

November 17, 2011

CURRICULUM VITAE

RAFAEL A. IRIZARRY

PERSONAL DATA

Web Page: <http://rafalab.org>
Email: rafa@jhu.edu
Mailing Address: Department of Biostatistics
Johns Hopkins Bloomberg School of Public Health
615 North Wolfe St. E3620
Baltimore, MD 21205
Phone: 410-614-5157
Fax: 410-955-0958

EDUCATION AND TRAINING

PhD	1998	University of California, Berkeley	Statistics
BS	1993	University of Puerto Rico, Río Piedras	Mathematics

PROFESSIONAL EXPERIENCE

2007- Professor, Department of Biostatistics
 Johns Hopkins Bloomberg School of Public Health

2008- Preceptor, Department of Human Genetics
 Johns Hopkins School of Medicine

2010- Joint Appointment, Department of Medicine
 Johns Hopkins School of Medicine

2004-2007 Associate Professor, Department of Biostatistics
 Johns Hopkins Bloomberg School of Public Health

Summer 2006 Visiting Professor, Department of Statistics, Stanford University

1998-2004 Assistant Professor, Department of Biostatistics
 Johns Hopkins Bloomberg School of Public Health

1997-1998 Instructor, Department of Statistics
 University of California, Berkeley

PROFESSIONAL ACTIVITIES

Society Membership
American Statistical Association

Institute of Mathematical Statistics

Consultations

The Collection, Storage, Management, and Distribution Of Next-Generation Sequence Data NIH Workshop. Gaithersburg, MD (2011)

Organized and moderated *Controversies in Public Health due to Misinterpretation of Statistical Information* Session at the American Public Health Association Meeting *Denver, CO* (2010)

NHGRI Informatics and Analysis Planning Meeting (2010)

Organizing Committee for the *Conference on Research in Computational Molecular Biology (RECOMB)* (2007)

Conference Committee for *NSF Sponsored International Conference on Bioinformatics in Zhejiang University, HangZhou, China* (2007)

Statistical Consulting on Microarray Data Analysis for *Recinto de Ciencias Médicas, Universidad de Puerto Rico, Rio Piedras, PR* (2006)

Software development for Nimblegen Systems Inc. (2005)

Organizer of “The 2003 Affymetrix GeneChip Microarray Low-Level Workshop”

Biostatistics Department Liaison to Johns Hopkins University Microarray Core

Statistical Consulting for Lucent Technologies (2000)

Statistical Consulting for Center for New Music and Audio Technology (1998)

Project Development

Microarray Quality Control (MAQC) II

GAIN Alternative Calling Algorithms Working Group

EMERALD Project scientific advisory board

MGED Advisory Board

Bioconductor Project Co-Founder and Co-leader

Member of External RNA Control Consortium (ERCC)

EDITORIAL ACTIVITIES

Peer Review Activities

Associate Editor for Annals of Applied Statistics 09/2006-1/2010

Associate Editor for Biostatistics 02/2002-11/2009

Editorial Board for BMC Bioinformatics 05/2005-Present

Served as *referee* for:

Annals of Biomedical Engineering
American Statistician
BMC Bioinformatics
Bayesian Analysis
Bioinformatics
Biometrics
Biometrika
Biostatistics
Biotechniques
Conference on Research in Computational Molecular Biology (RECOMB)
Epidemiology
Envirometrics
Expert Review of Molecular Diagnostics
Functional & Integrative Genomics
Genome Biology
Genome Research
Genomics
Journal of the American Association of Cancer Research (AACR)
Journal of the American Statistical Association (JASA)
Journal of Clinical Cancer Research
Journal of Clinical Epidemiology
Journal of Computational and Graphical Statistics
Journal of the National Cancer Institute (JNCI)
Molecular Cellular Probes
Nature
Nature Biotechnology
Nature Genetics
Nature Genetics Reviews
Nature Methods
Nature Nanotechnology
New England Journal of Medicine
Nucleic Acids Research
The Lancet
The Pharmacogenomics Journal

Physiological Genomics
PLoS Medicine
Proceedings of the National Academy of Science (PNAS)
Science
Statistical Applications in Genetics and Molecular Biology
Trends in Genetics

Review of Proposals

NIH GCAT Study Section - Regular member – 2010-present

National Human Genome Research Institute's Special Review Panel for "1000 Genomes Project Data Processing". October 26, 2009.

Ad-hoc review of NIH Challenge Grant applications received in response to the RFA on NIH Challenge Grants in Health and Science Research (American Recovery and Reinvestment Act of 2009)

National Human Genome Research Institute's Special Review Panel for 1000 Genomes Project Data Processing. March 19, 2009.

National Human Genome Research Institute's Genome Research Review Committee. GCAT section February 9, 2009

National Cancer Institute Review Panel for TCGA Data Analysis and Visualization Methods. April 2, 2008.

Alberta Heritage Foundation for Medical Research Grant Review. January 2006

National Human Genome Research Institute's Genome Research Review Committee. March 8, 2005

National Institute of Health Center for Scientific Review Special Emphasis Panel: Software Development. October 15, 2004.

National Institute of Arthritis and Musculoskeletal and Skin Disease Special Emphasis Panel: Microarray Awards (NIH) August 21-22, 2003.

Bioinformatics Study Section for the National Genomic Program sponsored by the National Science Council, Taiwan, R.O.C. March 29-30, 2002.

HONORS AND AWARDS

- 2010 Ranked second-most cited mathematical scientist in the world by Essential Science Indicators.
- 2010 The Daily Record's Very Important Professionals, Successful before 40, List

- 2009 COPSS President's Award presented to a young member of the statistical community in recognition of an outstanding contribution to the profession.
- 2009 Mortimer Spiegelman Award which recognizes a statistician age 40 years or younger who has made outstanding contributions to public health statistics.
- 2009 American Statistical Association Fellow
- 2009 Distinguished Alumni. College of Natural Sciences, University of Puerto Rico, Río Piedras.
- 2009 Main author of Fast Breaking Paper in Mathematics awarded by Thomson Essential Science Indicators (ESI).
- 2008 Faculty Spotlight Presenter at Johns Hopkins University Board of Trustees Meeting
- 2007 ASA Youden Award in Interlaboratory Testing
- 2005 Faculty Research Initiatives Fund, Johns Hopkins Bloomberg School of Public Health
- 2004 ASA Outstanding Statistical Application Award which recognizes a paper that is an outstanding application of statistics in any substantive field.
- 2003 Dean's Lecture: Bloomberg School of Public Health
- 2003 Main author of Fast Breaking Paper and New Hot Paper in Mathematics awarded by Thomson Essential Science Indicators (ESI).
- 2003 Insightful Innovation Award. This award from the Insightful Corporation recognizes innovation in information sciences. Awarded to Bioconductor.
- 2001 American Statistical Association Noether Young Scholar Award for researcher, younger than 35 years of age, who has significant research accomplishments in nonparametrics statistics
- 1999 Faculty Innovation Fund, Johns Hopkins University School of Public Health
- 1998 Outstanding Graduate Student Instructor Award, University of California, Berkeley
- 1996 Chancellor's Predoctoral Opportunity Fellowship, University of California, Berkeley
- 1993 National Science Foundation Graduate Fellow
- 1993 Facundo Bueso Medal, School of Natural Science, University of Puerto Rico
- 1993 Mathematics Medal, University of Puerto Rico
- 1992 First Prize Inter-collegiate Advanced Programming Competition, University of Puerto Rico, Río Piedras
- 1990 First Prize University Mathematics Olympics, University of Puerto Rico, Cayey

PUBLICATIONS

Journal Articles:

Niranjan TS, Adamczyk A, Bravo HC, Taub MA, Wheelan SJ, **Irizarry R**, Wang T. (2011) Effective detection of rare variants in pooled DNA samples using Cross-pool tailcurve analysis. *Genome Biology* 12(9):R93.

McCall MN, **Irizarry RA** (2011) Thawing Frozen Robust Multi-array Analysis (fRMA) *BMC Bioinformatics* 12:369.

Hansen KD, Timp W, Corrada Bravo H, Sabunciyan S, Langmead B, McDonald OG, Wen B, Wu H, Liu Y, Diep D, Briem E, Zhang K, **Irizarry RA**, Feinberg AP (2011) Increased methylation variation in epigenetic domains across cancer types. *Nature Genetics* 43(8):768-75

Jaffe AE, Feinberg AP, **Irizarry RA**, Leek JT (2011) Significance analysis and statistical dissection of variably methylated regions. *Biostatistics*. [Epub ahead of print]

Yegnasubramanian S, Wu Z, Haffner MC, Esopi D, Aryee MJ, Badrinath R, He TL, Morgan JD, Carvalho B, Zheng Q, De Marzo AM, **Irizarry RA**, Nelson WG (2011) Chromosome-wide mapping of DNA methylation patterns in normal and malignant prostate cells reveals pervasive methylation of gene-associated and conserved intergenic sequences. *BMC Genomics*. 2011 Jun 13;12(1):313.

Guerrero-Preston R, Soudry E, Acero J, Orera M, Moreno-Lopez L, Macia-Colon G, Jaffe A, Berdasco M, Ili-Gangas C, Brebi-Mieville P, Fu Y, Engstrom C, **Irizarry R**, Esteller M, Westra WH, Koch WM, Califano JA, Sidransky D (2011) NID2 and HOXA9 promoter hypermethylation as biomarkers for prevention and early detection in Oral Cavity Squamous Cell Carcinoma tissues and saliva. *Cancer Prev Res* (To appear)

Halper-Stromberg E, Frelin L, Ruczinski I, Scharpf R, Jie C, Carvalho B, Hao H, Hetrick K, Jedlicka A, Dziejczak A, Doheny K, Scott AF, Baylin S, Pevsner J, Spencer F, **Irizarry RA** (2011) Performance assessment of copy number microarray platforms using a spike-in experiment. *Bioinformatics* 27(8):1052-60.

Scharpf RB, **Irizarry RA**, Ritchie ME, Carvalho B, Ruczinski I (2011) Using the R Package crlmm for Genotyping and Copy Number Estimation. *Journal of Statistical Software* 40(12):1-32.

Shan L, Yang HC, Rabi SA, Bravo HC, **Irizarry RA**, Zhang H, Margolick JB, Siliciano JD, Siliciano RF (2011) Influence of host gene transcription level and orientation on HIV-1 latency in a primary cell model. *J Virol*. (To appear)

Ritchie ME, Liu R, Carvalho BS; The Australia and New Zealand Multiple Sclerosis Genetics Consortium (ANZgene), **Irizarry RA** (2011) Comparing genotyping algorithms for Illumina's Infinium whole-genome SNP BeadChips. *BMC Bioinformatics* 12(1):68.

McCall MN, Uppal K, Jaffee HA, Zilliox MJ, **Irizarry RA** (2011) The Gene Expression Barcode: leveraging public data repositories to begin cataloging the human and murine transcriptomes. *Nucleic Acids Res* (Database issue):D1011-5.

Louis TA, Carvalho BS, Fallin MD, Irizarry RA, Li Q, Ruczinski I (2010). Association tests that accommodate genotyping errors. *Bayesian Statistics 9*: 393-413 (Bernardo JM, Bayarri MJ, Berger JO, Dawid AP, Heckerman D, Smith AF, West M, Eds), Oxford University Press, Oxford UK.

Taub MA, Corrada Bravo H, **Irizarry RA** (2010) Overcoming bias and systematic errors in next generation sequencing data. *Genome Med.* 10;2(12):87.

Aryee MJ, Wu Z, Ladd-Acosta C, Herb B, Feinberg AP, Yegnasubramanian S, **Irizarry RA** (2010) Accurate genome-scale percentage DNA methylation estimates from microarray data. *Biostatistics* 12(2):197-210.

Feinberg AP, **Irizarry RA**, Fradin D, Aryee MJ, Murakami P, Aspelund T, Eiriksdottir G, Harris TB, Launer L, Gudnason V, Fallin MD (2010) Personalized epigenomic signatures that are stable over time and covary with body mass index. *Sci Transl Med.* 2(49):49ra67.

Leek JT, Scharpf RB, Bravo HC, Simcha D, Langmead B, Johnson WE, Geman D, Baggerly K, **Irizarry RA** (2010) Tackling the widespread and critical impact of batch effects in high-throughput data. *Nat Rev Genet.* 2010 11(10):733-9.

Ji H, Ehrlich LI, Seita J, Murakami P, Doi A, Lindau P, Lee H, Aryee MJ, **Irizarry RA**, Kim K, Rossi DJ, Inlay MA, Serwold T, Karsunky H, Ho L, Daley GQ, Weissman IL, Feinberg AP (2010) Comprehensive methylome map of lineage commitment from haematopoietic progenitors. *Nature* 467(7313):338-42

Carvalho BS, **Irizarry RA** (2010) A Framework for Oligonucleotide Microarray Preprocessing. *Bioinformatics* 26(19):2363-7.

MAQC Consortium (2010) The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. *Nature Biotechnology.* 28(8):827-38.

Scharpf RB, Ruczinski I, Carvalho B, Doan B, Chakravarti A, **Irizarry RA** (2010) A multilevel model to address batch effects in copy number estimation using SNP arrays. *Biostatistics* (To appear)

Kim K, Doi A, Wen B, Ng K, Zhao R, Cahan P, Kim J, Aryee MJ, Ji H, Ehrlich LI, Yabuuchi A, Takeuchi A, Cunniff KC, Hongguang H, McKinney-Freeman S, Naveiras O, Yoon TJ, Irizarry RA, Jung N, Seita J, Hanna J, Murakami P, Jaenisch R, Weissleder R, Orkin SH, Weissman IL, Feinberg AP, Daley GQ (2010) Epigenetic memory in induced pluripotent stem cells. *Nature* 467(7313):285-90.

Wu H, **Irizarry RA**, Bravo HC (2010) Intensity normalization improves color calling in SOLiD sequencing. *Nature Methods* 7(5):336-7.

Schafer E, **Irizarry RA**, Negi S, McIntyre E, Small D, Figueroa ME, Melnick A, Brown P (2010) Promoter hypermethylation in MLL-r infant acute lymphoblastic leukemia: biology and therapeutic targeting. *Blood*. 2010 115(23):4798-809.

Wu H, Caffo B, Jaffee HA, Feinberg AP, **Irizarry RA** (2010) Redefining CpG islands using hidden Markov models. *Biostatistics* 11(3):499-514.

López-Romero P, González MA, Callejas S, Dopazo A, **Irizarry RA** (2010) Processing of Agilent microRNA array data. *BMC Research Notes* 3:18

McCall MN, Bolstad BM, **Irizarry RA** (2010) Frozen robust multiarray analysis (fRMA). *Biostatistics* 11(2):242-53

Feinberg AF and **Irizarry RA** (2010) Stochastic epigenetic variation as a driving force of development, evolutionary adaptation, and disease. *Proceeding of the National Academy of Science* 107 Suppl 1:1757-64

Corrada-Bravo H, **Irizarry RA** (2010) Model-based quality assessment and base calling for second-generation sequencing data. *Biometrics* 66(3):665-74.

Sah S, McCall MN, Eveleigh D, Wilson M, Irizarry RA (2010) Performance evaluation of commercial miRNA expression array platforms. *BMC Research Notes* 18;3:80.

Carvalho B, Louis TA, **Irizarry RA** (2010) Quantifying Uncertainty in Genotype Calls. *Bioinformatics* 26(2):242-9

Irizarry RA, Wang C, Zhou Y, Speed TP (2009) Gene set enrichment analysis made simple. *Stat Methods Med Res*. 18(6):565-75

Doi A, Park IH, Wen B, Murakami P, Aryee MJ, **Irizarry RA**, Herb B, Ladd-Acosta C, Rho J, Loewer S, Miller J, Schlaeger T, Daley GQ, Feinberg AP (2009) Differential methylation of tissue- and cancer-specific CpG island shores distinguishes human induced pluripotent stem cells, embryonic stem cells and fibroblasts. *Nature Genetics*. 41(12):1350-3

Irizarry RA, Wu H, Feinberg AP (2009) A species-generalized probabilistic model-based definition of CpG islands. *Mammalian Genome* 20(9-10):674-80

Ritchie ME, Carvalho BS, Hetrick KN, Tavaré S, **Irizarry RA** (2009) R/Bioconductor software for Illumina's Infinium whole-genome genotyping BeadChips. *Bioinformatics* 25(19):2621-3

Irizarry RA, Ladd-Acosta C, Wen B, Wu Z, Montano C, Onyango P, Cui H, Gabo K, Rongione M, Webster M, Ji H, Potash J, Sabunciyan S, Feinberg AP (2009) Genome-wide methylation analysis of human colon cancer reveals similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. *Nature Genetics*. 41(2):246-50.

Wen B, Wu H, Shinkai Y, **Irizarry RA**, and Feinberg AP (2009) Large histone H3 lysine-9 dimethylated chromatin blocks distinguish differentiated from embryonic stem cells. *Nature Genetics*. 41(2):178-86.

Yegnasubramanian S, Haffner MC, Zhang Y, Gurel B, Cornish TC, Wu Z, **Irizarry RA**, Morgan J, Hicks J, DeWeese TL, Isaacs WB, Bova GS, De Marzo AM, Nelson WG (2008) DNA hypomethylation arises later in prostate cancer progression than CpG island hypermethylation and contributes to metastatic tumor heterogeneity. *Cancer Research* 68(21):8954-67.

Wen B, Wu H, Bjornsson H, Green RD, **Irizarry RA**, Feinberg AP (2008) Overlapping euchromatin/heterochromatin-associated marks are enriched in imprinted gene regions and predict allele-specific modification. *Genome Research*. 18(11):1806-13.

Bjornsson HT, Sigurdsson MI, Fallin MD, **Irizarry RA**, Aspelund T, Cui H, Yu W, Rongione MA, Ekström TJ, Harris TB, Launer LJ, Eiriksdottir G, Leppert MF, Sapienza C, Gudnason V, Feinberg AP (2008) Intra-individual change over time in DNA methylation with familial clustering. *Journal of the American Medical Association* 299(24):2877-83.

Wang W, Carvalho B, Miller N, Pevsner J, Chakaravarti A, **Irizarry RA** (2008) Estimating Genome-wide Copy Number using Allele Specific Mixture Models. *Journal of Computational Biology* 15(7):857-866.

McCall MN, **Irizarry RA** (2008) Consolidated strategy for the analysis of microarray spike-in data. *Nucleic Acids Research*. 36(17):e108.

Meluh PB, Pan X, Yuan DS, Tiffany C, Chen O, Sookhai-Mahadeo S, Wang X, Peyser BD, **Irizarry RA**, Spencer FA, Boeke JD (2008) Analysis of genetic interactions on a genome-wide scale in budding yeast: diploid-based synthetic lethality analysis by microarray. *Methods in Molecular Biology* 416:221-247.

Bjornsson HT, Albert TJ, Ladd-Acosta CM, Green RD, Rongione MA, Middle CM, **Irizarry RA**, Broman KW, Feinberg AP (2008) SNP-specific array-based allele-specific expression analysis. *Genome Research* 18(5):771-779.

Lin S, Carvalho B, Cutler D, Arking D, Chakravarti A, **Irizarry RA** (2008) Validation and Extension of an Empirical Bayes Method for SNP Calling on Affymetrix Microarrays. *Genome Biology* 9(4):R63.

Irizarry RA, Ladd-Acosta C, Carvalho B, Wu H, Brandenburg SA, Wen B, Feinberg AP (2008) Comprehensive High-throughput Arrays for Restriction endonuclease-based Methylation (CHARM). *Genome Research*. 18(5):780-790.

Rodriguez-Quinones JF, **Irizarry RA**, Diaz-Blanco NL, Rivera-Molina FE, Gomez-Garzon D, Rodriguez-Medina JR (2008) Global mRNA expression analysis in myosin II deficient strains of *Saccharomyces cerevisiae* reveals an impairment of cell integrity functions. *BMC Genomics* 9(1):34

Bengtsson H, **Irizarry R**, Carvalho B, Speed TP (2008) Estimation and assessment of raw copy numbers at the single locus level. *Bioinformatics*. 15;24(6):759-767.

Peysers BD, **Irizarry R**, Spencer FA (2007) Statistical Analysis of Fitness Data Determined by TAG Hybridization on Microarrays. *Methods in Molecular Biology* 416:369-382.

Wu Z, **Irizarry RA** (2007) A Statistical Framework for the Analysis of Microarray Probe-Level Data. *Annals of Applied Statistics* 1(2) 333-357.

Zilliox MJ, **Irizarry RA** (2007) A Gene Expression Bar Code for Microarray Data. *Nature Methods* 4(11):911-913.

Carvalho B, Bengtsson H, Speed TP, **Irizarry RA** (2007) Exploration, Normalization, and Genotype Calls of High Density Oligonucleotide SNP Array Data. *Biostatistics* 8(2):485-99.

Loyo-Berrios N, **Irizarry RA**, Hennessey JG, Tao XG, Matanoski G. (2007) Air Pollution Sources and Childhood Asthma Attacks in Cataño Puerto Rico. *American Journal of Epidemiology* 165(8):927-35.

Rayner TF, Rocca-Serra P, Spellman PT, Causton HC, Farne A, Holloway E, **Irizarry RA**, Liu J, Maier DS, Miller M, Petersen K, Quackenbush J, Sherlock G, Stoeckert CJ Jr, White J, Whetzel PL, Wymore F, Parkinson H, Sarkans U, Ball CA, Brazma A (2006) A simple spreadsheet-based, MIAME-supportive format for microarray data: MAGE-TAB *BMC Bioinformatics*, 7:489

Yuan DS, **Irizarry RA** (2006) High-Resolution Spatial Normalization for Microarrays. *Bioinformatics* 22(24):3054-60.

Katz S, **Irizarry RA**, Lin X, Tripputi M, Porter MW (2006) A summarization approach for Affymetrix GeneChip data using a reference training set from a large, biologically diverse database. *BMC Bioinformatics* 7:464.

Wheelan S, Scheifele L, Martinez-Murillo F, **Irizarry RA**, Boeke J (2006) The Transposon Insertion site Profiling Chip (TIP-chip). *Proceeding of the National Academy of Science* 103(47):17632-7.

Wheelan S, **Irizarry RA**, Martinez-Murillo F, Boeke J (2006) Stacking the deck: double-tiled DNA microarrays. *Nature Methods* 3(11):903-7.

Irizarry RA, Cope LM, Wu Z (2006) Feature-level exploration of a published Affymetrix GeneChip control dataset. *Genome Biology* 7(8):404

Quackenbush J, **Irizarry RA** (2006) Response to Shields: 'MIAME, we have a problem. *Trends in Genetics* 22(9): 471-472.

Takahashi H, McCaffery JM, **Irizarry RA**, Boeke JD (2006) Nucleocytosolic acetyl-coenzyme a synthetase is required for histone acetylation and global transcription. *Molecular Cell* 23(2):207-217.

Quackenbush J, Stoeckert C, Ball C, Brazma A, Gentleman R, Huber W, **Irizarry R**, Salit M, Sherlock G, Spellman P, Winegarden N (2006) Top-down standards will not serve systems biology. *Nature* 440(7080):24.

Zeger SL, **Irizarry RA**, Peng RD (2006) On time series analysis of public health and biomedical data. *Annual Review of Public Health*. 27:57-79.

DiPietro JA, Caulfield LE, **Irizarry RA**, Chen P, Merialdi M, Zavaleta N (2006). Prenatal development of intra- and inter-individual synchrony. *Behavioral Neuroscience* 20(3):687-701.

Irizarry RA, Zhijin Wu, Jaffee, H (2006) Comparison of Affymetrix GeneChip Expression Measures. *Bioinformatics* 22(7):789-94.

Cope L, Hartman SM, Golmann HWH, Tiesman JP, **Irizarry RA** (2006) Analysis of Affymetrix GeneChip Data Using Amplified RNA. *Biotechniques* 40:165-70.

Lechtzin N, John M, **Irizarry RA**, Merlo C, Diette GB, Boyle MP (2006) Outcomes of Adults with Cystic Fibrosis Infected with Antibiotic-Resistant *Pseudomonas aeruginosa*. *Respiration*. 73(1):27-33.

Ooi SL, Pan X, Peyser BD, Ye P, Meluh PB, Yuan DS, **Irizarry RA**, Bader JS, Spencer FA, Boeke JD (2005) Global synthetic-lethality analysis and yeast functional profiling. *Trends in Genetics* 22(1):56-63.

Baker SC, Bauer SR, Beyer RP, Brenton JD, Bromley B, Burrill J, Causton H, Conley MP, Elespuru R, Fero M, Foy C, Fuscoe J, Gao X, Gerhold DL, Gilles P, Goodsaid F, Guo X, Hackett J, Hockett RD, Ikonomi P, **Irizarry RA**, Kawasaki ES, Kaysser-Kranich T, Kerr K, Kiser G, Koch WH, Lee KY, Liu C, Liu ZL, Lucas A, Manohar CF, Miyada G, Modrusan Z, Parkes H, Puri RK, Reid L, Ryder TB, Salit M, Samaha RR, Scherf U, Sendera TJ, Setterquist RA, Shi L, Shippy R, Soriano JV, Wagar EA, Warrington JA, Williams M, Wilmer F, Wilson M, Wolber PK, Wu X, Zadro R. Nat Methods (2005) The External RNA Controls Consortium: a progress report. *Nature Methods* 2(10): 731-4.

Peysen BD, **Irizarry RA**, Tiffany CW, Chen O, Yuan DS, Boeke JD, Spencer FA (2005) Improved statistical analysis of budding yeast TAG microarrays revealed by defined spike-in pools. *Nucleic Acids Research* 33(16):e140.

Yuan DS, Pan X, Ooi SL, Peysen BD, Spencer FA, **Irizarry RA**, Boeke JD (2005) Improved microarray methods for profiling the Yeast Knockout strain collection. *Nucleic Acids Research* 33:e103

Irizarry RA, Warren D, Spencer F, Kim IF, Biswal S, Frank BC, Gabrielson E, Garcia JG, Geoghegan J, Germino G, Griffin C, Hilmer SC, Hoffman E, Jedlicka AE, Kawasaki E, Martinez-Murillo F, Morsberger L, Lee H, Petersen D, Quackenbush J, Scott A, Wilson M, Yang Y, Ye SQ, Yu W (2005) Multiple-laboratory comparison of microarray platforms. *Nature Methods* 2:329-30.

Hansel NN, Hilmer SC, Georas SN, Cope LM, Guo J, **Irizarry RA**, Diette GB (2005) Oligonucleotide-microarray analysis of peripheral-blood lymphocytes in severe asthma. *Journal of Lab Clinical Medicine*. May;145(5): 263-74.

Grigoryev DN, Ma SF, Simon BA, **Irizarry RA**, Ye SQ, Garcia JG (2005) In vitro identification and in silico utilization of interspecies sequence similarities using GeneChip technology. *BMC Genomics* 6:62.

Kittleson MM, Minhas KM, **Irizarry RA**, Ye SQ, Edness G, Breton E, Conte JV, Tomaselli G, Garcia JG, Hare JM (2005) Gene expression in giant cell myocarditis: Altered expression of immune response genes. *International Journal of Cardiology* 102(2): 333-40.

Kittleson MM, Minhas KM, **Irizarry RA**, Ye SQ, Edness G, Breton E, Conte JV, Tomaselli G, Garcia JG, Hare JM (2005) Gene expression analysis of ischemic and nonischemic cardiomyopathy: shared and distinct genes in the development of heart failure. *Physiology Genomics* 21:299-307.

Kendzierski C, **Irizarry RA**, Chen K-S, Haag JD, Gould MN (2005) On the utility of pooling biological samples in microarray experiments. *Proceedings of the National Academy of Science* 102: 4252-4257.

Wu Z, **Irizarry RA** (2005) Stochastic Models Inspired by Hybridization Theory for Short Oligonucleotide Arrays. *Journal of Computational Biology*. 12(6): 882-93.

Irizarry RA (2004) Parameters with Musical Interpretations. *Chance* 17: 30-38.

Wu Z, **Irizarry RA** (2004) Processing of oligonucleotide array data. *Nature Biotechnology* 22: 4-5.

Cummings DA, **Irizarry RA**, Endy TP, Nisalak A, Burke D (2004) Traveling waves in dengue hemorrhagic fever incidence in Thailand. *Nature* 427: 344-347.

Wu Z, **Irizarry RA**, Gentleman R, Martinez Murillo F, Spencer F (2004) A model based background adjustment for oligonucleotide expression arrays. *Journal of the American Statistical Association* 99: 909-917.

Kittleson MM, Ye SQ, **Irizarry RA**, Minhas KM, Edness G, Conte JV, Parmigiani G, Miller LW, Chen Y, Hall JL, Garcia JG, Hare JM (2004) Identification of a gene expression profile that differentiates between ischemic and nonischemic cardiomyopathy. *Circulation* 110 (22):3444-51.

Gentleman RC, Carey VJ, Bates DJ, Bolstad B, Dettling M, Dudoit S, Ellis B, Gautier L, Ge Y, Gentry J, Hornik K, Hothorn T, Huber W, Iacus S, **Irizarry RA**, Leisch F, Li C, Maechler M, Rossini AJ, Sawitzki G, Smith C, Smyth GK, Tierney L, Yang YH, Zhang J (2004) Bioconductor: Open software development for computational biology and bioinformatics. *Genome Biology* 5:R80

Bolstad, BM, Collin, F, Simpson, KM, **Irizarry RA**, Speed, TP (2004) Experimental design and low-level analysis of microarray data. *International Review of Neurobiology* 60:25-58.

Grigoryev DN, Ma SF, **Irizarry RA**, Ye SQ, Quackenbush J, Garcia JG (2004) Orthologous gene-expression profiling in multi-species models: search for candidate genes. *Genome Biology* 5:R34.

Warren CD, Eckley DM, Lee MS, Hanna JS, Hughes A, Peyser B, Jie C, **Irizarry RA**, Spencer FA (2004) S-Phase checkpoint genes safeguard high fidelity sister chromatid cohesion. *Molecular Biology of the Cell* 15:1724-35.

DiPietro JA, **Irizarry RA**, Costigan KA, Gurewitsch ED (2004) The psychophysiology of the maternal-fetal relationship. *Psychophysiology* 41:510-20.

Cope LM, **Irizarry RA**, Jaffee H, Wu Z, Speed TP (2004) A benchmark for Affymetrix GeneChip expression measures. *Bioinformatics* 20: 323-331.

Gautier L, Cope LM, Bolstad BM, **Irizarry RA** (2004) affy - An R package for the analysis of Affymetrix GeneChip data at the probe level. *Bioinformatics*. 20: 307-315.

Chen H, **Irizarry RA**, Luo L, Zirkin BR (2004) Leydig cell gene expression: Effects of age and caloric restriction. *Experimental Gerontology* 39:31-43.

Sidransky D, **Irizarry RA**, Califano JA, Li X, Ren H, Benoit N, Mao L (2003) Serum protein MALDI profiling distinguishes upper aerodigestive tract cancer patients from controls. *Journal of the National Cancer Institute* 95:1711-1777.

Cappola TP, Cope L, Cernetich A, Barouch LA, Minhas, K, **Irizarry RA**, Parmigiani G, Durrani S, Lavoie T, Hoffman EP, Ye SQ, Garcia JGN, Hare JM (2003) Deficiency of different nitric oxide synthase isoforms activates divergent transcriptional programs in cardiac hypertrophy. *Physiological Genomics* 14:25-34

Scharfstein DO, **Irizarry RA** (2003) Generalized additive selection models for the analysis of non-ignorable missing data. *Biometrics* 59: 610-613

Irizarry RA, Ooi SL, Wu Z, Boeke JD (2003) Use of mixture model in a genome-wide DNA microarray-based genetic screen for components of the NHEJ pathway in yeast. *Statistical Applications in Genetics and Molecular Biology* 2:Article 1

Irizarry RA, Bolstad BM, Collin F, Cope LM, Hobbs B, Speed TP (2003) Summaries of Affymetrix GeneChip probe level data. *Nucleic Acids Research* 31:e15

Bolstad BM, **Irizarry RA**, Astrand M, Speed TP (2003) A comparison of normalization methods for high density oligonucleotide array data based on bias and variance. *Bioinformatics* 19:185-193

Tankersley C, **Irizarry RA**, Flanders S, Rabold R, Frank R (2003) Unstable heart rate and temperature regulation predict mortality in ARK/J mice. *American Journal of Physiology-Regulatory, Integrative, and Comparative Physiology* 284:R742-750.

Irizarry RA, Hobbs B, Collin F, Beazer-Barclay YD, Antonellis KJ, Scherf U, Speed TP (2003) Exploration, normalization, and summaries of high density oligonucleotide array probe level data. *Biostatistics* 4:249-264

Irizarry RA (2002) Weighted estimation of harmonic components in a musical sound signal. *Journal of Time Series Analysis* 23:29-48

Irizarry RA, Tankersley CG, Frank R, Flanders SE (2001) Assessing homeostasis through circadian patterns. *Biometrics* 57:1228-1238

Tankersley CG, **Irizarry RA**, Flanders S, Rabold R (2001) Circadian rhythm variation in activity, body temperature and heart rate between C3H/HeJ and C57BL/6J inbred strains. *Journal of Applied Physiology* 92: 870-877

Brillinger DR, Chiann C, **Irizarry RA**, Morettin PA (2001) Automatic methods for generating seismic intensity maps. *Probability, Statistics, and Seismology: Journal of Applied Probability* 38A:189-202

DiPietro JA, **Irizarry RA**, Hawkins M, Costigan KA, Pressman EK (2001) Cross-correlation of fetal and somatic activity as an indicator of antenatal neural development. *American Journal of Obstetrics and Gynecology* 185:1421-8

Crone NE, Hao L, Hart J Jr, Boatman D, Lesser RP, **Irizarry RA**, Gordon B (2001) Electrographic gamma activity during word production in spoken and sign language. *Neurology* 57:2045-2053

Irizarry RA (2001) Local harmonic estimation in musical sound signals. *Journal of the American Statistical Association* 96:357-367

Irizarry RA (2001) Information and posterior probability criteria for model selection in local likelihood estimation. *Journal of the American Statistical Association* 96: 303-315

Irizarry RA (2001) Local regression with meaningful parameters. *The American Statistician* 55: 72-79

Irizarry RA (2000) Asymptotic distribution of estimates for a time-varying parameter in a harmonic model with multiple fundamentals. *Statistica Sinica* 10: 1041-1067

Brillinger DR, Morettin PA, **Irizarry RA**, Chiann C (2000) Some wavelet-based analyses of markov chain data. *Signal Processing* 80: 1607-1627

Katinas GS, Cornelissen G, **Irizarry RA**, Schaffer E, Homans D, Rhodus N, Schwartzkopff O, Siegelova J, Palat M, Halberg F (1999) Case report of coexisting elderly MESOR-hypertension and circadian amplitude-hypertension (CHAT) *Geronto-Geriatrics* 2: 68-86

Brillinger DR, **Irizarry RA** (1998) An investigation of the second- and higher-order spectra of music. *Signal Processing* 65: 161-178

Proceedings and Book Chapters

Irizarry RA (2007) Comparison of Microarray Data from Multiple Labs and Platforms in *Validation of Toxicogenomic Technologies: A Workshop Summary* (pp 49-57). The National Academies Press. Washington DC.

Peysner, BD, **Irizarry RA**, Spencer FA (2006) Statistical Analysis of Fitness Data Determined by TAG Hybridization on Microarrays in *Gene Essentiality at Genome Scale: Protocols and Bioinformatics*. Osterman, A.; Gerdes S. (Eds.), Totowa, NJ.

Huber W, **Irizarry RA**, Gentleman R (2005) Preprocessing Overview in *Bioinformatics and Computational Biology Solutions Using R and Bioconductor* (pp 3-12) Gentleman, R.; Carey, V.; Huber, W.; Irizarry, R.; Dudoit, S. (Eds.) Springer. NY.

Bolstad BM, **Irizarry RA**, Gautier L, Wu Z (2005) Preprocessing High-density Oligonucleotide Arrays in *Bioinformatics and Computational Biology Solutions Using R and Bioconductor* (pp 13-32) Gentleman, R.; Carey, V.; Huber, W.; Irizarry, R.; Dudoit, S. (Eds.) Springer. NY.

Bolstad BM, Collin F, Brettschneider J, Simpson K, Cope L, **Irizarry RA**, Speed TP (2005) Quality Assessment of Affymetrix GeneChip Data in *Bioinformatics and Computational Biology Solutions Using R and Bioconductor* (pp 33-47) Gentleman, R.; Carey, V.; Huber, W.; Irizarry, R.; Dudoit, S. (Eds.) Springer. NY.

Irizarry RA (2005) From CEL Files to Annotated Lists of Interesting Genes in *Bioinformatics and Computational Biology Solutions Using R and Bioconductor* (pp 431-442) Gentleman, R.; Carey, V.; Huber, W.; Irizarry, R.; Dudoit, S. (Eds.) Springer. NY.

Wu Z, **Irizarry RA**. Stochastic Models Inspired by Hybridization Theory for Short Oligonucleotide Arrays (2004) *Proceedings of the 8'th International Conference on Computational Molecular Biology (RECOMB)*.

Irizarry RA (2003) Measures of expression for Affymetrix high density oligonucleotide arrays. IMS Lecture Notes Volume 40. Monograph Series, Science and Statistics: A Festschrift for Terry Speed. Ed. Darlene R. Goldstein.

Irizarry RA, Gautier L, and Cope L (2003) An R package for analyses of Affymetrix oligonucleotide arrays in *The Analysis of Gene Expression Data: Methods and Software*, eds. Parmigiani G, Garrett ES, Irizarry RA, and Zeger SL. Springer. NY.

Irizarry RA, Parmigiani G, Guo M, Dracheva T, Jen J. A statistical analysis of radiolabeled gene expression data. *Proceeding of Interface 2001* Volume 33.

Tankersley C, Flanders S, Rabold R, **Irizarry RA**, Berger R, Frank R (1999) Bradycardia, hypothermia, and imminent death in AKR/J inbred mice. In *Proceedings of the third colloquium on particulate air pollution and human health*. Edited by: Robert Phalen and Yvonne Bell. University of California. Irvine, CA. pp. 6-97 - 6-106.

Books

Gentleman R, Carey V, Huber W, **Irizarry RA**, Dudoit, S (2005) *Bioinformatics and Computational Biology Solutions using R and Bioconductor*, eds. Springer. NY.

Parmigiani G, Garrett ES, **Irizarry RA**, Zeger SL (2003) *The Analysis of Gene Expression Data: Methods and Software*, eds. Springer. NY.

Licensed Software

Web Tool and R Package: Graphics Toolbox for Assessment of Affymetrix Expression Measures. Version 1.0 released May, 2003. (web tool has over 5,000 hits)

R Package for Analyses of Affymetrix Oligonucleotide Arrays. Version 1.0 released May, 2002 (Over 10,000 downloads).

Articles and Editorials not peer reviewed:

Irizarry RA, Gautier L (2002) Affy (R Package for Analyses of Affymetrix Oligonucleotide Arrays) Reference Manual.

Irizarry RA (1998) The power of math. *Berkeley Scientific*. vol. 2 issue 1.

Rubio I, **Irizarry RA** (1997) The computer in the teaching of Pre-Calculus. *Revista Arista* num. 4.

CURRICULUM VITAE

RAFAEL A. IRIZARRY
Part II

TEACHING

Master's Advisees

Peter Murakami, ScM Biostatistics 2008, Evaluation of Microarray Quality Assessment Methods

Daniel Yuan, ScM Biostatistics, 2006, High-Resolution Spatial Normalization for Microarrays Containing Embedded Technical Replicates

Richard Ittenbach, MHS, Biostatistics, 2001

PhD Thesis Advisees

Zhijin Wu, Biostatistics, 2005, Probe Level Models for DNA Microarrays

Benilton Carvalho, Biostatistics, 2008, Statistical Methods and Software for High Density Oligonucleotide Arrays

Matthew McCall, Biostatistics, 2010, Preprocessing and Barcoding of Data from a Single Microarray

Hao Wu, Biostatistics, 2010 (expected)

Samara Kiihl, Biostatistics, 2011 (Expected)

Eitan Halper-Stromberg, Human Genetics, 2012 (Expected)

Postdoctoral Students

Héctor Corrada-Bravo, 2008-2010

Martin Aryee (joint with Vasana Yegnasubramanian), 2008-2010

Christopher Barr, 2008-2009

Vasyl Pihur (joint with Aravinda Chakravarti) 2009-2011

Kasper Daniel Hansen, 2009-Present

Margaret Taub (joint with Ingo Ruczinski) 2009-Present

David Hiller (joint with Andrew Feinberg) 2010-Present

Final Oral Participation:

Matthew Marcello, Biochemistry and Molecular Biology, 2009

Christine Ladd-Acosta, Cellular and Molecular Medicine, 2009

Aristide Achy-Brou, Department of Biostatistics, 2008

Brian Peyser, Department of Cellular and Molecular Biology, 2007

Michelle Kittleson, Department of Clinical Investigation, 2005

Zhijin Wu, Department of Biostatistics, 2005

Hongling Zhou, Biostatistics, 2005

Nilsa Loyo-Berrios, Epidemiology, 2004.

Dr. Asghar Nazeer, Doctor of Public Health, 2001.

Melissa Hawkins, Population and Family Health Sciences, 2000.

Preliminary Oral Participation:

Diane Heiser, Cellular & Molecular Medicine, 2009

Samara Kiihl, Department of Biostatistics, 2009

Matthew McCall, Department of Biostatistics, 2008

Hao Wu, Department of Biostatistics, 2008

Brian Herb, Department of Molecular Biology and Genetics, 2009

Brian A. Roelofs, Department of Biochemistry and Molecular Biology, 2008

Christine Ladd-Acosta, Cellular and Molecular Biology, 2008

Aristide Achy-Brou, Department of Biostatistics, 2007

Benilton Carvalho, Department of Biostatistics, 2006.

Ani Manichaikul, Department of Biostatistics, 2005.

Yun Lu, Department of Biostatistics, 2005.

Laura E. LaRosa, Department of Environmental Health Sciences, 2003.

Varduhi Petrosyan, Department of Health Policy & Management, 2003.

Zhijin Wu, Biostatistics, 2002.

Chryssanthi Stylianopoulos, International Health, 2002.

Laura Kresch, Epidemiology, 2000.

Mildred Maisonet, Epidemiology, 1999.

Brad Astor, Epidemiology, 1999.

Member of Master Thesis Committee:

Dr. Thomas Peter Cappola, 2003.
Clinical and Genomic Approaches in Human Heart Failure
Master of Science in Clinical Investigation

Laura Plantinga, 2001.
Inference of Clusters of Related Individuals with Dominant Genetic Marker Data
ScM in Biostatistics

Jian Wang, 2003
Comparison of Alternative Approaches in Classification Analysis Using Microarray
Data
ScM in Biostatistics

Classroom Instruction:

2007-Present	Advanced Methods in Biostatistics I
2006	Methods in Clinical Research II (with others)
2006-2008	Bioinformatics and Computational Biology Solutions Using R and Bioconductor
2004-2005	Statistics for Gene Expression
2004-2005	Statistical Learning: Nonparametric and Algorithmic Approaches
2002	Statistical Reasoning in Public Health II
2002	Statistical Reasoning in Public Health I
2002	Introduction to Public Health Statistics Regression Analysis in Public Health Research.
2000-2001	Germanized Linear Models IV
1999	Graduate Summer Institute of Epidemiology and Biostatistics: Longitudinal Data Analysis
1999	Generalized Linear Models III

1997 University of California, Berkeley: Introduction to Probability and Statistics.

Workshops and Short Courses:

Integrative Statistical Analysis for Genome Scale Data. *Cold Spring Harbor Laboratory, NY*. June 12-13, 2009

Gene Expression Analysis with R/ Bioconductor. *Short Course on Mathematical Approaches to the Analysis of Complex Phenotypes. The Jackson Laboratory, Bar Harbor, Maine* October 16-18 2007

Computational and Statistical Aspects of Microarray Analysis. *Bressanone-Brixen, Italy*. June 18-22 2006 (with Robert Gentleman and Wolfgang Huber)

Top 10 things you need to know about microarrays series. *Johns Hopkins Schools of Medicine and Public Health*. Monthly seminar 2003-Present.

Gene Expression Analysis with R/ Bioconductor. *Short Course on Mathematical Approaches to the Analysis of Complex Phenotypes. The Jackson Laboratory, Bar Harbor, Maine* September 16 - 22, 2006

Array Quality Metrics Tutorial and Workshop. *MGED 9, Seattle, WA* September 9, 2006 (with Wolfgang Huber)

Hands-On Bioconductor Workshop. *Center for Information Technology. NIH, Bethesda, MD*, January 9, 2006

Gene Expression Analysis with R/ Bioconductor. Short Course on Mathematical Approaches to the Analysis of Complex Phenotypes. *The Jackson Laboratory, Bar Harbor, Maine*. October 5-11, 2005

Preprocessing and quality assessment of Affymetrix probe level data. *BioC2005 Conference. Fred Hutchinson Cancer Research Center - Seattle, WA*. August 16 and 17, 2005

Computational and Statistical Aspects of Microarray Analysis. *Bressanone-Brixen, Italy*. June 19-24 2005 (with Robert Gentleman and Wolfgang Huber)

Hands-On Bioconductor Workshop. *Center for Information Technology. NIH, Bethesda, MD*, November 15, 2004

Gene Expression Analysis with R/ Bioconductor. *Short Course on Mathematical Approaches to the Analysis of Complex Phenotypes. The Jackson Laboratory, Bar Harbor, Maine* September 16 - 22, 2004

Gene Expression Analysis, *The Interface, Baltimore, MD*, March, 2004

Bioconductor Workshop. *Department of Biology, University of Puerto Rico, Río Piedras, PR*, May 20-21 2004

The Bioconductor Project: Open-Source Statistical Software for the Analysis of Microarray Data. *CIT NIH, Bethesda, MD*, April 29, 2004

The Bioconductor Project: Open-Source Statistical Software for the Analysis of Microarray Data. *School of Public Health, University of Louisville, Louisville, KY*, April 23, 2004.

Bioconductor Training Workshop. *NIH, Bethesda, MD*, June 9, 2003

Statistical Methods and Software for the Analysis of DNA Microarray Experiments. *ENAR, Tampa, FL* 2003 (with Sandrine Dudoit)

Analysis of Genetic Microarray Data. *Mathematics and Statistics Department at Lancaster University*, 2002

Bioconductor Workshop. *Bloomberg School of Public Health*, 2002 (with Sandrine Dudoit and Robert Gentleman)

Analyzing DNA Microarray Data Using Bioconductor. *Short Course on Mathematical Approaches to the Analysis of Complex Phenotypes. The Jackson Laboratory, Bar Harbor, Maine* September 18 - 24, 2002 (with Sandrine Dudoit)

Análisis de Datos Longitudinales. *Instituto Politécnico Nacional. México D.F, México*, 2000

Modelaje Estadístico usando S-Plus. *Instituto Nacional de Salud Pública. Cuernavaca, Mexico*, 2000

Análisis de Datos Longitudinales. *Instituto Nacional de Salud Pública. Cuernavaca, Mexico*, 1999.

RESEARCH GRANT PARTICIPATION

Title: Analysis Tools and Software for Second Generation Sequencing Data

Period: 12/01/2009-11/30/2013

Sponsoring Agency: NIH

Principal Investigator: Rafael A. Irizarry

The goal of this project is to create a sound and unified statistical and computational methodology for representing and managing uncertainty throughout the sec-gen sequencing data analysis pipeline built on a robust, modular and extensible software platform.

Title: Predoctoral Biostatistics Training in Genetics/Genomics

Period: 07/01/2006-06/30/2010

Sponsoring Agency: NHI

Principal Investigator: Rafael A. Irizarry

Training grant for Biostatistics PhD program with focus on Genetics/Genomics

Title: Preprocessing and Analysis Tools for Contemporary Microarray Applications

Period: 07/01/2007-06/30/2011

Sponsoring Agency: NHI

Principal Investigator: Rafael A. Irizarry

The goal of this project is to improve the quality of results obtained using microarray experiments via the use of improved statistical methodology.

Title: Software for the Statistical Analysis of Microarray Probe Level Data

Period: 04/01/2007 – 03/31/2011

Sponsoring Agency: NIH

Principal Investigator: Rafael A. Irizarry

The goal of this project is to continue the support of our software and further develop our tools to increase their usefulness to the research community.

Title: Bioconductor: An Open Computing Resource for Genomics

Period: 07/1/2006 – 06/30/2011

Sponsoring Agency: NIH

Principal Investigator: Robert Gentleman

The Bioconductor project provides an open resource for the development and distribution of innovative reliable software for computational biology and bioinformatics.

Title: Center for the Epigenetics of Common Human Diseases

Period: 05/14/2004 – 04/30/2009

Sponsoring Agency: NHGRI

Principal Investigator: Andrew Feinberg

Funding Level: 10%

The goals of this project are to develop high through put tools for epigenome analysis; to develop the novel field of quantitative epigenetics; and to develop methods to apply these epigenetic tools to psychiatric disease.

Title: Yeast Genetic Interaction Map

Period: 1/31/2007 – 01/31/2009

Sponsoring Agency: NCHGR

Principal Investigator: Jef Boeke

Funding Level: 19%

The major goals of this project are to establish a genetic interaction map using computational analysis of synthetic interactions.

Title: Nucleating a discipline: Creating leadership in Bioinformatics and Computational

Biology

Period: 09/01/2008- 09/01/2009

Sponsoring Agency: Johns Hopkins University's Framework for the Future Initiative

Principal Investigator: Sarah Wheelan

Amount: \$250,000 per year

The purpose of this project is to create a PhD program and a Research Center in Computational Genomics

Title: The Johns Hopkins Individualized Medicine Program

Period: 09/01/2008- 09/01/2009

Sponsoring Agency: Johns Hopkins University's Framework for the Future Initiative

Principal Investigator: David Valle

Amount: \$250,000 per year

The purpose of this project is to create a program in individualized medicine at JHU.

Title: Ventilator Associated Lung Injury: Molecular Approaches: Cores B and E

Period: 09/30/2003 - 12/31/2006

Sponsoring Agency: NIH/NHLBI

Principal Investigator: Roy Brower

Funding Level: 25%

Acute lung injury (ALI) is a devastating illness occurring in the context of sepsis and other systemic inflammatory disorders with a clear contribution of mechanical ventilation-mediated stress to adverse patient outcomes. This SCCOR application is focused on understanding the complex interplay between mechanical ventilation and the increased morbidity and mortality noted in patients with ALI. We anticipate our work will facilitate development of new strategies, uncover new therapeutic targets and define new prognostic indicators that will limit the adverse effects of mechanical ventilation on the acutely injured lung.

Title: Center for Childhood Asthma in the Urban Environment

Period: 05/7/2004 -10/31/2008

Sponsoring Agency: NIH/NIEHS

Principal Investigator: Peyton Eggleston

Funding Level: 8%

The long term goals of this Center are to examine how exposures to environmental pollutants and allergens may relate to airway inflammation and respiratory morbidity in children with asthma living in the inner city of Baltimore, and to search for new ways to reduce asthma morbidity by reducing exposure to these agents.

Title: Applied Genomics in Cardiopulmonary Medicine

Period: 09/30/00-07/31/04

Sponsoring Agency: NIH

Principal Investigator: Joe Garcia

Funding Level: 50%

The overall objective of this award is to understand the genetics of cardiopulmonary disease through the use of microarray data.

Title: Electrographic Studies of Human Cortical Function

Period: 4/2001-4/2003

Sponsoring Agency: NINDS

Principal Investigator: Nathan E. Crone, M.D.

Funding Level: 25%

The objectives of this project are to determine what indices of cortical electrical activity reflect regional cortical processing in humans and to use these indices to analyze the processes and subprocesses involved in human cognition.

Title: Fetal Neurobehavioral Development and Postnatal Continuity

Period: 03/01/02-02/28/07

Sponsoring Agency: NIH

Principal Investigator: J. DiPietro

Funding Level: 9%

Documents the normal ontogeny of neurobehavioral development before birth and investigates the mediating role of maternal psychological and physiological factors in development before and after birth.

Title: Yeast Genetic Interaction Map

Period: 02/01/02-01/31/05

Sponsoring Agency: NIH

Principal Investigator: Boeke

The major goals of this project are: To construct a complete set of YKO mutations bearing a URA3 marker, to generate a yeast map of YKO synthetic lethality interactions and data base of these. Also, double mutant pools will be provided in the community for further studies.

Title: Supplemental Zinc and Fetal Development: Four-Year Follow-up

Period: 08/01/02-06/30/06

Sponsoring Agency: NIH

Principal Investigator: L. Caulfield

Title: The Merck Program in Quantitative Methods for Complex Biomedical Systems

Period: 1/1/98-12/31/01

Sponsoring Agency: Merck Company Foundation

Principal Investigator: Scott Zeger

Funding Level: 40%

The overall objective of this award is to support young faculty working in novel areas of biomedical research where modern statistical methodology has potentially valuable application.

ACADEMIC SERVICES

Biostatistics Admission Committee (2009-present)

Faculty Senate (2008-present)

JHU Strategic Plan (Framework for the Future) People Working Group (2007)

Biochemistry and Molecular Biology Departmental Chair Search Committee (2007)

Biochemistry and Molecular Biology Departmental Review Committee (2006-2007)

Department of Biostatistics Faculty Search Committee (2006-2007)

Committee on Affirmative Action (2001-2004)

Committee on Information Technology (2000-2001)

Biostatistics Information Technology (1999-2005)

PRESENTATIONS

Invited Seminars:

Dealing with systematic errors, bias, and variability in measurements from high throughput technologies. Pathology Seminar University of New Mexico. *Albuquerque, New Mexico*. November 3, 2011

Epigenetic Variation as a Driving Force for Development, Evolutionary Adaptation, and Cancer. Stanford University for the Bio-X "Frontiers in Interdisciplinary Biosciences" series (elected by students). *Stanford, CA*. October 27, 2011

Extracting Signal from High Throughput DNA Methylation Data. Center for Excellence in Genomics Sciences Meeting. *Boston, MA*. October 20, 2011.

Epigenetic Variation as a Driving Force for Development, Evolutionary Adaptation, and Cancer. The Lewis-Sigler Institute for Integrative Genomics, Princeton University. *Princeton, NJ*. October 17, 2011.

Bump hunting in the Epigenome. Department of Biostatistics Seminar. Columbia University. *New York, NY*. October 13, 2011

Some challenges related to next-generation sequencing data. Next-Generation Sequencing Technology and Algorithms for Primary Data Analysis. IPAM UCLA. *Los Angeles, CA*. October 3, 2011

Epigenetic Variation as a Driving Force for Development, and Cancer. Penn Bioinformatics Forum. University of Pennsylvania. *Philadelphia, PA*. September 28, 2011

Statistical approaches for analyzing epigenetic data. Epigenomics of Common Diseases. Wellcome Trust. *Cambridge, England*. September 14, 2011.

Epigenetic Variation as a Driving Force for Development, Evolutionary Adaptation, and Cancer. Garvan Institute of Medical Research. *Sydney, Australia*. July 26, 2011
7/26 Garvan talk

Epigenetic Variation as a Driving Force for Development, Evolutionary Adaptation, and Cancer. Walter and Eliza Hall Institute Bioinformatics Seminar. *Melbourne, Australia*. July 12, 2011.

Deciphering the cancer epigenome through data exploration. Very Large Data Conference. *Baltimore MD*. June 1, 2011.

Epigenetic Variation as a Driving Force for Development, Evolutionary Adaptation, and Cancer. Keynote speaker at Case Western Reserve University Joint Biostatistics Symposium. *Cleveland, OH*. May 5, 2011.

Tackling the widespread and critical impact of batch effects in high-throughput data. Biospecimen Research Network symposium. *Bethesda, MD*. March 29, 2011.

Stochastic Epigenetic Variation as a Driving Force for Evolutionary Adaptation and Disease. ENAR 2010. *Miami, FL*. March 21, 2011

How Genomics and High-Throughput Technologies are Useful in Understanding Epigenetic Alterations in Disease. RISE Conference. *San Juan, PR*, March 18, 2011.

Tackling the widespread and critical impact of batch effects in high-throughput data. Transplantomics Meetings. *Barcelona, Spain*. March 14, 2011.

Towards practical computational solutions for cancer diagnostics and prognosis based on anti-profiles. Department of Biostatistics and Computational Biology Seminar. *Boston, MA*. January 23 2011.

How can Bioinformatics, Genomics, and high-throughput technologies be useful to environmental health scientists. JHBSPPH EHS Department Retreat. *Baltimore, MD* January 19, 2011.

Overcoming bias and systematic errors in microarray and next generation sequencing data. The Winter 2011 OSA Molecular Biology Seminar. MITRE, *Crystal City, Virginia*. January 19, 2011.

The Role of Stochastic Epigenetic Variation in Evolution, Cancer, and Common Disease (with Andrew Feinberg and Dani Fallin). Department of Biostatistics Grand Rounds. Johns Hopkins Bloomberg School of Public Health. December 15, 2010.

Consequences of batch effects on extrapolating genomic signatures. 12th MAQC/SEQC project meeting, Silver Springs, MD. December 7, 2010.

Epigenetic variation as a driving force for development, evolutionary adaptation, cancer, and common disease. Keynote speaker at Harvard PQG Conference. *Boston, MA*. November 15, 2010.

Stochastic epigenetic variation as a driving force of development, evolutionary adaptation, and disease. NHGRI Seminar, Bethesda, MD. September 30, 2010.

The Role of Statistics in the Measurement Revolution. Keynote speaker at Association Mexicana de Estadísticos. Cuernavaca, Mexico. September, 2010

What the 1000 genomes project tells us about systematic bias and batch effects in sec-gen data. Statistical Challenges Arising from Genome Resequencing. Isaac Newton Institute for Mathematical Sciences. Cambridge, England. July 2010

Preprocessing High-throughput Data: Rescuing Signal From a Sea of Noise. Bioinformatics and Genetic Epidemiology in Puerto Rico. San Juan, PR. May 2010

Stochastic epigenetic variation as a driving force of development, evolutionary adaptation, and disease. Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor Laboratory, NY. March 27, 2010.

Stochastic epigenetic variation in evolutionary adaptation and common disease. Mathematical Biosciences Institute (MBI) colloquium. Ohio State University. Columbus, OH. March 1, 2010.

Stochastic epigenetic variation as a driving force of development, evolutionary adaptation, and common disease. Biostatistics Seminar. Yale University. New Haven CT. February 16, 2010

Stochastic epigenetic variation as a driving force of development, evolutionary adaptation, and common disease. Biostatistics Seminar. Emory University. Atlanta GA. February 4, 2010.

Stochastic epigenetic variation as a driving force of development, evolutionary adaptation, and common disease. DFCI Center for Cancer Computational Biology Series. Boston, MA. January 21, 2009.

Cancer diagnosis tools based on integrating public microarray datasets. AACR Frontiers in Cancer Prevention Meeting, Houston, TX. December 6, 2009.

Measuring Genome-wide DNA Methylation: Some Statistical Issues. Genome Informatics Meeting, *Cold Spring Harbor Laboratory, NY*. October 27, 2009.

Quantitative Problems in Epigenetic (Keynote Speaker) Modern Math Workshop at the Society for the Advancement of Chicanos and Native Americans in Science (SACNAS) conference, *Dallas, TX*. October 14, 2009.

Model-Based Quality Assessment and Base-Calling for Second-Generation Sequencing Data. BioC 2009, Seattle, WA. July 27, 2009.

Detecting Tissue and Cancer Specific Differentially Methylated Regions with Microarray Data. Department of Biochemistry. *Recinto de Ciencias Médicas, Universidad de Puerto Rico, Río Piedras, PR*. July 1, 2009.

Clinical predictions based on data from one microarray. Seminary IDIPABS. *Barcelona, Spain*. June 22, 2009.

Detecting Differentially Methylated Regions with Microarray Data. Mathematical Genomics. *Berkeley, California*, April 13-15, 2009.

The Role of Statistics in the Genomic Revolution: Rescuing Signal From a Sea of Noise. Dean's Lecture. Department of Mathematics, University of Puerto Rico. *Río Piedras, Puerto Rico*. March 13, 2009.

Detecting Differentially Methylated Regions with Microarray Data. Oncology Department Combo Talks. Johns Hopkins University. *Baltimore, MD*. February 26, 2009.

Detecting Differentially Methylated Regions with Microarray Data. Center for Computational Biology and Bioinformatics. Columbia University. *New York, NY*. February 25, 2009.

The Role of Statistics in the Genomic Revolution: Rescuing Signal From a Sea of Noise. Dean's Lecture. Johns Hopkins Bloomberg School of Public Health. *Baltimore, MD*. January 28, 2009.

Genotype Calling and Copy Number Estimation with Affymetrix SNP arrays. Department of Human Genetics Seminar. University of Chicago. *Chicago, IL*. December 5, 2008.

A Species-Generalized Probabilistic Model-Based Definition of CpG Islands. Department of Biostatistics and Medical Informatics. UW Madison. *Madison, WI*. November 21, 2008.

Genotyping and Copy Number Estimation with SNP chips. NYU Biology Seminar. NYU. *New York, NY*. October 27, 2008

Hidden Markov Model-based CpG islands definition substantially increases overlap with functional elements in the genome. UC Berkeley Statistics and Genomics Seminar. *Berkeley, CA*. October 9, 2008

A Gene Expression Barcode for Microarray. Weill Medical College of Cornell University Institute for Computational Biomedicine Seminar. New York, New York. September 15, 2008

A Gene Expression Barcode for Microarray Data. BioC 2008 Conference. *Fred Hutchinson Cancer Research Center - Seattle, WA*. August, 2008.

A Gene Expression Barcode for Microarray Data. SAMSI Summer Program on Meta-Analysis, *SAMSI, Research Triangle, NC*. June 9, 2008.

A Gene Expression Barcode for Microarray Data. BIRS Workshop: Emerging Statistical Challenges in Genome and Translational . *Banff, Canada*. June 5, 2008.

A Gene Expression Barcode for Microarray Data. NIH Microarray Special Interest Group Seminar, *Bethesda, Maryland*. April 9, 2008.

How Normalization and Batch Effects Affect Prediction. The 8th Meeting MicroArray Quality Control (MAQC) Project. *Rockville, MD*, March 25, 2008.

A Gene Expression Barcode for Microarray Data. ENAR, *Crystal City, Virginia*. March 17, 2008.

Statistics for the Genomics Revolution: Some Examples. Department of Mathematics, Tulane University, *New Orleans, LA*. November 15, 2007.

Applications of Affymetrix SNP chips. Department of Biostatistics, University of Minnesota, *Minneapolis, MN*. November 7, 2007.

High Precision Genome-Wide DNA Methylation Analysis. Centers for Excellence in Genomic Science (CEGS) Conference. Johns Hopkins University, *Baltimore, MD*. October 10, 2007.

Genome-wide Copy Number using Allele Specific Mixture Models. BioC 2007 Conference. *Fred Hutchinson Cancer Research Center - Seattle, WA*. August 7, 2007.

Epigenomics: Some Statistical Applications. Joint Statistical Meetings. *Salt Lake City, Utah*. August 1, 2007.

Applications of Affymetrix SNP chips. Department of Epidemiology, NICHD. *Rockville, MD*. July 12, 2007.

Epigenomics: Some Statistical Applications. Workshop Statistics for Biomolecular Data Integration and Modeling. *Ascona, Switzerland*. June 12, 2007.

Multiple Laboratory Comparisons of Microarray Platforms. 39th Symposium on the Interface: Computing Science and Statistics, *Philadelphia, PA*. May 23, 2007

Using Spike-in Experiments to Assess Microarray Data. *National Institute for Standards and Technology, Gaithersburg, Maryland*. May 3, 2007.

Assessing and improving genotype calls. Affymetrix Low Level Analysis Workshop. *Oakland, CA*. April 21, 2007.

Statistics for the Genomics Revolution. Seminario Interuniversitario de Investigación en Ciencias Matemáticas (SIDIM), *Ponce, Puerto Rico*. February 23-24, 2007.

Mathematics and Music. *Department of Mathematics, University of Puerto Rico, Humacao*. February 26, 2007.

Statistics for the Genomics Revolution. *Society for the Advancement of Chicanos and Native Americans in Science (SACNAS) conference*, *Tampa, Fl*. October 27, 2006.

Microarrays for Everything. *Department of Biostatistics and Epidemiology, University of Pennsylvania*, October 3, 2006.

Preprocessing Affymetrix SNP Chips: Improving Genotype Calling. *Perlegen Sciences, Mountain View, CA*, August 17, 2005.

Preprocessing Affymetrix SNP Chips: Improving Genotype Calling. *Affymetrix, Santa Clara CA*, August 9, 2006.

Preprocessing Microarrays: Expression and Beyond. *BioC2006 Conference, Seattle, WA*, August 4, 2006.

Preprocessing Microarrays: Expression and Beyond. *Department of Statistics, Stanford University, Stanford, CA*, July 27, 2006.

Microarray Data Normalization. *OBE Seminar, FDA, Bethesda, MD*. May 11, 2006.

Assessing and Improving Measurements made with Microarray Technology. *Department of Biostatistics, MD Anderson Cancer Center, Houston, TX.* March 13, 2006.

Gene Expression Data Analysis: The State of the Art. The Ninth US-Japan Cellular and Gene Therapy Conference on Genomics and Proteomics Technology in Biomarker Discovery, *National Institutes of Health Bethesda, MD.* February 23, 2006

Multiple Lab Comparison of Microarray Technology. *Recinto de Ciencias Médicas, Universidad de Puerto Rico, Rio Piedras, PR.* January 17, 2006.

Microarray Data Normalization. *FDA, Rockville, MD.* January 9, 2006.

Assessing and Improving Measurements made with Microarray Technology. *Department of Statistics, University of California. Berkeley, California.* November 22, 2005.

Using Stochastic Models to Improving Microarray Measurement. Computational Biology and Bioinformatics Discussion Group. *New York Academy of Sciences.* November 9, 2005.

Thoughts on ERCC related data analysis. External RNA Controls Consortium (ERCC) open meeting. *Bethesda, Maryland.* October 4, 2005.

Data Analysis and Probe Effects. 8th International Meeting of the Microarray Gene Expression Data Society. *Bergen, Norway.* September 11, 2005.

Bioconductor Overview. . BioC2005 Conference. *Fred Hutchinson Cancer Research Center - Seattle, WA.* August 16 and 17, 2005. (with Robert Gentleman and Vince Carey)

Data Normalization. Microarrays in Transcriptional Profiling: A joint FDA/Johns Hopkins University/PhRMA Workshop. *Johns Hopkins University, Montgomery County, MD,* July 20-21, 2005.

Multiple Lab Comparison of Microarray Platforms. 10th Meeting of the Committee on Emerging Issues and Data on Environmental Contaminants. *National Academy of Science, Washington D.C.,* July 7-8, 2005.

Getting Usable Data from Microarrays. *Department of Biology, Universidad de Puerto Rico, Rio Piedras, PR,* May 6, 2005.

Getting Usable Data from Microarrays. *Recinto de Ciencias Médicas, Universidad de Puerto Rico, Rio Piedras, PR,* March 21, 2005.

Assessment and Development of Microarray Methodology: The Role of Statisticians. *ISDS, Duke University, Raleigh, NC*, January 14, 2005

Analyzing Affymetrix GeneChip Data. *Department of Biostatistics, Georgetown University, Georgetown, DC*. November 19, 2004.

Software and Methods for the Analysis of Affymetrix GeneChip Data. *The Computational Genomics Conference, Reston, VA*, October, 24, 2004.

Putting Knowledge of Microarray Probe Hybridization Properties to Good Use. *Department of Physics and Mathematical Biology, Rockefeller University, NY, NY*. October 5, 2004.

Assessment and Development of Microarray Methodology: The Role of Statisticians. *Department of Biostatistics, Memorial Sloan Kettering, NY, NY*, October 4, 2004

Getting Usable Data from Microarrays: The Role of Statisticians. *Simposio Nacional de Probabilidade e Estatística. Caxambu, Minas de Gerais, Brazil*, July 29, 2004.

Microarray Data Analysis. *Instituto do Coração do Hospital das Clínicas da Faculdade de Medicina da Universidade de São Paulo, São Paulo, Brazil*. July 24, 2004.

From CEL files to lists of interesting genes. *Gene Expression Center, Madison, WI*, July 21, 2004

Affymetrix GeneChip Data Analysis. *University of Washington Expression Array Workshop, Seattle, WA*, June 24, 2004

The Role of Statistics in Bioinformatics: Some Case Studies. *Johns Hopkins University Symposium on Computational Biology, Systems Biology and Bioinformatics, Baltimore, MD*, May 24, 2004

New Developments in Affymetrix Probe Level Analysis. *International Conference on Analysis of Genomic Data, The Conference Center at Harvard Medical School, Boston, MA*, May 10-11, 2004.

Getting Usable Data from Microarrays: The Role of Statisticians. *School of Public Health, University of Louisville, Louisville, KY*, April 23, 2004.

Some Musical Applications of Statistics. *Department of Statistics, Yale University, New Haven, CT*, April 19, 2004.

Analyzing Affymetrix Data: From probe level data to lists of interesting genes. *PhRMA/FDA Genomics (Microarray) Biostatistics Workshop. Shady Grove, MD*, April 15, 2004.

Microarray Data Analysis. *Introduction to Biomedical Research and Careers Course. Biophysics Department, JHU, Baltimore, MD, March 1, 2004*

Getting Usable Data from Microarrays: The Role of Statisticians. *Department of Statistics, UMBC, Baltimore County, MD. February 13, 2004*

Affymetrix Probe Level Analysis. *Johnson and Johnson, Raritan, NJ. December 5, 2003.*

The Bioconductor Project: Open-source Statistical Software for the Analysis of Microarray Data. *Johnson and Johnson, Raritan, NJ. December 5, 2003.*

Getting Usable Data from Microarrays: The Role of Statisticians. *Center for Statistical Science, Brown University, Providence, RI. December 1, 2003.*

The Bioconductor Project: Open-source Statistical Software for the Analysis of Microarray Data. *USAMRMC Bioinformatics Workshop, Frederick, MD. November 4, 2003*

New Developments in Affymetrix GeneChip Probe Level Data Analysis. *Cambridge Healthtech Institute's Third Annual Microarray Data Analysis meeting. Baltimore, MD. September 23, 2003*

Getting Usable Data from Microarrays: The Role of Statisticians. *The 1st joint statistical meeting of IMS and ISBA. San Juan, PR. July 26, 2003*

A Model Based Background Adjustment for Oligonucleotide Expression Arrays. *RSS workshop on Gene expression, Wye, England. July 12, 2003*

Music and Stochastic Processes. *BIRS Workshop on Point Processes - Theory and Applications. Banff, Canada. June 22, 2003*

Software for Affymetrix Data: From CEL files to lists of candidate genes. *Affymetrix User Group, Bloomberg School of Public Health. June 6, 2003*

Getting Usable Data from Microarrays: The Role of Statisticians. *Department of Biostatistics, University of Rochester, April 10, 2003*

Microarray Data Analysis: Buyer Beware. *Dean's Lecture, Johns Hopkins Bloomberg School of Public Health. 2003*

Exploration, Normalization, Summaries and Software of Affymetrix GeneChip Probe Level Data. *35th Symposium on the Interface. Salt Lake City, Utah.* March 13, 2003

Microarray Data Analysis: Buyer Beware. *Preventive Medicine/Public Health Ground Rounds. Bloomberg School of Public Health.* March 5, 2003

Getting Usable Data from Microarrays: The Role of Statisticians. *Workshop on Statistical Aspects of Microarray Data. Department of Mathematical Sciences, University of Aarhus,* February 22, 2003

Some Musical Applications of Statistics. *Mathematics and Statistics Department at Lancaster University,* February 14, 2003

Assessments Using Spike-In Experiments. *Critical Assessment of Microarray Data Analysis (CAMDA 02), Durham, North Carolina,* November 14-15, 2002

Exploration, Normalization, and Summaries of Affymetrix GeneChip Probe Level Data. *Fred Hutchinson Cancer Center, Seattle,* November 8, 2002

Some Musical Applications of Statistics. *Department of Biostatistics University of Washington, Seattle,* November 7, 2002

Summaries of Affymetrix GeneChip Array Probe Level Data. *The Second Bi-Annual Symposium on Array Technology in Research and Diagnostics. Aarhus University Hospital, Skejby, Denmark.* October 26, 2002

Getting Usable Data from Microarrays: It's not as easy as you think. *Cancer Prevention and Control Colloquia Lecture Series (NCI) Bethesda, MD,* September 4, 2002

Choosing Smoothness Parameters for Smoothing Splines by Minimizing an Estimate of Risk. *Joint Statistical Meetings, NY, NY,* August 14, 2002

Summarizing Affymetrix GeneChip Data. *Proctor and Gamble. Cincinnati, OH,* July 19, 2002

Use of Mixture Model in a Genome-Wide DNA Microarray-Based Genetic Screen for Components of the NHEJ Pathway in Yeast. *24th Annual Midwest Biopharmaceutical Statistics Workshop. Muncie, IN,* May 24, 2002

Exploration, Normalization, and Summaries of High Density Oligonucleotide Array Probe Level Data. *2nd Annual UMASS Bioinformatics Conference, Lowell, MA.* May 3, 2002

Comparing Summaries of High Density Oligonucleotide Array Probes. *ASA Chapter Meetings, Albany, NY*. March 2002

Statistical Analyses of Microarray Data. *ASA chapter meetings, Albany, NY*, March 2002

A journey from gene expression to protein structure. (with Ingo Ruczinski). *Albany, NY*, March 2002

Comparing Summaries of High Density Oligonucleotide Array Probes. *Wadsworth Center for Labs and Research Albany, NY*,. March 2002

Statistical Analyses of Microarray Data. *General Electric, Schenectady, NY*. March 2002

Statistical Analyses of Microarray Data. *Department of Biochemistry and Molecular Biology, Bloomberg School of Public Health*, February 2002

Statistical Analyses of High Density Oligonucleotide Arrays. *Department of Biomedical Engineering, JHU*, December 2001

Exploration, Normalization, and Summaries of High Density Oligonucleotide Array Probe Level Data. *Gene Logic-sponsored workshop on low-level Affymetrix analysis, Bethesda, MD*, November 2001

Use of Mixture Model in a Genome-Wide DNA Microarray-Based Genetic Screen for Components of the NHEJ Pathway in Yeast. *Genetics and Bioinformatics Group, Walter and Eliza Hall Institute, Melbourne, Australia*, October 2001

Exploratory Data Analysis of High Density Oligonucleotide Array. *Genetics and Bioinformatics Group, Walter and Elize Hall Institute, Melbourne, Australia*. September 2001

Musically Meaningful Parameterizations of Sound. *American Association for the Advancement of Science Meetings, San Francisco*, 2001

Mathematical Representations of Music. Mathematics Departments. *Swarthmore College, Swarthmore, PA*, November 2000

Statistical Representations of Music and their Applications. *Statistics Research Department, Lucent Technologies, Murray Hill, NJ*, December 1999

A Study of Circadian Patterns Using REACT Estimators. *Department of Biostatistics, Columbia University, New York*, December 1999

Local regression with meaningful parameterizations. *Department of Statistics, UCLA*, November 1999

Som Musical e Estatística. Instituto de Matemática e Estatística. *Universidade de São Paulo*, July 1999 (in Portuguese)

Some Musical Applications of Statistics. Statistics Seminar. *Mathematics Department, University of Maryland, College Park*, February 1999

Statistics and Music: Fitting a Local Harmonic Model to Sound Signals. *Neyman Seminar. Department of Statistics, University of California, Berkeley*, February 1998

Scientific Meetings:

Stochastic Models Based on Molecular Hybridization Theory for Short Oligonucleotide Microarrays. *RECOMB, San Diego, CA, March 29, 2004*. (with Zhijin Wu)

Background Adjustment, Normalization, and Summaries: How Do We Know What's Best? *The 2003 Affymetrix GeneChip Microarray Low-Level Workshop*. Berkeley, California. August 7- 8

Analyzing Affymetrix GeneChip Data: From Probe Intensities to Lists of Candidate Genes. *From Genome to Disease: A Symposium on High Throughput Biology*. Bethesda, MD 2003 (with Leslie Cope).

Exploration, Normalization, and Summaries of High Density Oligonucleotide Array Probe Level Data. *ENAR, Arlington, VA* 2002.

A statistical analysis of radiolabeled gene expression data. *Interface 2001, Costa Mesa, California*, June 2001

Assessing homeostasis through circadian patterns: An application of REACT. *Simposio Nacional de Probabilidade e Estatística. Caxambu, Minas de Gerais, Brazil*, July 2000

The Psychophysiology of the Maternal-Fetal Relationship. *International Conference on Infant Studies, Brighton, England* July 2000 (presented by DiPietro, JA with Hawkins, M, and Costigan, K).

A Study of Circadian Patterns Using REACT Estimators. *ENAR, Chicago, IL*, March 2000

Local regression with meaningful parameterizations. *8ª Escola de Series Temporais e Econometria. Nova Friburgo - Rio de Janeiro, Brazil*, July 1999

Statistical analysis of sound signals using a local harmonic model. *105th Convention of the Audio Engineering Society, San Francisco, CA, September 1998*

The additive sinusoidal plus residual model: A statistical analysis. *International Computer Music Conference. Ann Arbor, MI, October 1998*

Estatística e música: Ajustando un modelo harmónico local aos sinais dos sons musicais. *Simposio Nacional de Probabilidade e Estatística, Caxambu, Minas de Gerais, Brazil. July 1998 (in Portuguese)*

ADDITIONAL INFORMATION

I enjoy playing music. I play Puerto Rican Cuatro, Guitar, Piano, and Latin Percussion. I also enjoy cooking: one of my recipes won an award from Better Homes and Gardens. I speak fluent Spanish, English and Portuguese.