OLGA V. SAZONOVA, PH.D.

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I am a driven bioinformatics data scientist with a diverse computational/experimental skill set, industry experience in translational genomics, and outstanding communication skills. I seek challenging opportunities to transform genomics data into clinical knowledge in a dynamic and collaborative environment.

EXPERIENCE

Scientist 1, Translational Genomics, Onyx Pharmaceuticals, South San Francisco, CA 2014 – present

- Lead the application of machine learning and data visualization algorithms to diverse genomics data sets (RNA-Seq, Exome-Seq, expression arrays) to discover drug response biomarkers as part of a cross-functional research team in oncology drug discovery. Collaborate with biologists to translate computational studies into hypothesis-driven validation.
- Design and implement a computational approach to interrogate multi-dimensional parameter space for optimizing copy number variant detection (CNV) from Exome-Seq using aCGH as a gold standard. The resulting pipeline has enabled ongoing biomarker discovery from clinical samples through close collaboration with other computational scientists.

Postdoctoral Research Fellow, Cardiovascular Genomics, Stanford University, CA 2011 – 2014

- Developed software and statistical methods to discover novel mechanisms of transcriptional regulation in coronary smooth muscle from combination of in-house NGS data (ChIP-Seq, RNA-Seq, ATAC-Seq, DNase-Seq) and public databases (ENCODE, 1000Genomes, HapMap, ROADMAP, JASPAR).
- Created computational pipelines combining custom and open source software for NGS data analysis, including: alignment, QC, replicate validation/comparison, transcription factor binding site discovery, motif discovery, gene enrichment analysis, allele-specific expression, and differential gene expression.
- Published first-author study in *PLoS Genetics*; presented findings at national conferences; secured highly competitive NIH NRSA postdoctoral fellowship to fund research and training.

Doctoral Candidate, Biomedical Engineering, Boston University, MA 2005 – 2011

- Led the discovery of novel mechanisms of mechanotransduction in aortic smooth muscle cells using diverse cell biology, biochemistry, molecular biology, and computational assays.
- Applied statistical tests to diverse data sets measuring nano-mechanics, molecular imaging, cellular morphology, protein and gene expression.
- Published first- and second-author studies in *Biophysical Journal* and *Biomaterials*; presented findings in podium and poster presentations at national conferences.

TECHNICAL SKILLS

- **Computational expertise** in data manipulation, statistical analysis, machine learning, and visualization: Proficient in R (including Bioconductor), Python, and MATLAB in Windows, OSX, and UNIX environments. Broad knowledge of NGS tools including SAMTools, BEDtools, BWA, STAR, HOMER, ANNOVAR, IGV, Omicsoft. Additional expertise in Igor, ImageJ, GIMP. Familiar with C++ and Mathematica.
- **Laboratory experience** in cellular/molecular biology, biomaterials, and microscopy: Immunoprecipitation, ELISA, qPCR, Western blotting, immunocytochemistry, wide-field and confocal fluorescence microscopy, atomic force microscopy, polymer synthesis, cell culture.

LEADERSHIP AND MENTORING

- **Stanford University:** Mentored graduate student in RNA-Seq analysis and algorithm development.
- **Boston University:** Recruited, trained, and supervised five undergraduate students to carry out wet-lab and computational studies on cellular response to extracellular matrix mechanics.
- **Other:** As Assistant Debate Coach, lead team of high school students to victory in the Illinois High School Association Debate Meet (2003-2004).

EDUCATION AND BACKGROUND

- Ph.D. in Biomedical Engineering, Boston University, 2011.
- B.S. in Biomedical Engineering, Northwestern University, 2005.
- U.S. Citizen; also fluent in Russian.

GRANTS AND HONORS

- Illumina Integrated Biology Grant Finalist, 2013
- NIH NRSA F32 Postdoctoral Fellowship, 2012 – 2014
- NIH Predoctoral Training Grant in Cardiovascular Biology, 2010 – 2011
- NSF GK-12 Graduate Teaching Fellowship, 2007 – 2008
- BU BME Whitaker Fellowship, 2005 – 2006
- Northwestern Undergraduate Research Grant, Summer 2004

PUBLICATIONS

1. **Sazonova OV**, Zhao Y, Nürnberg ST, Miller C, Pjanic M,Castano VG, Kim JB, Salfati EL, Kundaje AB, Bejerano G, Assimes T, Yang X, Quertermous T. (2015) Characterization of TCF21 downstream target regions identifies a transcriptional pathway linking multiple independent coronary heart disease loci. In press, *PLOS Genetics*.
2. **Sazonova OV,** Raiesdana A, Nuernberg ST, Smith KS, Anaya VI, Quertermous T, Montgomery SB. Differential allele specific expression analysis from RNA-Seq identifies potential gene-by-environment mechanisms of coronary heart disease risk. In preparation for submission to *Genome Research.*
3. **Sazonova OV**, Isenberg BC, Herrmann J, Lee KL, Hartman CD, Valentine AD, Wong JY, Nugent MA. (2015) Extracellular matrix presentation modulates vascular smooth muscle cell mechanotransduction. *Matrix Biology* 41:36-43.
4. **Sazonova OV,** Lee KL, Isenberg BC, Rich CB, Nugent MA, and Wong JY. (2011) Cell-cell interactions mediate the response of vascular smooth muscle cells to substrate stiffness. *Biophysical Journal* 101(3):622-30.
5. Pageau SC, **Sazonova OV,** Wong JY, Soto AM, Sonnenschein C. (2011) The effect of stromal components on the modulation of the phenotype of human bronchial epithelial cells in 3D culture. *Biomaterials* 32(29):7169-80.
6. Lin JB, Isenberg BC, Shen Y, Schorsch K, **Sazonova OV,** Wong, JY. (2012) Poly(N -isopropylacrylamide) grafted from microtextured polydimethylsiloxane for aligned cell sheet engineering. *Colloids and Surfaces B: Biointerface* 99:108-115.
7. **Sazonova OV**, Nugent MA, and Wong JY. (2008) Methods to investigate the effect of matrix mechanics and composition on cell signaling. *Proceedings of the 34th Annual Northeast Bioengineering Conference* 2008.

SELECT CONFERENCE PARTICIPATION

1. **Sazonova OV**, Raiesdana A, Nurnberg ST, Smith KS, Anaya VI, Quertermous T, Montgomery SB. A novel approach for detecting gene-by-environment interactions from RNA-Seq. The Biology of Genomes; May 6-10 2014, Cold Spring Harbor Laboratory, Long Island, NY.
2. Nurnberg ST, Cheng K, Kundu RK, **Sazonova OV**, Carcamo-Orive I, Shankman LS, Raiesdana A, Kundu S, Owens GK, Quertermous T. The CDH-associated transcription factor TCF21 regulates disease-related genes and may contribute to the migration of SMC progenitors to the fibrous cap. Arteriosclerosis, Thrombosis, and Vascular Biology Annual Meeting; May 1-3 2014; Toronto, Canada
3. **Sazonova OV**, Raiesdana A, Nurnberg ST, Smith KS, Anaya VI, Quertermous T, Montgomery SB. Analysis of allele specific expression and transcription factor activity identifies potential gene-by-environment mechanisms of coronary heart disease risk. ASHG Annual Meeting; October 23-26, 2013; Boston, MA.
4. **Sazonova OV**, Lee KL, Isenberg BC, Rich CB, Nugent MA, Wong JY. Vascular smooth muscle cell behavior is jointly regulated by substrate stiffness and cell-cell interactions. Biomedical Engineering Society 2011 Annual Meeting; October 12-15, 2011; Hartford, CT.
5. **Sazonova OV**, Herrmann J, Isenberg BC, Wong JY, Nugent MA. Substrate stiffness and cell-cell interactions regulate vascular smooth muscle cell behavior in an ECM dependent manner. Biomedical Engineering Society 2011 Annual Meeting; October 12-15, 2011; Hartford, CN.
6. **Sazonova OV**, Lee KL, Nugent MA, and Wong JY. Matrix mechanics modulate expression of ECM receptors and contractile markers in VSMCs. Biomedical Engineering Society 2009 Annual Meeting; October 7-10, 2009; Pittsburgh, PA.