

Andrew B. Nobel

Paul Ziff Distinguished Professor
Department of Statistics and Operations Research
University of North Carolina
Chapel Hill, NC 27599-3260

Fax: 919.962.1279
Telephone: 919.962.1352
E-mail: nobel@email.unc.edu

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Education

Ph.D., Electrical Engineering, Stanford University, 1992
Masters, Electrical Engineering, Stanford University, 1988
Certificate of Study, Mathematics, Cambridge University, England, 1986
Bachelor of Science (with honors), Electrical Engineering, Cornell University, 1985

Academic Appointments

Professor, Department of Biostatistics, UNC Chapel Hill, 2007 - 2012
Member, UNC Computational Genomics Program, 2019-present
Professor, Department of Statistics and Operations Research, UNC Chapel Hill, 2006 - 2020
Adjunct Professor, Department of Computer Science, UNC Chapel Hill, 2006 - 2010
Full Member, Lineberger Comprehensive Cancer Center, UNC Chapel Hill, 2003 - present
Associate Professor, Department of Statistics, UNC Chapel Hill, 2000 - 2006
Visiting Associate Professor of Statistics, University of Chicago, Fall 2000
Assistant Professor, Department of Statistics, UNC Chapel Hill, 1994 - 2000
Postdoctoral Fellow, Beckman Institute, University of Illinois Urbana-Champaign, 1992 - 1994

Honors

Fellow of the Institute of Mathematical Statistics (IMS), 2008
Lucent Distinguished Lecturer, EECS Department, University of Michigan, 2002
National Science Foundation CAREER Grant, 1995
Beckman Institute Fellow, University of Illinois, 1992-1995
IBM Doctoral Fellow, 1988
National Science Foundation Graduate Fellow, 1985-1988
Churchill Scholar, Cambridge University, 1985-1986

External Professional Activities

Associate Editor, Journal of the Royal Statistical Society, Series B, 2020-2024

Associate Editor, The Annals of Statistics, 2013-2019

Member and UNC co-PI, NIH Genotype-Tissue Expression (GTEx) Consortium, 2010-2019

Associate Editor, Electronic Journal of Statistics, 2007-2009

Institute of Mathematical Statistics (IMS)

Program Secretary and Member of the Executive Committee, 2003 - 2006

Committees on Special Lectures (06-09), Nominations (08-09), Selection of Officers (11-13), Funding Advisory (12-13), Publications (15-18), Diversity (20-22), Fellows (25-27)

Associate Editor, IEEE Transactions on Information Theory, 2002-2004

Visiting Assistant Professor, Université de Paris-Sud, Orsay, May-June 2000

Winston Churchill Scholarship

National Selection Committee, Chicago, IL, December, 2002

UNC Selection Committee, 1998-present

Conferences:

Session organizer “Theory at the Intersection of Machine Learning and Statistics” at JSM 2018, Vancouver.

Scientific Advisory Committee for *Probability Theory and Combinatorial Optimization*, Duke University, 2015.

Program Committee for the *Joint World Congress of the Bernoulli Society and Annual Meeting of the Institute for Mathematical Statistics*, National University of Singapore, 2008.

Program Committee for the *Third IMS-ISBA Joint Meeting*, Bormio, Italy, 2007.

Organizing Committee for the *IMS Special Topics Meeting, 50th Anniversary Commemorative Conference*, Department of Statistics, University of North Carolina, Chapel Hill, 1996.

Statistics and Applied Mathematical Sciences Institute (SAMSI)

Local Scientific Coordinator and Faculty Fellow, Program on Low Dimensional Structure in High Dimensional Systems, 2013-2014

Advisory Committee and Faculty Fellow, Program on Computational Biology of Infectious Diseases, 2004-2005

Local Development Committee, 2002-2003

Reviewing:

Grant applications: NIH, NSF, and NSA

National Science Foundation: Grant review panels 2012, 2014, 2016.

Journals: Annals of Statistics; Probability Theory and Related Fields; Proceedings of the U.S. National Academy of Sciences; IEEE Transactions on Information Theory, Pattern Analysis and Machine Intelligence, and Computational Biology and Bioinformatics; Machine Learning; Journal of Machine Learning Research; Journal of Multivariate Analysis; Annales de l'Institut Henri Poincaré; Electronic Journal of Statistics; Applied and Computational Harmonic Analysis; Statistics and Probability Letters; Annals of Applied Probability; Annals of the Institute of Statistical Mathematics; Bernoulli; Bioinformatics; Dynamical Systems; Statistics; Statistica Neerlandica; Computational Statistics; Journal of Theoretical Probability; Journal of Theoretical Statistics; Scandinavian Journal of Statistics; Journal of Nonparametric Statistics.

University and Departmental Activities

Administrative Board of the Graduate School, 2015-2021

Advisory Board of the Odum Institute for Research in Social Science, 2014-2016

Applied Physical Sciences Strategic Planning Advisory Committee, 2013

Director of Graduate Studies, Statistics and Operations Research, 2005 - 2019

Select External Funding

Network Analysis via Optimal Transport of Markov Embeddings

National Science Foundation, DMS-2413928

A.B. Nobel and K. McGoff PIs

Grant period 2024-2027

Inference for Stationary Processes: Optimal Transport and Generalized Bayes

National Science Foundation, DMS-2113676

A.B. Nobel, K. McGoff, and S. Mukherjee PIs

Grant period 2021-2024

Multi-tissue and network models for next-generation eQTL studies

NIH R01 HG009125-01

A.B. Nobel and F.A. Wright, PIs

Grant period 2016-2020

Iterative testing procedures and high-dimensional scaling limits of extremal random structures

National Science Foundation, DMS-1613072
A.B. Nobel and S. Bhamidi, PIs
Grant period 2016-2020

Random dynamical systems and limit theorems for optimal tracking
National Science Foundation, DMS-1613261
K. McGoff (UNC-C) PI, A.B. Nobel and S. Mukherjee (Duke), co-PIs
Grant period 2016-2020

Systems Approaches to Link Tissue-Specific Expression to Disease
NIH R01 MH101819-01
A.B. Nobel and F.A. Wright, PIs
Grant period 2013-2017

Optimality Landscapes and Exploratory Data Analysis
National Science Foundation, DMS-1310002
A.B. Nobel and S. Bhamidi, PIs
Grant period 2013-2017

PRODUCTS AND PRESENTATIONS

A. Refereed Publications and Proceedings

Graph optimal transport with transition couplings of random walks, K. O'Connor, Bongsoo Yi, K. McGoff, and A.B. Nobel. *JRSSB*, vol.87, 2025.

CoCoNest: A Continuous Structural Connectivity-based Nested Parcellation of the Human Cerebral Cortex, A. Allen, Z. Zhang, and A.B. Nobel, *Network Neuroscience*, vol.8, 2024.

Estimation of stationary optimal transport plans, K. O'Connor, K. McGoff, and A.B. Nobel, *Information and Inference*, vol.13, 2024.

Control of false discoveries in grouped hypothesis testing for eQTL data, P. Rudra, Y-H. Zhou, A.B. Nobel, and F.A. Wright *BMC Bioinformatics*, vol.25, 2024.

Finding stable groups of cross-correlated features in multi-view data, M. Dewaskar, J. Palowitch, M. He, M.I. Love, and A.B. Nobel, *JMLR*, vol.24, pp.1-47, 2023.

Optimal transport for stationary Markov chains via policy iteration, K. O'Connor, K. McGoff, and A.B. Nobel, *JMLR*, vol.23, 2022.

Gibbs posterior convergence and the thermodynamic formalism, K. McGoff, S. Mukherjee, A.B. Nobel, *Annals of Applied Probability*, vol.32, 2022.

Community modulated recursive trees and population dependent branching processes, S. Bhamidi, R. Fan, N. Fraiman, and A.B. Nobel, *Random Structures and Algorithms*, vol.60, 2022.

ACTOR: a latent Dirichlet model to compare expressed isoform proportions to a reference panel, S.D. McCabe, A.B. Nobel, and M.I. Love, *Biostatistics*, 2021 May 5:kxab013.

Variational analysis of inference from dynamical systems, K. McGoff and A.B. Nobel, *Information and Inference*, iaaa043, 2021.

Memoryless sequences for general losses. R.M. Frongillo and A.B. Nobel. *Journal of Machine Learning Research*, vol.21, pp.1-28, 2020.

Empirical risk minimization and complexity of dynamical models, K. McGoff and A.B. Nobel. *Annals of Statistics*, vol.48, pp.2031-2054, 2020.

I-Boost: an integrative boosting approach for predicting survival time with multiple genomics platforms. K.Y. Wong, C. Fan, M. Tanioka, J.S. Parker, A.B. Nobel, D. Zeng, D-Y. Lin, and C.M. Perou. *Genome Biology* vol.20, 2019.

The continuous configuration model: a null model for community detection on weighted networks, J. Palowitch, S. Bhamidi, and A.B. Nobel. *Journal of Machine Learning Research*, vol.18, pp.1-48, 2018.

A testing-based approach to the discovery of differentially correlated variable sets, K. Bodwin, K. Zhang, and A.B. Nobel. *The Annals of Applied Statistics*, vol.12, pp.1180-1203, 2018.

HT-eQTL: Integrative eQTL analysis in a large number of human tissues, G. Li, D.D. Jima, F.A. Wright, A.B. Nobel. *BMC Bioinformatics*, vol.19, 2018.

Change point detection in network models: preferential attachment and long range dependence, S. Bhamidi, J. Jin, and A.B. Nobel. *Annals of Applied Probability*, vol.28, pp.35-78, 2018.

Estimation of interpretable eQTL effect sizes using a log of linear model, J. Palowitch, A. Shabalina, Y. Zhou, A.B. Nobel, and F.A. Wright. *Biometrics*, vol.74, pp.616-625, 2018.

An empirical Bayes approach for multiple tissue eQTL analysis, G. Li, A.A. Shabalina, I. Rusyn, F.A. Wright, and A.B. Nobel. *Biostatistics*, vol.16, pp.391-406, 2018.

Memoryless Sequences for Differentiable Losses, R. Frongillo and A.B. Nobel. *Proceedings of Machine Learning Research*, vol.65, pp.1-15, 2017. (Presented at COLT 2017.)

Entropy and the uniform mean ergodic theorem for a family of sets, T.M. Adams and A.B. Nobel. *Transactions of the American Mathematical Society*, vol.369, pp.605-622, 2017.

Energy landscape for large average submatrix detection problems in Gaussian random matrices, S. Bhamidi, P.S. Dey and A.B. Nobel. *Probability Theory and Related Fields*, vol.168, pp.919-983, 2017.

Supervised singular value decomposition and its asymptotic properties, G. Li, D. Yang, A.B. Nobel, and H. Shen. *Journal of Multivariate Analysis*, vol.146, pp.7-17, 2016.

Consistency of maximum likelihood estimation for some dynamical systems, K. McGoff, S. Mukherjee, A.B. Nobel, and N. Pillai, *The Annals of Statistics*, vol.43, pp.1-29, 2015.

Fine-mapping additive and dominant SNP effects using group-LASSO and fractional re-sample model averaging, J. Sabourin, A.B. Nobel, and W. Valdar. *Genetic Epidemiology*, vol.39, pp.77-88, 2015.

The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans, The GTEx Consortium, *Science*, vol.348, pp.648-660, 2015.

A permutation approach for selecting the penalty parameter in penalized model selection, J. Sabourin, W. Valdar, and A.B. Nobel. *Biometrics*, vol.71, pp.1185-1194, 2015.

Consistent testing for recurrent genomic aberrations, V. Walter, F.A. Wright, and A.B. Nobel. *Biometrika*, vol.102, pp.783-796, 2015.

A testing based extraction algorithm for identifying significant communities in networks, J.D. Wilson, S. Wang, P.J. Mucha, S. Bhamidi, A.B. Nobel, *The Annals of Applied Statistics*, vol.8, pp.1853-1891, 2014.

On the size of large-average and ANOVA-fit submatrices in Gaussian random matrices, X. Sun and A.B. Nobel, *Bernoulli*, vol.19, pp.275-294, 2013.

Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple Datatypes, E.F. Lock, K.A. Hoadley, J.S. Marron, A.B. Nobel, *The Annals of Applied Statistics*, vol.7, pp.523-542, 2013.

Reconstruction of a low-rank matrix in the presence of Gaussian noise, A.A. Shabalin and A.B. Nobel, *Journal of Multivariate Analysis*, vol.118, pp.67-76, 2013.

Uniform approximation of Vapnik-Chervonenkis classes, T.M. Adams and A.B. Nobel, *Bernoulli*, vol.18, pp.1310-1319, 2012.

Basal-like Breast cancer DNA copy number losses identify genes involved in genomic instability, response to therapy, and patient survival, V. Weigman, H.H. Chao, A.A. Shabalin, X. He, J.S. Parker, S.H. Nordgard, T. Grushko, D. Huo, C. Nwachukwu, A.B. Nobel, V.N. Kristensen, A.L. Børresen-Dale, O.I. Olopade, C.M. Perou, *Breast Cancer Research and Treatment*, vol.133, pp.865-880, 2012.

Reprioritizing genetic associations in hit regions using LASSO-based resample model averaging, W. Valdar, J. Sabourin, A.B. Nobel, and C.C. Holmes, *Genetic Epidemiology*, vol.36, pp.451-462, 2012.

DiNAMIC: A Method for assessing the statistical significance of DNA copy number aberrations, V.A. Walter, A.B. Nobel, and F.A. Wright, *Bioinformatics*, vol.27, pp.678-685, 2011.

Uniform convergence of Vapnik-Chervonenkis classes under ergodic sampling, T.M. Adams and A.B. Nobel, *Annals of Probability*, vol.38, pp.1345-1367, 2010.

Heading down the wrong pathway: on the influence of correlation within gene sets, D.M. Gatti, W.T. Barry, A.B. Nobel, I. Rusyn, F.A. Wright, *BMC Genomics*, vol.11:574, 10 pages, 2010.

Supervised risk predictor of breast cancer based on intrinsic subtypes, J.S. Parker, M. Mullins, M.C.U. Cheang, S. Leung, D. Voduc, T. Vickery, S. Davies, C. Fauron, X. He, Z. Hu, J.F. Quackenbush, I.J. Stijleman, J. Palazzo, J.S. Marron, A.B. Nobel, E. Mardis, T.O. Nielsen, M.J. Ellis, C.M. Perou, P.S. Bernard, *Journal of Clinical Oncology*, JCO.2008.18.1370, 2009.

The Set2/Rpd3S pathway suppresses cryptic transcription without regard to gene length or transcription frequency, C.R. Lickwar, B. Rao, A.A. Shabalin, A.B. Nobel, B.D. Strahl, J.D. Lieb, *PLoS One*, 4(3):e4886, 2009.

Finding large average submatrices in high dimensional data, A.A. Shabalin, V.J. Weigman, C.M. Perou and A.B. Nobel, *Annals of Applied Statistics*, vol.3, pp.985-1012, 2009.

A Bayesian model for cross-study analysis of differential gene expression (with discussion and rejoinder), R.B. Scharpf, H. Tjelmeland, G. Parmigiani and A.B. Nobel, *Journal of the American Statistical Association*, vol.104, pp.1295-1310, 2009.

A statistical framework for testing functional categories in microarray data, W.T. Barry, A.B. Nobel and F.A. Wright, *The Annals of Applied Statistics*, vol. 2, pp.286-315, 2008.

Sequential procedures for aggregating arbitrary estimators of a conditional mean, F. Bunea and A.B. Nobel, *IEEE Transactions on Information Theory*, vol. 54, pp.1725-1735, 2008.

Merging two gene expression studies via cross platform normalization, A.A. Shabalin, H. Tjelmeland, C. Fan, C.M. Perou and A.B. Nobel, *Bioinformatics*, vol. 24, pp.1154-1160, 2008.

Statistical significance of clustering for high dimension low sample size data, Y. Liu, D.N. Hayes, A.B. Nobel and J.S. Marron, *Journal of the American Statistical Association*, vol. 103, pp.1281-1293, 2008.

On the Size and Recovery of Submatrices of Ones in a Random Binary Matrix, X. Sun and A.B. Nobel, *Journal of Machine Learning Research*, vol. 9, pp.2431-2453, 2008.

FastMap: Fast eQTL Mapping in homozygous populations, D.M. Gatti, A.A. Shabalin, T-C. Lam, F.A. Wright, I. Rusyn and A.B. Nobel, *Bioinformatics*, vol. 25, pp.482-489, 2008.

Mining approximate frequent itemsets in the presence of noise: Algorithms and analysis, J. Liu, S. Paulsen, X. Sun, W. Wang, A.B. Nobel and J. Prins. *Proceedings of the 2006 SIAM Conference on Data Mining (SDM)*, Bethesda, MD, April 2006.

Hypothesis testing for families of dependent processes, A.B. Nobel, *Bernoulli*, vol. 12, pp.251-269, 2006.

The Molecular Portraits of Breast Tumors Are Conserved Across Microarray Platforms, Z. Hu, C. Fan, D.S. Oh, J.S. Marron, X. He, B.F. Qaqish, C. Livasy, L.A. Carey, E. Reynolds, L. Dressler, A. Nobel, J. Parker, M.G. Ewend, L.R. Sawyer, D. Xiang, J. Wu, Y. Liu, R. Nanda, M. Tretiakova, A.R. Orrico, D. Dreher, J.P. Palazzo, L. Perreard, E. Nelson, M. Mone, H. Hansen, M. Mullins, J.F. Quackenbush, O.I. Olopade, P.S. Bernard and C.M. Perou, *BMC Genomics*, 7:96, 2006.

Different gene expression-based predictors for breast cancer patients are concordant, C. Fan, D.S. Oh, L. Wessels, A. Nobel, L.J. van't Veer, and C.M. Perou, *The New England Journal of Medicine*, vol. 355, pp.560-569, 2006.

Significance and Recovery of Block Structures in Binary Matrices with Noise, X. Sun and A.B. Nobel, *Proceedings of the 19th Annual Conference on Learning Theory (COLT)*, pp.109-122, H.U. Simon and G. Lugosi editors, Springer, 2006.

Denosing deterministic time series, S.P. Lalley and A.B. Nobel, *Dynamics of Partial Differential Equations*, vol. 3, pp.259-279, 2006.

Gene expression profiles do not consistently predict the clinical treatment response in locally advanced breast cancer, T. Sørlie, C.M. Perou, C. Fan, S. Geisler, T. Aas, A. Nobel, G. Anker, L.A. Akslen, D. Botstein, A-L. Børresen-Dale, and P.E. Lønning, *Molecular Cancer Therapeutics*, vol. 5, pp.2914-2918, 2006.

Understanding Patterns of TCP Connection Usage with Statistical Clustering, F. Hernandez Campos, A.B. Nobel, F.D. Smith, K. Jeffay. *Proceedings of the Thirteenth MASCOTS Symposium*, Atlanta, GA, September 2005.

Significance analysis of functional categories in gene expression studies: a structured permutation approach, W.T. Barry, A.B. Nobel and F.A. Wright, *Bioinformatics*, vol. 21, pp.1943-1949, 2005.

ChIPOTle: A user-friendly tool for the analysis of ChIP-chip data, M.J. Buck, A.B. Nobel and J.D. Lieb, *Genome Biology*, vol. 6, R97, 2005.

Mining Approximate Frequent Itemsets from Noisy Data, J. Liu, S. Paulsen, W. Wang, A.B. Nobel and J. Prins (short paper). *Proceedings of the Fifth IEEE International Conference on Data Mining (ICDM)*, Houston, TX, November, 2005.

Some statistical properties of memoryless individual sequences, A.B. Nobel, *IEEE Transactions on Information Theory*, vol. 50, pp.1497-1505, 2004.

On optimal sequential prediction schemes for general processes, A.B. Nobel, *IEEE Transactions on Information Theory*, vol. 49, pp.83-98, 2003.

Indistinguishability of absolutely continuous and singular distributions, S.P. Lalley and A.B. Nobel, *Statistics and Probability Letters*, vol. 62, pp.145-154, 2003.

Repeated Observation of Breast Tumor Subtypes in Independent Gene Expression Data Sets, T. Sørlie, R. Tibshirani, J. Parker, T. Hastie, J.S. Marron, A. Nobel, S. Deng, H. Johnsen, R. Pesich, S. Geisler, C.M. Perou, P.E. Lønning, P.O. Brown, A-L. Børresen-Dale and D. Botstein, *Proceedings of the U.S. National Academy of Sciences*, vol. 100, pp.8418-8423, 2003.

Analysis of a complexity based pruning method for classification trees, A.B. Nobel, *IEEE Transactions on Information Theory*, vol. 48, pp.2362-2368, 2002.

Finitary reconstruction of a measure preserving transformation, T.M. Adams and A.B. Nobel, *Israel Journal of Mathematics*, vol. 126, pp.309-326, 2001.

Estimating a function from ergodic samples with additive noise, A.B. Nobel and T.M. Adams, *IEEE Transactions on Information Theory*, vol. 47, pp.2895-2902, 2001.

Adaptive model selection using empirical complexities, G. Lugosi and A.B. Nobel, *Annals of Statistics*, vol. 27, pp.1830-1864, 1999.

Limits to classification and regression estimation from ergodic processes, A.B. Nobel, *Annals of Statistics*, vol. 27, pp.262-273, 1999.

Regression estimation from an individual stable sequence, G. Morvai, S.R. Kulkarni, and A.B. Nobel, *Statistics*, vol. 33, pp.99-118, 1999.

Density estimation from an individual numerical sequence, A.B. Nobel, G. Morvai and S. Kulkarni, *IEEE Transactions on Information Theory*, vol. 44, no. 2, pp.537-541, 1998.

On density estimation from an ergodic process, T.M. Adams and A.B. Nobel, *Annals of Probability*, vol. 26, no. 2, pp.794-804, 1998.

Recursive partitioning to reduce distortion, A.B. Nobel, *IEEE Transactions on Information Theory*, vol. 43, no. 4, pp.1122-1133, 1997.

Histogram regression estimation using data-dependent partitions, A.B. Nobel, *Annals of Statistics*, vol. 24, pp.1084-1105, 1996.

Vanishing distortion and shrinking cells, A.B. Nobel, *IEEE Transactions on Information Theory*, vol. 42, no. 4, pp.1303-1305, 1996.

Consistency of data-driven histogram methods for density estimation and classification, G. Lugosi and A.B. Nobel, *Annals of Statistics*, vol. 24, no. 2, pp.687-706, 1996.

Termination and continuity of greedy growing for tree-structured vector quantizers, A.B. Nobel and R.A. Olshen, *IEEE Transactions on Information Theory*, vol. 42, no. 1, pp.191-205, 1996.

A counterexample concerning uniform ergodic theorems for a class of functions, A.B. Nobel, *Statistics and Probability Letters*, vol. 24, pp.165-168, 1995.

A note on uniform laws of averages for dependent processes, A.B. Nobel and A. Dembo, *Statistics and Probability Letters*, vol. 17, pp.169-172, 1993.

A Recurrence theorem for dependent processes with applications to data compression, A.B. Nobel and A.D. Wyner, *IEEE Transactions on Information Theory*, vol. 38, pp. 1561-1564, 1992.

Evaluating the performance of a simple inductive procedure in the presence of overfitting error, A.B. Nobel. In *Proceedings of the Fourth Annual Conference on Learning Theory*, pp.267-274, Santa Cruz, CA, 1991.

B. Submitted Papers and Preprints

Graph Disjointness with Applications to Reversible Markov Chains, Y. Xiang, K. McGoff, A.B. Nobel. Submitted for publication.

Optimal graph joining with application to graph isomorphism detection and identification, P. Hoàng, Y. Xiang, B. Yi, A.B. Nobel, K. McGoff. Submitted for publication.

Cross-species alignment of structural connectomes using network optimal transport, A. Allen, Z. Zhang, A.B. Nobel. Preprint.

Latent association mining in binary data, C. Mosso, K. Bodwin, S. Chakraborty, K. Zhang, and A.B. Nobel. Preprint available at arXiv:1711.10427.

Large subgraphs in pseudo-random graphs A. Basak, S. Bhamidi, S. Chakraborty, A.B. Nobel. Preprint available at arXiv:1610.03762.

C. Lightly Refereed Publications

Exploratory methods to integrate multi-source data, E.F. Lock and A.B. Nobel, in *Integrating Omics Data*, G. Tseng, D. Ghosh, and X.J. Zhou editors, Cambridge University Press, 2015.

Measuring the statistical significance of local connections in directed networks, J.D. Wilson, S. Bhamidi, and A.B. Nobel, *NIPS 2013, Workshop on Frontiers of Network Analysis*, December, 2013.

A Counterexample concerning the extension of uniform strong laws to ergodic processes, T.M. Adams and A.B. Nobel, in *A Festschrift in Honor of Jon A. Wellner*, IMS collections vol.9, pp.1-4, 2013.

Identification of recurrent DNA copy number aberrations in tumors, V. Walter, A.B. Nobel, D.N. Hayes, and F.A. Wright, in *Statistical Diagnostics for Cancer: Analyzing High-Dimensional Data*, M. Dehmer and F. Emmert-Streib editors, pp.241-260, Wiley-Blackwell, 2013.

Discussion of “Population value decomposition, a framework for the analysis of image populations” (by C.M. Crainiceanu, B.S. Caffo, S. Luo, V. Zipunnikov and N.M. Punjabi), E.F. Lock, A.B. Nobel, and J.S. Marron, *Journal of the American Statistical Association*, vol.106, pp.798-802, 2011.

Discussion of “Adaptive confidence intervals for the test error in classification” (by E.B. Laber and S.A. Murphy), S. Wei and A.B. Nobel, *Journal of the American Statistical Association*, vol.106, pp.931-936, 2011.

Consistent estimation of a dynamical map, A.B. Nobel. In *Nonlinear Dynamics and Statistics*, pp.267-280, A.I. Mees editor, Birkhauser, Boston, 2001.

Histogram density estimation using data-dependent partitions, A.B. Nobel and G. Lugosi. In *Proceedings of the 1994 Conference on Information Science and Systems*, pp.775-780, Princeton University, Princeton, NJ, 1994.

D. Technical Reports

The gap dimension and uniform convergence under ergodic sampling, T.M. Adams and A.B. Nobel, arXiv:1007.2964, 2010.

First order predictive sequences and induced transformations, A.B. Nobel, Technical Report #2367, Department of Statistics, UNC Chapel Hill, 1999.

A.B. Nobel and A.D. Wyner, *On the Asymptotic Behavior of Block Codes*, Bell Labs Technical Memorandum, 1990.

E. United States Patents

Gene expression profiles to predict breast cancer outcomes, P. Bernard, M. Cheang, M. Ellis, E. Mardis, J.S. Marron, T. Nielsen, A.B. Nobel, J. Parker, and C. Perou. U.S. Patent No. 2297359

Methods, systems and computer program products for modeling and simulating application-level traffic characteristics in a network based on transport and network layer header information, F. Hernandez-Campos, K. Jeffay, F.D. Smith, and A.B. Nobel. U.S. Patent No. 7447209.

F. Software packages (all publicly available)

ACME: Fast procedure that uses a log-of-linear model to estimate interpretable cis-eQTL effect sizes.

MT-eQTL: Empirical Bayes method for multi-tissue expression quantitative trait loci (eQTL) analysis.

DCM: Method for finding sets of differentially correlated variables in case-control data.

JIVE: Expresses multiple data matrices on a common set of samples into a sum of low-moderate rank matrices capturing joint and individual variation.

SWITCHdna: A sequential method, based on change-point detection, for segmenting copy number data and identifying regions of copy number aberration.

LAS: Biclustering algorithm that finds statistically significant large average submatrices in high dimensional data.

SigClust: Permutation based method for assessing the significance of clustering results.

SAFE: Permutation based procedure for assessing the significance of functional categories in gene expression data.

XPN: Cross-platform normalization method for combining gene expression data from different studies.

XDE: Bayesian method for assessing the differential expression of genes using data from multiple studies.

FastMap: Fast method for performing eQTL analyses in homozygous populations, including permutation based assessment of significance.

ChIPOTle: Peak finding algorithm for ChIP-chip microarray data.