# Schuyler D. Smith, Ph.D.

DuPont Pioneer - Willmar, Minnesota

Willmar Research Station

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#### Education

#### Ph.D. **Bioinformatics and Computational Biology** 2021 Iowa State University, Ames, IA Characterization of environmental microbiomes impacted by lowa agriculture. M.S. **Plant Breeding** 2015 Texas A&M University, College Station, TX Molecular Characterization of the Texas Maize Breeding Program. B.S. 2012 **Genetics** Iowa State University, Ames, IA Experience **Senior Computational Scientist, Bioinformatics** 2022 – present Nutrien Ag Solutions - Champaign, Illinois Agronomic and Environmental Sciences Full-stack bioinformatician, in charge of building data-pipelines and setting up cloud-computing environments for AWS and GCP, developing custom software and packages for analyses of microbiome data to present to stakeholders. 2017 - 2021Graduate Research Assistant - Ph.D. Iowa State University - Ames, Iowa Genomics and Environmental Research in Microbial Systems Laboratory Developed pipeline for processing 16S sequencing data on a SLURM HPCC, conducted research on antibiotic-resistance genes, harmful algal blooms, and developed an R-packages for enabling microbiome research. 2015 - 2016Graduate Research Assistant - Ph.D. University of Wisconsin - Madison - Madison, Wisconsin Potato Breeding and Genetics Laboratory Developed a pipeline for processing NGS sequencing data and SNP-calling for auto-tetraploid crops, GWAS, and ML methods for auto-tetraploid genotyping. **Biological Science Technician - Internship** 2014 United States Department of Agriculture - Maricopa, Arizona Arid-Land Agricultural Research Center Evaluated high-throughput phenotyping platforms and image analysis. **Graduate Research Assistant - M.S.** 2013 - 2015 Texas A&M University - College Station, Texas Maize Breeding and Genetics Program Molecular characterization of Texas maize germplasm. **Maize Breeding Intern** 2012 Monsanto Company - Huxley, Iowa **Huxley Research Station** Maize Product Trait Development Intern - 6 month 2011

### Applicable Skills

| python | AWS / GCP / SLURM       | Shiny / Dash / Power BI |
|--------|-------------------------|-------------------------|
| R      | NextFlow / SnakeMake    | Markdown / HTML / CSS   |
| C      | AirFlow / MetaFlow      | latex                   |
| Shell  | CI / CD (Git / Jenkins) | Image J                 |
| SQL    | Docker / Singularity    | Linux / Windows / MacOS |

## Software

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

NextFlow Workflows: Workflows I am building for various bioinformatics analyses.

**smartchip\_analyzer**: C<sup>-</sup> 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<sup>-</sup> 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.

#### Selected Publications

Valeria Velásquez-Zapata, **Schuyler D. Smith**, Priyanka Surana, Antony V. E. Chapman, Roger P. Wise. *Transcriptome-based host epistasis and pathogen co-expression in barley-powdery mildew interactions.* bioR<sub>x</sub>iv preprint 2023.

**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.

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*. 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 phyloseg-objects. 2019.

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

# Workshops Taught

| <u> </u>  |             |
|---|-------------|
| Data Carpentry: Genomics, Oklahoma State University, online   |             |
| Software Carpentry: Shell, Git, R for Reproducible Scientific Analysis, University of Idaho, online |             |
| Data Carpentry: Ecology, Merck & Co., online  |             |
| Data Carpentry: Genomics, George Washington University, Washington, D.C.                            | 2020        |
| Data Carpentry: Ecology, Merck & Co., Upper Gwynedd, PA   |             |
| Girls in Science Initiaive, 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                              |             |
| Explorations in Data Analyses for Metagenomic Advances in Microbial Ecology                         |             |