Olga G. Troyanskaya, Ph.D.

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EDUCATION

1999-2003	Ph.D. Biomedical Informatics Stanford University, Stanford CA
1995-1999	B.S. Computer Science and Biology, *Summa Cum Laude,* Phi Beta Kappa University of Richmond, Richmond, VA

HONORS AND AWARDS

2008	PHI BETA KAPPA TEACHING AWARD, PRINCETON UNIVERSITY
2008	MYRA SAMUELS MEMORIAL LECTURE, DEPARTMENT OF STATISTICS, PURDUE UNIVERSITY
2007	BARNETT LECTURE (DECLINED), DEPARTMENT OF MATHEMATICAL SCIENCES, UNIVERSITY OF CINCINNATI
2006	HOWARD WENTZ FACULTY AWARD
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
1997	ACM 1997 UNDERGRADUATE SCHOLARSHIP Washington, D.C. Chapter of the Association for Computer Machinery

RESEARCH EXPERIENCE

Since 9/03 **Assistant Professor, Princeton University, NJ**
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**
5/98-7/98 & 6/97-8/97 **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

ADVISING EXPERIENCE

Graduated Ph.D. advisees
Chad Myers (now faculty, Department of Computer Science, University of Minnesotta)
Matthew Hibbs (with Kai Li, from 1/08 - faculty, Jackson Laboratory)
Zafer Barutcuoglu (with Rob Shapire, from 9/08 in financial industry)

Current Ph.D. advisees
Curtis Huttenhower
Maria Chikina
Patrick Bradley (with Josh Rabinovitz)
Yuanfang Guan
Chris Park
Ana Pop

Postdoctoral advisees
Edo Airoldi (from 1/08 - faculty, Harvard University)
Florian Markowetz (from 1/08 - faculty, Cancer UK Cambridge Research Institute and Cambridge University)
David Hess
Matthew Hibbs
Lars Bongo (with Kai Li)

Undergraduate senior thesis advisees
Adam Wible ‘05, Drew Robson ‘05, Conall O'Callaghan ‘05, Shannon Morales ’06, Rachel Sealfon ’07, Samuel Grossberg (’07)

Undergraduate research advisor and/or JP advisor
Adam Wible (Fall ’03, Spring ’04, Summer ‘04), Drew Robson (Summer ’04), Nicholas Stroustrap (Summer ’04, Fall ’05, Spring ’05), Xing Chen (Summer ’04), Conall O'Callaghan (Fall ’03, Spring ’04), Sharon Wilkes (Summer ’05), Rajiv Ayyandgar (Summer ’05, Fall ’05), Rachel Sealfon (Summer ’05, ’06,’07, JP ‘06-07), Daniel Berrett (Summer ’05,’06,’07 JP ’06-07), John Ulman (JP ’06-07),

UNIVERSITY SERVICE

Since 12/05	Executive committee of the Quantitative and Computational Biology training program
Since 12/06	Steering committee of the Princeton Institute for Computational Science and Engineering
10/05-6/07	SEAS search committee for a transformative hire in the life sciences
Since 9/05	Princeton Institute for Computational Science and Engineering steering committee
Since 9/05	Committee on the Princeton University Community (CPUC)
9/05-9/07	Executive committee of the CPUC
9/05-9/07	Faculty Advisory Committee on Policy
Since 11/03	Executive committee for Program in Applications of Computing
Since 9/03	Genomics integrated curriculum planning committee

PROFESSIONAL SERVICE AND COMMITTEE MEMBERSHIP

2009	PC member, RECOMB 2009
	PC track Chair, 2009 Summit on Translational Bioinformatics
2008	PC co-Chair, Transcriptomics, International Conference on Intelligent Systems for Molecular Biology (ISMB) 2008
	Organizing Committee, Yeast Genetics and Molecular Biology Meeting, 2008
	PC track Chair, 2008 Summit on Translational Bioinformatics
	PC member, 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.
Since 2005	Conference Committee, International Society for Computational Biology (ISCB)
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 2006	Associate Editor, *Bioinformatics*
Since 2006	Editor, *PLOS Computational Biology*
1/06, 1/07	EU-Siemens Health-e-Child Project reviewer
10/07	NSF Biological Databases and Informatics review panel

2/06, 6/06, 1/07 Biomedical Data Management and Analysis NIH study section

Since 2006 Editorial Board member, *Briefings in Bioinformatics*

Since 2005 Editorial Board member, *Bioinformatics*

Since 2005 Editorial Board member, *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: *Nature, Nature Genetics, Nature Oncogene, Bioinformatics, Protein Science, Pacific Symposium on Biocomputing, Nucleic Acids Research, BioMed Central Bioinformatics, Journal of Biomedical Informatics, Genome Research.*

RESEARCH GRANTS

6/06-6/11 NSF CAREER award: An Integrated Approach to the Study of Biological Process Specific Networks. (PI) $1,000,692

9/05-8/07 Alfred P. Sloan Foundation Research Fellowship: Computational Functional Genomics is *S. cerevisiae*. $45,000

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). $471,442

4/05-3/10 NIH NIGMS RO1: Integration and Visualization of Diverse Biological Data. (PI, co-PI Kai Li). $1,125,000

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). $900,000

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). $500,000

SOFTWARE RELEASED

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 analyis framework for simultaneously exploring multiple microarray datasets

2007 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

1. Hibbs MA*, Myers CL*, Huttenhower C*, Hess DC, Li K, Caudy AA, **Troyanskaya OG**. Analysis of Computational Functional Genomic Approaches for Directing Experimental Biology: a Case Study in Mitochondrial Inheritance. *PLOS Computational Biology*, in press, 2008.

2. Guan Y, Myers CL, Lu R, Lemischka IR, Bult CJ, **Troyanskaya OG**. A genome-wide functional network for the laboratory mouse. *PLOS Computational Biology*, in press, 2008.

3. 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: S3, 2008.

4. 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: S2, 2008.

5. Huttenhower C, **Troyanskaya OG**. Assessing the functional structure of genomic data. *Bioinformatics.* 24: i330-8, 2008.

6. Huttenhower C, Schroeder M, Chikina MD, **Troyanskaya OG**. The Sleipnir library for computational functional genomics. *Bioinformatics*. 24:1559-61, 2008.

7. 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.

8. Myers CL, **Troyanskaya OG**. Context-sensitive data integration and prediction of biological networks. *Bioinformatics*. 23: 2322-30, 2007.

9. Brauer MJ, Huttenhower C*, Airoldi EM*, Rosenstein R, Matese JC, Gresham D, Boer VM, **Troyanskaya OG**, Botstein D. Coordination of Growth Rate, Cell Cycle, Stress Response, and Metabolic Activity in Yeast. *Mol Biol Cell*. 19(1):352, 2008, Epub 2007.

10. Markowetz F, Kostka D, **Troyanskaya OG**, Spang R. Nested effects models for high-dimensional phenotypic screens. *Bioinformatics*. 23: i305-12, 2007.

11. Huttenhower C, Flamholz AI, Landis JN, Sahi S, Myers CL, Olszewski KL, Hibbs MA, Siemers NO, **Troyanskaya OG**, Coller HA. Nearest Neighbor Networks: clustering expression data based on gene neighborhoods. *BMC Bioinformatics*. 8:250, 2007.

12. Markowetz F, Troyanskaya OG. Computational identification of cellular networks and pathways. Mol Biosyst. 3:478, 2007

13. 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.

14. Guan Y, Dunham MJ, **Troyanskaya OG**. Functional analysis of gene duplications in Saccharomyces cerevisiae. *Genetics*. 175:933, 2007.

15. Chi A*, Huttenhower CH*, Geer LY, Coon JJ, Syka JEP, Bai1 DL, Shabanowitz1 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.

16. 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.

17. Huttenhower C, Hibbs MA, Myers CL, **Troyanskaya OG**. A Scalable Method for Integration and Functional Analysis of Multiple Microarray Data Sets. *Bioinformatics*. 22: 2890, 2006.

18. 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*. 21:148-159, 2006.

19. 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.

20. Myers CL, Barrett D, Hibbs MA, Huttenhower C, **Troyanskaya OG**. Finding function: evaluation methods for functional genomic data. *BMC Genomics*. 7:187, 2006.

21. Huttenhower C, **Troyanskaya OG**. Bayesian Data Integration: A Functional Perspective. *Computational Systems Bioinformatics Conf*. 4:341, 2006.

22. 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, **Troyanskya 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):10, 2006.

23. Barutcuoglu Z, Schapire RE, **Troyanskaya OG**. Hierarchical Multi-label Prediction of Gene Function. Bioinformatics. 22(7): 830, 2006.

24. Brown JA, Sherlock G, Myers CL, Burrows NM, Deng C, Wu HI, McCann KE, **Troyanskaya OG**, Brown MG. Global analysis of gene function in yeast by quantitative phenotypic profiling. Molecular Systems Biology. 2: doi:10.1038/msb4100043.

25. Barutcuoglu Z, Schapire RE, **Troyanskaya OG**. Using hierarchies to improve classifier predictions in genomics. NIPS Workshop on Computational Biology and the Analysis of Heterogeneous Data. 2005.

26. Myers CL, Dolinski K, **Troyanskaya OG**. Discovery of biological networks from diverse functional genomic data. NIPS Workshop on Computational Biology and the Analysis of Heterogeneous Data. 2005.

27. Myers CL, Robson D, Wible A, Chiriac C, Theesfeld CL, Dolinski K, **Troyanskaya OG**. Discovery of biological networks from diverse functional genomic data. Genome Biology. 6(13):R114, 2005.

28. Myers CL, Chen X, **Troyanskaya OG**. Visualization-based discovery and analysis of genomic abberations in microarray data. BMC Bioinformatics. 6:146, 2005.

29. Hibbs, MA, Dirksen NC, Li K, **Troyanskaya OG**. Visualization Methods for Statistical Analysis of Microarray Clusters. BMC Bioinformatics. 6:115, 2005.

30. Wallace G, Chen H, Chen Y, Liu Z, Samanta R, Bi P, Gupta A, Hibbs M, Li K, Finkelstein A, Funkhouser T, Cook P, Sukthankar R, and **Troyanskaya OG**. Tools and Applications for Large Scale Display Walls. Special Issue on Large Format Displays, IEEE Computer Graphics and Applications. July/August 2005.

31. Li K, Hibbs M, Wallace G, **Troyanskaya OG**. Dynamic Scalable Visualization for Collaborative Scientific Applications. IPDPS 2005 Workshop on Next Generation Software Proceedings. 2005.

32. Troyanskaya OG. Putting the 'bio' into bioinformatics. Genome Biology 6(10):351, 2005.

33. **Troyanskaya OG**. Unsupervised machine learning to support functional characterization of genes. In: Data analysis and visualization methods in genomics and proteomics, Azuaje F & Dopazo J, Eds. John Wiley & Sons. 2005.

34. **Troyanskaya OG**. Putting microarrays in a context: integrated analysis of diverse biological data. Briefings in Bioinformatics. 6 (1): 34-43, 2005.

35. Dolinski K, **Troyanksya OG**. In: Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics, Jorde LB, Little PFR, Dunn MJ, Subramaniam S, Eds. John Wiley & Sons. 2005.

36. Myers CL, Dunham M, Kung SY, **Troyanskaya OG**. Accurate detection of aneuploidies in array CGH and gene expression microarray data. Bioinformatics. 20:3533-3543, 2004.

37. Liang MP, **Troyanskaya OG**, Laederach A, Brutlag DL, Altman RB. Computational Functional Genomics. IEEE Signal Processing. 21 (6): 62-69, 2004.

38. **Troyanskaya OG**, Dolinski K, Owen AB, Altman RB, and Botstein D. A Bayesian framework for combining heterogeneous data sources for gene function prediction (in S. cerevisiae). Proc Natl Acad Sci USA 100(14): 8348-53, 2003.

39. Whitfield ML, Finlay DR, Murray JI, **Troyanskaya OG**, Chi JT, Pergamenschikov A, McCalmont TH, Brown PO, Botstein D, Connolly MK. Systemic and cell type-specific gene expression patterns in scleroderma skin. Proc Natl Acad Sci USA 100(21):12319-24, 2003.

40. Chi JT, Chang HY, Haraldsen G, Jahnsen FL, **Troyanskaya OG**, Chang DS, Wang Z, Rockson SG, van de Rijn M, Botstein D, Brown PO. Endothelial cell diversity revealed by global expression profiling. Proc Natl Acad Sci USA 100(19):10623-8, 2003.

41. Chen X, Leung SY, Yuen ST, Chu KM, Ji J, Li R, Chan SY, Law S, **Troyanskaya OG**, Wong J, Botstein D, So S, Brown PO. Variation in gene expression patterns in human gastric cancers. Mol Biol Cell 14(8):3208-15, 2003.

42. Bohen SP, **Troyanskaya OG**, Alter O, Warnke R, Botstein D, Brown PO, Levy R. Variation in gene expression patterns in follicular lymphoma and the response to rituximab. Proc Natl Acad Sci USA 100(4): 1926-30, 2003.

43. **Troyanskaya OG**, Garber ME, Brown PO, Botstein D, Altman RB. Nonparametric methods for identifying differentially expressed genes in microarray data. Bioinformatics 18:1454-61, 2002.

44. Leung SY, Chen X, Chu KM, Yuen ST, Mathy J, Ji J, Chan ASY, Li R, Law S, **Troyanskaya OG**, Tu IP, Wong J, So S, Botstein D, Brown PO. Phospholipase A2, Group IIA expression in gastric adenocarcinoma is associated with prolonged survival and less frequent metastasis. Proc Natl Acad Sci USA 99(25):16203-8, 2002.

45. **Troyanskaya OG**, Botstein D, Altman RB. Missing value estimation. In: A practical approach to microarray data analysis, D Berrar, W Dubitzky, M Granzow, Eds. Kluwer Academic Publishers, London, pp. 65-75, 2002.

46. **Troyanskaya OG**, Arbell O, Koren Y, Landau GM, Bolshoy A. Sequence complexity profiles of prokaryotic genomic sequences: A fast algorithm for calculating linguistic complexity. Bioinformatics 18:679-88, 2002.

47. Garber ME, **Troyanskaya OG**, Schluens K, Petersen S, Thaesler Z, Pacyna-Gengelbach M, van de Rijn M, Rosen GD, Perou CM, Whyte RI, Altman RB, Brown PO, Botstein D, Petersen I. Diversity of gene expression in adenocarcinoma of the lung. Proc Natl Acad Sci USA 98(24):13784-9, 2001.

48. **Troyanskaya O**, Cantor M, Sherlock G, Brown P, Hastie T, Tibshirani R, Botstein D, Altman RB. Missing value estimation methods for DNA microarrays. Bioinformatics 17:520-5, 2001.