

Sarah Stevens

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Education

University of Wisconsin - Madison

PhD Candidate - Microbiology Doctoral Training Program - 2012-Present

SciMed GRS Fellow

MDTP Recruiting Committee - **2014-2015**

MDTP Steering Committee - **2015-2016**

University of Illinois Urbana - Champaign

Bachelor of Science - Molecular and Cellular Biology - 2007-2011

Minor in Informatics

James Scholar Honors

Research

University of Wisconsin - Madison, [McMahon Lab](#)

Graduate Research Assistant - 2012-Present

Obtaining and classifying reference genomes (composite genomes from metagenomes and single-cell genomes) for unculturable but common freshwater bacteria and understanding how the related populations change through time using our metagenomic time series.

University of Illinois Urbana - Champaign, [Metcalf Lab](#)

Visiting Researcher - 2011-2012

Assembled genomes from isolates belonging to the archaeal genus *Methanosarcina* and analyzed shared genomic content of members of this genus.

University of Illinois Urbana - Champaign, [Whitaker Lab](#)

Undergraduate Research Assistant - 2010-2011

Studied insertion sequences in *Sulfolobus islandicus* in an independent project, Culturing archaea, organized sample/culture database, cleaned-up and prepped lab equipment.

Organizations

[Computational Biology, Ecology, and Evolution \(ComBEE\)](#) group

Co-Chair/Founder - 2014-Present

- [ComBEE](#) provides an opportunity for researchers to discuss new computational tools and learn bioinformatics skills together.

- [ComBEE Python Study Group](#) - **2014-Present**

- [ComBEE R Study Group](#) - **2015-Present**

[Software Carpentry](#)

Instructor - 2015-Present

[Data Carpentry Genomics Hack-a-thon](#)

Contributor - Mar. 23-25, 2015

Teaching

Software Carpentry Workshop - University of Wisconsin - Madison

Instructor - Jan. 14-15, 2016, Jun. 08-09, 2016

Helper - Jan. 13-16 2015, Jun. 3-4, 2015

Data Carpentry Workshop - University of Wisconsin - Madison

Helper - Jan. 11-12 2016, Jun. 01-02 2016

Software Carpentry Workshop - University of Wisconsin - Milwaukee

Instructor - Apr. 25-26, 2016

Software Carpentry Workshop - Northwestern University

Instructor - Nov. 10-11 2015

Bioinformatics Basics: Microbial Ecology and Evolution - Illinois Mathematics and Science Academy Intersession

Instructor/Course Designer - Jan. 2015

Microbiology 304: Biology of Microorganisms Laboratory - University of Wisconsin - Madison

Teaching Assistant/Instructor - Fall 2013

Selected Presentations

Stevens, S. L. R., Garcia, S. L., ... McMahon, K. D. Tracking Distinct Freshwater Populations Through Time by Mapping Metagenomes to Single-cell Genomes (Poster Presentation). DOE Joint Genome Institute User Meeting 2016. Walnut Creek, CA. <https://goo.gl/ShUQVn>

Stevens, S. L. R., Bendall, M. L., Chan, L.-K., Malfatti, S., Schwientek, P., Tremblay, J., ... McMahon, K. D. Malmstrom, R. R. Tracking Microbial Populations Through Time Using Single-cell Genomes and Metagenomics. UW Center for Limnology Seminar. December 2015. Madison, WI. <https://goo.gl/0ge2LZ>

Stevens, S. L. R., Bendall, M. L., Chan, L.-K., Malfatti, S., Schwientek, P., Tremblay, J., ... McMahon, K. D. Malmstrom, R. R. Genome-wide and Gene-specific Selective Sweeps in Freshwater Bacterial Populations Revealed Using Metagenomics. 14 Symposium Society for Aquatic Microbial Ecology. August 2015. Uppsala, Sweden <https://goo.gl/RcrxhJ>

Stevens, S. L. R., Bendall, M. L., Chan, L.-K., Malfatti, S., Schwientek, P., Tremblay, J., ... McMahon, K. D. Malmstrom, R. R. Genome-wide Selective Sweeps in Natural Bacterial Populations Revealed by Time-series Metagenomics. 15th International Symposium on Microbial Ecology. August 2014. Seoul, South Korea. <https://goo.gl/6iunz0>

Publications

Bendall, M. L.*, **Stevens, S. L. R.***, Chan, L.-K., Malfatti, S., Schwientek, P., Tremblay, J., Schackwitz, W., Martin, J., Pati, A., Bushnell, B., Froula, J., Kang, D., Tringe, S. G., Bertilsson, S., Moran, M. A., Shade, A., Newton, R. J., McMahon, K. D., Malmstrom, R. R. (2016). Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. ISMEJ. doi:10.1038/ismej.2015.241 **featured article** *Equal contributors

Garcia, S. L.*, **Stevens, S. L. R.***, Crary, B., Martinez-Garcia, M., Stepanauskas, R., Woyke, T., Tringe, S. G., Andersson, S., Bertilsson, Malmstrom, R. R., McMahon, K. D. (*prepared for submission*). Contrasting patterns of genome-level diversity across distinct co-occurring freshwater bacterial populations. *Equal contributors
