

# Schuyler D. Smith, Ph.D.

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## Education

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|---|------|
| <b>Ph.D. Bioinformatics and Computational Biology</b> | 2021 |
| Iowa State University, Ames, IA                       |      |
| <b>M.S. Quantitative Genetics</b>                     | 2015 |
| Texas A&M University, College Station, TX             |      |
| <b>B.S. Genetics</b>                                  | 2012 |
| Iowa State University, Ames, IA                       |      |

## Experience

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|   |                |
|---|----------------|
| <b>Senior Computational Scientist, Bioinformatics</b>   | 2021 – present |
| Agronomic and Environmental Sciences<br>Nutrien Ag Solutions - Champaign, Illinois<br><i>Full-stack bioinformatician, in charge of building pipelines in NextFlow and setting up cloud-computing environments for AWS and GCP, developing custom software and packages for analyses, and analyses of microbiome data to present to stakeholders.</i>      |                |
| <b>Graduate Research Assistant - Ph.D.</b>  | 2017 – 2021    |
| Genomics and Environmental Research in Microbial Systems Laboratory<br>Iowa State University - Ames, Iowa<br><i>Implemented and maintained pipeline for processing sequencing data on a SLURM HPCC, conducted research on environmental antibiotic-resistance genes, harmful algal blooms, and developed R-packages for enabling microbiome research.</i> |                |
| <b>Graduate Research Assistant - Ph.D.</b>  | 2015 – 2016    |
| Potato Breeding and Genetics Laboratory<br>University of Wisconsin - Madison - Madison, Wisconsin<br><i>Developed a pipeline for processing NGS sequencing data and SNP-calling for auto-tetraploid crops, performed GWAS, and investigated ML methods for imputation of auto-tetraploid genotypes.</i>   |                |
| <b>Biological Science Technician - Internship</b>   | 2014           |
| Arid-Land Agricultural Research Center<br>United States Department of Agriculture - Maricopa, Arizona<br><i>Evaluated high-throughput phenotyping platforms for crop traits such as canopy cover, plant height, and seed counting.</i>  |                |
| <b>Graduate Research Assistant - M.S.</b>   | 2013 - 2015    |
| Maize Breeding and Genetics Program<br>Texas A&M University - College Station, Texas<br><i>Conducted a molecular characterization of the Texas maize germplasm and oleic-acid screening using near-infrared spectroscopy.</i>   |                |

## Applicable Skills

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|--------|--------------------------------|---------------------------------|
| R      | AWS / GCP / Slurm              | Markdown                        |
| python | NextFlow / SnakeMake / AirFlow | HTML / CSS                      |
| C++    | CI / CD (Git / Jenkins)        | L <sup>A</sup> T <sub>E</sub> X |
| BASH   | Docker / Singularity           | Image J                         |
| SQL    | Shiny / Dash / Power BI        | Linux / Windows / MacOS         |

## Software

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**phylosmith**: R package for reproducible and efficient microbiome analysis with phyloseq-objects.

**NextFlow Workflows**: Nextflow Workflows I've built for various bioinformatics analyses.

**smartchip\_analyzer**: C++ program for processing data from a SmartChip qPCR.

**weather\_api**: python package with modules for accessing a weather-data API.

**ssBLAST**: R package wrapping functions written in C++ to parse BLAST outputs and manipulate corresponding FASTQ/FASTA files.

**simple.dada**: R package for streamlined implementation of the dada2 processing pipeline.

**schuyIR**: R package of various functions that I often find useful.

**linux\_box\_sync**: BASH program to sync a local Box directory on a Linux machine to the cloud.

**hpcc\_R\_setup**: BASH program to setup R on the MSU-HPCC.

## Selected Publications

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**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*. Communications Biology 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*. 2019.

**Schuyler D. Smith** *phylosmith: an R-package for reproducible and efficient microbiome analysis with phyloseq-objects*. 2019.

**Schuyler D. Smith**, Heffner, E., Murray, S.C. *Molecular analysis of genetic diversity in a Texas maize breeding program*. 2015.

## Workshops Taught

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|---|-------------|
| Data Carpentry: Genomics, Oklahoma State University, online   | 2021        |
| Software Carpentry: Shell, Git, R for Reproducible Scientific Analysis, University of Idaho, online | 2021        |
| Data Carpentry: Ecology, Merck & Co., online  | 2020        |
| Data Carpentry: Genomics, George Washington University, Washington, D.C.                            | 2020        |
| Data Carpentry: Ecology, Merck & Co., Upper Gwynedd, PA   | 2019        |
| Girls in Science Initiative, Science Center of Iowa, Des Moines, IA                                 | 2019        |
| Introduction to Data Analysis, 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        |
| Explorations in Data Analyses for Metagenomic Advances in Microbial Ecology                         | 2017 & 2018 |