

# ERNEST FRAENKEL

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## EDUCATION

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1991 - 1998 Ph.D. in Biology, Massachusetts Institute of Technology  
1987 - 1990 A.B. in Chemistry and Physics, Harvard College, *summa cum laude*

## CURRENT POSITIONS

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2010 - present Associate Professor, MIT Department of Biological Engineering  
2009 - present Associate Member, Broad Institute  
2002 - present Research Affiliate, MIT Computer Science and Artificial Intelligence Laboratory

## PRIOR RESEARCH POSITIONS

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2006 - 2010 Assistant Professor, MIT Department of Biological Engineering  
2001 - 2005 Whitehead Fellow, Whitehead Institute  
1998 - 2001 Postdoctoral Fellow in the laboratory of Professor Stephen Harrison,  
Harvard University  
1991 - 1998 Graduate student in the laboratory of Professor Carl Pabo,  
Massachusetts Institute of Technology  
1990 - 1991 Research Assistant in the laboratory of Professor Michael Weiss,  
Harvard Medical School

## AWARDS AND FELLOWSHIPS

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2015 Fulbright Distinguished Chair (Turin, Italy)  
2009 Merrimack-CSB2 Prize  
2008 Eugene Bell Career Development Chair  
2002 - 2005 Pfizer/Whitehead Computational Biology Fellow  
2001, 2002 Whitehead Institute Skeggs Fellow  
1999 - 2001 Damon Runyon-Walter Winchell Postdoctoral Fellowship  
1999 Cancer Research Institute Postdoctoral Fellowship  
1991 - 1996 Howard Hughes Medical Institute Predoctoral Fellow  
1990 Phi Beta Kappa (one of 24 Harvard College students selected for early admission)  
1989, 1990 John Harvard Scholarship  
1985 Bausch & Lomb Science Award

## PUBLICATIONS

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1. Gosline SJ, Oh C, Fraenkel E. SAMNetWeb: identifying condition-specific networks linking signaling and transcription. *Bioinformatics*. 2014 Nov 19. pii: btu748. PMID: 25414365 PMCID: In Process
2. Gao R1, Chen S, Kobayashi M, Yu H, Zhang Y, Wan Y, Young SK, Soltis A, Yu M, Vemula S, **Fraenkel E**, Cantor A, Antipin Y, Xu Y, Yoder MC, Wek RC, Ellis SR, Kapur R, Zhu X, Liu Y. Bmi1 promotes erythroid development through regulating ribosome biogenesis. *Stem Cells*. 2015 Mar;33(3):925-38. doi: 10.1002/stem.1896. PMID: 25385494 PMCID: In Process
3. Gitter A, Braunstein A, Pagani A, Baldassi C, Borgs C, Chays J, Zecchina R and **Fraenkel E**. Sharing information to reconstruct patient-specific pathways in heterogeneous diseases. *Pac Symp Biocomput*. 2014:39-50. PMCID: PMC3910098
4. Lo KA, Labadorf A, Kennedy NJ, Han MS, Yap YS, Matthews B, Xin S, Sun L, Davis RJ, Lodish HF and **Fraenkel E**. Analysis of In Vitro Insulin-Resistance Models and Their Physiological Relevance to In Vivo Diet-Induced Adipose Insulin Resistance. *Cell Reports*. 2013. 5(1): 259-70. PMCID: PMC3874466
5. Vashishtha M, Ng CW, Yildirim F, Gipson TA, Kratter IH, Bodai L, Song W, Lau A, Labadorf A, Vogel-Ciernia A, Troncosco J, Ross CA, Bates GP, Krainc D, Sadri-Vakili G, Finkbeiner S, Marsh JL, Housman DE, **Fraenkel E** and Thompson LM. Targeting H3K4 trimethylation in Huntington disease. *Proc Natl Acad Sci U S A*. 2013 Aug 6;110(32):E3027-36. PMCID: PMC3740882
6. Wilson JL, Hemann MT, **Fraenkel E**, Lauffenburger DA. Integrated network analyses for functional genomic studies in cancer. *Semin Cancer Biol*. 2013 Jun 27. PMCID: PMC3844556
7. Zhen AW, Nguyen NH, Gibert Y, Motola S, Buckett P, Wessling-Resnick M, **Fraenkel E** and Fraenkel PG. The small molecule, genistein, increases hepcidin expression in human hepatocytes. *Hepatology*. 2013 May 22. PMCID: PMC3770762
8. Lodato MA, Ng CW, Wamstad JA, Cheng AW, Thai KK, **Fraenkel E**, Jaenisch R and Boyer LA. Sox2 Co-occupies Distal Enhancer Elements with Distinct POU Factors in ESCs and NPCs to Specify Cell State. In press at *PLOS Genetics*. *PLoS Genet*. 2013 Feb;9(2):e1003288. PMCID: PMC3578749
9. Ng CW, Yildirim F, Yap YS, Dalin S, Matthews BJ, Velez PJ, Labadorf A, Housman D and **Fraenkel E**. Extensive changes in DNA methylation are associated with expression of mutant huntingtin. *Proc Natl Acad Sci USA*. 2013 Feb 5;110(6):2354-9. PMCID: PMC3568325
10. Huang SSC, Clarke DC, Gosline SJC, Labadorf A, Chouinard CR, Gordon W, Lauffenburger DA and **Fraenkel E**. Linking proteomic and transcriptional data through the interactome and epigenome reveals a map of oncogene-induced signaling. *PLoS Comput Biol*. 2013 Feb;9(2):e1002887. PMCID: PMC3567149
11. Gosline SJ, Spencer SJ, Ursu O, **Fraenkel E**, SAMNet: a network-based approach to integrate multi-dimensional high throughput datasets. *Integr Biol (Camb)*. 2012 Oct 22;4(11):1415-27. PMID: 23060147 PMCID: PMC3501250

12. Tuncbag N, Braunstein A, Pagnani A, Huang SSC, Chayes J, Borgs C, Zecchina R, and **Fraenkel E**. Simultaneous Reconstruction of Multiple Signaling Pathways via the Prize-collecting Steiner Forest Problem. *J Comput Biol.* 2013 Feb;20(2):124-36. PMID: PMC3576906
13. Riva L, Koeva M, Yildirim F, Dinesh D, Mazor T, Duennwald ML, and **Fraenkel E**. Poly-glutamine expanded huntingtin dramatically alters the genome-wide binding of HSF1. *Journal of Huntington's Disease.* 2012. 1:33-45. PMID: PMC3537492
14. Mendillo ML, Santagata S, Koeva M, Bell GW, Hu R, Tamimi RM, **Fraenkel E**, Ince TA, Whitesell L, Lindquist S., HSF1 Drives a Transcriptional Program Distinct from Heat Shock to Support Highly Malignant Human Cancers. *Cell.* 2012 Aug 3;150(3):549-62. PMID: PMC3438889
15. Tuncbag N, McCallum S, Huang SS, **Fraenkel E**. SteinerNet: a web server for integrating 'omic' data to discover hidden components of response pathways. *Nucleic Acids Res.* 2012 Jul;40(Web Server issue):W505-9. Epub 2012 May 25. PMID: PMC3394335
16. Huang SS, **Fraenkel E**. Swimming upstream: identifying proteomic signals that drive transcriptional changes using the interactome and multiple "-omics" datasets. *Methods Cell Biol.* 2012;110:57-80. PMID: PMC3870464
17. Yu M, Mazor T, Huang H, Huang HT, Kathrein KL, Woo AJ, Chouinard CR, Labadorf A, Akie TE, Moran TB, Xie H, Zacharek S, Taniuchi I, Roeder RG, Kim CF, Zon LI, **Fraenkel E**, Cantor AB., Direct recruitment of polycomb repressive complex 1 to chromatin by core binding transcription factors. *Mol Cell.* 2012 Feb 10;45(3):330-43. PMID: PMC3278717
18. Carlson SM, Chouinard CR, Labadorf A, Lam CJ, Schmelzle K, **Fraenkel E**, White FM., Large-scale discovery of ERK2 substrates identifies ERK-mediated transcriptional regulation by ETV3. *Sci Signal.* 2011 Oct 25;4(196):rs11. PMID: PMC3779841
19. Lo KA, Bauchmann MK, Baumann AP, Donahue CJ, Thiede MA, Hayes LS, des Etages SA, **Fraenkel E**., Genome-wide profiling of H3K56 acetylation and transcription factor binding sites in human adipocytes. *PLoS ONE* 2011 6(6): e19778. doi:10.1371/journal.pone.0019778 PMID: PMC3107206
20. Lan A, Smoly IY, Rapaport G, Lindquist S, **Fraenkel E**, Yeger-Lotem E., ResponseNet: revealing signaling and regulatory networks linking genetic and transcriptomic screening data. *Nucleic Acids Res.* 2011 Jul;39 (Web Server issue):W424-9. Epub 2011 May 16. PMID: PMC3125767
21. Ling G, Sugathan A, Mazor T, **Fraenkel E**, Waxman DJ. Unbiased, genome-wide in vivo mapping of transcriptional regulatory elements reveals sex differences in chromatin structure associated with sex-specific liver gene expression. *Mol Cell Biol.* 2010 Sep 27. **30**:5531-44. PMID: PMC2976433
22. Macisaac KD, **Fraenkel E**., Sequence analysis of chromatin immunoprecipitation data for transcription factors. *Methods Mol Biol.* 2010;674:179-93. PMID: PMC3922641
23. MacIsaac KD, Lo KA, Gordon W, Motola S, Mazor, T. **Fraenkel E**. A quantitative model of transcriptional regulation reveals the influence of binding location on expression. *PLoS Computational Biology.* 2010 Apr; 6(4):e1000773. PMID: PMC2861697.
24. Hartwig S, Ho J, Pandey P, Macisaac K, Taglienti M, Xiang M, Alterovitz G, Ramoni M, **Fraenkel E**, Kreidberg JA., Genomic characterization of Wilms' tumor suppressor 1 targets in nephron

progenitor cells during kidney development. *Development*. 2010 Apr;137(7):1189-203. PMID: PMC2835332

25. Su LJ, Auluck PK, Outeiro TF, Yeger-Lotem E, Kritzer JA, Tardiff DF, Strathearn KE, Liu F, Cao S, Hamamichi S, Hill KJ, Caldwell KA, Bell GW, **Fraenkel E**, Cooper AA, Caldwell GA, McCaffery JM, Rochet JC, Lindquist S., Compounds from an unbiased chemical screen reverse both ER-to-Golgi trafficking defects and mitochondrial dysfunction in Parkinson's disease models. *Dis Model Mech*. 2010 Mar-Apr;3(3-4):194-208. Epub 2009 Dec 28. PMID: PMC2869493
26. Yu M, Riva L, Xie H, Schindler Y, Moran TB, Cheng Y, Yu D, Hardison R, Weiss MJ, Orkin SH, Bernstein BE, **Fraenkel E**, Cantor AB. Insights into GATA-1-mediated gene activation versus repression via genome-wide chromatin occupancy analysis. *Mol Cell*. 2009 Nov 25;36(4):682-95. PMID: 2800995
27. Huang, S.-S.C. and **Fraenkel E**. Integrating proteomic, transcriptional, and interactome data reveals hidden components of signaling and regulatory networks. *Science Signaling*, 2, ra40, 2009. PMID: PMC2889494.
28. Yeger-Lotem E, Riva L, Su LJ, Gitler AD, Cashikar A, King OD, Auluck PK, Geddie ML, Valastyan JS, Karger DR, Lindquist SL, **Fraenkel E**. Bridging high-throughput genetic and transcriptional data reveals cellular responses to alpha-synuclein toxicity. *Nature Genetics*. 2009 Mar; 41(3): 316-323. PMID: PMC2733244
29. Romer KA, Kayombya GR, **Fraenkel E**., WebMOTIFS: automated discovery, filtering and scoring of DNA sequence motifs using multiple programs and Bayesian approaches. *Nucleic Acids Res*. 2007 Jul;35(Web Server issue):W217-20. Epub 2007 Jun 21. PMID: PMC1933171
30. Odom DT, Dowell RD, Jacobsen ES, Gordon W, Danford TD, MacIsaac K, Rolfe A, Conboy CM, Gifford, DK, **Fraenkel E**. Tissue-specific transcriptional regulation has diverged significantly between human and mouse. *Nature Genetics* 2007 Jun; 39(6): 730 - 732. PMID: PMC3797512
31. Marson A, Kretschmer K, Frampton GM, Jacobsen ES, Polansky JK, MacIsaac KD, Levine SS, **Fraenkel E**, von Boehmer H, Young RA. Foxp3 occupancy and regulation of key target genes during T-cell stimulation. *Nature*. 2007 Feb 22; 445(7130): 931-935. PMID: PMC3008159
32. Qi Y, Rolfe PA, MacIsaac KD, Gerber GK, Pokholok D, Zeitlinger J, Danford T, Dowell RD, **Fraenkel E**, Jaakkola TS, Young RA, Gifford DK. High-resolution computational models of genome binding events. *Nature Biotechnology*. 2006 Aug; 24(8): 963-970. PMID: 16900145
33. Odom DT, Dowell RD, Jacobsen ES, Nekludova L, Rolfe PA, Danford TW, Gifford DK, **Fraenkel E**, Bell GI, Young RA. Core Transcriptional Regulatory Circuitry in Human Hepatocytes. *Molecular Systems Biology*. 2006 2:2006.0017. PMID: PMC1681491
34. MacIsaac KD, **Fraenkel E**., Practical strategies for discovering regulatory DNA sequence motifs. *PLoS Comput Biol*. 2006 Apr;2(4):e36. No abstract available. PMID: PMC1447654
35. MacIsaac KD, Wang T, Gordon DB, Gifford DK, Stormo GD, **Fraenkel E**., An improved map of conserved regulatory sites for *Saccharomyces cerevisiae*. *BMC Bioinformatics*. 2006 Mar 7;7:113. PMID: PMC1435934

36. Macisaac KD, Gordon DB, Nekludova L, Odom DT, Schreiber J, Gifford DK, Young RA, **Fraenkel E.**, A hypothesis-based approach for identifying the binding specificity of regulatory proteins from chromatin immunoprecipitation data. *Bioinformatics*. 2006 Feb 15;22(4):423-9. Epub 2005 Dec 6. PMID: 16332710
37. Gordon DB, Nekludova L, McCallum S, **Fraenkel E.**, TAMO: a flexible, object-oriented framework for analyzing transcriptional regulation using DNA-sequence motifs. *Bioinformatics*. 2005 Jul 15;21(14):3164-5. Epub 2005 May 19. PMID: 15905282
38. Harbison CT, Gordon DB, Lee TI, Rinaldi NJ, MacIsaac KD, Danford TW, Hannett NM, Tagne JB, Reynolds, DB, Yoo J, Jennings EG, Zeitlinger J, Pokholok DK, Kellis M, Rolfe PA, Takusagawa KT, Lander ES, Gifford DK, **Fraenkel E**, Young RA. Transcriptional regulatory code of a eukaryotic genome. *Nature* 2004 Sep 2; 431(7004): 99-104. PMCID: PMC3006441  
\*Corresponding author
39. Odom DT, Zizlsperger N, Gordon DB, Bell GW, Rinaldi NJ, Murray HL, Volkert TL, Schreiber J, Rolfe PA, Gifford DK, **Fraenkel E**, Bell GI, Young RA. Control of pancreas and liver gene expression by HNF transcription factors. *Science*. 2004 Feb 27; 303(5662): 1378-1381.PMCID: PMC3012624
40. Bar-Joseph Z, Gerber G, Lee TI, Yoo J, Robert F, Gordon DB, **Fraenkel E**, Jaakkola TS, Young RA, Gifford DK. Computational discovery of gene modules and regulatory networks. *Nature Biotechnology*. 2003 Nov; 21(11): 1337-1342. PMID: 14555958
41. Lee TI, Rinaldi NJ, Robert F, Odom DT, Bar-Joseph Z, Gerber GK, Hannett NM, Harbison CT, Thompson CM, Simon I, Zeitlinger J, Jennings EG, Murray HL, Gordon DB, Ren B, Wyrick JJ, Tagne J, Volkert T, **Fraenkel E**, Gifford DK, Young RA. Transcriptional regulatory networks in *Saccharomyces cerevisiae*. *Science*. 2002 Oct 25; 298(5594): 799-804. PMID: 12399584
42. Lin CH, Hare BJ, Wagner G, Harrison SC, Maniatis T, **Fraenkel E.**, A small domain of CBP/p300 binds diverse proteins: solution structure and functional studies. *Mol Cell*. 2001 Sep;8(3):581-90.PMID: 11583620
43. Falvo JV, Parekh BS, Lin CH, **Fraenkel E**, Maniatis T., Assembly of a functional beta interferon enhanceosome is dependent on ATF-2-c-jun heterodimer orientation. *Mol Cell Biol*. 2000 Jul;20(13):4814-25. PMCID: PMC85927
44. Zheng N, **Fraenkel E**, Pabo CO, Pavletich NP., Structural basis of DNA recognition by the heterodimeric cell cycle transcription factor E2F-DP. *Genes Dev*. 1999 Mar 15;13(6):666-74. PMCID: PMC316551
45. **Fraenkel E**, Rould MA, Chambers KA, Pabo CO., Engrailed homeodomain-DNA complex at 2.2 Å resolution: a detailed view of the interface and comparison with other engrailed structures. *J Mol Biol*. 1998 Nov 27;284(2):351-61. PMID: 9813123
46. **Fraenkel E**, Pabo CO., Comparison of X-ray and NMR structures for the Antennapedia homeodomain-DNA complex. *Nat Struct Biol*. 1998 Aug;5(8):692-7. PMID: 9699632
47. Jasanoff A, Kochoyan M, **Fraenkel E**, Lee JP, Weiss MA., Aromatic-aromatic interactions in the zinc finger motif. Analysis of the two-dimensional nuclear magnetic resonance structure of a mutant

domain. J Mol Biol. 1992 Jun 20;225(4):1035-47. PMID: 1613788

## RELEASED SOFTWARE

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- **TAMO** (Tools for Analysis of MOTifs) is an object-oriented computational framework for interpreting transcriptional regulation using DNA-sequence motifs. It provides tools for integrating motif analysis with diverse data sources including genomic sequences, microarrays and various databases. Downloaded approximately 230 times in the first year after publication.
- **WebMotifs** is an online tool for motif discovery hosted on my lab's website. It makes many features of the TAMO package accessible for those who do not wish to use a programming environment.
- **ResponseNet** is an online tool for integrated network-based analysis of transcriptional and genetic data. It identifies known molecular interactions that link two disparate types of data, providing an underlying molecular basis for the experimental observations.
- **SteinerNet**: A website providing easy access for network modeling of diverse experimental data by solving the prize-collecting Steiner tree problem.

## INVITED TALKS

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- MIT CSBI Seminar Series on Computational and Systems Biology, Cambridge, MA. May 2003.
- Gordon Research Conference: "Bioinformatics: From Predictive Models To Inference" Queen's College, Oxford, UK. August 2003.
- First Andrew Viterbi Computational Symposium, University of Southern California, Los Angeles, CA. December 2003.
- Banbury meeting: Finding the Functional Elements of the Genome, Cold Spring Harbor, NY. March 2004.
- ALALabFusion 2004, Boston, MA. June 2004.
- Broad Institute, Cambridge, MA. November 2004.
- Biological Engineering Seminar Series, Cambridge, MA. February 2005.
- Vertex Pharmaceuticals, Cambridge, MA. May 2005.
- Philips Research, Briarcliff Manor, NY. April 2006.
- Seoul National University, Seoul, South Korea. September 2006.
- BIOINFO 2006, Pohang, South Korea. September 2006.
- University of Vermont, Burlington, VT. October 2006.
- BMES 2006 (Biomedical Engineering Society Annual Meeting). October 2006.
- San Raffaele Institute, Milan, Italy. January 2007.
- Technion, Haifa, Israel. January 2007.
- Hadassah Medical Center, Jerusalem, Israel. January 2007.
- European Conference on Computational Biology, Eilat, Israel. January 2007.
- Cistrome Meeting, Dana-Farber Cancer Institute, Boston MA. May 2007.
- Gordon Research Conference: "Structural, Functional and Evolutionary Genomics", Cambridge UK. August 2007.
- Engineering Cell Biology – The cell in context; Engineering Conferences International, Cambridge MA. August 2007.
- Pfizer, Groton CT. August 2007.
- Boston College Biology Department, Newton, MA. October 2007.
- Association of Biomolecular Resource Facilities. Salt Lake City, UT. February 2008.
- Association for Research in Otolaryngology MidWinter Meeting. Phoenix, AZ. February 2008.

- Uniformed Services University of the Health Sciences. Bethesda, MD. March 2008
- Georgia Institute of Technology, Distinguished Lecture Series in Systems Biology. Atlanta GA. April, 2008.
- University of Maryland, Baltimore County. Baltimore, MD. April 2008.
- Gulbenkian Institute for Science. Lisbon, Portugal. April 2008.
- National Cancer Institute-Integrated Cancer Biology Program Meeting. Columbus, OH. May 2008.
- Merck-MIT Symposium. Boston, MA. November, 2008.
- Broad Institute. Cambridge, MA. December, 2008.
- Cells, Circuits and Computation. Cambridge, MA. January, 2009.
- UCLA Bioinformatics Seminar Series. Los Angeles, CA. January, 2009.
- Boston University Systems Biology Seminars. Boston, MA. May, 2009.
- Systems Biology of Human Disease 2009. Boston, MA. June, 2009.
- MIT Science and Engineering Program for Teachers. Cambridge, MA. June, 2009.
- Merrimack Pharmaceuticals, Cambridge, MA. August, 2009.
- Gordon Research Conference: "Mechanisms of Cell Signaling." Oxford, UK. August, 2009.
- Princeton University, Princeton, MA. February, 2010.
- Fox Chase Cancer Center, Philadelphia, PA. April, 2010.
- Intelligent Systems for Molecular Biology (ISMB 2010), Boston, MA. July 2010.
- NIH NCI ICBP Mathematical Modeling Meeting, Berkeley, CA. October 2010.
- Workshop on "Identification of Aberrant Pathway and Network Activity from High-Throughput Data," Pacific Symposium on Biocomputing, Big Island, HI. January, 2011.
- Statistical Physics of Complexity, Optimization and Systems Biology," Turin, Italy. February, 2011.
- AACR "Systems Biology: Confronting the Complexity of Cancer," San Diego, CA. February, 2011.
- Vertex Pharmaceuticals, Cambridge, MA. March, 2011.
- MIT Industrial Liason Program Conference: "Tools and Approaches for Discovery," Cambridge, MA. May, 2011.
- Yale University Department of Biomedical Engineering Seminar Series. New Haven, CT. May, 2011.
- "Molecular Mechanisms of Neurodegeneration." Milan, Italy. May, 2011.
- "Systems Biology in Cancer Research," Hong Kong Baptist University. Hong Kong. June, 2011.
- Codexis, Inc. Redwood City, CA. June, 2011.
- IEEE Engineering in Medicine and Biology Society (IEEE EMBC 2011), Boston, MA. September, 2011.
- Microsoft Research 20<sup>th</sup> Anniversary Symposium, Cambridge, MA. September, 2011.
- Merrimack Pharmaceuticals, Cambridge, MA. October, 2011.
- University of Washington, Seattle, WA. December, 2011.
- Carnegie Mellon University, Pittsburgh, PA. January, 2012.
- Lincoln Laboratory, Lexington, MA. February, 2012.
- University of California, Berkeley, CA. March 2012
- American Association for Cancer Research Annual Meeting, Chicago IL. April 2012.
- NIH Integrative Cancer Biology Program Principal Investigator Meeting, San Francisco, CA. May 2012.
- Society for *in vitro* Biology. Seattle, WA. June 2012.
- Roche Pharmaceuticals, Nutley NJ. June 2012.
- Ben Gurion University, Beersheba, Israel. June 2012.



- Tel Aviv University, Tel Aviv, Israel. June 2012.
- Hebrew University, Jerusalem, Israel. June 2012.
- Weizmann Institute, Rehovot, Israel. June 2012.
- Technion – Israel Institute of Technology, Haifa, Israel. June 2012.
- Epigenomics, Sequencing & SNiPs-2012, Boston, MA. July 2012.
- Hereditary Disease Foundation Conference HD2012, Cambridge, MA. August 2012.
- Workshop on Common Concepts in Machine Learning and Statistical Physics, The Abdus Salam International Centre for Theoretical Physics, Trieste, Italy. August 2012.
- National Brain Tumor Society 2012 Summit, Boston, MA. October 2012.
- Keynote address at RECOMB Conference on Regulatory and Systems Genomics, San Francisco, CA. November 2012.
- University of Massachusetts, Worcester, MA. May 2013.
- NGS Translate, Cambridge, MA. May 2013.
- World Biotechnology Congress, Boston, MA. June 2013.
- Gordon Research Conference on CAG Triplet Repeat Disorders, Waterville Valley, NH. June 2013.
- NGX Applying Next-Generation Sequencing, Providence, RI. August 2013.
- IEEE Information Theory Workshop, Seville, Spain. September 2013.
- Whitehead Fellows Reunion, Cambridge, MA. October, 2013.
- Servier, Paris, France. October, 2013
- École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland. October, 2013.
- Microsoft Research New England, Cambridge, MA. November, 2013.
- Broad Institute, Cambridge, MA. February, 2014.
- 9th Annual Huntington's Disease Therapeutics Conference: A Forum for Drug Discovery & Development. Palm Springs, CA. February, 2014.
- Sanford-Burnham Medical Research Institute, La Jolla, CA. February, 2014.
- Bio-IT World. Boston, MA. May, 2014.
- NIH NINDS Parkinson's Disease Genetics and Systems Biology Workshop. Bethesda, MD. June, 2014.
- European Huntington's Disease Network, Biological Modifiers Meeting, Barcelona, Spain. September, 2014.
- EMBL-EBI Industry Workshop: Causal Inference: Algorithms, Methods and Cambridge, Massachusetts. November 2014.
- Stanford Center for Cancer Systems Biology Stanford University, Stanford, CA. November, 2014.
- Regulation and Inference in Biological Networks, Bardonecchia, Italy. February 2015.

## TEACHING

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### **Current Teaching:**

Analysis of Biomolecular & Cellular Systems (Course number: 20.320), *MIT*.

Foundations of Computational and Systems Biology (Course number: 20.390/7.36/7.91J/20.490J), *MIT*.

Member, Board of Tutors in Biochemical Sciences, *Harvard University*.

(I teach a required tutorial to Harvard College students).

### **Past Teaching:**

2008,2009      Perspectives in Biological Engineering (Course number: 20.400), *MIT*.

2007            Introduction to Computer Science and Programming (Course number: 6.00), *MIT*.

- 1998, 1999 Teaching Assistant, Structure and Function of Proteins and Nucleic Acids, *Harvard University*.
- 1994 Teaching Assistant, Graduate Biochemistry (Course number: 7.51), *MIT*.
- 1992 Teaching Assistant, Biophysical Chemistry (Course number: 7.71/5.64), *MIT*.
- 1990 Teaching Assistant, Laboratory Electronics, *Harvard University*.

## **PROFESSIONAL ACTIVITIES**

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- NSF Review Panel, 2005, 2006.
- NIH NIDA Special Emphasis Panel 2006.
- Invited workshop participant: "Future of Molecular Machines: Understanding Biomolecular Complexes and Interactions" Oak Ridge National Labs, 2006.
- Reviewer for Nature, Science, Cell, Nature Genetics, BMC Bioinformatics, Bioinformatics, FEBS Letters, Genome Research, Genome Biology and Molecular Systems Biology.
- Reviews Editor and Associate Editor: PLoS Computational Biology.
- Editor: Journal of Statistical Mechanics: Theory and Experiments
- Program Committee: ISMB 2006, 2012.
- Conference Organizing Committees: BMES 2006, PSB 2007, PSB2008.
- MIT Biological Engineering Computing Facilities Committee, Chair.
- Associate Chair of the MIT Biological Engineering Undergraduate Educational Program Committee.
- Co-chair Council for Systems Biology in Boston (CSB2).

## **GRADUATE STUDENTS AND POSTDOCTORAL ASSOCIATES**

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### **Current Graduate Students:**

- Amanda Daigle. Ph.D candidate in Computational and Systems Biology, MIT.
- Gabriela Pregernig. Ph.D. candidate in Biological Engineering, MIT.
- Chris Ng: Ph.D. candidate in Biological Engineering, MIT.
- Anthony Soltis: Ph.D. candidate in Biological Engineering, MIT.
- Leila Pirhaji: Ph.D. candidate in Biological Engineering, MIT.

### **Former Graduate Students:**

- Alice (Kin Yui) Lo: Ph.D. candidate in Biological Engineering, MIT, January 2012.
- Carol (Shao-shan) Huang: Ph.D. in Computational and Systems Biology, MIT, May 2011.
- Kenzie D. MacIsaac: Ph.D. in Electrical Engineering and Computer Science, MIT, June 2009.
- Laura Riva: Ph.D. in Biomedical Engineering at the Politecnico di Milano, Milan, Italy, June 2007.
- Esther Lou Pass: M.Sc. in Computer Science, Royal Institute of Technology, Stockholm Sweden, December, 2006.

### **Postdoctoral Associates:**

- Pamela Milani: 2013-present
- Xiaofeng Xin: 2011-present
- Sara Gosline: 2010-present
- Ferah Yildirim: 2010-present
- Nurcan Tuncbag: 2010-present

- Martina Koeva: 2010-present
- Tatjana Degenhardt: 2009-2010
- Shmulik Motola: 2008-2012
- Laura Riva: 2007-2010
- Esti Yeger-Lotem: 2005-2009
- (David) Ben Gordon: 2002-2005

**Thesis Committees:**

- Scott Carlson, Biological Engineering, MIT.
- Francesca Cordero, University of Turin, Italy.
- Robin Friedman, Computational and Systems Biology Initiative, MIT.
- Nancy Guillen, Biological Engineering, MIT.
- Yuchun Guo, Electrical Engineering and Computer Science, MIT.
- Paul Huang, Biological Engineering, MIT.
- Bo Kim, Electrical Engineering and Computer Science, MIT.
- Melody Morris, Biological Engineering, MIT.
- Seymour de Picciotto, Biological Engineering, MIT.
- Justin Pritchard, Biology, MIT.
- Alex Rolfe, Electrical Engineering and Computer Science, MIT.
- Ramon Salsas-Escat, Computational and Systems Biology Initiative, MIT.
- Wu Song, National University Singapore.
- Sarah Schrier, Biological Engineering, MIT
- Aarathi Sugathan, Boston University.
- Sonia Timberlake, Biological Engineering, MIT.
- Leah Octavio, Computational and Systems Biology Initiative, MIT.
- Bryan Owens, Biological Engineering, MIT.
- Justin Pritchard, Biological Engineering, MIT
- Chandni Rajan Valiathan, Computational and Systems Biology Initiative, MIT.
- Joel Wagner, Biological Engineering, MIT.
- Tracy Washington, Computational and Systems Biology Initiative, MIT.
- Jennifer Wilson, Biological Engineering, MIT.
- Grace Zheng, Computational and Systems Biology Initiative, MIT.