

Yuliya Karpievitch

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EDUCATION

Ph.D., Bioinformatics, December 2007
Department of Biostatistics, Bioinformatics and Epidemiology
Medical University of South Carolina, Charleston, SC 29425
Thesis Title: Computational Tools for MS-based Proteomics

Research Interests: Statistical models for normalization and missing value imputation in mass spectrometry-based proteomics data; differential expression analysis at single time point and across time, machine learning using non-parametric algorithms; biomarker identification

MS, Computer Science, 2003
College of Charleston, Charleston, SC 29424
Project Title: Solving Global Optimization Problems Using Interval Arithmetic

BS, Computer Information Systems, 2001
College of Charleston, Charleston, SC 29424

PROGRAMMING SKILLS

Matlab, R, C++, C, PHP, Java, Bash shell scripting
Developing Matlab stand-alone (compiled) executables
PHP scripting for HTTP database front-end, SQL
Linux system programming including system calls and kernel modules

EXPERIENCE

Jan 2010 - present

Senior Scientist, Fundamental & Computational Sciences Directorate, Pacific Northwest National Lab, Richland, WA.

- Computational mass spectrometry (MS)-based proteomics
- Statistical methods for MS-based proteomics

Aug 2007 – Jan 2010

Post Doctoral Fellow, Department of Statistics, Texas A&M University

- MS data interpretation and development of analysis tools
- Normalization, missing (censored) value imputation, and significance analysis of the MS-based proteomics data

Feb 2006 – Aug 2007

Graduate Research assistant, Department of Bioinformatics and Computational Biology, M. D. Anderson Cancer Center, University of Texas

- Preprocessing and normalization of MALDI data
- Clustering and biomarker identification in mass spectrometry and microarray data

Aug 2003 - Dec 2007

Graduate student, Medical University of South Carolina, Charleston, SC

Jan 2003 - Dec 2005

Adjunct Instructor, Computer Science Department, College of Charleston

- Object Oriented Design with C++
- Java Programming Lab

Aug 2001 - Dec 2003

Graduate Teaching Assistant (teaching beginning Java Lab),

Computer Science Department, College of Charleston

Spring 2001

Programming Intern, Information Technology Lab, MUSC, Charleston, SC

- Provide restricted access to MySQL database via web using Perl, PHP

Summer 2000

Programming Intern (C++), Automated Trading Desk, Mt. Pleasant

- Develop parsers to process incoming text data stream
- Use Object Oriented Design Patterns in software development process

Fall 1999 - Spring 2001

Teaching Assistant (assisting instructor in Java Programming Lab),
Computer Science Department, College of Charleston

PEER-REVIEWED PUBLICATIONS

Karpievitch YV, Dabney AR and Smith RD. Normalization and Missing Value Imputation for label-free LC-MS Analysis. *Springer Methods in Molecular Biology Series (submitted)*.

Andreev VP, Petyuk VA, **Karpievitch YV**, Clarke J, Camp DG, Smith RD, Lieberman A, Albin R, Myers AJ. Quantitative Proteomics reveals 197 Proteins with Significantly Altered Abundances in Cortical Samples of Alzheimer's Disease versus Normally Aged Human Brains. *Molecular Psychiatry (submitted)*.

Karpievitch YV, Polpitiya AD, Anderson GA, Smith RD, Dabney AR. Liquid Chromatography Mass Spectrometry-Based Proteomics: Biological and Technological Aspects. *Annals of Applied Statistics*, 2010.

Karpievitch YV, Hill EG, Leclerc AP, Dabney AR, Almeida JS. An Introspective Comparison of Random Forest-based Classifiers for the Analysis of cluster-correlated data by Way of RF++. *PLoS ONE* 2009.

Karpievitch YV, Taverner T, Adkins JN, Callister S, Anderson GA, Smith RD, Dabney AR. Normalization of peak intensities in bottom-up MS-based proteomics using singular value decomposition. *Bioinformatics* 2009.

Karpievitch YV, Stanley J, Taverner T, Huang J, Adkins J, Ansong C, Heffron F, Metz T, Qian W-J, Yoon H, Smith RD, Dabney AR. A Statistical Framework for Protein Quantitation in Bottom-Up MS-Based Proteomics. *Bioinformatics* 2009.

Karpievitch YV, Hill EG, Smolka AJ, Morris JS, CoombesKR, Baggerly KR, Almeida JS. PrepMS: Mass Spectrometry Graphical Preprocessing Tool. *Bioinformatics* 2006.

Karpievitch YV, Almeida JS. mGrid: A parallel Matlab library for user code distribution. *BMC Bioinformatics* 2006.

PUBLICATIONS IN PROGRESS

Karpievitch YV, Dabney AR. An Overview of Statistical Issues in Quantitative Proteomics. *In preparation*.

INVITED TALKS

Missing Values in Shotgun Proteomics Data Analysis, Barcelona Science Park, September 2010.

Shotgun Proteomic Data Analysis and Statistical Approaches to Protein Quantification, Purdue University, Department of Statistics, October 2010.

Normalization and Missing Value Imputation for Proteomics Analysis, JSM 2010.

GRANT SUPPORT

National Institute of Health, Microbial Community Proteomics grant proposal (*submitted*).

National Cancer Institute Postdoctoral Bioinformatics Training Grant (2007-2010)

National Library of Medicine Training Grant: Toolmakers for Bioinformatics (2003-2007) T15-LN07438

ISMB 2009 Travel Fellowship, Stockholm, Sweden

ISMB 2008 Travel Fellowship, Toronto, Canada

ISMB 2007 Travel Fellowship, Vienna, Austria

FASEB(MARC) Travel Award for ISMB 2006, Fortaleza, Brazil

F. Hoffmann-La Roche AG Travel Award for HUPO 2006, Long Beach, CA