# Sarah Stevens

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## Education

University of Wisconsin - Madison
*PhD Candidate - Microbiology Doctoral Training Program* - **2012-Present**
SciMed GRS Fellow

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

Molecular Microbial Ecology and Evolution (MoMiEE) focus group
*Co-Chair* - **2014-Present**
MoMiEE provides an opportunity for researchers to discuss new computational tools and learn bioinformatics skills together. In addition, I lead python study group for those interesting in learning python.

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

McMahon Git Workshop
*Instructor* - **July 2015**

Software Carpentry Workshop - University of Wisconsin - Madison
*Helper* - **Jan. 13-16 2015** , **Jun. 3-4, 2015**

Bioinformatics Basics: Microbial Ecology and Evolution - Illinois Mathematics and Science Academy Intersession
*Instructor* - **Jan. 2015**

Microbiology 304: Biology of Microorganisms Laboratory - University of Wisconsin - Madison
*Teaching Assistant/Instructor* - **Fall 2013**

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## Presentations

**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 (Oral Presentation). 15th International Symposium on Microbial Ecology. August 24, 2014. Seoul, South Korea. https://goo.gl/6iunz0

**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 24, 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. Sept. 03, 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

**Stevens, S. L. R.** and K. D. Malmstrom. Complementing Metagenomes with Single Amplified Genomes (Poster Presentation). Raper Symposium 2013. University of Wisconsin - Madison.

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## Publications

Bendall, M. L.*, **Stevens, S. L. R.***, Chan, L.-K., Malfatti, S., Schwientek, P., Tremblay, J., ... Malmstrom, R. R. (*in review at ISMEJ*). Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. *Equal contributors

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