

Donna K. Slonim

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Education	Massachusetts Institute of Technology Ph.D. in Computer Science, minor in Genetics, Advisor: Ron Rivest. Dissertation: <i>Learning from Imperfect Data in Theory and Practice.</i>	1996
	University of California at Berkeley M.S. in Computer Science	1991
	Yale University B.S. in Computer Science	1990
Appointments	Tufts University <i>Professor, 2016-</i> , Computer Science <i>Professor, 2016-</i> , Tufts School of Medicine <i>Genetics Faculty</i> , Sackler School of Graduate Biomedical Sciences <i>Associate Professor, 2005-2016</i> , Computer Science and Pathology	2005–present
	Boston Children’s Hospital <i>Visiting Associate Professor</i> , Medicine	2011-2012
	Wyeth Research (formerly Genetics Institute) <i>Principal Scientist</i> , Bioinformatics	2000-2004
	MIT/Whitehead Institute Center for Genome Research <i>Research Scientist</i>	1996-2000
Teaching	Tufts University Courses taught at Tufts include: <ul style="list-style-type: none">• an introductory bioinformatics course for undergraduates in the life sciences,• undergraduate data structures,• the introductory computer science class for majors,• a senior/graduate course in algorithms for computational biology• graduate research seminars on research techniques and on biological networks	Medford, MA
Professional Activities	Systems Theme Chair, ISMB 2016. Highlights chair, RECOMB 2016. Scientific Advisory Board member, The Gene Ontology, 2016-. Special Sessions Chair, <i>ISMB</i> 2014. NIH Reviewer, Modeling and Analysis of Biological Systems (MABS), June 2014. Program Co-Chair, <i>ACM-BCB</i> 2013. Advisory board member, <i>Mouse Genome Database</i> , The Jackson Laboratory, Bar Harbor,	

ME, 2012–2015.

Gene Regulation Area Co-Chair, *ISMB* 2012.

Member of the Board of Directors, International Society of Computational Biology, 2010 – 2013 and 2000 – 2003.

Program committee, *Conference on Research in Computational Biology (RECOMB)*, 2015, 2009 – 2011, and 1999 – 2001.

Reviewer for NIH's BioData Management and Analysis (BDMA) study section, June, 2007; June, 2010; Feb., 2012.

Session Co-Chair, Dynamics of Biological Networks, *Pacific Symposium on Biocomputing (PSB)*, 2010.

Associate Editor, *PLoS Computational Biology*, June 2008 – present.

Editorial Board Member, *Journal of Biomedical Informatics*, November 2006 – January 2013.

Editorial Board Member/Advisor, *BMC Bioinformatics*, May 2005 – present.

Associate Editor of the ACM/IEEE journal *Transactions on Computational Biology and Bioinformatics (TCBB)*, February 2004 – February 2008.

Selected Publications

Noto K, Majidi S, Edlow AG, Wick HC, Bianchi DW, Slonim DK. CSAX: characterizing systematic anomalies in expression data. *Journal of Computational Biology*, 22(5):402-13, 2015.

Park J, Wick HC, Kee DE, Noto K, Maron JL, Slonim DK. Finding novel molecular connections between developmental processes and disease. *PLoS Comp. Biol.*, 10(5):e1003578, 2014.

Wick HC, Drabkin H, Ngu H, Sackman M, Fournier C, Haggett J, Blake JA, Bianchi DW, Slonim DK. DFLAT: functional annotation for human development. *BMC Bioinformatics*, Feb 7;15:45, 2014.

Pritchard S, Wick HC, Slonim DK, Johnson KL, Bianchi DW. Comprehensive analysis of genes expressed by rare microchimeric fetal cells in maternal lung. *Biol. of Reproduction*, Aug 23;87(2):42, 2012.

Hui L, Slonim DK, Wick HC, Johnson KL, Bianchi DW. The amniotic fluid transcriptome: a source of novel information about human fetal development. *Obstetrics and Gynecology*, Jan 119(1):111-8, 2012.

Noto KN, Brodley C, Slonim DK. FRaC: A feature-modeling approach for semi-supervised and unsupervised anomaly detection. *Data Mining and Knowl. Disc.*, 25(1):109-133, 2012.

Andrew D. Fox, Benjamin J. Hescott, Anselm Blumer, and Donna K. Slonim. Connectedness of PPI network neighborhoods identifies regulatory hub proteins. *Bioinformatics*, Apr 15;27(8):1135-42, 2011.

Koide K, Slonim DK, Johnson KL, Tantravahi U, Cowan JM, Bianchi DW. Transcriptomic analysis of cell-free fetal RNA suggests a specific molecular phenotype in trisomy 18. *Hum Genet.*, 129(3):295-305, Mar. 2011.

Sevin Turcan, Doug E. Vetter, Jill L. Maron, Xintao Wei, and Donna K. Slonim. Mining functionally relevant gene sets for analyzing physiologically novel clinical expression data. *Pacific Symposium on Biocomputing*, 16:50-61, Jan. 2011.

Keith Noto, Carla Brodley, and Donna K. Slonim. Anomaly detection using an ensemble of feature models. *Int'l Conf on Data Mining*, pp. 953-8, Sydney, Australia, Dec. 2010.

Andrew D. Fox, William A. Baumgartner Jr., Helen Johnson, Lawrence E. Hunter and Donna

- K. Slonim. Mining protein-protein interactions from GeneRIFs with OpenDMAP. *Lecture Notes in Computer Science*, 6004:43-52, May, 2010.
- Teresa M. Przytycka, Mona Singh, and Donna K. Slonim. Toward the dynamic interactome: It's about time. *Brief Bioinform* Jan;11(1):15-29, 2010.
- Donna K. Slonim*, Keiko Koide*, Kirby L. Johnson, Umadevi Tantravahi, Janet M. Cowan, Zina Jarrah, and Diana W. Bianchi. Functional genomic analysis of amniotic fluid cell-free mRNA suggests that oxidative stress is significant in Down syndrome fetuses. *Proc. Natl. Acad. Sci. USA* 106(23):9425-9, June, 2009.
- Andrew Fox, Daniel Taylor, and Donna K. Slonim. High throughput interaction data reveals degree conservation of hub proteins. *Pacific Symposium on Biocomputing* 14:391-402, 2009.
- Jill L. Maron, Kirby L. Johnson, Donna K. Slonim, Chaoqiang Lai, Marco Ramoni, Zina Jarrah, Zinger Yang, and Diana W. Bianchi. Gene expression analysis in pregnant women and their infants identifies unique fetal biomarkers that circulate in maternal blood. *Journal of Clinical Investigation*, 117(10):3007-19, October, 2007.
- Margot O'Toole, Derek B. Janszen, Donna K. Slonim, Padmalatha S. Reddy, Debra K. Ellis, Holly M. Legault, Andrew A. Hill, Maryann Z. Whitley, William M. Mounts, Krystyna Zuberek, Frederick W. Immermann, Ronald S. Black, and Andrew J. Dorner. Risk Factors Associated with Beta-Amyloid(1-42) Immunotherapy in Pre-immunization Gene Expression Patterns of Blood Cells. *Archives of Neurology*, 62:1531-36, October, 2005.
- Donna K. Slonim. From patterns to pathways: gene expression data analysis comes of age. *Nature Genetics*, 32(S):502-508, December, 2002.
- Jane E. Staunton, Donna K. Slonim, Hilary A. Collier, Pablo Tamayo, Michael J. Angelo, Johnny Park, Uwe Scherf, Jae K. Lee, William O. Reinhold, John N. Weinstein, Eric S. Lander, Todd R. Golub. Chemosensitivity prediction by transcriptional profiling. *Proc. Natl. Acad. Sci. USA*, 98(19):10787-10792, September, 2001
- Atul J. Butte, Pablo Tamayo, Donna Slonim, Todd R. Golub, Isaac S. Kohane. Discovering functional relationships between RNA expression and chemotherapeutic susceptibility using relevance networks. *Proc. Natl. Acad. Sci. USA* 97(22):12182-12186, October, 2000.
- Todd R. Golub*, Donna K. Slonim*, Pablo Tamayo, Christine Huard, Michelle Gaasenbeek, Jill P. Mesirov, Hilary Collier, Mignon L. Loh, James Downing, Mark Caligiuri, Clara Bloomfield, and Eric S. Lander. Molecular classification of cancer: Class discovery and class prediction by gene expression monitoring. *Science*, 286:531-537, October, 1999.
- Chad Nusbaum*, Donna Slonim*, Katrina Harris, Bruce Birren, Robert Steen, Lincoln Stein, Joyce Miller, *et al.*. A YAC-based physical map of the mouse genome. *Nature Genetics*, 22(4):388-393, August, 1999.
- Pablo Tamayo, Donna Slonim, Jill Mesirov, Qing Zhu, Sutisak Kitareewan, Ethan Dmitrovsky, Eric S. Lander, and Todd R. Golub. Interpreting gene expression with self-organizing maps: Methods and application to hematopoietic differentiation. *PNAS*, 96(6):2907-2912, March, 1999.
- Donna Slonim, Leonid Kruglyak, Lincoln Stein, and Eric Lander. Building human genome maps with radiation hybrids. *Journal of Computational Biology*, 4(4):487-504, Dec., 1997.
- Thomas J. Hudson, Lincoln Stein, Sebastian Gerety, Junli Ma, Andrew Castle, James Silva, Donna K. Slonim, *et al.* An STS-based map of the human genome. *Science*, 270(5244):1945-1954, Dec., 1995.

* These authors contributed equally to this work.