

Vasyl Pihur

CONTACT INFORMATION	The McKusick-Nathans Institute of Genetic Medicine The Johns Hopkins University Broadway Research Building, Suite 543 733 N. Broadway Baltimore, MD 21205	<i>Mobile:</i> (502) 322-6178 <i>Office:</i> (443) 287-4420 <i>E-mail:</i> vpihur@gmail.com www.vpihur.com/biostat
CITIZENSHIP	USA	
RESEARCH INTERESTS	Genomics, statistical genetics, computational statistics, Bayesian statistics	
EDUCATION AND TRAINING	The Johns Hopkins University , Baltimore, Maryland USA Postdoctoral Fellow (2009 - 2011) <ul style="list-style-type: none">• McKusick-Nathans Institute of Genetic Medicine• Bloomberg School of Public Health - Department of Biostatistics• Joint mentors: Professor Aravinda Chakravarti and Professor Rafael Irizarry The University of Louisville , Louisville, Kentucky USA Ph.D., Biostatistics (2009) <ul style="list-style-type: none">• Dissertation: <i>Statistical Methods for High-dimensional Genomics Data Analysis</i>• Advisors: Professor Somnath and Susmita Datta The Northeastern Illinois University , Chicago, Illinois USA B.S., Computer Science (2004) <ul style="list-style-type: none">• Graduated with <i>Summa cum Laude</i>• Minor in Mathematics	
AWARDS	1st place at the annual Research!Louisville meeting, 2007 <ul style="list-style-type: none">• <i>Reconstruction of Genetic Association Networks from Microarray Data: A Partial Least Squares Approach.</i>	
PROFESSIONAL EXPERIENCE	Google/YouTube , San Bruno, California USA <i>Quantitative Analyst</i> July 2011 to present <ul style="list-style-type: none">• projects related to Youtube consumer behavior and experience The University of Louisville , Louisville, Kentucky USA <i>Statistical Consultant</i> September 2007 to July 2009 <ul style="list-style-type: none">• several collaborative projects with biomedical researchers that involved study design advising and practical hands-on high-throughput data analysis in genomics and proteomics contexts. <i>Research Assistant</i> July 2005 to July 2009 <ul style="list-style-type: none">• contributed to several research projects and grants (PI: Professor Susmita Datta)	

- Turner, T., **Pihur, V.**, Chakravarti, A. (2011) Testing for birth order effect in autism families. *Plos ONE*.
- The International Consortium for Blood Pressure Genome-Wide Association Studies (2011) Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature*.
- Wain, LV., ... , **Pihur, V.**, et al. Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*.
- Fox, ER., Young, JH, ... , **Pihur, V.**, ... , et al. (2011) Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. *Human Molecular Genetics*. **20**(11):2273-2284.
- Pihur, V.**, Datta, S., Datta, S. (2011) Meta analysis of Chronic Fatigue Syndrome through integration of clinical, gene expression, SNP and proteomic data. *Bioinformatics*. **6**:3.
- Warner, D., Brock, GN., **Pihur, V.** Green, RM. (2011) TGF β -1 and Wnt-3a interact to induce unique gene expression profiles in murine embryonic palate mesenchymal cells. *Reproductive Toxicology*. **31**(2):128-33.
- Kidd, LC., VanCleave, T., Doll, MA., Srivastava, DS., Thacker, B., Komolafe, O., **Pihur, V.**, Brock, GN., Hein, DW. (2011) No association between variant N-acetyltransferase genes, tobacco smoking and PCa susceptibility among men of African descent. *Biomarkers in Cancer*. **3**:1-13.
- Mukhopadhyay, P., Brock, GN., **Pihur, V.**, Webb, C., Pisano, MM., Greene, RM. (2010) Developmental microRNA expression profiling of murine embryonic orofacial tissue. *Birth Defects Res A Clin Mol Teratol*, **88**(7):511-534.
- Datta, S., **Pihur, V.**, Datta, S. (2010) An adaptive optimal ensemble classifier via bagging and rank aggregation with applications to high dimensional data. *BMC Bioinformatics*, **11**:427.
- Pihur, V.**, Datta, S. Datta, S. (2009) *RankAggreg*, an R package for weighted rank aggregation. *BMC Bioinformatics*, **10**:62.
- Pihur, V.**, Datta, S., Datta, S. (2008) Reconstruction of genetic networks from microarray data: A Partial Least Squares approach. *Bioinformatics*, **24**(4):561-568.
- Pihur, V.**, Datta, S., Datta, S. (2008) Finding cancer genes through meta-analysis of microarray experiments: rank aggregation via the cross entropy algorithm. *Genomics*, **92**:400-403.
- Pihur, V.**, Datta, S., Datta, S. (2007) Weighted rank aggregation of cluster validation measures: a monte carlo cross-entropy approach. *Bioinformatics*, **23**(13):1607-1615.
- Brock, GN., **Pihur, V.**, Datta, S., Datta, S. (2007) *clValid*, an R package for cluster validation. *Journal of Statistical Software*, **25**:4.
- McCabe, S., Uebele, A., **Pihur, V.**, Rosales RS., Atroshi, I. (2007) Epidemiologic associations of carpal tunnel syndrome and sleep position: Is there a case for causation? *HAND*, **2**:127-134.

- BOOK CHAPTERS Datta, S. and **Pihur, V.** (2010) Feature selection and machine learning with mass spectrometry data. In *Clinical Proteomics: Methods, Applications and Tools*, (Matthiesen, R. ed.), pp. 205-229.
- Brock, GN., **Pihur, V.**, Kubatko, L. (2009) Detecting gene regulatory networks from microarray data using fuzzy logic. In *Fuzzy Systems in Bioinformatics, Bioengineering and Computational Biology. Studies in Fuzziness and Soft Computing*, (Jin, Y and Wang, L, ed.), Springer-Verlag, Berlin Heidelberg, pp. 141-164.
- Pihur, V.**, Brock, GN., Datta, S., Datta, S. (2009) Cluster validation for microarray data: an appraisal. In *Multivariate Statistical Methods*, (A. SenGupta, ed.), ISI Platinum Jubilee series, World Scientific Press, pp. 79-94.
- IN PREPARATION **Pihur, V.** (2011) Estimating the number of null hypotheses in multiple testing. In preparation.
- Pihur, V.** and Chakravarti, A. (2011) Third-generation genome-wide association studies. Preprint.
- Bravo HC., **Pihur, V.**, McCall, M., Irizarry, R., Leek, J. (2011) Universal cancer classifier. In preparation.
- Nguyen, KH., **Pihur, V.**, Ehret, GB., Ganesh, SK., Weder, AB., Coresh, J., Kao, WHL, Young, JH., Chakravarti, A. (2011) Effects of rare, putatively damaging variants in essential hypertension in the population-based CLUE and the family-Based FBPP samples. Preprint.
- CHARGE consortium (2011) Long-term average analysis of blood pressure in the CHARGE consortium. In preparation.
- PRESENTATIONS IISA Conference on Probability, Statistics, and Data Analysis 2011, Raleigh, NC (invited)
- *Estimating and improving power in genome-wide association studies.*
- ASHG 2010, Washington, DC
- *Neither ‘rare’ nor ‘common’ variants can explain much of phenotypic variation.*
- JSM 2010, Vancouver, BC
- *Estimating the number of null hypotheses in multiple testing.*
- ENAR 2008 Spring Meeting, Arlington, VA
- *Reconstruction of genetic association networks from microarray data: a Partial Least Squares approach.*
- ENAR 2007 Spring Meeting, Atlanta, GA
- *Weighted rank aggregation of cluster validation measures: a Monte Carlo cross-entropy approach.*
- R PACKAGES *RankAggreg*
- weighted rank aggregation of ordered lists using several different algorithms
- clValid*
- statistical and biological validation of clustering results
- office2010*
- natively read and write xlsx files in R
- WORKSHOPS NIEHS SNPs Workshop
- *University of Louisville, Kentucky USA (2008)*

- PROFESSIONAL MEMBERSHIP
- *American Statistical Association (ASA)*
 - *Eastern North American Region of International Biometric Society (ENAR/IMS)*
 - *American Society of Human Genetics (ASHG)*
- REFEREE SERVICE
- *Bioinformatics*
 - *Computational Statistics and Data Analysis*
 - *Statistics & Probability Letters*
 - *Communications in Statistics - Theory and Methods*
 - *BMC Bioinformatics*
 - *Statistics in Medicine*