Steven B Smith
sbs@stevenbsmith.net http://stevenbsmith.net

INDUSTRY EXPERIENCE

LabCorp, Baltimore, MD May 2023 - Present
Bioinformatics Scientist

- Design, develop, test, and maintain software, databases and computational & bioinformatic pipelines.
- Develop and apply methods, algorithms, and software to support company products and services.
- Analyze sequencing data using established and newly developed workflows.

Output Biosciences, New York, NY June 2022 - April 2023
Computational Biology Lead

- Designed, executed and compiled statistical analysis reports communicated to leadership (Python).
- Built bioinformatics and computational infrastructure to extract value from raw sample data (AWS, Python, Docker).

Kaleido Biosciences, Lexington, MA August 2021-April 2022
Principal Scientist, Computational Biology

- Instrumental in the discovery of novel therapeutics that modulate the microbiome for the treatment of immunological diseases by using computational and statistical pipelines.
- Lead the design and build of a platform-wide analytical toolbox enabling biologists and chemists to query, integrate, analyze, visualize, and export experimental data (R, RShiny app development).
- Computationally analyzed 16S rRNA, shallow shotgun and RNA sequencing data from mouse and *ex vivo* experiments across multiple project disease areas (R, Python, Linux, AWS).

Teva Pharmaceuticals, West Chester, PA July 2020-August 2021
Principal Computational Biology Data Scientist

- Developed methods to prioritize, predict and evaluate both internal and external disease indication prioritization efforts using AI methods such as Deep Learning and embeddings (Python/TensorFlow).
- Identified candidate clinical biomarkers using genomics, transcriptomics and proteomics from patient data (R, RShiny app development).
- Supported and consulted various on-going translational statistics studies (R, Python).

Personal Genome Diagnostics, Baltimore, MD June 2017-June 2020
Computational Biology Scientist February 2020 - June 2020

- Developed innovative ctDNA NGS-based machine learning and computational methods to detect key genetic cancer signatures in liquid biopsies (Python, R, Linux).
- Responsible for ensuring product and customer requirements are met for several RUO assays.

Bioinformatics Scientist June 2017- February 2020

- Designed both lab and *in silico* studies to evaluate performance of bioinformatic pipeline outputs.
- Managed a team of software engineers to develop NGS bioinformatics pipelines.
- Development Lead delivering a Minimal Residual Disease (MRD) IUO monitoring assay that leveraged both tissue and ctDNA plasma approaches.

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.

COMPUTATIONAL & BIOINFORMATIC EXPERIENCE

- Used computational methods to evaluate and prioritize Next Gen Seq gene expression data, genomics data and proteomics data in a variety of computer languages including **Python** and **R**; implemented **machine learning and AI** techniques to generate hypotheses using **TensorFlow** & **R** (Graph Neural Networks, Random Forest).
- Investigated host-microbiome interactions using **RNA- and DNA-seq** approaches using pipelines implementing Tophat/BWA, DESeq, edgeR and Bayesian and machine learning algorithms.
- Designed/implemented functional algorithms, workflows, and databases using **Docker** along with **Perl, Python, Linux, and SQL** to make processes automated, repeatable, traceable, and transparent. Utilized cloud/distributed computing services such as **AWS**.

LABORATORY EXPERIENCE

- Optimized an RNA extraction method to sequence small RNA on Illumina HiSeq 4000 platform.
- Designed experiments for quantifying microRNA and microbial species using qPCR.
- Executed cell and bacterial culture experiments.

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

Thesis Title: Identification and Characterization of Regulatory miRNAs and mRNAs in the Longitudinal Human Host Response to Vaginal Microbiota.

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

Edwards VL*, **Smith SB**,* (*contributed equally), et al. (2019) *The cervicovaginal microbiota-host interaction modulates Chlamydia trachomatis infection.* mBio, doi:10.1128/mBio.01548-19

Delgado-Diaz, D.J, … **Smith SB**, et al. (2022) *Lactic acid from vaginal microbiota enhances cervicovaginal epithelial barrier integrity by promoting tight junction protein expression.* Microbiome, doi:10.1186/s40168-022-01337-5

Smith SB and Ravel, J (2017) *The vaginal microbiota, host defense and reproductive physiology.* J Physiol, 595: 451–463. 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.