

# Noah M. Daniels

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## CONTACT INFORMATION

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## INTERESTS

Computational biology, applied machine learning, functional programming

## EDUCATION

B.S. *cum laude* Computer Science, Tufts University, 2001  
M.S. Computer Science, Tufts University, 2006  
Ph.D. Computer Science, Tufts University, 2013

## HONORS, AWARDS, & FELLOWSHIPS

Best Poster Award, RECOMB 2009  
Fellow, Graduate Institute for Teaching, Tufts University 2010  
NSF Travel Grant, RECOMB 2012  
SIGPLAN PAC Travel Grant, ICFP 2012  
Outstanding Contributor to Engineering Education, Tufts University 2013

## ACADEMIC EXPERIENCE

**Teaching Assistant** Introduction to Bioinformatics, with Donna Slonim, Spring 2009  
**Guest Lecturer** Introduction to Bioinformatics Spring 2009  
**Research Assistant** with Lenore Cowen, Since May 2009.  
**GIFT practicum instructor** Machine Structure & Assembly-Language Programming, with Norman Ramsey, Fall 2010  
**Guest Lecturer** Exploring Computer Science - Introduction to Machine Learning, Fall 2010, Summer 2010  
**Course Head & Lecturer** Exploring Computer Science, Spring 2011  
**Guest Lecturer** Discrete Mathematics Spring 2012  
**Course Head & Lecturer** Machine Structure & Assembly-Language Programming, Fall 2012

## PROFESSIONAL EXPERIENCE

**Systems Engineer** Analog Devices, Inc. Wilmington, Massachusetts USA 2001-2004  
**Vice President - Research** IntrinsicQ Financial, LLC. Waltham, Massachusetts USA 2004-2007  
**Director of Data Analysis** Panjiva, Inc. New York, NY USA 2006-2008

## PUBLICATIONS

Couch A, Daniels N (2001). *The Maelstrom: Network Service Debugging via "Ineffective Procedures"*, Proceedings of LISA 2001, San Diego, CA.  
Zhou W, Wu W, Palmer N, Mower E, Daniels N, Cowen L, Blumer A (2003). *Microarray Data Analysis of Survival Times of Patients with Lung Adenocarcinomas Using ADC and K-Medians Clustering*, Proceedings of CAMDA 2003, Durham, NC.  
Brady A, Maxwell K, Daniels N, Cowen L (2009). *Fault Tolerance in Protein Interaction Networks: Stable Bipartite Subgraphs and Redundant Pathways*, PLoS One 4(4): e5364.  
Daniels N, Kumar A, Cowen L, Menke M (2010). *Touring Protein Space with Matt*, Bioinformatics Research and Applications. Lecture Notes in Computer Science, 2010, Volume 6053/2010, 18-28  
Daniels N, Kumar A, Cowen L, Menke M (2011). *Touring Protein Space with Matt*, IEEE/ACM Trans Comput Biol Bioinform. 2011 Apr 1  
Nadimpalli S, Daniels N, Cowen L (2011). *Format: Correcting Protein Multiple Structural Alignments by Sequence Peeking*, Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine, Aug 2011

Daniels N, Hosur R, Berger B, Cowen L (2012). *SMURFLite: combining simplified Markov random fields with simulated evolution improves remote homology detection for beta-structural proteins into the twilight zone*, *Bioinformatics* (2012) 28 (9): 1216-1222.

Daniels N, Gallant A, Ramsey N (2012) *Experience Report: Haskell in Computational Biology*, Proceedings of the International Conference on Functional Programming, Sep 2012.

Daniels N, Nadimpalli S, Cowen L (2012). *Formatt: Correcting Protein Multiple Structural Alignments by Incorporating Sequence Alignment*, *BMC Bioinformatics*. 2012, 13:259

Daniels N, Gallant A, Peng J, Baym M, Cowen L, Berger B (2013). *Compressive Genomics for Protein Databases*, Proceedings of ISMB 2013, To Appear

WORKING PAPERS  
AND PAPERS UNDER  
REVIEW

*MRfY: Protein Remote Homology Detection Using Markov Random Fields and Stochastic Search*, with Andrew Gallant, Norman Ramsey Lenore Cowen

*Going the distance for protein function prediction*, with Mengfei Cao, Hao Zhang, Jisoo park, Mark Crowella, Lenore Cowen, Benjamin Hescott

CONFERENCE  
PRESENTATIONS

*Fault Tolerance in Protein Interaction Networks: Stable Bipartite Subgraphs and Redundant Pathways*

RECOMB 2009 (poster session, **Best Poster Award**).

Tucson, AZ, May 18, 2009.

*Touring Protein Space with Matt*

International Symposium on Molecular Biology, 3D SIG (poster session)

Boston, MA, July 9, 2010.

*Touring Protein Space with Matt*

International Symposium on Bioinformatics Research and Applications

Storrs, CT, May 24, 2010.

*Formatt: Correcting Protein Multiple Structural Alignments by Sequence Peeking*

ACM Conference on Bioinformatics, Computational Biology and Biomedicine

Chicago, IL, August 2, 2011.

*SMURFLite: combining simplified Markov random fields with simulated evolution improves remote homology detection for beta-structural proteins*

RECOMB 2012 (poster session)

Barcelona, Spain April 21, 2012.

*Experience Report: Haskell in Computational Biology*

ICFP 2012

Copenhagen, Denmark September 11, 2012.

INVITED TALKS

Massachusetts Institute of Technology, Computer Science and Artificial Intelligence Laboratory, Computation and Biology group, October 2010

Tufts University, Graduate School of Arts & Sciences and School of Engineering, Plenary Session of the 16th Annual Graduate Research Symposium, April 2012

PROFESSIONAL  
ACTIVITIES

**Reviewer**, Workshop on Algorithms for Bioinformatics, 2012  
**Reviewer**, Nucleic Acids Research, 2012  
**Reviewer**, Research in Computational Molecular Biology, 2013  
**Reviewer**, ACM Transactions in Computational Biology and Bioinformatics, 2013  
**Member**, International Society for Computational Biology, since 2010.  
**Member**, Association for Computing Machinery, Since 2011.  
**Student Representative**, Faculty Research Support and Facilities Advisory Committee, Tufts University, 2010-2012  
**Student Representative**, Educational Policy Committee, Tufts University, 2011-2012  
**Chair**, Academic Committee, Graduate Student Council, Tufts University, 2010-2011.  
**Member**, Academic Committee, Graduate Student Council, Tufts University, 2011-2012.  
**Chair**, Graduate Research Symposium, Tufts University, 2011

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