

EDUCATION

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

Ph.D., Biological Oceanography

2011–2016

- 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

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

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 intercompare microbial abundance data with trait-based models and statistically infer microbial interaction networks

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

Graduate Research Assistant

2011–2016

- Incubated deep-sea hydrothermal vent chemoautotrophic communities at *in situ* pressure and temperature to infer their ecophysiology and biogeochemical impact
- Cultivated *Sulfurimonas denitrificans* in a custom-built chemostat to validate a theoretical model of energy conservation for this organism

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 hydrothermal fluid incubations in collaboration with Stefan Dyksma and Marc Mußmann who developed a [novel method](#) that combines ^{14}C incubations and CARD-FISH/FACS to quantify activity

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 and GC-FID quantification
- 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; Sackville, NB, Canada

Summer Research Student 2007-2008

- Quantified iron accumulation in *Cyanobacteria* grown under high and low light under the supervision of Dr. Zoe Finkel

TEACHING
EXPERIENCE

Woods Hole Oceanographic Institution; Woods Hole, MA, USA

Graduate Teaching Assistant

Biological Oceanography (Spring 2015)

Instructors: Dr. Lauren Mullineaux and Dr. Stace Beaulieu

- Taught two classes on microbial biogeochemistry and metabolism
- Developed and marked assignments / exam questions; held weekly review sessions

Marine Microbiology and Biogeochemistry (Fall 2013)

Instructors: Dr. Stefan Sievert and Dr. Amy Apprill

- Taught class on coupling microbial identity to function
- Developed and marked assignments / exam questions; held weekly review sessions

Mount Allison University; Sackville, NB, Canada

Undergraduate Teaching Assistant, Native Flora (Fall 2007)

Instructor: Dr. Robert Thompson

- Assisted students to identify vascular plant species in the field

RESEARCH
MENTORING
EXPERIENCE

(Dec 2019 - present, USC): Mentoring undergraduate Bruce Yanpui Chan in bioinformatic analyses and assisted with a successful funding application to the program Student Opportunities for Academic Research (SOAR).

(Jan 2018 - present, USC): Assisted graduate students Selene Sanchez-Garcia (Technical University Braunschweig) and Felix Milke (University of Oldenburg) with amplicon analysis, data interpretation, and [conference presentations](#).

(Jan 2018 - present, USC): Assisted Fuhrman lab graduate students in 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 and local sediments.
*Equivalent of Honours thesis.

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

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

PEDAGOGICAL &
RESEARCH
TRAINING

edX Online Learning Platform

Becoming a More Equitable Educator: Mindsets and Practices (Spring 2021)

- Exploring mindsets and strategies used by effective educators to reflect on and address issues of educational equity in the classroom, with an emphasis on how race, ethnicity and other differences affect student outcomes.

CyVerse Learning Network

Foundational Open Science Skills Online (Spring 2021)

- Learned technical and pedagogical skills for collaborative data science projects using open-source cyberinfrastructure.

University of Southern California, Center for Excellence in Teaching

Future Faculty Teaching Institute (Spring 2020)

- Studied paradigms and practical approaches for instructional design in addition to strategies for providing online course offerings.

OTHER
EDUCATIONAL
EXPERIENCE

Joint Educational Project, University of Southern California (Jan 2021 - present)

- Tutoring local third grade student in Math, English and Science.

Chinese Summer Language Village, Mount Allison University (2008)

- Collaboratively developed and taught a language immersion camp for native English speakers ages 8-16 to learn Mandarin Chinese.

Planet Performers environmental drama, Mount Allison University (2007-2008)

- Taught and discussed environmental issues (biofuels, global warming) with students in grades 6-8, and created two public performances in collaboration with other undergraduate students.

PREPRINTS &
IN-REVIEW
PUBLICATIONS

McNichol, J.^{1,2}, Dyksma S.¹, Mußmann M., Seewald, J., Sylva, S., Sievert S.², 2020. [Group-Specific Carbon Fixation Activity Measurements Reveal Distinct Responses to Oxygen Among Hydrothermal Vent *Campylobacter*](#). bioRxiv (In revision for *Applied and Environmental Microbiology*). ¹Co-first authors. ²Co-corresponding authors.

McNichol, J.*, Sievert, S.M.*, 2019. [Reconciling a Model of Core Metabolism with Growth Yield Predicts Biochemical Mechanisms and Efficiency for a Versatile Chemoautotroph](#). *bioRxiv* (In revision for *mSystems*). *Co-corresponding authors.

PEER-REVIEWED
PUBLICATIONS

McNichol, J.*, Berube, P., Biller, S., Fuhrman, J., 2021. [Evaluating and Improving SSU rRNA PCR Primer Coverage for Bacteria, Archaea, and Eukaryotes Using Metagenomes from Global Ocean Surveys](#). *mSystems*. 6(3), e00565-21. *Corresponding author.

Yeh, Y.C., McNichol, J., Needham, D., Fichot, E., Berdjeb, L., Fuhrman, J., 2021. [Comprehensive single-PCR 16S and 18S rRNA community analysis validated with mock communities, and estimation of sequencing bias against 18S](#). *Environmental Microbiology*. doi: 10.1111/1462-2920.15553.

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*. 115, 6756-6761. *Co-corresponding authors.

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.

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](#). *Analytical and Bioanalytical Chemistry* 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. *Journal of Applied Phycology* 24, 339–348.

PUBLICATIONS
IN PREP

Lin, X.Q., Chu, X., McNichol, J., Qian, Y., Luo, H.W. Cryptic niches in intertidal sediments support differentiation of a novel ecotype of *Ruegeria pomeroyi*.

Charoenpong, C.N., McNichol, J., Sievert, S.M., Seewald, J., Wankel, S. Subsurface modifications of NH_4^+ at low-temperature, diffuse vents at 9°50'N East Pacific Rise.

BOOK
CHAPTERS &
EDUCATIONAL
WRITING

Sievert, S.M., McNichol, J., Thomas, F., Panayotova, E., Watson R., 2018. [How Do Deep-Sea Hot Spring Ecosystems Work?](#) *Environmental Science Journal for Teens*.

McNichol, J., 2017. [Breaking the Oxygen Barrier in Microbial Cultivation](#), Small Things Considered Blog, American Society for Microbiology.

McNichol, J., 2014. [A First-Time Diver's Experience](#). Blog for research cruise AT26-23 (R/V *Atlantis*).

McNichol, J., 2014. “Mail Buoy” responses to gradeschool student questions about deep-sea hydrothermal vent ecosystems: [Jan 12th](#), [Jan 13th](#), [Jan 20th](#), [Jan 30th](#). Research cruise AT26-10 (R/V *Atlantis*).

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.

McNichol, J., 2008. [Primordial soup, fool's gold, and spontaneous generation](#). *Biochemistry and Molecular Biology Education* 36, 255–261.

SCIENTIFIC
WORKFLOWS
AND TOOLS

McNichol, J., Yeh Y.C., Aleman, M., 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 metagenomes with amplicons ([pipeline link](#)).

McNichol, J., 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](#)). [Implementation and coding by Ken](#), [concept and ASV generation by Jesse](#), [R “oce” code template provided by Clark Richards](#).

SELECTED DATA PRODUCTS	<p>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 to transform ASV tables into CMAP format are available here.</p> <p>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.</p> <p>McNichol, J., Dyksma S., Mußmann 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.</p> <p>McNichol, J. 2019. Curated GTDB ssu_r86.1_20180911 qiime2 classification artifacts and pipeline.</p>
TECHNICAL COMMENTS	<p>McNichol, J., Sievert, S.M. Comment on PMID 26929299: Carbon Fixation Driven by Molecular Hydrogen Results in Chemolithoautotrophically Enhanced Growth of <i>Helicobacter pylori</i>. In: PubMed Commons [Internet]. Bethesda (MD): National Library of Medicine; 2017 Feb 16. Available from: Permalink.</p>
GRANTS & FELLOWSHIPS	<p>JGI Small-Scale Microbial/Metagenome Program <i>Investigating the Genetic Basis of Differential Oxygen Tolerance in Sulfurimonas Ecotypes from the Subseafloor Biosphere Using Single-Cell Genomics</i> (502884) 2016</p> <p>NASA Earth Systems Science Fellowship <i>Quantifying Energy Metabolism and Associating Function with Taxonomy for Chemosynthetic Microbial Communities at Deep-Sea Hydrothermal Vents</i> (PLANET14F-0075) 2014-2016</p> <p>Natural Sciences and Engineering Research Council of Canada, Post-Graduate Scholarship (Doctoral level) <i>Quantifying Energy Metabolism and Associating Function with Taxonomy for Chemolithoautotrophic Microbial Communities at Deep-Sea Hydrothermal Vents</i> (PGSD3-439487-2013) 2013-2016</p> <p>Canadian Meteorological and Oceanographic Society Scholarship Supplement 2013-2014</p> <p>Natural Sciences and Engineering Research Council of Canada, Post-Graduate Scholarship (Master's level) <i>Psychrophilic bacteria in the Canadian Arctic</i> (PGSM-405117-2011) 2011-2012</p>
INVITED TALKS	<p>Institute for Chemistry and Biology of the Marine Environment (ICBM); Oldenburg, Germany (COVID e-seminar). <i>Using Global Metagenomes to Evaluate and Improve PCR Primer Coverage and the Application of 3-Domain Amplicon Data to Trait-Based Models</i> Nov 25th, 2020</p>

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
AND WORKSHOP
ACTIVITY

Ocean Sciences Meeting (2020) San Diego, CA, USA
Testing model predictions and revealing basin-scale biogeography with whole-community PCR amplicons from GEOTRACES (Oral Presentation; [Abstract](#))

Ocean Nucleic Acids ‘omics Intercalibration and Standardization Workshop (2020)
 UNC Chapel Hill, NC, USA (Participant; [Workshop website](#))

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, Journal of Open-Source Science, Nature Communications, PeerJ, Molecular Ecology Resources, Environmental Microbiology, ISME Journal.

PROFESSIONAL
AFFILIATIONS

American Society for Microbiology (ASM), Canadian Society for Microbiology (CSM), The Oceanography Society (TOS)

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

LABORATORY
EXPERIENCE

Skills I am comfortable teaching / supervising:

- Aquatic microbial field sampling, preservation, and DNA extraction
- SSU rRNA amplicon / metagenomic / -transcriptomic library preparation
- Microbial pure culture isolation, including for oxygen-sensitive microorganisms
- Physiological growth experiments, including both batch and chemostat methods
- Incubations for measuring biogeochemical rates and microbial growth, including both stable/radioisotope methods
- Microscopic enumeration and identification of environmental microorganisms, including Fluorescence *In Situ* Hybridization methods (e.g. CARD-FISH) and subsequent single-cell activity measurements (e.g. NanoSIMS)

SOFTWARE
COMPETENCIES

Scripting and Plotting Languages: Python, bash, R.

Selected Bioinformatics Software Experience: qiime2, jupyter, conda/mamba, snake-make, anvi'o, (meta)SPAdes, look@NanoSIMS, GTDB-tk, phyloFlash, bbtools.

LANGUAGES

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