Schuyler D. Smith, Ph.D.

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Education

Ph.D. **Bioinformatics and Computational Biology** 2021
Iowa State University, Ames, IA
Characterization of environmental microbiomes impacted by Iowa agriculture.

M.S. **Quantitative Genetics and Plant Breeding** 2015
Texas A&M University, College Station, TX
Molecular Characterization of the Texas Maize Breeding Program.

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
- 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
- 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
- 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 Cente | Maricopa, Arizona
- 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
- 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	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++ 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.
schuylR: 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 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	2017
Explorations in Data Analyses for Metagenomic Advances in Microbial Ecology	2017 & 2018

Conferences Attended

International Phytobiomes Conference | Denver, Colorado	2022
International Society for Computational Biology | Basel, Switzerland	2019
Midwest Bioinformatics Conference | Kansasy City, Missouri	2019
Great Lakes Bioinformatics Conference | Madison, Wisconsin	2019
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	2018
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:

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

M.S. Plant Breeding and Quantitative Genetics:

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

Awards, Fellowships, Honors, & Recognitions

Iowa State University

- 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

- Willie May Harris Fellow 2013 - 2014