Donna K. Slonim

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Education

Massachusetts Institute of Technology 1996
Ph.D. in Computer Science, minor in Genetics, Advisor: Ron Rivest.
Dissertation: *Learning from Imperfect Data in Theory and Practice.*

University of California at Berkeley 1991
M.S. in Computer Science

Yale University 1990
B.S.in Computer Science

Appointments

Tufts University 2005–present
Professor, 2016-, Computer Science; Immunology (secondary)
Genetics Faculty, Tufts Graduate School Biomedical Sciences
Associate Professor, 2005-2016, Computer Science; Medicine

Broad Institute 2018-2019
Visiting Professor

Boston Children's Hospital 2011-2012
Visiting Associate Professor, Medicine

Wyeth Research (formerly Genetics Institute) 2000-2004
Principal Scientist, Bioinformatics

MIT/Whitehead Institute Center for Genome Research 1996-2000
Research Scientist

Selected Professional Activities

Fellow, International Society for Computational Biology, 2025.
Proceedings Co-Chair, *ISMB* 2020.
NCBI Board of Scientific Counselors, Member, 2018-2023.
Systems Theme Chair, *ISMB* 2016.
Highlights Chair, *RECOMB* 2016.
Scientific Advisory Board Member, *The Gene Ontology*, 2016-.
Special Sessions Chair, *ISMB* 2014.
NIH Reviewer, Modeling and Analysis of Biological Systems (MABS), June 2017; June 2014.
Program Chair, *ACM-BCB* 2013.
Advisory Board Member, *Mouse Genome Database*, The Jackson Laboratory, Bar Harbor, ME, 2012–2015.
Board of Directors, Int'l Society of Computational Biology, 2010 – 2013 and 2000 – 2003.
Program Committee, *RECOMB*, 2015-2019, 2009 – 2011, and 1999 – 2001.
NIH Reviewer, BioData Management and Analysis (BDMA), 3x 2007-2012.
Session Chair, Dynamics of Biological Networks, *Pacific Sympos. 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 – March 2015.

Teaching

Tufts University: courses taught include Medford, MA

- an introductory bioinformatics course for undergraduates in the life sciences
- a senior/graduate course in algorithms for computational biology
- undergraduate data structures
- the introductory computer science class for majors
- graduate seminars on research techniques and on biological networks
- statistical methods in bioinformatics for data science students

Selected Publications

Zhu H and Slonim DK. From noise to knowledge: probabilistic diffusion-based neural inference of gene regulatory networks. *J Comput Biol*, 31(11):1087-1103, 2024.

Zitnik M, Li MM, Wells A, Glass K, Morselli G, Krishnan A, Murali TM, Radivjac P, Roy S, Baudot A, *et al.*. Current and future directions in network biology. *Bioinfx. Advances*, 4(1):vbae099, 2024.

Batorsky R, Ceasrine AM, Shook LL, Kislal S, Bordt EA, Devlin B, Perlis RH, Slonim DK, Bilbo S, Edlow AG. Hofbauer cells and fetal brain microglia share transcriptional profiles and responses to maternal diet-induced obesity. *Cell Reports*, 43(6):114326, June, 2024.

Sapashnik D*, Newman R*, Pietras CM*, Zhou D, Qu F, Devkota K, Kofman L, Boudreau S, Fried I, Slonim DK. Cell-specific imputation of drug connectivity mapping with incomplete data. *PLOS One*; 18(2):e0278289, 2023.

Bumin A, Ritz A, Slonim D, Kahveci T, Huang K. FiT: fiber-based tensor completion for drug repurposing. ACM-BCB, Aug. 2022, 31:1-10. Best student-led paper award.

Pietras CM, Power L, Slonim DK. aTEMPO: pathway-specic temporal anomalies for precision therapeutics. *Pacific Symposium on Biocomputing*, 25:683-694, Jan. 2020.

Choobdar S, *et al.* Assessment of network module identification across complex diseases. *Nat. Methods.* 2019 Sep;16(9):843-852.

Park J, Hescott BJ, Slonim DK. Pathway centrality in protein interaction networks identifies functional mediators of pulmonary disease. *Scientific Reports*, 9:5863, 2019.

B Peters, SE Brenner, E Wang, D Slonim, MG Kann. Putting benchmarks in their rightful place: The heart of computational biology. *PLoS Comp. Biol.* 14 (11), e1006494, 2018.

CM Pietras, F Ocitti, DK Slonim. TEMPO: Detecting pathway-specific temporal dysregulation of gene expression in disease. *ACM-BCB* 2018:79-88.

Tarui T, Kim A, Flake A, McClain L, Stratigis J, Fried I, Newman R, Slonim DK, Bianchi DW. Amniotic fluid transcriptomics reflects novel disease mechanisms in fetuses with myelomeningocele. *Am J Obst & Gynec.*, 217(5):587, Nov. 2017.

Park J, Hescott BJ, Slonim DK. Towards a more molecular taxonomy of disease. *Journal of Biomedical Semantics*, Jul 27;8(1):25, 2017.

Slonim DK. Time is money: designing cost-effective time series experiments. *Cell Systems* 3(1):15-6, 2016.

Guedj F, Pennings JL, Ferres MA, Graham LC, Wick HC, Miczek KA, Slonim DK, Bianchi DW. The fetal brain transcriptome and neonatal behavioral phenotype in the Ts1Cje mouse model of Down syndrome. *Am J Med Genet Part A*, 167A(9):1993-2008, Sep. 2015.

Noto K, Majidi S, Edlow AG, Wick HC, Bianchi DW, Slonim DK. CSAX: characterizing systematic anomalies in expression data. *Journal of Comput. Biol.*, 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 CompBiol.*, 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.

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.

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.

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. Coller, 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 Coller, 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. *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.