CURRICULUM VITAE
SUSAN MARIE HUSE

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Education

1986	B.S. Yale University, Special Divisional Major
1995	Ph.D. University of California, Berkeley, Environmental Planning Robert Twiss, *GRASSLinks*: *Public Access GIS*

Academic Appointments

2012 – present	Assistant Professor (Research), Pathology and Laboratory Medicine Brown University, Providence, Rhode Island
2009 – 2013	Assistant Research Scientist, Josephine Bay Paul Center, Marine Biological Laboratory, Woods Hole, Massachusetts.
2007 - 2009	Scientific Informatics Analyst, Josephine Bay Paul Center, Marine Biological Laboratory, Woods Hole, Massachusetts.
2007 - 2007	Research Associate in Bioinformatics, Josephine Bay Paul Center, Marine Biological Laboratory, Woods Hole, Massachusetts.
2005 - 2006	Research Assistant III in Bioinformatics, Josephine Bay Paul Center, Marine Biological Laboratory, Woods Hole, Massachusetts

Other Appointments

1996 - 2005	Biologist, Alaska Support Office, National Park Service, Anchorage, Alaska

Publications List

Original Publications in Peer-Reviewed Journals

1. **Huse SM**, Young VB, Morrison HG, Antonopoulos DA, Kwon J, Dalal S, Arrieta R, Hubert NA, Shen L, Vineis JH, Koval JC, Sogin ML, Chang EB, Raffals, L (in press) Comparison of brush and biopsy sampling methods of the ileal pouch for assessment of mucosa-associated microbiota of human subjects. *Microbiome*
2. **Huse SM**, Mark Welch DB, Voorhis A, Shipunova A, Morrison HG, Eren AM, Sogin ML (2014) VAMPS: a website for visualization and analysis of microbial communities. *BMC Bioinformatics* **15**(1):41
3. Catlin, NR, **Huse SM**, Boekelheide K (in press) The stage-specific testicular germ cell apoptotic response to low dose X-irradiation and 2,5-hexanedione combined exposure. I. Improved laser capture microdissection method for qRT-PCR array application. *Toxicological Pathology*
4. Catlin, NR, **Huse SM**, Boekelheide K (in press) The stage-specific testicular germ cell apoptotic response to low dose radiation and 2,5-hexanedione combined exposure. II. qRT-PCR array analysis reveals dose dependent adaptive alterations in the apoptotic pathway. *Toxicological Pathology*
5. Spade DJ, Hall SH, Saffarini C, **Huse SM**, McDonnell-Clark EV, Boekelheide K. (2014) Differential

response to abiraterone acetate and di-*n*-butyl phthalate in an androgen-sensitive human fetal testis xenograft bioassay. *Toxicological Science*s doi: 10.1093/toxsci/kft266

6. Glass, E. M., Y. Dribinsky, P. Yilmaz, H. Levin, R. Van Pelt, D. Wendel, A. Wilke, J. A. Eisen, S. Huse, A. Shipanova, M. Sogin, J. Stajich, R. Knight, F. Meyer and L. M. Schriml (2014) MIxS-BE: a MIxS extension defining a minimum information standard for sequence data from the built environment. *ISME J* 8(1): 1-3.
7. Newton RJ, **Huse SM**, Morrison HG, Peake CS, Sogin ML and McLellan SL (2013) Shifts in the microbial community composition of Gulf Coast beaches following beach oiling. *PLoS ONE* **8**(9):e74265
8. Saffarini CM, McDonnell EV, Amin A, Spade DJ, **Huse SM**, Kostadinov S, Hall SJ, Boekelheide K (2013) Maturation of the developing human fetal prostate in a rodent xenograft model. *The Prostate* **73**(16):1761-75
9. Eren AM, Morrison HG, **Huse SM**, and Sogin ML (2013) DRISEE overestimates errors in metagenomic sequencing data. *Briefings in Bioinformatics* doi:10.1093/bib/bbt010
10. Young VB, Raffals LH, **Huse SM**, Vital M, Dai D, Schloss PD, Brulc JM, Antonopoulous DA, Arrieta RL, Kwon JH, Reddy KG, Hubert NA, Grimm SL, Vineis JH, Dalal S, Morrison HG, Eren AM, Meyer F, Schmidt TM, Tiedje JM, Chang EB and Sogin, ML (2013) Multiphasic Analysis of the Temporal Development of the Distal Gut Microbiota in Patients Following Ileal Pouch Anal Anastomosis. *Microbiome* **1**(1):9 http://www.microbiomejournal.com/content/1/1/9
11. McLellan SL, Newton RJ, Vandewalle JL, Shanks OC, **Huse SM**, Eren AM, and Sogin ML (2013) Sewage reflects the distribution of human faecal *Lachnospiraceae*. *Environmental Microbiology*
12. Shanks, OC, Newton, RJ, Kelty, CA, **Huse, SM**, Sogin, ML, and McLellan, SL (2013) Comparison of the microbial community structures of untreated wastewaters from different geographic locales. *Applied and Environmental Microbiology* **79**(9):2906-2913.
13. **Huse SM**, Ye Y, Zhou Y, and Fodor, AA (2012) A Core human microbiome as viewed through 16S rRNA sequence clusters. *PLoS ONE* 7(6): e34242. PMC3374614
14. Human Microbiome Project Consortium (2012) A Framework for human microbiome research. *Nature* 486:215-221.
15. Human Microbiome Project Consortium (2012) Structure, function and diversity of the healthy human microbiome. *Nature* 486:207-214. PMC3564958
16. VandeWalle JL, Goetz GW, **Huse SM**, Morrison HG, Sogin ML, Hoffman RG, Yan K, and McLellan SL (2012) *Acinetobacter*, *Aeromonas* and *Trichococcus* populations dominate the microbial community within urban sewer infrastructure. *Environmental Microbiology.* Epub 2012 Apr 24.
17. Ozok AR, Persoon IF, **Huse SM**, Keijser BJ, Wesselink PR, Crielaard W, and Zaura E (2012) Ecology of the microbiome of the infected root canal system: a comparison between apical and coronal root segments. *International Endodontic Journal* 45(6):530-541.
18. Amend AS, Oliver TA, Amaral-Zettler LA, Boetius A, Fuhrman J, Horner-Devine MC, **Huse SM**, Mark Welch DB, Martin, AC, Ramette A, Zinger L, Sogin M, and Martiny JH (2012) Macroecological patterns of marine bacteria on a global scale. *Journal of Biogeography*.
19. Brandt BW, Bonder MJ, **Huse SM**, and Zaura E (2012) TaxMan: a server to trim metagenomic rRNA reference databases and inspect taxonomic coverage. *Nucleic Acids Research* Epub 2012 May 22. PMC3394339
20. Finkel O, Burch A, Elad T, **Huse S**, Lindow S, Post, A and Belkin, S (2012) Distance-decay diversity patterns of phyllosphere bacteria on Tamarisk trees across the Sonoran Desert. *Appl and Environ Microbiol.*
21. Freitas S, Hatosy S, Fuhrman J, Huse S, Sogin M, Mark Welch D, and Martiny, AC (2012) Global distribution and diversity of marine *Verrucomicrobia*. *ISME J* 6(8):1499-505.
22. Gobet A, Boer SI, **Huse SM**, van Beusekomm JEE, Quince C, Sogin ML, Boetius A, and Ramette, R (2012) Diversity and dynamics of rare and of resident bacterial populations in coastal sands. *ISME J* 6:542-553.
23. Sun Y, Cai Y, **Huse SM**, Knight R, Farmerie WG, Wang X, and Mai V (2012) A Large-scale Benchmark Study of Existing Algorithms for Taxonomy Independent Analysis. *Briefings in Bioinformatics* 13: 107-121.
24. Post AF, Penno S, Zandbank K, Paytan A, **Huse S**, and Mark Welch D (2011) Long term seasonal dynamics of *Synechococcus* population structure in the Gulf of Aqaba, Northern Red Sea. *Frontiers in Aquatic Microbiology*.
25. Gilbert JA, Steele JA, Caporaso JG, Steinbruck L, Reeder J, Temperton B, **Huse S**, McHardy AC, Knight R,

Joint I, Somerfield P, Fuhrman JA, Field D (2011) Defining seasonal marine microbial community dynamics. *ISME J* 6(2):298-308.

26. Shanks OC, Kelty CA, Archibeque S, Jenkins M, Newton RJ, McLellan SL, **Huse SM**, and Sogin ML. (2011) Community structure of cattle fecal bacteria from different animal feeding operations. *Appl Environ Microbiol*: AEM.02988-02910.
27. White J, Gilbert J Hill G, Hill E, **Huse SM**, Weightman AJ, Mahenthiralingam E (2011) Culture-independent analysis of bacterial fuel contamination provides insight into the level of concordance with the standard industry practice of aerobic cultivation. *Appl Environ Microbiol* 77(13): 4527-38.
28. Crielaard W, Zaura E, Schuller A, **Huse S**, Montijn R, and Keijser B (2011) Exploring the oral microbiota of children at various developmental stages of their dentition in the relation to their oral health. *BMC Medical Genomics* 4: 22. PMC3058002
29. Bogaert D, Keijser B, **Huse S**, Rossen J, Veenhoven R, van Gils E Bruin J, Montijn R, Bonten M and Sanders E (2011) Variability and diversity of nasopharyngeal microbiota in children: a metagenomic analysis. *PLoS ONE* 6: e17035. PMC3046172
30. Zinger L, Amaral-Zettler LA, Fuhrman JA Horner-Devine MC, **Huse SM**, Mark Welch DB, Martiny JB, Sogin ML, Boetius A, and Ramette A (2011) *PLoS ONE* 6(0):e24570.
31. **Huse SM**, Mark Welch D, Morrison HG, and Sogin ML (2010) Ironing out the wrinkles in the rare biosphere through improved OTU clustering. *Environmental Microbiology* 12:1889-1898. PMC2909393 ***Top Cited***
32. Huber JA, Cantin HV, **Huse SM**, Mark Welch DB, Sogin ML, and Butterfield DA (2010) Isolated communities of Epsilonproteobacteria in hydrothermal vent fluids of the Mariana Arc seamounts. *FEMS microbiology ecology* 73: 538-549.
33. Gilbert JA, Field D, Swift P, Thomas S, Cummings D, Temperton B, Weynber K, **Huse S**, Hughes M, Joint I, Somerfield PJ, and Muhling M (2010) The taxonomic and functional diversity of microbes at a temperate coastal site: a 'multi-omic' study of seasonal and diel temporal variation. *PLoS ONE* 5.
34. Zaura E, Keijser B, **Huse S**, and Crielaard W (2009) Defining the healthy "core microbiome" of oral microbial communities. *BMC Microbiology* 9: 259. PMC2805672
35. McLellan SL, **Huse SM**, Mueller-Spitz SR, Andreishcheva EN, and Sogin ML (2009) Diversity and population structure of sewage-derived microorganisms in wastewater treatment plant influent. *Environmental Microbiology* 12: 378-392.
36. Lazarevic V, Whiteson K, **Huse S**, Hernandez D, Farinelli L, Osteras M et al. (2009) Metagenomic study of the oral microbiota by Illumina high-throughput sequencing. *Journal of Microbiological Methods* 79: 266-271.
37. Huber JA, Morrison HG, **Huse SM**, Neal PR, Sogin ML, and Mark Welch DB (2009) Effect of PCR amplicon size on assessments of clone library microbial diversity and community structure. *Environmental Microbiology* 11: 1292-1302. PMC2716130 ***Top Cited***
38. Gilbert JA, Dawn F, Paul S, Lindsay N, Anna O, Tim S, Somerfield P, **Huse S**, and Joint I (2009) The seasonal structure of microbial communities in the Western English Channel. *Environmental Microbiology* 11: 3132-3139.
39. Antonopoulos DA, **Huse SM**, Morrison HG, Schmidt TM, Sogin ML, and Young VB (2009) Reproducible Community Dynamics of the Gastrointestinal Microbiota Following Antibiotic Perturbation. *Infect Immun*: IAI.01520-01508. PMC2687343
40. Amaral-Zettler LA, McCliment EA, Ducklow HW, and **Huse SM** (2009) A Method for Studying Protistan Diversity Using Massively Parallel Sequencing of V9 Hypervariable Regions of Small-Subunit Ribosomal RNA Genes. *PLoS ONE* 4: e6372.
41. Keijser BJF, Zaura E, **Huse SM**, van der Vossen JMBM, Schuren FHJ, Montijn RC, ten Cate JM, and Crielaard W (2008) Pyrosequencing analysis of the oral microflora of healthy adults. *Journal of Dental Research* 87: 1016-1020.
42. **Huse SM**, Dethlefsen L, Huber JA, Mark Welch DB, Relman DA, and Sogin ML (2008) Exploring Microbial Diversity and Taxonomy Using SSU rRNA Hypervariable Tag Sequencing. *PLoS Genetics* 4: e1000255. PMC2577301
43. Dethlefsen L, **Huse S**, Sogin ML, and Relman DA (2008) The Pervasive Effects of an Antibiotic on the

Human Gut Microbiota, as Revealed by Deep 16S rRNA Sequencing. *PLoS Biology* 6: e280 PMC2586385

44. Morrison HG, McArthur AG, Gillin FD, Aley SB, Adam RD, Olsen GJ, Best AA, Cande WZ, Chen F, Cipriano MJ, Davids BJ, Dawson SC, Elmendorf HG, Hehl AB, Holder ME, **Huse** SM, Kim UU, Lasek-Nesselquist E, Manning G, Nigam A, Nixon JEJ, Palm D, Passamaneck NE, Prabhu A, Reich CL, Reiner DS, Samuelson J, Svard SG, Sogin ML (2007) Genomic Minimalism in the Early Diverging Intestinal Parasite Giardia lamblia. *Science* 317: 1921-1926. PMID: 17901334
45. **Huse S**, Huber J, Morrison H, Sogin M, and Mark Welch D (2007) Accuracy and quality of massively parallel DNA pyrosequencing. *Genome Biology* 8: R143. PMC2323236 ***Highly Accessed***
46. Huber JA, Mark Welch DB, Morrison HG, **Huse SM**, Neal PR, Butterfield DA, and Sogin ML (2007) Microbial Population Structures in the Deep Marine Biosphere. *Science* 318: 97-100.
47. Sogin ML, Morrison HG, Huber JA, Mark Welch D, **Huse SM**, Neal PR Arrieta J, and Herndl G (2006) Microbial diversity in the deep sea and the underexplored "rare biosphere". *Proceedings of the National Academy of Sciences* 103: 12115-12120. PMC1524930

Books and Book Chapters

1. **Huse SM**, Mark Welch DB, Sogin ML (2013) Sequencing errors, diversity estimates and the rare biosphere. In *The Science and Applications of Microbial Genomics*. Institute of Medicine, Washington, DC: The National Academies Press.
2. **Huse SM**, and Mark Welch DB. (2011) Accuracy and quality of massively parallel DNA pyrosequencing. In *Handbook of Molecular Microbial Ecology I: Metagenomics and Complementary Approaches*. de Bruijn, F.J. (ed): Wiley and Sons.
3. Mark Welch DB, and **Huse SM** (2011) Microbial diversity in the deep sea and the underexplored “rare biosphere". In *Handbook of Molecular Microbial Ecology II: Metagenomics in Different Habitats*. de Bruijn, F.J. (ed): Wiley and Sons.
4. Shanks OC, McLellan SL, **Huse SM**, and Sogin ML (2011) Characterization of microbial community structures in recreational waters and primary sources of faecal pollution with a next-generation sequencing approach. In *Environmental Microbiology: Current Technology and Water Applications*. Sen, K., and Ashbolt, N.J. (eds). Norfolk, UK: Caister Academic Press.

Publications in Review or Submission

1. He Y, Jiang X-T, Caporaso JG, Sheng H-F, **Huse SM**, Edgar RC, Knight R, Zhou H-W (in review) Stable operational taxonomic units for studying microbial ecology. *Molecular Biology and Evolution*
2. Saffarini, CM, McDonnell-Clark EV, Amin A, **Huse SM**, Boekelheide K (in submission) Developmental exposure to estrogen alters differentiation and epigenetic programming in a human fetal prostate xenograft model. *Endocrinology*

Invited Presentations

October 23, 2013	“Identifying the role of functional microbial clades in Ulcerative Colitis”, Center for Computational and Molecular Biology, Brown University, Providence, RI
February 7, 2013	“How to Measure the Human Microbiome in Clinical Research Projects”, Liver Research Center, Division of Gastroenterology, Brown University, Providence, RI
October 17, 2012	“Marker Gene Analysis: Best Practices” Microbiome of the Built Environment. Boulder, CO
September 27, 2012	“The Human Microbiome in Health and Disease” Brown University, Providence, RI
June 13, 2012	“The Impact Of Sequencing Errors On Estimates Of Diversity In The Rare Biosphere (And Potential Solutions)” The Science and Applications of Microbial Genomics, Institute of Medicine, National Academy of Sciences.
January 25, 2012	“What’s at the Core of the Human Microbiome?” Institute for Genome Studies, University of Maryland.
December 12, 2011	“Exploring the Human Microbiome via Next-Gen rRNA Sequence Tags”,

	University of Colorado, Boulder.
December 9, 2011	“Comparing Microbial Communities using DNA Clustering”, Argonne National Laboratory, Chicago, IL
November 29, 2011	“New Techniques for Taxonomic-Independent Analyses of the Microbiome” University of Idaho, Moscow.
June 17, 2010	“Effect of Clustering Method on the Estimated Richness of Microbial Communities.” Classification Society 2010, Saint Louis, MO
March 26, 2010	“454 Pyrosequencing rRNA Tags of Microbial Communities: Lessons Learned” University of North Carolina, Charlotte, NC
Feb. 25, 2010	“Improved Sequence-Based Clustering of rRNA Tags from Next-Generation Sequencing for Studying Microbial Diversity” Academic Center for Dentistry Amsterdam (ACTA), Holland.

Grants

NSF Biological Databases and Infrastructure. *Expanding visualization and analysis tools for comparative microbial ecology*. S Huse, PI. $769,827 ($508.832 direct) over 3 years. (09/01/2011 – 09/30/2013)

University Teaching Roles

BIOL2860: Molecular Mechanisms of Human Disease, Brown University, guest lecture: Bioinformatics and the Analysis of RT^2 PCR Microarrays; 2012

Strategies and Techniques for Analyzing Microbial Population Structures, Marine Biological Laboratory Special Topics Course - “NextGen QAQC: Quality filtering and trimming next-gen reads”; “Assigning taxonomy with 16S genes”; “SSU rRNA Clustering”; “Visualization and Analysis of Microbial Population Structures”. 2011, 2012, 2013

Molecular Evolution – Marine Biological Laboratory Summer Course: “Introduction to Perl programming”. 2010

Using GIS in Alaska National Parks, National Park Service - weeklong introduction to GIS.

Using Remote Sensing Data, Department of Water Resources, State of California - short course for government agency professionals.

GIS Applications in Anthropology, University of California, Berkeley – section of graduate class in applied anthropology.

Introduction to GIS Laboratory, University of California, Berkeley – graduate-level laboratory in applied GIS for environmental planning.

Introductory Biology Laboratory, University of California, Berkeley – lab course on ecology and plant physiology.

Professional Societies

American Society for Microbiology

Service to the Profession

Referee of grants - NSF Advances in Biological Informatics.

Referee of manuscripts – journals include: Bioinformatics, BMC Bioinformatics, Journal of the International Society for Microbial Ecology, Microbiome, Molecular Ecology, Nature Methods, Nucleic Acids Research, PLoS ONE, Proceedings B of the Royal Society

Postgraduate Honors and Awards

2002	Time Off Award, National Park Service “in acknowledgement of exceptional performance”
2000	Special Achievement Award, National Park Service “for performance substantially exceeding job requirements.”

2000	Star Award, National Park Service "for creative efforts, tireless energy and dedication."
1999	Best GIS in Alaska, ESRI, Awarded to the National Park Service Alaska Support Office GIS Team primarily for the *GIS Theme Manager* and the *AlaskaPak* toolset. Presented at the annual ESRI International User Conference.
1999	Certificate of Achievement, National Park Service "for outstanding performance, achievement, and contributions as a Federal Employee."
1999	On the Spot Award, National Park Service "in acknowledgement of exceptional performance."
1998	Special Achievement Award, National Park Service "for performance substantially exceeding job requirements."
1996	Best University Website, GIS World. Awarded to the Regional Program in Environmental Planning at University of California, Berkeley for *GRASSLinks*.