

Curriculum Vitae—Nir Friedman

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Professional History

Professor	2009–present
Institute of Life Sciences Hebrew University, Jerusalem	
Professor	2007–present
School of Computer Science & Engineering Hebrew University, Jerusalem	
Associate Professor	2002–2007
School of Computer Science & Engineering Hebrew University, Jerusalem	
Senior Lecturer	1998–2002
School of Computer Science & Engineering Hebrew University, Jerusalem	
Postdoctoral Scholar	1996–1998
Division of Computer Science University of California, Berkeley	

Education

Ph.D. Computer Science, Stanford University	1992–1997
M.Sc. Math. & Computer Science, Weizmann Institute of Science	1990–1992
B.Sc. Math. & Computer Science, Tel-Aviv University	1983–1987

Awards

Michael Bruno Memorial Award	2010
European Research Council research award	2009-2014
Juludan Prize for Advancing Technology in Medicine	2007
Sir Zelman Cowen Universities Fund Prize for Discovery in Medical Research	2007
Yoram Ben-Porat Presidential Prize for Outstanding Young Researcher	2002

Best Paper Award <i>Intelligent Systems in Molecular Biology</i>	2001
“Inferring subnetworks from perturbed expression profiles” with D. Pe’er, A. Regev, and G. Elidan	
Best Paper Award <i>Uncertainty in Artificial Intelligence</i>	2001
“Multivariate information bottleneck” with O. Mosenzon, N. Slonim, and T. Tishby	
Harry & Abe Sherman Senior Lectureship in Computer Science	2000–2002
Alon Fellowship	1999–2002
Young Distinguished Researcher Sacher Trust’s prize	1998–1999
Outstanding Dissertation in Language, Logic and Computation	1998
1’st Annual FoLLI Prize	
IBM Graduate Fellowship	1995–1996

Visiting and Part-Time Positions

- Visiting Associate Professor, **Broad Institute, MIT and Harvard** Summer, 2007
- Visiting Associate Professor, **Harvard University** Summer, 2006
- Consultant, **Agilent Life Sciences** 2005-2008
- Visiting Researcher, **Microsoft Research** Summer, 2004
- Visiting Associate Professor, **Harvard University** 2003-2005
- Visiting Associate Professor, **Stanford University** Summer, 2003
- Visiting Assistant Professor, **Stanford University** Summers, 2001-2
- Visiting Research Associate, **Stanford University** Summer 1999
- Research Associate, **Stanford University** 1998
- 1997

Editorial Positions

- **Associate Editor:** *Journal of Artificial Intelligence Research* (2002–2005), *ACM Transactions on Computational Biology and Bioinformatics* (2004–2007), *Journal of Machine Learning Research* (2004–2007).
- **Editorial Board:** *Journal of Artificial Intelligence Research* (1999–2002), *Machine Learning* (2000–2001), *Journal of Machine Learning Research* (2000–2004).
- **Program Co-Chair:** Uncertainty in Artificial Intelligence (UAI), 2002.
- **Meeting Co-organizer:** Systems Biology: Global Regulation of Gene Expression, (Cold Spring Harbor Labs), 2006 and 2007.
- **Senior Program Committee:** Uncertainty in Artificial Intelligence (UAI): 2000, 2001, 2005, 2006, 2007, 2008 and 2009; National Conference on Artificial Intelligence (AAAI): 2006. Intelligent Systems for Molecular Biology (ISMB) 2009. Neural Information Processing Systems (NIPS) 2009.
- **Program Committee:** Uncertainty in Artificial Intelligence (UAI): 1996, 1997, 1998, 1999, 2003, and 2004; National Conference on Artificial Intelligence (AAAI): 1997, 1998, 1999, 2000, and 2002; International Conference on Machine Learning (ICML): 1997, 1998, 2001, and 2006; AI and Statistics: 1999, 2000, 2002, and 2005; Workshop on Algorithms in Bioin-

formatics (WABI): 2002; European Conference on Computational Biology (ECCB): 2002, 2003, 2006; Joint Conference on Artificial Intelligence (IJCAI): 2003, and 2005; Conference on Computational Molecular Biology (RECOMB): 2003, 2005, 2006, 2007, 2008 and 2009.

Refereeing

- **Journals:** *Artificial Intelligence*, *Machine Learning*, *Bioinformatics*, *Journal of Artificial Intelligence Research*, *Journal of Machine Learning Research*, *Journal of Computational Biology*, *Information and Computation*, *Games and Economic Behavior*, *Annals of Mathematics and Artificial Intelligence*, *Journal of the ACM*, *ACM Trans. Neural Networks*, *Systematic Biology*, *Proc. National Academy of Sciences USA*, *Journal of the American Statistical Association*, *Statistics and Computing*, *Nature Genetics*, *Nature*, *PLoS Biology*, *Genome Research*, *Nature Biotechnology*, *PLoS Computational Biology*, *Science*.
- **Conferences:** International Joint Conference on Artificial Intelligence (IJCAI), Annual Conference on Neural Information Processing Systems (NIPS), Annual Conference on Computational Learning Theory (COLT), International Conference on Computational Molecular Biology (RECOMB).

Invited Tutorials

- **Annual Conference on Neural Information Processing Systems (NIPS) '06:** “Computational Methods in Systems Biology: Prospects and Challenges” (with M. Schuldiner).
- **International Conference on Systems Biology (ICSB) '05:** “Graphical Probabilistic Models in Systems Biology”.
- **Uncertainty in Artificial Intelligence (UAI) '04:** “Graphical Models in Computational Molecular Biology”
- **Annual Conference on Neural Information Processing Systems (NIPS) '01:** “Learning Bayesian Networks from Data” (with D. Koller).
- **International Joint Conference on Artificial Intelligence (IJCAI) '99:** “Learning Bayesian Networks” (with M. Goldszmidt).
- **National Conference on Artificial Intelligence (AAAI) '98:** “Learning Bayesian Networks” (with M. Goldszmidt).

Selected Invited Talks

- Workshop on Machine Learning in Systems Biology **October, 2010**
- International Conference on Machine Learning **June, 2010**
- Systems Biology: Genomic Approaches to Transcriptional Regulation, Cold Spring Harbor Labs, **March, 2008**
- RECOMB Satalite Meeting On Regulatory Genomics **September, 2007**
- IEEE Statistical Signal Processing Workshop **August, 2007**
- Nineteenth International Joint Conference on Artificial Intelligence (IJCAI) **August, 2005**
- Tenth Conference on Artificial Intelligence and Statistics (AISTAT) **January, 2005**
- Integrative Post-Genomics: A multidisciplinary approach to living systems, Lyon **October, 2004**
- Lausanne Genomics Days, Lausanne **October, 2004**
- Systems Biology: Genomic Approaches to Transcriptional Regulation Cold Spring Harbor Labs, **March, 2004**
- 2nd Annual Pittsburgh International Lung Conference on “Functional Genomics of Lung Diseases: Bench to Bedside”, **October, 2003.**
- 2nd European Conference on Computational Biology (ECCB) **September, 2003**
- 4th Scandinavian Bioinformatics Meeting. **April, 2002**
- Computer Science Department, Stanford. **October, 2001**
“Broad Area Colloquium for Artificial Intelligence, Geometry, Graphics, Robotics and Vision”
- Ernest Schering Foundation, Berlin. **June, 2001**
“Workshop on Bioinformatics and Genome Analysis”
- Division of Informatics, University of Edinburgh. **May, 2001**
“Distinguished Speaker Series in Bioinformatics”

Selected Publications

Number of citations according to ISI citation index (ISI) and Google Scholar (GS).

- **N. Friedman**, M. Linial, I. Nachman, and D. Pe'er. "Using Bayesian networks to analyze expression data." *Journal of Computational Biology* **7**:601–620, 2000. **ISI: 715, GS: 1645**.
- **N. Friedman**, D. Geiger, and M. Goldszmidt. "Bayesian networks classifiers." *Machine Learning* **29**:131–163, 1997. **ISI: 647, GS: 1574** .
- E. Segal, M. Shapira, A. Regev, D. Pe'er, D. Botstein, D. Koller, and **N. Friedman**. "Module networks: identifying regulatory modules and their condition specific regulators from gene expression data". *Nature Genetics* **34**:166-178, 2003. **ISI: 554 , GS: 917**.
- A. Ben-Dor, L. Bruhn, **N. Friedman**, I. Nachman, M. Schummer, and Z. Yakhini. "Tissue classification with gene expression profiles." *Journal of Computational Biology* **7**:559–584, 2000. **ISI: 271, GS: 538**.
- **N. Friedman**. "Inferring cellular networks using probabilistic graphical models", *Science*, **303**:799-805, 2004. (Review) **ISI: 263, GS: 519**.
- E. Segal, **N. Friedman**, D. Koller, and E. Regev. "A module map showing conditional activity of expression modules in cancer." *Nature Genetics*, **36**:1090–8, 2004. **ISI: 257, GS: 341**.
- C.-L. Liu, T. Kaplan, M. Kim, S. Buratowski, S.L. Schreiber, **N. Friedman**, and O.J. Rando. "Single-nucleosome mapping of histone modifications in *S. cerevisiae*" *PLoS Biology*. **3**(10):e328, 2005. **ISI: 168, GS: 189**.
- I. Wapinski, A. Pfeffer, **N. Friedman**, and A. Regev. "Natural history and evolutionary principles of gene duplication in fungi" *Nature*, **449**:54-61, 2007. **ISI: 129, GS: 163**.
- E. Segal, **N. Friedman**, N. Kaminski, A. Regev and D. Koller. "From Signatures to Models: Understanding Cancer using Microarrays" *Nature Genetics*, **37 Suppl**:S38–45, 2005. (Review) **ISI: 116, GS: 209**.
- **N. Friedman** and D. Koller. "Being Bayesian about Bayesian network structure: A Bayesian approach to structure discovery in Bayesian networks." *Machine Learning* **50**:95-126, 2003. **ISI: 111, GS: 408**.
- M. Dion, T. Kaplan, M. Kim, S. Buratowski, **N. Friedman**, and O.J. Rando. "Dynamics of replication-independent histone turnover in budding yeast" *Science*, **315**:1405-8, 2007. **ISI: 92, GS: 102**.
- **N. Friedman**, L. Getoor, D. Koller, and A. Pfeffer. "Learning probabilistic relational models." *Proc. Sixteenth International Joint Conference on Artificial Intelligence*, 1999. **GS: 513**.
- **N. Friedman**. "The Bayesian structural EM algorithm." *Fourteenth Conf. on Uncertainty in Artificial Intelligence*, pp. 129–138, 1998. **GS: 423**.

Publications

Books

- [A1] D. Koller and **N. Friedman**. “Probabilistic Graphical Models: Principles and Techniques”, MIT Press, 2009.
- [A2] A. Darwiche and **N. Friedman**, editors. “Proceedings of the Eighteenth Conference on Uncertainty in Artificial Intelligence”, Morgan Kaufmann, 2002.

Peer-Reviewed Journal Papers

- [B1] N. Novershtern, A. Subramanian, L.N. Lawton, R.H. Mak, W.N. Haining, M.E. McConkey, N. Habib, N. Yosef, C.Y. Chang, T. Shay, G.M. Frampton, A.C. Drake, I. Leskov, B. Nilsson, F. Pfeffer, D. Dombkowski, J.W. Evans, T. Liefeld, J.S. Smutko, J. Chen, **N. Friedman**, R.A. Young, T.R. Golub, A. Regev, and B.L. Ebert. “Densely interconnected transcriptional circuits control cell States in human hematopoiesis” *Cell* **144**(2):296-309, 2011.
- [B2] B.R. Carone, L. Fauquier, N. Habib, J.M. Shea, C.E. Hart, R. Li, C. Bock, C. Li, H. Gu, P.D. Zamore, A. Meissner, Z. Weng, H.A. Hofmann, **N. Friedman**, and O.J. Rando. “Paternally induced transgenerational environmental reprogramming of metabolic gene expression in mammals” *Cell*. **143**(7):1084-96, 2010.
- [B3] I. Cohn, T. El-Hay, **N. Friedman**, and R. Kupferman. “Mean field variational approximation for continuous-time Bayesian networks.” *Journal of Machine Learning Research*, in press, 2010.
- [B4] M. Yassour, J. Pfiffner, J.Z. Levin, X. Adiconis, A. Gnirke, C. Nusbaum, D.A. Thompson, **N. Friedman**, A. Regev. “Strand-specific RNA sequencing reveals extensive regulated long antisense transcripts that are conserved across yeast species” *Genome Biology* **11**:R87, 2010.
- [B5] J.Z. Levin, M. Yassour, X. Adiconis, C. Nusbaum, D.A. Thompson, **N. Friedman**, A. Gnirke, and A. Regev. “Comprehensive comparative analysis of strand-specific RNA sequencing methods.” *Nature Methods*, **7**:109-115, 2010.
- [B6] A. Jaimovich, R. Rinott, M. Schuldiner, H. Margalit and **N. Friedman**. “Modularity and directionality in genetic interaction maps” *Bioinformatics* **26**:i228-36, 2010.
- [B7] T.S. Kim, C.L. Liu, M. Yassour, J. Holik, N. Friedman, S. Buratowski, and O.J. Rando. “RNA polymerase mapping during stress responses reveals widespread nonproductive transcription in yeast” *Genome Biology*, **11**:R75, 2010.
- [B8] M. Radman-Livaja, C.-L. Liu, **N. Friedman**, S.L. Schreiber, and O.J. Rando. “Replication and active demethylation represent partially overlapping mechanisms for erasure of H3K4me3 in budding yeast”. *PLoS Biology*, 2010.
- [B9] A. Weiner, A. Hughes, M. Yassour, O.J. Rando, and **N. Friedman**. “High-resolution nucleosome mapping reveals transcription-dependent promoter packaging”, *Genome Research* **20**:90-100, 2010.

- [B10] M. Garber, M. Guttman, M. Clamp, M.C. Zody, **N. Friedman** and X. Xie. “Identifying novel constrained elements by exploiting biased substitution patterns” *Bioinformatics* **25**:i54-62, 2009.
- [B11] R.H. Segman, T. Goltser-Dubner, I. Weiner, L. Canetti, E. Galili-Weisstub, A. Milwidsky, V. Pablov, **N. Friedman**, and D. Hochner-Celnikier. “Blood mononuclear cell gene expression signature of postpartum depression.” *Molecular Psychiatry*, **15**:93-100 2010.
- [B12] M. Yassour, T. Kaplan, H.B. Fraser, J.Z. Levin, J. Pfiffner, X. Adiconis, G. Schroth, S. Luo, I. Khrebtukova, A. Gnirke, C. Nusbaum, D.A. Thompson, **N. Friedman**, and A. Regev. “*Ab initio* construction of a eukaryotic transcriptome by massively parallel mRNA sequencing.” *Proc Natl Acad Sci U S A* **106**:3264-9, 2009.
- [B13] T. Kaplan, C-L. Liu, J.A. Erkmann, J. Holik, M. Grunstein, P.D. Kaufman, **N. Friedman**, and O.J. Rando. “Cell cycle- and chaperone-mediated regulation of H3K56ac incorporation in yeast” *PLoS Genetics* **4**(11):e1000270, 2008.
- [B14] A.P. Capaldi, T. Kaplan, Y. Liu, N. Habib, A. Regev, **N. Friedman**, and E.K. O’Shea.” Structure and function of a transcriptional network activated by the MAPK Hog1” *Nature Genetics* **40**(11):1300-6, 2008.
- [B15] I. Eisenberg, N. Novershtern, Z. Itzhaki, M. Becker-Cohen, M. Sadeh, P.H. Willems, **N. Friedman**, W.J. Koopman, and S. Mitrani-Rosenbaum. “Mitochondrial processes are impaired in hereditary inclusion body myopathy” *Human Molecular Genetics* **17**(23):3663-74, 2008.
- [B16] M. Yassour, T. Kaplan, A. Jaimovich, and **N. Friedman**. “Nucleosome positioning from tiling microarray data” *Bioinformatics* **24**:i139–146, 2008.
- [B17] N. Habib, T. Kaplan, H. Margalit, and **N. Friedman**. “A Novel Bayesian DNA Motif Comparison Method for Clustering and Retrieval” *PLoS Computational Biology* **4**(2):e1000010, 2008.
- [B18] N. Novershtern, Z. Itzhaki, O. Manor, **N. Friedman**, and N. Kaminski. “A Functional and Regulatory Map of Asthma” *American Journal of Respiratory and Cell Molecular Biology*, **38**(3):324-336, 2007.
- [B19] I. Wapinski, A. Pfeffer, **N. Friedman**, and A. Regev. “Natural history and evolutionary principles of gene duplication in fungi” *Nature*, **449**:54-61, 2007.
- [B20] I. Wapinski, A. Pfeffer, **N. Friedman**, and A. Regev. “Genome-wide reconstruction of phylogenetic gene trees” *Bioinformatics*, **23**:i549-58, 2007.
- [B21] M. Dion, T. Kaplan, M. Kim, S. Buratowski, **N. Friedman**, and O.J. Rando. “Dynamics of replication-independent histone turnover in budding yeast” *Science*, **315**:1405-8, 2007.
- [B22] M. Ninio, E. Privman, T. Pupko, and **N. Friedman**. “Phylogeny Reconstruction: Increasing the Accuracy of Pairwise Distance Estimation Using Bayesian Inference of Evolutionary Rates” *Bioinformatics*, **23**:e136-41, 2007.
- [B23] N. Slonim, **N. Friedman**, and N. Tishby. “Multivariate information bottleneck”, *Neural Computation*, **18**:1739–89, 2006.

- [B24] A. Jaimovich, G. Elidan, H. Margalit, and **N. Friedman**. “Towards an Integrated Protein-protein Interaction Network: A Relational Markov Network Approach” *Journal of Computational Biology*, **13**:2, 145–164, 2006.
- [B25] I. Mayrose, **N. Friedman**, and T. Pupko. “A Gamma mixture model better accounts for among site rate heterogeneity”. *Bioinformatics* **21 Suppl 2**:ii151-ii158, 2005.
- [B26] C.-L. Liu, T. Kaplan, M. Kim, S. Buratowski, S.L. Schreiber, **N. Friedman**, and O.J. Rando. “Single-nucleosome mapping of histone modifications in *S. cerevisiae*” *PLoS Biology*. **3**(10):e328, 2005.
- [B27] T. Kaplan, **N. Friedman**, and H. Margalit “Ab initio prediction of transcription factor targets using structural knowledge” *PLoS Computational Biology* **1**(1):e1, 2005.
- [B28] E. Segal, D. Pe’er, A. Regev, D. Koller and **N. Friedman**. “Learning Module Networks” *Journal of Machine Learning Research* **6**: 557–588, 2005.
- [B29] R.H. Segman, N. Shefi, T. Goltser-Dubner, **N. Friedman**, N. Kaminski, and A. Y. Shalev. “Peripheral blood mononuclear cell gene expression profiles identify emergent post-traumatic stress disorder among trauma survivors”. *Molecular Psychiatry*, **10**:500–13, 2005.
- [B30] G. Elidan and **N. Friedman**. “Learning hidden variable networks: The information bottleneck approach”. *Journal of Machine Learning Research*, **6**:81–127, 2005.
- [B31] G. Bejerano, **N. Friedman**, and N. Tishby. “Efficient exact p-value computation for small sample, sparse, and surprising categorical data” *Journal of Computational Biology* **11**:867–886, 2004.
- [B32] E. Segal, **N. Friedman**, D. Koller, and E. Regev. “A module map showing conditional activity of expression modules in cancer.” *Nature Genetics*, **36**:1090–8, 2004.
- [B33] Y. Barash, G. Elidan, T. Kaplan, and **N. Friedman**. “CIS: Compound importance sampling method for protein-DNA binding site p-value estimation.” *Bioinformatics*, **21**:596-600, 2004.
- [B34] R.M. Marion, A. Regev, E. Segal, Y. Barash, D. Koller, **N. Friedman**, and E.K. O’Shea. “Sfp1 is a stress- and nutrient-sensitive regulator of ribosomal protein gene expression.” *Proc Natl Acad Sci U S A.*, **101**:14315–22, 2004.
- [B35] M. Horowitz, L. Eli-Berchoer, I. Wapinski, **N. Friedman**, and E. Kodesh. “Stress related genomic responses during the course of heat acclimation and its association with ischemic/reperfusion cross-tolerance”. *J Appl Physiol*, **97**:1496–507, 2004.
- [B36] I. Nachman, A. Regev, and **N. Friedman**. “Inferring quantitative models of regulatory networks from expression data” *Bioinformatics*, **20** suppl 1:I248-I256, 2004.
- [B37] A. Achiron, M. Gurevich, **N. Friedman**, N. Kaminski, M. Mandel. “Blood transcriptional signatures of multiple sclerosis: Unique gene expression of disease activity”. *Annals of Neurology*, **55**:410-7, 2004.
- [B38] Y. Barash, E. Dehan, M. Krupsky, W. Franklin, M. Geraci, **N. Friedman**, and N. Kaminski. “Comparative analysis of algorithms for signal quantitation from oligonucleotide microarrays”. *Bioinformatics*, **20**:839-46, 2004.

- [B39] E. Segal, M. Shapira, A. Regev, D. Pe’er, D. Botstein, D. Koller, and **N. Friedman**. “Module networks: identifying regulatory modules and their condition specific regulators from gene expression data”. *Nature Genetics* **34**:166-178, 2003.
- [B40] B. Dekel, T. Burakova, F. Arditti, S. Reich-Zeliger, S. Aviel-Ronen, G. Rechavi, **N. Friedman**, N. Kaminski, J. Passwell, Y. Reisner. “Human and porcine early kidney precursors as a new source for transplantation”. *Nature Medicine* **9**:53-60, 2003.
- [B41] **N. Friedman** and D. Koller. “Being Bayesian about Bayesian network structure: A Bayesian approach to structure discovery in Bayesian networks.” *Machine Learning* **50**:95-126, 2003.
- [B42] L. Getoor, **N. Friedman**, B. Taskar, and D. Koller. ”Learning probabilistic models of link structure.” *Journal of Machine Learning Research* **3**:679–707, 2002.
- [B43] Y. Barash and **N. Friedman**. “Context-specific Bayesian clustering for gene expression data”. *Journal of Computational Biology* **9**(2):169-191, 2002.
- [B44] **N. Friedman**, M. Ninio, I. Pe’er, and T. Pupko. “A structural EM algorithm for phylogenetic inference”. *Journal of Computational Biology* **9**(2):331-353, 2002.
- [B45] T. Pupko, I. Pe’er, M. Hasegawa, D. Graur, and **N. Friedman**. “A branch-and-bound algorithm for the inference of ancestral amino-acid sequences when the replacement rate varies among sites: Application to the evolution of five families”. *Bioinformatics* **18**:1116-1123, 2002.
- [B46] D. Pe’er, A. Regev, G. Elidan, and **N. Friedman**. “Inferring subnetworks from perturbed expression profiles”. *Bioinformatics* **17**, suppl. 1 S215-24, 2001.
- [B47] E. Segal, B. Taskar, A. Gasch, **N. Friedman**, and D. Koller. “Rich probabilistic models for gene expression”. *Bioinformatics*, **17**, suppl. 1 S243-52, 2001.
- [B48] A. Ben-Dor, L. Bruhn, **N. Friedman**, I. Nachman, M. Schummer, and Z. Yakhini. “Tissue classification with gene expression profiles.” *Journal of Computational Biology* **7**:559–584, 2000.
- [B49] **N. Friedman**, M. Linial, I. Nachman, and D. Pe’er. “Using Bayesian networks to analyze expression data.” *Journal of Computational Biology* **7**:601–620, 2000.
- [B50] **N. Friedman** and J. Y. Halpern. “Plausibility measures and default reasoning.” *Journal of the ACM* **48**:4, 2001, pp. 648–685.
- [B51] R. I. Brafman and **N. Friedman**. “On decision-theoretic foundations for defaults.” *Artificial Intelligence* **133**:1-33, 2001.
- [B52] **N. Friedman**, J. Y. Halpern, and D. Koller. “Conditional first-order logic revisited”. *ACM Trans. Computational Logic(TOCL)* **1**:175-207, 2000.
- [B53] **N. Friedman** and J. Y. Halpern. “Belief revision: A critique.” *Journal of Logic, Language, and Information* **8**:401–420, 1999.
- [B54] **N. Friedman** and J. Y. Halpern. “Modeling beliefs in dynamic systems. Part II: Revision and update.” *Journal of Artificial Intelligence Research* **10**:117–167, 1999.

- [B55] **N. Friedman**, D. Geiger, and M. Goldszmidt. “Bayesian networks classifiers.” *Machine Learning* **29**:131–163, 1997.
- [B56] **N. Friedman** and J. Y. Halpern. “Modeling beliefs in dynamic systems. Part I: Foundations.” *Artificial Intelligence* **95**:257–316, 1997.

Invited Papers and Book Chapters

- [C1] **N. Friedman** and M. Schuldiner. “The DNA Damage Road Map” (Perspective). *Science* **330**:1327-8, 2010.
- [C2] A. Jaimovich and **N. Friedman**. “From Large-scale Assays to Mechanistic Insights: Computational Analysis of Interactions” *Current Opinion in Biotechnology*, in press, 2010.
- [C3] E. Segal, **N. Friedman**, N. Kaminski, A. Regev and D. Koller. “From Signatures to Models: Understanding Cancer using Microarrays” *Nature Genetics*, **37 Suppl**:S38–45, 2005.
- [C4] A. Regev and **N. Friedman**. “Identifying Regulatory Networks Lessons from Yeast to Humans”. *American Journal of Respiratory and Cell Molecular Biology* **31**:125–132, 2004.
- [C5] **N. Friedman**. “Inferring cellular networks using probabilistic graphical models”, *Science*, **303**:799-805, 2004.
- [C6] **N. Friedman**. “Probabilistic models for identifying regulation networks”. *Bioinformatics* **19 Suppl 2**:II57, 2003.
- [C7] N. Kamniski, and **N. Friedman**. “Practical approaches to analyzing results of microarray experiments”. *American Journal of Respiratory and Cell Molecular Biology* **27**:125–132, 2002.
- [C8] **N. Friedman** and N. Kamniski. “Statistical methods for analyzing gene expression data for cancer research”. In H. W. Mewes, H. Seidel, and B. Weiss, eds. *Ernest Schering Foundation Workshop: Volume 38: Bioinformatics and Genome Analysis*, 2002.
- [C9] **N. Friedman** and R. Kohavi. “Bayesian classification”. In *Handbook of Data Mining and Knowledge Discovery*, Oxford University Press, 2002.
- [C10] **N. Friedman** and J. Halpern. “Plausibility measures and default reasoning: an overview”. In *Proceedings of the 14th IEEE Symposium on Logic in Computer Science*, pp. 130-135, 1999.

Peer-Reviewed Book Chapters

- [D1] L. Getoor, **N. Friedman**, D. Koller, and A. Pfeffer. “Learning probabilistic relational models.” In S. Dzeroski and N. Lavrac, eds. *Relational Data Mining*, Springer-Verlag, pp. 307–337, 2001.
- [D2] **N. Friedman** and M. Goldszmidt. “Learning Bayesian networks with local structure.” In M. I. Jordan ed. *Learning in Graphical Models*, Kluwer Academic Press, 1998, pp. 421–460.

Peer-Reviewed Conference Proceedings

- [E1] T. El-Hay, I. Cohn, **N. Friedman**, and R. Kupferman. “Continue-time belief propagation” *Proc. Twenty Seventh International Conf. on Machine Learning*, 2010.
- [E2] I. Cohn, T. El-Hay, **N. Friedman**, and R. Kupferman. “Mean field variational approximation for continuous-time Bayesian networks.” *Twenty Fifth Conference on Uncertainty in Artificial Intelligence*, 2009.
- [E3] O. Meshi, A. Jaimovich, A. Globerson, and **N. Friedman**. “Convexifying the Bethe free energy.” *Twenty Fifth Conference on Uncertainty in Artificial Intelligence*, 2009.
- [E4] T. El-Hay, **N. Friedman**, and R. Kupferman. “Gibbs sampling in factorized continuous-time Markov processes” *Twenty Fourth Conference on Uncertainty in Artificial Intelligence*, 2008.
- [E5] A. Jaimovich, O. Meshi, and **N. Friedman**. “Template based inference in symmetric relational Markov random fields” *Twenty Third Conference on Uncertainty in Artificial Intelligence*, 2007.
- [E6] T. El-Hay, **N. Friedman**, D. Koller, and R. Kupferman. “Continuous time Markov networks” *Twenty Second Conference on Uncertainty in Artificial Intelligence*, 2006.
- [E7] **N. Friedman** and R. Kupferman. “Dimension reduction in singularly perturbed continuous-time Bayesian networks” *Twenty Second Conference on Uncertainty in Artificial Intelligence*, 2006.
- [E8] A. Jaimovich, G. Elidan, H. Margalit, and **N. Friedman**. “Towards an integrated protein-protein interaction network” *Ninth Annual International Conference on Computational Molecular Biology*, 2005.
- [E9] T. Kaplan, **N. Friedman**, and H. Margalit. “Predicting transcription factor binding sites using structural knowledge” *Ninth Annual International Conference on Computational Molecular Biology*, 2005.
- [E10] I. Nachman, G. Elidan, and **N. Friedman**. “Ideal parent structure learning for continuous variable networks” *Twentieth Conference on Uncertainty in Artificial Intelligence*, 2004.
- [E11] E. Segal, R. Yelensky, A. Kaushal, T. Pham, A. Regev, D. Koller, and **N. Friedman**. “GeneXPress: A Visualization and Statistical Analysis Tool for Gene Expression and Sequence Data” *Eleventh Inter. Conf. on Intelligent Systems for Molecular Biology (ISMB)*, 2004.
- [E12] Y. Barash, G. Elidan, **N. Friedman**, and T. Kaplan. “Modeling Dependencies in Protein-DNA Binding Sites”. *Seventh Annual International Conference on Computational Molecular Biology*, 2003.
- [E13] G. Elidan and **N. Friedman**. “The information bottleneck EM Algorithm”. *Nineteenth Conference on Uncertainty in Artificial Intelligence*, 2003.
- [E14] E. Segal, D. Pe’er, A. Regev, D. Koller, and **N. Friedman**. “Learning Module Networks”. *Nineteenth Conference on Uncertainty in Artificial Intelligence*, 2003.
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