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

Stevens, S. L. R., Kuzak, M., Martinez, C., Moser, A., Bleeker, P., Galland, M. (*in prep*). Building a local community of practice in scientific programming for life scientists.

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. (Online 08 December 2017). Contrasting patterns of genome-level diversity across distinct co-occurring freshwater bacterial populations. ISMEJ. doi:10.1038/s41396-017-0001-0 *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. 2014-Mar. 2014

Teaching

Software Carpen-

University of Wisconsin - Madison

try Workshops

- *Instructor* - Jan. 14-15, 2016, Jun. 08-09, 2016, Jan. 12-13, 2017, Jan. 10-11, 2018

- *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 Ba- Sics IntersessionIllinois 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

Sarah Stevens - sarahlrstevens@gmail.com - sarahlrstevens.info