CONTACT INFORMATION	Department of Statistics *Room:* 315, Philip E. Austin Building

CONTACT INFORMATION

Department of Statistics
University of Connecticut
Storrs, CT, 06269-4120

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Web site: `https://haim-bar.uconn.edu/`

RESEARCH INTERESTS

Statistical models; shrinkage estimation; Bayesian High-Dimensional Data; high throughput applications in biology;applications in econometrics; Bayesian statistics; machine learning.

EDUCATION

Cornell University, Ithaca, New York USA

Ph.D. in Statistics, 2012

Dissertation Topic: "*Parallel Testing, and Variable Selection – a Mixture-Model Approach with Applications in Biostatistics*"
Advisors: James Booth (Chair), Martin T. Wells, Robert L. Strawderman

M.Sc. in Statistics

Yale University, New Haven, Connecticut USA

M.Sc. in Computer Science

The Hebrew University, Jerusalem, Israel

B.Sc. in Mathematics, Cum Laude

ACADEMIC EXPERIENCE

University of Connecticut, Storrs, Connecticut, USA

Associate Professor	**August 2013 - Present**
Assistant Professor	**August 2013 - 2019**

I am an associate professor at the University of Connecticut, in the Department of Statistics. I am affiliated with the Institute for Systems Genomics (ISG), the Institute for Collaboration on Health, Intervention, and Policy (InCHIP), and the CT Institute for the Brain and Cognitive Sciences.
Teaching:

    STAT 5005: Introduction to Applied Statistics
    STAT 5505: Applied Statistics I
    STAT 5605: Applied Statistics II
    STAT 3515Q/5515: Design of Experiments (*Excellence in teaching recognition - Spring 2014, Spring 2017*)
    STAT 3675Q: Statistical Computing (*Excellence in teaching recognition - Spring 2016*)
    STAT/BIST 5225: Data Management in SAS and R (*Excellence in teaching recognition - Fall 2017*)
    STAT/BIST 5215: Statistical Consulting (*Excellence in teaching recognition - Spring 2018, Fall 2018*)

Cornell University, Ithaca, New York, USA

Statistical Consultant	**July 2011 - July 2013**

    As a member of the Cornell Statistical Consulting Unit (CSCU) I provided statistical consulting to Cornell faculty and staff. I handled a diverse range of applications, including economics, business, genomics, nutrition, sociology, etc. I presented a wide range of topics in workshops, and as a guest lecturer in courses at Cornell, including on Bayesian statistics, missing data, multiple testing, etc.
Teaching: BTRY 6020: Statistical Methods II

PostDoc, Department of Statistical Science **August 2012 - July 2013**

I collaborated with the Melnick Lab at the Weill Cornell Medical College. I developed new methods and applied existing techniques to analyze very large data sets involving up to millions of features. Primarily, we focused on methylation data for epigenetic analysis, and RNA sequencing for transcription regulation analysis.

Research Assistant **July 2011 - December, 2011**

I worked with Professor Francesca Molinari on the theory and application of sharp identification regions. Implemented a fast and accurate estimation method based on Support Vector Machines. We applied the method to linear prediction, and game theory problems.

Graduate Student **August 2005 - December 2011**

M.Sc. and Ph.D. programs.

Head Teaching Assistant **August 2009 - December 2010**

BTRY 6010, Statistical Methods I (*Outstanding TA Award* 2010-2011).

Teaching Assistant **August, 2005 - May 2010**

BTRY 6020, Statistical Methods II (graduate level class).
BTRY 6010, Statistical Methods I (graduate level class).
ORIE 474, Statistical Data Mining.
CS 101M, Introduction to Computer Programming (*Outstanding TA Award*, 2006).
MATH 335/COMS 480, An Introduction to Cryptology.

PUBLICATIONS

Bar, H.; Wang, H. *Reproducible Science with LATEX*. J. data sci. 2021; 19, no. 1, 111-125, DOI 10.6339/21-JDS998

Bar H.; Bang S. *A mixture model to detect edges in sparse co-expression graphs with an application for comparing breast cancer subtypes.* 2021; PLOS ONE 16(2): e0246945.
https://doi.org/10.1371/journal.pone.0246945

McLaughlin, P.; Bar, H. *A spatial capture–recapture model with attractions between individuals.* Environmetrics. 2021; 32(1):e2653. https://doi.org/10.1002/env.2653

Bar, H.; Zweifach, A. *Z' Does Not Need to be > 0.5.* SLAS Discovery, 2020
https://journals.sagepub.com/doi/full/10.1177/2472555220942764
DOI: 10.1177/2472555220942764

Katneni, Upendra; Holcomb, David; Hernandez, Nancy E.; Hamasaki-Katagiri, Nobuko ; Hunt, Ryan C.; Bar, Haim; Ibla, Juan C.; Kimchi-Sarfaty, Chava . *In silico features of ADAMTS13 contributing to plasmatic ADAMTS13 levels in neonates with congenital heart disease.* Thrombosis Research, 2020, Vol. 193, 66-76

Bar, H.; Booth, J.; Wells, M. T. *A Scalable Empirical Bayes Approach to Variable Selection in Generalized Linear Models.* Journal of Computational and Graphical Statistics, 2020. DOI: 10.1080/10618600.2019.1706542

Kames, J; Holcomb, D.D.; Alexaki, A; Santana-Quintero, L; Athey, J.C; Hamasaki-Katagiri, N; Katneni, U; Golikov, A; Ibla, J.C.; Bar, H.; Kimchi-Sarfaty, C. *TissueCoCoPUTs: Novel Human Tissue-Specific Codon and Codon-Pair Usage Tables Based on Differential Tissue Gene Expression.* Journal of Molecular Biology. 2020 Jan 23; S0022-2836(20) 30041-3

Hunt, R.; Hettiarachchi, G.; Katneni, U.; Hernandez, N.; Holcomb, D; Kames, J.; Alnifaidy, R.; Lin, B.; Hamasaki-Katagiri, N.; Wesley, A.; Kafri, T.; Morris, C.; Bouché, L.; Panico, M.; Schiller, T.; Ibla, J.; Bar, H.; Ismail, A.; Morris, H.; Komar, A.; Kimchi-Sarfaty, C. *A single synonymous variant (c.*354*G > A[p.P*118*P]) in ADAMTS13 confers enhanced specific activity.* The International Journal of Molecular Sciences. 2019, 20(22), 5734; https://doi.org/10.3390/ijms20225734

Alexaki, A.; Hettiarachchi, G.K.; Athey, J.C.; Katneni, U.K.; Simhadri, V.; Hamasaki-Katagiri, N.; Nanavaty, P.; Lin, B.; Takeda, K.; Freedberg, D.; Monroe, D.; McGill, J.R.; Peters, R.; Kames, J.M.; Holcomb, D.D.; Hunt, R.C.; Sauna, Z.E.; Gelinas, A.; Janjic, N.; DiCuccio, M.; Bar, H.; Komar, A.A.; Kimchi-Sarfaty, C.. *Effects of codon optimization on coagulation factor IX translation and structure: Implications for protein and gene therapies.* Nature Research's Scientific Reports, 9, 15449 (2019) doi:10.1038/s41598-019-51984-2

Bar, H. and Schifano, E. D. *Differential variation and expression analysis.* 2019. Stat. DOI:10.1002/sta4.237

Korach-Rechtman, H.; Freilich, S.; Gerassy-Vainberg, S.; Buhnik-Rosenblau, K.; Danin-Poleg, Y.; Bar, H.; Kashi, Y. *Murine Genetic Background has a Stronger Impact on the Composition of the Gut Microbiota than Maternal Inoculation or Exposure to Unlike Microbiota.* 2019. Applied and Environmental Microbiology. DOI: 10.1128/AEM.00826-19

Katneni, U.; Liss, A.; Holcomb, D.; Katagiri, N.; Hunt, R.; Bar, H.; Ismail, A.; Komar, A.A.; Kimchi-Sarfaty, C. *Splicing dysregulation contributes to the pathogenicity of several F9 exonic point variants.* 2019. Molecular Genetics & Genomic Medicine. DOI:10.1002/mgg3.840

Alexaki, A.; Kames, J.M.; Holcomb, D.D.; Athey, J.; Santana-Quintero, L.V.; Lam. P.V.; Hamasaki-Katagiri, N.; Osipova, E.; Simonyan, V.; Bar, H.; Komar, A.A.; Kimchi-Sarfaty, C. *Codon and Codon-Pair Usage Tables (CoCoPUTs): facilitating genetic variation analyses and recombinant gene design.* 2019. Journal of Molecular Biology. pii: S0022-2836(19)30228-1. doi: 10.1016/j.jmb.2019.04.021

Poole, A.C.; Goodrich, J.K.; Youngblut, N. D.; Luque, G.G.; Ruaud, A.; Sutter, J.L.; Waters, J.L.; Shi, Q.; El-Hadidi, M.; Johnson, L.M.; Bar, H.; Huson, D.H.; Booth, J.G.; Ley, R.E. *Human Salivary Amylase Gene Copy Number Impacts Oral and Gut Microbiomes.* 2019. Cell Host & Microbe. 25, 553–564.

Bar, H.; Liu, K. *Empirical Bayes Methods in Variable Selection.* 2019. WIREs Computational Statistics. Volume 11, Issue 2. doi: 10.1002/wics.1455

Hettiarachchi, G. K.; Katneni, U. K.; Hunt, R. C.; Kames, J. M.; Athey, J. C.; Bar, H.; Sauna, Z. E.; McGill, J. R.; Ibla, J. C.; Kimchi-Sarfaty, C. *Translational and transcriptional responses in human primary hepatocytes under hypoxia.* 2019. American Journal of Physiology-Gastrointestinal and Liver Physiology. doi:10.1152/ajpgi.00331.2018.

Bar, H.; Booth, J.; Wells, M. T.; Liu, K. *Facilitating High Dimensional Transparent Classification Via Empirical Bayes Variable Selection.* 2018. Applied Stochastic Models in Business and Industry. Volume 34, Issue 6. Pages 949-961. https://doi.org/10.1002/asmb.2393

Fox, E. L.; Pelto, G. H.; Bar, H.; Rasmussen, K. M.; Young, S. L.; Debrosse, M. G.; Rouzier, V. A.; Pape, J. W.; Pelletier, D. L. *Capturing changes in HIV-infected, breastfeeding mothers' cognitive processes from before delivery to five months postpartum: An application of the pile sorting technique in Haiti.* 2018. Current Developments in Nutrition; Volume 2, Issue 6, 1 June 2018, nzy017, https://doi.org/10.1093/cdn/nzy017. **Editor's Choice**.

Chen, K.; Mishra, N.; Smyth, J.; Bar, H.; Schifano, E.; Kuo, L.; Chen, M.-H. *A tailored multivariate mixture model for detecting proteins of concordant change in the pathogenesis of Necrotic Enteritis.* 2018. Journal of the American Statistical Association. Volume 113, Issue 522. Pages 546-559. http://dx.doi.org/10.1080/01621459.2017.1356314

Bar, H. *Missing Data - Mechanisms and Possible Solutions.* 2017. Cultura y Educación / Culture and Education, 29(3), pages 492-525.

Bar, H. and Mentch, L. *R-CMap - An Open-Source Software for Concept Mapping.* 2017. Evaluation and Program Planning - Special Issue on: Concept Mapping at 25: Development, Applications, and Future Directions. 60:284-292. doi: 10.1016/j.evalprogplan.2016.08.018. Epub 2016 Aug 28.

Rom, O.; Korach Rechtman, H.; Hayek;, T.; Danin-Poleg, Y.; Bar, H.; Kashi, Y.; Aviram, M. *Acrolein increases macrophage atherogenicity in association with gut microbiota remodeling in atherosclerotic mice: protective role for the polyphenol-rich pomegranate juice.* 2017. Archives of Toxicology, 2017 Apr; 91(4):1709-1725. doi: 10.1007/s00204-016-1859-8. Epub 2016 Sep 30.

Hamasaki-Katagiri, N.; Lin, B.; Simon, J.; Hunt, R.; Schiller, T.; Russek-Cohen, E.; Komar, A.; Bar, H.;Kimchi-Sarfaty, C. *The Importance of mRNA Structure in Determining the Pathogenicity of Synonymous and Non-synonymous Mutations in X-linked Genes.* 2017. Haemophilia 2017 Jan; 23(1):e8-17

Tako, E.; Bar, H.; Glahn, R. P. *The combined application of the Caco-2 cell bioassay coupled with in vivo (Gallus gallus) feeding trial represents an effective approach to predicting Fe bioavailability in humans.* 2016 (Nov), Nutrients. 18;8(11). pii: E732.

Molinari, E.; Bar, H.; Pyle, A. M.; Patrizio, P. *Transcriptome analysis of human cumulus cells reveals hypoxia as the main determinant of follicular senescence.* 2016. Molecular Human Reproduction Vol 22 (8): pages 866-876 doi:10.1093/molehr/gaw038

Schifano, E. D.; Bar, H.; Harel, O.. *Methods for analyzing secondary outcomes in public health case-control studies.* 2015, "Innovative Statistical Methods for Public Health Data", Ding-Geng Chen and Jeffrey Wilson, editors. Springer. Pages 3-15.

Bar, H.; Booth, J.; Wells, M. T. *A Bivariate Model for Simultaneous Testing in Bioinformatics Data.* 2014 (June), Journal of the American Statistical Association. Vol. 109, No. 506, Applications and Case Studies. DOI: 10.1080/01621459.2014.884502

Finkelstein, J. L.; Pressman, E. K.; Cooper, E. M.; Kent, T. R.; Bar, H.; O'Brien, K.y O. *Vitamin D Status Affects Serum Metabolomic Profiles in Pregnant Adolescents* 2014. Reproductive Sciences. doi: 10.1177/1933719114556477

Alexander, E. L.; Gardete, S.; Bar, H.; Wells, M. T.; Tomasz, A.; Rhee, K. Y. *Intermediate-Type Vancomycin Resistance (VISA) in Genetically-Distinct Staphylococcus aureus Isolates is Linked to Specific, Reversible Metabolic Alterations.* May 9, 2014. PLOS ONE. Vol. 9, No. 5, pages e97137.

Coate, J. E.; Bar, H.; Doyle, J. J. *Extensive Translational Regulation of Gene Expression in an Allopolyploid (Glycine dolichocarpa).* 2014. The Plant Cell Online. Vol. 26, No. 1.

Athiphunamphai, N; Bar, H.; Cooley, H. J.; Padilla-Zakour, O. I. *Heat treatment and turbo extractor rotational speed effects on rheological and physico-chemical properties of varietal applesauce.* 2014. Journal of Food Engineering. Vol. 136, Pages 19-27.

Garrett-Bakelman, F. E.; Li, S.; Hricik, T.; Chung, S. S.; Bar, H.; Brown, A. L.; Patel, J. P.; Rapoport, F.; Liu, L,; Sheridan, C.; Ishii, J.; Zumbo, P.; Gandara, J.; Lewis, I. D.; To, L. B.; Becker, M. W.; Guzman, M. L.; D'Andrea, R. J.; Michor, F.; Park, C. Y.; Carroll, M.; Levine, R. L.; Mason, C. E.; Melnick, A. M . *Epigenetic deregulation in relapsed acute myeloid leukemia.* 2013. Blood. Vol. 122(21), pages 2499-2499.

Jiang, X.; Bar, H.; Yan, J.; Jones, S.; Brannon, P. M.; West, A.; Perry, C. A.; Ganti, A.; Pressman, E.; Devapatla, S.; Vermeylen, F.; Wells, M. T.; Caudill, M. A. *A higher maternal choline intake among third-trimester pregnant women lowers placental and circulating concentrations of the antiangiogenic factor fms-like tyrosine kinase-1 (sFLT1).* 2013. The FASEB Journal, Vol. 27, No. 3, pages 1245-1253.

Bar H. and Lillard D. *Accounting for Heaping in Retrospectively Reported Event Data – A Mixture Model Approach.* 2012. Statistics in Medicine, DOI: 10.1002/sim.5419.

Bar, H.; Booth, J.; and Wells, M. T. *A Mixture-Model Approach for Parallel Testing for Unequal Variances.* 2012 (Jan.) Statistical Applications in Genetics and Molecular Biology: Vol. 11, Iss. 1, Article 8.

Jiang, X.; Bar, H.; Yan, J.; West, A.; Perry, C. A.; Malysheva, O. V.; Devapatla, S.; Pressman, E.; Vermeylen, F. M.; Wells, M. T.; Caudill, M. A. *Pregnancy Induces Transcriptional Activation of the Peripheral Innate Immune System and Increases Oxidative DNA Damage among Healthy Third Trimester Pregnant Women.* 2012. PLoS ONE 7(11): e46736. doi:10.1371/journal.pone.0046736

Jiang, X.; Yan, J.; West, A.; Perry, C.; Malysheva, O.; Bar, H.; Wells, M.; Devapatla, S.; Pressman, E.; Caudill, M. *Pregnancy status and choline intake alter DNA integrity, epigenetic marks and gene expression.* 2012 (March), The FASEB Journal, Vol. 26:116.1,

Rosenbaum M.; Bar H.; Beg Q.; Segré D.; Booth J.; Cotta M.; Angenent L., *Transcriptional analysis of Shewanella oneidensis MR-1 with an electrode compared to soluble Fe(III) or oxygen as terminal electron acceptor.* 2012 (Feb.), PLoS ONE, 7(2):e30827.

Bar H. and Schifano E. D. *Empirical and fully Bayesian approaches for random effects models in microarray data analysis.* 2011 (Feb.), Statistical Modelling 11(1):71-88.

Jiang, X.; Yan, J.; West, A.; Perry, C.; Malysheva, O.; Bar, H.; Wells, M.; Devapatla, S.; Pressman, E.; Caudill, M. *A higher maternal choline intake favorably alters placental gene expression of biological pathways related to disease risk.* 2011, The FASEB Journal, Vol. 25:599.5,

Menda G.; Bar H.; Arthur B.; Rivlin P.; Wyttenbach R.; Strawderman R.; Hoy R. *Classical Conditioning Through Auditory Stimuli in Drosophila: Methods and Models* 2011, The Journal of Experimental Biology 214:2864-2870.

Bar H.; Booth J.; Schifano E. D.; Wells M. T. *Laplace Approximated EM Microarray Analysis: An Empirical Bayes Approach for Comparative Microarray Experiments.* 2010, Statistical Science 2010, 25(3):388-407.

Rosenbaum M. A.; Bar H.; Beg Q. K.; Segré D.; Booth J.; Cotta M. A.; Angenent L. T. *Shewanella oneidensis in a lactate-fed pure-culture and a glucose-fed co-culture with Lactococcus lactis with an electrode as electron acceptor.* 2010 (Oct.), Bioresource Technology, 102(3):2623-2628.

Bar H.; Miranker W.; Ambash A. *Competition and Cooperation in Neuronal Processing.* 2003, IEEE Transactions on Neural Networks 14(4):860-8.

UNDER REVIEW OR IN PREPARATION	Liu, K.; Bar, H. *Large-P Variable Selection in Two-Stage Models.*

Bar, H.; Booth, J.; Wells, M. T. *Mixed Effect Modeling and Variable Selection for Quantile Regression.* https://arxiv.org/abs/1910.11479

Bar, H.; Schifano, E. D. *DVX: an R package for Differential Variation and eXpression analysis.* https://haim-bar.uconn.edu/software/DVX/, 2018.

Bar, H. *Robust Variance Estimation.*

GRANTS AND CONTRACTS

NIH Award: *Characterization of the ventricular-subventricular stem cell niche during human brain development.* PI: J. Conover. H. Bar (co-Investigator.) Funding period: April 2020-March 2024.

NSF Award #: 1612625. PI. *Variable Selection in the High Dimensional, Low Sample Size Setting - Beyond the Linear Regression and Normal Errors Model.* Funding period: 8/15/16-7/31/19. Funding amount $150,000.

National Science Center - Poland. *Identification of transcriptomic markers of maize resistance to cereal aphids.* PI Dr. Hubert Sytykieticz. Funding period: 2/9/17-2/8/20.

Travelers. *Modeling and analysis of large insurance claim and occurrence data: A partnership between UConn and Travelers.* 2018 – PI: Dr. Dipak Dey, co-PIs: Haim Bar, Kun Chen, Elizabeth Schifano, Xiaojing Wang. Funding period: 8/1/17-7/31/18. Funding amount $137,881.
2019 – PI: Dey, D. Co-Investigators: Haim Bar, Kun Chen, Victor Hugo Lachos Davilla. Funding period: 8/1/2018 - 7/31/2019. Funding amount $146,451.

PATENTS

- U.S. Patent 9384677 (granted July 5, 2016)
  U.S. Patent 20150213730 A1 (Publication Date: July 30, 2015)
  U.S. Patent 9076342 B2 (granted July 7, 2015)
  U.S. Patent 20090208910 A1 (Publication Date: August 20, 2009)
  Automated execution and evaluation of network-based training exercises.
  Inventors: Brueckner, S. K.; Adelstein, F. N.; Bar, H.; Donovan, M.
- U.S. Patent 20150143355 (Publication Date: May 21, 2015)
  Service Oriented Architecture Version and Dependency Control.
  Inventors: Tingstrom, D. J.; Joyce, R. A.; Stillerman, M. A.; Brueckner, S. K.; Bar, H.
- U.S. Patent 8,984,396 (granted March 17, 2015)
  Identifying and representing changes between extensible markup language (XML) files using symbols with data element indication and direction indication.
  Inventors: Tingstrom, D. J.; Joyce, R. A.; Stillerman, M. A.; Brueckner, S. K.; Bar, H.
- U.S. Patent 8,898,285 (granted November 25, 2014)
  Service oriented architecture version and dependency control
  Inventors: Tingstrom, D. J.; Joyce, R. A.; Stillerman, M. A.; Brueckner, S. K.; Bar, H.
- U.S. Patent 8,286,249 (granted October 9, 2012)
  U.S. Patent 7,748,040 (granted June 29, 2010);
  Attack correlation using marked information.
  Inventors: Adelstein F. N., Bar H., Alla P. and Proskourine N.

SHORT COURSES

Advanced statistical modeling ideas (session on missing data). The University of Barcelona, Spain. January, 2019.
Advanced topics in R and Machine Learning. The Technion, Haifa, Israel. July, 2018.
R/Bioconductor workshop - the Technion, Haifa. November, 2016 (co-taught with Dr. Martin Morgan).

INVITED TALKS

Large-P Variable Selection in Two-Stage Models.
- CMStatistics, London, UK, December 2020.
- University of Connecticut, March 2020.
- University of Haifa, Israel. May, 2020.

Quantile Regression Modelling via Location and Scale Mixtures of Normal Distributions.
- Cornell University, October 2019.

A Mixture Model to Detect Edges in Sparse Co-expression Graphs.
- The 3rd Eastern Asia Meeting on Bayesian Statistics, Seoul, South Korea. July, 2018.
- Yonsei University, Seoul, South Korea. July, 2018.
- Korea University, Seoul, South Korea. July, 2018.
- Bayesian Modeling, Computation, and Applications, Storrs, CT, May 2018.

A Scalable Empirical Bayes Approach to Variable Selection in Generalized Linear Models.
- The 34th Quality and Productivity Research Conference, Storrs, CT, June 2017.
- The 10th ICSA International Conference, Shanghai, China. December, 2016.
- Temple University, Research Colloquium, Department of Statistical Science, April 2017.
- Baruch College, CUNY, Colloquium, Department of Information Systems and Statistics Zicklin School of Business, November 2016.

A Scalable Empirical Bayes Approach to Variable Selection.
- 2016 Joint Statistical Meetings, Chicago, IL. July, 2016.
- Joint UCONN/UMASS Statistics Colloquium, University of Massachusetts Amherst, MA. October 7, 2015
- Statistics Seminar, Department of Mathematics - University of Maryland. October 1, 2015.
- Colloquium - Mathematical Biosciences Institute - The Ohio State University. Sep. 21, 2015

An Empirical Bayes Approach to Variable Selection and QTL Analysis.
- Purdue University, Research Colloquium, Statistics Department, October 2014.
- Modern Modeling Methods (M^3) Conference, Storrs, CT, May 2014.

Model-based approaches for big-data problems, with applications in genomics. University of Connecticut, Institute for Systems Genomics Annual Networking Workshop. Storrs, CT. May 13, 2014.

A Bivariate Model for Simultaneous Testing in Bioinformatics Data
- 3rd International Conference and Exhibition on Biometrics & Biostatistics, Baltimore, MD, October 2014.
- University of Iowa, February 2013
- NIH/NCI, March 2013
- University of Connecticut, February 2013
- University of Rochester, February 2013
- Cornell University, October 2012

Accounting for Heaping in Retrospectively Reported Event Data - A Mixture Model Approach. ICSA Applied Statistics Symposium in New York City, NY, USA. June 2011.

A Heap of Trouble? Accounting for Mismatch Bias in Retrospectively Collected Data on Smoking. 3rd Biennial Conference of the American Society of Health Economists, Ithaca, NY, June 2010.

CONFERENCE PRESENTATIONS

An Empirical Bayes Approach to Variable Selection and QTL Analysis. Frontiers Of Hierarchical Modeling In Observational Studies, Complex Surveys And Big Data: A Conference Honoring Professor Malay Ghosh. College Park, MD. May 29-31, 2014.

A Mixture-Model Approach for Testing for Unequal Variances in Microarray Data. Conference of Applied Statistics Ireland, Galway, Ireland, 2011.

An Empirical Bayes Approach to Variable Selection and QTL Analysis. In the Proceedings of the 25th International Workshop on Statistical Modelling, Glasgow, Scotland, 2010.

JOURNAL REFEREE	Annals of Applied Statistics; Bayesian Analysis; Bioinformatics; Biometrics; Behavior Research Methods; BMC bioinformatics; Conservation Biology; Evaluation and Program Planning; International Journal of Environmental Research and Public Health; International Statistical Review; Journal of Agricultural, Biological, and Environmental Statistics; Journal of Computational and Graphical Statistics; Journal of Statistical Modeling; Journal of Statistical Planning and Inference; Journal of Statistical Theory and Practice; Journal of the American Statistical Association; Methodology & Computing in Applied Probability; PLOS ONE; Statistical Analysis and Data Mining; Statistical Modelling; Statistics and Its Inference; Statistics in Medicine; Stats.
REFEREE - OTHER	- National Science Foundation (NSF), 2017. - The Donaghue Medical Research Foundation: 　　"Greater Value Portfolio" - Review Board Member, 2015, 2016, 2017. 　　"Another Look" - Review Board Member, 2016. - National Aeronautics and Space Administration - Review Board Member, 2016. - International Chinese Statistical Association - Student Award Committee for the 2016 ICSA International Conference in Shanghai, China, Dec. 19-22, 2016. - New England Statistics Symposium - IBM Student Award Committee, 2015.
CONFERENCE ACTIVITIES	Organizing committee: The 33rd New England Statistics Symposium, Hartford, CT, 2019. Co-chair of the organizing committee: The 31st New England Statistics Symposium, Storrs, CT, 2017. Co-chair of the organizing committee: The 34th Quality and Productivity Research Conference, Storrs, CT, 2017. Session chair - Joint Statistical Meeting, 2016 (Chicago, IL). Session title: R Tools for Statistical Computing Session chair - Joint Statistical Meeting, 2015 (Seattle, WA). Session title: Methods in Machine Learning and Data Mining. Session chair - 3rd International Conference and Exhibition on Biometrics & Biostatistics, 2014.
DEPARTMENT AND UNIVERSITY COMMITTEES	Distinguished Statistician Colloquium - the Pfizer Series (Chair). Graduate program curriculum - applied statistics (Chair). Computing. New England Statistics Society. New England Statistics Symposium, 2017. Gratis faculty appointment (Chair). Visiting assistant professor search committee. Graduate students and distinguished alumni awards. UConn's Q-Center. Environmental health and safety (Chair). Library / tech reports (Chair).
OTHER SERVICES	Sankhya Series A, the Indian Journal of Statistics. (2018-) Associate Editor. Health Policy Statistics Section communication officer (July 2016-June 2019). Health Policy Statistics Section - best student paper review board (for JSM 2017). The 10th ICSA International Conference - Young Researcher Award review committee. New England Statistics Society - co-chair of the committee to establish the society's journal. Eastern North American Region (ENAR) 2019: Program committee member. (2018).

PH.D. ADVISING

Liu, Kangyan, 2019 (major advisor)
McLaughlin, Paul, 2019 (major advisor)
Chaoran Hu, 2020 (associate advisor)
Yulia Sidi, 2020 (associate advisor)
Jieying Jiao, 2020 (associate advisor)
Renjie Chen, 2019 (associate advisor)
Zha, Ruochen, 2018 (associate advisor)
Luo, chongliang, 2017 (associate advisor)
Mishra, Aditya, 2017 (associate advisor)
Mishra, Neha, 2017 (associate advisor)
Larose, Chantal, 2015 (associate advisor)
Ouyang, Guang, 2015 (associate advisor)

PROFESSIONAL
EXPERIENCE

ATC-NY, Ithaca, New York USA

Principal Scientist   **September 2003 - December 2010**

Involved in several government-funded research projects, mostly related to secure and survivable computer systems. For example, in the SPRINT project ("Secure Programming Using Artificial Intelligence Techniques") I designed and prototyped a tool to support secure programming with SPARK (SRI's Procedural Agent Realization Kit). In "Policy Projector", a Phase I OSD-funded effort, I was involved in the design of a tool that rapidly reveals potential problems with network policy changes prior to their implementation. In "Software Pedigree Analysis" (SPAN), a DARPA Phase I SBIR effort, I developed a prototype that maintains software pedigree to support future forensic investigations; and in "Active Smart Targets for Effective Response" (ASTER), a DARPA-funded Phase II SBIR, I developed a prototype to identify hackers by feeding them traceable information during exploratory probes.

MicroPatent LLC, East Haven, Connecticut USA

Director of Software Development   **January 2002 - December 2003**

Responsible for all software development projects, leading a team of 15-20 programmers. Designed and implemented an extensive patent-family database with over 50 million records, merging several different sources of data. Developed analytical tools for advanced patent searchers.

Special Projects Manager   **October 2000 - January 2002**

Led a team of five people to develop a large-scale system to deliver patent databases in XML format. The project included designing a database, writing a program to convert the data to XML, writing programs to validate the XML, and programs to automate and monitor the delivery process.

Team Leader   **February 1999 - September 2000**

Led a team that designed and implemented comprehensive patent and trademarks databases and web interfaces. In addition to developing web-based applications, I was involved in other projects, including the design and implementation of a Client/Server application to provide customers with direct access to the patent database (using OpenText's "Bibliographic Retrieval Services (BRS)/Search"); design and implementation of an SQL-based database to save user queries, and a corresponding web interface that allows users to construct complicated searches by combining results from previous searches, and share searches with colleagues; and an information-theoretic approach to improve retrieval of records.

Unix Programmer   **November 1997 - February 1999**

Involved in almost all the development projects in the company, including programs to enable our web customers to download patent data in PDF format (the first web site in the industry to do that), and in Lotus Notes format.

Motorola Israel - Wireless Access Systems Division, Tel Aviv, Israel

Software Engineer   **May 1995 - July 1997**

As part of the Software Quality Assurance (SQA) team in the "Wireless Local Loop" (WiLL) project, I was involved in a wide range of activities, including extensive test and integration of wireless and land telephony systems, from the operating system of the base stations to the end-user wireless equipment; software engineering practices and procedures; writing a graphic user interface for the WiLL system; writing a program to automate the analysis of massive log files in order to detect anomalies; and integration and testing of an encryption device in the fixed wireless terminals.

OTHER SKILLS   Statistical Packages: R, BUGS, Matlab, JMP, SAS, Stata, SPSS.
Programming languages: Perl, Pyhton, C, Java, JavaScript, Unix shell scripts, SQL, PHP, HTML/XML, Tcl/Tk.