

**EDUCATION****Ph.D., Bioinformatics, May 2005**

North Carolina State University Raleigh, NC

**M.S., Molecular and Cellular Biology, September 1989**

Long Island University Brooklyn, NY

**B.S., Zoology, May 1984**

University of Massachusetts Amherst, MA

**RESEARCH EXPERIENCE****September 2006-Present      National Institute of Environmental Health Sciences, RTP, NC***Biologist-Bioinformatics/Computational Biology      Biostatistics and Computational Biology  
Branch,**Head, Microarray and Genome Informatics Group**Clarice Weinberg*

Managed a share of the bioinformatics operations to analyze array-based data, genomic and next generation sequence data using cutting-edge statistical and computational methodologies.

Led a bioinformatics group with a statistician performing statistical modeling, bioinformaticians performing data analysis, computational biologists developing analytical application tools, scientific programmer developing software, a scientific systems administrator overseeing computer hardware and server software hosting data files, and several graduate bioinformatics and genomic students in the development of bioinformatics methodologies as well as the analysis of genomic data sets.

Conceived and designed custom bioinformatics resources to facilitate the integrated analysis of genomic and ancillary biological information.

Developed cutting-edge statistical methods and computational algorithms to analyze and predict toxicogenomics data.

Coordinated and presented a biyearly short course in pathway analysis and a bioinformatics e-bulletin.

Consulted and collaborated with biologists and biostatisticians as the NIEHS bioinformatics expert through the Biostatistics and Bioinformatics Consulting Service.

Formulated collaborations with investigators within government, public, non-profit, private and academic establishments.

- Head of the Microarray and Genome Informatics Group offering NIEHS and NTP investigators bioinformatics support with the management and analysis of gene expression, other array-based data, next generation RNA-Seq data, and genetic/genotype data.
- Led a bioinformatics staff consisting of statisticians, bioinformaticians, IS administrator, computational biologists and graduate students.
- Co-coordinated the organization and training of bioinformatics for NIEHS through bioinformatics short courses, the NIEHS Bioinformatics E-Bulletin, institute presentations and web presences.
- Developed and/or collaborated in the development of EPIG, PAGE, ExP, Mod-k-prototypes, cc-biclustering, SVN, PVAC and PVCA computational tools many of which are tailed specifically for data from toxicogenomics-based studies. Developed the novel transcript-regulator eQTL approach for SNP association on a genome-wide scale. Designed and led the development of RATEmiRs (miRNA database), EPIG-Seq (pattern analysis), goSTAG (GO annotation labeling),

PIPERS (RNA-Seq processing pipeline) and TEMPORA (integration of gene expression, gene ontology and literature mining).

- Formulated bioinformatics collaborations with SAS, FDA/National Center for Toxicological Research, NCI, ILSI/HESI, NCSU and the Harvard School of Public Health.
- Served on the NIEHS Scientific Advisory Committee, Assembly of Scientists and the Trans-NIH Biomedical Informatics Coordinating Committee (as the NIEHS bioinformatics representative).
- Participant in the international MGED standardization society, MicroArray Quality Control consortium, the SEquence Quality Control effort, and the NIEHS computing and IT division computational biology facility meetings/discussion.

**September 2008-December 2008 Harvard School of Public Health, Cambridge, MA**

*Assistant Professor*

*Department of Biostatistics, Louise Ryan*

*Department of Environmental Health, Douglas Dockery*

Yerby Visiting professorship in bioinformatics and computational biology.

- Collaborated with statisticians and bioinformaticians in the development of bioinformatics and genomic annotation resources for genome-wide association studies.
- Developed a novel methodology to integrate gene expression data with SNP genotype data for elucidation of expression Quantitative trait loci under the control of transcript-regulators.
- Presented two lectures/workshops on bioinformatics for genomic data analysis and also served as leader for a round-table discussion on the future of bioinformatics in public health efforts.
- Consulted with biostatistics graduate students on ways to integrate bioinformatics into their graduate research projects.

**April 2000-September 2006 National Institute of Environmental Health Sciences, RTP, NC**

*Staff Scientist*

*Microarray Group, Cindy Afshari and Richard S. Paules*

Managed the daily bioinformatics operations to acquire and validate microarray gene expression data. Responsible for microarray image analysis software, data acquisition methods, data analysis procedures and management of data.

Supervised a statistician performing statistical modeling, a bioinformatician performing microarray data analysis and developing informatics application tools, a scientific programmer developing computational algorithms, an information systems administrator overseeing the computer hardware and server software hosting data files, and several graduate bioinformatics/statistics students tracking microarray project and experimental information as well as compiling and analyzing gene expression data sets.

Developed an enterprise version of the MicroArray Project System with added statistical computations implemented to validate microarray gene expression data.

Designed computational software and processes for classifying/predicting microarray gene expression data.

Served as expert bioinformatics advisor to ILSI/HESI, National Center for Toxicogenomics and the International Microarray Gene Expression Database working group designing and developing state-of-the-art microarray gene expression databases.

- Supervised a bioinformatics staff consisting of a statistician, bioinformatician, IS administrator, computational biologist and part-time graduate students in the analysis and management of gene expression data as well as classification of gene sequences into sub-categories.
- Developed and acquired database systems, computational methodologies and statistical approaches for analysis and mining of genomics data.
- Directed the development and implementation of computational software, algorithms and bioinformatics resources for support of NIEHS gene expression analysis.

- Responsible for the justification and acquisition of microarray IT, IS systems, computers and servers.
- Drafted the NCT informatics contract and serves as technical project officer as well as the resident bioinformatics expert on the NCT staff and the NIEHS microarray group Toxicogenomics Research Consortium component.
- Served on the NIEHS Scientific Advisory Committee, Assembly of Scientists and as an ILSI working group member.
- Formulated informatics collaborations with SAS, NCTR, NIAID, NHGRI, Boehringer Ingelheim Pharmaceutical Institute, Phase-1 corporation and Molecular Mining.
- Participant in the international MGED standardization society, NIEHS computing and IT divisions programs and projects.

**November 1998-April 2000**     **OAO Corporation, Durham, NC**  
*Bioinformatics Scientist*     *NIEHS Microarray Center, Hunter Robinson*

Engaged in providing bioinformatics, computational biology, and molecular biology support to the National Institute of Environmental Health Sciences and primarily the NIEHS Microarray Center (NMC). Services rendered involved interfacing with computer support personnel and scientist, database and application development, and genome microarray analysis.

Responsible for management of bioinformatics group projects and leadership of informatics team efforts.

- Represented the microarray cDNA database with EST clones corresponding to environmental genome candidate genes, detoxifying enzymes, and cell cycle senescence genes.
- Evaluated, demonstrated, and trained users on image acquisition software and gene analysis applications.
- Designed and developed MAPS, a MicroArray Project System to manage microarray gene expression experiment information as well as integrate biological data from distributed resources.
- Implemented an Oracle version of the publicly available ArrayDB as a NMC laboratory information management system and repository for environmental and mechanistic gene expression data.
- Developed Perl scripts, computer applications, and web client programs to obtain and parse internet database records and reorganize system flat-files.

**June 1998-August 1998**     **SYNAPTIC, Paramus, NJ**  
*Manager/Genome Analyst*     *Automated DNA Sequencing, T.V. Venkatesh*

Managed the daily activities of the automated DNA sequencing core lab and oversee the high-throughput DNA sequencing efforts of three internal GPCR subclone library projects.

Supervised the DNA sequencing and bioinformatics scientists.

Responsible for providing bioinformatics support and genome analysis assistance to the genomics program as well as designing programs and scripts to process, analyze, and manage DNA sequencing data.

- Supervised five Research Associates in a two-shift team approach.
- Updated and organized the in-house Oracle GPCR database by categorizing the families and species of GPCRs as well as expanding the database of ligands used to query sequence homology searches.
- Performed data mining of internal, commercial, and public databases to identify and annotate new GPCRs from sequence homology searches.

- Facilitated genome data analysis with the design and use of a PERL program to parse through a one-year backlog of BLAST reports and update clients with GPCR status reports.
- Stream-lined the processing, analyzing, management, and reporting of DNA sequencing data to scientists with a network of Microsoft software, proprietary applications, and shell scripting.
- Utilized Phred bases calling software and CrossMatch SWAT algorithm to monitor the qualitative and quantitative DNA sequencing efforts.

**April 1996-February 1998**      **NOVARTIS, RTP, NC**  
*Scientist/Genome Analyst*      *Automated DNA Sequencing, Steve Goff*

Responsible for leading a production DNA sequencing team and coordinate the assembly of sequence reads into contigs. In addition, responsible for the BLAST, analysis, and annotation of DNA sequence reads.

- Supervised a team of four Scientists to clone, sequence, and assemble genomic DNA into contigs.
- Designed PERL and C++ scripts and programs to automate genome sequence analysis and annotation.
- Reported sequencing results to clients by designing FTP retrieval sites and Intranet web postings.
- Localized the asthma/allergy susceptible gene by sequencing PCR fragments and using proprietary applications to quality screen and process assembled sequence pairs.

**August 1990-April 1996**      **SCHERING-PLOUGH, Kenilworth, NJ**  
*Associate Scientist*      *Tumor Biology Department, Chandra Kumar*

Utilized molecular and cellular biology to identify proteins and transcriptional regulatory elements. Developed protein over-expression and two-hybrid systems, as well as high-throughput solid phase receptor and filter binding assays to screen for lead compounds.

- Utilized reporter gene assay systems to localize, identify, and characterize transcriptional response elements of the  $\alpha$ -actin promoter in ras-transformed cells.
- Developed high-throughput solid phase receptor and filter binding assays using over-expressed SRF, G-proteins, and signal transduction receptors to screen 20,000 compounds and subsequently identify two lead agents which block binding to receptors or transcriptional regulatory elements.
- Used receptor pharmacology, binding kinetics, controls and test to validate drug-screening assays as reliable means to identify novel therapeutic agents.
- Developed a yeast two-hybrid system to screen cDNA libraries for SRF accessory factors and other protein-protein interactions.
- Published results in peer review journals and presented findings to the scientific community.

**September 1986-August 1990**      **COLLEGE of PHYSICIANS AND SURGEONS of  
 COLUMBIA UNIVERSITY, Hammer Health Sciences Center  
 New York, NY**  
*Technician*      *Human Genetics and Medicine, Arthur Bank and Maggie Allan*

Responsible for supervising the daily activities of the molecular biology training lab designed to teach Medical Doctors molecular biology techniques and procedures.

Managed the supplies, resources, equipment, and service contracts used to maintain the training lab.

Responsible for identifying transcriptional regulatory elements involved in erythroid differentiation and development as well as screening of Sickle Cell Anemia.

- Trained Medical Doctors fundamental molecular biology techniques and procedures.
- Created a molecular biology protocol and procedure training manual.
- Managed the contract purchase ordering and communicated with vendor representatives.
- Organized the daily activities of the training lab and maintained the equipment/service contracts.
- Utilized reporter gene constructs to identify  $\beta$ - and  $\epsilon$ - transcriptional regulatory elements.
- Performed sterile tissue culture techniques on cell lines maintained in culture.

## HONORS AND AWARDS

- National Institutes of Health Award of Merit, NIEHS, December 2000, 2001 & 2003
- National Institutes of Health Director's Award, NIH, Bethesda Maryland June 2002

## PROFESSIONAL ACTIVITIES

Member, Trans-NIH Biomedical Informatics Coordinating Committee, at the National Institutes of Health, Bethesda MD 2007 and Present

Member, Scientific Advisory Committee for the Carolina Environmental Bioinformatics Center, at the University of North Carolina- Chapel Hill. 2008 and 2009

Journal associate editor for: *Frontiers in Toxicogenomics*, July 2011 – Present

Advisory Board member for: *OA Bioinformatics*, January 2013 - Present

Journal referee for:

*Bioinformatics*

*BMC Bioinformatics*

*BMC Genomics*

*BMC Systems Biology*

*BMC Medical Genomics*

*Cancer Informatics*

*Genome Biology*

*PLoS Genetics and PLoS One*

*Physiological Genomics*

*Toxicological Sciences*

*Molecular and Cellular Probes*

*Bioinformatics and Biology Insights*

Ph.D. Dissertation Committees:

Matthew McElwee – Duke University, Nicholas School of the Environment and Earth Sciences, Integrated Toxicology and Environmental Health Program

“Molecular and Toxicological Responses to Mercuric and Methyl-Mercury” 2009-2010.

Lingkang Huang – North Carolina State University, Bioinformatics Program

“Variable Selection in Multiclass Support Vector Machine and Applications in Genomic Data Analysis”. 2004 – 2008.

Co-founder and co-organizer of the Toxicogenomics Integrated with Environmental Sciences (TIES) conferences:

2007 at North Carolina State University, Raleigh NC

2009 with the International Conference on Toxicogenomics in Seoul, South Korea

2011 at the University of North Carolina - Chapel Hill NC

## PUBLICATIONS IN PEER-REVIEWED JOURNALS

**\*Denotes equal contribution**

Smith A, Calley J, Mathur S, Qian HR, Wu H, Farnen M, Caiment F, **Bushel PR**, Li J, Fisher C, Kirby P, Koenig E, Hall DG, Watson DE. The Rat microRNA body atlas; Evaluation of the microRNA content of rat organs through deep sequencing and characterization of pancreas enriched miRNAs as biomarkers of pancreatic toxicity in the rat and dog. *BMC Genomics*. 2016 Aug 30;17:694.

Kim SH, Trinh A, Larsen M, Mastrocola A, Jefcoate C, **Bushel PR**, Tibbetts, R. Tunable regulation of CREB DNA binding activity couples genotoxic stress response and metabolism, *NAR*, published online July 18th, 2016

Ciencewicki JM, Verhein KC, Gerrish KE, McCaw ZR, Li J, **Bushel PR**, Kleeberger SR. Effects of mannose-binding lectin on pulmonary gene expression and innate immune inflammatory response to ozone. *Am J Physiol Lung Cell Mol Physiol*. 2016 Apr 22

Li J, **Bushel PR**. EPIG-Seq: extracting patterns and identifying co-expressed genes from RNA-Seq data. *BMC Genomics*. 2016 Mar 22;17(1):255.

**Bushel PR**, Fannin RD, Gerrish K, Watkins PB, Paules RS. Blood gene expression profiling of an early acetaminophen response. *Pharmacogenomics J*. 2016 Mar 1.

Fannin RD, Gerrish K, Sieber SO, **Bushel PR**, Watkins PB, Paules RS. Blood transcript immune signatures distinguish a subset of people with elevated serum ALT from others given acetaminophen. *Clin Pharmacol Ther*. 2015 Dec 21.

Hewitt SC, Winuthayanon W, Pockette B, Kerns RT, Foley JF, Flagler N, Ney E, Suksamrarn A, Piyachaturawat P, **Bushel PR**, Korach KS. Development of phenotypic and transcriptional biomarkers to evaluate relative activity of potentially estrogenic chemicals in ovariectomized mice. *Environ Health Perspect*. 2015 Apr;123(4):344-52.

Verhein KC, McCaw Z, Gladwell W, Trivedi S, **Bushel PR**, Kleeberger SR. Novel Roles for Notch3 and Notch4 Receptors in Gene Expression and Susceptibility to Ozone-Induced Lung Inflammation in Mice. *Environ Health Perspect*. 2015 Aug;123(8):799-805.

Davis M, Li J, Knight E, Eldridge SR, Daniels KK, **Bushel PR**. Toxicogenomics profiling of bone marrow from rats treated with topotecan in combination with oxaliplatin: a mechanistic strategy to inform combination toxicity. *Front Genet*. 2015 Feb 12;6:14.

Bourdon-Lacombe JA, Moffat ID, Deveau M, Husain M, Auerbach S, Krewski D, Thomas RS, **Bushel PR**, Williams A, Yauk CL. Technical guide for applications of

gene expression profiling in human health risk assessment of environmental chemicals. *Regul Toxicol Pharmacol*. 2015 Jul;72(2):292-309.

Yang J, Bennett BD, Luo S, Inoue K, Grimm SA, Schroth GP, **Bushel PR**, Kinyamu HK, Archer TK. LIN28A Modulates Splicing and Gene Expression Programs in Breast Cancer Cells. *Mol Cell Biol*. 2015 Sep;35(18):3225-43.

\*Wang C, \*Gong B, \***Bushel PR**, Thierry-Mieg J, Thierry-Mieg D, Xu J, Fang H, Hong H, Shen J, Su Z, Meehan J, Li X, Yang L, Li H, Labaj PP, Kreil DP, Megherbi D, Gaj S, Caiment F, van Delft J, Kleinjans J, Scherer A, Devanarayan V, Wang J, Yang Y, Qian HR, Lancashire LJ, Bessarabova M, Nikolsky Y, Furlanello C, Chierici M, Albanese D, Jurman G, Riccadonna S, Filosi M, Visintainer R, Zhang KK, Li J, Hsieh JH, Svoboda DL, Fuscoe JC, Deng Y, Shi L, Paules RS, Auerbach SS, Tong W. The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. *Nat Biotechnol*. 2014 Sep;32(9):926-32.

SEQC/MAQC-III Consortium; SEQC/MAQC-III Consortium. A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. *Nat Biotechnol*. 2014 Sep;32(9):903-14

Lowe JM, Menendez D, **Bushel PR**, Shatz M, Kirk EL, Troester MA, Garantziotis S, Fessler MB, Resnick MA. p53 and NF- $\kappa$ B coregulate proinflammatory gene responses in human macrophages. *Cancer Res*. 2014 Apr 15;74(8):2182-92.

Williams-Devane CR, Reif DM, Cohen Hubal E, **Bushel PR**, Hudgens EE, Gallagher JE, Edwards SW. Decision tree-based method for integrating gene expression, demographic, and clinical data to determine disease endotypes. *BMC Syst Biol*. 2013 Nov 4;7(1):119.

Huang L, Zhang HH, Zeng ZB, **Bushel PR**. Improved Sparse Multi-Class SVM and Its Application for Gene Selection in Cancer Classification. *Cancer Inform*. 2013 Aug 4;12:143-53.

Huda A, **Bushel PR**. Widespread exonization of transposable elements in human coding sequences is associated with epigenetic regulation of transcription. *Transcriptomics*: 2013: 101.

Zhang L, Simpson DA, Innes CL, Chou J, Bushel PR, Paules RS, Kaufmann WK, Zhou T. Gene expression signatures but not cell cycle checkpoint functions distinguish AT carriers from normal individuals. *Physiol Genomics*. 2013 Oct 1;45(19):907-16.

Lu J, **Bushel PR**. Dynamic expression of 3' UTRs revealed by Poisson hidden Markov modeling of RNA-Seq: implications in gene expression profiling. *Gene*. 2013 Sep 25;527(2):616-23.

Arana ME, Kerns RT, Wharey L, Gerrish KE, **Bushel PR**, Kunkel TA. Transcriptional responses to loss of RNase H2 in *Saccharomyces cerevisiae*. *DNA Repair (Amst)*. 2012 Dec 1;11(12):933-41.

Davis BJ, Risinger JI, Chandramouli GV, **Bushel PR**, Baird DD, Peddada SD. Gene expression in uterine leiomyoma from tumors likely to be growing (from black women over 35) and tumors likely to be non-growing (from white women over 35). *PLoS One*. 2013 Jun 13;8(6):e63909. doi: 10.1371/journal.pone.0063909. Print 2013. PubMed PMID: 23785396; PubMed Central PMCID: PMC3681799.

Zhang, L., **Bushel PR.**, Chou, J., Zhou, T. & Watkins, P.B. Identification of identical transcript changes in liver and whole blood during acetaminophen toxicity. *Front Genet*, 2012.

Pandiri AR, Sills RC, Ziglioli V, Ton TV, Hong HH, Lahousse SA, Gerrish KE, Auerbach SS, Shockley KR, **Bushel PR**, Peddada SD, Hoenerhoff MJ. Differential Transcriptomic Analysis of Spontaneous Lung Tumors in B6C3F1 Mice: Comparison to Human Non-Small Cell Lung Cancer. *Toxicol Pathol*. 2012 Jun 11.

**Bushel PR**, McGovern R, Liu L, Hofmann O, Huda A, Lu J, Hide W, Lin X. Population differences in transcript-regulator expression quantitative trait loci. *PLoS One*. 2012;7(3):e34286. Epub 2012 Mar 27.

Hewitt SC, Li L, Grimm SA, Chen Y, Liu L, Li Y, **Bushel PR**, Fargo D, Korach KS. Research resource: whole-genome estrogen receptor  $\alpha$  binding in mouse uterine tissue revealed by ChIP-seq. *Mol Endocrinol*. 2012 May;26(5):887-98. Epub 2012 Mar 22.

Corton JC, **Bushel PR**, Fostel J, O'Lone RB. Sources of variance in baseline gene expression in the rodent liver. *Mutat Res*. 2012 Aug 15;746(2):104-12. Epub 2012 Jan 5.

Kerns RT, **Bushel PR**. The impact of classification of interest on predictive toxicogenomics. *Front Genet*. 2012;3:14. Epub 2012 Feb 7

Chang C, Wang J, Zhao C, Fostel J, Tong W, **Bushel PR**, Deng Y, Pusztai L, Symmans WF, Shi T. Maximizing biomarker discovery by minimizing gene signatures. *BMC Genomics*. 2011 Dec 23;12 Suppl 5:S6. Epub 2011 Dec 23.

Hoenerhoff MJ, Pandiri AR, Lahousse SA, Hong HH, Ton TV, Masinde T, Auerbach SS, Gerrish K, **Bushel PR**, Shockley KR, Peddada SD, Sills RC. Global gene profiling of spontaneous hepatocellular carcinoma in B6C3F1 mice: similarities in the molecular landscape with human liver cancer. *Toxicol Pathol*. 2011 Jun;39(4):678-99. Epub 2011 May 13. PubMed

Lu J, Kerns RT, Peddada S and **Bushel PR**. Principal Component Analysis-based Filtering Improves Detection for Affymetrix Gene Expression Arrays. *Nucleic Acids Research* 2011; doi: 10.1093/nar/gkr241

Eggesbo M, Moen B, Peddada S, Baird D, Rugtveit J, Midtvedt T, **Bushel PR**, Sekelja M and Rudi K. Development of gut microbiota in infants not exposed to medical interventions. *APMIS* 2011 Jan;119(1):17-35.

Afshari CA, Hemadeh HK and **Bushel PR**. The Evolution of Bioinformatics in Toxicology: Advancing Toxicogenomics. *Toxicol Sci*. 2011 Mar;120 Suppl 1:S225-37. Epub 2010 Dec 22

Huang J, Shi W, Zhang J, Chou JW, Paules RS, Gerrish K, Li J, Luo J, Wolfinger RD, Bao W, Chu TM, Nikolsky Y, Nikolskaya T, Dosymbekov D, Tsyganova MO, Shi L, Fan X, Corton JC, Chen M, Cheng Y, Tong W, Fang H, **Bushel PR**. Genomic indicators in the blood predict drug-induced liver injury. *Pharmacogenomics J*. 2010 Aug;10(4):267-77.

Fan X, Lobenhofer EK, Chen M, Shi W, Huang J, Luo J, Zhang J, Walker SJ, Chu TM, Li L, Wolfinger R, Bao W, Paules RS, **Bushel PR**, Li J, Shi T, Nikolskaya T, Nikolsky Y, Hong H, Deng Y, Cheng Y, Fang H, Shi L, Tong W. Consistency of predictive signature genes and classifiers generated using different microarray platforms. *Pharmacogenomics J*. 2010 Aug;10(4):247-57.

Luo J, Schumacher M, Scherer A, Sanoudou D, Megherbi D, Davison T, Shi T, Tong W, Shi L, Hong H, Zhao C, Elloumi F, Shi W, Thomas R, Lin S, Tillinghast G, Liu G, Zhou Y, Herman D, Li Y, Deng Y, Fang H, **Bushel P**, Woods M, Zhang J. A comparison of batch effect removal methods for enhancement of prediction performance using MAQC-II microarray gene expression data. *Pharmacogenomics J*. 2010 Aug;10(4):278-91.

Shi L and the MAQC Consortium. The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. *Nat Biotechnol*. 2010 Aug;28(8):827-38. Epub 2010 Jul 30.

**Bushel PR**, Heard NA, Gutman R, Liu L, Peddada SD, Pyne S. Dissecting the fission yeast regulatory network reveals phase-specific control elements of its cell cycle *BMC Systems Biology*. 2009 Sept 16;3:93.

Chou JW, **Bushel PR**. Discernment of possible mechanisms of hepatotoxicity via biological processes over-represented by co-expressed genes. *BMC Genomics*. 2009 Jun 18;10:272.

Chou J.W. and **Bushel P.R**. Discernment of possible mechanisms of hepatotoxicity via biological processes over-represented by co-expressed genes. *BMC Genomics*. 2009 Jun 18;10:272.

**Bushel, P.R.**, Nielsen, D, Tong, W. Proceedings of the First International Conference on Toxicogenomics Integrated with Environmental Sciences (TIES-2007). *BMC Proceedings* 2009 3(Suppl 2):S1.

**Bushel, P.R.**, Clustering of Gene Expression Data and End-Point Measurements by Simulated Annealing. *JBCB* 2009 7(1): 193-215.

Lobenhofer E.K., Auman J.T., Blackshear P.E., Boorman G.A., **Bushel P.R.**, Cunningham M.L., Fostel J.M., Gerrish K., Heinloth A.N., Irwin R.D., Malarkey D.E., Merrick B.A., Sieber S.O.,

Tucker C.J., Ward S.M., Wilson R.E., Hurban P., Tennant R.W., Paules R.S. Gene Expression Response in Target Organ and Whole Blood Varies as a Function of Target Organ Injury Phenotype. *Genome Biol.* 2008 Jun 20;9(6):R100.

Huang L., Heinloth A.N., Zeng Z.B., Paules R.S., **Bushel P.R.** Genes Related to Apoptosis Predict Necrosis of the Liver as a Phenotype Observed in Rats Exposed to a Compendium of Hepatotoxicants. *BMC Genomics.* 2008 Jun 16;9(1):288.

Boedigheimer M.J., Wolfinger R.D., Bass M.B., **Bushel P.R.**, Chou J.W., Cooper M., Corton J.C., Fostel J., Hester S., Lee J.S., Liu F., Liu J., Qian H.R., Quackenbush J., Pettit S., Thompson K.L. Sources of Variation in Baseline Gene Expression Levels from Toxicogenomics Study Control Animals Across Multiple Laboratories. *BMC Genomics.* 2008 Jun 12;9(1):285.

Jin Y.H., Dunlap P.E., McBride S.J., Al-Refai H., **Bushel P.R.**, Freedman J.H. Global Transcriptome and Deletome Profiles of Yeast Exposed to Transition Metals. *PLoS Genetics* 2008 Apr 25;4(4):e1000053.

\***Bushel, P.R.**, \*Heinloth, A.N., Li, J., Huang, L., Chou, J.W., Boorman, G.A., Malarkey, D.E., Houle C.D., Ward S.M., Wilson R.E., Tennant R.W., Paules, R.S. Blood Gene Expression Signatures Predict Exposure Levels. *PNAS* 2007 Nov;104(46):18211-18216. Epub 2007 November 2.

**Bushel P.R.**, Wolfinger R.D., Gibson G.C. Simultaneous Clustering of Gene Expression Data with Clinical Chemistry and Pathological Evaluations Reveals Phenotypic Prototypes. *BMC Systems Biology* 2007, 1:15.

Chou J.W., Zhou, T., Kaufmann, W.K., Paules R.S., **Bushel P.R.** Extracting gene expression patterns and identifying co-expressed genes from microarray data reveals biologically responsive processes. *BMC Bioinformatics* 2007, 8:427.

Zhou T., Chou J., Zhou Y., Simpson D.A., Cao F., **Bushel P.R.**, Paules R.S., Kaufmann W.K. Ataxia telangiectasia-mutated dependent DNA damage checkpoint functions regulate gene expression in human fibroblasts. *Mol Cancer Res.* 2007 Aug;5(8):813-22.

Fostel J.M., Burgoon L., Zwickl C., Lord P., Corton J.C., **Bushel P.R.**, Cunningham M., Fan L., Edwards S.W., Hester S., Stevens J., Tong W., Waters M., Yang C., Tennant R. Toward a checklist for exchange and interpretation of data from a toxicology study. *Toxicol Sci.* 2007 Sep;99(1):26-34. Epub 2007 Apr 17.

Zhou T., Chou J., Mullen T.E., Elkon R., Zhou Y., Simpson D.A., **Bushel P.R.**, Paules R.S., Lobenhofer E.K., Hurban P., Kaufmann W.K. Identification of primary transcriptional regulation of cell cycle-regulated genes upon DNA damage. *Cell Cycle.* 2007 Apr 15;6(8):972-81. Epub 2007 Apr 19.

Zhou T, Chou JW, Simpson DA, Zhou Y, Mullen TE, Medeiros M, **Bushel PR**, Paules RS, Yang X, Hurban P, Lobenhofer EK, Kaufmann WK. Profiles of global gene expression in ionizing-

radiation-damaged human diploid fibroblasts reveal synchronization behind the G1 checkpoint in a G0-like state of quiescence. *EHP*. 2006 Apr;114(4):553-9.

Innes CL, Heinloth AN, Flores KG, Sieber SO, Deming PB, **Bushel PR**, Kaufmann WK, Paules RS. ATM requirement in gene expression responses to ionizing radiation in human lymphoblasts and fibroblasts. *Mol Cancer Res*. 2006 Mar;4(3):197-207.

Xirasagar S, Gustafson SF, Huang CC, Pan Q, Fostel J, Boyer P, Merrick BA, Tomer KB, Chan DD, Yost KJ 3rd, Choi D, Xiao N, Stasiewicz S, **Bushel P**, Waters MD. Chemical effects in biological systems (CEBS) object model for toxicology data, SysTox-OM: design and application. *Bioinformatics*. 2006 Apr 1;22(7):874-82. Epub 2006 Jan 12.

Chou J.W, Paules R.S., **Bushel P.R.** "Systematic Variation Normalization in Microarray Data to Get Gene Expression Comparison Unbiased". *JBCB* 3, 1-17, 2005.

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## BOOK CHAPTERS

**Bushel, PR.** Bioinformatics of Genomics in the Assessment of Cancer. In *Toxicogenomics in Predictive Carcinogenicity Subtitle: Current Issues and Future Applications*. Michael D. Waters and Russell S. Thomas. The Royal Society of Chemistry. 2016.

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## INVITED TALKS

“Predicting Exposure to and Adverse Effects of Acetaminophen: The Power and Potential of Gene Expression”. Triangle Statistical Genetics conference. Theme: Environmental Statistical Genetics and Bioinformatics. SAS Institute, Cary, North Carolina, October 31, 2016.

“Bioinformatics Applications Reveal Gene Regulation Complexities in Response to Toxicant Exposures”. Environmental Mutagenesis and Genomics Society: Integrating Environmental, Genomic, and Health Research. 45th Annual Meeting, September 13-17, 2014, Orlando Florida.

“State-of-the-art Biological Processes Enrichment Using Gene Ontology”. Program in Quantitative Genomics. Department of Biostatistics, Harvard School of Public Health, Harvard University, December 14, 2009.

“Delineation of Perturbed Biological Systems that Govern Hepatotoxic Potential”. Bioinformatics Core Forum. Department of Biostatistics, Harvard School of Public Health, Harvard University, December 16, 2008.

“Bioinformatics from a Toxicogenomics Perspective”. Training Initiative for Biomedical and Biological Sciences. Molecular Biology Department, University of North Carolina- Chapel Hill, Chapel Hill, North Carolina, March 20, 2007.

“Careers and Jobs in Bioinformatics”. The Science and Career Seminar Series Partnership for Minority Advancement in the Biomolecular Sciences. Shaw University, Raleigh North Carolina, November 16, 2005.

“Classification and Prediction of Gene Expression Profiles for Toxicogenomics”. 10th Annual Hewitt Symposium and Toxicology Colloquium. Department of Pharmaceutical Sciences, University of Connecticut, Storres, Connecticut, May 16, 2003.

“A Bioinformatics Approach to Identify Microarray Gene Expression Toxicant Signature Patterns”. TestSmart- Pharmaceuticals: An Efficient and Humane Approach to Predictors of Potential Toxic Effects of Drugs, Pier 5 Hotel, Baltimore, Maryland, May 7, 2001.

“Informatics Implementations for Microarray Gene Expression and Toxicogenomics Efforts”. Department of Toxicoinformatics, Functional Genomics and Toxicoinformatics Centers, National Center for Toxicological Research, Jefferson, Arkansas, July 24, 2002.