Ziv Bar-Joseph

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Research Areas

Machine learning, systems biology and algorithms in nature
My work focuses on developing new computational methods for modeling and analyzing very large biological datasets. As part of this effort I have worked on the analysis of high throughput genomics and imaging data and on using machine learning, statistical algorithms and signal processing techniques to address problems ranging from experimental design to data analysis, pattern recognition and systems biology. Over the last few years and I have also looked at the other direction: How can we derive new AI algorithms from insights regarding the way biological systems operate and compute.

Employment

9/2017 - FORE Systems Professor of Computational Biology and Machine Learning, School of Computer Science, Carnegie Mellon University

9/16-2/17 - Weston Visiting Professor, Department of Molecular Cell Biology, Weizmann Institute of Science, Israel

7/2015 - Professor, Computational Biology Department and Machine Learning Department, School of Computer Science, Carnegie Mellon University

2009-2015 Associate Professor, Lane Center for Computational Biology and Machine Learning Department, School of Computer Science, Carnegie Mellon University

9/2004- Adjunct Assistant Professor (Associate Prof., 2009, Prof. 2015), Department of Biology, Carnegie Mellon University

9/2003-2009 Assistant professor, Machine Learning Department and Department of Computer Science, School of Computer Science, Carnegie Mellon University

6/2003-9/03 Postdoctoral associate, MIT CSAIL and Whitehead Institute for Biomedical Research, Cambridge, MA

Education

Massachusetts Institute of Technology, Cambridge, MA (1999 – 2003)
Ph.D. in Computer Science
Advisors: Prof. David K. Gifford and Prof. Tommi S. Jaakkola
Thesis title: Inferring Interactions, Expression Programs and Regulatory Networks from High Throughput Biological Data.

Hebrew University, Jerusalem, Israel (1997 – 1999)
M.Sc. in Computer Science

Advisor: Dr. Dani Lischinski
Thesis title: Statistical Learning of Multi-Dimensional Textures.

Hebrew University, Jerusalem, Israel (1994 – 1997)
B.Sc. in Computer Science, Mathematics and "Amirim" special honors program
Advisor: Prof. Michael Ben-Or
Thesis Title: A Tight Lower Bound for Randomized Synchronous Consensus.

Awards and Honors

F1000 Best Presentation Award, Conference on Intelligent Systems for Molecular Biology (ISMB) (2019)

FORE Systems Chair, School of Computer Science, Carnegie Mellon University (2017)

Best Paper Award, 20th ACM International Conference on Research in Computational Molecular Biology (RECOMB) (2016)

Overton Prize (2012)

NSF CAREER Award (2005)

DIMACS-Celera Genomics Graduate Student Award in Computational Molecular Biology (2003)

Program in Mathematics and Molecular Biology (PMMB), National Fellow (2001-2003)

Best Student Paper Award - Seventeenth ACM Symposium on Principles of Distributed Computing (PODC) (1998)

Professional service

Consultant, Astarte Medical (2020-present)

Consultant, Oxford Nanopore Technologies (2020-present)

Advisory Board Member, Salk / Allen Center for Aging and Alzheimer's Disease (2019-present)

Leading the Computational Tools Center, NIH Human BioMolecular Atlas Program (overseeing 6 academic groups and several software engineers in the US and the UK) (2018-present)

Scientific Advisory Board Member, Cancer Systems Biology Center, UC Irvine (2018-present)

Chair, Highlight Papers track, RECOMB (2018)

Director, The Joint CMU-Pitt Ph.D. Program in Computational Biology (over 60 students and 70 affiliated faculty) (2017-present)

Director, Big Data for Better Health (BD4BH) in Pennsylvania (overseeing the work of 15 faculty members and their groups in three institutions) (2015-2019)

Stirring Committee Member: NIAID Systems Biology Program (2014-2017)

Standing Member: Modeling and Analysis of Biological Systems Study Section (MABS), NIH (2014-2018)

Associate Editor: *Bioinformatics* (2013-2017)

Organizer and Program committee co-chair: 1st-9th Workshop on Biological Distributed Algorithms (BDA) (2013-2021)

Editorial board member: *Bioinformatics* (2008-2012)

Organizer and Program committee co-chair: *Recomb regulatory genomics and systems biology* (2009, 2010)

Published Papers in Refereed Journals and Conferences

[137] Y. Yuan and Z. Bar-Joseph. Deep learning of gene relationships from single cell time-course expression data. *Briefings in Bioinformatics*. In press, 2021

[136] D. Ruiz-Perez, J. Lugo-Martinez, N. Bourguignon, K. Mathee, B. Lerner, Z. Bar-Joseph*, G. Narasimhan*.
Dynamic Bayesian Networks for Integrating Multi-omics Time Series Microbiome Data. *mSystems*, epub ahead of print, 2021.
*corresponding authors

[135] G. Songwei, H. Wang, A. Alavi, E. Xing and Z. Bar-Joseph. Supervised Adversarial Alignment of Single-Cell RNA-seq Data. *J Comput Biol.*, to appear, 2021.
Preliminary version in Proceedings of the 24th Annual International Conference on Research in Computational Molecular Biology (RECOMB), pp 72-87, 2020.

[134] S. Rashid, G. Taubenfeld, Z. Bar-Joseph. Genome-Wide Epigenetic Modifications as a Shared Memory Consensus Problem. *Proceedings of the 28th International Colloquium on Structural Information and Communication Complexity (SIROCCO),* to appear, 2021.

[133] Y. Yuan, Z. Bar-Joseph. GCNG: graph convolutional networks for inferring gene interaction from spatial transcriptomics data. *Genome Biology*, 21(1), 1-16, 2020.

[132] A. Alavi, Z. Bar-Joseph. Iterative point set registration for aligning scRNA-seq data. *PLoS Comput Biol.* 16(10):e1007939, 2020

[131] D. Li, J. Ding, Z. Bar-Joseph. Identifying signaling genes in spatial single cell expression data. *Bioinformatics,* in press, 2020.

[130] J Ding, Z Bar-Joseph. Analysis of time series regulatory networks. *Current Opinion in Systems Biology,* 21, 16-24, 2020.

[129] H. Zafar, C. Lin, Z. Bar-Joseph. Single-cell lineage tracing by integrating CRISPR-Cas9 mutations with transcriptomic data. *Nature Communications*, 11:3055, 2020.

[128] M. Zander, M.G. Lewsey, N.M. Clark, L. Yin, A. Bartlett, J.P. Saldierna Guzmán, E. Hann, A.E. Langford, B. Jow, A. Wise, J.R. Nery, H. Chen, Z. Bar-Joseph, J.W. Walley, R. Solano, J.R. Ecker. Integrated multi-omics framework of the plant response to jasmonic acid. *Nature Plants*. 6(3):290-302. 2020

[127] C. Lin, J. Ding, Z. Bar-Joseph. Inferring TF activation order in time series scRNA-Seq studies. *PLoS Comput Biol.* 16(2):e1007644, 2020

[126] K. Hurley, J. Ding, C. Villacorta-Martin, M.J. Herriges, A. Jacob, M. Vedaie, K.D. Alysandratos, Y.L. Sun, C. Lin, R.B. Werder, J. Huang, A.A. Wilson, A. Mithal, G. Mostoslavsky, I. Oglesby, I.S. Caballero, S.H. Guttentag, F. Ahangari, N. Kaminski, A. Rodriguez-Fraticelli, F. Camargo, Z. Bar-Joseph*, D.N. Kotton*. Reconstructed Single-Cell Fate Trajectories Define Lineage Plasticity Windows during

Differentiation of Human PSC-Derived Distal Lung Progenitors. *Cell Stem Cell*, S1934-5909(19)30527-2, 2020.
* corresponding author

[125] Y. Yuan, and Z. Bar-Joseph. Deep learning for inferring gene relationships from single-cell expression data. *Proceedings of the National Academy of Science (PNAS)*, 116 (52) 27151-27158, 2019

[124] C. Lin and Z. Bar-Joseph. Continuous State HMMs for Modeling Time Series Single Cell RNA-Seq Data. *Bioinformatics*. 35(22):4707-4715, 2019.

[123] S. Rashid, Z. Long, S. Sing, M. Kohram, H. Vashistha, S. Navlakha, H. Salman, Z. N. Oltvai, and Ziv Bar-Joseph. Adjustment in tumbling rates improves bacterial chemotaxis on obstacle-laden terrains. *Proceedings of the National Academy of Science (PNAS)*, 16(24):11770-11775, 2019.

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* corresponding author

[121] J.E. McDonough, F. Ahangari, Q. Li, S. Jain, W.E. Verleden, J. Herazo-Maya, M. Vukmirovic, G. DeIuliis, A. Tzouvelekis, N. Tanabe, F. Chu, X. Yan, J. Verschakelen, R.J. Homer, D.V. Manatakis, J. Zhang, J. Ding, K. Maes, L. De Sadeleer, R. Vos, A. Neyrinck, P.V. Benos, Z. Bar-Joseph, D. Tantin, J.C. Hogg, B.M. Vanaudenaerde, W.A. Wuyts, N. Kaminski. Transcriptional regulatory model of fibrosis progression in the human lung. *JCI Insight*, 4(22):e131597, 2019.

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[118] J. Lugo-Martinez, J. Dengjel, Z. Bar-Joseph, R.F. Murphy. Integration of Heterogeneous Experimental Data Improves Global Map of Human Protein Complexes. *Proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (BCB)*, pp144-53, 2019

[117] M. Ruffalo and Z. Bar-Joseph. Protein interaction disruption in cancer. *BMC Cancer*. 19(1):370, 2019

[116] J. Ding, C. Lin, and Z. Bar-Joseph, Cell lineage inference from SNP and scRNA-Seq data. *Nucleic Acids Researc*, 47(10):e56, 2019.

[115] J. Lugo-Martinez, D. Ruiz-Perez, G. Narasimhan and Ziv Bar-Joseph. Dynamic interaction network inference from longitudinal microbiome data. *Microbiome*, 7(1):54, 2019.

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[112] S. Rashid, S. Shah, Z. Bar-Joseph, R. Pandya. Dhaka: Variational Autoencoder for Unmasking Tumor Heterogeneity from Single Cell Genomic Data .*Bioinformatics, Epub ahead of print, 2019*. Previous version in *Proceedings of the RECOMB-Computational Cancer Biology (CCB) meeting*, 2018

[111] M. Ray, M.M. Ruffalo and Ziv Bar-Joseph. Construction of integrated microRNA and mRNA immune cell signatures to predict survival of patients with breast and ovarian cancer. *Genes, Chromosomes and Cancer*, 58(1):34-42, 2019

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[106] J. Ding, J.S. Hagood, N. Ambalavanan, N. Kaminski, Z. Bar-Joseph. iDREM: Interactive visualization of dynamic regulatory networks. *PLoS Comput Biol.* 14(3):e1006019, 2018

[105] S. Navlakha, Z. Bar-Joseph, A.L. Barth. Network Design and the Brain. *Trends Cogn Sci.* 22(1):64-78 2018.

[104] J.D. Herazo-Maya, J. Sun , P.L. Molyneaux, Q. Li, J.A. Villalba, … Z. Bar-Joseph, K.F. Gibson, H. Zhao, E.L. Herzog, I.O. Rosas, T.M. Maher, N. Kaminski. Validation of a 52-gene risk profile for outcome prediction in patients with idiopathic pulmonary fibrosis: an international, multicentre, cohort study. *Lancet Respir Med.* 2600(17)30349-1, 2017

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[92] E. Sefer, M. Kleyman and Z. Bar-Joseph. Tradeoffs between dense and replicate sampling strategies for high throughput time series experiments. *Cell Systems*, 3(1):35-42, 2016.
Prior version in *Proceedings of the 20th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, 2016
*Recipient of the 'Best Paper Award' in *RECOMB* 2016

[91] S. Navlakha A. Barth and Z. Bar-Joseph. Decreasing-Rate Pruning Optimizes the Construction of Efficient and Robust Distributed Networks. *PLoS Comput Biol.*, 11(7):e1004347, 2015

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Unbiased, High-Throughput Electron Microscopy Analysis of Experience-Dependent Synaptic Changes in the Neocortex. *The Journal of Neuroscience*, 35(50):16450-62, 2015
^Cover story for the issue

[88] N.J. Venkatachari, J.M. Zerbato, S. Jain, A.E. Mancini, A. Chattopadhyay, N. Sluis-Cremer, Z. Bar-Joseph, and V. Ayyavoo. Temporal transcriptional response to latency reversing agents identifies specific factors regulating HIV-1 viral transcriptional switch. *Retrovirology*. 12(1):85, 2015

[87] A. Wise and Z. Bar-Joseph. cDREM: Inferring dynamic combinatorial gene regulation. *Journal of Computational Biology*, 22(4): 324-333, 2015
Also appeared in: *Proceedings of the 7th RECOMB/ISCB Conference on Regulatory and Systems Genomics,* 2014.

[86] S. Navlakha, C. Faloutsos and Z. Bar-Joseph. MASSEXODUS: Modeling evolving networks in adversarial environments. *Data Mining and Knowledge Discovery (DAMI)*, 29(5): 1211-1232, 2015

[85] A. Gitter and Z. Bar-Joseph. The SDREM method for reconstructing signaling and regulatory response networks: Applications for studying disease progression. *Chapter in: The Systems Biology of Alzheimers disease*, Humana / Springer press, 1303:493-506, 2015

[84] S. Navlakha, and Z. Bar-Joseph. Distributed information processing in biological and computational systems. *Communications of the ACM (CACM)*, 58(1): 94-102, 2015.

[83] A. Wise and Z. Bar-Joseph. SMARTS: Reconstructing disease response networks from multiple individuals using time series gene expression data. *Bioinformatics*, 31(8):1250-7, 2015
A preliminary version appeared as: Reconstructing dynamic regulatory developmental networks in multiple brain regions. In *Proceedings of the NIPS 2014 workshop on Analyzing the omics of the brain*, 2014.

[82] S. Jain, A. Gitter and Z. Bar-Joseph. Multitask Learning of Signaling and Regulatory Networks with Application to Studying Human Response to Flu. *PLoS Computational Biology*, 10.1371, 2014

[81] B.D. Modena, J.R. Tedrow, J. Milosevic, E.R. Bleecker, D.A. Meyers, W. Wu, Z. Bar-Joseph, S.C. Erzurum, B.M. Gaston, W.W. Busse, N.N. Jarjour, N. Kaminski and S.E. Wenzel. Gene Expression in Relation to Exhaled NO Identifies Novel Asthma Phenotypes with Unique Biomolecular Pathways. *Am J Respir Crit Care Med*, 190(12):1363-72, 2014

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[79] S. Navlakha, X. He, C. Faloutsos, and Z. Bar-Joseph. Topological Properties of Robust Biological and Computational Networks. *J. R. Soc. Interface*, 11(96):20140283, 2014.

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* Highlighted on the cover of *PNAS* and discussed in a published commentary in the same issue: U. Ohler, Using machine learning to identify disease-relevant regulatory RNAs, *PNAS* 110(39) 15516–15517, 2014.

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[76] A. Gitter, M. Carmi, N. Barkai, Z. Bar-Joseph. Linking the signaling cascades and dynamic regulatory networks controlling stress responses. *Genome Research*, 23: 365-376, 2013
* Selected as one of the Top Ten Papers in the field of Regulatory and Systems Genomics for 2013 by the RECOMB/ISCB Conference on Regulatory and Systems Genomics.

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[69] K. Duskova, P. Nagilla, H.S. Le, P. Iyer, A. Thalamuthu, J. Martinson, Z. Bar-Joseph, W. Buchanan, C. Rinaldo and V. Ayyavoo. MicroRNA regulation and its effects on cellular transcriptome in Human Immunodeficiency Virus-1 (HIV-1) infected individuals with distinct viral load and CD4 cell counts. *BMC Infectious Diseases*, 13:250, 2013

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*names in alphabetical order

[6]7 H.S. Le*, M. H. Schulz*, B.M. McCauley, V.F. Hinman, Z. Bar-Joseph. Probabilistic error correction for RNA sequencing. *Nucleic Acids Research*, 41(10):e109, 2013

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[64] M.H. Schulz, W.E. Devanny, A. Gitter, S. Zhong, J. Ernst, Z. Bar-Joseph. DREM 2.0: Improved reconstruction of dynamic regulatory networks from time-series expression data. *BMC Systems Biology*, 6:1, 2012

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* Perspective discussing this paper appeared in *Science*. Selected as a highlight paper by the editors at *Science Signaling* and *Cell*.

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*Selected as Featured Article (top 5% of NAR papers).

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*corresponding authors

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^ equal contribution, * corresponding authors

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*corresponding authors

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Teaching

10701 – Introduction to Machine Learning, PhD level
10601 - Introduction to Machine Learning, MSc level
15780 - Graduate Artificial Intelligence, PhD level
15-381 - Artificial Intelligence: Representation and Problem Solving (Undergraduate AI)
02710 - Graduate Computational Genomics, PhD level
02-717 / 10-811 - Algorithms in Nature
02-716 - Cross species analysis of genomics data

Group

Currently supervising 1 Junior Faculty, 3 Postdocs, 5 SCS PhD students, 3 MSc students and 3 Software Engineers.

Alumni

1. Yanjun Qi, Ph.D. 2008 (co-advised with J. Klein).
Current Position: Associate Prof., Department of Computer Science, University of Virginia, Charlottesville, VA.
2. Jason Ernst, Ph.D. 2008.
Current Position: Associate Prof., Biological Chemistry and Computer Science, UCLA, Los-Angeles, CA.
3. Yong Lu, Ph.D. 2008 (co-advised with R. Rosenfeld).
Current Position: Staff Scientist, National Institute of Health (NIH), Bethesda, MD.
4. Henry Lin, Ph.D. 2011 (co-advised with B. Murphy).
Current Position: Google, CA.
5. Anthony Gitter, Ph.D. 2012.
Current Position: Assistant Prof. Department of Biostatistics & Medical Informatics and Department of Computer Science, University of Wisconsin, Madison, WI.

6. Guy Zinman, Ph.D. 2012.
Current Position: Head of Global Initiatives and Senior Data Scientist, SparkBeyond, Tel-Aviv, Israel.
7. Marcel Schulz, Postdoc. 2010-2013.
Current Position: Professor of Computational Biology, Frankfurt University, Frankfurt, Germany.
8. Shan Zhong, Ph.D. 2013.
Current Position: Scientist, Foundation Medicine, Cambridge, MA.
9. Hai-Son Le, Ph.D. 2013.
Current Position: Analyst, Sunrise Futures LLC, Chicago, IL.
10. Xin He, Postdoc 2011-2014, (co-advised with K. Roeder)
Current Position: Assistant Prof., Department of Human Genetics, University of Chicago, Chicago, IL.
11. Saket Navlakha, Postdoc 2011-2014
Current Position: Associate Prof. Cold Spring Harbor Laboratory, Long Island, NY.
12. Ercument Cicek, Postdoc 2013-2015, (co-advised with K. Roeder)
Current Position: Assistant Prof., Department of Computer Science, Bilkent University, Ankara, Turkey
13.. Emre Sefer, Postdoc 2015-2016
Current Position: Assistant Professor, Department of Computer Science, Ozyegin University, Istanbul, Turkey
14. Aaron Wise, PhD 2015
Current Position: Bioinformatics Scientist at Illumina
15. Siddhartha Jain, Ph.D. 2017.
Current Position: Postdoc, Computer Science, MIT.
16. Sabrina Rashid*, Ph.D. 2019
Current Position: Deep Learning Scientist - AI Therapeutics
*School of Computer Science Distinguished Dissertation Award : Honorable Mention (1 of 4 selected from the entire school)
17. Hamim Zafar, Postdoc 2018-2019
Current Position: Assistant Prof., Department of Computer Science, IIT Kanpur, India
18. Chieh Lin*, PhD 2020
Current Position: Machine Learning researcher, Google
* School of Computer Science Distinguished Dissertation Award : Honorable Mention (1 of 4 from the entire school)
19. Jun Ding, postdoc 2016-2020
Current Position: Assistant Prof., Department of Medicine, McGill University, Montreal, CA
20. Ye Yuan, postdoc 2017-2020
Current Position: Assistant Prof., Department of Automation, Shanghai Jiao Tong University (SJTU), Shanghai, China
21. Jose Lugo-Martinez, Postdoc, 2018-2021
Current Position: Assistant Prof. Department of Mathematics and Computer Science, University of Puerto Rico-Rio Piedras, Puerto Rico

Selected Invited Talks (last 5 years)

05/21 “Hidden Markov Model for integrating longitudinal, clinical, and microbiome data to predict Growth Faltering

in preterm infants" AI in Heath Conference, Ohio State University, Columbus, OH
04/21 "Analysis of time series microbiome data" Biomolecular Sciences Institute Symposium, Florida International University, Miami, FL
04/21 "Reconstructing dynamic regulatory and signaling networks from time-series single-cell data", University of Rochester CTSI Analytics Colloquium, Rochester, NY
04/21 "Functional genomics based personal medicine", Conference on Advancing Research through Computing, University of Pittsburgh, Pittsburgh PA
02/21 ''Reconstructing dynamic regulatory networks from time series single cell data' PENN Bioinformatics Colloquium, , UPenn, Philadelphia, PA
11/20 'Analysis of single cell spatial expression data', Keynote, RECOMB/ISCB Conference on Regulatory and Systems Genomics, Pittsburgh, PA.
05/20 'Reconstructing dynamic regulatory networks from time series single cell data' MIT Bioinformatics Seminar, MIT, Cambridge, MA
09/19 'The HuBMAP pipelines for uniformly processing genomics data', Annual HuBMAP Consortium Meeting, Stanford University, CA
03/19 'Learning from Nature: Distributed Algorithms Based on Bacterial Food Search', Center for Cyber-Physical Systems and the Internet-of-Things (CCI) seminar, University of Southern California (USC), Los Angeles, CA
05/18 'Graphical models for reconstructing developmental regulatory networks', Machine Learning And Data Science Seminar Series, Mount Sinai, NY, NY
05/18 'Reconstructing regulatory networks from bulk and scRNA-Seq data', Salk Science Seminar Series, Salk Institute, San Diego, CA
5/18 'Reconstructing Dynamic Signaling and Regulatory Disease and Developmental Networks', LJI Seminar Series, La Jolla Institute for Allergy & Immunology, La Jolla, CA
03/18 'Reconstructing developmental regulatory networks from scRNA-Seq data', Duke Computational Biology Seminar, Durham, NC
12/17 'Analyzing and modeling biological processes using scRNA-Seq data', Biomedical Engineering seminar series, Washington University in St. Louis, MO.
10/17 'Reconstructing regulatory networks from bulk and scRNA-Seq data', Translational Genomics and Epigenomics Symposium, Buffalo, NY.
08/17 'Modeling lung development using bulk and single cell data' Gordon conference on Lung Development, Injury & Repair New London, NH
08/17 'Modeling dynamic signaling and regulatory immune response networks' Gordon conference on Posttranslational Modification Networks. Hong Kong University of Science and Technology, Hong Kong, China
02/17 'Analysis and modeling of single cell developmental networks', Biochemistry & Molecular Biology Department seminar, University of Texas Medical Branch, Galveston, TX
09/16 'Distributed gradient descent in bacterial food search', Keynote, 10th International Workshop on Machine Learning in Systems Biology (MLSB), Hague, Netherlands.
05/16 'Design issues in studying dynamic biological systems', Biostatistics Department seminar, Harvard University, Cambridge, MA.
04/16 'Reconstructing Dynamic Signaling and Regulatory Immune Response Networks', Computational Biology & Bioinformatics (CBB) seminar, Yale University, New-Haven, CT.
03/16 ''Reconstructing Dynamic Signaling and Regulatory Immune Networks in Development and Disease Response', Simmons Institute in Berkeley workshop on Regulatory Genomics and Epigenomics, Berkeley, CA.

Grants and Contract Support (when not the PI totals refer to our part)

Three Lakes Foundation. 'The Pulmonary Fibrosis Connectome' to Naftali Kaminski (PI). Role: Investigator. 2021-2023

C3.AI Digital Transformation Institute. ‘Effective cocktail treatments for SARS-CoV-2 based on modeling lung single cell response data’ to Ziv Bar-Joseph (PI), 2020-2021

Astarte Medical (Contract) ‘Development of predictive computational models using time series clinical and microbiome data’ to Ziv Bar-Joseph (PI), 2020-2021

U01HL146002 National Institute of Health (NIH, NHLBI) ‘Immunometabolic phenotypes in adult severe asthma and disease progression’ to Bruce Levy (PI), role – investigator 2019-2024

2T32EB009403 National Institute of Health NIH (NIBIB) ‘Integrated interdisciplinary, inter-university phd program computational biology’ to Ziv Bar-Joseph (MPI) and Jim Faeder, 2019-2024

OT2OD026682 National Institute of Health NIH (Common Fund) ‘Comprehensive, Flexible and FAIR Tools for the HuBMAP HIVE’ to Ziv Bar-Joseph (PI), 2018-2024

1R01HL127349 - National Institute of Health (NIH, NHLBI), ‘Normal Aging Lung Cell Atlas (NALCA)’ to Naftali Kaminski (PI), role – co-PI, 2018-2022

1R01GM122096, National Institute of Health (NIH, NIGMS), ‘Reconstructing regulatory networks from time series single cell data’ to Ziv Bar-Joseph (PI), 2017-2022

CURE, PA Department of Health, ‘Big Data for Better Health (BD4BH) in Pennsylvania’, to Ziv Bar-Joseph (MPI) and Greg Cooper, 2015-2019

1R01HL127349 - National Institute of Health (NIH, NHLBI), ‘Genomic Analysis of Tissue and Cellular Heterogeneity in IPF’ to Naftali Kaminski (PI), role – co-PI, 2015-2019

1R01HL128172- National Institute of Health (NIH, NHLBI), ‘Epigenenomic and transcriptomic networks in normal and defective lung development’, to Darrell Kotton (PI), Role: co-PI, 2015-2020

ProSEED/BrainHub, CMU, “Understanding the topology of neural networks: An information processing approach” to Ziv Bar-Joseph (PI), 2015-2016

DBI- 1356505, National Science Foundation (NSF) “ABI Innovation: BCSP: Understanding the design and usage of distributed biological networks” to Ziv Bar-Joseph (PI). 2014-2018

1 U01 HL122626-01 - National Institute of Health (NIH, NHLBI) “Alveolar DevMAP” to Namasivayam Ambalavanan (PI). Role - Investigator. 2014-2020

1 U54 HL127624-01U54 National Institute of Health (NIH, NIGMS) “Modeling Signaling and Regulatory Response Networks” to Avi Ma’ayan (PI). Role: Investigator. 2014-2016

James S. McDonnell Foundation Scholars Award in Studying Complex Systems “Exploring similarities of network based information processing in biology and computer systems” to Ziv Bar-Joseph (PI). 2013-2021

Ziv Bar-Joseph

I-Corps 1242525, National Science Foundation (NSF) “ExpressionBlast” to Ziv Bar-Joseph (PI). 2012-2013

1U01HL108642 - National Institute of Health (NIH, NHLBI) “Gene networks beyond organ boundaries; heart, lung and pulmonary vascular disease” to Naftali Kaminski (PI). Role – Investigator. 2011-2015

DBI-0965316, National Science Foundation (NSF) “Cross species analysis of gene expression data” to Ziv Bar-Joseph (PI). 2010-2014

The Pittsburgh Foundation “A Pittsburgh Collaborative Network to Combat Right Heart Failure in Pulmonary Hypertension" to Ziv Bar-Joseph (PI’s) and Ahmad Ferhaan (UPitt). 2010-2013

1R01GM085022 - National Institute of Health (NIH, NIGMS) "Reconstructing dynamic regulatory networks". RO1 grant to Ziv Bar-Joseph (PI). 2008-2014

United States – Israel Binational Science Foundation (BSF). “Genome-wide analysis of the human cell cycle in primary cells”. To Ziv Bar-Joseph and Itamar Simon (PIs). 2006-2008

National Institute of Health (NIH) " Tools for Machine Learning of Subcellular Targeting Motifs". To Robert Murphy, PI. Role: Investigator. 2006-2007

National Science Foundation (NSF) CAREER Award "Modeling dynamic systems in the cell". To Ziv Bar-Joseph. 2005-2011

National Institute of Health (NIH, NIAID) "Center for Modeling Immunity for Biodefense: Innate Immune Response". To Penelope Morel (UPitt) PI. Role: co-PI. 2005-2010

Pennsylvania Department of Health. "Comparative analysis of the cell cycle system with application to cancer”. To Ziv Bar-Joseph (PI) and Roni Rosenfeld. 2005-2007