Michael Shaffer, Ph.D.

Postdoctoral Research Associate
Wrighton Lab
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Education

Ph.D.	Computational Bioscience University of Colorado Denver - Anschutz Medical Campus November 2018 *Advisor:* Catherine Lozupone *Dissertation:* Detecting and Understanding Microbiome and Metabolome Interactions via Networks	Denver, CO
B.S.	Bioinformatics, Biology with Molecular Biology Emphasis *magna cum laude* Loyola University Chicago May 2013	Chicago, IL

Professional Experience

2019-Ongoing	Postdoctoral Research Associate	Colorado State University, Fort Collins, CO
2013-2018	Graduate Research Assistant	University of Colorado Denver - Anschutz Medical Campus, Aurora, CO
2011-2013	Research Assistant	Loyola University Chicago, Chicago, IL

Teaching Experience

Summer 2021	Course designer and guest lecturer, Soil Microbiome Research Experience (SOCR 481)	Colorado State University, Fort Collins, CO
April 2021	Workshop speaker, Ohio State University Microbiome Informatics webinar series	Online
Spring 2021	Course designer and instructor of record, Current Methods in Microbial Community Genomics (SOCR 545)	Colorado State University, Fort Collins, CO
July 2020	Instructor for Virtual Multiscale Microbial Dynamics Modeling Summer School	Online
Spring 2016	Teaching Assistant for Research Methods in Biomedical Informatics (CPBS 7712)	University of Colorado Denver - Anschutz Medical Campus, Aurora, CO

Honors/Awards

2009-2013	ExCEL Scholarship, Loyola University
2009-2011	Presidential Scholarship, Loyola University
Fall 2011-Spring 2013	Dean's List
2012-2013	Damen Scholarship, Loyola University
2015-2018	NLM Bioinformatics Training Grant

Fellowships

2012	LUROP Travel Fellowship	Loyola University Chicago
2012-2013	Mulcahy Undergraduate Research Scholar	Loyola University Chicago
Summer 2012	Biology Summer Research Fellowship	Loyola University Chicago
2016	ISME16 Travel Grant	International Society of Microbial Ecology

Leadership

2017	Translational Bioinformatics Year in Review Literature Search Committee
2018	University of Colorado Anschutz Medical Campus Computational Bioscience Program Admissions Committee Student Representative
2020	Front Range Microbiology Symposium Steering Committee (Cancelled due to COVID-19)

Workshops Attended

2015	SSPPS Metabolomics Training Course	Denver, CO
2018	QIIME2 Developers and Teaching Workshop	San Diego, CA

Current Research

Postdoctoral Research Associate – Colorado State University
Mentor: Kelly Wrighton
January 2019 – Ongoing
My work in the Wrighton lab is split into two main areas: software development on a tool that curates annotations of metabolism and an integrative multi-omics project investigating the progression of Salmonella infection and its effect on the gut microbiome in mice. The software development project is based around the tool for the Distillation and Refinement of Annotations of Metabolism (DRAM). DRAM is a genome annotator for (meta)genomes of microbes and viruses but more importantly it distills those annotations to generate visualizations of microbial

function. DRAM for viruses (DRAM-v) is an extension to DRAM that detects auxiliary metabolic genes in viral genomes. My other research project investigating the effects of Salmonella infection progression on the gut microbiome in mice has been highly collaborative. We have worked with experts in Salmonella physiology, metabolomics and proteomics to conduct an experiment where mice infected with Salmonella infection have been sampled daily and have conducted measurements of the microbiome (16S, metagenomic and metatranscriptomic sequencing), metabolome (untargeted LC/MS) and proteome as well as immunological readouts. I have lead the processing and analysis of microbiome measurements as well as the integration of all data types. In the lab I have also had opportunities to mentor graduate students via the teaching of computational skills and help with professional development.

Previous Research

Doctoral Candidate - University of Colorado Denver - Anschutz Medical Campus
Mentor: Catherine Lozupone
June 2014 – December 2018
I focused on improving the quality of correlation based integrative microbiome experiments. I approached this from two angles: improving the statistical power of correlational analyses and using database information to provide biological context for the detected correlations. To address the first point we have developed a tool for finding and summarizing modules of cooccurring microbes or other features called SCNIC (github.com/shafferm/SCNIC). This tool includes the SparCC correlation metric which is designed for compositional data, like we observe in 16S ribosomal RNA microbiome data, as well as traditional correlation metrics. It also uses a novel modularity detection metric to detect groups of tightly cooccurring microbes and detects modules that are enriched in biologically relevant signals. I am most interested in finding associations between the microbiome and the metabolome. To provide biological context for correlations between the microbiome and metabolome, I have used the PICRUSt and KEGG databases in order to determine whether microbes (or modules of microbes) encode genes, or are enriched in genes of a pathway, that can metabolize the associated compounds.

Rotation Student - University of Colorado Denver - Anschutz Medical Campus
Mentor: Christopher Miller
March 2014 – June 2014
During my rotation I sought to first assess quality metrics for metagenomic shotgun sequencing. Then I designed a sequencing simulation to test if treatment of subsets of DNA extracted from total bacterial DNA treated with various restriction enzymes, sequenced and assembled separately and then coassembled could increase bacterial community assembly quality. This is based on the idea that bacterial genomes are made of varying nucleotide compositions and would be differentially digested by restriction enzymes with recognition sites of various nucleotide compositions. This has the potential to both make assembly easier, as only smaller subsets of metagenomic sequencing needs to be assembled de novo, and increase the assembly quality of individual bacterial genomes, as the complexity of assembling the different subsets digested with different restriction enzymes would be reduced.

Rotation Student - University of Colorado Denver - Anschutz Medical Campus
Mentor: Catherine Lozupone

January 2014 – March 2014
While multiple papers analyzing the bacterial content of the stool HIV microbiome, measured via 16S sequencing, had been published at this point, no analyses of the change in functional capabilities as measured by microbial gene content had been presented. We used the, at the time, new tool PICRUSt to predict the gene functional content, in terms of KEGG genes and COGs, to determine changes in abundance of specific genes encoded by bacterial present in our 16S analyses as well as pathways that these genes are a part of. We expanded on the PICRUSt analysis to create total microbial community metabolic networks. Using knowledge in the KEGG database we were able to find reactions encoded by the genes found and used those to create a reaction network. We found areas of the network that were differentially abundant in the stool of HIV infected individuals which lead to functional hypothesis to investigate the effect of microbial community changes in HIV.

Research Assistant – Loyola University Chicago
Mentor: Catherine Putonti
May 2011 – August 2013
My research within the Putonti lab included divergent projects utilizing my skills in bioinformatics and software development. I worked on searching for the viral origin of spacer sequences in bacterial CRISPR systems. Developing fuzzy string matching algorithms in order to find related sequences between viruses and the integrated viral sequence present in CRISPR spacers. I identified regions of genomic and pathogenicity islands in *Neisseria* species and created of heat maps in order to show islands of similarity between divergent species. I also created of evolutionary trees of alphoid sequences in the centromere of human chromosome 21 including the development of scripts to facilitate of the display of trees with 10,000+ nodes.

Publications

Journal Publications

1. **Shaffer M**, Borton MA, McGivern BB, Zayed AA, La Rosa SL, Solden LM, et al. DRAM for distilling microbial metabolism to automate the curation of microbiome function. Nucleic Acids Res. 2020;48:8883–900.2.
2. Li SX, Sen S, Schneider JM, Xiong K-N, Nusbacher NM, Moreno-Huizar N, et al. Gut microbiota from high-risk men who have sex with men drive immune activation in gnotobiotic mice and in vitro HIV infection. PLoS Pathog. 2019;15.3.
3. **Shaffer M**, Thurimella K, Quinn K, Doenges K, Zhang X, Bokatzian S, et al. AMON: annotation of metabolite origins via networks to integrate microbiome and metabolome data. BMC Bioinformatics. 2019;20:1–11.4.
4. Armstrong AJ, **Shaffer M**, Nusbacher NM, Griesmer C, Fiorillo S, Schneider JM, et al. An exploration of Prevotella-rich microbiomes in HIV and men who have sex with men. Microbiome. 2018;8:1–2.5.
5. Bolyen E, Rideout JR, Dillon MR, Bokulich NA, Abnet CC, Al-Ghalith GA, et al. QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science. Nature Publishing Group; 2018.6.
6. Kang D-W, Ilhan ZE, Isern NG, Hoyt DW, Howsmon DP, **Shaffer M**, et al. Differences in fecal microbial metabolites and microbiota of children with autism spectrum disorders. Anaerobe. 2018;49:121–31.7.

7. **Shaffer M**, Lozupone C. Prevalence and source of fecal and oral bacteria on infant, child, and adult hands. mSystems. 2018;3.8.
8. **Shaffer M**, Armstrong AJS, Phelan VV, Reisdorph N, Lozupone CA. Microbiome and metabolome data integration provides insight into health and disease. Transl Res. 2017;189.9.
9. Li SX, Armstrong AJS, Neff CP, **Shaffer M**, Lozupone CA, Palmer BE. Complexities of Gut Microbiome Dysbiosis in the Context of HIV Infection and Antiretroviral Therapy. Clin Pharmacol Ther. 2016;99.10.
10. Putonti C, Nowicki B, **Shaffer M**, Fofanov Y, Nowicki S. Where does Neisseria acquire foreign DNA from: an examination of the source of genomic and pathogenic islands and the evolution of the Neisseria genus. BMC Evol Biol. 2013;13:184.

Presented Talks

1. **Shaffer, M.**, Putonti, C. Detecting the Source of Infections Past. Proceedings of the 2013 Midwest Ecology and Evolution Conference (Notre Dame, IN), 2013

2. **Shaffer, M.,** Putonti, C. Detecting the Source of Infections Past. Proceedings of the Undergraduate Research & Engagement Symposium (Chicago, IL), 2013

3. **Shaffer, M.**, Lozupone, C. Integrating Data in a Microbiome Context. Proceedings of the 2014 Rocky Mountain Bioinformatics Conference (Aspen, CO), 2012

4. **Shaffer, M.**, Lozupone, C. Exploring the functional effect of chronic untreated HIV on the human gut microbiome. CPBS Rotation Talk 1 (Denver, CO), 2014.

5. **Shaffer, M.**, Miller, C. Combining Molecular and Computational Techniques to Improve Metagenomic Assembly Quality. CPBS Rotation Talk 2 (Denver, CO), 2014.

6. **Shaffer, M.**, Lozupone, C. Multi-omic Analysis of the Human Nasal Microbiome. Research Update Talk (Denver, CO). 2015.

7. **Shaffer, M.**, Lozupone, C. Improving Integrative Analyses of Microbiome and Metabolome Data to Discover Functional Effects of Microbiomes on Disease. CPBS Comprehensive Examination (Denver, CO). 2015.

8. **Shaffer, M.**, Lozupone, C. SCNIC: finding and summarizing modules of correlated observations. Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis (New York, NY). 2016

9. **Shaffer, M.**, Lozupone, C. Discovering the Contribution of the Gut Microbiome to the Plasma Metabolome. Proceedings of the 2017 Rocky Mountain Bioinformatics Conference (Aspen, CO), 2017

10. **Shaffer, M.**, Lozupone, C. SCNIC: Collapsing modules of cooccuring microbes to increase statistical power. QIIME2 Developers Workshop (San Diego, CA), 2018.

Poster Presentations

1. **Shaffer, M.,** Putonti, C. Investigating the Prevalence of CRISPRs in Bacterial Genomes.

Proceedings of the 2012 Great Lakes Bioinformatics Conference (Ann Arbor, MI), 2012: B49.

2. **Shaffer, M.,** Putonti, C. Investigating the Prevalence of CRISPRs in Bacterial Genomes. Proceedings of the 2012 Rocky Mountain Bioinformatics Conference (Aspen, CO), 2012.

3. **Shaffer, M.,** Putonti, C. Detecting the Source of Infections Past. Proceedings of the 2013 Midwest Ecology and Evolution Conference (Notre Dame, IN), 2013.

4. **Shaffer, M.,** Putonti, C. Detecting the Source of Infections Past. Proceedings of the Undergraduate Research & Engagement Symposium (Chicago, IL), 2013.

5. Baltrusaitis, D., **Shaffer, M.,** Kelly, J., and Putonti, C. Evaluating the occurrence of the CRISPR/Cas systems in the environment. Proceedings of the 2013 Midwest Ecology and Evolution Conference (Notre Dame, IN), 2013.

6. **Shaffer, M.**, Lozupone, C. SCNIC: finding and summarizing modules of correlated observations. Proceedings of ISME 16 (Montreal, CA), 2016.

7. **Shaffer, M.**, Lozupone, C. SCNIC: finding and summarizing modules of correlated observations. Department of Medicine Research Day 2016 (Denver, CO), 2016.

8. **Shaffer, M.**, Lozupone, C. SCNIC: finding and summarizing modules of correlated observations. Proceedings of the 2016 Rocky Mountain Bioinformatics Conference (Aspen, CO), 2016.

9. **Shaffer, M.**, Lozupone, C. Discovering the Contribution of the Gut Microbiome to the Plasma Metabolome. Proceedings of the 2017 Rocky Mountain Bioinformatics Conference (Aspen, CO), 2016.

10. **Shaffer, M.**, Reisdorph, N., Lozupone, C. Providing genomic context for microbiome and metabolome crosscorrelations. Proceedings of ISME 17 (Leipzig), 2018.

11. **Shaffer, M.**, Sabag-Daigle, A., Borton ,MA., Wu, J., Wyosocki, V., Ahmer, BMM., and Wrighton, KC. Metagenomics Increases the Power of Metatranscriptomics: Building Understanding of the Dynamics of Salmonella Infection in Mice. Proceddings of the 2019 Salmonella GRC (Easton, MA), 2019.