

**Olga G. Troyanskaya, Ph.D.**

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**Professor**  
**Lewis-Sigler Institute for Integrative Genomics &**  
**Department of Computer Science**  
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**EDUCATION**

- 2003 Ph.D. Biomedical Informatics  
Stanford University, Stanford, CA
- 1999 B.S. Computer Science and Biology, with Honors, *Summa Cum Laude*, Phi Beta Kappa  
University of Richmond, Richmond, VA

**HONORS AND AWARDS**

- 2014 IRA HERSKOWITZ AWARD, Genetic Society of America  
Awarded bi-annually “for outstanding contributions in the field of yeast research in the last 20 years. This award is usually given to scientists under 50.”
- 2011 THE OVERTON PRIZE, International Society of Computational Biology  
Awarded annually “for outstanding accomplishment” by an early to mid career scientist who “has already made significant contribution to the field of computational biology”
- 2011 BLAVATNIK AWARD FOR YOUNG SCIENTISTS (FINALIST AWARD)
- 2011 THE 35<sup>TH</sup> ANNUAL CARL F. SCHMIDT HONORARY LECTURE, UNIVERSITY OF PENNSYLVANIA MEDICAL SCHOOL
- SINCE 2009 SENIOR FELLOW, CANADIAN INSTITUTE FOR ADVANCED RESEARCH
- 2008 PHI BETA KAPPA TEACHING AWARD, PRINCETON UNIVERSITY
- 2008 MYRA SAMUELS MEMORIAL LECTURE, DEPARTMENT OF STATISTICS, PURDUE UNIVERSITY
- 2006 HOWARD WENTZ FACULTY AWARD, PRINCETON UNIVERSITY
- 2006 NSF CAREER AWARD
- 2005 SLOAN RESEARCH FELLOWSHIP
- 2004 MIT TECHNOLOGY REVIEW MAGAZINE TR35 AWARD  
List of top technology innovators in the world under the age of 35
- 1999 – 2003 HOWARD HUGHES MEDICAL INSTITUTE PREDOCTORAL FELLOWSHIP  
Howard Hughes Medical Institute
- 1999-2002 STANFORD GRADUATE FELLOWSHIP  
Stanford University
- 1999 THE MAZE AWARD  
Annual award to the most outstanding graduate of the University of Richmond
- 1999 GOLDEN KEY HONOR SOCIETY, *SCHOLAR AWARD*  
Annual award for outstanding leadership, scholarship, and service
- 1995-1999 JEPSON INTERNATIONAL & INTERNATIONAL STUDENT SCHOLARSHIPS  
Full tuition, room & board scholarships at the University of Richmond

**RESEARCH EXPERIENCE**

- 2/13- **Professor, Princeton University, NJ**  
Department of Computer Science & Lewis-Sigler Institute for Integrative Genomics

10/13- **Consultant, Simons Center for Data Analysis, NY**

7/09-1/13 **Associate Professor, Princeton University, NJ**  
Department of Computer Science & Lewis-Sigler Institute for Integrative Genomics

6/10- **Visiting Associate Professor, Tromso University, Norway**

9/03-6/09 **Assistant Professor, Princeton University, NJ**  
Department of Computer Science & Lewis-Sigler Institute for Integrative Genomics

9/99-8/03 **Doctoral Student, Stanford University, CA**  
Dissertation: "Improving the Specificity of Biological Signal Detection from Microarray Data".

5/99-9/99 **Research Fellow, University of Haifa, Israel**  
Department of Computer Science and Genome Diversity Center

Sum '97&'98 **Summer Fellow, The Institute for Genomic Research (TIGR), MD**

## TEACHING EXPERIENCE

Since 09/04 **COS 231/COS 232 An integrated, quantitative intro to natural sciences**  
Development and teaching of computer science component of the novel integrated 1st year curriculum that integrates computer science, physics, chemistry and biology

Spring 2004 **COS 554 Computational analysis of biological networks**  
Graduate course on analysis and modeling of biological networks from static and dynamic perspectives

Since 10/03 **Cold Spring Harbor Laboratory Advanced Bioinformatics course**  
Teaching the microarray analysis component of the Advanced Bioinformatics course

Since 09/03 **COS 557 Visualization and analysis of large-scale genomics data sets**  
Upper-level undergraduate and graduate course on analysis of genomic data from computational perspective

7/02-8/02 **Advanced Bioinformatics, California State University, Hayward, CA**  
Lecture and laboratory course on analysis of microarray datasets

## PROFESSIONAL SERVICE, BOARD, AND COMMITTEE MEMBERSHIP

2012 co-Chair, NHGRI workshop "Integrating Functional Data for Connecting Genotype to Phenotype"

2012 Chair, Late Breaking Research Track, Intelligent Systems for Molecular Biology (ISMB) 2012

2011 Steering Committee, ISMB/ECCB 2011 conference  
Chair, Late Breaking Research Track, ISMB/ECCB 2011 conference

Since 2010 ENCODE/modENCODE External Consultants Panel

2010 Conference Chair, ISMB 2010 Conference  
Advisory Committee, AMIA Summit on Translational Bioinformatics 2011  
Program Committee, Yeast Genetics and Molecular Biology Meeting, 2010

Since 2010 Scientific Advisory Board, The Gene Ontology Consortium

Since 2010 Scientific Advisory Group, GenomeSpace Consortium (SAG Chair since 8/2012)

2009 Program Committee, RECOMB 2009  
Track Chair, 2009 Summit on Translational Bioinformatics

2008 Track co-Chair, Transcriptomics, ISMB 2008  
Program Committee, Yeast Genetics and Molecular Biology Meeting, 2008  
Track Chair, 2008 Summit on Translational Bioinformatics

- Program Committee, RECOMB Systems Biology
- 2007 Organizing Committee member, IPAM Workshop: Search and Knowledge Building for Biological Datasets  
PC co-Chair, Transcriptomics, ISMB and European Conference on Computational Biology (ECCB) 2007  
PC member, Computational Systems Bioinformatics Conference (CSB) 2007  
PC member, 7th Workshop on Algorithms in Bioinformatics (WABI) 2007
- Since 2006 Board of Directors member, International Society for Computational Biology (ISCB)
- 2006 PC co-Chair, Proteomics, ISMB 2006  
PC member, CSB 2006  
PC member, WABI 2006  
Organizer, NYAS Computational Biology and Bioinformatics Discussion Group Meetings
- 2005 PC member, IEEE CSB 2005  
PC member, ISMB 2005.
- 2004 PC member, ISMB 2004
- Since 2003 Member, Center for Discrete Mathematics and Theoretical Computer Science
- 2000 Founding co-chairwoman, Biomedical Computation @ Stanford conference.

## EDITORIAL AND REVIEWING EXPERIENCES

- Since 2012 Series Editor (with A. Dress, M. Linial, and M. Vingron), Computational Biology series, Springer.
- Since 2006 Associate Editor, *Bioinformatics*
- Since 2006 ISCB Editor, *PLOS Computational Biology*
- Since 09 Panels member, European Commission FP7 Systems Biology evaluations
- 1/06, 1/07 EU-Siemens Health-e-Child Project reviewer
- 10/07 NSF Biological Databases and Informatics review panel
- Since 2009 The Genomics, Computational Biology and Technology NIH study section ad-hoc reviewer
- Since 2006 Biomedical Data Management and Analysis NIH study section ad-hoc reviewer
- Since 2008 Editorial Board member, *Journal of Biomedical Informatics*
- Since 2006 Editorial Board member, *Briefings in Bioinformatics*
- Since 2005 Editorial Board member, *Bioinformatics*, *Biology Direct*
- 7/05-9/05 HHMI-NIBIB Interfaces Initiative Graduate Training Programs grant review panel
- 9/05 Continued Development and Maintenance of Software NIH study section
- 6/05 National Centers for Systems Biology NIH study section
- 3/05 Modeling and Analysis of Biological Systems NIH study section
- Since 2001 Reviewer: *Science*, *Nature*, *Nature Genetics*, *Nature Oncogene*, *Nature Biotechnology*, *Cell*, *Bioinformatics*, *Protein Science*, *Pacific Symposium on Biocomputing*, *Nucleic Acids Research*, *BioMed Central Bioinformatics*, *Journal of Biomedical Informatics*, *Genome Research*.

## RESEARCH GRANTS

- 8/12-5/17 NIH NHLBI U54: Personalization of Therapeutic Efficacy and Risk (**co-PI and Director** of the Systems, Modeling, and Computation Core and of the Centralized PENTACON database, PI is Garret FitzGerald at the University of Pennsylvania School of Medicine)

- 11/12-11/13 2 Million Dogs Foundation: Molecular Study of Canine Mammary Tumor Development and Progression: from Genome To Clinical Outcome (**PI**)
- 4/05-1/16 NIH NIGMS RO1: Integration and Visualization of Diverse Biological Data (**PI**, co-PI Matthias Kretzler at the University of Michigan at Ann Harbor School of Medicine).
- 1/11-1/14 NIH NHGRI RO1: Context-Sensitive Search of Human Expression Compendia (**PI**, co-PI Kai Li)
- 12/10-12/11 Google Research Award: Social Systems for Complex Information Processing (**PI**, w. Sep Kamvar)
- 9/10-9/15 NIH NIAID: Modeling Immunity for Biodefense (PI: Stuart Sealfon, Mount Sinai Medical School)
- 8/07-5/12 NIH NCI RO1: Predicting and testing gene function in the human cell division cycle (co-PI, PI is Michael Whitfield, Dartmouth Medical School)
- 12/09-12/11 Project X, Princeton University Benign or Malignant: A Predictive Molecular Model of Breast Cancer Progression (**PI**)
- 1/07-1/08 Google Research Award. Context-sensitive search engine for cancer micro array data. (**PI**)
- 6/06-6/11 NSF CAREER award: An Integrated Approach to the Study of Biological Process Specific Networks. (**PI**)
- 9/05-8/07 Alfred P. Sloan Foundation Research Fellowship: Computational Functional Genomics in *S. cerevisiae*. (**PI**)
- 8/05-8/08 NSF Science and Engineering Informatics (BIO): Integrated analysis of heterogeneous genomic data for accurate prediction of gene function and interactions between proteins. (**PI**, co-PI Robert Schapire).
- 2/05-2/09 CSR-PDOS-Content-Searchable Storage for Feature-Rich Data. (co-PI along with Moses Charikar, Perry Cook, PI is Kai Li).
- 4/04-4/08 NGS: Software Tools for New-Generation, Display-Centric Applications. (co-PI along with Thomas Funkhouser, Szymon Rusinkiewicz, PI is Kai Li).

## SOFTWARE RELEASED

- 2014 giant.princeton.edu – a web-based interactive system for analysis of tissue-specific protein function and interactions, providing functional networks in 144 tissues and cell types, and enabling analysis of tissue-specific rewiring
- 2013 seek.princeton.edu – a “google-like” search system for thousands of human gene expression datasets across >50 microarray and sequencing technology platforms
- 2013 nano.princeton.edu – a web server for predicting tissue- and cell-lineage-specific gene expression from large collections of expression compendia that are not necessarily resolved for that tissue
- 2012 IMP – a web-based system for multi-species prediction of functional relationship networks and function, using functional-knowledge based annotation transfer
- 2011 PILGRM – a web-based system enabling advanced machine learning analysis of large expression compendia by expert biologists
- 2011 Network Homologs server – a web-based system for identifying functional analogs of genes across model organisms
- 2010 ARAGraphle – a web-based system for tissue- and development- specific investigation of functional networks in the plant *Arabidopsis thaliana*.
- 2009 HEFaIMp – a web-based system for interactive visualization and investigation of human functional maps in a process and disease-specific way
- 2008 Sleipnir – a library for very large-scale data integration and analysis
- 2008 MouseNET – a system for integration and analysis of biological networks in mouse

2008	HIDRA - visualization and analysis framework for simultaneously exploring multiple microarray datasets
2008	Software for analysis of cellular growth rate based on microarray data
2007	SPELL – a context-sensitive search system for very large microarray compendia
2006	MEFIT – a web-based system for microarray data integration and functional analysis
2006	GOLEM – a system for Gene Ontology navigation and analysis
2006	GRIFN – a general framework for evaluation and analysis of functional genomics data
2006	bioPIXIE – a general web-based system for data storage, integration, and methodology for prediction, visualization, and functional coherence analysis of biological pathways
2005	GeneVAND – software for visualization-based statistical analysis of microarray datasets
2005	ChARMView – software for visualization-based genome-scale discovery of aneuploidies
2004	ChARM – software for identification of chromosomal abnormalities from microarray data
2001	KNNimpute – software for missing value estimation for microarray datasets

## PUBLICATIONS

\*=co-corresponding authors

1. Zhou J and **Troyanskaya OG**. Global quantitative modeling of chromatin factor interactions. *PLoS Comput Biol*. 2014;10(3):e1003525. doi: 10.1371/journal.pcbi.1003525. 2014.
2. Vandersluis B, Hess DC, Pesyna C, Krumholz EW, Syed T, Szappanos B, Nislow C, Papp B, **Troyanskaya OG**, Myers CL, Caudy AA. Broad metabolic sensitivity profiling of a prototrophic yeast deletion collection. *Genome Biol*. 2014;15(4):R64.
3. Zhou J and **Troyanskaya OG**. Deep supervised and convolutional generative stochastic network for protein secondary structure prediction. *Proceedings of the International Conference on Machine Learning* (refereed conference paper publication). 2014.
4. Ju W, Casey CS, Eichinger F, Nair V, Hodgin JB, Bitzer M, Lee Y, Zhu Q, Kehata M, Li M, Rastaldi MP, Cohen CD, **Troyanskaya OG\***, Kretzler M\*. Defining cell-type specificity at the transcriptional level in human disease. *Genome Research*. 23(11). 2013  
**Highlighted in: Nature Rev Genet**. 2013 Oct; 14(10):678.
5. Lee YS, Krishnan A, Zhu Q, **Troyanskaya OG**. Ontology-aware classification of tissue and cell-type signals in gene expression profiles across platforms and technologies. *Bioinformatics*. 2013 Dec 1;29(23):3036-44. doi: 10.1093/bioinformatics/btt529
6. Aure MR, Leivonen SK, Fleischer T, Zhu Q, Overgaard J, Alsner J, Tramm T, Louhimo R, Alnæs GI, Perälä M, Busato F, Touleimat N, Tost J, Børresen-Dale AL, Hautaniemi S, **Troyanskaya OG**, Lingjærde OC, Sahlberg KK, Kristensen VN. Individual and combined effects of DNA methylation and copy number alterations on miRNA expression in breast tumors. *Genome Biology*. 2013 Nov 20;14(11):R126.
7. Park CY, Wong AK, Greene CS, Rowland J, Guan Y, Burdine RD, **Troyanskaya OG**. Functional knowledge transfer for high-accuracy prediction of under-studied biological processes. *PLOS Comput Biol* 9(3), 2013.
8. Caudy AA\*, Guan Y, Jia Y, Hansen C, Desevo C, Hayes AP, Agee J, Alvarez-Dominguez JR, Arellano H, Barrett D, Bauerle C, Bisaria N, Bradley PH, Breunig JS, Bush EC, Cappel DA, Capra E, Chen W, Clore J, Combs PA, Doucette C, Demuren O, Fellowes P, Freeman S, Frenkel E, Gadala-Maria D, Gawande R, Glass D, Grossberg S, Gupta A, Hammonds-Odie L, Hoisos A, Hsi J, Hsu YH, Inukai S, Karczewski KJ, Ke X, Kojima M, Leachman S, Lieber D, Liebowitz A, Liu J, Liu Y, Martin T, Mena J, Mendoza R, Myhrvold C, Millian C, Pfau S, Raj S, Rich M, Rokicki J, Rounds W, Salazar M, Salesi M, Sharma R, Silverman SJ,

- Singer C, Sinha S, Staller M, Stern P, Tang H, Weeks S, Weidmann M, Wolf A, Young C, Yuan J, Crutchfield C, McClean MN, Murphy CT, Llinás M, Botstein D, **Troyanskaya OG\***, Dunham MJ\*. A New System for Comparative Functional Genomics of Saccharomyces Yeasts. *Genetics*. Sep;195(1):275-87
9. Guan Y, Dunham MJ\*, **Troyanskaya OG\***, Caudy AA\*. Comparative gene expression between two yeast species. *BMC Genomics*. 14(1), 2013.
10. Greene GS, **Troyanskaya OG**. Data-driven view of disease biology. *PLoS Comput Biol*. 9(12), 2012.
11. Guan Y, Grenshteyn D, Schimenti J, Handel MA, Bult C, Hibbs M, **Troyanskaya OG**. Tissue-specific functional networks for prioritizing phenotype and disease genes. *PLoS Comput Biol*. 8(9): e1002694. doi:10.1371/journal.pcbi.1002694. 2012. 2012.
12. Nair VD, Ge Y, Balasubramanian N, Kim J, Okawa Y, Chikina M, **Troyanskaya O**, Sealfon SC. Involvement of Histone Demethylase LSD1 in Short-Time-Scale Gene Expression Changes during Cell Cycle Progression in Embryonic Stem Cells. *Mol Cell Biol*. 32(23):4861-76, 2012.
13. Wong AK, Park CY, Greene CS, Bongo LA, Guan Y, **Troyanskaya OG**. IMP: A multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. *Nucl Acids Res*. 40: W484-90, 2012.
14. Chikina M, **Troyanskaya OG**. An effective statistical evaluation of ChIPseq dataset similarity. *Bioinformatics*. 28(5): 607-613, doi: 10.1093/bioinformatics/bts009, 2012
15. Greene CS, **Troyanskaya OG**. Accurate evaluation and analysis of functional genomics data and methods. *Annals of the NYAS*. Vol.1260, Number 1, 95-100, 2012.
16. Kristensen VN, Vaske CJ, Ursini-Siegel J, Van Loo P, Nordgard SH, Sachidanandam R, Sørlie T, Wärnberg F, Haakensen VD, Helland Å, Naume B, Perou CM, Haussler D, **Troyanskaya OG**, and Børresen-Dale AL. Integrated molecular profiles of invasive breast tumors and ductal carcinoma in situ (DCIS) reveal differential vascular and interleukin signaling. *PNAS*. 109(8): 2802-7, 2012.
17. Chikina M, **Troyanskaya OG**. Accurate quantification of functional analogy among close homologs. *PLOS Comput Biol*, 7(2): e1001074. doi:10.1371/journal.pcbi.1001074, 2011.
18. Greene CS, **Troyanskaya OG**. PILGRM: an interactive data-driven discovery platform for expert biologists. *Nuc. Acids Res*. Vol.39: W369-W374, doi: 10.1093/nar/gkr440, 2011.
19. **Troyanskaya OG**. Don't fear the command line! *Cell*. 144(6): 842-843, 2011.
20. Guan Y, Yao V, Tsui K, Gebbia M, Dunham MJ, Nislow C, **Troyanskaya OG**. Nucleosome-coupled expression differences in closely-related species. *BMC Genomics*. 12:466, 2011.
21. Baryshnikova A, Costanzo M, Kim Y, Ding, H, Koh J, Toufighi K, Youn JY, Ou J, San Luis BJ, Bandyopadhyay S, Hibbs M, Hess D, Gingras AC, Bader GD, **Troyanskaya OG**, Brown GW, Andrews B, Boone C, Myers CL. Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. *Nature Methods*. 7: 1017-1024, 2010.
22. Pop A, Huttenhower C, Iyer-Pascuzzi A, Benfey PN, **Troyanskaya OG**. Integrated functional networks of process, tissue, and developmental stage specific interactions in *Arabidopsis thaliana*. *BMC Systems Biology*. 4: 180, 2010.
23. Greene CS, **Troyanskaya OG**. Integrative systems biology for data-driven knowledge discovery. *Semin Nephrol*. 30(5):443-54, 2010.
24. Markowitz F, Mulder K, Airoidi E, Lemischka I, **Troyanskaya OG**. Mapping Dynamic Histone Acetylation Patterns to Gene Expression in Nanog-depleted Murine Embryonic Stem Cells. *PLoS Comput Biol*. 6(12): e1001034, 2010.
25. Guan Y, Dunham M, Caudy A, **Troyanskaya OG**. Systematic planning of genome-scale experiments in poorly-studied species. *PLoS Comput Biol*. 6(3): e1000698, 2010.

**Highlighted in:** *Nature Rev Genet.* 11(5):315, 2010.

26. Park C, Hess D, Huttenhower C, **Troyanskaya OG**. Simultaneous Genome-Wide Inference of Physical, Genetic, Regulatory, and Functional Pathway Components. *PLoS Comput Biol.* 6(11): e1001009, 2010.
27. Guan Y, Ackert-Bicknell CL, Kell B, **Troyanskaya OG**, Hibbs MA Functional Genomics Complements Quantitative Genetics in Identifying Disease-Gene Associations. *PLoS Comput Biol.* 6(11): e1000991, 2010.
28. Costanzo M, Baryshnikova A, Bellay J, Kim Y, Spear ED, Sevier CS, Ding H, Koh JL, Toufighi K, Mostafavi S, Prinz J, St Onge RP, VanderSluis B, Makhnevych T, Vizeacoumar FJ, Alizadeh S, Bahr S, Brost RL, Chen Y, Cokol M, Deshpande R, Li Z, Lin ZY, Liang W, Marback M, Paw J, San Luis BJ, Shuteriqi E, Tong AH, van Dyk N, Wallace IM, Whitney JA, Weirauch MT, Zhong G, Zhu H, Houry WA, Brudno M, Ragibzadeh S, Papp B, Pál C, Roth FP, Giaever G, Nislow C, **Troyanskaya OG**, Bussey H, Bader GD, Gingras AC, Morris QD, Kim PM, Kaiser CA, Myers CL, Andrews BJ, Boone C. The genetic landscape of a cell. *Science.* 327(5964):425-31, 2010.
29. Huttenhower C, Mehmood SO, **Troyanskaya OG**. Graphlet: Interactive exploration of large, dense graphs. *BMC Bioinformatics.* 10: 417, 2009.
30. Lu R, Markowitz F, Unwin RD, Leek JT, Airoidi EM, MacArthur BD, Lachmann A, Rozov R, Ma'ayan A, Boyer LA, **Troyanskaya OG**, Whetton AD, Lemischka IR. Systems-level dynamic analyses of fate change in murine embryonic stem cells. *Nature.* 462: 358-62, 2009.
31. Huttenhower C, Mutungu KT, Indik N, Yang W, Schroeder M, Forman JJ, **Troyanskaya OG**, Collier HA. Detailing regulatory networks through large scale data integration. *Bioinformatics.* 25: 3267-74, 2009.
32. Huttenhower C, Haley EM, Hibbs MA, Dumeaux V, Barrett DR, Collier HA, **Troyanskaya OG**. Exploring the human genome with functional maps. *Genome Res.* 19(6): 1093-106, 2009. Epub Feb 26.
33. Barutcuoglu Z, Schapire RE, Airoidi EM, **Troyanskaya OG**. Aneuploidy prediction and tumor classification with heterogeneous hidden conditional random fields. *Bioinformatics.* 25(10): 1307-13, 2009.
34. Chikina MD, Huttenhower C, Murphy CT, **Troyanskaya OG**. Global Prediction of Tissue-Specific gene expression and context-dependent Gene Networks in *C. elegans*. *PLoS Comput Biol.* 5(6): e1000417, 2009.
35. Huttenhower C, Hibbs NA, Myers CL, Caudy AA, Hess DC, **Troyanskaya OG**. The impact of incomplete knowledge on evaluation: an experimental benchmark for protein function prediction. *Bioinformatics.* 25(18): 2404-10, 2009.
36. Hess DC, Myers CL, Huttenhower C, Hibbs MA, Hayes AP, Paw J, Clore JJ, Mendoza RM, Luis BS, Nislow C, Giaever G, Costanzo M, **Troyanskaya OG**, Caudy AA. Computationally driven, quantitative experiments discover genes required for mitochondrial biogenesis. *PLoS Genet.* 5(3): e1000407, 2009.
37. Hibbs MA, Myers CL, Huttenhower C, Hess DC, Li K, Caudy AA, **Troyanskaya OG**. Directing experimental biology: a case study in mitochondrial biogenesis. *PLoS Comput Biol.* 5(3): e1000322, 2009.
38. Huttenhower C, Myers CL, Hibbs MA, **Troyanskaya OG**. Computational analysis of the yeast proteome: understanding and exploiting functional specificity in genomic data. *Methods Mol Biol.* 548: 273-93, 2009.
39. Myers CL, Chiriac C, **Troyanskaya OG**. Discovering biological networks from diverse functional genomic data. *Methods Mol Biol.* 563:157-75, 2009.
40. Airoidi EM, Huttenhower C, Gresham D, Lu C, Caudy AA, Dunham MJ, Broach JR, Botstein D, **Troyanskaya OG**. Predicting cellular growth rates from gene expression. *PLoS Comput Biol.* 5(1): e1000257, 2009.
41. Bradley BH, Brauer MJ, Rabinowitz JD, **Troyanskaya OG**. Coordinated concentration changes of transcripts and metabolites in *Saccharomyces cerevisiae*. *PLoS Comput Biol.* 5(1): e1000270, 2009.

42. Huttenhower C, Schroeder M, Chikina MD, **Troyanskaya OG**. The Sleipnir library for computational functional genomics. *Bioinformatics*. 24:1559-61, 2008.
43. Guan Y, Myers CL, Lu R, Lemischka IR, Bult CJ, **Troyanskaya OG**. A genome-wide functional network for the laboratory mouse. *PLOS Comput Biol*. 4(9): e1000165, 2008.
44. Guan Y, Myers CL, Hess D, Barutcuoglu Z, Caudy A, **Troyanskaya OG**. Predicting gene function in a hierarchical context with an ensemble of classifiers. *Genome Biology*. 9 Suppl 1: S3, 2008.
45. Pena-Castillo L, Tasan M, Myers CL, Lee H, Joshi T, Zhang C, Guan Y, ..., Blake JA, Deng M, Jordan MI, Noble WS, Morris Q, Klein-Seetharaman J, Bar-Joseph Z, Chen T, Sun F, **Troyanskaya OG**, Marcotte EM, Xu D, Hughes TR, Roht FP. A critical assessment of *Mus musculus* gene function prediction using integrated genomic evidence. *Genome Biology*. 9 Suppl 1: S2, 2008.
46. Huttenhower C, **Troyanskaya OG**. Assessing the functional structure of genomic data. *Bioinformatics*. 24: i330-8, 2008.
47. Brauer MJ, Huttenhower C, Airoidi EM, Rosenstein R, Matese JC, Gresham D, Boer VM, **Troyanskaya OG**, Bostein D. Coordination of Growth Rate, Cell Cycle, Stress Response, and Metabolic Activity in Yeast. *Mol Biol Cell*. 19: 352–367, 2008.
48. Hibbs MA, Hess DC, Myers CL, Huttenhower C, Li K, **Troyanskaya OG**. Exploring the functional landscape of gene expression: directed search of large microarray compendia. *Bioinformatics*. 23 (20): 2692-9, 2007.
49. Myers CL, **Troyanskaya OG**. Context-sensitive data integration and prediction of biological networks. *Bioinformatics*. 23: 2322-30, 2007.
50. Markowitz F, Kostka D, **Troyanskaya OG**, Spang R. Nested effects models for high-dimensional phenotypic screens. *Bioinformatics*. 23: i305-12, 2007.
51. **Troyanskaya OG**. “Getting Started In...”: A Series Not to Miss. *PLoS Comput Biol*. 3(10): e224, 2007.
52. Huttenhower C, Flamholz AI, Landis JN, Sahi S, Myers CL, Olszewski KL, Hibbs MA, Siemers NO, **Troyanskaya OG**, Collier HA. Nearest Neighbor Networks: clustering expression data based on gene neighborhoods. *BMC Bioinformatics*. 8: 250, 2007.
53. Markowitz F, **Troyanskaya OG**. Computational identification of cellular networks and pathways. *Molecular Biosystems*. 3(7): 478-82, 2007.
54. Bongo LA, Wallace G, Larsen T, Li K, **Troyanskaya OG**. Systems Support for Remote Visualization of Genomics Applications over Wide Area Networks. *Proceedings of the International Workshop on Distributed, High-Performance and Grid Computing in Computational Biology*, 2007.
55. Hibbs MA, Wallace G, Dunham M, Li K, **Troyanskaya OG**. Viewing the Larger Context of Genomic Data through Horizontal Integration. *Proceedings of the 11th Int. Conf. on Information Visualization (IV07)*, 2007.
56. Guan Y, Dunham MJ, **Troyanskaya OG**. Functional analysis of gene duplications in *Saccharomyces cerevisiae*. *Genetics*. 175(2): 933-43, 2007.
57. Chi A\*, Huttenhower CH\*, Geer LY, Coon JJ, Syka JEP, Bail DL, Shabanowitz J, Burke DJ, **Troyanskaya OG**, Hunt DF. Analysis of phosphorylation sites on proteins from *Saccharomyces cerevisiae* by electron transfer dissociation (ETD) mass spectrometry. *PNAS*. 104(7): 2193-8, 2007.
58. Bongo LA, Wallace G, Larsen T, Li K, **Troyanskaya OG**. Systems Support for Remote Visualization of Genomics Applications over Wide Area Networks. *Proceedings of the International Workshop on Distributed, High-Performance and Grid Computing in Computational Biology*, 2007.
59. Huttenhower C, Hibbs MA, Myers CL, **Troyanskaya OG**. A Scalable Method for Integration and Functional Analysis of Multiple Microarray Data Sets. *Bioinformatics*. 22(23): 2890-7, 2006.

60. Haarer B, Viggiano S, Hibbs MA, **Troyanskaya OG**, Amberg DC. Modeling Complex Genetic Interactions in a Simple Eukaryotic Genome: Actin Displays a Rich Spectrum of Complex Haploinsufficiencies. *Genes & Development*. 21(2):148-159, 2006.
61. Sealfon RSG, Hibbs MA, Huttenhower C, Myers CL, **Troyanskaya OG**. GOLEM: an interactive graph-based gene-ontology navigation and analysis tool. *BMC Bioinformatics*. 7: 443, 2006.
62. Myers CL, Barrett D, Hibbs MA, Huttenhower C, **Troyanskaya OG**. Finding function: evaluation methods for functional genomic data. *BMC Genomics*. 7:187, 2006.
63. Huttenhower C, **Troyanskaya OG**. Bayesian Data Integration: A Functional Perspective. *Computational Systems Bioinformatics Conf*. Vol. 5, 341-351, 2006.
64. Reguly T, Breitkreutz A, Boucher L, Breitkreutz B, Hon G, Myers CL, Parsons A, Friesen H, Oughtred R, Tong A, Ho Y, Botstein D, Andrews B, Boone C, **Troyanskaya OG**, Ideker T, Dolinski K, Batada NN, Tyers M. Comprehensive Curation and Analysis of Global Interaction Networks in *Saccharomyces cerevisiae*. *Journal of Biology*. 5(4):11, 2006.
65. Barutcuoglu Z, Schapire RE, **Troyanskaya OG**. Hierarchical Multi-label Prediction of Gene Function. *Bioinformatics*. 22(7): 830-6, 2006.
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## SELECTED RECENT INVITED TALKS

1. Opening keynote at the Yeast Genetics 2014 meeting. The awesome power of yeast genetics for developing genomic technologies and understanding human disease. 7/2014.
2. Invited speaker at the Systems Biology of Human Disease. Cell-lineage and Tissue-specific View of Human Disease on the Whole-genome Scale. 6/2014.
3. Invited speaker at the NIH BD2K Meeting on Challenges in Data Integration. Challenges of data integration: extracting context-specific biological signal from heterogeneous data compendia. 6/2014.

4. Invited speaker at the NCI meeting Ras Pathway Modeling and Quantitative Measurements. Mapping signaling pathways in a tissue-specific context. 6/2014.
5. Invited speaker at the OMICS meets Cell Biology: Applications to Human Health and Disease Keystone Symposium. From Functional Genomics Studies to the Cell-Lineage Specific View of Human Disease. 2/2014.
6. Invited speaker at the Introduction to Network Medicine course through the Harvard Catalyst program at the Harvard Clinical and Translational Science Center. 10/2013.
7. Invited speaker at the MAGE 2013: Models and Algorithms for Genome Evolution. Title: Understanding gene function across organisms with functional networks. 8/2013.
8. Invited speaker at the Moscow Conference on Computational Molecular Biology 2013. Title: Tissue-specific understanding of human disease from functional genomic data. 7/2013.
9. Invited speaker at the Annual Meeting of the NIH/NIGMS National Centers for Systems Biology. Title: Molecular-level understanding of human disease through Integrated analysis of heterogeneous “omics” data. 7/2013.
10. Keynote speaker at the Dynamics of Biological Networks conference, Edinburgh, Scotland. Title: From functional genomics data to understanding human disease: Modeling tissue-specificity in gene expression and interactions. 6/2013.
11. Invited speaker at the Biological Sequence Analysis & Probabilistic Models Conference, Janelia Farms. Title: Identifying cell-lineage specific gene expression and function on the genomic scale. 3/2013.
12. Keynote speaker at the LINCS Data Forum 2013, Harvard Medical School. Title: Understanding of Human Disease in a Tissue-Specific Context Through the Integration of Diverse Functional Genomics. 3/2013.
13. Seminar at the Penn Genome Frontiers Institute. Title: Integrated, tissue-specific view of human disease. 2/2013.
14. Seminar at the Johns Hopkins University Biomedical Engineering Institute. Title: Understanding of human disease in a tissue-specific context through the integration of diverse functional genomics data. 2/2013.
15. Keynote speaker at the 10<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference. Title: From Tissue-specific Functional Networks to Understanding Human Disease. 12/2012
16. Seminar at Stanford University Systems Medicine/Department of Pediatrics. Title: Cell-lineage specifically in functional genomics: from networks to understanding human disease. 10/2012
17. Keynote speaker at the Translational Bioinformatics Conference. Title: Understanding complex human disease through cell-lineage specific networks. 10/2012
18. Invited speaker at the 13<sup>th</sup> International Conference on Systems Biology. Title: Tissue-specific modeling of functional genomics data: from networks to understanding human disease. 8/2012
19. Keynote Speaker at the Critical Assessment of Massive Data Analysis 2012 conference. Title: Dissecting cell-lineage specific signals in functional genomics data compendia. 7/2012
20. Seminar at the Department of Systems Biology at the Harvard Medical School. Title: Cell-lineage specificity in functional genomics: from networks to understanding human disease. 6/2012
21. Seminar at the UCLA Bioinformatics Seminar Series. Title: Cell-lineage specificity in functional genomics, or how can all these networks help us understand complex human disease. 6/2012

22. Distinguished Seminar at the Center for Bioinformatics and Computational Biology, University of Maryland, College Park. Title: Integrative analysis of functional genomics data: from yeast to tissue-specific modeling of human disease. 4/2012
23. Seminar at The J. David Gladstone Institutes and UCSF. Title: Integrative cell-lineage specific view of human disease. 3/2012
24. Invited speaker at the 56<sup>th</sup> Annual Meeting of the Biophysical Society. Title: From cell-lineage specific models to understanding of human disease. 2/2012
25. Invited speaker at the Experimental models of cancer course, The Jackson Laboratory. 8/2012
26. Keynote, Overton Award Lecture, Intelligent Systems for Molecular Biology conference. Title: Integrating computation and experiments for a molecular-level understanding of human disease. 7/2011
27. The 35th Annual Carl F. Schmidt Honorary Lecture, University Of Pennsylvania Medical School. Title: The tale of many "omes": Molecular understanding of disease from heterogeneous functional genomics data. 2/2011
28. Seminar at the Department of Genome Sciences, University of Washington, Seattle. Title: From Data to Networks to Understanding Complexity of Human Disease. 10/2010
29. Invited speaker at the Experimental models of cancer course, The Jackson Laboratory. 8/2011
30. Invited speaker at the 21<sup>st</sup> Annual European Association for Cancer Research Conference. Title: Analyzing functional genomics data and networks to understand disease. 6/2010.
31. Invited speaker at the Systems Biology and New Sequencing Technologies Symposium, Barcelona, Spain. Title: Understanding biology of disease based on diverse functional genomics data. 6/2010
32. Seminar in IGSB-GGSB Seminar Series, University of Chicago. Title: From networks to pathways and understanding disease. 6/2010
33. Invited speaker at the Keystone Symposium on Bimolecular Interaction Networks: Function and Disease. Title: From integrated functional networks to understanding disease. 3/2010
34. Seminar at the Genome Center, Columbia University. Title: Integrated Analysis of Functional Genomics Data: on the Road to Systems - Level Understanding of Disease and Enabling Molecular Medicine. 2/2010
35. Invited speaker at the High-Throughput Genomic Technologies meeting, Australia. Title: Understanding tissue-specific gene expression and disease from large microarray compendia. 10/2009
36. Seminar in the Computational Medicine and Bioinformatics Seminar Series, University of Michigan at Ann Arbor Medical School. Title: Making sense of biology and disease in genomics: from functional networks to tissue-specific gene expression.
37. Invited speaker at the Experimental models of cancer course, The Jackson Laboratory. 8/2010
38. Invited speaker at the Systems Biology of Human Disease conference, Harvard University. Title: Understanding human disease through functional networks. 6/2009
39. Seminar, Albert Einstein College of Medicine. Title: The tale of a thousand microarrays or How to get from functional networks to understanding biology and disease. 5/2009
40. Invited Speaker, AMIA Summit on Translational Bioinformatics, San Francisco, CA. Title: From data to networks and understanding of disease in functional genomics. 3/2009