

## 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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2017 - present Professor, MIT Department of Biological Engineering  
2009 - present Associate Member, Broad Institute

### PRIOR RESEARCH POSITIONS

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2010 - 2017 Associate Professor, MIT Department of Biological Engineering  
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 Senior Member, International Society for Computational Biology  
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. Pirhaji, L., et al., Identifying therapeutic targets by combining transcriptional data with ordinal clinical measurements. *Nat Commun*, 2017. 8(1): p. 623. PMID: 5606996. <http://www.ncbi.nlm.nih.gov/pubmed/28931805>
2. Northcott, P.A., et al., The whole-genome landscape of medulloblastoma subtypes. *Nature*, 2017. 547(7663): p. 311-317. <http://www.ncbi.nlm.nih.gov/pubmed/28726821>
3. Lim, R.G., et al., Huntington's Disease iPSC-Derived Brain Microvascular Endothelial Cells Reveal WNT-Mediated Angiogenic and Blood-Brain Barrier Deficits. *Cell Rep*, 2017. 19(7): p. 1365-1377. PMID: 5646270. <http://www.ncbi.nlm.nih.gov/pubmed/28514657>
4. Khurana, V., et al., Genome-Scale Networks Link Neurodegenerative Disease Genes to alpha-Synuclein through Specific Molecular Pathways. *Cell Syst*, 2017. 4(2): p. 157-170 e14. PMID: 5388136. <http://www.ncbi.nlm.nih.gov/pubmed/28131822>
5. The HD iPSC Consortium, Developmental alterations in Huntington's disease neural cells and pharmacological rescue in cells and mice. *Nat Neurosci*, 2017. 20(5): p. 648-660. PMID: 5610046. <http://www.ncbi.nlm.nih.gov/pubmed/28319609>
6. Akhmedov, M., et al., PCSF: An R-package for network-based interpretation of high-throughput data. *PLoS Comput Biol*, 2017. 13(7): p. e1005694. PMID: 5552342. <http://www.ncbi.nlm.nih.gov/pubmed/28759592>
7. Wilson, J.L., et al., Functional Genomics Approach Identifies Novel Signaling Regulators of TGFalpha Ectodomain Shedding. *Mol Cancer Res*, 2017. [Http://www.ncbi.nlm.nih.gov/pubmed/29018056](http://www.ncbi.nlm.nih.gov/pubmed/29018056)
8. Ursu, O., et al., Network modeling of kinase inhibitor polypharmacology reveals pathways targeted in chemical screens. *PLoS One*, 2017. 12(10): p. e0185650. PMID: 5638242. <http://www.ncbi.nlm.nih.gov/pubmed/29023490>
9. Soltis, A.R., et al., Hyper- and hypo- nutrition studies of the hepatic transcriptome and epigenome suggest that PPARalpha regulates anaerobic glycolysis. *Sci Rep*, 2017. 7(1): p. 174. PMID: 5428070. <http://www.ncbi.nlm.nih.gov/pubmed/28282965>
10. Wong, A.S., et al., Multiplexed barcoded CRISPR-Cas9 screening enabled by CombiGEM. *Proc Natl Acad Sci U S A*, 2016. 113(9): p. 2544-9. PMID: 4780610. <http://www.ncbi.nlm.nih.gov/pubmed/26864203>
11. Wilson, J.L., et al., Pathway-based network modeling finds hidden genes in shRNA screen for regulators of acute lymphoblastic leukemia. *Integr Biol (Camb)*, 2016. 8(7): p. 761-74. PMID: 5224708. <http://www.ncbi.nlm.nih.gov/pubmed/27315426>
12. Tuncbag, N., et al., Network Modeling Identifies Patient-specific Pathways in Glioblastoma. *Sci Rep*, 2016. 6: p. 28668. PMID: 4926112. <http://www.ncbi.nlm.nih.gov/pubmed/27354287>

13. Tuncbag, N., et al., Network-Based Interpretation of Diverse High-Throughput Datasets through the Omics Integrator Software Package. *PLoS Comput Biol*, 2016. 12(4): p. e1004879. PMID: 4838263. <http://www.ncbi.nlm.nih.gov/pubmed/27096930>
14. Pirhaji, L., et al., Revealing disease-associated pathways by network integration of untargeted metabolomics. *Nat Methods*, 2016. 13(9): p. 770-6. PMID: 5209295. <http://www.ncbi.nlm.nih.gov/pubmed/27479327>
15. Milani, P., et al., Cell freezing protocol suitable for ATAC-Seq on motor neurons derived from human induced pluripotent stem cells. *Sci Rep*, 2016. 6: p. 25474. PMID: 4857123. <http://www.ncbi.nlm.nih.gov/pubmed/27146274>
16. Hanaford, A.R., et al., DiSCoVERing Innovative Therapies for Rare Tumors: Combining Genetically Accurate Disease Models with In Silico Analysis to Identify Novel Therapeutic Targets. *Clin Cancer Res*, 2016. 22(15): p. 3903-14. PMID: 5055054. <http://www.ncbi.nlm.nih.gov/pubmed/27012813>
17. Gosline, S.J., et al., Elucidating MicroRNA Regulatory Networks Using Transcriptional, Post-transcriptional, and Histone Modification Measurements. *Cell Rep*, 2016. 14(2): p. 310-9. PMID: 4831719. <http://www.ncbi.nlm.nih.gov/pubmed/26748710>
18. Gosline, S.J., C. Oh, and E. Fraenkel, SAMNetWeb: identifying condition-specific networks linking signaling and transcription. *Bioinformatics*, 2015. 31(7): p. 1124-6. PMID: 4382899. <http://www.ncbi.nlm.nih.gov/pubmed/25414365>
19. Gao, R., et al., Bmi1 promotes erythroid development through regulating ribosome biogenesis. *Stem Cells*, 2015. 33(3): p. 925-38. PMID: 4380436. <http://www.ncbi.nlm.nih.gov/pubmed/25385494>
20. Gitter, A., et al., Sharing information to reconstruct patient-specific pathways in heterogeneous diseases. *Pac Symp Biocomput*, 2014: p. 39-50. PMID: 3910098. <http://www.ncbi.nlm.nih.gov/pubmed/24297532>
21. Zhen, A.W., et al., The small molecule, genistein, increases hepcidin expression in human hepatocytes. *Hepatology*, 2013. 58(4): p. 1315-25. PMID: 3770762. <http://www.ncbi.nlm.nih.gov/pubmed/23703590>
22. Wilson, J.L., et al., Integrated network analyses for functional genomic studies in cancer. *Semin Cancer Biol*, 2013. 23(4): p. 213-8. PMID: 3844556. <http://www.ncbi.nlm.nih.gov/pubmed/23811269>
23. Vashishtha, M., et al., Targeting H3K4 trimethylation in Huntington disease. *Proc Natl Acad Sci U S A*, 2013. 110(32): p. E3027-36. PMID: 3740882. <http://www.ncbi.nlm.nih.gov/pubmed/23872847>
24. Tuncbag, N., et al., Simultaneous reconstruction of multiple signaling pathways via the prize-collecting steiner forest problem. *J Comput Biol*, 2013. 20(2): p. 124-36. PMID: 3576906. <http://www.ncbi.nlm.nih.gov/pubmed/23383998>

25. Ng, C.W., et al., Extensive changes in DNA methylation are associated with expression of mutant huntingtin. *Proc Natl Acad Sci U S A*, 2013. 110(6): p. 2354-9. PMID: 3568325. <http://www.ncbi.nlm.nih.gov/pubmed/23341638>
26. Lodato, M.A., et al., SOX2 co-occupies distal enhancer elements with distinct POU factors in ESCs and NPCs to specify cell state. *PLoS Genet*, 2013. 9(2): p. e1003288. PMID: 3578749. <http://www.ncbi.nlm.nih.gov/pubmed/23437007>
27. Lo, K.A., et al., Analysis of in vitro insulin-resistance models and their physiological relevance to in vivo diet-induced adipose insulin resistance. *Cell Rep*, 2013. 5(1): p. 259-70. PMID: 3874466. <http://www.ncbi.nlm.nih.gov/pubmed/24095730>
28. Huang, S.S., et al., Linking proteomic and transcriptional data through the interactome and epigenome reveals a map of oncogene-induced signaling. *PLoS Comput Biol*, 2013. 9(2): p. e1002887. PMID: 3567149. <http://www.ncbi.nlm.nih.gov/pubmed/23408876>
29. Yu, M., et al., Direct recruitment of polycomb repressive complex 1 to chromatin by core binding transcription factors. *Mol Cell*, 2012. 45(3): p. 330-43. PMID: 3278717. <http://www.ncbi.nlm.nih.gov/pubmed/22325351>
30. Tuncbag, N., et al., SteinerNet: a web server for integrating 'omic' data to discover hidden components of response pathways. *Nucleic Acids Res*, 2012. 40(Web Server issue): p. W505-9. PMID: 3394335. <http://www.ncbi.nlm.nih.gov/pubmed/22638579>
31. Riva, L., et al., Poly-glutamine expanded huntingtin dramatically alters the genome wide binding of HSF1. *J Huntingtons Dis*, 2012. 1(1): p. 33-45. PMID: 3537492. <http://www.ncbi.nlm.nih.gov/pubmed/23293686>
32. Mendillo, M.L., et al., HSF1 drives a transcriptional program distinct from heat shock to support highly malignant human cancers. *Cell*, 2012. 150(3): p. 549-62. PMID: 3438889. <http://www.ncbi.nlm.nih.gov/pubmed/22863008>
33. Huang, S.S. and E. Fraenkel, Swimming upstream: identifying proteomic signals that drive transcriptional changes using the interactome and multiple "-omics" datasets. *Methods Cell Biol*, 2012. 110: p. 57-80. PMID: 3870464. <http://www.ncbi.nlm.nih.gov/pubmed/22482945>
34. Gosline, S.J., et al., SAMNet: a network-based approach to integrate multi-dimensional high throughput datasets. *Integr Biol (Camb)*, 2012. 4(11): p. 1415-27. PMID: 3501250. <http://www.ncbi.nlm.nih.gov/pubmed/23060147>
35. Lo, K.A., et al., Genome-wide profiling of H3K56 acetylation and transcription factor binding sites in human adipocytes. *PLoS One*, 2011. 6(6): p. e19778. PMID: 3107206. <http://www.ncbi.nlm.nih.gov/pubmed/21655096>
36. Lan, A., et al., ResponseNet: revealing signaling and regulatory networks linking genetic and transcriptomic screening data. *Nucleic Acids Res*, 2011. 39(Web Server issue): p. W424-9. PMID: 3125767. <http://www.ncbi.nlm.nih.gov/pubmed/21576238>

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38. Su, L.J., et al., 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. 3(3-4): p. 194-208. PMID: 2869493. <http://www.ncbi.nlm.nih.gov/pubmed/20038714>
39. MacIsaac, K.D., et al., A quantitative model of transcriptional regulation reveals the influence of binding location on expression. *PLoS Comput Biol*, 2010. 6(4): p. e1000773. PMID: 2861697. <http://www.ncbi.nlm.nih.gov/pubmed/20442865>
40. MacIsaac, K.D. and E. Fraenkel, Sequence analysis of chromatin immunoprecipitation data for transcription factors. *Methods Mol Biol*, 2010. 674: p. 179-93. PMID: 3922641. <http://www.ncbi.nlm.nih.gov/pubmed/20827592>
41. Ling, G., et al., 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. 30(23): p. 5531-44. PMID: 2976433. <http://www.ncbi.nlm.nih.gov/pubmed/20876297>
42. Hartwig, S., et al., Genomic characterization of Wilms' tumor suppressor 1 targets in nephron progenitor cells during kidney development. *Development*, 2010. 137(7): p. 1189-203. PMID: 2835332. <http://www.ncbi.nlm.nih.gov/pubmed/20215353>
43. Yu, M., et al., Insights into GATA-1-mediated gene activation versus repression via genome-wide chromatin occupancy analysis. *Mol Cell*, 2009. 36(4): p. 682-95. PMID: 2800995. <http://www.ncbi.nlm.nih.gov/pubmed/19941827>
44. Yeger-Lotem, E., et al., Bridging high-throughput genetic and transcriptional data reveals cellular responses to alpha-synuclein toxicity. *Nat Genet*, 2009. 41(3): p. 316-23. PMID: 2733244. <http://www.ncbi.nlm.nih.gov/pubmed/19234470>
45. Huang, S.S. and E. Fraenkel, Integrating proteomic, transcriptional, and interactome data reveals hidden components of signaling and regulatory networks. *Sci Signal*, 2009. 2(81): p. ra40. PMID: 2889494. <http://www.ncbi.nlm.nih.gov/pubmed/19638617>
46. Romer, K.A., G.R. Kayombya, and E. Fraenkel, WebMOTIFS: automated discovery, filtering and scoring of DNA sequence motifs using multiple programs and Bayesian approaches. *Nucleic Acids Res*, 2007. 35(Web Server issue): p. W217-20. PMID: 1933171. <http://www.ncbi.nlm.nih.gov/pubmed/17584794>
47. Odom, D.T., et al., Tissue-specific transcriptional regulation has diverged significantly between human and mouse. *Nat Genet*, 2007. 39(6): p. 730-2. PMID: 3797512. <http://www.ncbi.nlm.nih.gov/pubmed/17529977>
48. Marson, A., et al., Foxp3 occupancy and regulation of key target genes during T-cell stimulation. *Nature*, 2007. 445(7130): p. 931-5. PMID: 3008159. <http://www.ncbi.nlm.nih.gov/pubmed/17237765>

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50. Odom, D.T., et al., Core transcriptional regulatory circuitry in human hepatocytes. *Mol Syst Biol*, 2006. 2: p. 2006 0017. PMID: 1681491. <http://www.ncbi.nlm.nih.gov/pubmed/16738562>
51. Maclsaac, K.D., et al., An improved map of conserved regulatory sites for *Saccharomyces cerevisiae*. *BMC Bioinformatics*, 2006. 7: p. 113. PMID: 1435934. <http://www.ncbi.nlm.nih.gov/pubmed/16522208>
52. Macisaac, K.D., et al., A hypothesis-based approach for identifying the binding specificity of regulatory proteins from chromatin immunoprecipitation data. *Bioinformatics*, 2006. 22(4): p. 423-9. <Http://www.ncbi.nlm.nih.gov/pubmed/16332710>
53. Maclsaac, K.D. and E. Fraenkel, Practical strategies for discovering regulatory DNA sequence motifs. *PLoS Comput Biol*, 2006. 2(4): p. e36. PMID: 1447654. <http://www.ncbi.nlm.nih.gov/pubmed/16683017>
54. Gordon, D.B., et al., TAMO: a flexible, object-oriented framework for analyzing transcriptional regulation using DNA-sequence motifs. *Bioinformatics*, 2005. 21(14): p. 3164-5. <Http://www.ncbi.nlm.nih.gov/pubmed/15905282>
55. Odom, D.T., et al., Control of pancreas and liver gene expression by HNF transcription factors. *Science*, 2004. 303(5662): p. 1378-81. PMID: 3012624. <http://www.ncbi.nlm.nih.gov/pubmed/14988562>
56. Harbison, C.T., et al., Transcriptional regulatory code of a eukaryotic genome. *Nature*, 2004. 431(7004): p. 99-104. PMID: 3006441. <http://www.ncbi.nlm.nih.gov/pubmed/15343339>
57. Bar-Joseph, Z., et al., Computational discovery of gene modules and regulatory networks. *Nat Biotechnol*, 2003. 21(11): p. 1337-42. <Http://www.ncbi.nlm.nih.gov/pubmed/14555958>
58. Lee, T.I., et al., Transcriptional regulatory networks in *Saccharomyces cerevisiae*. *Science*, 2002. 298(5594): p. 799-804. <Http://www.ncbi.nlm.nih.gov/pubmed/12399584>
59. Lin, C.H., et al., A small domain of CBP/p300 binds diverse proteins: solution structure and functional studies. *Mol Cell*, 2001. 8(3): p. 581-90. <Http://www.ncbi.nlm.nih.gov/pubmed/11583620>
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61. Zheng, N., et al., Structural basis of DNA recognition by the heterodimeric cell cycle transcription factor E2F-DP. *Genes Dev*, 1999. 13(6): p. 666-74. PMID: 316551. <http://www.ncbi.nlm.nih.gov/pubmed/10090723>
62. Fraenkel, E., et al., 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. 284(2): p. 351-61. <Http://www.ncbi.nlm.nih.gov/pubmed/9813123>

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[Http://www.ncbi.nlm.nih.gov/pubmed/9699632](http://www.ncbi.nlm.nih.gov/pubmed/9699632)

64. Jasanoff, A., et al., 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. 225(4): p. 1035-47. [Http://www.ncbi.nlm.nih.gov/pubmed/1613788](http://www.ncbi.nlm.nih.gov/pubmed/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.
- **Omics Integrator**: A software package that discovers novel and annotated response pathways from high-throughput data including proteomics, transcriptomics and genetic screens.
- **PIUMet**: A tool for analyzing untargeted metabolomics data alone or in combination with other omics to reveal biological pathways.

## 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 Liaison 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.
- Bristol-Myers Squibb, New Jersey. March, 2015.

- ICBP Principal Investigators Meeting, Bethesda MD. May 2015.
- German Cancer Research Center (DKFZ), Heidelberg, Germany. July, 2015.
- Simons Institute Workshop on Dynamic Biological Modeling: Abstractions, Algorithms and Logic, Berkeley, CA. August, 2015.
- 2015 MIT Digital Health Conference, Cambridge, MA. September, 2015.
- F.Hoffmann-La Roche Ltd. Basel, Switzerland. October, 2015.
- Imuneering, Cambridge, MA. October, 2015.
- Medullo in the Mountains, Waterville Valley, NH. January, 2016.
- Answer ALS Inaugural Meeting, Baltimore, MD. February, 2016.
- Network Biology Workshop, Simons Institute, Berkeley, CA. April, 2016.
- Horizons in Genomic Research. International Laboratory for Human Genome Research (LIIGH-UNAM), Queretaro, Mexico. May, 2016.
- Hebrew University, Jerusalem Israel. May, 2016.
- Novartis, Cambridge, MA. June, 2016.
- HD2016: Hereditary Disease Foundation Symposium, Cambridge, MA. August, 2016.
- St. Jude Children's Research Hospital, Memphis, TN. August, 2016.
- Bioinformatics in Health and Disease, Heidelberg, Germany. November, 2017.
- EMBL, Heidelberg, Germany. March, 2017.
- Dana Farber Cancer Center, Boston, MA. May, 2017.
- HIBIT, North Cyprus. June, 2017.
- Gordon Research Conference on Amyotrophic Lateral Sclerosis (ALS) & Related Motor Neuron Diseases, Stowe, VT. July, 2017.

## TEACHING

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### Current Teaching:

Biomolecular Kinetics & Cellular Dynamics (Course number: 20.420), *MIT*.

Laboratory Fundamentals in Biological Engineering (Course number: 20.109), *MIT*.

Member, Board of Tutors in Biochemical Sciences, *Harvard University*. (I teach a required tutorial to Harvard College students).

### Past Teaching:

2016 Analysis of Biological Networks (Course number: 20.440), *MIT*.

2015 Introduction to Computational Biology, *Politecnico di Torino, Italy*.

2007-2014 Analysis of Biomolecular & Cellular Systems (Course number: 20.320), *MIT*.

2010-2014 Foundations of Computational and Systems Biology (Course number: 20.390/7.36/7.91J/20.490J), *MIT*.

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).
- Scientific advisor to Sanford-Burnham Institute, geneLAB, National Aeronautics and Space Administration (NASA), AriSLA International Scientific Committee (Italy), Associazione Italiana per la Ricerca sul Cancro (Italy), United States - Israel Binational Science Foundation
- Consultant for Microsoft Research, Pfizer, Roche, Servier, Vertex

## **GRADUATE STUDENTS AND POSTDOCTORAL ASSOCIATES**

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### **Current Graduate Students:**

- Tobi Ehrenberger: Ph.D. candidate in Biological Engineering, MIT.
- Amanda Kedaigle: Ph.D. candidate in Computational and Systems Biology, MIT.
- Jonathan Li: Ph.D. candidate in Computational and Systems Biology, MIT.
- Natasha Patel-Murray: Ph.D.: candidate in Computational and Systems Biology, MIT.
- Divya Ramamoorthy: Ph.D. candidate in Biological Engineering, MIT.
- Maxwell Gold: Ph.D. candidate in Computational and Systems Biology, MIT.
- Bryce Hwang: M.Sc. candidate in Electrical Engineering and Computer Science, MIT.

### **Former Graduate Students:**

- Gabriela Pregonig: Ph.D. in Biological Engineering, MIT.
- Anthony Soltis: Ph.D. in Biological Engineering, MIT.
- Leila Pirhaji: Ph.D. in Biological Engineering, MIT, May 2016.
- Chris Ng: Ph.D. candidate in Biological Engineering, MIT, December 2014.
- 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. Maclsaac: 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.

### **Current Postdoctoral Associates:**

- No current postdoctoral associates

### **Former Postdoctoral Associates:**

- Renan Antonio Escalante-Chong: 2015-2016
- Leila Pirhaji: 2016-2017
- Pamela Milani: 2013-2016
- Xiaofeng Xin: 2011-2015
- Sara Gosline: 2010-2015
- Ferah Yildirim: 2010-2015
- Nurcan Tuncbag: 2010-2014
- Martina Koeva: 2010-2015
- Tatjana Degenhardt: 2009-2010
- Shmulik Motola: 2008-2012
- Laura Riva: 2007-2010
- Esti Yeger-Lotem: 2005-2009
- (David) Ben Gordon: 2002-2005

### **FUNDING**

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- Embryonal Brain Tumor Networks (U01)
- Epigenetic Pathology and Therapy in Huntington's Disease (R01)
- Neuron and Glial Cellular Signatures from Normal and Diseased iPS Cells (U54)
- Answer ALS Analytics (Johns Hopkins University)
- Regulation of RUX1 Multiprotein Complex Formation during Hematopoiesis. Children's Hospital Boston (RSTFD0000705651)
- Integrative Multi-Omic Discovery of Proximal Mechanisms Driving Age-Dependent Neurodegeneration (RF1AG057331)