

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

Determining the forces that shape population structure and how wild bacterial populations change through time in lakes as a model system using reference genomes (composite genomes from metagenomes and single-cell genomes) for unculturable but common freshwater bacteria and metagenomic timeseries.

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, Cultured 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**

Oral Presentations

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. JF Crow Institute for the Study of Evolution Seminar Series. October 2015. Madison, WI. <https://goo.gl/oSnDYG>

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>

Poster 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., ... McMahon, K. D. Malmstrom, R. R. Dynamics of Sequence-Discrete Bacterial Populations Inferred Using Metagenomes (Poster Presentation). 15th International Symposium on Microbial Ecology. August 2014. Seoul, South Korea. <https://goo.gl/qsYL32>

Stevens, S. L. R., Bendall, M. L., ... McMahon, K. D. Malmstrom, R. R. Dynamics of Sequence-Discrete Bacterial Populations Inferred Using Metagenomes (Poster Presentation). SciMed GRS Poster Session 2014. September 2014. Madison, WI.

Stevens, S. L. R., Bendall, M. L., ... McMahon, K. D. Malmstrom, R. R. Dynamics of Sequence-Discrete Bacterial Populations Inferred Using Metagenomes (Poster Presentation). DOE Joint Genome Institute User Meeting 2014. Walnut Creek, CA. <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

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