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 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

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

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

Organizations

Computational Biology, Ecology, and Evolution (ComBEE) group

Co-Chair/Founder - 2014-Present

- ComBEE provides an opportunity for researchers to discuss new computational tools and learn bioinformatics skills together.
- ComBEE Python Study Group 2014-Present
- ComBEE R Study Group 2015-Present

Software Carpentry and Data 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

ComBEE Git/Github Workshop - University of Wisconsin - Madison Instructor - Mar. 2-3, 2017

Software Carpentry Workshop - 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

Data Carpentry Workshop - University of Wisconsin - Madison Instructor - Jan. 10-11, 2017

Software Carpentry Instructor Training - University of Wisconsin - Madison *Helper* - Oct. 24-25, 2016

Data Carpentry Workshop - University of Wisconsin - Madison

Helper - Jan. 11-12 2016, Jun. 01-02 2016

Software Carpentry Workshop - University of Wisconsin - Milwaukee

Instructor - Apr. 25-26, 2016

Software Carpentry Workshop - Northwestern University

Instructor - Nov. 10-11 2015

McMahon Lab Git Workshop

Instructor - July 2015

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. https://goo.gl/0ge2LZ

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. https://goo.gl/oSnDYG

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. 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. Contrasting Patterns fo Genome-level Diversity across Distinct Co-occurring Populations. 16th International Symposium on Microbial Ecology. August 2016. Montreal, Canada. https://goo.gl/8JGS52

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. 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. 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. 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. https://goo.gl/6iunz0

Awards

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**

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