

## EDUCATION

**Massachusetts Institute of Technology - Woods Hole Oceanographic Institution,**  
Cambridge/Woods Hole, Massachusetts, USA

*Ph.D., Biological Oceanography*

2011–2016

- Cumulative GPA: 4.4/5.0
- Thesis: [Productivity, Metabolism and Physiology of Free-Living Chemoautotrophic \*Epsilonproteobacteria\*](#)
- Advisor: Dr. Stefan M. Sievert

**Mount Allison University,** Sackville, New Brunswick, Canada

*Bachelor of Science, First Class Honours with Distinction, Biology*

2003–2008

- Cumulative GPA: 3.8/4.0; Minor in Chinese Studies
- Honours Thesis: Endophytic Fungi of Liverworts (*Bryophyta*) in a Copper-Contaminated Environment
- Advisors: Dr. Felix J. Bärlocher and Dr. Robert Thompson

## PROFESSIONAL EXPERIENCE

**University of Southern California, Fuhrman Lab;** Los Angeles, CA, USA

*Postdoctoral Scholar - Research Associate*

January 2018 - present

- Compiling an atlas of microbial biogeography based on existing meta-'omics datasets and newly generated amplicon sequence libraries
- Developing software pipelines for the analysis of amplicon sequences, intercomparison with metagenomes, and *in-silico* evaluation of primer performance
- Working with other CBIOMES investigators to compare microbial abundance data with trait-based models

**Chinese University of Hong Kong, Luo Lab;** Shatin, New Territories, HK

*Research Assistant*

November 2016 - Nov 2017

- Developed plate-based isolation methods for high-throughput isolation of fastidious chemoautotrophic *Campylobacteria*
- Isolated sulfur-oxidizing microorganisms from hydrothermal vents and coastal sediments for pangenome and population genetic analysis
- Developed a high-throughput isolation system for selective enrichment of roseobacter-group bacteria from local sediments

**Woods Hole Oceanographic Institution, Sievert Lab;** Woods Hole, MA, USA

*Guest Investigator*

November 2016 - present

- Studying the population genetics of a collection of 9 *Sulfurovum* single-cell genomes sampled in 2008 and again in 2014 from the same deep-sea study site
- Studying activity and community changes for short-term hydrothermal fluid incubations - in collaboration with Stefan Dykstra and Marc Mussmann who developed a [novel method](#) that combines <sup>14</sup>C incubations and CARD-FISH/FACS to quantify activity

**Woods Hole Oceanographic Institution, Sievert Lab; Woods Hole, MA, USA**

*Graduate Research Assistant*

2011-2016

- Studied the biogeochemistry/ecophysiology of chemoautotrophic *Campylobacteria* in the field at deep-sea hydrothermal vents using incubations at *in situ* pressure and temperature
- Cultivated *Sulfurimonas denitrificans* in a custom-built chemostat to validate a theoretical model of energy conservation for this organism

**National Research Council of Canada; Halifax, NS, Canada**

*Technical Officer, National Bioproducts Program*

2009-2011

- Cultivated and harvested kilogram quantities of microalgal biomass
- Developed protocols for lipid extraction from microalgae
- Isolated pure cultures of microalgae from environmental samples

**Environment Canada; Moncton, NB, Canada**

*Environmental Technician, Atlantic Lab for Environmental Testing*

2009

- Conducted toxicology assays and counted sea urchin larvae microscopically

**Atlantic Canada Conservation Data Center; Sackville, NB, Canada**

*Assistant Field Botanist*

2008

- Identified native flora in the field, with an emphasis on rare species

**Marine Macroecology and Biogeochemistry Lab (Finkel Lab); Sackville, NB, Canada**

*Summer Research Student*

2007-2008

- Quantified iron accumulation in *Cyanobacteria* grown under high and low light

TEACHING  
EXPERIENCE

**Woods Hole Oceanographic Institution; Woods Hole, MA, USA**

*Graduate Teaching Assistant*

*Biological Oceanography*

(Spring 2015 with Dr. Lauren Mullineaux and Dr. Stace Beaulieu)

- Taught two classes on microbial biogeochemistry and metabolism
- Marked assignments, developed exam questions, and held weekly review session

*Marine Microbiology and Biogeochemistry*

(Fall 2013 with Dr. Stefan Sievert and Dr. Amy Apprill)

- Taught class on coupling microbial identity to function
- Marked assignments, developed exam questions, and held weekly review session

**Mount Allison University; Sackville, NB, Canada**

*Teaching Assistant*

*Native Flora*

(Fall 2007 with Dr. Robert Thompson)

- Assisted students to identify vascular plant species in the field

MENTORING  
EXPERIENCE

(Jan 2018 - present): Assisted Fuhrman lab students implementing a qiime2 workflow for the analysis of PCR amplicon data.

(May 2017 - May 2018, CUHK): Guided the final-year undergraduate project of Annie Wing-Yi Lo, which tested the effect of microoxic conditions on the isolation of sulfur-oxidizing microbes from shallow-water hydrothermal vents.

(2015-2016, WHOI): Supervised the independent research project of volunteer Dali Smolsky to isolate novel autotrophic *Campylobacteria* from salt marsh and hydrothermal vent environments.

(2010, NRC): Taught students techniques for lipid extraction and transesterification of microalgal biomass with bio-compatible solvents.

PUBLICATIONS

McNichol, J., Berube, P., Biller, S., Chisholm, S.W., and Fuhrman, J., 2020. Evaluating Environmental Coverage of SSU rRNA PCR Primers Across Global Ocean Basins with Shotgun Metagenomes. In preparation (snakemake pipeline available [here](#)).

McNichol, J.\*, Dykma S.\*, Mussmann M., and Sievert S., 2020. Taxon-Specific Radiocarbon Uptake Reveals Three Clades of *Campylobacteria* are Simultaneously Active During Short-Term Incubations of Hydrothermal Vent Fluids. In preparation. \*Co-first authors.

Yeh, Y.C., McNichol, J., Fichot, E., Needham, D., and Fuhrman, J., 2019. Comprehensive single-PCR 16S & 18S rRNA community analysis validated with mock communities and metagenomes. In review.

McNichol, J., Sievert, S.M., 2019. [Reconciling a Model of Core Metabolism with Growth Yield Predicts Biochemical Mechanisms and Efficiency for a Versatile Chemoautotroph](#). In review.

Götz, F., Pjevac, P., Markert, S., McNichol, J., Becher, D., Schweder, T., Mussmann, M., Sievert, S.M., 2019. [Transcriptomic and proteomic insight into the mechanism of cyclooctasulfur- versus thiosulfate-oxidation by the chemolithoautotroph \*Sulfurimonas denitrificans\*](#). Environmental Microbiology 21, 244–258.

Labonté, J.M., Pachiadaki, M., Fergusson, E., McNichol, J., Grosche, A., Gulmann, L.K., Vetriani, C., Sievert, S.M., Stepanauskas, R., 2019. [Single Cell Genomics-Based Analysis of Gene Content and Expression of Prophages in a Diffuse-Flow Deep-Sea Hydrothermal System](#). Frontiers in Microbiology. 10.

McNichol, J., Stryhanyuk, H., Sylva, S.P., Thomas, F., Musat, N., Seewald, J.S., Sievert, S.M., 2018. [Primary Productivity Below the Seafloor at Deep-Sea Hot Springs](#). Proceedings of the National Academy of Sciences. 201804351.

Götz, F., Longnecker, K., Soule, M.C.K., Becker, K.W., McNichol, J., Kujawinski, E.B., Sievert, S.M., 2018. [Targeted metabolomics reveals proline as a major osmolyte in the chemolithoautotroph \*Sulfurimonas denitrificans\*](#). Microbiology Open e586.

- McNichol, J., Sylva, S.P., Thomas, F., Taylor, C.D., Sievert, S.M., Seewald, J.S., 2016. [Assessing microbial processes in deep-sea hydrothermal systems by incubation at \*in situ\* temperature and pressure](#). Deep Sea Research Part I: Oceanographic Research Papers 115, 221–232.
- McNichol, J., MacDougall, K.M., Melanson, J.E., McGinn, P.J., 2012. [Suitability of soxhlet extraction to quantify microalgal fatty acids as determined by comparison with \*in situ\* transesterification](#). Lipids 47, 1–13.
- McNichol, J., McGinn, P.J., 2012. [Adapting Mass Algaculture for a Northern Climate](#), in: Gordon, R., Seckbach, J. (Eds.), The Science of Algal Fuels, Cellular Origin, Life in Extreme Habitats and Astrobiology. Springer Netherlands, pp. 131–146.
- McNichol, J., Gordon, R., 2012. [Are We from Outer Space?: A Critical Review of the Panspermia Hypothesis](#), in: Seckbach, J. (Ed.), Genesis - In The Beginning, Cellular Origin, Life in Extreme Habitats and Astrobiology. Springer Netherlands, pp. 591–619.
- MacDougall, K.M., McNichol, J., McGinn, P.J., O’Leary, S.J.B., Melanson, J.E., 2011. [Triacylglycerol profiling of microalgae strains for biofuel feedstock by liquid chromatography–high-resolution mass spectrometry](#). Anal Bioanal Chem 401, 2609–2616.
- Park, K.C., Whitney, C., McNichol, J., Dickinson, K.E., MacQuarrie, S., Skrupski, B.P., Zou, J., Wilson, K.E., O’Leary, S.J.B., McGinn, P.J., 2011. [Mixotrophic and photoautotrophic cultivation of 14 microalgae isolates from Saskatchewan, Canada: potential applications for wastewater remediation for biofuel production](#). J Appl Phycol 24, 339–348.
- McNichol, J., 2008. [Primordial soup, fool’s gold, and spontaneous generation](#). Biochem Mol Biol Educ 36, 255–261.

SCIENTIFIC  
WORKFLOWS/  
TOOLS

- McNichol, J., Yeh Y.C., Aleman, M., and Fuhrman J. A custom bash pipeline to process 515Y/926R mixed 16S/18S amplicons with cutadapt/bbsplit/qiime2/DADA2 into ASVs ([protocol link](#)).
- McNichol, J. *MGPrimerEval*: A reproducible snakemake pipeline to compare amplicon primer sequences with metagenomes to quantify their *in-silico* coverage and real-world performance by comparing actual metagenomes with amplicons ([pipeline link](#)). Usage instructions are available upon request (to be made public upon paper publication).
- McNichol, J., and Youens-Clark, K. *C-Microbial-MAP*: A tool that takes as input 16S sequences of interest, and generates as output oceanographic section plots of related ASVs ([tool link](#)). This currently works with ANT28-5 data (see below), but will be extended to amplicons from BioGEOTRACES cruises. **Implementation and coding by Ken, concept and ASV generation by Jesse, R ”oce” code template provided by Clark Richards.**

## SELECTED

## DATA PRODUCTS

McNichol, J. 2019. [Exact Amplicon Sequence Variant Abundances from the ANT28-5 Latitudinal Transect of the Atlantic Ocean](#), an ASV dataset derived from publicly-accessible amplicon sequence data from the ANT28-5 cruise. This is the first example of amplicon sequence data to be integrated into the Simons Collaborative Marine Atlas (CMAP) project. Scripts used to generate the ASVs and transform the tables into CMAP format are available [here](#) and [here](#), respectively.

McNichol, J. 2019. [bioGEOTRACES SSU rRNA extracted with phyloFlash, sorted with bbsplit into EUK, BACT, CYANO, and ARCH categories, with 16S additionally subsetted to 515Y/926R amplicon region.](#)

McNichol, J., Dykstra S., Musmann M., and Sievert S., 2020. [CARD-FISH Images from Incubations of Deep-Sea Hydrothermal Vent Fluid and Testing of Novel Probes for Arcobacter, Sulfurimonas, and Sulfurovum.](#)

McNichol, J. 2019. [Curated GTDB ssu\\_r86.1\\_20180911 qiime2 classification artifacts and pipeline.](#)

TECHNICAL  
COMMENTS

McNichol, J., Sievert, S.M. Comment on PMID 26929299: Carbon Fixation Driven by Molecular Hydrogen Results in Chemolithoautotrophically Enhanced Growth of *Helicobacter pylori*. In: PubMed Commons [Internet]. Bethesda (MD): National Library of Medicine; 2017 Feb 16. Available from: [Permalink](#).

GRANTS &  
FELLOWSHIPS

**JGI Small-Scale Microbial/Metagenome Program**  
*Investigating the Genetic Basis of Differential Oxygen Tolerance in Sulfurimonas Ecotypes from the Subseafloor Biosphere Using Single-Cell Genomics* (502884)  
2016

**NASA Earth Systems Science Fellowship**  
*Quantifying Energy Metabolism and Associating Function with Taxonomy for Chemosynthetic Microbial Communities at Deep-Sea Hydrothermal Vents* (PLANET14F-0075)  
2014-2016

**Natural Sciences and Engineering Research Council of Canada, Post-Graduate Scholarship (Doctoral level)**  
*Quantifying Energy Metabolism and Associating Function with Taxonomy for Chemolithoautotrophic Microbial Communities at Deep-Sea Hydrothermal Vents* (PGSD3-439487-2013)  
2013-2016

**Canadian Meteorological and Oceanographic Society Scholarship Supplement**  
2013-2014

**Natural Sciences and Engineering Research Council of Canada, Post-Graduate Scholarship (Master's level)**  
*Psychrophilic bacteria in the Canadian Arctic* (PGSM-405117-2011)  
2011-2012

INVITED  
TALKS

- Scripps Institution of Oceanography**; San Diego, CA (COVID e-seminar).  
*Using Global Metagenomes to Quantify PCR Primer Coverage and Integrating 3-Domain Amplicon Data with Models* June 17th, 2020
- CBIOMES e-meeting**; (online seminar).  
*Biogeography of Exact Amplicon Sequence Variants* ([video link](#)) Dec 12th, 2018
- The Swire Institute of Marine Science**; Hong Kong S.A.R., China  
*Brimstone Bacteria: Primary Productivity and Microbial Ecology of Deep-Sea Hydrothermal Vents* Mar 20th, 2016
- University of Hong Kong, School of Biological Sciences**; Hong Kong S.A.R., China  
*Brimstone Bacteria: Primary Productivity and Microbial Ecology of Deep-Sea Hydrothermal Vents* Jan 29th, 2016
- Max Planck Institute for Marine Microbiology**; Bremen, Germany  
*Insights into chemolithoautotrophy at deep-sea hydrothermal vents from in-situ experiments and metabolic modeling* July 8th, 2014

CONFERENCE  
ACTIVITY

- Ocean Sciences Meeting** San Diego, CA, USA (2020)  
*Testing model predictions and revealing basin-scale biogeography with whole-community PCR amplicons from GEOTRACES* (Oral Presentation; [Abstract](#))
- Gordon Research Conference/Seminar in Marine Molecular Ecology** (2017) Hong Kong S.A.R., China  
*Primary Productivity and Ecophysiology of Chemosynthetic Campylobacteria* (Poster Presentation)
- International Society for Microbial Ecology** (2016) Montreal, QC, Canada  
*Primary Productivity and Ecology of the Seafloor Biosphere at Deep-Sea Hydrothermal Vents, 9 °N East Pacific Rise* (Oral Presentation)
- Gordon Research Conference in Marine Molecular Ecology** (2015) Hong Kong S.A.R., China  
*Bacterial Chemosynthesis at Deep-Sea Hydrothermal Vents Quantified by Cultivation at in-situ Pressure and NanoSIMS Analysis* (Poster Presentation)
- Gordon Research Seminar in Marine Molecular Ecology** (2015) Hong Kong S.A.R., China  
*Incubations of Hydrothermal Vent Communities at In-situ Pressure and Temperature Quantify Community Primary Productivity of the Seafloor Biosphere* (Oral Presentation)
- American Society for Microbiology General Meeting** (2015) New Orleans, LA, USA  
*Simulated Seafloor Conditions Reveal Epsilonproteobacteria as Dominant Chemoautotrophs in Fluids from the Seafloor Biosphere at Deep-Sea Vents* (Young Investigator Oral Presentation)



**American Society for Microbiology General Meeting (2014)** Boston, MA, USA  
*A Genome-Scale Metabolic Model of Sulfurimonas denitrificans Provides Insight into the Process of Autotrophic Denitrification* (Young Investigator Oral Presentation)

**DEPARTMENTAL SEMINARS** **Woods Hole Oceanographic Institution;** Woods Hole, MA, USA  
*Productivity, Metabolism and Physiology of Free-Living Chemoautotrophic Epsilonproteobacteria* (Thesis defense) Aug 1st, 2016

**Woods Hole Oceanographic Institution;** Woods Hole, MA, USA  
*Simulated Seafloor Conditions Reveal Epsilonproteobacteria as Dominant Chemoautotrophs in Fluids from the Subseafloor Biosphere at Deep-Sea Vents* Feb 19th, 2015

**PROFESSIONAL SERVICE** Reviewer for: Scientific Reports, PLoS One, Frontiers in Microbiology, International Journal of Systematic and Evolutionary Microbiology

**PROFESSIONAL AFFILIATIONS** American Association for the Advancement of Science (AAAS), American Society for Microbiology (ASM), Canadian Society for Microbiology (CSM)

**RESEARCH CRUISES** **November 2014**, East Pacific Rise 9°N, R/V *Atlantis*: AT26-23, Chemoautotrophic Carbon Production at Deep-Sea Hydrothermal Vents  
**January 2014**, East Pacific Rise 9°N, R/V *Atlantis*: AT26-10, Dimensions of Biodiversity, An Integrated Study of Energy Metabolism, Carbon Fixation, and Colonization Mechanisms in Chemosynthetic Microbial Communities at Deep-Sea Vents  
**July-Aug 2012**, Rhode Island Continental Shelf, R/V Endeavor: Deep Ocean Benthic Sampler Cruise

**COMPUTATIONAL EXPERIENCE** **Scripting Languages:** Python, bash, R.  
**Bioinformatics Software Experience:** qiime/qiime2, SPAdes/metaSPAdes, Redundans, ARB, BLAST, BWA-MEM, CheckM, EMIRGE, FIJI, graftM, Integrative Genomics Viewer, Jspecies, KaKs Calculator, komplexity, look@NanoSIMS, Prokka, RAxML, SAMtools, Snippy, TMHMM.

**LANGUAGES** Written Chinese (functional with traditional and simplified characters), Mandarin Chinese (conversational), Cantonese (basic spoken), French (conversational), Spanish (functional)