

Schuyler D. Smith

Ph.D. Candidate - Bioinformatics and Computational Biology
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Education

Ph.D.	Bioinformatics and Computational Biology	ABD
	Iowa State University of Science and Technology, Ames, IA	
M.S.	Quantitative Genetics	2015
	Texas A&M University, College Station, TX	
B.S.	Genetics	2012
	Iowa State University of Science and Technology, Ames, IA	

Experience

Iowa State University of Science and Technology	2017 - pres.
Genomics and Environmental Research in Microbial Systems Lab, Ames, Iowa Graduate Research Assistant - Ph.D.	
University of Wisconsin-Madison	2015 - 2016
Potato Breeding and Genetics Laboratory, Madison, Wisconsin Graduate Research Assistant - Ph.D.	
United States Department of Agriculture - ARS	2014
Arid-Land Agricultural Research Center. Maricopa, Arizona Biological Science Technician (Internship)	
Texas A&M University	2013 - 2015
Maize Breeding and Genetics Program, College Station, Texas Graduate Research Assistant - M.S.	
Monsanto Company	2012
Huxley Research Station. Huxley, Iowa Maize Breeding Intern	
DuPont Pioneer	2011
Willmar Research Station. Willmar, Minnesota Maize Product Trait Development Intern - 6 month	
United States Department of Agriculture - ARS	2010 - 2011
Soybean Genomics Laboratory - Graham Lab. Ames, Iowa Undergraduate Research Assistant	

Publications

- Schuyler D. Smith**, Choi, J., Howe, A. *Diversity of Antibiotic Resistance genes and Transfer Elements-Quantitative Monitoring (DARTE-QM): a method for sequencing microbiome functional profiles*. Preparing submission. 2021.
- Yu, W., Lawrence, N. C., Sooksa-nguan, T., **Smith, S.D.**, Tenesaca, C., Howe, A. C., Hall, S. J. *Microbial linkages to soil biogeochemical processes in a poorly drained agricultural ecosystem*. Soil Biology and Biochemistry, 108228. March, 2021.
- Schuyler D. Smith**, Colgan, P., Yang, F., Rieke, E.L., Soupier, M.L., Moorman, T.B., Allen, H.K., Howe, A. *Investigating the dispersal of antibiotic resistance associated genes from manure application to soil and drainage waters in simulated agricultural farmland systems*. PLOS One. journal.pone.0222470 September, 2019.
- Schuyler D. Smith** *phylosmith: an R-package for reproducible and efficient microbiome analysis with phyloseq-objects*. Journal of Open Source Software. 10.21105/joss.01442 June, 2019.
- Choi, J., Rieke, E.L., Moorman, T.B., Soupier, M.L., Allen, H.K., **Smith, S.D.**, Howe, A. *Practical implications of erythromycin resistance gene diversity on surveillance and monitoring of resistance*. FEMS microbiology ecology. 10.1093/femsec/fiy006 January, 2018.
- Schuyler D. Smith**, Heffner, E., Murray, S.C. *Molecular analysis of genetic diversity in a Texas maize breeding program*. Maydica. cabdirect.org/abstract/201 2015.

Posters

- Smith, S.D.** *phylosmith: an R-package for reproducible and efficient microbiome analysis with phyloseq-objects*. Presented at the 27th ISMB/18th ECCB. 2019, July 21-25. Basel, Switzerland.
- Smith, S.D.**, Villanueva, P.E., Fukami, T., Howe, A. *Co-Occurrence Networks Reveal Key OTUs in Flower Nectar Microbiomes Across Dispersal Treatments*. Presented at the 17th ISME. 2018, August 12-17. Leipzig, Germany & the NSF Research Traineeship (NRT) Annual Meeting. 2018, September 27-28. Arlington, Virginia.
- Smith, S.D.**, Howe, A. *Examining Antibiotic Resistance Gene (ARG) horizontal transfer and introduction through farmland soil microbiomes as a result of modern farming practices*. Presented at the 3rd Annual Front Rang Computational & Systems Biology Symposium: Microbiome. 2017, June 12-13. Fort Collins, Colorado.
- Smith, S.D.**, Endelman, J.B. *Genotyping by Sequencing for Autotetraploid Species*. Presented at the 5th International Conference on Quantitative Genetics. 2016, June 12-17. Madison, Wisconsin. & the 11th Annual National Association of Plant Breeders Meeting. 2016, August 15-18. Raleigh, North Carolina.

Software

- phylosmith: an R-package for reproducible and efficient microbiome analysis with phyloseq-objects.
- ssBLAST: an R-package of efficient c++ functions to parse BLAST outputs and wrangle corresponding FASTQ/FASTA files.
- schuylR: an R-package of various functions I've written, that I often find useful.

Skills

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| • R | • Shell (BASH) | • L ^A T _E X | • Linux |
| • C++ | • SQL | • Markdown | • Windows |
| • Python | • html | • Git | • MacOS |

Workshops Instructed

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| • Data Carpentry: Genomics
George Washington University, Washington, D.C. | 2020 |
| • Data Carpentry: Ecology
Merck & Co Upper Gwynedd, PA | 2019 |
| • Data Carpentry: Ecology
Merck & Co Online | 2020 |
| • Girls in Science Initiative
Science Center of Iowa, Des Moines, IA | 2019 |
| • Data Analyses for Metagenomic Advances in Microbial Ecology
Kellogg Research Station, Hickory Corners, MI | 2017 & 2018 |
| • Introduction to Data Analysis for Biology Graduate Students.
Iowa State University, Ames, IA | 2017 & 2018 |
| • Iowa State BCB Data Analysis Language Workshops
Introduction to Unix | 2017 & 2018 |
| • Iowa State BCB Data Analysis Language Workshops
Introduction to Python | 2017 |

Awards, Fellowships, Honors, & Recognitions

Iowa State University of Science and Technology

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| • Selected P3 representative for 2018 NSF-NRT Annual Meeting | 2018 |
| • College of Engineering Interdepartmental Research Fellow | 2017 - 2020 |
| • NSF-NRT Predictive Plant Phenomics Fellow | 2017 - 2018 |
| • Academic Recognition Award | 2008 - 2012 |

Texas A&M University

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| • Willie May Harris Fellow | 2013 - 2014 |
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Certifications

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| • Data Carpentry - Course Instructor | 2017 |
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