

Sarah Stevens

Webpage – sarah.lr.stevens@gmail.com – [CV weblink](#)

Education

- 2012-2018 (expected) PhD, Microbiology Doctoral Training Program;**
University of Wisconsin - Madison
SciMed GRS Fellow
MDTP Recruiting Committee - **2014-2015**
MDTP Steering Committee - **2015-2016**
- 2007-2011 Bachelor of Science - Molecular and Cellular Biology;**
University of Illinois Urbana - Champaign
Minor in Informatics
James Scholar Honors

Research Experience

University of Wisconsin - Madison, [McMahon Lab](#)

Graduate Research Assistant - **2012-Present**
Server Administrator - *2014-2017*

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 uncultivated but common freshwater bacteria and metagenomic time series from several lakes.

University of Illinois Urbana - Champaign, [Metcalf Lab](#)

Laboratory Technician/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.

Publications

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. (*accepted at ISME Journal*). Contrasting patterns of genome-level diversity across distinct co-occurring freshwater bacterial populations. *Equal contributors

He, S., **Stevens, S. L. R.**, Chan, L.-K., Bertilsson, S., Glavina del Rio, T., Tringe, S. G., Malmstrom, R. R., McMahon, K. D. (2017). Ecophysiology of Freshwater Verrucomicrobia Inferred from Metagenome-Assembled Genomes. mSphere. doi:[10.1128/mSphere.00277-17](https://doi.org/10.1128/mSphere.00277-17)

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](https://doi.org/10.1038/ismej.2015.241) **featured article**

*Equal contributors

Organizations

Software Carpentry and Data Carpentry

Instructor - **2015-Present**

- **DC Genomics Hack-a-thon Contributor** - **Mar. 23-25, 2015**

Computational Biology, Ecology, and Evolution (ComBEE) group

Founder/Co-Chair - **2014-2017**

- **ComBEE** provides an opportunity for researchers to discuss new computational tools and learn bioinformatics skills together.

- **ComBEE Python Study Group** - **2014-2017**

- **ComBEE R Study Group** - **2015-2017**

DOE Joint Genome Institute

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

Teaching

Software Carpentry Workshops

University of Wisconsin - Madison

- *Instructor* - **Jan. 14-15, 2016, Jun. 08-09, 2016, Jan. 12-13, 2017**

- *Helper* - **Jan. 13-16, 2015, Jun. 3-4, 2015, Aug. 29-30, 2016, Oct. 24-25, 2016, Jun. 28-29, 2017, Aug. 30-31, 2017**

Federal Reserve Bank, Chicago - *Instructor* - **Aug. 2-3, 2017**

University of Wisconsin - Milwaukee - *Instructor* - **Apr. 25-26, 2016**

Northwestern University - *Instructor* - **Nov. 10-11, 2015**

Data Carpentry Workshops

University of Wisconsin - Madison

- *Instructor* - **Jan. 10-11, 2017, Aug. 22-23, 2017**

- *Helper* - **Jan. 11-12, 2016, Jun. 01-02, 2016, Jun. 19-20, 2017**

ComBEE Anvio Workshop

University of Wisconsin - Madison

- *Instructor* - **May. 24, 2017**

ComBEE Git/Github Workshop

University of Wisconsin - Madison

- *Instructor* - **Mar. 2-3, 2017**

McMahon Lab Git Workshop

University of Wisconsin - Madison

- *Instructor* - **July 2015**

Bioinformatics Basics Intersession

Illinois Mathematics and Science Academy

- *Instructor/Course Designer* - **Jan. 2015**

Microbiology 304

University of Wisconsin - Madison

- *Teaching Assistant/Instructor* - **Fall 2013**

Oral Presentations

Stevens, S. L. R. Starting Your Own Study Group. Rebecca J. Holz series in Research Data Management. October 2016. Madison, WI. [Link to Webpage/Slides](#)

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. [Link to Slides](#)

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. [Link to Slides](#)

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 [Link to Slides](#)

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. [Link to Slides](#)

Poster Presentations

Stevens, S. L. R., Egan, R., Malmstrom, R.R., McMahon, K. D. Comparative Genomics of Selected Bacterial Populations from Several Freshwater Bog Lakes. 2017 Microbial Population Biology Gordon Research Conference. July 2017. Andover, NH. [Link to Poster](#)

Stevens, S. L. R., Egan, R., Malmstrom, R.R., McMahon, K. D. Comparative Genomics of Selected Bacterial Populations from Several Freshwater Bog Lakes. 2017 Microbial Population Biology Gordon Research Seminar. July 2017. Andover, NH. [Link to Poster](#)

Stevens, S. L. R., Garcia, S. L., ... McMahon, K. D. Contrasting Patterns fo Genome-level Diversity across Distinct Co-occurring Populations. 16th International Symposium on Microbial Ecology. August 2016. Montreal, Canada. [Link to Poster](#)

Stevens, S. L. R., Garcia, S. L., ... McMahon, K. D. Tracking Distinct Freshwater Populations Through Time by Mapping Metagenomes to Single-cell Genomes. DOE Joint Genome Institute User Meeting 2016. Walnut Creek, CA. [Link to Poster](#)

Stevens, S. L. R., Bendall, M. L., ... McMahon, K. D. Malmstrom, R. R. Genome-wide and Gene-specific Selective Sweeps in Freshwater Bacterial Populations Revealed Using Metagenomics. 2015 Microbial Population Biology Gordon Research Conference. July 2015. Andover, NH. [Link to Poster](#)

Stevens, S. L. R., Bendall, M. L., ... McMahon, K. D. Malmstrom, R. R. Dynamics of Sequence-Discrete Bacterial Populations Inferred Using Metagenomes. 15th International Symposium on Microbial Ecology. August 2014. Seoul, South Korea. [Link to Poster](#)

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

Awards

UW-Madison Dept. of Bacteriology Travel Award - **Spring 2017**

UW-Madison Dept. of Bacteriology Betley-Allen Fellowship - **2016-2017**

UW-Madison Graduate School Travel Award - **Fall 2015**

UW-Madison Dept. of Bacteriology Travel Award - **Spring 2014**

Proficiencies

Bioinformatics

Blast, BBtools, Metabat, Anvi'o, MCL, Phylosift, CheckM

Other Computational

Bash, Python, R, Git, Markdown, Docker, HTCondor, UGE, Slurm, Microsoft Office Suite, Adobe Illustrator, SQL, openRefine

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