

# 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

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## 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.

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## Organizations

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

*Co-Chair - 2014-Present*

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

[ComBEE Python Study Group](#)

*Chair - 2014-Present*

[ComBEE R Study Group](#)

*Chair - 2015-Present*

[Software Carpentry](#)

*Instructor - 2015-Present*

Data Carpentry Genomics Hack-a-thon

Contributor - **Mar. 23-25, 2015**

DOE Joint Genome Institute

Intern/Affiliate - **Jan. 2015-Mar. 2015**

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## 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**

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## 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.

**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.

**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>

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## 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>

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## 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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