

VASYL ZHABOTYNSKY

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ADDRESS

University of North Carolina-Chapel Hill
Department of Biostatistics
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INTERESTS

Applied statistics, Statistical genetics, and computationally intensive statistics.

EXPERTISE

- Statistical modeling
- Implementation of advanced computational algorithms for statistical analysis
- Development of study materials
- Data source analysis, modeling, analysis, reporting, and presentation

SKILLS SUMMARY

- **Tools:** R, SAS, SQL*Plus
- **Languages:** C, C++, Python, Java, SQL, PL/SQL, Basic, FORTRAN
- **RDBMS:** Oracle 9i, Oracle 8i
- **OS:** Linux SUSE, Red Hat, Sun Solaris, UNIX System V, Windows

EDUCATION

University of North Carolina at Chapel Hill

- DrPH in Biostatistics, March 2020

University of Iowa

- MS in Statistics, May 2007

Central College-Iowa

- BA in Mathematics and Computer Science, May 2004

PROFESSIONAL EXPERIENCE

UNC Department of Biostatistics, Chapel Hill, NC

Mar 2020 to Mar 2021

Postdoctoral Trainee

- Model development and analysis of genetic and haloperidol effects in a diverse mouse crosses (RIX).
- Model development and analysis of genetic effects based on GTEx and 1000Genomes human datasets incorporating total and allele-specific counts and providing a framework for a more detailed study of allelic imbalances based on other factors of interests

UNC Department of Biostatistics, Chapel Hill, NC

Aug 2014 to Feb 2020

Graduate Research Assistant, Dissertation Completion Fellowship

- Statistical algorithms development, implementation and analysis for several projects involving several human genomic data projects and mice genomic data projects.

UNC Lineberger Comprehensive Cancer Center, Chapel Hill, NC

May 2016 to Aug 2018

Graduate Research Assistant

- Proteomic and NextGen (RNAseq, RRBS, etc.) data processing and analysis.
- Statistical algorithms development, implementation and analysis for several projects involving several human genomic data projects and mice genomic data projects.

UNC Department of Genetics, Chapel Hill, NC

Sep 2009 to Jul 2014

Biostatistician

- Worked at statistical algorithms development, implementation and analysis for a CISGen project in a generalized mixed models framework. Work includes development of highly computationally intensive algorithms primarily for NextGen (RNAseq, RRBS, etc.) and for microarrays. Perform various permutation based and pathway analysis of the data.
- Participate in method development of the integrative analysis of GWAS and sequencing data.
- Collaborated in drPathway toxicological project for pathway detection in eQTL microarrays and GODOT twin study project.

University of Iowa, Iowa City, IA

Aug 2005 to Jun 2009

Research Assistant

- Worked with a group developing Bayesian spatial model for the prediction radon levels by combining multiple sources and multiple data types. Worked with highly computationally intensive algorithms that required the development of parallel algorithm.
- Participated in several consulting projects.

Teaching Assistant

- Worked with discussion groups, developed study materials and quizzes, graded exams, quizzes and homework, prepared review sessions and tutored students of the undergraduate level courses.

Infogate, Buffalo Grove, IL

Jun 2004 to May 2005

Software Engineer

- Designed, developed and maintained Order Entry and Processing System. Analyzed requirements, created weekly, monthly and on-request reports, developed testing plan to ensure data quality, designed, developed and tested user interface software. Was responsible for integration of the new system into the existing Administrative User interface.

MyPoints.com, Inc., Schaumburg, IL

Jun 2003 to Aug 2003

Business Analyst Intern

- Designed, developed, implemented and maintained reports for Company and Clients in Data Warehouse environment. Created and executed ad-hoc queries. Verified execution plans for ad-hoc queries and for default SQL-queries created by Business Object. Worked with DBA team on SQL-queries' modifying and tuning.

OTHER PROJECTS

Z++, Highland Park, IL

Aug 2009 to Sep 2009

Statistician

- Consulted graduate students.
- Developed illustrative materials.
- Developed custom statistical software.

PUBLICATIONS

ORCID ID: 0000-0003-1575-5732

- 1. Giusti-Rodríguez, P, Xenakis, J, Crowley, JJ, Nonneman, RJ, DeCristo, DM, Ryan, A., Quackenbush, CR, Miller, DR, Shaw, GD, Zhabotynsky, V. and Sullivan, P
Antipsychotic behavioral phenotypes in the mouse Collaborative Cross recombinant inbred inter-crosses (RIX). *BioRxiv* (2019): 761353. (accepted *G3 (Bethesda): Genes | Genomes | Genetics*) (2020)
- 2. Zhabotynsky V, Sun W, Inoue K, Magnuson T, Calabrese M
A statistical method for joint estimation of cis-eQTLs and parent-of-origin effects using RNA-seq human data under family trio design. (2019)
Biometrics PMID: 30666629
- 3. Sun W, Bunn P, Jin C, Little P, Zhabotynsky V, Perou CM, Hayes DN, Chen M, Lin DY
The Association between Copy Number Aberration, DNA Methylation, and Gene Expression (2018)
Nucleic Acids Research doi: 10.1093/nar/gky131 PMID: 29529299
- 4. Sun W, Yufeng Liu, Crowley JJ, Chen TH, Zhou H, Chu H, Huang S, Kuan PF, Li Y, Miller D, Shaw G, Wu Y, Zhabotynsky V, McMillan L, Zou F, Sullivan PF, Pardo-Manuel de Villena F
IsoDOT Detects Differential RNA-isoform Expression/Usage with respect to a Categorical or Continuous Covariate with High Sensitivity and Specificity. (2015)
Journal of the American Statistical Association PMID: 26617424
- 5. Crowley JJ, Zhabotynsky V, Sun W, Huang S, Pakatci I, Kim Y, Wang J, Morgan A, Calaway J, Aylor D, Yun Z, Bell T, Buus R, Calaway M, Didion J, Gooch T, Hansen S, Robinson N, Shaw G, Spence J, Quackenbush C, Barrick C, Xie Y, Valdar W, Lenarcic A, Wang W, Welsh C, Fu C, Zhang Z, Holt J, Guo Z, Threadgill D, Tarantino L, Miller D, Zou F, McMillan L, Sullivan PF, Pardo-Manuel de Villena F
Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. (2015)
Nature Genetics 47, 353–360 PMID: 25730764
- 6. Zou F, Sun W, Crowley JJ, Zhabotynsky V, Sullivan PF, and Pardo-Manuel de Villena F
A novel statistical approach for jointly analyzing RNA-Seq data from F1 reciprocal crosses and inbred lines. (2014)
Genetics 197 (1), 389-399. PMID: 24561482
- 7. Collaborative Cross Consortium.
The Genome Architecture of the Collaborative Cross Mouse Genetic Reference Population. (2012)
Genetics 190(2):389-401. PMID: 22345608
- 8. Sun W, Lee S, Zhabotynsky V, Zou F, Wright FA, Crowley JJ, Yun Z, Buus RJ, Miller DR, Wang J, McMillan L, Pardo-Manuel de Villena F, Sullivan PF (2012)
Transcriptome Atlases Of Mouse Brain Reveals Differential Expression Across Brain Regions And Genetic Backgrounds.
G3 (Bethesda): Genes | Genomes | Genetics 2 (2), 203-211. PMID: 22384399

CONFERENCES

- 1. Zhabotynsky V, Sun W, Xenakis JG, Crowley JJ, Giusti P, Sullivan PF, Pardo-Manuel De Villena F, Zou F
Analysis of Genetic Responses to the Antipsychotic Medicine Haloperidol with RNA-Seq Data from Diverse Mouse Recombinant Inbred Crosses (RIX) (2020) *The Allied Genetics Conference 2020*
- 2. Xenakis JG, Kim K, Zhabotynsky V, Mi X, Cotney PA, Kashfeen A, McMillan L, Crowley JJ, Sullivan PF, Zou F, Pardo-Manuel De Villena F
The Role of Allele-Specific CpG Methylation in the Silencing of Recent Endogenous Retrovirus Insertions (2020) *The Allied Genetics Conference 2020*
- 3. Xenakis JG, Kim KS, Zhabotynsky V, Mi X, Crowley JJ, Sullivan PF, Pardo-Manuel De Villena F
A Statistical Model of Methylation Sequencing Data Identifies Novel Differentially Methylated CpG's and Provides Insights into the Role of Methylation in X-chromosome Inactivation and the Silencing of Transposable Elements (2019) *The 33th International Mammalian Genome Conference*
- 4. Giusti Rodriguez P, Xenakis JG, Crowley JJ, Nonneman RJ, DeCristo DM, Ryan A, Quackenbush CR, Miller DR, Shaw GD, Zhabotynsky V, Sullivan PF, Fernando Pardo Manuel de Villena, Zou F
Antipsychotic behavioral phenotypes of Collaborative Cross recombinant inbred intercrosses (RIX) (2018) *The 32th International Mammalian Genome Conference*
- 5. Zhabotynsky V, Hu YJ, Zou F, Sun W
eQTL Analysis Using Human RNA-seq Data with TReCASE and RASQUAL (2018)
ENAR 2018 Spring Meeting with IMS and sections of ASA
- 6. Zhabotynsky V, Sun W, Inoue K, Magnuson T, Calabrese M
Unbiased Estimation of Parent-of-Origin Effects Using RNA-seq Data from Human (2017) *ENAR 2017 Spring Meeting with IMS and sections of ASA*
- 7. Peng XL, Zhabotynsky V, East MP, Voltzke KJ, Sprague D, Herrera Loeza SJ, Moffitt RA, Rashid NU, Graves LM, Johnson GJ, Yeh JJ
Kinome profiling in pancreatic cancer reveals subtype-specific drug (2017) *2017 UNC Lineberger Comprehensive Cancer Center Scientific Retreat*
- 8. Sun W, Bunn P, Jin C, Little P, Zhabotynsky V, Perou CM, Hayes DN, Chen M, Lin D
Tissue Purity and cell composition challenges in estimation of association between somatic copy number aberration, DNA methylation and gene expression (2016) *2016 UNC Lineberger Annual Scientific Retreat*
- 9. Xenakis JG, Zhabotynsky V, Zou F
A score statistic for testing variance components in the shared random effects setting with applications to a complex mouse study (2016) *2016 Joint Statistical Meetings*
- 10. Zou F, Sun W, Crowley JJ, Zhabotynsky V, Sullivan PF, Pardo-Manuel de Villena F, Xenakis J, Giusti P
TReCASE: a powerful method to detect differential gene expression using total and allele specific RNA-seq data (2014) *The 12th Annual Centers of Excellence in Genomic Science Grantee Meeting*
- 11. Crowley JJ, Zhabotynsky V, Sun W, Huang S, Pakatci I, Kim Y, Wang J, Morgan A, Calaway J, Aylor D, Yun Z, Bell T, Buus R, Calaway M, Didion J, Gooch T, Hansen S, Robinson N, Shaw G, Spence J, Quackenbush C, Barrick C, Xie Y, Valdar W, Lenarcic A, Wang W, Welsh C, Fu CP, Zhang Z, Holt J, Guo Z, Threadgill D, Tarantino L, Miller D, Zou F, McMillan L, Sullivan P, Pardo-Manuel de Villena F
Pervasive Allelic Imbalance Revealed By Allele-Specific Gene Expression In Highly Divergent Mouse Crosses (2013) *The 27th International Mammalian Genome Conference*
- 12. Holt JM, Wang J, Zhabotynsky V, Kim Y, Crowley JJ, Zou F, Sullivan P, Pardo-Manuel de Villena F, McMillan L
A Visualization Tool For Exploring the Gene Expression Landscape in a Full Three-Founder Diallele (2013) *The 27th International Mammalian Genome Conference*

SOFTWARE DEVELOPMENT

- 1. Sun W, Zhabotynsky V (2013)
asSeq: A set of tools for the study of allele-specific RNA-seq data.
<http://www.bios.unc.edu/~weisun/software/asSeq.pdf>
- 2. Zhabotynsky V, Sun W, Zou F (2013)
rxSeq: Reciprocal Cross in RNA-seq.
<https://cran.r-project.org/package=rxSeq>
- 3. Wright F, Sypa M, Li Z, Zhabotynsky V, Zhou Y, Rudra P, Idowu S, Rusyn I (2013)
DR Pathway GUI.
<http://comptox.unc.edu/DRPathway.php>

AFFILIATIONS

- American Statistical Association from 2005
- Genetics Society of America from 2016
- ENAR International Biometric Society from 2016