Curriculum Vitae—Nir Friedman

School of Computer Science and Engineering
Alexander Silberman Institute of Life Sciences
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Professional History

Professor **2009–present**
Alexander Silberman Institute of Life Sciences **The Hebrew University of Jerusalem**

Professor **2007–present**
School of Computer Science & Engineering **The Hebrew University of Jerusalem**

Associate Professor **2002–2007**
School of Computer Science & Engineering **The Hebrew University of Jerusalem**

Senior Lecturer **1998–2002**
School of Computer Science & Engineering **The Hebrew University of 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

Alexander von Humboldt Foundation Research Award **2015**

Fellow of the *International Society of Computational Biology* **2014**

European Research Council “Advanced Grant” research award **2014-2018**

“Test of Time” Award *Research in Computational Molecular Biology (RECOMB)* **2012**
Most cited paper in 12-year window in RECOMB

Michael Bruno Memorial Award **2010**
“Israeli scholars and scientists of truly exceptional promise, whose achievements to date suggest future breakthroughs in their respective fields” [age < 50]

European Research Council “Advanced Grant” research award **2009-2013**

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 *Intelligent Systems in Molecular Biology* **2001**

Best Paper Award *Uncertainty in Artificial Intelligence* **2001**

Harry & Abe Sherman Senior Lectureship in Computer Science **2000–2002**

Alon Fellowship **1999–2002**

Young Distinguished Researcher Sacher Trust's prize **1998–1999**
Hebrew University President's prize for Young faculty.

Outstanding Dissertation in Language, Logic and Computation **1998**

IBM Graduate Fellowship **1995–1996**

Visiting and Part-Time Positions

- Visiting Professor, **Max Delbruck Center for Molecular Medicine** **Fall 2016, 2017**.
- Visiting Professor, **Broad Institute, MIT and Harvard** **Fall, 2015 - Fall, 2016**
- Visiting Associate Professor, **Broad Institute, MIT and Harvard** **Summer, 2007**
- Consultant, **Agilent Life Sciences** **2005-2008**
- Visiting Researcher, **Microsoft Research** **Summer, 2004**
- Visiting Associate Professor, **Harvard University** **2003-2005; Summer, 2006**
- Visiting Professor, **Stanford University** **Summers, 1999, 2001-3**

Scientific Leadership

- **Lead PI and Coordinator** ISF I-CORE Excellence Center "The role of chromatin, RNA modifications and non-coding RNAs in regulation of gene expression in development and disease". **2013–2018**
- **Coordinator** Etgar excellence program in Life Sciences, Hebrew U. **2012–present**
- **Co-founder and coordinator** Interdisciplinary program for B.Sc. in Computer Science and Computational Biology, Hebrew U. **1999–2016**

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), *eLife* (2014–2016).
- **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.
- **Meeting Co-organizer**: Broad-ISF Annual Cell Circuit Symposium. 2013–present.

Refereeing

- **Journals:** *ACM Trans. Neural Networks, Annals of Mathematics and Artificial Intelligence, Artificial Intelligence, Bioinformatics, Cell, Cell Systems, eLife, Games and Economic Behavior, Genome Research, Information and Computation, J. ACM, J. American Statistical Association, J. Artificial Intelligence Research, J. Computational Biology, J. Machine Learning Research, Machine Learning, Molecular Cell, Molecular Systems Biology, Nature, Nature Biotechnology, Nature Genetics, Nucleic Acid Research, PLoS Biology, PLoS Computational Biology, Proc. National Academy of Sciences USA, Science, Statistics and Computing, Systematic Biology* .
- **Funding organizations:** Israel Science Foundation, Israeli Ministry of Science, European Research Council.
- **Scientific Advisory Board:** Max Planck Institute for Informatics, Cluster of Excellence "Multimodal Computing and Interaction" (University of Saarbrucken).

Students

PHD Students:

- Dana Pe'er (1998–2003), currently Professor Memorial Sloan Kettering Cancer Center
- Gal Elidan (1998–2004), currently Associate Professor, Hebrew University
- Iftach Nachman (1998–2004), currently Assistant Professor, Tel Aviv University
- Yoseph Barash (1999– 2006), currently Associate Professor, U. Penn.
- Tommy Kaplan (2002–2008), currently Associate Professor, Hebrew University
- Matan Ninio (2002–2010), currently Researcher at IBM Research
- Noa Shefi (2004–2010), currrently Research Associate, Weizmann Institute of Science
- Ariel Jaimovich (2004-2010), currently Researcher in Guardant Health
- Tal El-Hay (2005–2012), currently Researcher at IBM Research
- Naomi Habib (2007–2012), currently Assistant Professor, Hebrew University
- Moran Yassour (2007–2012), currently Assistant Professor, Hebrew University
- Ofer Meshi (2006–2013), currently Researcher at Google
- Assaf Weiner (2010–2015), currently Postdoctoral Fellow, Weizmann Institute of Science
- Avital Klein (2011–2018), currently in MobileEye.
- Jenia Gutin (2013–present)
- Alon Appleboim (2014–present)
- Gavriel Fialkoff (2018–present)

MSC Students:

- Tal El-Hay (1998–2001)
- Matan Ninio (1999–2001)
- Ori Mosenzon (1999–2004)
- Tomer Naveh (2001–2004)
- Noa Shefi (2002–2004)
- Ariel Jaimovich (2002–2004)
- Omri Peleg (2002-2005)
- Naomi Habib (2005–2007)
- Moran Yasour (2005–2007)
- Ofer Meshi (2006–2007)
- Ido Cohn (2007–2010).
- Assaf Weiner (2007–2010)
- Ruty Rinott (2008–2010)
- Aharon Novogrodski (2008–2010)
- Avital Klein (2009-2011)
- Jenia Gutin (2010-2013)
- Daniel Haimovich (2012–2015)
- Alon Appleboim (2013–2014)
- Maayan Baral (2014–2017)

- Noa Moriel (2016–2018)
- Gavriel Fialkoff (2016–2018)
- Dana Perez (2017–present)
- Michal Bazir (2017–present)

Impact and Scholarly Contributions

More than 100 publications in peer-reviewed journals, edited books, and conferences. **These publications are highly cited — H-index: 49/86** according to ISI and Google Scholar, respectively (the discrepancies are due to peer-reviewed conference papers that are not processed by ISI).

Selected Publications

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

- **N. Friedman**, D. Geiger, and M. Goldszmidt. “Bayesian networks classifiers.” *Machine Learning* **29**:131–163, 1997. **ISI: 1733, GS: 4365**.
- **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: 1523, GS: 3594**.
- 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: 1012 , GS: 1789**.
- **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: 316, GS: 793**.
- **N. Friedman**. “Inferring cellular networks using probabilistic graphical models”, *Science*, **303**:799-805, 2004. (Review) **ISI: 619, GS: 1220**.
- 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: 479, GS: 732**.
- 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: 324, GS: 493**.
- 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: 390, GS: 529**.
- 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: 334, GS: 463**.
- 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. **ISI: 122, GS: 170**.
- D. Koller and **N. Friedman**. “Probabilistic Graphical Models: Principles and Techniques”, MIT Press, 2009. **GS: 4809**.
- 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. **ISI: 212, GS: 295**.

- M.G. Grabherr, B.J. Haas, M. Yassour, J.Z. Levin, D.A. Thompson, I. Amit, X. Adiconis, L. Fan, R. Raychowdhury, Q. Zeng, Z. Chen, E. Mauceli, N. Hacohen, A. Gnirke, N. Rhind, F. di Palma, B.W. Birren, C. Nusbaum, K. Lindblad-Toh, **N. Friedman** and A. Regev. "Full-length transcriptome assembly from RNA-Seq data without a reference genome", *Nature Biotechnology* **29**:644-652, 2011. **ISI: 4370, GS: 5897**.

- M. Radman-Livaja. K. Verrzijlbergen, A. Weiner, **N. Friedman**, O.J. Rando, and, F. van Leeuwen. "Patterns and mechanisms of ancestral histone protein inheritance in budding yeast", *PLoS Biology*, **9**:e1001075, 2011. **ISI: 75, GS: 96**.

- A. Weiner, H.V. Chen, C-L. Liu, A. Rahat, A. Klein, L. Soares, M. Gudipati, J. Pfeffner, A. Regev, S. Buratowski, J.A. Pleiss5, **N. Friedman**, and O.J. Rando. "Systematic dissection of roles for chromatin regulators in a yeast stress response", *PLoS Biology* **10**:e1001369, 2012 **ISI: 70, GS: 93**.

- D. Lara-Astiaso, A. Weiner, E. Lorenzo-Vivas, I. Zaretsky, D.A. Jaitin, E. David, H. Keren-Shaul, A. Mildner, D. Winter, S. Jung, **N. Friedman**, I. Amit. "Chromatin state dynamics during blood formation" *Science* **345**:943-949, 2014. **ISI: 233, GS: 307**.

- J. Gutin, A. Sadeh, A. Rahat, A. Aharoni, and **N. Friedman**. "Condition-specific genetic interaction maps reveal crosstalk between the cAMP/PKA and the HOG MAPK pathways in the activation of the general stress response" *Molecular Systems Biology* **11**:829, 2015. **ISI: 5, GS: 8**

- A. Weiner, T.-H. Hsieh, A. Appleboim, H.V. Chen, A. Rahat, I. Amit, O.J. Rando, and **N. Friedman**. "High-Resolution chromatin dynamics during a yeast stress response" *Molecular Cell* **58**:371-386, 2015. **ISI: 25, GS: 37**

- R. Sadeh, R. Launer-Wachs, H. Wandel, A. Rahat, and **N. Friedman**. "Elucidating Combinatorial Chromatin States at Single-Nucleosome Resolution" *Molecular Cell* **63**:1080-1088, 2016 **ISI: 5, GS: 12**

- A. Dixit, O. Parnas, B. Li, J. Chen, C.P. Fulco, L. Jerby-Arnon, N.D. Marjanovic, D. Dionne, T. Burks, R. Raychowdhury, B. Adamson, T.M. Norman, E.S. Lander, J.S. Weissman, **N. Friedman**, and A. Regev. "Perturb-seq: dissecting molecular circuits with scalable single-cell RNA profiling of pooled genetic screens" *Cell* **7**:1853-1866. e17, 2016 **ISI:71 , GS: 112**

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] A. Klein-Brill, D. Joseph-Strauss, A. Appleboim, and **N. Friedman**. “Dynamics of Chromatin and Transcription during Transient Depletion of the RSC Chromatin Remodeling Complex” *Cell Reports* **26**:279-292, 2019.

[B2] M. Radzinski, R. Fassler, O. Yogev, W. Breuer, N. Shai, J. Gutin, S. Ilyas, Y. Geffen, S. Tsytkin-Kirschenzweig, Y. Nahmias, T. Ravid, **N. Friedman**, M. Schuldiner, D. Reichmann “Temporal profiling of redox-dependent heterogeneity in single cells” *eLife* **7**, e37623, 2018.

[B3] J. Gutin, R. Sadeh, N. Bodenheimer, D. Joseph-Strauss, A. Klein-Brill, A. Alajem, O. Ram, and **N. Friedman**. “Fine-Resolution Mapping of TF Binding and Chromatin Interactions” *Cell Reports* **22**:2797-2807, 2018.

[B4] Y. Ichikawa, C,F. Connelly, A. Appleboim, T.C.R. Miller, H. Jacobi, N.A. Abshiru, H-J. Chou, Y. Chen, U. Sharma, Y. Zheng, P.M. Thomas, H.V. Chen, V. Bajaj, C.W. Muller, N.L. Kelleher, **N. Friedman**, D.N.A. Bolon, O.J. Rando, and P.D. Kaufman. “A synthetic biology approach to probing nucleosome symmetry” *eLife* 6:e28836, 2017

[B5] A. Dixit, O. Parnas, B. Li, J. Chen, C.P. Fulco, L. Jerby-Arnon, N.D. Marjanovic, D. Dionne, T. Burks, R. Raychowdhury, B. Adamson, T.M. Norman, E.S. Lander, J.S. Weissman, **N. Friedman**, and A. Regev. “Perturb-seq: dissecting molecular circuits with scalable single-cell RNA profiling of pooled genetic screens” *Cell* **7**:1853-1866. e17, 2016

[B6] Y. Geffen, A. Appleboim, R.G. Gardner, **N. Friedman**, R. Sadeh, and T. Ravid. “Mapping the Landscape of a Eukaryotic Degronome” *Molecular Cell* **6**:1055-1065, 2016

[B7] G. Levy, N. Habib, M.A. Guzzardi, D. Kitsberg, D. Bomze, E. Ezra, B.E. Uygun, K. Uygun, M. Trippler, J.F. Schlaak, O. Shibolet, E.H. Sklan, M. Cohen, J. Timm, **N. Friedman**, and Y. Nahmias. “Nuclear receptors control pro-viral and antiviral metabolic responses to hepatitis C virus infection” *Nature Chemical Biology* **12**:1037-1045, 2016

[B8] R. Sadeh, R. Launer-Wachs, H. Wandel, A. Rahat, and **N. Friedman**. “Elucidating Combinatorial Chromatin States at Single-Nucleosome Resolution” *Molecular Cell* **63**:1080-1088, 2016

[B9] J. Gutin, A. Sadeh, A. Rahat, A. Aharoni, and **N. Friedman**. ”Condition-specific genetic interaction maps reveal crosstalk between the cAMP/PKA and the HOG MAPK pathways in the activation of the general stress response” *Molecular Systems Biology* **11**:829, 2015.

[B10] A. Weiner, T.-H. Hsieh, A. Appleboim, H.V. Chen, A. Rahat, I. Amit, O.J. Rando, and **N. Friedman**. ”High-Resolution chromatin dynamics during a yeast stress response” *Molecular Cell* **58**:371-386, 2015.

[B11] T.-H. Hsieh, A. Weiner, B. Lajoie, J. Dekker, **N. Friedman**, and O.J. Rando. ”Mapping nucleosome resolution chromosome folding in yeast by Micro-C” *Cell* **162**:108-119, 2015.

[B12] I. Lerner, O. Bartok, V. Wolfson, J.S. Menet, U. Weissbein, S. Afik, D. Haimovich, C .Gafni, **N. Friedman**, M. Rosbash, and S. Kadener. ”Clk post-transcriptional control denoises circadian transcription both temporally and spatially” *Nature Communications* **6**, 2015.

[B13] M. Rege, V. Subramanian, C. Zhu, T.-H. Hsieh, A. Weiner, **N. Friedman**, S. Clauder-Munster, L.M. Steinmetz, O.J. Rando, L.A. Boyer, and C.L. Peterson. ”Chromatin dynamics and the RNA exosome function in concert to regulate transcriptional homeostasis” *Cell Reports* **8**:1610-1622, 2015.

[B14] M. Rabani, R. Raychowdhury, M. Jovanovic, M. Rooney, D.J. Stumpo, A. Pauli, N. Hacohem, A.F. Schier, P.J. Blackshear, **N. Friedman**, I. Amit, and A. Regev. “High-resolution sequencing and modeling identifies distinct dynamic RNA regulatory strategies” *Cell* **159**:1698-1710, 2014.

[B15] D. Lara-Astiaso, A. Weiner, E. Lorenzo-Vivas, I. Zaretsky, D.A. Jaitin, E. David, H. Keren-Shaul, A. Mildner, D. Winter, S. Jung, **N. Friedman**, and I. Amit. “Chromatin state dynamics during blood formation” *Science* **345**:943-949, 2014.

[B16] A. Shalek, R. Satija, J. Shuga, J.J. Trombetta, D. Gennert, D. Lu, P. Chen, R.S. Gertner, J.T. Gaublomme, N. Yosef, S. Schwartz, B. Fowler, S. Weaver, J. Wang, X. Wang, R. Ding, R .Raychowdhury, **N. Friedman**, N. Hacohen, H. Park, A.P. May, and A. Regev. “Single-cell RNA-seq reveals dynamic paracrine control of cellular variation”. *Nature* **510**:363-369, 2014.

[B17] B.J. Haas, A. Papanicolaou, M. Yassour, M. Grabherr, P.D. Blood, J. Bowden, M.B. Couger, D. Eccles, B. Li, M. Lieber, M.D. Macmanes, M. Ott, J. Orvis, N. Pochet, F. Strozzi, N. Weeks, R. Westerman, T. William, C.N. Dewey, R. Henschel, R.D. Leduc, **N. Friedman**, and A. Regev. “De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis.” *Nat Protoc* **8**:1494-512, 2013

[B18] N. Habib, I. Wapinski, H. Margalit, A. Regev and **N. Friedman**. “A functional selection model explains evolutionary robustness despite plasticity in regulatory networks”, *Molecular Systems Biology* **8**:1, 2012

[B19] M. Garber, N. Yosef, A. Goren, R. Raychowdhury, A. Thielke, M. Guttman, J. Robinson, B. Minie, N. Chevrier, Z. Itzhaki, R. Blecher-Gonen, C. Bornstein, D. Amann-Zalcenstein, A. Weiner, D. Friedrich, J. Meldrim, O. Ram, C. Cheng, A. Gnirke, S. Fisher, **N. Friedman**, B. Wong, B.E. Bernstein, C. Nusbaum, N. Hacohen, A. Regev, and I. Amit.”A high-throughput chromatin immunoprecipitation approach reveals principles of dynamic gene regulation in mammals”, *Molecular Cell*, **47**:810-22, 2012

[B20] A. Weiner, H.V. Chen, C-L. Liu, A. Rahat, A. Klein, L. Soares, M. Gudipati, J. Pfeffner, A. Regev, S. Buratowski, J.A. Pleiss5, **N. Friedman**, and O.J. Rando. “Systematic dissection of roles for chromatin regulators in a yeast stress response”, *PLoS Biology* **10**:e1001369, 2012

[B21] G.A. Brar, M. Yassour, **N. Friedman**, A. Regev, N.T. Ingolia and J.S. Weissman. "High-resolution view of the yeast meiotic program revealed by ribosome profiling", *Science* **335**:552-7, 2012.

[B22] J. Sivriver, N. Habib and **N. Friedman**. "An integrative clustering and modeling algorithm for dynamical gene expression data", *Bioinformatics* **27**:i392, 2011.

[B23] N. Novershtern, A. Regev and **N. Friedman** "Physical Module Networks: an integrative approach for reconstructing transcription regulation", *Bioinformatics* **27**:i177, 2011.

[B24] B. Celona, A. Weiner, F. Di Felice, F.M. Mancuso, E. Cesarini, R.L. Rossi, L. Gregory, D. Baban, G. Rossetti, P. Grianti, M. Pagani, T. Bonaldi, J. Ragoussis, **N. Friedman**, G. Camilloni, M.E. Bianchi and A. Agresti. "Substantial histone reduction modulates genomewide nucleosomal occupancy and global transcriptional output", *PLoS Biology* **9**:e1001086, 2011.

[B25] Y. Zhang, D. Handley, T. Kaplan, H. Yu, A.S. Bais, T. Richards, K.V. Pandit, Q. Zeng, P.V. Benos, **N. Friedman**, O. Eickelberg and N. Kaminski. "High throughput determination of TGFβ1/SMAD3 targets in A549 lung epithelial cells", *PloS One* **6**:e20319, 2011.

[B26] N. Rhind, Z. Chen, M. Yassour, D.A. Thompson, BJ. Haas, N. Habib, I. Wapinski, S. Roy, M.F. Lin, D.I. Heiman, S.K. Young, K. Furuya, Y. Guo, A. Pidoux, H. Mei Chen, B. Robbertse, J.M. Goldberg, K. Aoki, E.H. Bayne, A.M. Berlin, C.A. Desjardins, E. Dobbs, L. Dukaj, L. Fan, M.G. FitzGerald, C. French, S. Gujja, K. Hansen, D. Keifenheim, J.Z. Levin, R.A. Mosher, C.A. Mller, J. Pfiffner, M. Priest, C. Russ, A. Smialowska, P. Swoboda, S.M. Sykes, M. Vaughn, S. Vengrova, R. Yoder, Q. Zeng, R. Allshire, D. Baulcombe, B.W. Birren, W. Brown, K. Ekwall, M. Kellis, J. Leatherwood, H. Levin, H. Margalit, R. Martienssen, C.A. Nieduszynski, J. W Spatafora, **N. Friedman**, J. Z Dalgaard, P. Baumann, H. Niki, A. Regev and C. Nusbaum. "Comparative functional genomics of the fission yeasts" *Science* **332**:930, 2011.

[B27] M.G. Grabherr, B.J. Haas, M. Yassour, J.Z. Levin, D.A. Thompson, I. Amit, X. Adiconis, L. Fan, R. Raychowdhury, Q. Zeng, Z. Chen, E. Mauceli, N. Hacohen, A. Gnirke, N. Rhind, F. di Palma, B.W. Birren, C. Nusbaum, K. Lindblad-Toh, **N. Friedman** and A. Regev. "Full-length transcriptome assembly from RNA-Seq data without a reference genome", *Nature Biotechnology* **29**:644-652, 2011.

[B28] M. Rabani, J.Z. Levin, L. Fan, X. Adiconis, R. Raychowdhury, M. Garber, A. Gnirke, C. Nusbaum, N. Hacohen, **N. Friedman**, I. Amit and A. Regev. "Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells", *Nature Biotechnology* **29**:436-442, 2011.

[B29] M. Radman-Livaja. K. Verrzijlbergen, A. Weiner, **N. Friedman**, O.J. Rando, and, F. van Leeuwen. "Patterns and mechanisms of ancestral histone protein inheritance in budding yeast", *PLoS Biology*, **9**:e1001075, 2011.

[B30] R. Rinott, A. Jaimovich and **N. Friedman**. "Exploring transcription regulation through cell-to-cell variability" *Proc Natl Acad Sci USA* **108**(15):6329-34, 2011.

[B31] M. Radman-Livaja, G. Ruben G, A. Weiner, **N. Friedman**, R. Kamakaka, O.J. Rando. "Dynamics of Sir3 spreading in budding yeast: secondary recruitment sites and euchromatic localization" *EMBO J* **30**:1012-26, 2011.

[B32] 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. Preffer, 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.

[B33] 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.

[B34] I. Cohn, T. El-Hay, **N. Friedman**, and R. Kupferman. "Mean field variational approximation for continuous-time Bayesian networks." *Journal of Machine Learning Research*, **11**:2745-2783, 2010.

[B35] 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.

[B36] 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.

[B37] A. Jaimovich, R Rinott, M Schuldiner, H Margalit and **N. Friedman**. "Modularity and directionality in genetic interaction maps" *Bioinformatics* **26**:i228-36, 2010.

[B38] 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.

[B39] 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 Genetics*, **6**(2):e1000837, 2010.

[B40] 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.

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