

## Dr. Steven James Hallam

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### Employment and Education

- Marine Biological Laboratory, Strategies and Techniques for Analyzing Microbial Population Structure (2014)
- Associate Professor, Microbiology & Immunology, University of British Columbia (2012-present)
- Program Faculty, Genome Science & Technology, University of British Columbia (2008-present)
- Program Faculty, Bioinformatics, University of British Columbia (2008-present)
- Marine Biological Laboratory, Microbial Diversity Course (2008)
- Assistant Professor, Microbiology & Immunology, University of British Columbia (2006-2012)
- Postdoctoral Fellow, Massachusetts Institute of Technology (2004-2005)
- Research Associate, Monterey Bay Aquarium Research Institute (2002-2004)
- Postdoctoral Fellow, Monterey Bay Aquarium Research Institute (2000-2002)
- Ph.D., Molecular Genetics, University of California Santa Cruz (1995-2000)
- School for Field Studies, El Cielo Biosphere Reserve, Tamaulipas Mexico (1994)
- Research Associate, Department of Oncology Montefiore Medical Center (1992-1995)
- B.A., Liberal Arts, focus on Religion & Biology, Sarah Lawrence College (1988-1992)

### Fieldwork

- Northeast subarctic Pacific Ocean, Line-P transect, CCGS John P Tulley (2007-present)
- Sakinaw Lake, Sunshine Coast BC (2007-present)
- Saanich Inlet, Vancouver Island BC, Monthly time-series, HMS John Strickland (2006-present)
- Gulf of California (GoC) MBARI Expedition R/V Western Flyer (2003)
- Gulf of Mexico (GoM) USGS Gas Hydrate Expedition, R/V Marion Dufresne (2002)
- Mid-Atlantic Ridge (MAR) Expedition, R/V Atlantis (2001)

### Teaching and Training

*"Go to the people. Learn from them. Live with them. Love them. Start with what they know. Build with what they have. But the best of leaders when the job is done, when the task is accomplished, the people will all say we have done it ourselves."* Lao Tzu, 604 B.C.

I have a particular interest in network and scaling relationships in biological systems. This brings me to teach about microbial genomes, pathways and communities in relation to ecosystem functions and the services that humans enjoy.

- Lead Instructor, MICB425 Microbial Ecological Genomics and Genetics (2012-present)
- Co-instructor, MICB405 Bioinformatics (2012-present)
- Lead Instructor, SCIE113 First-Year Seminar in Science (2011)
- Lead Instructor, MICB409 Microbial Genetics (2007-2010)

In addition to classroom instruction I am committed to student training across undergraduate, graduate and postgraduate levels and encourage my trainees to participate in the design and implementation of MICB425.

- Graduate students supervised (17 total; 9 PhD and 8 MSc; 12 current)
- Postdoctoral fellows supervised (12 total; 5 current)
- Technicians, co-op, interns and undergraduates supervised (54 total; 15 current)
- Directed Studies students supervised (18 total; 4 current)

Recently I became a faculty mentor for the UBC International Genetically Engineered Machine (iGEM) team. Working with the team has helped me refocus my own research program to include the paradigm of emergent or distributed metabolism in natural and engineered ecosystems (<http://www.hallam.microbiology.ubc.ca/iGEM>).

- Mentor, International Genetically Engineered Machine Team (2012-present)

### Research Program

*"We have to do better at producing tools to support the whole research cycle—from data capture and data curation to data analysis and data visualization." Jim Gray The Fourth Paradigm, 2009*

My lab investigates the ecological and biogeochemical roles of uncultivated microbial communities in natural and engineered ecosystems with a particular emphasis on defining metabolic interactions. We combine plurality and single-cell genome sequencing with functional screening and the development of computational tools to predict latent and expressed metabolic potential and recover genomic scaffolds with biotechnological applications. To permit improved metabolic pathway prediction from environmental sequence information we have developed MetaPathways, a modular annotation and analysis pipeline for pathway inference that uses the PathoLogic algorithm to map functional annotations onto the MetaCyc collection of reactions and pathways, and construct environmental Pathway/Genome Databases (ePGDBs) compatible with the editing and navigation features of Pathway Tools. We use MetaPathways to predict metabolic interactions between sequenced isolates or environmental clones that can be validated in co-culture experiments using traditional genetic and biochemical methods. Other project space includes the use of microfluidic digital chip technology for single-cell genome sequencing and the use of biosensors to detect small molecule production or substrate conversion by environmental clones in plate-based or cell-sorting screens. In 2013, the lab spun-off a synthetic biology company called MetaMixis Biologics (<http://www.metamixis.com>), that uses proprietary platform screening technology to discover and evolve small molecules and industrial catalysts from uncultivated microbial communities inhabiting natural and engineered ecosystems. In 2014, the lab spun off a second computation intelligence company called MetaMixis Informatics that designs and provides ecoinformatics tools and services in the cloud.

### Selected Publications

I have been cited 4,091 times since 1995 with 2,655 of those citations occurring since 2010, resulting in a cumulative h-index of 25 and i10-index of 43. Trainees are underlined. For a complete citation index see <http://scholar.google.ca/citations?user=YsgFAIUAAA&hl=en>

- **Hallam, S. J.** and J. P. McCutcheon. 2015. *Microbes don't play solitaire: How cooperation trumps isolation in the microbial world*. **EM Reports** 7(1), 26-28 doi:10.1111/1758-2229.12248
- **Kim, D., K. M. Kishori, N. W. Hanson, and S. J. Hallam.** 2014. *Koonkie: An Automated Software Tool for Processing Environmental Sequence Information using Hadoop*. **Academy of Science and Engineering 2104 ASE Conference on BigData and Social Informatics**.
- **Gies E. A., K. M. Konwar, J. T. Beatty, and S. J. Hallam.** 2014 *Illuminating microbial dark matter in meromictic Sakinaw Lake*. **AEM** 80 (21), 6807-6818 doi: 10.1128/AEM.01774-14
- **Strachan C.R., D. VanInsberghe, R. Singh, K. Ievdokymenko, K. Budwill, W.W. Mohn, L.D. Eltis & S.J. Hallam.** 2014. *Metagenomic scaffolds enable combinatorial lignin transformation by Escherichia coli*. **PNAS**. 111(28):10143–10148 doi: 10.1073/pnas.1401631111
- **Hanson, N.W., K. M. Konwar, A. K. Hawley, T. Altman, P. Karp, and S. J. Hallam.** 2014. *Metabolic pathways for the whole community*. **BMC Bioinformatics** 15:619 doi:10.1186/1471-2164-15-619
- **Hawley, A. K., H M. Brewer, A.D. Norbeck, L. Pasa-Tolic and S. J. Hallam.** 2014. *Metaproteomics reveals differential modes of metabolic coupling among ubiquitous oxygen minimum zone microbes*. **PNAS** doi: 10.1073/pnas.1322132111
- **Hanson, N.W., K. M. Konwar, S. Wu, and S. J. Hallam.** 2014. *Metapathways 2.0: A master-worker model for environmental Pathway/Genome Database construction on grids and clouds*. **Computational Intelligence in Bioinformatics and Computational Biology, 2014 IEEE Conference on**. doi: 10.1109/CIBCB.2014.6845516
- **Hurwitz, B.L., S.J. Hallam\*** and **M.B. Sullivan\***. 2013. *Metabolic reprogramming by viruses in the sunlit and dark ocean*. **Genome Biology**. 14(11):R123 doi:10.1186/gb-2013-14-11-r123 [corresponding author (\*)]
- **Wright, J.J., K. Mewis, N. W. Hanson, K. M. Konwar, K. R. Mitchell and S. J. Hallam.** 2013. *A potential role for Marine Group A bacteria in the marine sulfur cycle*. **ISME Journal** 8(2):455-468 doi:10.1038/ismej.2013.152
- **Mewis, K., Z. Armstrong, Y.C. Song, S.A. Baldwin, S. Withers and S. J. Hallam.** 2013. *Biomining active cellulases from a passive mining bioremediation system*, **Journal of biotechnology** 167(4):462-471 doi:p11: S0168-1656(13)00311-8. 10.1016/j.jbiotec.2013.07.015
- **An D., S. M. Caffrey, J. Soh, A. Agrawal, D. Brown, K. Budwill, X. Dong, P. F. Dunfield, J. Foght, L. M. Gieg, S. J. Hallam, et al.** 2013. *Metagenomics of Hydrocarbon Resource Environments Indicates Aerobic Taxa and Genes to be Unexpectedly Common*. **Environ. Sci. Technol.** 47(18):10708–10717 doi:10.1021/es4020184
- **Konwar, K. M., N. W. Hanson, A. P. Pagé, and S. J. Hallam.** 2013. *MetaPathways: A modular pipeline for constructing Pathway/Genome Databases from environmental sequence information*. **BMC Bioinformatics** 14(1):202. doi: 10.1186/1471-2105-14-202
- **Swan B.K., B. Tupper, A. Sczyrba, F. M. Lauro, M. Martinez-Garcia, J. M. González, H. Luo, J. J. Wright, Z. C. Landry, N. W. Hanson, B. P. Thompson, N. J. Poulton, P. Schwientek, S. G. Acinas, S. J. Giovannoni, M. A. Moran, S. J. Hallam, R. Cavicchioli, T. Woyke and R. Stepanauskas.** 2013. *Prevalent genome streamlining and latitudinal divergence of marine bacteria in the surface ocean*. **Proc. Natl. Acad. Sci. USA** 110(28):11463-8. doi: 10.1073/pnas.1304246110
- **Rinke, C., P. Schwientek, A. Sczyrba, N. N. Ivanova, I. J. Anderson, J. Cheng, A. Darling, S. Malfatti, B. K. Swan, E. A. Gies, J. A. Dodsworth, B. P. Hedlund, G. Tsiamis, S. M. Sievert, W. Liu, J. A. Eisen, S. J. Hallam, N. C. Kyrpides, R. Stepanauskas, E. M. Rubin, P. Hugenholtz and T. Woyke.** 2013. *Insights into the Phylogeny and Coding Potential of Microbial Dark Matter*. **Nature** 499(7459):431-7 doi:10.1038/nature12352

- Durno E., N. W. Hanson, K. M. Konwar and S. J. Hallam. 2013. *Expanding the boundaries of local similarity analysis*, **BMC Genomics** 14 Suppl 1:S3. doi: 10.1186/1471-2164-14-S1-S3
- Allers, E<sup>+</sup>, J. J. Wright<sup>+</sup>, K. M. Konwar, C. G. Howes, E. Beneze, S. J. Hallam\* and Matthew J. Sullivan\*. 2012. *Diversity and population structure of Marine Group A bacteria in the oxygen minimum zone of the Northeast subarctic Pacific Ocean*. **ISME Journal** 7(2):256-68. doi: 10.1038/ismej.2012.108 [co-first author (+), corresponding author (\*)]
- Hartmann, M., C. G. Howes, D. VanInsberghe, H. Yu, D. Bachar, R. Christen, R. H. Nilsson, S. J. Hallam and W.W. Mohn. 2012. *Significant and Persistent Impact of Timber Harvesting on Soil Microbial Communities in Northern Coniferous Forests*. **ISME Journal**. 6:2199-2218 doi:10.1038/ismej.2012.84
- Leung, K., H. Zahn, T. Leaver, K. M. Konwar, N. W. Hanson, A.P. Pagé, C. Lo, P. S. Chain, S.J. Hallam, and C. L. Hansen. 2012. *Programmable droplet-based microfluidic device applied to multiparameter analysis of single microbes and microbial communities*. **Proc. Natl. Acad. Sci. USA** 109(20):7665-70 doi: 10.1073/pnas.1106752109
- Orsi, W<sup>+</sup>, Y.C. Song<sup>+</sup>, S.J. Hallam and V. Edgcomb. 2012. *Effect of Oxygen Minimum Zone Formation on Communities of Marine Protists*. **ISME Journal** 6(8):1586-1601 doi:10.1038/ismej.2012.7
- Schulze-Makuch, D., S. Haque, M. Resendes de Sousa Antonio, D. Ali, R. Hosein, Y.C. Song, J. Yang, E. Zaikova, D.M. Beckles, E. Guinan, H.J. Lehto and S.J. Hallam. 2011. *Microbial life in a liquid asphalt desert*, **Astrobiology** Apr;11(3):241-58 doi:10.1089/ast.2010.0488
- Zaikova, E., D. A. Walsh, C. P. Stilwell, W.W. Mohn, P. D. Tortell, and S. J. Hallam, 2010. *Microbial community dynamics in a seasonally anoxic fjord: Sannich Inlet British Columbia*, **Environmental Microbiology**, 12(1):172-91 doi: 10.1111/j.1462-2920.2009.02058.x
- Walsh, D. A., E. Zaikova, C. G. Howes, Y. C. Song., J.J. Wright, S. Tringe, P. D. Tortell, and S. J. Hallam, 2009. *Metagenome of a versatile chemolithoautotroph from expanding oceanic dead zones*, **Science**, 326(5952):578-82 DOI: 10.1126/science.1175309

### Selected Book Chapters and Reviews

- Hawley, A. K., S. Kheirndish, A. Mueller, A.D. Norbeck, H. Brewer, L. Pasa-Tolic and S. J. Hallam. 2013. *Molecular tools for investigating microbial community structure and function in oxygen-deficient marine waters*. **Meth. Enzymol.** 531:305-329 doi.org/10.1016/B978-0-12-407863-5.00016-2
- Wright, J.J. K. Konwar, and S.J. Hallam. 2012 *Microbial Ecology of Expanding Oxygen Minimum Zones*. **Nat. Rev. Microbiol.** 10, 381-94 doi:10.1038/nrmicro2778
- Walsh D.A. and S.J. Hallam. 2011. *Bacterial community diversity and population dynamics in a seasonally anoxic fjord: Saanich Inlet*, Chapter 25:253-267 **Handbook of Molecular Microbial Ecology II: Metagenomics and Complementary Approaches**, Wiley-Blackwell, Ed. Frans de Bruijn
- Taupp, M., K. Mewis and S.J. Hallam. 2011. *The art and design of functional metagenomic screens*. **Curr. Opin. Biotechnol.** Jun;22(3):465-72, doi:10.1016/j.copbio.2011.02.010.
- Taupp, M., L. Constan, S.J. Hallam. 2010. *The biochemistry of anaerobic methane oxidation* Part 17 in the **Handbook of Hydrocarbon Microbiology**, doi: 10.1007/978-3-540-77587-4\_63

### Selected Speaking Engagements

- *Single-Cell Genomics Reveals Co-Metabolic Innovations Within Uncultivated Marine Group A Bacteria* (2015) AAAS Annual Meeting
- *Oceans of Information* at the ASM General Meeting, (2014), Boston, MA, USA

- *Analysis of environmental genomes using Pathway Tools*, Conference on Predicting Cell Metabolism and Phenotypes SRI International (2013), Menlo Park, CA, USA
- *The nuts and bolts of ecological design*, University of British Columbia Civil and Environmental Engineering Department (2013), Vancouver, BC, CA
- *Oceans of Information*, EuroEEFG Conference “Frontiers in Ecological and Evolutionary Genomics” (2013), Noordwijkerhout, Netherlands, (**Keynote**)
- *Microbial community responses to changing levels of water column oxygen-deficiency in the northeastern subarctic pacific ocean*, Marine Microbes Gordon Research Conference (2012), Renaissance Tuscany Il Ciocco Resort, Barga, Italy
- *Microbial ecology of expanding oxygen minimum zones*, Bigelow Laboratory for Ocean Science (2012), East Boothbay, Maine, USA
- *Oceans of Information*, OECD Global forum on Biotechnology: Enabling Solutions for ocean productivity and sustainability, Wosk Centre for Dialogue (2012), Vancouver, BC, CA
- *From Fjords to open seas: Ecological genomics of expanding oxygen minimum zones*, SAME-12 (2011), Leibniz Institute of Baltic Sea Research, Rostock-Warnemünde, Germany, (**Keynote**)
- *Microbial sentinels of environmental change*, University of Washington (2011), Seattle WA, USA
- *Connecting the dots: patterns and processes in microbial systems ecology*, Institute of Molecular Life Sciences University of Zurich (2011), Zurich, Switzerland
- Genome BC 7<sup>th</sup> Annual Genomics Forum (2009), Vancouver, BC, CA, (**Panel member**)

#### Patents and Invention Disclosures

- Sequential screening for co-culture based detection of metagenomic elements conferring heterologous metabolite secretion. 14-036 (Tech 14-0238) and Modular protein class structures for combinatorial lignin transformation in *E. coli*. 14-076 (Tech 14-0465)
- Provisional patents based on 14-036 and 14-076 has been filed in the United States and Canada with serial numbers 61/936,448 and 62/013,369, respectively.

#### Honors & Awards

- UBC Research Fellow (2014)
- Leopold Leadership Fellow (2104)
- American Association for the Advancement of Science (AAAS) Fellow (2013)
- UBC Killam Teaching Prize (2013)
- Canadian Society for Microbiology (CSM) Fisher Scientific Early Career Award (2010)
- Peter Wall Institute for Advanced Studies Early Career Scholar (2007)
- Canadian Institute for Advanced Research (CIFAR) Fellow, Integrated Microbial Diversity (2007)
- Canada Research Chair in Environmental Genomics (2006)
- MBARI Postdoctoral Fellowship (2000)

#### Professional Activities

- Organizer: Scientific Committee on Oceanographic Research (SCOR) [Microbial Community Responses to Ocean Deoxygenation](#) 2014
- Steering committee member: [Moore Foundation Microbial ecology and biogeochemistry of oxygen-deficient marine waters, Santa Cruz, Chile, March 18-22, 2013](#)

- Co-convenor: [Systems Ecology of Expanding Marine Oxygen Minimum Zones at the 13th international symposium of the International Society of Microbial Ecology \(ISME13\), Seattle WA USA, August 22-27, 2010](#)
- Organizer: [CIFAR bigDATA workshop, Vancouver BC, Canada, May 28-30<sup>th</sup>, 2010](#)
- Reviewer for 18 journals including Bioinformatics, BMC Genomics, PLoS Biology, PNAS, Environmental Microbiology, ISME, Nature Geomicrobiology, Nature Methods and Science
- Grant reviewer for CIHR Genomics Panel (GMX 2008, 2009), JGI Community Sequencing Program Panel (2007, 2008, 2009), EMSL User Program (2007, 2008, 2009)
- Centre for Microbial Diversity and Evolution board member (2007-present)
- Program committee member for Biodiversity Training Program (BRITE) (2009-present)

### Science Outreach

- [The Power of Microbial Cooperation](#) (TEDx) October 25, 2014
- Straight talk with Adam Stirling (CFAX1070 Radio) October 23, 2009
- Studio4 with Fanny Kiefer (Shaw Television) April 6, 2010
- [Quirks and Quarks with Bob MacDonald CBC April 24, 2010](#)