# 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

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

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

## 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 Carpen- University of Wisconsin - Madison

try Workshops - 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 Work- University of Wisconsin - Madison

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

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

ComBEE Anvio Work- University of Wisconsin - Madison

shop - Instructor - May. 24, 2017

ComBEE Git/Github University of Wisconsin - Madison

Workshop - Instructor - Mar. 2-3, 2017

McMahon Lab Git University of Wisconsin - Madison

Workshop - 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 Genespecific 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 Computa- Bash, Python, R, Git, Markdown, Docker, HTCondor, UGE, Slurm, Mi-

tional crosoft Office Suite, Adobe Illustrator, SQL, openRefine

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