

Schuyler D. Smith, Ph.D.

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Education

Ph.D. Bioinformatics and Computational Biology	2021
Iowa State University, Ames, IA	
<i>Characterization of environmental microbiomes impacted by Iowa agriculture.</i>	
M.S. Quantitative Genetics and Plant Breeding	2015
Texas A&M University, College Station, TX	
<i>Molecular Characterization of the Texas Maize Breeding Program.</i>	
B.S. Genetics	2012
Iowa State University, Ames, IA	

Experience

Senior Computational Scientist, Bioinformatics	January, 2022 – present
Nutrien Ag Solutions Agronomic and Environmental Sciences Champaign, Illinois	
<ul style="list-style-type: none">• Project lead for development end-to-end NGS data pipelines for metagenomic samples.• Built NextFlow workflows in cloud-computing environments on AWS and GCP.• Optimized existing workflows, resulting in a 40% reduction in processing time.• Authored custom software in C++ to assist wet-lab team processing qPCR data.• Authored packages in both R and python for advanced microbiome data analysis.• Project lead for soil-biome report generation platform.• Developed models and algorithms for product placement using biome metrics.• Project lead for development of metagenomic results discovery database.• Developed analyses and presentations for stakeholders.• Mentored junior colleagues and summer interns.	
Graduate Research Assistant - Ph.D.	January, 2017 – December, 2021
Iowa State University GERMS Laboratory Ames, Iowa	
<ul style="list-style-type: none">• Developed pipeline for processing 16S sequencing.• Authored R-packages for microbiome data analysis.• Published research on antibiotic-resistance gene dispersal in environmental systems.• Conducted research on harmful algal bloom biome-community and predictors.• Published research evaluating large-scale marker detection for microbiome genes.• Mentored junior lab members.• Instructor for Data & Software Carpentries workshops.	
Graduate Research Assistant - Ph.D.	June, 2015 – December, 2016
University of Wisconsin - Madison Potato Genetics Laboratory Madison, Wisconsin	
<ul style="list-style-type: none">• Developed pipeline for NGS data and SNP-calling for autotetraploid crops.• Authored R-packages for ML methods for autotetraploid genotyping.	
Biological Science Technician - Internship	June, 2014 - December, 2014
USDA-ARS Arid-Land Agricultural Research Center Maricopa, Arizona	
<ul style="list-style-type: none">• Evaluated use of image-based high-throughput phenotyping platforms.	
Graduate Research Assistant - M.S.	January, 2013 - May, 2015
Texas A&M University Maize Genetics Laboratory College Station, Texas	
<ul style="list-style-type: none">• Published research characterizing markers of Texas maize germplasm.	
Maize Breeding Intern	May, 2012 - September, 2012
Monsanto Company Huxley Research Station Huxley, Iowa	
Maize Product Trait Development Intern – 6 month	June, 2011 - December, 2011
DuPont Pioneer Willmar Research Station Willmar, Minnesota	

Applicable Skills

python	AWS / GCP / SLURM	Shiny / Dash / Power BI
R	NextFlow / SnakeMake	Markdown / HTML / CSS
C++	AirFlow / MetaFlow	L ^A T _E X
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++ 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.

schuylerR: 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*. bioRxiv 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 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

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

Conferences Attended

NSF Research Traineeship (NRT) Annual Meeting Arlington, Virginia	2018
International Symposium on Microbial Ecology Leipzig, Germany	2018
Bioinformatics and Computational Biology Symposium: The Past and Future of Bioinformatics and Computational biology Ames, Iowa	2018
Front Range Computational & Systems Biology Symposium: Microbiome Fort Collin, Colorado	2017

Bioinformatics and Computational Biology Symposium: The Breadth and Depth of Bioinformatics Analysis Ames, Iowa	2017
National Association of Plant Breeders Meeting Raleigh, North Carolina	2016
International Conference on Quantitative Genetics Madison, Wisconsin	2016
American Seed Trade Association Annual Meeting Chicago, Illinois	2015
NCCC: Potato Breeding and Genetics Technical Committee Chicago, Illinois	2015

Graduate Coursework Completed

Ph.D. Bioinformatics and Computational Biology:

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| • Bioinformatic Algorithms | • Fundamentals of Predictive Plant Phenomics | • Biometric Procedures in Plant Breeding |
| • Statistical Bioinformatics | | |
| • Bioinformatic Systems | • Tools for Reproducible Research | • Advanced Plant Breeding |
| • Genomic Sciences | | |
| • Linear Mixed Models | • Plant Genetics | • Selection Theory |

M.S. Plant Breeding and Quantitative Genetics:

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| • Quantitative Genetics | • Plant Breeding I | • Molecular and Quantitative Genetics in Plant Breeding |
| • Statistics in Research I | • Plant Breeding II | |
| • Statistics in Research II | • Experimental Design | • Host-Plant Resistance |

Awards, Fellowships, Honors, & Recognitions

Iowa State University

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| • College of Engineering Interdepartmental Research Fellow | 2017 - 2021 |
| • Selected P3 representative for 2018 NSF-NRT Annual Meeting | 2018 |
| • 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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