# 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 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

 $Undergraduate\ Research\ Assistant$  -  ${f 2010-2011}$ 

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 - 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

## **Teaching**

Software Carpentry Workshop - University of Wisconsin - Milwaukee

Instructor - Apr. 25-26, 2016

Software Carpentry Workshop - University of Wisconsin - Madison

Instructor - Jan. 14-15, 2016

Software Carpentry Workshop - Northwestern University

Instructor - Nov. 10-11 2015

Git Workshop

Instructor - July 2015, Jan. 7 2015

Software Carpentry Workshop - University of Wisconsin - Madison

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

Data Carpentry Workshop - University of Wisconsin - Madison

Helper - Jan. 11-12 2016

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.

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 <a href="https://goo.gl/RcrxhJ">https://goo.gl/RcrxhJ</a>

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*). Genome level exploration of abundant and uncultivated freshwater bacteria reveals distinct and dynamic populations. \*Equal contributors

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