

CURRICULUM VITAE

Jeffrey H. Chuang, Ph. D.

Contact Information

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Professional appointments

9/2012 - : Associate Professor, Jackson Laboratory for Genomic Medicine, Farmington, CT.
2/2014 - : Associate Professor, University of Connecticut Health Center, Department of Genetics and Developmental Biology, Farmington, CT.
8/2014 - : Member, University of Connecticut Institute for Systems Genomics, Farmington, CT.
2005 – 8/2012: Assistant Professor, Department of Biology, Boston College, Chestnut Hill, MA.
2001 - 2005: Postdoctoral fellow, Department of Biochemistry and Biophysics, University of California, San Francisco, CA. Advisor: Hao Li.

EDUCATION

Ph. D. Massachusetts Institute of Technology (1996-2001) in Physics. Thesis title: Energy and Topology of Heteropolymers. Advisors: Alexander Grosberg, Toyochi Tanaka and Mehran Kardar
B.A. Harvard University (1992-1996) in Chemistry and Physics *summa cum laude*.

Individual Fellowships and Awards

National Science Foundation Postdoctoral Fellowship in Interdisciplinary Informatics, UCSF (2003-2005).
National Institutes of Health Biochemistry Postdoctoral Training Grant Recipient, UCSF (2001-2002).
National Science Foundation Graduate Fellowship, MIT (1997-1999).
American Association for the Advancement of Science Mass Media Fellowship (1997).
Karl Taylor Compton Graduate Fellowship for Theoretical Physics, MIT (1996-1997).
Phi Beta Kappa, Harvard University (1996).
National Science Scholar (1992-1996)

PROFESSIONAL SERVICE

Ad-hoc Journal Reviewer. PLoS Biology, PLoS Genetics, PLoS ONE, Bioinformatics, Genome Research, Genome Biology, Molecular Biology and Evolution, G3, Genome Biology and Evolution, Nucleic Acids Research, BMC Cancer, BMC Genomics, BMC Genetics, Journal of Cellular Biochemistry, Journal of Chemical Physics, Journal of Chromatography B, Physical Review E.

Professional Associations. New York Genome Center: Scientific and Clinical Steering Committee 2015- Present. American Association for Cancer Research, Human Genome Organization, International Society for Computational Biology, Society for Molecular Biology and Evolution, American Association for the Advancement of Science, Genetics Society of America, Sigma Xi Research Honor Society, American Physical Society.

Grant review panels

2017. Reviewer for National Cancer Institute Moonshot Initiative: R33 Integration and Validation of Emerging Technologies for Cancer Research.

2017. Ad-hoc reviewer for Genome Quebec -- Large-Scale Applied Research Project Competition: Genomics and Precision Health
2017. Reviewer for National Cancer Institute Special Emphasis Panel: U01 Cancer Target Discovery and Development Network.
2016. Ad-hoc reviewer for Netherlands Organisation for Scientific Research (NWO).
2016. Ad-hoc reviewer for U.S. Department of Veterans Affairs
2010. Panel Reviewer for NSF Postdoctoral Fellowship in Biological Informatics
2007. Ad-hoc reviewer for National Science Foundation DBI: Biological Databases and Informatics Cluster
2007. Ad-hoc reviewer for National Science Foundation MCB: Genes and Genome Systems Cluster
2007. Ad-hoc reviewer for NSF-sponsored Bioinformatics Education module at Oakland University

Conference organization

2018. PDXNet Consortium-wide Meeting, organizer.
2015. JAX-BIDMC Workshop on RNA Biology, faculty co-organizer.
2013. JAX-UCONN/BECAT/UCHC Joint Workshop on Computational Biology and Bioinformatics, conference co-organizer.
2009. Society of Molecular Biology and Evolution Conference, symposium organizer and session chair (Molecular Evolution of Functional Noncoding Sequences).
2007. New England Association of Parasitologists Meeting, conference co-organizer.
2007. Society of Molecular Biology and Evolution Conference, session chair (Methods in Comparative Genomics).
2006. Boston Area Pathogen and Vector Encounter, conference co-organizer.
2004. Biopathways Consortium at ISMB. Network evolution and regulatory networks, panel discussion member.

DEPARTMENTAL SERVICE – JACKSON LABORATORY FOR GENOMIC MEDICINE

JAX Scientific Advisory Council. Two year elected member of faculty group advising senior leadership on faculty concerns (2016-2018). Co-led faculty evaluations of JAX Computational Sciences and Graduate Admissions.

JAX Computational Sciences and Information Technology. Faculty advisor (2015-). Interviewed and evaluated many computational scientist and software engineer candidates (2012-present). Informal mentorship for several members of these teams. UCHC/Yale/JAX data center planning committee.

JAX Machine Learning Interest Group. Council member (2016-).

Research-oriented Data Management and Analysis Committee (2015-). Committee member.

Postdoc/Predoc Training Committee (2012-). Helped design new JAX postdoc scholars program. Reviewed applications. Committee chair (2016-).

Chair of Graduate Admissions for JAX-GM (2014-). Reviewed graduate admissions. Coordinated with UCHC and JAX education office to expand and develop program. Member of UCHC Genetics and Genome Sciences Graduate Committee. Member of UCHC MD/PhD Admissions Committee.

University of Connecticut Institute for Systems Genomics (2014-). Scientific steering committee.

Faculty Search Committees (2012-). Host for numerous faculty searches for JAX-GM. Additional review of multiple JAX bioinformatics candidates. Guest member for UCHC

Developmental Biology and Genetics search committee (2014). Computational/Systems Genomics search committee (2014-2015). JAX cancer domain review committee (2016-).

JAX Vice-President for Education Search Committee (2017-). Developed search criteria and interviewed candidates.

JAX Cancer Center Member (2013-). Contributions to multiple aspects of patient derived xenograft data analysis projects, including subtype classification, tumor/stromal interactions, and heterogeneity analysis. **Computational Sciences Co-Project Lead for Cancer Center Grant (2016-).**

Website Redesign Committee (2012-15). Provided faculty input for JAX website redesign and website vendor selection.

JGM Genomics Journal Club (2013-2014). Initiated and managed the first scheduled journal club / discussion group at JGM.

Research Grant Review Committee (2014). Internal JAX reviewer for research grant applications.

DEPARTMENTAL SERVICE - BOSTON COLLEGE

Biology Graduate Committee (2005 - 2012). Reviewed all applications to the Ph.D. and Masters programs in biology, including email, phone, video, and/or face-to-face interviews with all bioinformatics applicants. Co-designed the bioinformatics and biology admissions materials. Biology Graduate Student Technology Grant competition co-organizer.

Bioinformatics Curriculum Development Committee (2005-2012). Managed the course requirements for both the undergraduate and graduate students studying bioinformatics. Led an overhaul of the graduate requirements in 2009. Partnered with Computer Science and Math faculty to revise the undergraduate bioinformatics concentration in 2009 and 2010.

Academic Technology Fund (2006 – 2012). Biology department committee chair. Managed funds for the procurement of core resources and computer equipment for faculty and staff. Faculty Technology Contact (2006-2012). Member of committee to re-organize technology consultants for the sciences (2008).

Boston College High Performance Computing Committee (2007 – 2012). Biology representative for management of the university-wide computing cluster scorpio.bc.edu.

Bioinformatics Faculty Search Committee. Member for searches in 2007, 2010. Ad-hoc interviewer for faculty candidates in Chemistry Department (2008).

Biology Department External Review (2006-2007). Junior faculty development committee.

Biology Department Research Retreat (2007). Co-organizer.

Infectious Disease Group (2005-2007). Co-organizer of monthly intradepartmental seminars, paper discussions, etc.

Biology Department Computational Management: Co-manager of Jason Persampieri, scientific programmer (2006-2008). Co-manager of Tony Schreiner, Ph.D., UNIX system administrator (2006-2012).

FUNDING HISTORY

Current Grants

Agency: NIH
Title: Data Coordination Center for PDX Net (U24 CA224067-01)
Dates: 09/01/2017-08/30/2022
Role: PI (co-PI: Brandi-Davis Dusenbery, Seven Bridges Genomics)

Agency: NIH
Project Title: (PQ3) Cellular and Molecular Mechanisms Driving Myeloid Compartment Variation in Human Triple Negative Breast Cancer (R01 CA219880-01)
Dates: 09/01/2017 – 07/31/2022
Role: co-PI (PI: Palucka)

Agency: NIH
Title: Identification of Genomic Causes of Morphological Heterogeneity within Tumors (Genomics Data Commons supplement)
Dates: 09/01/2017-08/30/2018
Role: PI

Agency: JAX Scientific Services Innovation Fund
Title: Develop an Easy to Use Interface to Launch omics-Seq Analytics Pipelines & Visualize the Results
Dates: 2/1/2017-10/31/2017
Role: co-PI (PIs: Karuturi, Beane)

Agency: JAX Director's Innovation Fund
Title: Computational methods for comparing genomic structural ensembles
Dates: 8/1/2016-7/31/2018
Role: PI

Agency: NIH / NHGRI
Title: Big Genomic Data Skills Training for Professors (R25, EB022365)
Dates: 09/30/2015-06/30/2018
Role: PI

Agency: NIH / NINDS
Title: Ribosome Dysfunction in Neurological Disorders (R01, NS094637)
Dates: 09/01/2015-08/31/2020
Role: Co-PI (PI: Ackerman, UCSD)

Agency: NIH/NCI
Title: Dissection of Tumor Evolution Using Patient-Derived Xenografts (R21, CA191848)
Dates: 07/01/15-06/30/17 (extended through 6/30/2018)
Role: PI

Completed Grants

Agency: JAX Cancer Center
Title: Computing Phenotypically Important Immune Cell Populations from Tumor RNA-seq Data
Dates: 9/1/2016-8/31/2017
Role: PI (co-PI: Palucka)

Agency: NIH / NHGRI
Title: Big Genomic Data Skills Training for Professors - Supplement (R25, EB022365-02S1)
Dates: 08/01/2016-06/30/2017
Role: PI

Agency: Southwest Oncology Group
Title: Genomic Analysis of Inflammatory Breast Cancer
Dates: 01/01/2016-12/31/2016 (extension requested to 6/30/2017)
Role: Co-PI (Additional Co-PI's: Pusztai and Gerstein, Yale)

Agency: NIH/NCI
(PQB5) Epigenetic Drivers of Hematopoietic Stem Cell Transformation (R21, CA184851)
Dates: 05/05/14-04/30/16 (extended through 4/30/2017)
Role: Co-PI (PI: Trowbridge)

Agency: NIH
Title: Combinatorial RNA Structural Features That Control RNA-Protein Binding (R21, HG007554)
Dates: 01/25/2014 – 12/31/2015 (extended through 12/31/2016).
Role: PI

Agency: NIH/NCI
Title: TCGA-based Validation of a Mutation Filtering Pipeline for Accurate Resolution of Tumor Heterogeneity (R21, CA191848-01A1S1, Supplement to support evaluation of the NCI Cancer Genomics Cloud Pilots).
Dates: 02/03/2016-06/30/2016
Role: PI

Agency: JAX Cancer Center Pilot Project Fund
Title: Targeting Tumor Heterogeneity with Orthogonal Cell State-Specific Drugs
Dates: 11/01/2013-10/31/2014
Role: Collaborator

Agency: JAX-GM Interactive Fund
Title: Differential expression of isodecoder tRNAs in the mammalian brain
Dates: 9/2013-8/2015
Role: co-PI

Agency: JAX-GM Interactive Fund
Title: Epigenetic and Transcriptional Responses to Environmental Stresses
Dates: 9/2013-8/2015
Role: co-PI

Agency: National Science Foundation
Title: Computational and Experimental Approaches to Characterizing Noncoding Selection in Coding Sequences (EF-0850155)
Dates: 8/15/2009-7/31/2012 (extended through 7/2013).
Role: PI

Agency: PhRMA Foundation Informatics Starter Grant
Title: Deciphering Malaria Gene Regulation through Comparative Genomics
Dates: 1/01/08-12/31/09
Role: PI

Agency: National Science Foundation
Title: Computational Comparative Genomic Approaches to Identifying Functional and Neutral DNA (Research Starter Grant DBI-0708206)
Dates: 7/01/07-6/30/08
Role: PI

Agency: National Institutes of Health

Title: Role of Conserved Non-Coding Elements in Vertebrate Brain Development (R21
HD051835)
Dates: 7/01/2006 – 6/30/2008
Role: Consultant (PI : Guo, UCSF)

PUBLICATIONS

Journal Articles

40. SARNaClust: Semi-Automatic Detection of RNA Protein Binding Motifs From Immunoprecipitation Data. Ivan Dotu, Scott Adamson, Benjamin Coleman, Cyril Fournier, Emma Ricart-Altimiras, Eduardo Eyras, and **Jeffrey H Chuang**. *PLoS Comput Biol* 14 (3): e1006078. (2018)
39. Alterations in the Rho pathway contribute to Epstein-Barr virus-induced lymphomagenesis in immunosuppressed environments. Sung-Yup Cho, Chang Ohk Sung, Jeesoo Chae, Jieun Lee, Deukchae Na, Wonyoung Kang, Jinjoo Kang, Seoyeon Min, Ahra Lee, Eunhye Kwak, Jooyoung Kim, Boram Choi, Hyunsoo Kim, **Jeffrey H. Chuang**, Hyo-Kyung Pak, Chan-Sik Park, Sanghui Park, Young Hyeoh Ko, Dakeun Lee, Jin Roh, Min-Sun Cho, Seongyeol Park, Young Seok Ju, Yun-Suhk Suh, Seong-Ho Kong, Hyuk-Joon Lee, James Keck, Jacques Banchereau, Edison T. Liu, Woo-Ho Kim, Hansoo Park, Han-Kwang Yang, Jong-Il Kim and Charles Lee. *Blood* 131:1931-1941 (2018).
38. Mutations in DNA repair genes are associated with increased neo-antigen load and activated T cell infiltration in lung adenocarcinoma. Young Kwang Chae, Jonathan F. Anker, Preeti Bais, Sandeep Namburi, Francis J. Giles and **Jeffrey H. Chuang**. *Oncotarget*. 2018; 9:7949-7960 (2017).
37. Uncertainties in tumor allele frequencies limit power to infer evolutionary pressures. Javad Noorbakhsh and **Jeffrey H. Chuang**. *Nature Genetics* 49, 1288–1289 doi:10.1038/ng.3876 (2017).
36. CloudNeo: A cloud pipeline for identifying patient-specific tumor neoantigens. Preeti Bais, Sandeep Namburi, Daniel M. Gatti, Xinyu Zhang, **Jeffrey H. Chuang**. *Bioinformatics*, doi: 10.1093/bioinformatics/btx375 (2017).
35. Activation of GCN2 by Ribosome Stalling Links Translation Elongation with Translation Initiation. Ryuta Ishimura, Gabor Nagy, Ivan Dotu, **Jeffrey H. Chuang**, and Susan Ackerman. *eLife* 10.7554/eLife.14295. (2016)
34. The Tandem Duplicator Phenotype as a distinct genomic configuration associated with therapeutic response in cancer. Francesca Menghi, Koichiro Inaki, Xing Yi Woo, Pooja A. Kumar, Krzysztof R. Grzeda, Ankit Malhotra, Hyunsoo Kim, Eladio J. Marquez, Duygu Ucar, Phung T. Shreckengast, Joel P. Wagner, R. Krishna Murthy Karuturi, James Keck, **Jeffrey H. Chuang**, and Edison T. Liu. *PNAS* 113:17 E2373-E2382 (2016).
33. Genetic Architectures of Quantitative Variation in RNA Editing Pathways. Tongjun Gu, Daniel M. Gatti, Anuj Srivastava, Elizabeth M. Snyder, Narayanan Raghupathy, Petr Simecek, Karen L. Svenson, Ivan Dotu, **Jeffrey H. Chuang**, Mark P. Keller, Alan D. Attie, Robert E. Braun, and Gary A. Churchill. *Genetics* 202:787-798 (2016).
32. Identification of Tumor Subtypes of Endometrial Carcinoma by Integration of Heterogeneous Datasets. Kim H, Bredel M, Park H, **Chuang JH** (2015) *J Med Diagn Meth* 4:189 (2015). doi: 10.4172/2168-9784.1000189
31. Loss of Tumor Suppressive MicroRNA-31 Enhances TRADD/NF- κ B Signaling in Glioblastoma. Rajani Rajbhandari, Braden McFarland, Ashish Patel, G Gray, Samuel Fehling, Markus Bredel, Nicolas Berbari, Hyunsoo Kim, Margaret Marks, Gordon Meares, Tanvi Sinha, **Jeffrey H Chuang**, Etty Benveniste, and Susan Nozell. *Oncotarget* 6:17085 (2015).
30. Functional chromatin features are associated with structural mutations in cancer. Krzysztof R Grzeda, Beryl Royer-Bertrand, Koichiro Inaki, Hyunsoo Kim, Axel M Hillmer, Edison T Liu, **Jeffrey H Chuang**. *BMC Genomics* 15: 1013 (2014).

29. Ribosome stalling induced by mutation of a CNS-specific tRNA causes neurodegeneration. Ryuta Ishimura, Gabor Nagy, Ivan Dotu, Huihao Zhou, Xiang-Lei Yang, Paul Schimmel, Satoru Senju, Yasuharu Nishimura, **Jeffrey H. Chuang**, and Susan L. Ackerman. *Science* 345: 455–459 (2014).
28. Dynamics of the ethanolamine glycerophospholipid remodeling network. Lu Zhang, Kourosh Zarringhalam, Norberto Diaz-Diaz, and **Jeffrey H. Chuang**. *PLoS ONE* 7(12): e50858 (2012).
27. Integrating chemical footprinting data into RNA secondary structure prediction. Kourosh Zarringhalam, Michelle Meyer, Ivan Dotu, **Jeffrey H. Chuang**, and Peter Clote. *PLoS ONE* 7(10): e45160. (2012).
26. Statistical analysis of the processes controlling choline and ethanolamine glycerophospholipid molecular species composition. Kourosh Zarringhalam, Lu Zhang, Michael A Kiebish, Kui Yang, Xianlin Han, Richard W Gross, and **Jeffrey H. Chuang**. *PLoS ONE* 7(5): e37293 (2012).
25. Transcriptional Enhancers in Protein-Coding Exons of Vertebrate Developmental Genes Deborah I Ritter, Zhiqiang dong, Su Guo, and **Jeffrey H. Chuang**, *PLoS ONE* 7(5): e35202 (2012).
24. CodingMotif: Determination of Overrepresented Nucleotide Motifs in Coding Sequences. Yang Ding, William Lorenz, and **Jeffrey H. Chuang**. *BMC Bioinformatics* 13:32 (2012). *“Highly Accessed Article.”*
23. Expression Divergence Measured by Transcriptome Sequencing of Four Yeast Species. M.A. Busby, J. Gray, A.M. Costa, D. Stewart, M. Stromberg, D. Barnett, **Jeffrey H. Chuang**, M. Springer, G.T. Marth. 2011. *BMC Genomics* 12:635 (2011). *“Highly Accessed Article.”*
22. A mathematical model for the determination of steady-state cardiolipin remodeling mechanisms using lipidomic data. L. Zhang, R.J.A. Bell, M. A. Kiebish, T. N. Seyfried, X. Han, R. Gross, and **Jeffrey H. Chuang**. *PLoS ONE* 6:e21170 (2011).
21. The Importance of Being Cis: Evolution of Orthologous Fish and Mammalian Enhancer Activity. D. I. Ritter, Q. Li, D. Kostka, K. S. Pollard, S. Guo and **Jeffrey H. Chuang**. *Molecular Biology and Evolution* 27:2322 (2010). *Highlighted on the Nature Molecular Systems Biology Blog.*
20. A molecular-imprint nanosensor for ultrasensitive detection of proteins. D. Cai, L. Ren, H. Zhao, Chenjia Xu, L. Zhang, Y. Yu, H. Wang, Y. Lan, M. F. Roberts, **Jeffrey H. Chuang**, M. J. Naughton, Z. Ren and T. C. Chiles. *Nature Nanotechnology* 5:597 (2010). *Highlighted on Nature Chemistry and Nature Methods.*
19. Dynamic simulation of cardiolipin remodeling: Greasing the wheels for an interpretative approach to lipidomics. M. A. Kiebish, R. Bell, K. Yang, T. Phan, Z. Zhao, W. Ames, T. N. Seyfried, R. W. Gross, **Jeffrey H. Chuang**, and X. Han. *J. Lipid Res.* 51:2153 (2010).
18. A systematic approach to identify functional motifs within vertebrate developmental enhancers. Q. Li, D. Ritter, N. Yang, Z. Dong, H. Li, **Jeffrey H. Chuang**, S. Guo. *Developmental Biology* 337:484 (2010).
17. COMIT: Identification of Noncoding Motifs under Selection in Coding Sequences. D. Kural, Y. Ding, J. Wu, A. M Korpi, **Jeffrey H. Chuang**. *Genome Biology* 10:R133 (2009).

16. The effect of Plasmodium falciparum Sir2a histone deacetylase on clonal and longitudinal variation in expression of the var family of virulence genes. C. J. Merrick, R. Dzikowski, H. Imamura, **Jeffrey Chuang**, K. Deitsch, M. T. Duraisingh. *Int J Parasitol.* 40:35 (2009).
15. Weak preservation of local neutral mutation rates across mammalian genomes. H. Imamura, J. E. Karro and **Jeffrey H. Chuang**. *BMC Evolutionary Biology* 9:89 (2009).
14. Cardiolipin and electron transport chain abnormalities in mouse brain tumor mitochondria: Lipidomic evidence supporting the Warburg theory of cancer. M. A. Kiebish, X. Han, H. Cheng, **Jeffrey H. Chuang** and T. N. Seyfried. *Journal of Lipid Research*, 49:2545 (2008). *Cover article.*
13. cneViewer: A Database of Conserved Noncoding Elements for Studies of Tissue-Specific Gene Regulation. J. Persampieri, D. I. Ritter, D. Lees, J. Lehoczky, Q. Li, S. Guo, and **Jeffrey H. Chuang**. *Bioinformatics*, 24:2418 (2008).
12. Brain Mitochondrial Lipid Abnormalities in Mice Susceptible to Spontaneous Gliomas. M.A. Kiebish, X. Han, H. Cheng, **Jeffrey H. Chuang**, and T.N. Seyfried. *Lipids* 43:951 (2008).
11. Measuring the Prevalence of Regional Mutation Rates: An Analysis of Silent Substitutions in Mammals, Fungi, and Insects. A.K. Fox, B.B. Tuch, and **Jeffrey H. Chuang**. *BMC: Evolutionary Biology* 8:186 (2008). *“Highly accessed article.”*
10. Lipidomic Analysis and Electron Transport Chain Activities in C57BL/6J Mouse Brain Mitochondria. M.A. Kiebish, X. Han, H. Cheng, A. Lunford, C.F. Clarke, H. Moon, **Jeffrey H. Chuang**, and T.N. Seyfried. *Journal of Neurochemistry* 106:299 (2008).
9. Sequences Conserved by Selection across Mouse and Human Malaria Species. H. Imamura, J. Persampieri, and **Jeffrey H. Chuang**. *BMC: Genomics* 8:372 (2007).
8. Similarity of Synonymous Substitutions Rates Across Mammalian Genomes. **Jeffrey H. Chuang** and H. Li. *Journal of Molecular Evolution* 65:236 (2007).
7. Genome-wide Regulatory Complexity in Yeast Promoters: Separation of Functional and Neutral Sequence. C.S. Chin, **Jeffrey H. Chuang**, and H. Li. *Genome Research*, 15:205 (2005).
6. Functional Bias and Spatial Organization of Genes in Mutational Hot and Cold Regions in the Human Genome. **Jeffrey H. Chuang** and H. Li. *PLoS Biology*, 2(2):e29 (2004). *Faculty of 1000 highlighted article.*
5. Anomalous Dynamics of Translocation. **Jeffrey Chuang**, Y. Kantor, and M. Kardar. *Physical Review E* 65:011802 (2001).
4. Effect of Reversible Cross-linker, N,N'-Bis(acryloyl)-cystamine, on Calcium Ion Adsorption by Imprinted Gels. H. Hiratani, C. Alvarez-Lorenzo, **Jeffrey Chuang**, O. Guney, A. Yu.Grosberg, and T. Tanaka. *Langmuir* 17:4431 (2001).
3. Free Energy Self-Averaging in Protein-Sized Heteropolymers. **Jeffrey Chuang**, A. Yu. Grosberg, and M. Kardar. *Physical Review Letters* 87:078104 (2001).
2. Frustrations in Polymer Gels and Their Minimization through Molecular Imprinting. T. Enoki, K. Tanaka, T. Watanabe, T. Oya, T. Sakiyama, Y. Takeoka, K. Ito, G. Wang, M. Annaka, K. Hara, R. Du, **Jeffrey Chuang**, K. Wasserman, A. Yu. Grosberg, S. Masamune, and T. Tanaka. *Physical Review Letters* 85:5000 (2000).
1. Topological Repulsion between Polymer Globules. **Jeffrey Chuang**, A. Yu. Grosberg, and T. Tanaka. *Journal of Chemical Physics* 112:6434 (2000).

Reviews

2. Multiple Contact Adsorption of Target Molecules by Heteropolymer Gels. K. Ito, **Jeffrey Chuang**, C. Alvarez-Lorenzo, T. Watanabe, N. Ando, and A. Yu. Grosberg. *Macromolecular Symposia* 207:1 (2004).

1. Multiple point adsorption in a Heteropolymer Gel and the Tanaka Approach To Imprinting: Experiment and Theory. K. Ito, **Jeffrey Chuang**, C. Alvarez-Lorenzo, T. Watanabe, N. Ando, and A. Yu. Grosberg. *Progress in Polymer Science*, 28:1489 (2003).

Book chapters

1. Smart Polymers: Applications in Biotechnology and Biomedicine, Second Edition. Chapter title: Imprinting Using Smart Polymers. C. Alvarez-Lorenzo, A. Concheiro, **Jeffrey Chuang** and A. Yu. Grosberg. CRC Press: Boca Raton (2007).

SOFTWARE AND ONLINE RESOURCES DEVELOPED

11. PDXNet Data Commons and Coordination Center.

We are working with Seven Bridges to develop a large data and computational workflow resource for the NCI PDXNet.

<https://www.pdxnetwork.org>

10. SARNaClust: Semi-Automatic Detection Of RNA Protein Binding Motifs From Immunoprecipitation Data (Dotu et al 2018).

<https://github.com/idotu/SARNaClust>

9. CloudNeo – A cloud pipeline for identifying patient-specific tumor neoantigens. (Bais et al 2017).

<https://github.com/TheJacksonLaboratory/CloudNeo>

8. DLipid – Software to identify lipid remodeling pathways from lipidomic data (developed for Zhang et al 2012).

<http://nbidiaz.github.com/DLipid/>

7. CodingMotif – Software to identify overrepresented motifs important for post-transcriptional regulation of genes (developed for Ding et al 2011).

<http://bioinformatics.bc.edu/chuanglab/codingmotif.tar>

6. Cardiolipin Remodeling Simulator – Software to simulate the process by which the population of acyl chains evolves in lipids. This software allows one to test mechanistic hypotheses using lipidomic data (developed for Kiebish et al 2010).

<http://bioinformatics.bc.edu/~jchuang/dynamic.html>

5. COMIT – Software for the identification of noncoding motifs under selection in coding sequences (developed for Kural et al 2009).

<http://bioinformatics.bc.edu/chuanglab/COMIT/COMIT-v.0.02012010.tar.gz>

4. cneViewer – A database of conserved noncoding elements for studies of tissue-specific gene expression (developed for Persampieri et al 2008).

<http://bioinformatics.bc.edu/chuanglab/cneViewer/>

3. cneBrowser – A database of experimentally validated conserved noncoding elements in the zebrafish genome (developed for Ritter et al 2010 and Li et al 2009).

<http://bioinformatics.bc.edu/chuanglab/cneBrowser/>

2. Malaria Conserved Noncoding Sequences – A database of sequences under purifying selection across rodent and human malaria species (developed for Imamura et al 2007).

<http://bioinformatics.bc.edu/chuanglab/malaria/malaria.html>

1. Yeast Conserved Noncoding Sequences – A database of sequences under purifying selection across the *sensu stricto* yeasts (developed for Chin et al 2005).

<http://genome.ucsf.edu/YeastReg/>

PRESENTATIONS

Invited Talks and Seminars

75. Evolutionary Dynamics of Response to Chemotherapies in Breast Cancer Xenografts. International Society for Evolution, Ecology and Cancer Conference. Tempe, AZ. December 2017.
74. Sequencing the genome to fight cancer. Public outreach for Connecticut high school students. Farmington, CT. Oct 2017 (invited).
73. Patient-derived xenograft computational biology workshop. JAX Cancer Course. Bar Harbor, ME. August 2017 (invited).
72. Intratumoral evolution of breast cancer. JAX Scientific Symposium. Bar Harbor, ME. May 2017 (invited).
71. Interpreting tumor heterogeneity using the Cancer Genomics Cloud. American Medical Informatics Association Joint Summits on Translational Science. San Francisco, CA. March 2017 (invited).
70. Intratumoral evolution of breast cancer in response to therapy. Columbia University Medical School. New York, NY. January 2017 (invited).
69. Intratumoral evolution of breast cancer in response to therapy. Pompeu Fabra University. Barcelona, Spain. December 2016 (invited).
68. Intratumoral evolution of breast cancer in response to therapy. University of Connecticut Health – Center for Molecular Medicine. Farmington, CT. October 2016 (invited).
67. Resolving Tumor Heterogeneity Using the Cancer Genomics Cloud. American Association for Cancer Research Conference. New Orleans, LA. April 2016 (invited).
66. Training Undergraduates in Big Data Genomics. University of Illinois. Urbana-Champaign, IL. April 2016 (invited).
65. Comparing sequence data from related tumors and xenografts. JAX Cancer Interest Group. The Jackson Laboratory for Genomic Medicine. Farmington, CT. January 2016.
64. Subclonal Selection in Patient-Derived Xenografts. JAX faculty retreat. Northport, ME. October 2015.
63. Computational Approaches to Tumor Heterogeneity. JAX Cancer Center External Advisory Board Meeting. Farmington, CT. August 2015.
62. Computational Approaches to Tumor Heterogeneity. JAX group visit to Bristol Myers Squibb. Princeton, NJ. June 2015.
61. Measures and Models of Tumor Evolution. JAX Scientific Director's Series. Farmington, CT. May 2015.
60. Evolution in Cancer Genomes. University of Connecticut Health Center, Department of Genetics and Genome Sciences. Farmington, CT. April 2015.
59. Patient-Derived Xenograft Genomics. Center for Quantitative Medicine / Jackson Laboratory for Genomic Medicine. Farmington, CT. January 2015.

58. Genomic Approaches to Tumor Heterogeneity Using Patient-Derived Xenografts. University of Connecticut Health Center – Center for Vascular Biology. Farmington, CT. December 2014 (invited).
57. Mechanism of a Translational Regulatory Defect Leading to Neurodegeneration. Rutgers University – Camden. Camden, NJ. December 2014 (invited).
56. Developing Individualized Cancer Therapies Using Patient Derived Xenografts. Leo & Anne Albert Institute for Bladder Cancer Care and Research 1st Annual Symposium. Hartford, CT. September 2014 (invited).
55. Genomic Approaches to Treating Breast Cancer. Connecticut Breast Health Initiative Seminar. New Britain, CT. August 2014 (invited).
54. Computational Challenges in Cancer Genomics. 23rd Annual Short Course on Experimental Models of Human Cancer. Bar Harbor, ME. August 2014 (invited).
53. Computational Studies in Cancer Genomics and Gene Regulation. University of Connecticut Institute for Systems Genomics Networking Workshop. Storrs, CT. May 2014 (invited).
52. Inferring Post-Transcriptional Regulatory Mechanisms from Genomics Data. Academia Sinica. Taipei, Taiwan. April 2014 (invited).
51. The PDX Model for Cancer Research. 6th Seoul Breast Cancer Symposium. Seoul, Korea. April 2014 (invited).
50. Solving Tumor Heterogeneity Using Patient-Derived Xenografts. Seoul National University Hospital. Seoul, Korea. April 2014 (invited).
49. Genomics of Evolving Xenografts. The Jackson Laboratory for Genomic Medicine - faculty seminar series. Farmington, CT. April 2014.
48. Mechanism of a Translational Regulatory Defect Leading to Neurodegeneration. University of Connecticut Department of Molecular and Cell Biology. Storrs, CT. April 2014 (invited).
47. New Approaches in Genomics and Bioinformatics at JAX-GM. Connecticut Children's Medical Center. Hartford, CT. March 2014 (invited).
46. Computational Approaches to Cancer Genomics. Connecticut College Workshop on Bridging the Gap Between Computer Science and the Life Sciences. New London, CT. January 2014 (invited).
45. Gene Regulation and Cancer Genomics. JAX/UCONN Workshop on Computational Biology. Storrs, CT. September 2013.
44. Integrating Chemical Footprinting Data into RNA Secondary Structure Prediction. Rutgers University Biological Physics Seminar Series. Piscataway, NJ. May 2013. (invited)
43. Gene Regulation and Cancer Genomics at JAX-GM. University of Connecticut Center for Cell Analysis and Modeling. Farmington, CT. February 2013. (invited)
42. The Prevalence of Hidden Functional Elements in Coding Regions. University of Connecticut Department of Cell and Genome Sciences. Farmington, CT. May 2012. (invited)
41. Statistical Approaches to Identifying Functional Elements in Coding Sequences. Harvard School of Public Health – Program in Quantitative Genomics. Boston, MA. April 2012. (invited)

40. Statistical Approaches to Identifying Functional Elements in Coding Sequences. Shanghai Jiao Tong University Bio-X Institute. Shanghai, China. April 2012. (invited)
39. The Functions of Enhancer Elements. Children's Hospital of Fudan University. Shanghai, China. April 2012. (invited)
38. Detecting Hidden Functional Elements in Coding Sequences. Genome Institute of Singapore. Singapore. March 2012. (invited)
37. Next Generation Sequencing and Its Applications to RNA Biology. Conference on Next Generation Sequencing Applications Asia. Singapore. March 2012. (invited)
36. The Prevalence of Hidden Functional Elements in Coding Regions. The Jackson Laboratory. Bar Harbor, ME. March 2012. (invited)
35. Computational Approaches to Identifying Functional Elements in Coding Sequences. Virginia Bioinformatics Institute at Virginia Tech. Blacksburg, VA. March 2012. (invited)
34. Computational Approaches to Identifying Functional Elements in Coding Sequences. Worcester Polytechnic Institute. Worcester, MA. February 2012. (invited)
33. Detecting Hidden Functional Elements in Coding Sequences. Michigan State University. East Lansing, MI. February 2012. (invited)
32. CodingMotif: Exact Determination of Overrepresented Motifs in Coding Sequences. Intelligent Systems for Molecular Biology Rocky Mountain Conference. Aspen, CO. December 2011.
31. Algorithms for Identifying Functional Elements in Coding Sequences. Miami University of Ohio. Miami, OH. December 2011. (invited)
30. The Prevalence of Hidden Functions in Coding Regions. National Institute of Environmental Health Sciences (NIH). Research Triangle Park, NC. November 2011. (invited)
29. Detecting Hidden Regulatory Functions in Coding Sequences. Virginia Commonwealth University. Richmond, VA. October 2011. (invited)
28. The Evolution of Enhancers in Vertebrate Coding Sequences. Presented at Stonehill College Biology Department. Easton, MA. September 2011. (invited)
27. Functional Elements in Vertebrate Coding Sequences. Presented at the Michigan State Summer Symposium on Transcriptional Dynamics, Evolution, and Systems Biology. East Lansing, MI. July 2011. (invited)
26. Whose Code Is It Anyway? Transcriptional Enhancers Are Embedded in Protein-Coding Exons of Vertebrate Developmental Genes. Presented at the Biology of Genomes Conference. Cold Spring Harbor Laboratory (talk given by lab student D. Ritter). May 2011.
25. Highly Conserved Coding Sequences Act as Enhancers. Presented at the RECOMB Satellite Meeting on Regulatory Genomics at Columbia University. New York, NY. November 2010.
24. Regulation, Evolution, and Networks: Some Insights from Computational Biology. Presented at the Boston College Biology Colloquium. Chestnut Hill, MA. October 2010.
23. Evolution of Orthologous Fish and Mammalian Enhancer Activity. Presented at the Society for Molecular Biology and Evolution Meeting. Lyon, France. July 2010.

22. Noncoding Selection on Motifs in Coding Regions. Presented at Dana Farber Cancer Institute, Boston, MA. June 2009. (invited)
21. Noncoding Selection on Motifs in Coding Regions. Presented at the Society for Molecular Biology and Evolution Meeting, Iowa City, Iowa. June 2009.
20. Comparative Analysis of Enhancers and Regulatory Motifs for Gene Expression in the Vertebrate Brain. Presented at the RECOMB Satellite Conference on Regulatory Genomics, Broad Institute of MIT and Harvard, Cambridge, MA. November 2008.
19. Sequences Conserved by Selection Across Mouse and Human Malaria Species. Presented at the Comparative Genomics of Malaria Parasites Meeting, American Museum of Natural History, New York, NY. September 2007. (invited)
18. Sequences Conserved by Selection Across Mouse and Human Malaria Species. Presented at the Society for Molecular Biology and Evolution Meeting, Halifax, Canada. June 2007.
17. Computational Identification of Malaria Gene Regulation. Presented at the New England Association of Parasitologists Meeting, Brown University, Providence, RI. November 2006.
16. Plasmodium Comparative Genomics and Gene Regulation. Presented at the Boston Pathogen and Vector Encounter, Boston College, Chestnut Hill, MA. July 2006. (invited, talk given by lab postdoc H. Imamura)
15. Selection in Synonymous Sites of Mammalian Genes. Presented at the Society for Molecular Biology and Evolution Meeting (Genomes, Evolution, and Bioinformatics), Tempe, AZ. May 2006.
14. Functional and Neutral Sequence in Genome Comparisons. Presented at Condensed Matter Theory Biophysics Seminar, Massachusetts Institute of Technology, Cambridge, MA. October 2005. (invited)
13. Insights from Comparative Genomics: From Genome Organization to Regulatory Complexity. Presented at CSAIL Computational Biology Seminar, Massachusetts Institute of Technology, Cambridge, MA. October 2005. (invited)
12. Computational Approaches to Comparative Genomics. Presented at Department of Physics Colloquium – Boston College, Chestnut Hill, MA. September 2005. (invited)
11. Insights from Comparative Genomics: From Genome Organization to Regulatory Complexity. Presented at New York University, Department of Biology, New York, NY. February 2005. (invited)
10. Insights from Comparative Genomics: From Genome Organization to Regulatory Complexity. Presented at Boston College, Department of Biology. Chestnut Hill, MA. February 2005. (invited)
9. Insights from Comparative Genomics: From Genome Organization to Regulatory Complexity. Presented at the Bauer Center for Genomics Research – Harvard University, Cambridge, MA. March 2005. (invited)
8. Insights from Comparative Genomics: From Genome Organization to Regulatory Complexity. Presented at Rice University, Department of Bioengineering, Houston, TX. March 2005. (invited)
7. Functional Significance of Spatial Variations in Mutation Rates: Mammals and Yeast.

Presented at the Intelligent Systems for Molecular Biology Workshop on Biopathways, Glasgow, Scotland. July 2004. (invited)

6. Functional Bias and Spatial Organization of Genes in Mutational Hot and Cold Regions in the Human Genome. Presented at the UCSF Research in Progress Seminar Series, San Francisco, CA. October 2003.

5. Multiple Point Adsorption in a Heteropolymer Gel and the Tanaka Approach to Imprinting. Presented at the Europolymer Conference, Gargnano, Italy. June 2002.

4. Entropic Slowdowns in Aggregation and Translocation of Biopolymers. Presented at the National Institute of Standards and Technology, Gaithersburg, Maryland. March 2001. (invited)

3. Free Energy Self-Averaging in Protein-Sized Random Heteropolymers. Presented at American Physical Society March Meeting, Seattle, WA. March 2001.

2. Free Energy Self-Averaging in Protein-Sized Random Heteropolymers. Presented at the 84th Statistical Mechanics Conference - Rutgers University, New Brunswick, NJ. December 2000.

1. Free Energy Self-Averaging in Protein-Sized Random Heteropolymers. Presented at the American Physical Society March Meeting, Minneapolis, Minnesota. March 2000.

Laboratory Personnel

| Name | Dates | Role | Subsequent Position |
|--------------------------|----------------------|-------------------------------------------------|----------------------------------------------------------------------------------------|
| Dr. Ada Zhan | 11/16- | Postdoc (joint with Y. Ruan) | |
| Dr. Minji Kim | 6/17- | Postdoc (joint with Y. Ruan) | |
| Dr. Javad Noorbakhsh | 1/15- | Postdoc; research scientist (as of 2017) | |
| Dr. Hyunsoo Kim | 1/13- | Research scientist | |
| Dr. Ziming Zhao | 2/17- | Research scientist | |
| Victor Wang | 7/17- | MD/PhD student | |
| Scott Adamson | 8/15- | PhD student (joint with B. Graveley) | |
| Sherry Zhang | 5/16-8/16, 6/17-8/17 | Student intern | Undergrad U. Connecticut |
| Smrithi Raman | 10/16-5/17 | Student intern | College at MIT |
| Lucas Melo | 6/17-8/17 | Summer intern | High school student |
| Aiszlyn Zupkus | 7/17-8/17 | Summer intern | High school student |
| Alex Iyabor | 6/16-8/16 | Summer intern | Undergrad, Stanford |
| Kathryn Rankin | 6/16-8/16 | Summer intern | |
| Victor Wang | 6/16-8/16 | Rotation student (joining as grad student 7/17) | |
| Benjamin Coleman | 6/15-8/15, 6/16-8/16 | Summer intern | High school student |
| Dr. Ivan Dotu | 9/12-6/17 | Visiting scientist | Startup company founder. |
| Dr. Houman Younessi | 8/14-12/15 | Visiting prof. | |
| Dr. Dong-Guk Shin | 12/14-12/15 | Visiting prof. | Professor, U. Conn. |
| Emma Ricart Altimiras | 3/15-8/15 | Research assistant. | Graduate student, ETH. |
| Cyril Fournier | 2/14-8/14 | Visiting masters student | |
| Meredith Shea | 6/14-8/14 | Summer intern | Undergraduate, Case Western |
| Jared Graveley | 6-8/13, 5/14-8/14 | Summer intern | Undergraduate, U. Conn. |
| Beryl Royer-Bertrand | 2/13-7/13 | Visit. masters stud. | PhD student, Universite de Lausanne |
| Dr. Krzysztof Grzeda | 11/12-6/15 | Research scientist | Bioinformatics consultant |
| Dr. Kourosh Zarringhalam | 6/10-8/12 | Postdoctoral | Asst Prof, UMass-Boston |
| Ningtao Shi | 2/11-6/12 | Masters student | Software consultant |
| David Gostine | 1/11-8/11 | Undergrad | |
| Lu Zhang | 2/08-6/12 | Ph.D. student | Scientist, Seven Bridges Genomics |
| Deborah Ritter | 4/07-9/11 | Ph.D. student | Postdoc, Wheeler Lab, Baylor College of Medicine |
| Norberto Diaz-Diaz | 7/11-10/11 | Visiting sci. | Asst. Prof., Universidad de Pablo de Olavide |
| Dr. Hideo Imamura | 3/06-12/08 | Postdoctoral | Inst. of Tropical Med.- Antwerp and Wellcome Trust Sanger Institute research scientist |
| Dr. Zehua Chen | 12/06-12/07 | Postdoctoral | Broad Institute of Harvard and MIT research scientist. |
| Dr. Jessica Lehoczky | 6/07-12/07 | Visit. Sci. | Harvard Medical School postdoc |
| Jason Persampieri | 12/06-6/08 | Programmer | Software engineer, Affinity Circles |
| Aleah Fox | 1/06-5/08 | Undergrad | UCSF Ph.D. student |
| Robert Bell | 9/06-7/09 | Undergrad | UCSF Ph.D. student (Winner, BC best senior biology thesis 2009) |
| Hwi Moon | 1/06-5/08 | Undergrad | Severance Hospital, Seoul, S. Korea |
| Alicia Korpi | 9/08-5/10 | Undergrad | U. S. Peace Corps |
| Toan Phan | 6/08-5/10 | Undergrad | Tufts U. pre-medical training |
| Daniel Lees | 6/06-8/06 | Undergrad | Technology consultant Exeter Group |
| Jeffrey Wang | 6/10-7/10 | Summer res. | Auburn H. S., Rockford, IL |
| Yuliana Tan | Fall 2017 | Rotation Student | |
| Victor Wang | Summer 2016 | Rotation Student | |
| Laura Urbanski | Summer 2015 | Rotation Student | |
| Scott Adamson | Summer 2015 | Rotation Student | |

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|-------------------|-------------|------------------|
| Bandita Adhikari | Fall 2015 | Rotation Student |
| Rohit Reja | Spring 2011 | Rotation Student |
| Shermin Pei | Fall 2010 | Rotation Student |
| Rashmi Dubey | Fall 2010 | Rotation Student |
| Ningtao Shi | Fall 2010 | Rotation Student |
| Mengyao Zhao | Fall 2009 | Rotation Student |
| Andrew Farrell | Fall 2009 | Rotation Student |
| Yi Qiao | Fall 2009 | Rotation Student |
| Deniz Kural | Fall 2008 | Rotation Student |
| Jiantao Wu | Fall 2008 | Rotation Student |
| Lu Zhang | Fall 2007 | Rotation Student |
| Yang Ding | Fall 2007 | Rotation Student |
| Genevieve Toutain | Summer 2007 | Rotation Student |
| Deborah Ritter | Spring 2007 | Rotation Student |
| Derek Barnett | Fall 2006 | Rotation Student |
| Michele Busby | Fall 2006 | Rotation Student |
| Aliz Axmann | Fall 2006 | Rotation Student |
| Michael Stromberg | Fall 2005 | Rotation Student |
| Didem Demirbas | Fall 2005 | Rotation Student |

Membership on Graduate Comprehensive Exam Committees

2006. Aaron Quinlan
2007. Michael Stromberg
2007. Didem Demirbas
2008. Derek Barnett
2008. Michele Busby
2008. Brooke Anderson-White
2009. Yang Ding
2010. Deniz Kural
2010. Amit Indap
2010. Jiantao Wu
2011. Mengyao Zhao
2011. Zeynep Akgoc
2014. Gopinath Rajadinakaran
2015. Jufen Zhu

Graduate research thesis committees

2006-2008 Aaron Quinlan (Ph.D.)
2007 Jayme Flynn (M.S.)
2007-2010 Michael Stromberg (Ph.D.)
2008 Michael Kiebish (Ph.D.)
2008 Manal Alamery (Ph.D.)
2008-2010 Yang Ding (M.S.)
2007-2011 Deborah Ritter (Ph.D.)
2008-2012 Lu Zhang (Ph.D.)
2010-2012 Ningtao Shi (M.S.)
2008-2012 Michele Busby (Ph.D.)
2008-2012 Derek Barnett (Ph.D.)
2010-2013 Amit Indap (Ph.D.)
2010-2014 Deniz Kural (Ph.D.)
2010-2012 Jiantao Wu (Ph.D.)
2010-2012 Chenjia Xu (Ph.D.)
2010-2012 Linh Ta (Ph. D.)
2015- Jufen Zhu (Ph.D.)
2014- Gopinath Rajadinakaran (Ph.D.)

Additional Mentoring

Summer 2010. Research Science Institute mentor. Mentored Jeffrey Wang, a student in the Research Science Institute summer program at MIT for advanced high school students. Guided entry of the project into the Siemens science competition.

Spring 2011. Outreach to the Pioneer Charter School of Science. As an education component of my NSF grant, I visited the Pioneer Charter School of Science (Everett, MA) to guest lecture on how to write about scientific topics (4/4/11) and to judge the science fair (4/15/11).

Courses Taught (Most courses at Boston College unless noted)

Undergraduate

BI420. Fall 2006. Introduction to Bioinformatics. Guest lecture on Computational Identification of Functional Sequences.

BI420. Fall 2007. Introduction to Bioinformatics. 15 students. 2.5 hours per week. Course co-taught with Prof. G. Marth, who taught a second section. 4 problem sets, 2 midterms, and a final presentation. Teacher rating 3.86 (Bio avg = 3.43)

BI420. Fall 2009. Introduction to Bioinformatics. 25 students. 2.5 hours per week. Course co-taught with Prof. G. Marth, who taught a second section. 3 problem sets, 2 midterms, and a final presentation. Teacher rating 4.00 (Bio avg = 3.49)

BI420. Spring 2011. Introduction to Bioinformatics. 39 students. 2.5 hours per week. 3 problem sets, 2 midterms, and a final presentation.

BI462. Spring 2006. Undergraduate Research. 2 students.

BI461. Fall 2006. Undergraduate Research. 3 students.

BI462. Spring 2007. Undergraduate Research. 3 students. Aleah Fox's research was honored by the Society of Molecular Biology and Evolution with a travel fellowship and poster presentation at SMBE 2007 in Halifax, Canada. It was also published in the BC undergraduate journal Elements.

BI461. Fall 2007. Undergraduate Research. 3 students.

BI462. Spring 2008. Undergraduate Research. 3 students. Aleah Fox wrote a senior thesis.

BI461. Fall 2008. Undergraduate Research. 3 students.

BI462. Spring 2009. Undergraduate Research. 3 students. Robert Bell wrote a senior thesis honored as the best in the BC Biology Department.

BI461. Fall 2009. Undergraduate Research. 2 students.

BI462. Spring 2010. Undergraduate Research. 2 students.

BI462. Spring 2011. Undergraduate Research. 1 student.

BI305. Spring 2006. Genetics. Guest lecture on Molecular Evolution.

BI529. Spring 2012. Molecular Driving Forces. 6 guest lectures on statistical mechanics of biomolecules.

Graduate

BI83201 Spring 2006. Literature of Computational Genomics Graduate Seminar. 6 students. 1.5 hours per week. Weekly paper presentations and discussions.

BI561. Spring 2007. Molecular Evolution. 10 students. 2.5 hours per week. 4 problem sets, one midterm, a final exam, and a final presentation. Rating 4.50 (Bio avg = 3.47)

BI561. Spring 2008. Molecular Evolution. 13 students. 2.5 hours per week. 4 problem sets, a midterm, a final exam, and a final presentation. Rating 4.00 (Bio avg = 3.49)

BI561. Spring 2009. Molecular Evolution. 5 students. 2.5 hours per week. 4 problem sets, a midterm, a final exam, and a final presentation. Rating 5.00 (Bio avg = 3.74)

BI561. Spring 2010. Molecular Evolution. 8 students. 2.5 hours per week. 4 problem sets, a midterm, a final exam, and a final presentation. Rating 4.71 (Bio avg = 3.63)

BI561. Fall 2011. Molecular Evolution. 13 students. 2.5 hours per week.

Note: BI561 is also open to advanced undergraduates.

MEDS 369. Spring 2017. UConn Health. Guest lecture on "Computationally Analyzing Tumor Heterogeneity."

MEDS 6498. Fall 2017. UConn Health. Guest lecture on "Patient Derived Xenograft Computational Biology."

Prior Teaching Experience

Math 22a. Fall 1993. Linear Algebra and Multivariable Calculus for Physics Majors. Harvard University, Teaching Fellow.

Physics 8.08. Spring 2000. Statistical Physics. Massachusetts Institute of Technology, Teaching Assistant.