

BIOGRAPHICAL SKETCH: CHRIS WIGGINS

PROFESSIONAL PREPARATION

Columbia College	Math/Physics	B.A. 1993
Princeton University	Theoretical Physics	Ph.D. 1998
Courant Institute, NYU	Biomathematics	1998-2001

APPOINTMENTS

2006-	Associate Professor, Department of Applied Physics and Applied Mathematics, and Center for Computational Biology and Bioinformatics (C2B2), Columbia University
2001-2006	Assistant Professor, Department of Applied Physics and Applied Mathematics, and Center for Computational Biology and Bioinformatics (C2B2), Columbia University
1998-2001	Assistant Professor/Courant Instructor, Courant Institute, NYU
1998-2001	NSF Mathematical Sciences Foundation Postdoctoral Research Fellow
1998	Visiting Postdoctoral Researcher, Institut Curie, Physico-Chimie Curie, Paris
1993-1998	Graduate student, Princeton University, Department of Physics

EDUCATION ACTIVITIES: COURSES TAUGHT

Columbia	2001-present	Introduction to Biophysical Modeling
	2003-present	Junior Seminar: problems in applied mathematics
	2003-present	Senior Seminar: problems in applied mathematics
NYU	Spring, 2001	Mathematical Neuroscience
	Fall, 2000	Chaos and Dynamical Systems
	Spring, 2000	Ordinary Differential Equations
	Fall, 1999	Linear Algebra

DISTINCTIONS

1989-1993	I. I. Rabi Scholar, Columbia College
1998-2001	NSF DMS Postdoctoral Research Fellow, Courant Institute, NYU
2007	Janette and Armen Avanesians Diversity Award (selected by Columbia SEAS undergraduates)

SYNERGISTIC ACTIVITIES

1. Workshop and Conference organizing:

- (i) "The facts of life: data-driven approaches to systems biology" (mini-symposium, APS march meeting, 2005);

- (ii) Co-organizer: “Machine Learning Approaches for Understanding Gene Regulation” (DIMACS workshop, 2005);
 - (iii) Co-organizer: Eighth Annual Japanese-American Beckman Frontiers of Science Symposium, 2005 (U.S. National Academy of Sciences/JSPP);
 - (iv) Co-organizer: DIMACS Conference on Networks January 2007;
 - (v) Co-organizer: The Boulder School for Condensed Matter and Materials Physics, July 2007.
 - (vi) Track Chair, IEEE EMBC 2006
 - (vii) Program Committee, The 2008 SIAM International Conference on Data Mining
2. Open source code available: InfoMod, MatStat, and NetBoost (all 3 through sourceforge.net); GeneClass, Robust-GeneClass, and MEDUSA (though www.cs.columbia.edu/compbio)
 3. Seminars/Colloquia Organized: “Applied Math Lab Seminar,” and “Genomics Journal Club” (NYU; 1999-2000); “Colloquium in Applied Mathematics” (Columbia; 2001-2003)
 4. Education – New courses: Mathematical Neuroscience with MATLAB (NYU); Biophysical Modeling (Columbia; textbook in development at <http://q-bio.myftp.org>). Curricular development: assisted development of computational biology PhD via Columbia’s C2B2.
 5. Extended visits at workshops both nationally and internationally, including (i) Institute for Theoretical Physics, June 1997; (ii) Institut Curie, May→October, 1998; (iii) Cargese Institute, July 1998; (iv) Hahn-Meitner Institut, Berlin 2001 (supported by INT01-07284); (v) Les Houches, July 2001; (vi) Institute for Theoretical Physics, Spring 2002; (vii) Kavli Institute for Theoretical Physics, Spring 2003; (viii) Aspen Center for Physics, August 2003; (ix) IPAM, UCLA, May 2006; (x) Stanford iCME, March 2007; and (xi) Boulder Center for Theoretical Physics, July 2007.
 6. Nontraditional training: Advised ten VIGRE undergraduates in projects involving machine learning/network classification (summer 2003), and information theory/spectral (graph theoretic) approaches to dimensionality reduction (summer 2004), with results published and presented at national and international conferences; advised four high school students in the Intel Science Competition, including a coauthor

PUBLICATIONS

1. Andrew Mugler, Etay Ziv, Ilya Nemenman, Chris H. Wiggins. Form, Function, and Information Processing in Small Stochastic Biological Networks. *IET Systems Biology (formerly IEE Proceedings - Systems Biology)*, 2008. To appear.
2. Chris H. Wiggins. Biological Modularity: Functional, Topological, and Statistical. *IET Systems Biology (formerly IEE Proceedings - Systems Biology)*, 2008. To appear.

3. A. Crut, D. A. Koster, R. Seidel, C. H. Wiggins, N. H. Dekker. Fast dynamics of supercoiled DNA revealed by single-molecule experiments. *Proc Natl Acad Sci U S A.*, 104(29):11957–62. Epub 2007 Jul 10., Jul 17 2007.
4. Lawrence David, Chris H. Wiggins. Benchmarking of Dynamic Bayesian Networks Inferred From Stochastic Time-Series Data. *Annals of The New York Academy of Sciences*, 2007. In press.
5. Benjamin J. Dubin-Thaler, Jake M. Hofman, Harry Xenias, Ingrid Spielman, Anna V. Shneidman, Lawrence A. David, Hans-Gunther Dobereiner, Chris H. Wiggins, Michael P. Sheetz. Quantification of Cell Movement Reveals Distinct Types of Edge Motility During Cell Spreading. 2007. Submitted.
6. Amy Rebecca Gansell, Irene K. Tamaru, Aleks Jakulin, Chris H. Wiggins. Predicting Regional Classification of Levantine Ivory Sculptures: A Machine Learning Approach. 2007. Submitted; coauthors include undergraduate; paper grew out of student project in seminar course taught by PI.
7. Jake M. Hofman, Chris H. Wiggins. A Bayesian Approach to Network Modularity. 2007. URL <http://arxiv.org/abs/0709.3512>.
8. Anshul Kundaje, Steve Lianoglou, Xuejing Li, David Quigley, Marta Arias, Chris H. Wiggins, Li Zhang, Christina Leslie. Learning regulatory programs that accurately predict differential expression with MEDUSA. *Annals of The New York Academy of Sciences*, 2007. In press.
9. T. N. Sims, T. J. Soos, H. S. Xenias, B. Dubin-Thaler, J. M. Hofman, J. C. Waite, T. O. Cameron, V. K. Thomas, R. Varma, C. H. Wiggins, M. P. Sheetz, D. R. Littman, M. L. Dustin. Opposing effects of PKC θ and WASp on symmetry breaking and relocation of the immunological synapse. *Cell.*, 129(4):773–85, May 18 2007.
10. Etay Ziv, Ilya Nemenman, Chris H. Wiggins. Optimal Signal Processing in Small Stochastic Biochemical Networks. *PLoS ONE*, 2(10):e1077, Oct 2007. URL <http://dx.doi.org/10.1371/journal.pone.0001077>.
11. A. S. Ada-Nguema, H. Xenias, Jake M. Hofman, Chris H. Wiggins, M. P. Sheetz, P. J. Keely. The small GTPase R-Ras regulates organization of actin and drives membrane protrusions through the activity of PLC- ϵ . *J Cell Sci.*, page 4364.<http://jcs.biologists.org/cgi/content/full/119/20/4364>, Apr 1 2006.
12. Y. Cai, N. Biais, G. Giannone, M. Tanase, G. Jiang, J. M. Hofman, C. H. Wiggins, P. Silberzan, A. Buguin, B. Ladoux, M. P. Sheetz. Nonmuscle myosin IIA-dependent force inhibits cell spreading and drives F-actin flow. *Biophys J.*, 91(10):3907–20. Epub 2006 Aug 18., Nov 15 2006.
13. H. G. Dobereiner, B. J. Dubin-Thaler, J. M. Hofman, H. S. Xenias, T. N. Sims, G. Giannone, M. L. Dustin, C. H. Wiggins, M. P. Sheetz. Lateral membrane waves constitute a universal dynamic pattern of motile cells. *Phys Rev Lett.*, 97(3):038102. Epub 2006 Jul 20., Jul 21 2006.
14. Daniel A. Koster, Chris H. Wiggins, Nynke H. Dekker. Multiple events on single molecules: Unbiased estimation in single-molecule biophysics. *Proc Natl Acad Sci U S A.*, 104:1750–1755, 2006.
15. A. Kundaje, M. Middendorf, M. Shah, C. H. Wiggins, Y. Freund, C. Leslie. A classification-based framework for predicting and analyzing gene regulatory response. *BMC Bioinformatics.*, 7 Suppl 1:S5., Mar 20 2006.

16. A. A. Margolin, I. Nemenman, K. Basso, C. Wiggins, G. Stolovitzky, Dalla R. Favera, A. Califano. ARACNE: an algorithm for the reconstruction of gene regulatory networks in a mammalian cellular context. *BMC Bioinformatics.*, 7 Suppl 1:S7., Mar 20 2006.
17. Tobias Munk, Oskar Hallatschek, Chris H. Wiggins, Erwin Frey. Dynamics of semiflexible polymers in a flow field. *Physical Review E*, 74(4):041911, 2006. Selected for the October 30, 2006 issue of Virtual journal of Nanoscale Science & Technology.
18. Anshul Kundaje, Manuel Middendorf, Feng Gao, Chris Wiggins, Christina Leslie. Combining sequence and time series expression data to learn transcriptional modules. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(3):194–202, Jul-Sep 2005. ISSN 1545-5963. doi:[bibinfo{doi}{http://dx.doi.org/10.1109/TCBB.2005.34}](http://dx.doi.org/10.1109/TCBB.2005.34). URL <http://www1.cs.columbia.edu/compbio/module-clust/>.
19. M. Middendorf, E. Ziv, C. H. Wiggins. Inferring network mechanisms: the *Drosophila melanogaster* protein interaction network. *Proc Natl Acad Sci U S A.*, 102(9):3192–7. Epub 2005 Feb 22., Mar 1 2005. q-bio/0408010, URL <http://www.pnas.org/cgi/content/abstract/102/9/3192>.
20. Manuel Middendorf, Anshul Kundaje, Mihir Shah, Yoav Freund, Chris H. Wiggins, Christina S. Leslie. Motif discovery through predictive modeling of gene regulation. In Satoru Miyano, editor, *Proceedings of Ninth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2005), special "Lecture notes in Bioinformatics" from Springer-Verlag*, volume 3500, pages 538–552. Springer, 2005. 39 papers are accepted from 217 submissions.
21. Manuel Middendorf, Anshul Kundaje, Chris Wiggins, Yoav Freund, Christina Leslie. Predicting genetic regulatory response using classification: Yeast stress response. *Regulatory Genomics*, 3318:1–13, 2005. Proceedings of the First Annual RECOMB Regulation Workshop 2004, q-bio/0406016.
22. E. Ziv, R. Koytcheff, M. Middendorf, C. Wiggins. Systematic identification of statistically significant network measures. *Phys Rev E Stat Nonlin Soft Matter Phys.*, 71(1 Pt 2):016110. Epub 2005 Jan 10., Jan 2005. Selected for the January 15, 2005 issue of Virtual journal of Biological Physics Research; coauthors include undergraduates advisees, cond-mat/0306610.
23. E. Ziv, M. Middendorf, C. H. Wiggins. Information-theoretic approach to network modularity. *Physical Review E*, 71(4 Pt 2):046117. Epub 2005 Apr 14., Apr 2005. Selected for the April 15, 2005 issue of Virtual journal of Biological Physics Research, q-bio/0411033.
24. Y. Bohbot-Raviv, W. Z. Zhao, M. Feingold, C. H. Wiggins, R. Granek. Relaxation dynamics of semiflexible polymers. *Phys Rev Lett.*, 92(9):098101. Epub 2004 Mar 3., Mar 5 2004.
25. Adam A. Margolin, Ilya Nemenman, Chris Wiggins, Gustavo Stolovitzky, Andrea Califano. On the Reconstruction of Interaction Networks with Applications to Transcriptional Regulation. 2004. Presented at the NIPS'04 Computational Biology Workshop, q-bio/0410036.
26. Manuel Middendorf, Anshul Kundaje, Chris Wiggins, Yoav Freund, Christina Leslie. Predicting Genetic Regulatory Response Using Classification. *Bioinformatics*, 20(suppl. 1):i232–240, 2004. Proceedings of the Twelfth International Conference on Intelligent Systems for Molecular Biology (ISMB 2004); long paper presentation, totals: 67 long and short papers accepted (14%), 496 submitted., q-bio/0411028.

27. Manuel Middendorf, Etay Ziv, Carter Adams, Jen Hom, Robin Koytcheff, Chaya Levovitz, Gregory Woods, Linda Chen, Chris Wiggins. Discriminative Topological Features Reveal Biological Network Mechanisms. *BMC Bioinformatics*, 5:181, Nov 22 2004. [q-bio/0402017](#).
28. J. P. Bennett, C. H. Wiggins. A Computational Study of Mixing Microchannel Flows. 2003. [cond-mat/0307482](#).
29. Chris H. Wiggins, Alberto Montesi, Matteo Pasquali. The stochastic spectral dynamics of bending and tumbling. 2003. [cond-mat/0307551](#).
30. Chris H. Wiggins, Ilya Nemenman. Process Pathway Inference via Time Series Analysis. *Journal of Experimental Mechanics*, 43:361–370, 2003. [physics/0206031](#).
31. Chris H. Wiggins, Loic Le Goff. Biopolymer Dynamics. In A. Deutsch, M. Falcke, J. Howard, W. Zimmermann, editors, *Function and Regulation of Cellular Systems: Experiments and Models*. Birkhaeuser-Verlag, 2002.
32. A. Belmonte, M. J. Shelley, S. T. Eldakar, C. H. Wiggins. Dynamic patterns and self-knotting of a driven hanging chain. *Phys Rev Lett.*, 87(11):114301. Epub 2001 Aug 24., Sep 10 2001.
33. Chris H. Wiggins. Biopolymer mechanics: stability, dynamics, and statistics. *Mathematical Methods in the Applied Sciences*, 24:1325–1335, 2001.
34. Chris H. Wiggins. Darboux's Frame and Schrodinger's Equation for Biopolymers. In M. Deville, R. Owens, editors, *Sixteenth IMACS World Congress 2000 on Scientific Computation, Applied Mathematics, and Simulation*. 2000. ISBN 3-9522075-1-9.
35. T. R. Powers, R. E. Goldstein, Chris H. Wiggins. Supercoiling Bacterial Filaments. In H. Frauenfelder, G. Hummer, R. Garcia, editors, *Biological Physics: Third International Symposium*, page 271. 1999.
36. Raymond E. Goldstein, Thomas R. Powers, Chris H. Wiggins. The Viscous Nonlinear Dynamics of Twist and Writhe. *Physical Review Letters*, 80:5232–5235, 1998. [cond-mat/9802084](#).
37. Chris H. Wiggins, Raymond E. Goldstein. Flexive and Propulsive Dynamics of Elastica at Low Reynolds numbers. *Physical Review Letters*, 80:3879–3882, 1998. [cond-mat/9707346](#).
38. Chris H. Wiggins, Daniel X. Riveline, Albrecht Ott, Raymond E. Goldstein. Trapping and Wiggling: Elastohydrodynamics of Driven Microfilaments. *Biophysical Journal*, 74(2 Pt 1)(2):1043–1060, Feb 1998. [cond-mat/9703244](#).
39. D. Riveline, Chris H. Wiggins, A. Ott, Raymond E. Goldstein. Elastohydrodynamic study of actin filaments using fluorescence microscopy. *Physical Review E*, 56:R1330–R1333, 1997. [cond-mat/9704225](#).
40. Chris Wiggins, M. Spiegelman. Magma Migration and magmatic solitary waves in 3D. *Geophysical Research Lett.*, 22:1289–1292, 1995. Cover figure; research completed while undergraduate (with support of I. I. Rabi Scholars program, Columbia University).
41. E. O'Brien, M. Bennett, V. Cherniatin, C. Y. Chi, A. Chikanian, B. Dolgoshein, S. Kumar, D. Lissauer, S. McCorkle, J. T. Mitchell, S. Nagamiya, V. Polychronakos, K. Pope, W. Sippach, H. Takai, M. Toy, D. Wang, Y. F. Wang, C. Wiggins, W. Willis. A Transition Radiation Detector which Features Accurate Tracking and dE/dx Particle Identification. *IEEE Transactions on Nuclear Science*, 40:153–157, 1993.

ADDITIONAL PUBLICATIONS

1. *Quantitative Biology: An Introductory Tour*. 2008. In development, <http://q-bio.myftp.org>
2. “Bayes’ theorem”, *Scientific American Online* 2006 <http://tinyurl.com/y28wlo>
3. “Ask the experts: Bayes’ theorem” *Scientific American*, April 2007, p.108

COLLABORATORS

Andrea Califano, Columbia; Linda Chen, Ohio; Riccardo Dalla Favera, Columbia; Nynke Dekker, Tu-Delft; Yoav Freund, UCSD; Rony Granek, Weizmann; Christina Leslie, MSKCC; Ilya Nemenman, LANL; Michael Sheetz, Columbia; Gustavo Stolovitzky, IBM;

ADVISING: CURRENT STUDENTS

1. Jacob Hofman: Expected PhD 2008. Applications of machine learning in network and image data.
2. Xuejing Li: Expected PhD 2009. Applications of machine learning for inferring predictive models of transcriptional regulatory networks from high-throughput biological datasets
3. Anil Raj: Expected PhD 2010. Applications of information theory for the analysis and organization of biological networks.
4. Andrew Mugler: Expected PhD 2010. Applications of information theory for relating topology and function in small biological networks.

ADVISING: PREVIOUS STUDENTS

1. Etay Ziv: MD/PhD student; 5 papers authored; first author on 3. Recipient of DOE and DOD (Krell CSGF) Fellowships. PhD 2006. Biological networks. Dissertation selected by unanimous vote of the committee for dean’s distinction.
2. Manuel Middendorf: 8 papers authored; first author on 5. PhD awarded 2005. Biological applications of machine learning. Currently at Psychogenics.
3. Robin Koytcheff: 2 papers authored; BS awarded 2005. Currently at Stanford (Math)
4. Lawrence David: 2 papers authored; BS awarded 2005. Currently at MIT (Computational and systems biology)

CURRENT SUPPORT

Project/Proposal Title: QSB: optimal information processing in biological networks

PI: Chris Wiggins

Source of Support: National Science Foundation

Total Award Amount: \$ 310,490

Total Award Period Covered: 09/01/04 - 08/31/07

Location of Project: Columbia University

Person-Months Per Year Committed to the Project

Cal: 1.00 Acad: 0.00 Sumr: 0.00

Goals: Theoretical and computational study of the relationships between, and constraints imposed by, the topology of biological networks and their biological functions

Responsibilities: Computational simulation of small genetic networks; discriminative classification of network topologies

Project/Proposal Title: MAGNET: a National Center for Biomedical Computation

PI: Andrea Califano

Source of Support: National Institutes of Health

Total Award Amount: \$ 18,500,000

Total Award Period Covered: 07/01/06 - 06/30/11

Location of Project: Columbia University

Person-Months Per Year Committed to the Project

Cal: 1.00 Acad: 0.00 Sumr: 0.00

Goals: Develop a national center for biomedical computation, centering on biological networks

Responsibilities: Co-PI

Project/Proposal Title: Genetic network inference with combined phenotypes

PI: Andrea Califano

Source of Support: National Institutes of Health, National Cancer Institute

Total Award Amount: \$1,179,208

Total Award Period Covered: 07/01/2003 - 06/30/2007

Location of Project: Columbia University

Person-Months Per Year Committed to the Project: Cal: 0.00 Acad: 0.00 Sumr: 1.00

Goals: Develop mathematical tools for the inference and analysis of biological networks from cancer-relevant microarray experiments performed at Columbia's Center for Computational Biology and Bioinformatics

Responsibilities: Co-PI

Project/Proposal Title: NanoMedicine Center for Mechanical Biology

PI: Michael Sheetz
Source of Support: National Institutes of Health, NIH Roadmap initiative
Total Award Amount: \$7,711,900
Total Award Period Covered: 09/30/2005 - 09/29/2010
Location of Project: Columbia University
Person-Months Per Year Committed to the Project: Cal: 0.00 Acad: 0.00 Sumr: 1.00
Goals: Develop strategies to alter the cellular level responses to correct defects, and define the role of mechanical force in the functional regulation of interconnected protein networks, which is crucial to systems biology.
Responsibilities: Co-PI

Project/Proposal Title: Temporal Transcriptomes of TBI and OGD for Dissemination

PI: Barclay Morrison
Source of Support: NINDS
Total Award Amount: \$100,000
Total Award Period Covered: 09/01/2006-08/31/2008
Location of Project: Columbia University
Person-Months Per Year Committed to the Project: Cal: 0.00 Acad: 0.00 Sumr: 0.00
Goals: Develop tools to build predictive and interpretable models of the cascade of genetic responses to traumatic brain injury based on expression data
Responsibilities: Co-PI

Project/Proposal Title: III-CXT: Learning from graph-structured data

PI: Christina Leslie
Source of Support: National Science Foundation
Total Award Amount: \$788,325
Total Award Period Covered: 09/01/2007-08/31/2010
Location of Project: Columbia University
Person-Months Per Year Committed to the Project: Cal: 0.00 Acad: 0.00 Sumr: 1.00
Goals: Develop new algorithms for modeling physical interactions in cellular networks
Responsibilities: Co-PI

INVITED PRESENTATIONS BY YEAR SINCE 2001

multiple mentions indicate multiple seminars in the same year

2008: Cornell Med (NYC)

2007: IBM, Temple University, Boulder Summer School, DIMACS Workshop on Networks and Applications (Coorganizer), Chicago Physics, Stanford, Berkeley, UCSF, NYU Med (Skirball institute), NIH All Hands meeting, Gulbenkian Institute, Columbia (Physics), Columbia (Inverse Problems Workshop), NetSci07, Siam Dynamical Systems Meeting, Interface 2007 (Philadelphia), Linnaeus Centre for Bioinformatics (Uppsala Sweden), University of Maryland, IPAM, LANL q-bio summer school and conference, SciFoo conference, Columbia University (APAM seminar), IHP (Paris)

- 2006:** CSHL, Columbia University (SPS– Physics), TTI-Chicago, UCSB, Harvard, Stanford, Princeton (Biophysics Seminar), Cambridge (DAMTP), Imperial College London, Arnold Sommerfeld Center (Ludwig-Maximilians-Universitat Munchen), Columbia University (APAM seminar)
- 2005:** Nehru University (Delhi), Kitano Systems Biology Institute (Tokyo), The Genome Institute of Singapore, ASIT (Tokyo), University of Tokyo, Genopole (France), CMU, University of Hawaii, University of Hawaii, University of Hawaii, IBM, Columbia University, NYU, Columbia University, Yale, Rutgers, Columbia University (APAM seminar)
- 2004:** UCSB, California Institute of Technology, Columbia University, Princeton, Brandeis, Columbia University, Columbia University, NYU, Princeton, Columbia University, Columbia University, NJIT, LLNL
- 2003:** Duke, Rockefeller University, NYU, Manhattanville College, IBM
- 2002:** Princeton, Columbia University (BME), Columbia University, Rutgers
- 2001:** NYU, Northwestern, Columbia University, NJIT, Rutgers, Columbia University, Sarah Lawrence