

LENORE JENNIFER COWEN
CURRICULUM VITAE
(3/17)

Lenore J. Cowen

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EDUCATION

Massachusetts Institute of Technology (9/87–5/93)

- Ph.D. in Applied Mathematics (5/93).
- Thesis title: *On Local Representations of Graphs and Networks*.
- Thesis Advisor: Daniel J. Kleitman.

Yale University (9/83–6/87)

- B.A. *Cum Laude* with honors in the Mathematics major (6/87).
- AT&T Bell Laboratories Summer Research Program (Summer, 1986).
- Budapest Semesters in Mathematics (Spring, 1986).

Hampshire College Summer Studies in Mathematics (1982–1983)

PROFESSIONAL EXPERIENCE

- Professor, Dept. of CS, Tufts University (7/09–present)
- Associate Professor, Dept. of CS, Tufts University (6/01–6/09)
- Joint Appointment, Tufts Dept. of Mathematics (1/04–present)
- Visiting Associate Professor, Dept. of EECS, Tufts University (9/00–12/00)
- Associate Professor, Dept. of Mathematical Sciences, Johns Hopkins University (5/00–6/01)
- Visiting Scientist, MIT Lab for Computer Science (Summer, 1998 and Year 1999–2000).
- Assistant Professor, Dept. of Mathematical Sciences, Johns Hopkins University (7/94–5/00). (Joint appointment in Computer Science 1/95–present). *On leave, academic year 1999–2000*.
- Postdoctoral Fellow, Dept. of Math. and DIMACS, Rutgers University (1/94–6/94), the Institute for Mathematics and Its Applications at the University of Minnesota (9/93 – 12/93).

- Consultant, Bell Laboratories, Murray Hill, New Jersey (Summer/Fall, 1992).

HONORS AND AWARDS

- **Best Performer, DREAM Disease Module Detection Challenge**, 2016
- **Emmaline Bigelow Conland Fellowship, Radcliffe Institute**, (9/99–8/00).
- **ONR Young Investigator** (6/96–6/99).
- **Robert S. Pond Teaching Award**, Johns Hopkins School of Engineering (1996).
- **Young Faculty Research Fellow**, Johns Hopkins School of Engineering (9/95–6/96).
- **NSF Postdoctoral Fellow** (9/93–7/96).
- **deForest Prize** for best graduating senior in Mathematics, Yale University (1987).
- **Anthony D. Stanley Prize** for Excellence in Pure and Applied Mathematics, Yale University (1985 and 1986).

PUBLICATIONS IN COMPUTATIONAL BIOLOGY

Note: paper authors alphabetized except in Computational Biology and Bioinformatics, where both the first and last authors have special importance.

1. P. Bradley, L. Cowen, M. Menke, J. King and B. Berger, "BETAWRAP: Successful prediction of parallel β -helices from primary sequence reveals an association with many microbial pathogens" *Proceedings of the National Academy of Sciences*, **98**(26), 2001: 14819-14824.

-Through computational methods, we predict a previously unsuspected role for the beta-helix fold in human infectious disease; the bacterial and fungal proteins identified include toxins, virulence factors, adhesins, and surface proteins of Chlamydia, Helicobacteria, Bordetella, Rickettsia and Neisseria.

2. L. Cowen, P. Bradley, M. Menke, J. King and B. Berger, "Predicting the Beta-Helix Fold From Protein Sequence Data," *Journal of Computational Biology*, **9**(2), 2002: 261-276.

-A spacial generalization of methods to predict protein fold superfamilies based on pairwise statistical dependencies yields the first successful prediction of a beta-structural fold.

3. M. Menke, J. King, B. Berger and L. Cowen, "Wrap-and-Pack: A New Paradigm for Beta Structural Motif Recognition with Application to Recognizing Beta Trefoils," *Journal of Computational Biology*, **12**(6), 2005: 777-795.

-More beta-structural motif recognition.

4. A. McDonnell, M. Menke, N. Palmer, L. Cowen and B. Berger, "Fold Recognition and Accurate Alignment of Sequences Directing Beta Sheet Folding by Profile Wrapping," *Proteins: Structure, Function, & Bioinformatics*, **63**, 2006: 976-985.

-This work was co-awarded the PDB Best Poster Award recognizing insight and innovation in structural computational biology at RECOMB 2005.

5. M. Menke, B. Berger and L. Cowen, "Matt: Multiple Structure Alignment with Translations and Twists" *PLOS Computational Biology*, Vol 4, No. 1, 2008.

-Local flexibility improves protein multiple structure alignment for more structurally divergent proteins. Editor's pick of the week.

6. G. Widmer, L. Cowen, G. Ge, and X. Feng, "Protein Coding Gene Nucleotide Substitution Patterin in the Apicomplexan Protozoa *Cryptosporidium parvum* and *Cryptosporidium hominis*," *Computational and Functional Genomics*, doi: 879023, 2008.

- Computational methods for measuring rates of evolution may point to genes involved in the difference in virulence and host specificity for two waterborne pathogens.

7. A. Bryan, M. Menke, L. Cowen, S. Lindquist and B. Berger, "Betascan: Probable Beta-Amyloids Identified by Pairwise Probabilistic Analysis," *PLOS Computational Biology*, **5**(3): e10000333, 2009.

-A method to computationally predict where amyloids will form in sequence using pairwise beta-sheet probabilities.

8. A. Brady, K. Maxwell, N. Daniels and L. Cowen, "Fault Tolerance in Protein Interaction Networks: Stable Bipartite Subgraphs and Redundant Pathways," *PLOS One*, **4**(4): e5364, 2009.

- A new graph-theoretic method to find structure in genetic interaction networks in yeast that might indicate fault tolerance in the form of redundant pathways.

9. A. Kumar and L. Cowen, "Augmented Training of Hidden Markov Models to Recognize Remote Homology Via Simulated Evolution," *Bioinformatics*, **25**(3): 1602-1608, 2009.

-A simple pointwise mutation model to create new artificial training data improves the performance of profile HMMs for protein structural motif recognition.

10. B. Hescott, M. Leiserson, L. Cowen and D. Slonim, "Evaluating Between-Pathway Models with Expression Data," *Journal of Computational Biology*, **17**(3): 477-487, 2010.

-We present a way to use microarray deletion data to validate BPM network motifs.

11. M. Menke, B. Berger and L. Cowen, "Markov Random Fields Reveal an N-terminal Double Beta-Propeller Motif as Part of a Bacterial Hybrid Two-Component Sensor System," *PNAS*, 107(9): 4069-4074, 2010.

-We introduce a framework that allows pairwise and HMM probabilities in the same objective function and used it to better recognize structures that fold into beta-propellers, with applications to an interesting family of bacterial HTCS proteins.

12. A. Kumar and L. Cowen, "Recognition of Beta-Structural Motifs Using Hidden Markov Models Trained with Simulated Evolution," *Bioinformatics*, 26: i287-i293, 2010.

-Simulated evolution (from paper 31) generalized to capture pairwise dependencies of beta-strands improves remote homology detection.

13. N. Daniels, A. Kumar, L. Cowen and M. Menke, "Touring Protein Space with Matt," *IEE/ACM Transactions on Bioinformatics and Computational Biology* 9: 286-293, 2012.

- The Matt structural alignment program is used to automatically cluster folds into hierarchical classes by similarity. Relation to the SCOP manual classification is discussed.

14. A. Bryan Jr., C. O'Donnell, M. Menke, L. Cowen, S. Lindquist and B. Berger, "STITCHER: Dynamic assembly of likely amyloid and prion beta-structures from secondary structure predictions," *Proteins: Structure, Function, and Bioinformatics* 80: 410-420, 2012.

-The Betascan method to identify amyloid regions is extended to assemble into full structural predictions.

15. N. Daniels, R. Hosur, B. Berger and L. Cowen, "SMURFLite: combining simplified Markov random fields with simulated evolution improves protein remote homology detection into the twilight zone," *Bioinformatics*, 28: 1216-1222, 2012.

-The SMURF method is generalized to design "shallow" Markov Random Fields for most SCOP mainly-beta structural superfamilies.

16. M. Leiserson, D. Tatar, L. Cowen and B. Hescott, "Inferring mechanisms of Compensation from E-MAP and SGA Data Using Local Search Algorithms for Max Cut," *Journal of Computational Biology*, Special issue, best papers in RECOMB 2011, 18: 1399-1409, 2011.

-Exploiting structural properties of the genetic interaction network in yeast to uncover functional modules and redundant pathways using new high-throughput E-MAP and SGA data.

17. S. Su, C. Gramazio, D. Extrum-Fernandez, C. Crumm, L. Cowen, M. Menke, and M. Strait, "Molli: Interactive Visualization for Exploratory Protein Analysis," *IEEE Computer Graphics and Applications*, 32: 62-69, 2012.

-2D visualization of aligned 3D protein structures using multiple views, and our Matt protein structure alignment program.

18. N. Daniels, S. Nadimpalli and L. Cowen, "Formatt: Correcting protein multiple structure alignments by incorporating sequence alignment" *BMC Bioinformatics*, 13: 259, 2013.

-Incorporating sequence information into our Matt protein structure alignment program.

19. A. Gallant, M. D. Leiserson, M. Kachalov, L. J. Cowen, and B. J. Hescott, "Genecentric: a package to uncover graph-theoretic structure in high-throughput epistasis data," *BMC Bioinformatics*, 14: 23, 2013.

-Software that implements the method in Paper #16, with example results on new biological E-MAP data.

20. N. Daniels, A. Gallant, J. Peng, L. J. Cowen, M. Baym and B. Berger, "Compressive genomics for protein databases," *Bioinformatics*, 29: i283-i290, 2013.

-Compressive genomics paradigm introduced for DNA sequence by Berger's group now adapted to protein sequence data. In Proceedings Track of 2013 ISMB conference.

21. M. Cao, H. Zhang, J. Park, N. Daniels, M. Crovella, L. Cowen and B. Hescott, "Going the Distance for Protein Function Prediction," *PLOS ONE*, 8: e76339, 2013.

-A new fine-grained diffusion-based metric for biological network analysis improves classical protein function prediction algorithms based on the yeast PPI network.

22. M. Cao, C. Pietras, X. Feng, K. Doroschak, T. Schaeffer, J. Park, H. Zhang, L. Cowen and B. Hescott, "New Directions for Diffusion-Based Network Prediction of Protein Function: Incorporating Pathways with Confidence" *Bioinformatics*, 30: i219-i227, 2014.

-How best to incorporate confidence measures and coherent pathways into the methods of paper 21.

23. N. Daniels, A. Gallant, N. Ramsey, and L. Cowen, "Remote homology detection for beta-structural proteins using Markov random fields and stochastic search" *IEEE/ACM Transactions on Bioinformatics and Computational Biology*, 12 : 4-16, 2015.

-Won Best Student Paper at the 4th ACM BCB-Conference. Invited to the Special Issue of best papers from the conference.

24. M. Cao, L. Cowen, "When should we NOT transfer functional Annotation between sequence paralogs", *Proceedings of the Pacific Symposium on Biocomputing*, 22: 15, 2016.

-The difficulty of functional annotation when false negatives are not systematically collected into available databases

SELECTED JOURNAL PUBLICATIONS IN GRAPH THEORY AND ALGORITHMS

1. L. Cowen, R. Cowen, and D. Woodall, "Defective Colorings of Planar Graphs in Surfaces: Partitions into Subgraphs of Bounded Valency," *Journal of Graph Theory*, **10**(2), 1986: 187–195.

-Introduced defective coloring and solved defective chromatic number for the plane.

2. B. Awerbuch, B. Berger, L. Cowen, and D. Peleg, "Low Diameter Graph Decomposition is in NC," *Random Structures and Algorithms*, **5**(3), 1994: 442–452.

-The probabilistic method yields a deterministic parallel algorithm for graph decomposition.

3. B. Awerbuch, L. Cowen, and M. Smith, "Efficient Asynchronous Distributed Symmetry-Breaking," In *Proceedings of the 26th ACM Symposium on the Theory of Computing*, Montréal, Québec, Canada, May 1994 (NY: ACM Press, 1994), 214–223.

-An optimal randomized algorithm for MIS and Dining Philosophers in general asynchronous networks.

4. B. Berger and L. Cowen, "Scheduling with Concurrency-based Constraints," *Journal of Algorithms*, **18**(1), 1995: 98–123.

-Scheduling unit tasks on a fixed number of machines with both pre- and co-requisites; also solves a scheduling problem on the Tera architecture.

5. D. Kleitman, F. Lasaga, and L. Cowen, "Asymptotic Enumeration of Full Graphs," *Journal of Graph Theory*, **20**(1), 1995: 59–69.

-Solved 10-year open conjecture of J. Lynch.

6. B. Awerbuch, B. Berger, L. Cowen, and D. Peleg, "Fast Distributed Network Decomposition," *Journal of Parallel and Distributed Computing*, **39**(2), 1996: 105–114.

-The construction of network decompositions in the distributed computation model.

7. L. Cowen and R. Mathar, "The Offset Problem," *Combinatorics, Probability, and Computing*, **6**(2), 1997: 159–164.

-Gave an optimal strategy for a placement of locally synchronized stations in packet radio networks.

8. L. Cowen, W. Goddard, and E. Jesurum, "Defected Coloring Revisited," *Journal of Graph Theory*, **24**(3), 1997: 205–219.

-Every toroidal graph is (3,2) and (5,1) colorable; defective chromatic number is within a constant of the number of colors needed for the maximum clique on the surface, NP-completeness results and approximation algorithms.

9. L. Cowen and C. Priebe, "Randomized Non-Linear Projections Uncover High-Dimensional Structure," *Advances in Applied Mathematics*, **19**(3), 1997: 319–331.

-Introduced the ADC method for randomized dimension reduction.

10. C. Cheng and L. Cowen, "On the Local Distinguishing Number of Cycles," *Discrete Mathematics*, **196**(1-3), 1999: 97–108.

-A local version of the Albertson-Collins distinguishing number.

11. B. Awerbuch, B. Berger, L. Cowen, and D. Peleg, "Near Linear Cost Construction of Neighborhood Covers and their Applications," *SIAM Journal of Computing*, **28**(1), 2000: 263–277.

-The first approximation scheme for the k-pairs shortest paths problem.

12. L. Cowen, "Compact Routing with Minimum Stretch," *Journal of Algorithms*, (2001): **38**, 2001: 170–183. *Special Issue: Best Papers in SODA 1999*.

-The first universal compact routing scheme for weighted undirected networks that achieves maximum stretch 3, with sublinear space at every node.

13. A. Cannon and L. Cowen, "Approximation Algorithms for the Class Cover Problem," *Annals of Mathematics and Artificial Intelligence*, **40**(3-4), 2004: 215-224.

-Special Issue: Best Papers in AMAI 2000.

14. L. Cowen and C. Wagner, "Compact Roundtrip Routing in Directed Networks," *Journal of Algorithms*, **50**(1), 2004: 79-95.

-The first algorithm for compact routing in directed graphs is achieved by considering roundtrip distances.

15. B. Bogstad and L. Cowen, "The Distinguishing Number of the Hypercube," *Discrete Mathematics*, **283**(1-3), 2004: 29-35.

-The distinguishing number of a graph G is the minimum number of colors for which there exists an assignment of colors to the vertices of G so that the group of color-preserving automorphisms of G consists only of the identity. We solve the distinguishing number exactly for hypercubic graphs and their squares.

16. M. Arias, L. Cowen, K. Laing, R. Rajaraman, and O. Taka, "Compact Routing with Name Independence," *SIAM Journal on Discrete Mathematics*, **20**(3), 2006: 705-726.

-Achieves name-independent compact routing with stretch 5 (down from 1000+). Generalizes to different ranges of stretch/space tradeoffs.

17. A. Brady and L. Cowen, "Compact Routing on Power Law Graphs with Additive Stretch," Proceedings of the Eighth Workshop on Algorithm Engineering and Experiments (ALENEX06), 119-128, 2006.

-Experimentally validated compact routing schemes that perform nearly optimally on Internet-like graphs.

18. M. Arias, L. Cowen and K. Laing, "Compact Roundtrip Routing with Topology-Independent Node Names," *Journal of Computer and Systems Sciences*, **74**(5), 2008: 775-795.

-First paper to achieve name-independent compact (roundtrip) routing in directed graphs

19. L. Cowen, R. Cowen and A. Steinberg, "Totally Greedy Coinsets and Greedy Obstructions," *Electronic Journal of Combinatorics*, R90, 2009.

-Exploration of algorithms to determine a hereditary greedy property of coinsets; proved that any 3-element non-greedy coinset cannot be extended by adding larger coin denominations to a greedy coinset.

PROFESSIONAL ACTIVITIES

- Conference Committee Co-Chair, 8th ACM Conference on Bioinformatics, Computational Biology and Health Informatics, 2017.
- Chair, Dénes König Prize Selection Committee, 2016
- Vice Chair, SIAM Activity Group in Discrete Mathematics, 2013-2015
- Program Committee member, RECOMB 2014-2017 and 2010-2012.
- Program Committee Member ISMB – co-chair of Protein Structure and Function Track, ISMB, 2012, 2013 and 2016; co-chair of Applied Bioinformatics Track, 2014, PC member 2017
- Program Committee Member, APBC 2016 and 2017
- Program Committee Member, co-chair of Protein and RNA Structure Track, ACM BCB 2012 and 2013, Program Committee 2015-2016.
- Program Committee Member, WABI, 2010-2014
- Conference Chair, SIAM Discrete Math 2012
- Program Committee member, WG 2012
- Chair, George Pólya Prize Selection Committee, 2012
- Co-Chair, 2008 SIAM Annual Meeting. Organizing Committee Member: SIAM Annual meeting 2009 and 2017.
- Editorial Board member, SIAM Review, January 2008–2013
- Program Committee member, SODA 2008
- Program Committee member, ICALP 2008
- Chair, Dénes König prize committee, 2008.
- Alumni Mentor, Graduate Women at MIT, 2010-present

PROFESSIONAL SOCIETY MEMBERSHIPS

- ACM Association for Computing Machinery
- AMS American Mathematical Society
- AWM Association for Women in Mathematics
- ICSB International Society for Computational Biology
- SIAM Society for Industrial and Applied Mathematics

COURSES TAUGHT AND EDUCATIONAL ACTIVITIES: LAST 10 YEARS

Theory of Computation, Computational Biology, Algorithms, Advanced Algorithms, Graph Theory, Discrete Mathematics, Current Topics in Bioinformatics and Computational Biology.

GRADUATE STUDENT THESIS SUPERVISION

Mengfei Cao (Ph.D. August 2016, Tufts)

Dissertation Title: New Graph Metrics Improve Network-Based Protein Function Prediction

Noah Daniels (Ph.D. May 2013, Tufts)

Dissertation Title: Remote Homology Detection in Proteins Using Graphical Models

Anoop Kumar (Ph.D. August 2010, Tufts)

Dissertation Title: Augmented Training Methods for Hidden Markov Models for the Detection of Remote Protein Homologs

Arthur Brady (Ph.D. August 2008, Tufts)

Dissertation title: Detecting High-Level Gene Function and Inferring Redundant Genetic Pathways using Machine Learning Methods

Christine Cheng (Ph.D., 1999, JHU)

Dissertation title: Three Problems in Graph Labelling

Christopher Wagner (joint with Mike Goodrich) (Ph.D., 1999, JHU)

Dissertation title: Drawing with Curves and Routing in Directed Networks

Adam Cannon (Ph.D., 2000, JHU)

Dissertation title: Approximate Distance Methods in Classification

Fredrick Crimins (Masters, 2002, Tufts)

Dissertation title: Sensor Registration for Vapor Classification with an Artificial Nose

Orjeta Taka (Masters, 2003, Tufts)

Dissertation title: Compact Routing with Name Independence

Andrew McDonnell (Masters, 2003, Tufts)

Dissertation title: Predicting the Structure of The Beta-Helix Protein Motif

Jake Crawford (Masters, 2017, Tufts)

Masters project: A Double Spectral Approach to Disease Module Detection

Guangtao Ge (PhD 2009), Bioinformatics PhD in the Tufts Interdisciplinary Doctorate Program (IDOC), co-supervised by me, Giovanni Widmer (Tufts Vet. School) and Susan Ernst (Tufts Biology). Dissertation title: Analysis of Genomic and Experimental Data for Identifying Positively Selected Genes, Early Cancer Diagnosis, and Screening for Improved Industrial Protein Production.

Supervise 1-3 Undergraduate Research students each year. Undergraduate research students have gone on to be NSF graduate fellowship winners (Max Leiserson, Emily Mower, Shilpa Nadimpalli) and honorable mentions (Nathan Palmer).

UNIVERSITY SERVICE: LAST 5 years

School of Arts, Science and Engineering University-Wide Committees:

- Undergraduate Admissions and Financial Aid Committee 2009-2012
- Tenure and Promotion Committee 2013-2014
- Committee on Committees 2011-2016

Departmental Service:

- Tufts Computer Science Colloquium organizer 2008-2011
- Chair, Computer Science Graduate Admissions 2010-2014
- Member, Computer Science Graduate Admissions Committee 2016-present
- Member, Faculty Search Committee 2017
- Faculty Advisor, Tufts ACM-W Student Chapter 2016-present

FEDERAL GRANT REVIEW COMMITTEE SERVICE: LAST 5 years

NIH Study Section Review:

- BCMB-P Challenge Grants Panel 6/2009
- BDMA Biodata Management and Analysis 1/2010
- BCMB-S Special Emphasis Panel 8/2011
- FOA-A Fellowship Applications Meeting 9/2011
- MSFE Macromolecular Structure and Function E 11/2011
- BDK U24 Data Discovery Index Coordination Panel 5/2014

NSF Committee of Visitors for CCF 3/2009

NSF Career Panel: AF (Computational Biology) 9/2010

NSF Graduate Research Fellowship Program Panel: Computer Science 1/2016

GRANTS AND CONTRACTS: LAST 5 years

Computational Methods for Wrapping and Threading Remote Protein Homologs, NIH R01 grant, \$1,047,386 (2008-2013). Role: PI.

Tufts Collaborates! Understanding and Harnessing the Inherent Diversity within Repetitive Proteins, with Stephen Fuchs, Biology department, \$20,995 (2013). Role: Secondary co-PI.