

Shengwei Hou

COMPUTATIONAL BIOLOGIST · BIOINFORMATICIAN

Fuhrman Lab, 3616 Trousdale Parkway AHF 230, USC, Los Angeles, CA 90089

□ (+1) 213-740-5759 | □ housw2010@gmail.com | □ www.shengweihou.com | □ shengwei.hou@hotmail.com



Education

FuhrmanLab, Marine Microbial Ecology, University of Southern California

Los Angeles, United States

PostDoc - RESEARCH ASSOCIATE IN BIOINFORMATICS

Apr. 2018 - present

- “Computational Biogeochemical Modeling of Marine Ecosystems (CBIOMES)” supervised by Prof. Jed A. Fuhrman

Freiburg Institute for Advanced Studies (FRIAS), Freiburg University

Freiburg, Germany

POSTDOCTORAL RESEARCHER IN BIOINFORMATICS

Oct. 2017 - Feb. 2018

- “Genome-Wide Map Pairwise sRNA-RNA Interactions in Staphylococcaceae aureus” supervised by Prof. Wolfgang R. Hess

Cyanolab, Freiburg University

Freiburg, Germany

Ph.D. IN BIOINFORMATICS

Sep. 2013 - Apr. 2018

- “Genomic and transcriptomic Analyses of Marine Microorganisms” supervised by Prof. Wolfgang R. Hess

- Ph.D. Defense Grading: Dissertation: 1.0, Examination: 1.0, Overall: 1.0 (scale 5.0-1.0).

XuLab, Institute of Hydrobiology, Chinese Academy of Sciences

Wuhan, China

MASTER OF MOLECULAR GENETICS

2009.09-2013.06

- “HetR Binding Site Upstream of patA Is Required for Heterocyst Patterning” supervised by Prof. Xudong Xu
- Master Defense Grading: 93.4 (scale 0.0-100.0).
- GPA: 3.38/4.0

Southwest University, China

Chongqing, China

BACHLOR OF BIOLOGY, MAJORING IN BIOLOGY AND BIOTECHNOLOGY

2005.09-2009.07

- “Cloning of IFN- γ from Newcastle Disease Virus(NDV) Stimulated Swine Lymphocytes” supervised by Prof. Huamao Du
- GPA (overall): 3.55/4.0
- GPA (major): 3.74/4.0

Conferences & Workshops

2019 CBIOMES Annual Meeting at Simons Foundation

New York, United States

UNPOSTER: “GENOME-RESOLVED MICROBIAL DYNAMICS DURING A COASTAL PHYTOPLANKTON BLOOM”

29th - 31st May. 2019

- Attended the second annual meeting of CBIOMES project
- Described the microbial succession during a coastal phytoplankton bloom

2019 “Speeding Up Science” in Environmental-Omics: a hackathon for compiling reproducible Jupyter/Binder workflows

Davis, United States

SELECTED PARTICIPANT FOR DEVELOPING REPRODUCIBLE BINDER WORKFLOWS

8th - 10st May. 2019

- MAGstats - an example binder project for visualizing basic information of metagenome assembled genomes (MAGs)
- DE Analysis - an example binder project for doing exploratory and differential expression analysis using DESeq2

2018 CBIOMES Annual Meeting at Simons Foundation

New York, United States

UNPOSTER: “COMPARATIVE METAGENOMICS AND METATRANSCRIPTOMICS OF MARINE MICROBIAL COMMUNITIES”

21st - 23rd May. 2018

- Attended the first annual meeting of CBIOMES project
- Introduced a draft metagenomic and metatranscriptomic data analysis pipeline

2017 ELIXIR-IIB Training Programme on Machine Learning

San Michele all'Adige, Italy

PARTICIPANT: “MACHINE LEARNING FOR BIOLOGISTS”

4th - 7th Sept. 2017

- Adopted basic machine learning skills for genomic and transcriptomic data analyses

2016 MaCuMBA “Marine Microbiome: Discovery & Innovation” International Conference

Berlin, Germany

POSTER: TAXONOMIC AND TRANSCRIPTIONAL DYNAMICS OF THE MICROBIAL COMMUNITY DURING A TRICHODESMIUM BLOOM

27th - 30th Jun. 2016

- Presented the primary analysis results of metagenomic and metatranscriptomic data sets

2015 Black Forest Summer School on “NGS data for phylogenetics”

Feldberg, Germany

POSTER: DIFFERENTIAL RNA-SEQ ANALYSIS OF MICROBIAL POPULATIONS (META-DRNA-SEQ)

14th - 17th Sept. 2015

- Presented the mdRNA-Seq results

2014 EU MaCuMBA Project General Assembly

Cadiz, Spain

PRESENTATION: METATRANSCRIPTOME ANALYSIS OF MARINE MICROBIAL POPULATIONS USING dRNA-SEQ APPROACH

- Introduced the dRNA-Seq method and its potential application in marine microbial communities

2013 Training Course of Bernstein Center Freiburg, Department of Neurobiology and Neurotechnology

Freiburg, Germany

PARTICIPANT: "SCIENTIFIC PROGRAMMING IN PYTHON"

14th Oct. - 1st Nov. 2013

- Learned basic Python syntax and scientific libraries

2013 International PHOTO.COMM Training Workshop

Freiburg, Germany

PARTICIPANT: "BIOINFORMATIC ANALYSIS OF TRANSCRIPTOMIC AND GENOMIC DATASETS IN METABOLIC CONTEXT"

8th - 12th Sept. 2013

- Adopted basic bioinformatics data analysis skills

Teaching Assistantships

"Genetics" and "Microbiology" given by Prof. Wolfgang R. Hess at Freiburg University

Freiburg, Germany

TEACHING ASSISTANT

2016 - 2017 semester

"Bioinformatics" for Bachelor Students given by Dr. Wolfgang Maier at Freiburg University

Freiburg, Germany

TEACHING ASSISTANT

Jun. 20th - Jul. 15th 2016

- Prepared course materials for image processing module

- Gave one-day lecture on image processing using CellProfiler

- Answered questions and solved problems during the hands on session

"Python Crash Course" for Biologists given by Dr. Björn Grüning at Freiburg University

Freiburg, Germany

TEACHING ASSISTANT

15th - 18th Dec. 2015

- Prepared the Jupyter notebooks for this course

- Answered questions and solved problems during the hands on session

Publications

Note: [§]Co-First Author, * Corresponding Author

Jens Georg[§], David Lalaouna[§], **Shengwei Hou**, Steffen C. Lott, Isabelle Caldelari, Stefano Marzi, Wolfgang R. Hess*, Pascale Romby*. The power of cooperation: Experimental and computational approaches in the functional characterization of bacterial sRNAs. (*under review*)

Andrew M. Long^{§*}, **Shengwei Hou**[§], J. Cesar Ignacio-Espinoza1, Jed A. Fuhrman. Benchmarking metagenomic marine microbial growth prediction from codon usage bias and peak-to-trough ratios. (*under review*)

Jin-Long Shang, Min Chen, **Shengwei Hou**, Tao Li, Yi-Wen Yang, Qi Li, Hai-Bo Jiang, Guo-Zheng Dai, Zhong-Chun Zhang, Wolfgang R. Hess and Bao-Sheng Qiu. Survival strategies of the free-living desiccation-tolerant cyanobacteria: Insights from comparative genomic and transcriptomic analyses. *Environ Microbiol.* 2019 Feb;21(2):845-863.

Jonna E. Teikari, Rafael V. Popin, **Shengwei Hou**, Matti Wählsten, Wolfgang R. Hess and Kaarina Sivonen*. Insight into the genome and brackish water adaptation strategies of toxic and bloom-forming Baltic Sea *Dolichospermum* sp. UHCC 0315. *Sci Rep.* 2019 Mar 20;9(1):4888.

Shengwei Hou, Manuel Brenes, Alicia M. Muro-Pastor, Wolfgang R. Hess*. CRISPR-Cas systems in multicellular cyanobacteria. *RNA Biol.* 2018 Aug 15:1-12.

Xiaoming Tan[§], **Shengwei Hou**[§], Kuo Song, Jens Georg, Stephan Klähn, Xuefeng Lu*, Wolfgang R. Hess*. The Primary Transcriptome of the Fast-Growing Cyanobacterium *Synechococcus elongatus* UTEX 2973. *Biotechnol Biofuels.* 2018 Aug 4;11:218.

Weichao Huang*, Ilka Haferkamp, Bernard Lepetit, Carolina Río Bártulos, **Shengwei Hou**, Wolfgang Jeblick, Peter G. Kroth. Reduced vacuolar β-1,3-glucan synthesis affects carbohydrate metabolism, plastid homeostasis and structure in *Phaeodactylum tricornutum*. *Proc. Natl. Acad. Sci.* April 18, 2018, ahead of print

Jonna E. Teikari, David P. Fewer, Rashmi Shrestha, **Shengwei Hou**, Niina Leikoski, Minna Hämäläinen, Asko Simojoki, Wolfgang R. Hess, and Kaarina Sivonen*. Strains of the toxic and bloom-forming *Nodularia spumigena* (cyanobacteria) can degrade methylphosphonate and release methane. *The ISME J* 2018 Feb 14:1.

Shengwei Hou[§], Mario López-Pérez[§], Ulrike Pfreundt, Natalia Belkin, Kurt Stüber, Bruno Huettel, Richard Reinhardt, Ilana Berman-Frank, Francisco Rodriguez-Valera and Wolfgang R. Hess*. Benefit from decline: The primary transcriptome of *Alteromonas macleodii* str. Te101 during *Trichodesmium* demise. *The ISME J* 2018 Jan 15:1

Dan Miller, Ulrike Pfreundt, **Shengwei Hou**, Steffen Lott, Wolfgang R. Hess and Ilana Berman-Frank*. Winter Mixing Induces Reshuffling and Impacts Gene Expression of Marine Microbial Populations in the Gulf of Aqaba. *Aquat Microb Ecol* 80:223-242.

Jonna E. Teikari[§], **Shengwei Hou**[§], Matti Wählsten, Wolfgang R. Hess* and Kaarina Sivonen*. Comparative genomics of the Baltic Sea toxic cyanobacteria *Nodularia spumigena* UHCC 0039 and its response on varying salinity. *Frontiers in microbiology* 2018 Mar 8;9:356

Tao Zhu^{\$}, **Shengwei Hou^{\$}**, Xuefeng Lu*, Wolfgang R. Hess*. Draft Genome Sequences of Nine Cyanobacterial Strains from Diverse Habitats. *Genome Announc.* 2017 Mar 2;5(9). pii: e01676-16.

Ulrike Pfreundt^{\$}, Dina Spungin^{\$}, **Shengwei Hou**, Björn Voß, Ilana Berman-Frank, Wolfgang R. Hess*. Genome of a giant bacteriophage from a decaying *Trichodesmium* bloom. *Marine Genomics* 2017 Feb 22. pii: S1874-7787(17)30033-8.

Shengwei Hou, Ulrike Pfreundt, Dan Miller, Ilana Berman-Frank, Wolfgang R. Hess*. mdRNA-Seq analysis of microbial communities. *Sci. Rep.* 2016 Oct 19;6:35470.

Shengwei Hou, Fang Zhou, Shan Peng, Hong Gao and Xudong Xu*. The HetR-binding site that activates expression of *patA* in vegetative cells is required for normal heterocyst patterning in *Anabaena* sp. PCC 7120. *Sci. Bull.* 2015 Jan;60(2):192-201.

Yun Wang, **Shengwei Hou**, Fei Ke and Hong Gao*. Bibliometric analysis of research on microcystins in China and worldwide from 1991 to 2011. *Desalination and water treatment* 53(1):1-12

Zhiwei Hou, Yun Wang, Hong Gao* and **Shengwei Hou***. The principle of dRNA-seq and its applications in prokaryotic transcriptome analyses. *Yi Chuan* 2013 Aug;35(8):983-91 (in Chinese).

Ye Du, Yan Cai, **Shengwei Hou** and Xudong Xu*. Identification of the HetR-recognition sequence upstream of hetZ in *Anabaena* sp. Strain PCC 7120. *J. Bacteriol.* 2012 May;194(9):2297-306.

Professional Service

I'm a frequent reviewer of *Microbiome*, and occasional reviewer of *Nature Microbiology*, *ISME J.*, *Freshwater Biology* and *Marine Genomics*. I collaborated with Prof. Jed A. Fuhrman in several peer review services under the permission of journal editors. Please check my publon profile for a summary of recorded peer review activities.