

Olga G. Troyanskaya, Ph.D.

Assistant Professor
Department of Computer Science &
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ACADEMIC POSITIONS

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

EDUCATION

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

RESEARCH EXPERIENCE

Since 9/03 **Assistant Professor, Princeton University, NJ**
Department of Computer Science & Lewis-Sigler Institute for Integrative Genomics
9/99-8/03 **Doctoral Student, Stanford University, CA**
Biomedical Informatics and Department of Genetics
5/99-9/99 **Research Fellow, University of Haifa, Israel**
Department of Computer Science and Genome Diversity Center
97 & 98 **Summer Fellow, The Institute for Genomic Research (TIGR), MD**

HONORS AND AWARDS

2006 NSF CAREER AWARD
2006 HOWARD WENZ FACULTY AWARD
2005-2007 SLOAN RESEARCH FELLOWSHIP
2004 MIT TECHNOLOGY REVIEW MAGAZINE TR35 AWARD
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

GRANTS AND FELLOWSHIPS

- 6/06-6/11 NSF CAREER award: An integrated approach to the study of biological process specific networks. \$1,000,692 (PI)
- 1/07-1/08 Google Research Award. Context-sensitive search engine for cancer micro array data. \$75,000 (PI)
- 9/05-8/07 Alfred P. Sloan Foundation Research Fellowship: Computational Functional Genomics in *S. cerevisiae*. \$45,000 (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). \$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 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 Kai Li). \$500,000

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

UNIVERSITY SERVICE

- Since 12/05 Executive committee of the Quantitative and Computational Biology training program
- Since 10/05 Transformative Hire in the Life Sciences search committee
- Since 9/05 Princeton Institute for Computational Science and Engineering steering committee
- Since 9/05 Committee on the Princeton University Community (CPUC)
- Since 9/05 Executive committee of the CPUC
- Since 9/05 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

- 2007 Program committee co-Chair, Transcriptomics, International Conference on Intelligent Systems for Molecular Biology (ISMB) 2007 and European Conference on Computational Biology (ECCB) 2007
- 2007 Program committee member, Computational Systems Bioinformatics Conference (CSB) 2007
- 2007 Program committee member, 7th Workshop on Algorithms in Bioinformatics (WABI) 2007
- Since 2006 Board of Directors, International Society for Computational Biology (ISCB)
- 2006 Program committee co-Chair, Proteomics, ISMB 2006
- 2006 Program committee member, CSB 2006
- 2006 Program committee member, WABI 2006
- 2006 Organizer, NYAS Computational Biology and Bioinformatics Discussion Group Meetings
- 2005 Program committee member, IEEE CSB 2005
- 2005 Program committee member, ISMB 2005.
- Since 2005 Conference Committee, International Society for Computational Biology (ISCB)
- 2004 Program committee member, ISMB 2004
- Since 2003 Member, Center for Discrete Mathematics and Theoretical Computer Science
- 2000 Founding co-chairwoman, Biomedical Computation @ Stanford conference. A student-organized research conference with approximately 500 attendees

REVIEWING EXPERIENCES

- Since 2006 Associate Editor, *Bioinformatics*
- Since 2006 Editor, *PLOS Computational Biology* ISCB pages
- 2/06, 6/06, 1/07 Biomedical Data Management and Analysis NIH study section
- Since 2006 Editorial Board member, *Briefings in Bioinformatics*
- Since 2006 Editorial Board member, *Journal of Biomedical Informatics*
- 2005-2006 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 Genetics*, *Nature Oncogene*, *Nature Biotechnology*, *Bioinformatics*, *Protein Science*, *Pacific Symposium on Biocomputing*, *Nucleic Acids Research*, *BioMed Central Bioinformatics*, *Journal of Biomedical Informatics*, *Genome Research*.

SOFTWARE RELEASED

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. Guan Y, Dunham MJ, **Troyanskaya OG**. Functional analysis of gene duplications in *Saccharomyces cerevisiae*. *Genetics*. Epub ahead of print doi:10.1534/genetics.106.064329, 2006.
2. 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 (GCCB)*, 2006.
3. 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.
4. Chi A*, Huttenhower CH*, Geer LY, Coon JJ, Syka JEP, Bai 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*, 2006 in press.
5. 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, 2006.
6. 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.
7. Myers CL, Barrett D, Hibbs MA, Huttenhower C, **Troyanskaya OG**. Finding function: evaluation methods for functional genomic data. *BMC Genomics*. 7:187, 2006.
8. Huttenhower C, **Troyanskaya OG**. Bayesian Data Integration: A Functional Perspective. *Series on Advances in Bioinformatics and Computational Biology: Computational Systems Bioinformatics*. 4: 341, 2006.
9. 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):10, 2006.
10. Barutcuoglu Z, Schapire RE, **Troyanskaya OG**. Hierarchical Multi-label Prediction of Gene Function. *Bioinformatics*. 22(7): 830, 2006.
11. 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: 2006.001, 2006.

12. 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.
13. 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.
14. 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.
15. Myers CL, Chen X, **Troyanskaya OG**. Visualization-based discovery and analysis of genomic aberrations in microarray data. *BMC Bioinformatics*. 6:146, 2005.
16. Hibbs MA, Dirksen NC, Li K, **Troyanskaya OG**. Visualization Methods for Statistical Analysis of Microarray Clusters. *BMC Bioinformatics*. 6:115, 2005.
17. 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.
18. Li K, Hibbs M, Wallace G, **Troyanskaya OG**. Dynamic Scalable Visualization for Collaborative Scientific Applications. *IPDPS 2005 Workshop on Next Generation Software Proceedings*. 2005.
19. **Troyanskaya OG**. Putting the 'bio' into bioinformatics. *Genome Biology* 6(10):351, 2005.
20. **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.
21. **Troyanskaya OG**. Putting microarrays in a context: integrated analysis of diverse biological data. *Briefings in Bioinformatics*. 6 (1): 34-43, 2005.
22. Dolinski K, **Troyanskaya OG**. In: *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*, Jorde LB, Little PFR, Dunn MJ, Subramaniam S, Eds. John Wiley & Sons. 2005.
23. 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.
24. Liang MP, **Troyanskaya OG**, Laederach A, Brutlag DL, Altman RB. Computational Functional Genomics. *IEEE Signal Processing*. 21 (6): 62-69, 2004.
25. **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.
26. 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.
27. 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.
28. 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.

29. 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.
30. **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.
31. 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.
32. **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.
33. **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.
34. 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.
35. **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.