# Schuyler D. Smith

Ph.D. Candidate - Bioinformatics and Computational Biology
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## Education

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

## Experience

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

# 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., Soupir, 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., Soupir, 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

- R
- C++
- Python

- Shell (BASH)
- SQL
- html

- LaTeX
- Markdown
- Git

- Linux
- Windows
- MacOS

## Workshops Instructed

- Data Carpentry: Genomics
  George Washington University, Washington, D.C.      2020
- Data Carpentry: Ecology
  Merck & Co Upper Gwynedd, PA      2019
  Merck & Co Online      2020
- Girls in Science Initiaive
  Science Center of Iowa, Des Moines, IA      2019
- Data Analyses for Metagenomic Advances in Microbial Ecology
  Kellog 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
  Introduction to Python      2017

## Awards, Fellowships, Honors, & Recognitions

Iowa State University of Science and Technology
- 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
- Willie May Harris Fellow      2013 - 2014

## Certifications

- Data Carpentry - Course Instructor      2017