

CONTACT INFORMATION	Box 357232 University of Washington Seattle, WA 98195-7232	e: avmikh@uw.edu w: http://staff.washington.edu/avmikh/
RESEARCH INTERESTS	My main research interests are in statistical genetics and pharmacogenomics. In particular, I am interested in developing and applying methodology for predicting gene expression in admixed populations, i.e. in individuals with ancestry derived from multiple previously isolated populations.	
EDUCATION	University of Washington, Seattle, WA	
	Ph.D, Biostatistics	September 2013 – present
	<ul style="list-style-type: none"> • Statistical genetics pathway • Advisor: Dr Timothy Thornton 	
	University of North Carolina at Greensboro, Greensboro, NC	
	B.S., Mathematics	January 2010 – May 2013
	<ul style="list-style-type: none"> • Minors: Biology, Chemistry • Full University Honors, summa cum laude 	
RESEARCH EXPERIENCE	University of Washington, Seattle, WA	
	<i>Research Assistant</i>	June 2016 – present
	<ul style="list-style-type: none"> • Statistical analyst for NHLBI TopMed WGS Project • Advisor: Dr Timothy Thornton 	
	<i>Research Associate</i>	September 2015 – May 2016
	<ul style="list-style-type: none"> • Virology Research Clinic • Supervisor: Dr Amalia Magaret 	
	<i>Research Assistant</i>	January 2014 – May 2015
	<ul style="list-style-type: none"> • Alzheimer's Disease and Learning Disabilities projects • Supervisor: Dr Ellen Wijsman 	
PUBLICATIONS *	<ol style="list-style-type: none"> 1. Mikhaylova AV and Thornton TA. Accuracy of gene expression prediction from genotype data with PrediXcan varies across and within continental populations. <i>Frontiers in Genetics</i> 10(2019):261. 2. Hill J, Sedlak RH, Magaret A, Mikhaylova A, Huang ML, Jerome K, Zerr D, Boeckh M. Large-scale identification and characterization of hematopoietic cell transplant recipients and their donors with inherited chromosomally integrated human herpesvirus 6. <i>Biology of Blood and Marrow Transplantation</i>. 23(3): S55-S56. 3. Ramchandani M, Kong M, Tronstein E, Selke S, Mikhaylova A, Magaret A, Huang ML, Johnston C, Corey L, Wald A. Herpes simplex virus type 1 shedding in tears and nasal and oral mucosa of healthy adults. <i>Sexually Transmitted Diseases</i>. 43(12):756-60. 4. Butler D, Shivaji R, Tuck A. S-shaped bifurcation curves for logistic growth and weak Allee effect growth models with grazing on an interior patch. <i>Electron. J. Differ. Equ., Conf.</i> 2013 (Vol. 20, pp. 15-25). 5. Gill TS, Tuck A, Gupta S, Crowe M, Figueroa J. A field test of optional unrelated question randomized response models: estimates of risky sexual behaviors. In <i>Topics from the 8th Annual UNCG Regional Mathematics and Statistics Conference 2013</i> (pp. 135-146). Springer New York. 6. Gupta S, Tuck A, Gill T, Crowe M. Optional unrelated-question randomized response models. <i>Involve, a Journal of Mathematics</i>. 6(4):483-92. 	

*Last name changed from Tuck to Mikhaylova in 2015

PREPRINTS

1. Keys KL, Mak ACY, White MJ, Eckalbar WL, Dahl A, Mefford J, **Mikhaylova AV**, Contreras MG, Elhawary JR, Eng C, Hu D, Huntsman S, Oh SS, Salazar S, Lenoir MA, Ye JC, Thornton TA, Zaitlen N, Burchard EG, Gignoux CR. On the cross-population portability of gene expression prediction models. *bioRxiv:10.1101/552042*

TEACHING
EXPERIENCE**University of Washington**, Seattle, WA*Teaching Assistant for UCONJ 510***June 2015 – August 2015**

- Introductory Biostatistics course for graduate students in biomedical sciences
- Instructor: Dr Lloyd Mancl

University of North Carolina at Greensboro, Greensboro, NC*Math Emporium Instructional Assistant***January 2013 – May 2013**

- Department of Mathematics and Statistics at UNCG
- Tutor for students in college algebra and precalculus

*Undergraduate Assistant***August 2011 – May 2013**

- Department of Mathematics and Statistics at UNCG
- Grader for introductory linear and abstract algebra courses and calculus

CONFERENCE
PRESENTATIONS

Predictive modeling of gene expression in admixed populations. Poster presentation at ASHG, San Diego, CA. Fall 2018.

Estimation of Genotyping Error Rate in SNP Data. Poster presentation at UW Biostatistics Retreat, Blaine, WA. Fall 2014.

Population Dynamics Model with Logistic Growth, Weak Allee Effect, and Grazing on an Interior Patch. MAA MD-DC-VA Section, Salisbury University, Salisbury, MD. Spring 2013.

Estimating Prevalence of Sensitive Behaviors with Optional Unrelated-Question Randomized Response Models. Poster presentation at 2013 Joint Mathematics Meeting, San Diego, CA. Winter 2013

Parameter Estimation for Quantitative and Binary Optional Unrelated-Question Randomized Response Model. International Conference on Statistics and Informatics in Agricultural Research, New Delhi, India. Fall 2012.

Estimating Parameters for Optional Unrelated-Question Randomized Response Models. Oral presentation at NIMBioS Undergraduate Research Conference at the Interface of Biology and Mathematics, University of Tennessee, Knoxville. Fall 2012.

Optional Unrelated-Question Randomized Response Models. Oral presentation at the 8th Annual Regional Undergraduate Mathematics Conference, University of North Carolina at Greensboro. Fall 2012.

A Quantitative Optional Unrelated-Question Randomized Response Model. Oral presentation at International Conference on Advances in Interdisciplinary Statistics and Combinatorics, University of North Carolina at Greensboro. Fall 2012.

A Statistical Method to Improve Truthful Responses to Surveys of Sensitive Information: A Quantitative Optional Unrelated-Question Randomized Response Model. Poster presentation at 2012 National Conference on Health Statistics, Washington, DC. Summer 2012.

A Quantitative Optional Unrelated-Question Randomized Response Model. Poster presentation at Undergraduate Research EXPO, University of North Carolina at Greensboro. Spring 2012.

Estimating Stimulant Medication Misuse Using RRT Models. Poster presentation at Undergraduate Research EXPO, University of North Carolina at Greensboro. Spring 2012.

An Optional Unrelated-Question Randomized Response Model. Oral presentation at International Conference on Applied Mathematics and Statistics (ICAPMS-2011). Gujarat University, India. Fall 2011.

An Optional Unrelated-Question Randomized Response Model. Oral presentation at the 7th Annual Regional Undergraduate Mathematics Conference, University of North Carolina at Greensboro. Fall 2011.

An Optional Unrelated-Question Randomized Response Model. Oral presentation at Duke-UNCG Math Biology Workshop, Duke University, Durham, NC. Summer 2011.

HONORS AND AWARDS	<p>Student Excellence Award, Spring 2012</p> <p>Phi Beta Kappa, Spring 2012</p> <p>Pi Mu Epsilon, Spring 2012</p> <p>NSF Math-Bio Undergraduate Fellowship, 2011 – 2012</p> <p>Best Paper Award in Undergraduate Student Category, Fall 2012</p> <p>Chancellor's List, 2010 – 2013</p> <p>Dean's List, 2010 – 2013</p> <p>Lloyd International Honors College Dean's List, 2011 – 2013</p> <p>Science Technology and Math Preparation Scholarship, 2011 – 2013</p> <p>Posey Mathematics Scholarship, 2012</p> <p>Women in Math and Science Scholarship, 2012</p> <p>Judith J. Mendenhall Scholarship, 2011</p> <p>Ruth Collins Scholarship, 2011</p> <p>Chris Velonis Miller Scholarship, 2010</p>	
RELATED EXPERIENCE	<p>UCLA Computational Genomics Summer Institute, Los Angeles, CA <i>Research talks and tutorials covering a variety of bioinformatics techniques</i></p> <p>UCLA Computational Genomics Summer Institute, Los Angeles, CA</p> <p>Summer Institute in Statistical Genetics, Seattle, WA <i>Modules</i></p> <p>'Integrative Genomics' by Dr Greg Gibson and Dr Michael Inouye 'Network and Pathway Analysis of Omics Data' by Dr Ali Shojaie and Dr Alison Motsinger-Rief</p> <p>Summer Institute in Statistics for Big Data, Seattle, WA <i>Modules</i></p> <p>'Big Data Wrangling with R' by Dr Andrew Jaffe and Dr Jeffrey Leek</p> <p>UCLA Computational Genomics Summer Institute, Los Angeles, CA</p> <p>Fifth Seattle Symposium in Biostatistics, Seattle, WA <i>Short courses</i></p> <p>'High-dimensional statistical learning' by Dr Noah Simon and Dr Ali Shojaie 'Overview of Omics data' by Dr Bruce Weir 'Promises and pitfalls of Omics experiments' by Dr Raphael Gottardo</p>	<p>July 2019</p> <p>July 2017</p> <p>July 2016</p> <p>July 2016</p> <p>July 2016</p> <p>July 2016</p> <p>November 2015</p>
COMPUTING SKILLS	<p>Statistical packages: R, can comprehend STATA</p> <p>Languages: shell scripting; can comprehend Python</p> <p>Version control: Git</p> <p>Applications: L^AT_EX, Microsoft Office</p> <p>Operating Systems: Unix/Linux, Windows, Mac OS</p>	
SERVICE	<p>Member, Diversity Committee, Department of Biostatistics, University of Washington, 2016 – 2019</p> <p>Senator, Graduate and Professional Student Services, University of Washington, 2016 – 2017</p> <p>High School Mentor, Community for Youth, Seattle, 2015 – 2016</p>	
LANGUAGES	<p>Fluent in English and Russian, intermediate Spanish.</p>	