

Steven B Smith

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http://stevenbsmith.net

CAREER OBJECTIVES

The ability to use computational and bioinformatic methods to solve clinical problems. The application of mathematical models and computer algorithms to “omic” data to make associations, predict outcomes, or prioritize experimentation. Ideally, the ability to also conduct experimental validation of computational findings.

EDUCATION

University of Maryland, College of Computer, Mathematical, and Natural Sciences

Doctor of Philosophy in Biological Sciences, Graduation: 2017 (Comp. Bio, Bioinformatics, & Genomics)

Mentor: Jacques Ravel, Institute for Genome Sciences, Baltimore, MD

University of Pennsylvania, School of Engineering & Applied Science

Master of Science in Engineering, Graduated August 2011 (Major: Bioengineering)

Thesis Title: Identification of Common Biological Pathways and Drug Targets in Respiratory Viral Infection Using Host mRNA Expression Profiles.

Drexel University, School of Biomedical Engineering, Science & Health Systems

Bachelor of Science in Engineering, Graduated Cum Laude June 2010 (Major: Biomedical Engineering)

PEER REVIEWED PUBLICATIONS

Smith SB and Ravel, J (2016) *The vaginal microbiota, host defense and reproductive physiology*. J Physiol. Accepted Author Manuscript. doi:10.1113/JP271694

Smith SB, Magid-Slav M, Brown JR (2013) *Host Response to Respiratory Bacterial Pathogens as Identified by Integrated Analysis of Human Gene Expression Data*. PLoS ONE 8(9): e75607.

Smith SB, Dampier W, Tozeren A, Brown JR, Magid-Slav M (2012) *Identification of Common Biological Pathways and Drug Targets Across Multiple Respiratory Viruses Based on Human Host Gene Expression Analysis*. PLoS ONE 7(3): e33174.

COMPUTATIONAL & BIOINFORMATIC EXPERIENCE

- Used computational methods to evaluate gene expression data in a variety of computer languages including Python and R; machine learning (Naïve Bayes, Random Forest), clustering, regression, and gene and pathway enrichment analysis. Identified and prioritized genes, proteins, functions, and pathways important in various disease states.
- Investigated host-microbiome interactions using RNA- and DNA-seq approaches. Analysis pipeline included sequence read-alignment using combinations of Tophat/BWA, DESeq, edgeR in addition to Bayesian and machine learning algorithms for estimating model parameters and ranking features.
- Designed/implemented functional algorithms, workflows, and databases using Perl, Linux, and MySQL to make processes automated, repeatable, traceable, and transparent.

LABORATORY EXPERIENCE

- Developed an RNA extraction method to sequence small RNA on Illumina HiSeq 4000 platform.
- Designed experiments for quantifying microRNA and microbial species using qPCR.
- Maintained eukaryotic and prokaryotic cell culture stocks in addition to the design and execution of *in vitro* experiments.

WORK EXPERIENCE

University of Maryland, Baltimore, MD

January 2013-Present

PhD Student- Jacques Ravel Lab

- Studied miRNA host response in vaginal microbiome events using RNA seq.
- Evaluated methods to efficiently extract and sequence RNA from clinical and cell culture samples.
- Designed a custom bioinformatic and computational pipeline to analyze RNA seq data.

Acidophil, LLC, Lutherville, MD

August 2014-Present

Intern

- Assisted company with various SharePoint tasks to help streamline virtual collaboration.
- Performed IP, due diligence and IP research on a myriad of projects to support ongoing efforts.

GlaxoSmithKline Pharmaceuticals, Upper Merion, PA

September 2010-July 2012

Computational Biology Intern

- Computationally discovered common genomic signatures of host responses after exposure to respiratory viruses and bacteria. Identified possible drug targets for follow-up studies.
- Identified potentially repurposed compounds that reverse viral- or bacterial- host gene signature using Connectivity-MAP analysis.
- Analyzed Next Generation Sequencing metagenomic data in diabetic and obese mouse models to elucidate the role of microbiome in chronic disease states.

AstraZeneca Pharmaceuticals, Wilmington, DE

March 2009-September 2009

Research Assistant

- Lead a study that quantified the effects of rat body temperature compensation in whole body plethysmography. Prospective impact to study design considerations during assessment studies.
- Evaluated the safety profile of seven candidate drug compounds *in vivo* using combinations of telemetry, automated blood sampling, and whole body plethysmography.
- Performed jugular vein and carotid artery cannulation surgery to support ongoing safety assessment studies.

Lyophilization Technology, Inc, Warminster, PA

September 2007 to March 2008

Laboratory Technician

- Assisted in formulation and filling of freeze-dried parental pharmaceuticals according to GMPs.
- Performed finished product testing such as Karl Fischer titration for moisture analysis on freeze-dried products to ensure proper moisture extraction for long-term preservation.
- Composed and executed qualification validation protocols and engineering studies to maintain compliance.

SEMINARS & CONFERENCES

Sequence-Based Analysis of Human MicroRNA Expression Associated with Dynamic Vaginal Microbiota. American Society for Microbiology Microbe Conference. Boston, Massachusetts. June 18, 2016.

Identifying Human Host Response Caused by Multiple Viruses. Computational Biology Seminar Series. GlaxoSmithKline Pharmaceuticals, King of Prussia, Pennsylvania. November 15, 2011.

Identification and Characterization of Arabidopsis Mutants with Known miRNA Phenotype. Genetics & Molecular Biology Lab Seminar. University of Pennsylvania, Philadelphia, Pennsylvania. April 21, 2011.

Effects of Varying Body Temperature in Whole Body Plethysmography. Safety Assessment Seminar. AstraZeneca Pharmaceuticals, Wilmington, Delaware. September 22, 2009.