

LENORE JENNIFER COWEN
CURRICULUM VITAE
(7/24)

Lenore J. Cowen

Department of Computer Science
177 College Avenue
Tufts University
Medford, MA 02155

Tel. (617) 627-2225
Email1: cowen@cs.tufts.edu
Email2: lenore.cowen@tufts.edu
URL: <http://cs.tufts.edu/~cowen/>

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)
- Joint Appointment, Tufts Graduate School in Biomedical Science (6/20–present)
- Associate Professor, Dept. of CS, Tufts University (6/01–6/09)
- Joint Appointment, Tufts Dept. of Mathematics (1/04–present)
- Visiting Scientist, Center for Genomic Regulation, Barcelona, Spain (9/14–6/15)
- 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

- **ISCB Fellow**(2023)
- **SIAM Fellow** (2023)
- **CRA-E Undergraduate Research Faculty Mentoring Award** (2020)
- **NCWIT Undergraduate Research Mentoring Award** (2020)
- **Best Performer: DREAM Disease Gene Module Identification Challenge**, to Tufts “Team Tusk” (Fall 2016)
- **BetaWrap declared one of the top ten Contributions of the year by NIH’s NIGMS** (2001)
- **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).

JOURNAL 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.

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 spatial generalization of methods to predict protein fold superfamilies based on pairwise statistical dependencies yields the first 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 Pattern 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.
-Combine pairwise and HMM probabilities to better recognize structures that fold into beta-propellers; applied 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, “Format: 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. L. Cowen, T. Ideker, B. Raphael, and R. Sharan, “Network Propagation: A Universal Amplifier of Genetic Associations” *Nature Reviews Genetics*, 18: 551, 2017.

-Review article on network diffusion in biological networks.

25. S. Choobdar, M. Ahsen, J. Crawford, M. Tomasoni, T. Fang, D. Lamparter, J. Lin, B. Hescott, X. Hu, J. Mercer, T. Natoli, R. Narayan, A. Subramian, J. Zhang, G. Stolovitzky,

Z. Kutanlik, K. Lage, D. Slonim, J. Saez-Rodriguez, L. Cowen, S. Bergmann, and D. Marbach, "Assessment of Network Module Identification Across Complex Disease," *Nature Methods*, 16: 843-852, 2019.

-Describes our winning the DREAM disease module challenge

26. J. Baskaran, A. Weldy, J. Guarin, G. Munoz, P. Shpilker, M. Kotik, N. Subbiah, A. Wishart, Y. Peng, M. Miller, L. Cowen and M. Oudin, "Cell Shape, and not 2D Migration, Predicts Extracellular Matrix-Driven 3D Cell Invasion in Breast Cancer," *APL Bioengineering*, 4: 026105, 2020.

27. K. Devkota, J. Murphy and L. Cowen, "GLIDE: Combining Local Methods and Diffusion State Embeddings to Predict Missing Interactions in Biological Networks," *Bioinformatics*, 36 (S1), pp. i464-i473, 2020.

-Link prediction in biological networks

28. J. Lazarsfeld, J. Rodriguez, M. Erden, Y. Liu, and L. Cowen, "Majority Vote Cascading: A Semi-Supervised Framework for Improving Protein Function Prediction," *IEEE/ACM Transactions in Computational Biology and Bioinformatics*, in press, doi: 10.1109/TCBB.2021.3059812, 2021.

-Special issue, Best papers in ACM BCB 2019. Also won "Best Poster" at the conference

29. S. Sledzieski, R. Singh, L. Cowen and B. Berger, "Sequence-Based Prediction of Protein-Protein Interactions: An Integrative Deep Learning Model," *Cell Systems*, 12, pp. 1-14, 2021.

- Cell Systems Special Issue of Best Papers in RECOMB 2021.

30. V. Arsenescu, K. Devkota, M. Erden, P. Shpilker, M. Werenski and L. Cowen, "MUNDO: Protein Function Prediction Embedded in a Multi-species World," *Bioinformatics Advances* vbab025, 2021.

-Co-embedding PPI networks for 2 species into a shared space improves protein function prediction beyond pointwise homologous functional annotation transfer.

31. K. Devkota, H. Schmidt, M. Werenski, J.M. Murphy, M. Erden, V. Arsenescu, and L. Cowen. "GLIDER: Function Prediction from GLIDE-based Neighborhoods," *Bioinformatics* 3395-3406, 2022.

-GLIDE-style embeddings improve protein function prediction

32. L. Cowen and H. Putnam, "Bioinformatics of Corals: Investigating Heterogeneous Omics Data from Coral Holobionts for Insight Into Reef Health and Resilience," *Annual Review of Biomedical Data Science* 5:205-231, 2022

-Review article that surveys the current state of the field, and approaches to understand coral stress

33. R. Singh, K. Devkota, S. Sledzieski, B. Berger and L. Cowen, "Topsy-Turvy: Integrating a Global View into Sequence-Based PPI Prediction," *Bioinformatics* 38 (Suppl. 1), i254-i272, 2022

-Augmented D-SCRIPT with training information from global PPI organization. Presented at ISMB 2022

34. L. Kumar, N. Brenner, S. Sledzieski, M. Olaosebikan, L.M. Roger, M. Lynn-Goin, R. Klein-Seetharaman, B. Berger, H. Putnam, JK Yang, N. Lewinski, R. Singh, N. Daniels, L. Cowen, J. Klein-Seetharaman, "Transfer of Knowledge from Model Organisms to Evolutionarily Distant Non-Model Organisms: The Coral *Pocillopora damicornis* membrane signaling receptome," *PLOS One*, 10.1371/journal.pone.0270965, 2023

-Do corals see, taste and smell? Comparative genomics with human proteins helps answer these questions

35. S. Sledzieski, K. Devkota, R. Singh, L. Cowen and B. Berger, "TT3D: Leveraging precomputed protein 3D sequence models to predict protein-protein interactions," *Bioinformatics*, 39(11). btad663, 2023.

-Improving Topsy-Turvy when 3D structure is available by adding backbone confirmation information from the Foldseek 3Di string

36. R. Singh, S. Sledzieski, B. Bryson, L. Cowen, and B. Berger, “Contrastive learning in protein language space predicts interactions between drugs and protein targets.” *Proceedings of the National Academy of Sciences*, 120(24), p.e2220778120, 2023.

-Adding a contrastive piece to a pre-trained language model yields state of the art rapid drug-target interaction prediction

37. J. Asheby, H. McKelvie, J. Freeman, P. Shpilker, L. Zane, D. Becker, L. Cowen, R. Richmond, V. Paul, F. Seneca and H. Putnam, “Characterizing transcriptomic responses to sediment stress across location and morphology in reef-building corals,” *PeerJ*, 12, e16654, 2024.

-Differentially expressed genes in two corals experiments in response to sediment stress

38. M. Hosahalli, S. Murthy, P. Jasbi, W. Lowe, L. Kumar, M. Olaosebikan, L. Roger, J. Yang, N. Lewinski, N. Daniels, L. Cowen, J. Klein-Seetharaman, “Insulin signaling and pharmacology in humans and in corals,” *PeerJ*, 12, e16804, 2024.

-Remote homology finds ancient insulin pathway genes in corals

39. K. Devkota, A. Blumer, X. Hu, L. Cowen, “Approximate IsoRank for Scalable and Functionally Meaningful Cross-Species Alignments of Protein Interaction Networks,” *Journal of Computational Biology*, in press, 2024

-Invited to special issue, best papers in Recomb 2024

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.

20. J. Lin, L. Cowen, B. Hescott, and X. Hu, “Computing the Diffusion State Distance on Graphs Via Algebraic Multigrid and Random Projections,” *Numerical Linear Algebra with Applications*, 25: e2156, 2018.

-Speeds up computation of the approximate DSD metric for large networks.

21. L. Cowen, K. Dekota, X. Hu, J. Murphy and K. Wu, “Diffusion State Distances and Multitemporal Analysis, Fast Algorithms, and Applications to Biological Networks” *SIAM Journal on Mathematics of Data Science*, 3: 142-170, 2021.

-Mathematical theory applied to DSD finds clustering structure across scales

22. C. Ratigan and L. Cowen, “The VOROS: Lifting ROC curves to 3D to summarize unbalanced classifier performance,” *Submitted for publication*, 2024

-Introduces volume over the ROC surface to measure competing binary classifier performance in face of uncertainty about class imbalance and cost

SELECTED INTERDISCIPLINARY DATA SCIENCE PAPERS

1. M. Olaosebikan, C. Aranda Barrios, B. Kolawole, L. Cowen and O. Shaer, “Identifying Cognitive and Create Support Needs for Remote Scientific Collaboration using VR: Practices, Affordances, and Design Implications,” *Creativity and Cognition*, 97-110, 2022.

-Exploring the needs of scientists studying rich multi-modal data meeting in VR.

2. N. Rabb, L. Cowen, J.P. deRuiter, M. Scheutz, “Cognitive Cascades: How to Model (and Potentially Counter) the Spread of Fake News,” *PLOS One*, **17**: e0261811, 2022.

-Adds a model of individual cognitive dissonance on top of standard network propagation models.

3. P. Shpilker, J. Freeman, H. McKelvie, J. Ashley, J.-M. Fonticella, H. Putnam, J. Greenberg, L. Cowen, A. Couch, N. Daniels, “MEDFORD: A Human and Machine Readable Markup Language,” *Database* baac065, 2022.

-Produced a new system for recording metadata that is both human and machine readable. Conference version in MTSR 2021

4. N. Rabb, L. Cowen and J.P. deRuiter, “Investigating the effect of selective exposure, audience fragmentation, and echo-chambers on polarization in dynamic media ecosystems,” *Applied Network Science*, 8(1), 78, 2024.

- In the Special Issue of the 11th International Conference on Complex Networks and their Applications

VOLUMES EDITED

1. Lenore J. Cowen (Ed), “Research in Computational Molecular Biology,” Proceedings of the 23rd Annual International Conference, Recomb 2019, May 2019, Washington DC. Springer Nature Switzerland, AG 2019, Lecture Notes in Bioinformatics Series, LNBI 11467.

PROFESSIONAL ACTIVITIES

Journal Editorial Boards

Editorial Board Member, Data Science in Science (Taylor & Francis), 2022-Present

Editorial Board Member, Bioinformatics (Oxford University Press), 2019-Present

Editorial Board Member, IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB), 2017-present

Editorial Board member, SIAM Review, January 2008–2013

Editorial Board member, SIAM Journal on Discrete Mathematics, January 2003–2012

Conference Technical Program Committee Service

Organizing Committee Co-Chair, 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2024)

Conference Co-Chair, SIAM Conference on Applied and Computational Discrete Algorithms (ACDA 2023)

Program Committee Chair, 23rd Annual International Conference on Research in Computational Molecular Biology (RECOMB 2019)

Conference Co-Chair: 7th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2017), Cambridge, MA, 8/2017.

Conference Chair, SIAM Discrete Math Conference 6/2012

Co-Chair, 2008 SIAM Annual Meeting

Program Committee Member ISMB and ECCB/ISMB: 2012-2023; co-chair of Protein Structure and Function Track, ISMB, 2012, 2013 and 2016; co-chair of Applied Bioinformatics Track, 2014, co-chair of Macromolecular Structure and Function Track, 2019 and 2020, co-chair of General Bioinformatics, 2023.

Program Committee member, RECOMB 2020-2023, 2014-2018 and 2010-2012.

Program Committee Member, WABI, 2010-2014, 2020-2022

Program Committee Member, Workshop on Mechanism Design for Social Good (MD4SG 19-20).

Organizing Committee Member, SIAM Annual Meeting (2017 and 2009)

Program Committee Member, co-chair of Protein and RNA Structure Track, ACM BCB 2012 and 2013, Programming Committee 2015-2016, 2021.

Program Committee member, SODA 2008

Program Committee member, ICALP 2008

Professional Society Service

Faculty Mentor, CSGrad4US Fellowship Program, Computing Research Association, 2021-present

Chair, Dénes König Prize Selection Committee, 2022

Vice Chair, SIAM Activity Group in Discrete Mathematics, 2021-2022, 2013-2015

Member, Dénes König Prize Selection Committee, 2020

Member, ISCB Ethics and Professional Conduct Committee, 2020

Chair, Dénes König Prize Selection Committee, 2008 and 2016

Chair, George Pólya Prize Selection Committee, 2012

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
- ICRS International Coral Reef Society

COURSES TAUGHT AND EDUCATIONAL ACTIVITIES: LAST 10 YEARS

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

GRADUATE STUDENT THESIS SUPERVISION

Christopher Ratigan (Ph.D. in progress, Tufts Mathematics) Dissertation Topic: Geometric measures of classifier performance

Mert Erden (Ph.D. in process, Tufts)
Dissertation Topic: Deep Learning for Molecular Structure and Function

Polina Shpilker (Ph.D. in progress, Tufts)
Dissertation Topic: The MEDFORD Metadata language for scientific data

Nicholas Rabb (Ph.D. May 2024, Tufts)
Dissertation Title: Modeling Media Influence on the Formation of Misinformed Attitudes

Kapil Devkota (Ph.D. August 2023, Tufts)
Dissertation Title: Computational Methods for the Prediction and Analysis of Protein-Protein Interaction Networks

Monsurat Olaosebikan (Ph.D. May 2023, Tufts)
Dissertation Title: Designing Immersive Tools for Supporting Remote Scientific Collaboration and Learning
Note: Co-advised by Orit Shaer

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

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.

Current pre-quals Ph.D. students: Faith Ocitti, Weiwei Lou.

Supervise 3-6 Undergraduate Research students each year. Undergraduate research students have gone on to be NSF graduate fellowship winners (Max Leiserson, Emily Mower, Shilpa Nadimpalli, Jonathan Rodriguez) and honorable mentions (Nathan Palmer).

UNIVERSITY SERVICE: LAST 10 years

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

- Undergraduate Admissions and Financial Aid Committee 2009-2012, 2023
- Tenure and Promotion Committee 2013-2014
- Committee on Undergraduate Advising and Co-Curricular Learning, 2019-2020
- Health Professions Recommendation Committee, 2017-2020
- Committee on Committees 2011-2016, 2018-2022 (chair, 2018-2020)
- DISC Faculty Advisory Committee, 2019-present
- Cummings Building Art Committee, 2020-2022

Departmental Service:

- Tufts Computer Science Colloquium organizer 2008-2011, Fall 2018.
- Chair, Computer Science Graduate Admissions 2010-2014
- Admissions director, MS in Computer Science 2017-2020, 2021-2023
- Core faculty, Tufts Programs in Data Science 2018-present
- Faculty advisor, Tufts ACM-W Chapter 2018-2022

FEDERAL GRANT REVIEW COMMITTEE SERVICE: LAST 10 years

NIH Study Section Review:

- BDK U24 Data Discovery Index Coordination Panel 5/2014
- NIH Member Conflict Panel 7/2018
- NSF/NIH Panel Supporting Research at the Interface of DMS/NIGMS 1/2019
- ZMH1 ERB-L BRAIN Initiative Review 10/2022
- ZMH1 ERB-G BRAIN Initiative Review 9/2023

NSF Panel Service:

- NSF GRFP Graduate Fellowship and CSGrad4US Fellowship Panels (Multiple Years)
- Serve on 1-3 NSF panels/year in BIO, DMS, CISE, and joint NSF/NIH panels

GRANTS AND CONTRACTS: LAST 10 years

Mining Multi-Layer Protein-Protein Association Networks: An Integrated Spectral Approach, \$210,000 (2018-2022). NSF DMS grant, with Xiaozhe Hu (Tufts Mathematics). Role: PI.

Harnessing Data Advances in Systems Biology to Design A Biological 3D Printer: The Synthetic Coral, NSF DIRSE-IL HDR grant, \$1,500,000 (Tufts portion: \$260,081), Judith Klein-Seetheraman, Colorado School of Mines (PI). (2019-2022) Role: coPI (Tufts PI).

HDR Tripods: Building the Theoretical Foundation for a Data-Intensive Studies Center, NSF HDR grant, \$1,500,000. With Misha Kilmer (Tufts Mathematics), Eric Miller (Tufts ECE), Kathleen Fisher and Bert Huang (Tufts CS). (2019-2023) Role: PI

REU Site: DIAMONDS: Directed and Mentored Opportunities in Data Science, NSF CISE REU grant, \$404,206. Ellise LaMotte, Tufts University (PI). (2022-2024) Role: coPI