

# Sarah Stevens

[Download PDF](#) – [sstevens2@wisc.edu](mailto:sstevens2@wisc.edu) – [sarah.lr.stevens@gmail.com](mailto:sarah.lr.stevens@gmail.com) – [sarahlrsteven.info](http://sarahlrsteven.info)

---

## 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

---

## 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

[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*

---

## Teaching

Software Carpentry Workshop - University of Wisconsin - Madison

*Instructor* - **Jan. 14-15, 2015**

Software Carpentry Workshop - Northwestern University

*Instructor* - **Nov. 10-11 2015**

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**

---

## 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. 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 (Oral Presentation). 15th International Symposium on Microbial Ecology. August 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 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>

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

---

## Publications

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

---

