Biology**  
ISMB/ECCB 2017, ISMB 2016, ISMB/ECCB 2015, ISMB 2014, ISMB/ECCB 2013,  
ISMB 2012, ISMB/ECCB 2011
- Intl. Society for Computational Biology Student Council Symposium,**  
SCS 2016, SCS 2015, SCS 2014, SCS 2013, SCS 2012
- Intl. Conf. on Research in Computational Molecular Biology.** RECOMB 2012, RECOMB 2009
- ACM Conf. on Bioinformatics, Computational Biology.**  
ACM-BCB 2016, ACM-BCB 2015, ACM-BCB 2014
- International Workshop on Algorithms in Bioinformatics.**  
WABI 2016, WABI 2015, WABI 2009

## **Professional Associations**

- |  |               |
|--|---------------|
| ACM, Member  | 2007-present  |
| SIGAct, Member   | 2009-present  |
| SIGBio, Member   | 2011-present  |
| IEEE, Member   | 2007-present  |
| Computer Society, Member                                   | 2008-present  |
| ISCB, Member   | 2011-present  |
| Upsilon Pi Epsilon, Computer Science Honor Society, Member | Inducted 2009 |