

CURRICULUM VITAE

PIERRE ROBERT BUSHEL

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EDUCATION:

Ph.D., Bioinformatics, May 2005
North Carolina State University Raleigh, NC
Advisor: Greg Gibson

M.S., Molecular and Cellular Biology, September 1989
Long Island University Brooklyn, NY
Advisor: Norman Rothwell

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 and Alison Motsinger-Reif*

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.

April 2000-September 2006 **National Institute of Environmental Health Sciences, RTP, NC**
Staff Scientist *Microarray Group, Cindy Afshari and Richard S. Paules*

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

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

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

August 1990-April 1996

Associate Scientist

SCHERING-PLOUGH, Kenilworth, NJ

Tumor Biology Department, Chandra Kumar

September 1986-August 1990

Technician

**COLLEGE of PHYSICIANS AND SURGEONS of
COLUMBIA UNIVERSITY, Hammer Health Sciences Center
New York, NY**

Human Genetics and Medicine, Arthur Bank and Maggie Allan

HONORS AND AWARDS:

- University of Massachusetts-Amherst Distinguished Alumni, May 2015
- National Institutes of Health Award of Merit, NIEHS, 2000, 2001, 2003 & 2014
- National Institutes of Health Director's Award, NIH, Bethesda Maryland June 2002
- North Carolina State University, College of Agriculture & Life Sciences, Association for the Concerns of African American Graduate Students Academic Achievement Award, April 2005

PROFESSIONAL ACTIVITIES:

- Member, Trans-NIH Biomedical Informatics Coordinating Committee, at the National Institutes of Health, Bethesda MD 2007 – 2017, Alternate representative 2018 - Present
- Member, Scientific Advisory Committee for the Carolina Environmental Bioinformatics Center, at the University of North Carolina- Chapel Hill. 2008 and 2009
- Adjunct Professor, Nicholas School of the Environment and Earth Science, Duke University, 2009 – 2010
- Journal associate editor for: *Frontiers in Toxicogenomics*, July 2011 – Present
- Advisory Board member for: *OA Bioinformatics*, January 2013 – Present
- Editorial Board member for: *Mutation Research-Reviews*, January 2017 – Present
- Adjunct Faculty, Department of Biological and Biomedical Sciences, School of Graduate Studies, North Carolina Central University, 2017 – Present
- Assembly of Scientists Council member for: NIEHS, 2017 - Present
- Advisory Board member for: *Bioinformatics Research Center*, North Carolina State University, 2018 – Present
- Adjunct Lecturer, Department of Biostatistics, T.H. Chan School of Public Health, Harvard University, 2019 – 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:

Tia A. Hudson – North Carolina Central University, Bioinformatics, Genomics and Computational Chemistry, Department of Biological and Biomedical Sciences

“Bioinformatics integration of triple-negative breast cancer tumor genomic data” 2017-present

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.

Student Interns:

Kaitlin Klotz– M.S. student at the University of North Carolina at Charlotte, Bioinformatics, Summer 2018

Mia Burks– Undergraduate at St. Augustine University, Public Health, Summer 2013 – Spring 2014

Michael Falk– Undergraduate at Georgia Institute of Technology, Materials Sciences and Engineering, Summer 2013

Alexander Nordquist– Undergraduate at North Carolina State University, Chemical Engineering, Summer 2012

Venus Welch– Ph.D. student at Tuskegee University, Integrative Biosciences, Summer 2007

Elo Leung– Ph.D. student at George Mason University, Bioinformatics and Computational Biology, Summers 2005 & 2006

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

RESEARCH INTERESTS:

- Toxicogenomics and systems toxicology
- Epigenetics and exonization of transposable elements
- Cancer genomics/signatures, miRNAs, UTR usage and alternative polyadenylation
- Genetical genomics/eQTLs and gene regulation
- Big data science analytics for knowledge discovery
- Mixed type data integration
- Sequence quality control
- Data modeling and algorithm development
- Database development for bioinformatics
- Software development for computational biology

PUBLICATIONS IN PEER-REVIEWED JOURNALS:

*Denotes equal contribution

Ramaiahgari SC, Auerbach SS, Saddler TO, Rice JR, Dunlap PE, Sipes NS, DeVito MJ, Shah RR, **Bushel PR**, Merrick BA, Paules RS, Ferguson SS. The Power of Resolution: Contextualized Understanding of Biological Responses to Liver Injury Chemicals using High-throughput Transcriptomics and Benchmark Concentration Modeling. *Toxicol Sci.* 2019 Mar 8. pii: kfz065

Grimm SA, Shimbo T, Takaku M, Thomas JW, Auerbach S, Bennett BD, Bucher JR, Burkholder AB, Day F, Du Y, Duncan CG, French JE, Foley JF, Li J, Merrick BA, Tice RR, Wang T, Xu X, NISC Comparative Sequence Program, **Bushel PR**, Fargo DC, Mullikin JC, Wade PA. Genetics, sex and life experience-based influences on DNA methylation in mice. *Nat Commun.* 2019 Jan 18;10(1):305

Davis M, Knight E, Eldridge SR, Li J, **Bushel PR**. Transcriptomic profiles of tissues from rats treated with anticancer drug combinations. *Sci Data.* 2019 Jan 8;6:180306

Bushel PR, Tong W. Editorial: Integrative Toxicogenomics: Analytical Strategies to Amalgamate Exposure Effects With Genomic Sciences. *Front Genet.* 2018 Nov 27;9:563

Bushel PR, Caiment F, Wu H, O'Lone R, Day F, Calley J, Smith A, Li J. RATEmiRs: the rat atlas of tissue-specific and enriched miRNAs database. *BMC Genomics.* 2018 Nov 19;19(1):825

Bushel PR, Paules RS, Auerbach SS. A Comparison of the TempO-Seq S1500+ Platform to RNA-Seq and Microarray Using Rat Liver Mode of Action Samples. *Front Genet.* 2018 Oct 30;9:485

Nguyen TT, Grimm SA, **Bushel PR**, Li J, Li Y, Bennett BD, Lavender CA, Ward JM, Fargo DC, Anderson CW, Li L, Resnick MA, Menendez D. Revealing a human p53 universe. *Nucleic Acids Res.* 2018 Sep 19;46(16):8153-8167

Funderburk KM, Auerbach SS, **Bushel PR**. Crosstalk between Receptor and Non-receptor Mediated Chemical Modes of Action in Rat Livers Converges through a Dysregulated Gene Expression Network at Tumor Suppressor Tp53. *Front Genet.* 2017 Oct 24;8:157

Duncan CG, Kondilis-Mangum HD, Grimm SA, **Bushel PR**, Chrysovergis K, Roberts JD, Tyson FL, Merrick BA, Wade PA. Base-Resolution Analysis of DNA Methylation Patterns Downstream of Dnmt3a in Mouse Naïve B Cells. *G3 (Bethesda).* 2018 Mar 2;8(3):805-813

Mav D, Shah RR, Howard BE, Auerbach SS, **Bushel PR**, Collins JB, Gerhold DL, Judson RS, Karmaus AL, Maull EA, Mendrick DL, Merrick BA, Sipes NS, Svoboda D, Paules RS. A hybrid gene selection approach to create the S1500+ targeted gene sets for use in high-throughput transcriptomics. *PLoS One.* 2018 Feb 20;13(2):e0191105

Muñoz MD, Della Vedova MC, **Bushel PR**, Ganini da Silva D, Mason RP, Zhai Z, Gomez Mejiba SE, Ramirez DC. The nitron spin trap 5,5-dimethyl-1-pyrroline N-oxide dampens lipopolysaccharide-induced transcriptomic changes in macrophages. *Inflamm Res.* 2018 Jun;67(6):515-530

Lozoya OA, Martinez-Reyes I, Wang T, Grenet D, **Bushel P**, Li J, Chandel N, Woychik RP, Santos JH. Mitochondrial nicotinamide adenine dinucleotide reduced (NADH) oxidation links

the tricarboxylic acid (TCA) cycle with methionine metabolism and nuclear DNA methylation. *PLoS Biol.* 2018 Apr 18;16(4):e2005707

Duncan CG, Grimm SA, Morgan DL, **Bushel PR**, Bennett BD; NISC Comparative Sequencing Program, Roberts JD, Tyson FL, Merrick BA, Wade PA. Dosage compensation and DNA methylation landscape of the X chromosome in mouse liver. *Sci Rep.* 2018 Jul 4;8(1):10138

Bennett BD, **Bushel PR**. goSTAG: gene ontology subtrees to tag and annotate genes within a set. *Source Code Biol Med.* 2017 Apr 13;12:6

Osgood RS, Upham BL, **Bushel PR**, Velmurugan K, Xiong KN, Bauer AK. Secondhand Smoke-Prevalent Polycyclic Aromatic Hydrocarbon Binary Mixture-Induced Specific Mitogenic and Pro-inflammatory Cell Signaling Events in Lung Epithelial Cells. *Toxicol Sci.* 2017 May 1;157(1):156-171

Manrai AK, Cui Y, **Bushel PR**, Hall M, Karakitsios S, Mattingly CJ, Ritchie M, Schmitt C, Sarigiannis DA, Thomas DC, Wishart D, Balshaw DM, Patel CJ. Informatics and Data Analytics to Support Exposome-Based Discovery for Public Health. *Annu Rev Public Health.* 2017 Mar 20;38:279-294

Smith A, Calley J, Mathur S, Qian HR, Wu H, Farmen 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- κ 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 α 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.

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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.

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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.

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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.

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BOOK CHAPTERS:

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INVITED TALKS:

“Prediction of a Toxic Response to a Pharmaceutical Using a Machine Learning Paradigm”, 3rd Annual Massive Analysis and Quality Control Society Conference in collaboration with CHARME, Riva Del Garda Congress Centre, Trentino, Italy, April 8-10, 2019

“A Mashup of Statistics and Bioinformatics Applied to Genomic and Genetic Data for Better Understanding of Biological Consequences” Department of Biostatistics Colloquium Seminar Series, T.H. Chan School of Public Health, Harvard University, Boston, Massachusetts, November 15, 2018

“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 for Toxicogenomics: an acetaminophen case example” Genomic Sciences Alumni Conference, North Carolina State University, Raleigh, North Carolina, April 27, 2015

“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, Orlando, Florida, September 13-17, 2014

“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