## **KEITH ARORA-WILLIAMS**

I'm interested in developing user-friendly tools that identify significant patterns in complex data and visualize them in ways that are both quantitative and intuitive.

#### CONTACT

★ karoraw1@gmail.com

**y** @karoraw1

github.com/karoraw1

**2**01-421-1770



2016

2018

2016

2013

2009

2009

2007

#### **EDUCATION**

PhD, Environmental Health and Engineering
Johns Hopkins University

Paltimore, MD

Advisor: Sarah Preheim

Title: Microbial Genes, Genomes and Taxa Associated With Key

Aspects Of Pathogenesis and Biogeochemical Cycles

MS, Environmental Sciences

Johns Hopkins University 

◆ Baltimore, MD

Advisor: Sarah Preheim

BE, Biomedical Engineering

SUNY: Stony Brook University 
◆ Stony Brook, NY

GPA: 3.50 (Cum Laude), Deans List 7 semesters

CUNY: Baruch College • New York, NY

- **GPA:** 3.85

- Transfer: from BS in Finance

### LANGUAGE SKILLS

**Expertise:** Python,

pandas, R, bash, Matlab

**Proficient:** Ruby, C/C++, Markdown, Git/Github,

SPSS, Perl



#### RESEARCH EXPERIENCE

under the Bay Bridge near Annapolis, MD.

### **Doctoral Research Projects**

Preheim Lab, EHE@JHU

2020 | 2018 Biogeochemical cycling potential of the Chesapeake Bay water column microbiome

- Assisted with pumping, filtering, sampling and transportation of water samples from field site
- Prepared amplicon and whole genome short read libraries from environmental samples and bacterial cell cultures.
- Developed bioinformatic pipelines for amplicon sequence-variant calling, performed genome binning, and taxonomic/functional annotation.
- Developed novel statistical methods for identifying significant spatiotemporal boundaries and synchronous abundance changes within the Chesapeake Bay microbiome.
- Provided preliminary data and written material for multiple grant applications
- See publications in prep #1, 3

2020 | 2019

The effects of intermittent aeration at different time scales on water column microbial community gene expression in Rock Creek

- Prepped, organized and managed a team of 15 student volunteers to participate in 3 weeks of daily sampling
- Trained/mentored 3 Masters & Undergraduate students in filtration, cell culture, DNA extraction, data management and analysis methods.
- Developed a flow cytometry-based bacterial cell staining and counting protocol

		- Provided preliminary data a	grant application		
2018 	•	Distribution of microbial populations affiliated anaerobic biogeochemical			
2016	1	cycling in Mystic Lake			
	1	<ul> <li>Developed bioinformatics pigenomes</li> </ul>	peline for producing and curating	metagenome-assembled	
	П	- Implemented multivariable optimization method for reactive transport model			
2020	•	Pathogen sequence signatures in persistent and Collaboration w/ Dr. Margaret			
 2018	ı	recurrent infections of Campylobacter spp. in Peruvian infants  Collaboration W/ Dr Kosek at University			
		<ul> <li>Used traditional statistical methods to quantify the effect sizes of host factors and quantify infection frequency in 300 subject cohort incidence data</li> <li>Utilized existing tools i.e. core-genome MLST, pangenomics, and small polymorphisms detection to identify enriched sequence signatures among relapsing infection strains</li> <li>Identified high incidence rate of multi-Campylobacter species coinfection</li> <li>See publication in prep #2</li> </ul>			
2015	•	Assistant Research Scien	tist <u>NYU Center for G</u>	enomics & Systems Biology	
2013		<ul> <li>Technical lead for <u>PowerBridgeNY</u> clean energy technology development team</li> <li>Developed and implemented a protocol for recursively isolating and culturing high-lipid algae cells using cell sorting to achieve adaptive laboratory evolution</li> <li>Performed all aspects of Arabidopsis cultivation, as well as imaging for projects as needed</li> </ul>			
2013	•	Research Aide	Cardiac Cell Engineering I	Lab, Stony Brook University	
2013   2012		- Developed software in MatL		ace with patch clamp hardware in	
Ī		- Developed software in MatL	ab Real-Time Workshop to interfa	ace with patch clamp hardware in	
2012	•	<ul> <li>Developed software in MatL order to deliver automated of</li> <li>Amgen Scholar</li> <li>Cultured microbial isolates a</li> </ul>	ab Real-Time Workshop to interfa	Division, NASA JPL/CalTech	
2012		<ul> <li>Developed software in MatL order to deliver automated of</li> <li>Amgen Scholar</li> <li>Cultured microbial isolates a</li> </ul>	ab Real-Time Workshop to interface optical stimulation to human embed planetary Protection and performed DNA extraction, and ned 16S rRNA sequences mapped	Division, NASA JPL/CalTech	
2012 2012		<ul> <li>Developed software in MatL order to deliver automated of Amgen Scholar</li> <li>Cultured microbial isolates at Vetted, assembled, and align</li> <li>Summer Intern</li> <li>Dissected, prepped, fixed, and align</li> </ul>	ab Real-Time Workshop to interface optical stimulation to human embed planetary Protection and performed DNA extraction, and ned 16S rRNA sequences mapped	Division, NASA JPL/CalTech evolutionary distances  Advanced Microscopy ssue samples for imaging	
2012 2012		<ul> <li>Developed software in MatL order to deliver automated of Amgen Scholar</li> <li>Cultured microbial isolates at Vetted, assembled, and align</li> <li>Summer Intern</li> <li>Dissected, prepped, fixed, and align</li> </ul>	ab Real-Time Workshop to interface optical stimulation to human embound performed DNA extraction, and ned 16S rRNA sequences mapped  U. of Sussex Centre form mounted various Drosophila tis 2D & 3D with confocal laser scan	Division, NASA JPL/CalTech evolutionary distances  Advanced Microscopy ssue samples for imaging	
2012 2012 2011		<ul> <li>Developed software in MatL order to deliver automated of Amgen Scholar</li> <li>Cultured microbial isolates at Vetted, assembled, and align</li> <li>Summer Intern</li> <li>Dissected, prepped, fixed, at Imaged fluorescent tissue in Life Sciences Fellow</li> <li>Transfected HeLa and skelet natural promoters with differences automated in the control of the control of</li></ul>	Planetary Protection and performed DNA extraction, and need 16S rRNA sequences mapped  U. of Sussex Centre for and mounted various Drosophila tis 2D & 3D with confocal laser scan	Division, NASA JPL/CalTech plification, and purification. evolutionary distances  Advanced Microscopy sue samples for imaging ning and wide-field microscope  Lab, University of Missouri smids containing a synthetic and	
2012 2012 2011		<ul> <li>Developed software in MatL order to deliver automated of Amgen Scholar</li> <li>Cultured microbial isolates at Vetted, assembled, and align</li> <li>Summer Intern</li> <li>Dissected, prepped, fixed, at Imaged fluorescent tissue in Life Sciences Fellow</li> <li>Transfected HeLa and skelet natural promoters with differences automated in the control of the control of</li></ul>	Planetary Protection and performed DNA extraction, and need 16S rRNA sequences mapped  U. of Sussex Centre for and mounted various Drosophila tise 2D & 3D with confocal laser scan  Duan and myoblast cells with custom plase rent fluorescent reporters eeding, whelping, handling, and D	Division, NASA JPL/CalTech plification, and purification. evolutionary distances  Advanced Microscopy sue samples for imaging ning and wide-field microscope  Lab, University of Missouri smids containing a synthetic and	



### **Publications and Patents**

# Microbial Community Assembly in the Chesapeake Bay: Beyond Seasonal Cycles and Spatial Gradients

- Arora-Williams, K., Zhang, Y., Secor, M., Unger, M., Sakowski, E., Xia, M., Ellis, J., Preheim, S.
- Status: In prep (#1)

#### Sulfur-oxidizing microbes are prevalent in the water column of the Chesapeake Bay

- Arora-Williams, K., Holder, C., Sakowski, E., Ellis, J., Gnanadesikan, A., Preheim, S.
- Status: In prep (#3)

# Host factors and genomic correlates of persistent Campylobacter jejuni and coli infection isolates in a pediatric cohort.

- Arora-Williams, K., Schiaffino, F., Gray, H., Parker, C., Olortegui, M., Peñataro-Yori, P., François, R., Preheim, S., Kosek, M.
- Status: In prep (#2)

# Capturing in situ Virus-Host Range and Interaction Dynamics through Gene Fusion with epicPCR.

- Sakowski, E., Arora-Williams, K., Tian, F., Zayed, A., Zablocki, O., Sullivan, M., Preheim, S., (2020) *Nature Microbiology*.
- Role: analysis support
- Status: In revision

## Contribution of time, taxonomy and selective antimicrobials to antibiotic and multidrug resistance in wastewater bacteria.

- Gray, H., Arora-Williams, K., Young, C., Bouwer, E., Davis, M., Preheim, S. (2020) Environmental Science and Technology
- Role: analysis support
- Status: Resubmitted

#### Dynamics of microbial populations mediating biogeochemical cycling in a freshwater lake.

Arora-Williams, K., Olesen, S., Scandella, B., Delwiche, K., Spencer, S., Myers, E., Abraham, S.,
 Sooklal, A., Preheim, S. *Microbiome* 6, 165 (2018). 10.1186/s40168-018-0556-7

#### Systems and methods for selecting cellular strains

- Birnbaum, K. and Arora-Williams, K., 2018, US20180058987A1
- Status: Pending

### 晃 Posters, Talks, & Workshops

Genomic variation among isolates from persistent Campylobacter infections in a pediatric cohort

- Arora-Williams, K., Schiaffino, F., Gray, H., François, R., Parker, C., Olortegui, M., Prehiem, S., Penataro-Yori, P., Kosek, M.
- Lightning Talk, Campylobacter and Helicobacter and Related Organisms. Belfast

2019

2019

Attendee, M3 Mid-Atlantic Microbiome Meetup. Johns Hopkins University, Baltimore

<ul> <li>Microbial and Water Quality Data Define Emergent Habitats in an Estuarine Water Column</li> <li>Arora-Williams, K., Holder, C., Sakowski, E., Preheim, S.</li> </ul>				
Destan Forting and all traditional Forting and Descaped Detact Delting and				
- <b>Poster,</b> Environmental Health and Engineering Research Retreat. Baltimore				
2018 • Attendee, M3 Mid-Atlantic Microbiome Meetup, University of Maryland, College Park				
2016 Participant, The First Traditional Anvi'o Colloquium Workshop. International Symposium on Microbial Ecology, Montreal				
2013 Genetic and Metabolic Profiles of Microbes Isolated from the Mars Exploration Rovers.	f Microbes Isolated from the Mars Exploration Rovers.			
<ul> <li>Arora-Williams, K., Schubert, W., Smith S., Childers, S., Paszczynski, A., Benardini, J.</li> <li>Poster, American Society for Microbiology General Meeting, Denver</li> </ul>				
Teaching and Awards	Teaching and Awards			
2018 TA and Grader for Environmental Health & Engineering Systems Design	TA and Grader for Environmental Health & Engineering Systems Design			
<ul> <li>Presented analytic techniques frequently for public decision making. Emphasis is on mathematical programming techniques e.g. linear, integer, mixed-integer, and multi-object programming. Spring term, graduate-level course</li> </ul>	ive			
2018 TA and Grader for Data Analytics in Environmental Health and Engineering				
- Presented approaches to model formulation, application, and interpretation in fields of computational statistics, data mining and machine learning. Fall term, graduate-level course	<b>2</b> .			
2016 National Science Foundation Graduate Research Fellowship: Honorable Mention				
2015 Recipient of M. Gordon Wolman Fellowship from Johns Hopkins University				
2015 Volunteer Judge in New York City Science and Engineering Fair				
2013 Tutor for Educational Opportunity Program at Stony Brook University				
2012 - Provided 1-on-1 supplemental lessons relating to Engineering Statics and Dynamics courses				