Haim Bar, Ph.D.

Associate Professor
Department of Statistics
University of Connecticut

haim.bar@uconn.edu · https://haim-bar.uconn.edu · https://github.com/haimbar

Research Interests

Statistical models; shrinkage estimation; Bayesian high-dimensional data; high throughput applications in biology; Bayesian statistics; machine learning.

Education

Cornell University, Ithaca, New York USA. Statistics: Ph.D. 2012, M.Sc. 2010.
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.

2019 – Present: Associate Professor.

2013 – 2019: Assistant Professor.

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 (IBACS).

Teaching: STAT 5005: Introduction to Applied Statistics; STAT 5505: Applied Statistics I; STAT 5605: Applied Statistics II; STAT 3515Q/5515: Design of Experiments; STAT 3675Q: Statistical Computing; STAT/BIST 5225: Data Management in SAS and R; STAT/BIST 5215: Statistical Consulting; STAT 5615: Categorical Data Analysis.

The Hebrew University, Jerusalem, Israel. 2022 (May-August). Visiting faculty.

Cornell University, Ithaca, New York, USA.

2011 – 2013: Statistical Consultant.

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.

2012 – 2013: PostDoc, Department of Statistical Science

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.

Publications

Bar, H., & Wells, M. T. (2023). On graphical models and convex geometry. *Computational Statistics & Data Analysis*, *187*, 107800. Retrieved from https://www.sciencedirect.com/science/article/pii/S0167947323001111 doi: https://doi.org/10.1016/j.csda.2023.107800

Bar, H., & Yan, J. (2023). Legendary career and colorful life: A conversation with dr. bob riffenburgh. *Journal of Data Science*, *21*(4), 818–837. doi: 10.6339/23-JDS1115

Witherow, M. A., Samad, M. D., Diawara, N., Bar, H. Y., & Iftekharuddin, K. M. (2023). Deep adaptation of adult-child facial expressions by fusing landmark features. *IEEE Transactions on Affective Computing*, 1-12. doi: 10.1109/TAFFC.2023.3297075

Fumagalli, S. E., Padhiar, N. H., Meyer, D., Katneni, U., Bar, H., DiCuccio, M., … Kimchi-Sarfaty, C. (2023). Analysis of 3.5 million SARS-CoV-2 sequences reveals unique mutational trends with consistent nucleotide and codon frequencies. *Virology Journal*(31). Retrieved from https://virologyj.biomedcentral.com/articles/10.1186/s12985-023-01982-8 doi: 10.1186/s12985-023-01982-8

Barrett, D., Wyatt, M., Bar, H., Haynes, M. K., Edwards, B. S., Sklar, L. A., & Zweifach, A. (2022). A phenotypic screen for compounds that reverse cAMP-mediated suppression of T cell functions. *SLAS Discovery*. Retrieved from https://www.sciencedirect.com/science/article/pii/S2472555222126596 doi: https://doi.org/10.1016/j.slasd.2022.03.008

Kateni, U., Alexaki, A., Hunt, R., Katagiri, N., Hettiarachchi, G., Kames, J., … Kimchi-Sarfaty, C. (2022, 04). Structural, functional, and immunogenicity implications of F9 gene recoding. *Blood Advances*. Retrieved from https://doi.org/10.1182/bloodadvances.2022007094 (bloodadvances.2022007094) doi: 10.1182/bloodadvances.2022007094

Cheng, J., Bar, H., & Tako, E. (2021). Zinc Status Index (ZSI) for Quantification of Zinc Physiological Status. *Nutrients*, *13*(10). Retrieved from https://www.mdpi.com/2072-6643/13/10/3399 doi: 10.3390/nu13103399

Bar, H., Booth, J. G., & Wells, M. T. (0). Mixed effect modelling and variable selection for quantile regression. *Statistical Modelling*, *0*(0), 1471082X211033490. Retrieved from https://doi.org/10.1177/1471082X211033490 doi: 10.1177/1471082X211033490

Meyer, D., Kames, J., Bar, H., Komar, A. A., Alexaki, A., Ibla, J., … Kimchi-Sarfaty, C. (2021). Distinct signatures of codon and codon pair usage in 32 primary tumor types in the novel database CancerCoCoPUTs for cancer-specific codon usage. *Genome Medicine*, *13*(122). doi: 10.1186/s13073-021-00935-6

Holcomb, D., Hamasaki-Katagiri, N., Laurie, K., Katneni, U., Kames, J., Alexaki, A., … Kimchi-Sarfaty, C. (2021). New approaches to predict the effect of co-occurring variants on protein characteristics. *The American Journal of Human Genetics*, *108*, 1502-1511. Retrieved from https://www.sciencedirect.com/science/article/pii/S0002929721002354 doi: https://doi.org/10.1016/j.ajhg.2021.06.011

Bar, H., & Wang, H. (2021). Reproducible Science with LATEX. *Journal of Data Science*, *19*(1), 111-125. doi: 10.6339/21-JDS998

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

McLaughlin, P., & Bar, H. (2021). A spatial capture-recapture model with attractions between individuals. *Environmetrics*, *32*(1), e2653. Retrieved from https://onlinelibrary.wiley.com/doi/abs/10.1002/env.2653 doi: https://doi.org/10.1002/env.2653

Bar, H. Y., Booth, J. G., & Wells, M. T. (2020). A Scalable Empirical Bayes Approach to Variable Selection in Generalized Linear Models. *Journal of Computational and Graphical Statistics*, *0*(0), 1-12. Retrieved from https://doi.org/10.1080/10618600.2019.1706542 doi: 10.1080/10618600.2019.1706542

Bar, H., & Zweifach, A. (2020). Z' Does Not Need to Be >0.5. *SLAS DISCOVERY: Advancing the Science of Drug Discovery*, *25*(9), 1000-1008. Retrieved from https://doi.org/10.1177/2472555220942764 (PMID: 32749188) doi: 10.1177/2472555220942764

Katneni, U. K., Holcomb, D. D., Hernandez, N. E., Hamasaki-Katagiri, N., Hunt, R. C., Bar, H., … Kimchi-Sarfaty, C. (2020). In silico features of ADAMTS13 contributing to plasmatic ADAMTS13 levels in neonates with congenital heart disease. *Thrombosis Research*, *193*, 66-76. Retrieved from https://www.sciencedirect.com/science/article/pii/S0049384820302140 doi: https://doi.org/10.1016/j.thromres.2020.05.042

Kames, J., Alexaki, A., Holcomb, D. D., Santana-Quintero, L. V., Athey, J. C., Hamasaki-Katagiri, N., … Kimchi-Sarfaty, C. (2020). TissueCoCoPUTs: Novel Human Tissue-Specific Codon and Codon-Pair Usage Tables Based on Differential Tissue Gene Expression. *Journal of Molecular Biology*, *432*(11), 3369-3378. Retrieved from https://www.sciencedirect.com/science/article/pii/S0022283620300413 (Computation Resources for Molecular Biology) doi: https://doi.org/10.1016/j.jmb.2020.01.011

Alexaki, A., Kames, J., Hettiarachchi, G. K., Athey, J. C., Katneni, U. K., Hunt, R. C., … Kimchi-Sarfaty, C. (2020). Ribosome profiling of HEK293T cells overexpressing codon optimized coagulation factor IX. *F1000 Research*.

Hunt, R., Hettiarachchi, G., Katneni, U., Hernandez, N., Holcomb, D., Kames, J., … Kimchi-Sarfaty, C. (2019). A Single Synonymous Variant (c.354G>A [p.P118P]) in ADAMTS13 Confers Enhanced Specific Activity. *International Journal of Molecular Sciences*, *20*(22). Retrieved from https://www.mdpi.com/1422-0067/20/22/5734 doi: 10.3390/ijms20225734

Alexaki, A., Hettiarachchi, G. K., Athey, J. C., Katneni, U. K., Simhadri, V., Hamasaki-Katagiri, N., … Kimchi-Sarfaty, C. (2019). Effects of codon optimization on coagulation factor IX translation and structure: Implications for protein and gene therapies. *Scientific Reports*, *9*, 15449. doi: 10.1038/s41598-019-51984-2

Bar, H., & Schifano, E. D. (2019). Differential variation and expression analysis. *Stat*, *8*(1), e237. Retrieved from https://onlinelibrary.wiley.com/doi/abs/10.1002/sta4.237 (e237 sta4.237) doi: https://doi.org/10.1002/sta4.237

Korach-Rechtman, H., Freilich, S., Gerassy-Vainberg, S., Buhnik-Rosenblau, K., Danin-Poleg, Y., Bar, H., & Kashi, Y. (2019). Murine genetic background has a stronger impact on the composition of the gut microbiota than maternal inoculation or exposure to unlike exogenous microbiota. *Applied and Environmental Microbiology*, *85*(18). Retrieved from https://aem.asm.org/content/85/18/e00826-19 doi: 10.1128/AEM.00826-19

Katneni, U. K., Liss, A., Holcomb, D., Katagiri, N. H., Hunt, R., Bar, H., … Kimchi-Sarfaty, C. (2019). Splicing dysregulation contributes to the pathogenicity of several F9 exonic point variants. *Molecular Genetics & Genomic Medicine*, *7*(8), e840. Retrieved from https://onlinelibrary.wiley.com/doi/abs/10.1002/mgg3.840 doi: https://doi.org/10.1002/mgg3.840

Alexaki, A., Kames, J., Holcomb, D. D., Athey, J., Santana-Quintero, L. V., Lam, P. V. N., … Kimchi-Sarfaty, C. (2019). Codon and Codon-Pair Usage Tables (CoCoPUTs): Facilitating Genetic Variation Analyses and Recombinant Gene Design. *Journal of Molecular Biology*, *431*(13), 2434-2441. Retrieved from https://www.sciencedirect.com/science/article/pii/S0022283619302281 (Computation Resources for Molecular Biology) doi: https://doi.org/10.1016/j.jmb.2019.04.021

Poole, A. C., Goodrich, J. K., Youngblut, N. D., Luque, G. G., Ruaud, A., Sutter, J. L., … Ley, R. E. (2019). Human salivary amylase gene copy number impacts oral and gut microbiomes. *Cell Host & Microbe*, *25*(4), 553-564.e7. Retrieved from https://www.sciencedirect.com/science/article/pii/S1931312819301131 doi: https://doi.org/10.1016/j.chom.2019.03.001

Bar, H., & Liu, K. (2019). Empirical Bayes methods in variable selection. *WIREs Computational Statistics*, *11*(2), e1455. Retrieved from https://onlinelibrary.wiley.com/doi/abs/10.1002/wics.1455 doi: https://doi.org/10.1002/wics.1455

Hettiarachchi, G., Katneni, U., Hunt, R., Kames, J., Athey, J., Bar, H., … Kimchi-Sarfaty, C. (2019). Translational and transcriptional responses in human primary hepatocytes under hypoxia. *Am J Physiol Gastrointest Liver Physiol.*, *316*(6), G720-G734. doi: 10.1152/ajpgi.00331.2018

Bar, H., Booth, J., Wells, M. T., & Liu, K. (2018). Facilitating high-dimensional transparent classification via empirical Bayes variable selection. *Applied Stochastic Models in Business and Industry*, *34*(6), 949-961. Retrieved from https://onlinelibrary.wiley.com/doi/abs/10.1002/asmb.2393 doi: https://doi.org/10.1002/asmb.2393

Fox, E. L., Pelto, G. H., Bar, H., Rasmussen, K. M., Young, S. L., Debrosse, M. G., … Pelletier, D. L. (2018). 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. *Current Developments in Nutrition*, nzy017. Retrieved from http://dx.doi.org/10.1093/cdn/nzy017 doi: 10.1093/cdn/nzy017

Chen, K., Mishra, N., Smyth, J., Bar, H., Schifano, E., Kuo, L., & Chen, M.-H. (2017). A tailored multivariate mixture model for detecting proteins of concordant change in the pathogenesis of Necrotic Enteritis. *Journal of the American Statistical Association*. doi: 10.1080/01621459.2017.1356314

Bar, H. (2017). Missing data - mechanisms and possible solutions / datos ausentes: mecanismos y posibles soluciones. *Culture and Education*, *29*(3), 492-525. Retrieved from https://doi.org/10.1080/11356405.2017.1365426 doi: 10.1080/11356405.2017.1365426

Bar, H., & Mentch, L. (2017). R-CMap - An open-source software for concept mapping. *Evaluation and Program Planning*, *60*(C), 284-292. Retrieved from https://EconPapers.repec.org/RePEc:eee:epplan:v:60:y:2017:i:c:p:284-292

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

Hamasaki-Katagiri, N., Lin, B., Simon, J., Hunt, R., Schiller, T., Russek-Cohen, E., … Kimchi-Sarfaty, C. (2017, January). The importance of mrna structure in determining the pathogenicity of synonymous and non-synonymous mutations in haemophilia. *Haemophilia : the official journal of the World Federation of Hemophilia*, *23*(1), e8-e17. Retrieved from https://europepmc.org/articles/PMC5226872 doi: 10.1111/hae.13107

Tako, E., Bar, H., & Glahn, R. P. (2016). 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. *Nutrients*, *8*(11). Retrieved from https://www.mdpi.com/2072-6643/8/11/732 doi: 10.3390/nu8110732

Molinari, E., Bar, H., Pyle, A., & Patrizio, P. (2016). Transcriptome analysis of human cumulus cells reveals hypoxia as the main determinant of follicular senescence. *MHR: Basic science of reproductive medicine*, *22*(8), 866-876. Retrieved from http://dx.doi.org/10.1093/molehr/gaw038 doi: 10.1093/molehr/gaw038

Schifano, E., Bar, H., & Harel, O. (2015). Methods for analyzing secondary outcomes in public health case-control studies. In C. DG. & W. J. (Eds.), *Innovative statistical methods for public health data. icsa book series in statistics.* (p. 3-15). Switzerland: Springer.

Bar, H. Y., Booth, J. G., & Wells, M. T. (2014, Feb). A Bivariate Model for Simultaneous Testing in Bioinformatics Data. *Journal of the American Statistical Association*, *109*(506), 537-547. Retrieved from http://dx.doi.org/10.1080/01621459.2014.884502 doi: 10.1080/01621459.2014.884502

Finkelstein, J. L., Pressman, E. K., Cooper, E. M., Kent, T. R., Bar, H. Y., & O'Brien, K. O. (2014, nov). Vitamin D Status Affects Serum Metabolomic Profiles in Pregnant Adolescents. *Reproductive Sciences*, *22*(6), 685–695. doi: 10.1177/1933719114556477

Alexander, E. L., Gardete, S., Bar, H. Y., Wells, M. T., Tomasz, A., & Rhee, K. Y. (2014). Intermediate-Type Vancomycin Resistance (VISA) in Genetically-Distinct Staphylococcus aureus Isolates Is Linked to Specific , Reversible Metabolic Alterations. *PloS one*, *9*(5), e97137. doi: 10.1371/journal.pone.0097137

Coate, J. E., Bar, H., & Doyle, J. J. (2014). Extensive Translational Regulation of Gene Expression in an Allopolyploid (Glycine dolichocarpa). *The Plant Cell*, *26*(1), 136–150. Retrieved from http://www.plantcell.org/content/26/1/136 doi: 10.1105/tpc.113.119966

Athiphunamphai, N., Bar, H. Y., Cooley, H. J., & Padilla-Zakour, O. I. (2014). Heat treatment and turbo extractor rotational speed effects on rheological and physico-chemical properties of varietal applesauce. *Journal of Food Engineering*, *136*, 19-27. Retrieved from https://www.sciencedirect.com/science/article/pii/S0260877414001290 doi: https://doi.org/10.1016/j.jfoodeng.2014.03.016

Garrett-Bakelman, F. E., Li, S., Hricik, T., Chung, S. S., Bar, H., Brown, A. L., … Melnick, A. M. (2013, 11). Epigenetic Deregulation In Relapsed Acute Myeloid Leukemia. *Blood*, *122*(21), 2499-2499. Retrieved from https://doi.org/10.1182/blood.V122.21.2499.2499 doi: 10.1182/blood.V122.21.2499.2499

Bar, H. Y., & Lillard, D. R. (2012). Accounting for heaping in retrospectively reported event data - a mixture-model approach. *Statistics in Medicine*, *31*(27), 3347-3365. Retrieved from https://onlinelibrary.wiley.com/doi/abs/10.1002/sim.5419 doi: https://doi.org/10.1002/sim.5419

Bar, H. Y., Booth, J. G., & Wells, M. T. (2012, Jan). A mixture-model approach for parallel testing for unequal variances. *Statistical applications in genetics and molecular biology*, *11*(1), Article 8. Retrieved from http://www.ncbi.nlm.nih.gov/pubmed/22499680 doi: 10.2202/1544-6115.1762

Jiang, X., Bar, H. Y., Yan, J., West, A. a., Perry, C. A., Malysheva, O. V., … Caudill, M. A. (2012, Jan). Pregnancy Induces Transcriptional Activation of the Peripheral Innate Immune System and Increases Oxidative DNA Damage among Healthy Third Trimester Pregnant Women. *PloS one*, *7*(11), e46736. Retrieved from http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=3487782&tool=pmcentrez&rendertype=abstract doi: 10.1371/journal.pone.0046736

Jiang, X., Yan, J., West, A. A., Perry, C. A., Malysheva, O., Bar, H. Y., … Vermeylen, F. (2012, Nov). Pregnancy status and choline intake alter DNA integrity, epigenetic marks and gene expression. *The FASEB Journal*, *26*(1), 116.1. Retrieved from http://www.ncbi.nlm.nih.gov/pubmed/23195033http://www.fasebj.org/content/early/2012/11/28/fj.12-221648.abstracthttp://www.fasebj.org/cgi/content/meeting_abstract/26/1_MeetingAbstracts/116.1 doi: 10.1096/fj.12-221648

Rosenbaum, M. A., Bar, H. Y., Beg, Q. K., Segrè, D., Booth, J., Cotta, M. A., & Angenent, L. T. (2012, Jan). Transcriptional analysis of Shewanella oneidensis MR-1 with an electrode compared to Fe(III)citrate or oxygen as terminal electron acceptor. *PloS one*, *7*(2), e30827. Retrieved from http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=3271074&tool=pmcentrez&rendertype=abstract doi: 10.1371/journal.pone.0030827

Bar, H., & Schifano, E. D. (2011). Empirical and fully Bayesian approaches for random effects models in microarray data analysis. *Statistical Modelling*, *11*(1), 71–78. doi: doi:10.1177/147108X1001100105

Jiang, X., Yan, J., West, A., Perry, C., Malysheva, O., Bar, H., … Caudill, M. (2011, Mar). A higher maternal choline intake favorably alters placental gene expression of biological pathways related to disease risk. *The FASEB Journal*, *25*(1), 599.5. Retrieved from http://www.fasebj.org/cgi/content/meeting_abstract/25/1_MeetingAbstracts/599.5

Menda, G., Bar, H. Y., Arthur, B. J., Rivlin, P. K., Wyttenbach, R. A., Strawderman, R. L., & Hoy, R. R. (2011, 09). Classical conditioning through auditory stimuli in Drosophila: methods and models. *Journal of Experimental Biology*, *214*(17), 2864-2870. Retrieved from https://doi.org/10.1242/jeb.055202 doi: 10.1242/jeb.055202

Bar, H., Booth, J., Schifano, E. D., & Wells, M. T. (2010). Laplace Approximated EM Microarray Analysis: An Empirical Bayes Approach for Comparative Microarray Experiments. *Statistical Science*, *25*(3), 388-407. doi: 10.1214/10-STS339

Rosenbaum, M. A., Bar, H. Y., Beg, Q. K., Segrè, D., Booth, J., Cotta, M. A., & Angenent, L. T. (2011, Feb). Shewanella oneidensis in a lactate-fed pure-culture and a glucose-fed co-culture with Lactococcus lactis with an electrode as electron acceptor. *Bioresource technology*, *102*(3), 2623–8. Retrieved from http://www.ncbi.nlm.nih.gov/pubmed/21036604 doi: 10.1016/j.biortech.2010.10.033

Bar, H., Miranker, W., & Ambash, A. (2003). Competition and cooperation in neuronal processing. *IEEE Transactions on Neural Networks*, *14*(4), 860-868. doi: 10.1109/TNN.2003.813822

Under review or in preparation

Bar, H.; Booth, J.; Wells, M.T. *Automated Model Building and Goodness-of-fit via Quantile Regression.*

Sasanka L Adikari; Norou Diawara; Haim Bar. *The geometry of dynamic time-dependent best-worst choice pairs.*

Bar, H. *Robust Variance Estimation.*

Grants and Contracts

- CLAS Research in Academic Themes 2022 funding initiative (January 2023-June 2024). PI. *A novel statistical approach to uncover the hidden language of long non-coding RNAs.* Funding amount $49,725.
- IBACS Seed Grant. PI. *Modeling and visualizing the formation of brain cavities covering from stem cells.* Funding period: 1/1/2022-12/31/2022. Funding amount $18,516.
- 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 20230041627 A1 (Publication Date: February 9, 2023)
  Assay Compound Screening.
- 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

On graphical models and convex geometry.
- Consortium for Data Analytics in Risk, Berkeley, CA. November, 2023.
- SIAM Conference on Financial Mathematics and Engineering. Philadelphia, PA. June, 2023.
- Mathematics and Statistics Department, Old Dominion University. March, 2023.
- Statistics Department, The Hebrew University, Jerusalem, Israel. June 2022.

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), CISE.
- 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 Department of Statistics 60th anniversary, University of Connecticut, Storrs, CT, 2022.
- 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 (Chair).
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

College of Liberal Arts and Sciences. Research Advisory Committee AY22-23.
The New England Journal of Statistics in Data Science - Software section. Editor.
Data Science in Science. Associate Editor.
Sankhya Series A, the Indian Journal of Statistics. (2018-2021) 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

Kangyan Liu, 2019 (major advisor)
Paul McLaughlin, 2019 (major advisor)
Cheng Huang, 2022 (associate advisor)
Srawan Bishoni, 2022 (associate advisor)
Ziqi Yang, 2021 (associate advisor)
Ellis Shaffer, 2020 (associate advisor)
Zhe Wang, 2020 (associate advisor)
Dakota Cintron, 2020 (associate advisor)
Chaoran Hu, 2020 (associate advisor)
Yulia Sidi, 2020 (associate advisor)
Jieying Jiao, 2020 (associate advisor)
Renjie Chen, 2019 (associate advisor)
Ruochen Zha, 2018 (associate advisor)
chongliang Luo, 2017 (associate advisor)

Aditya Mishra, 2017 (associate advisor)
Neha Mishra, 2017 (associate advisor)
Chantal Larose, 2015 (associate advisor)
Guang Ouyang, 2015 (associate advisor)

Professional Experience

ATC-NY, Ithaca, New York, USA.

2003 – 2010: Principal Scientist.

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.

2002 – 2003: Director of Software Development.

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.

2000 – 2002: Special Projects Manager.

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.

1999 – 2000: Team Leader

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.

1997 – 1999: Unix Programmer

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.

1995 – 1997: Software Engineer.

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: Pyhton, C, Perl, Java, JavaScript, Unix shell scripts, SQL, PHP, HTML/XML, Tcl/Tk.

Updated on December 11, 2023