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|  |  | Education**University of Chicago** PhD, biophysical sciences 2011-2015* advisers: Profs. Jack Gilbert and Maureen Coleman
* dissertation title: *Multiscale microbial systems ecology and evolution*.

**Uppsala University** MSc, microbiology2009-2010* adviser: Prof. Peter Lindblad
* thesis title: *Synthetic Biology for Renewable Energy*.

**The University of Montana** BA/BSc/BA, molecular biology/microbiology/French 2002-2008* undergraduate research adviser: Prof. James Gannon
* minor: chemistry
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|  |  | Research Experience **Institute for Systems Biology** 2018-presentWashington Research Foundation Innovation Faculty & Assistant Professor* Investigate eco-evolutionary feedbacks in microbial communities.
* Determine how gut microbiota influence human health and well-being.
* Design targeted strategies to engineer the gut microbiome for improved human health.

**Center for Microbiome Informatics and Therapeutics** 2015-2018MIT Dept. of Biological Engineering and The Broad Institute, Postdoctoral Research Associate* Adviser: Prof. Eric Alm
* Developed analytical/computational workflows for studying the dynamics of microbial populations in the gut.
* Coordinated multidisciplinary team investigating high-resolution eco-evolutionary dynamics of diverse microbial populations in the human gastrointestinal tract.
* Designed a series of mouse experiments looking at how combined dietary and antibiotic perturbations influence the structure and stability of the gut microbiome.
* Developed a model-free normalization method for high-throughput sequencing data.

**EPA STAR Graduate Research Fellow** 2011-2015University of Chicago Biophysical Sciences Program, Graduate Student* Advisers: Prof. Jack Gilbert and Prof. Maureen Coleman
* Led a study of marine microbial biogeography, investigating whether or not microbes are dispersal-limited across the globe.
* Established and coordinated outside collaborations on the influence of invasive plants on soil microbial communities and on how human land use activities alter river sediment microbial community structure and function.
* Developed and carried out a high-throughput bacterial microcosm experiment to test classic ecological theory on how environmental disturbances influence ecological diversity; collaborated with colleagues from the physics department to develop a mathematical formalism for modeling my empirical results.
* Worked on several of the first investigations of how the human microbiome interacts with our built environment.

**Institute for Genomics and Systems Biology** 2012-2015Argonne National Laboratory, Biological Sciences Division, Research Associate * Adviser: Prof. Jack Gilbert
* Senior data analyst for the [Earth Microbiome Project](http://www.earthmicrobiome.org) - coordinated collection and analysis of microbial community data from a variety of environments across planet Earth.
* Collaborated with researchers from the Knight and Caporaso labs to develop computational tools for processing very large sequencing data sets.

**Complex Systems Summer School** 2014Santa Fe Institute, Graduate Student * Team leader on a project that investigated tradeoffs between efficiency and robustness of complex, adaptive systems (i.e. from economics to ecology); report: <http://goo.gl/9S4Rmy>

**Molecular Ecology Laboratory** 2010-2011MPG Ranch, Research Scientist* Ran the molecular ecology wet-lab at MPG Ranch; supervisors: Dr. Ylva Lekberg & Dr. Philip Ramsey
* Studied the impacts of invasive plant species on grasslands soil microbial communities.
* Trained and managed research technicians in DNA extraction, PCR, next-generation sequencing library preparation, bioinformatics, and multivariate statistical analyses.

**Fulbright Graduate Research Fellow** 2009-2010Uppsala University, Ångström Laboratory, Graduate Student * Advisers: Prof. Peter Lindblad & Dr. Thorsten Heidorn.
* Conducted synthetic biology research geared toward engineering biohydrogen production pathways in cyanobacteria.

**Environmental and Industrial Microbiology Laboratory** The University of Montana, Laboratory Manager 2008-2009* Advisers: Prof. James Gannon and Dr. Philip Ramsey
* Managed the Environmental and Industrial Microbiology Laboratory at the University of Montana.
* Trained graduate students and postdocs in wet lab techniques.
* Developed wet-lab protocols and conducted independent research on the effects of heavy metals on microbial metabolism and community assembly.

The University of Montana, Laboratory Technician 2005-2008* Adviser: Prof. James Gannon
* Cultured and characterized novel bacterial strains from the Nyack Microbial Observatory in Glacier National Park, cleaned glassware, prepared media, and maintained/repaired equipment.
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|  |  | Teaching Experience**Computational Analysis Strategies for the Microbiome Workshop, University of Costa Rica** Fall, 2017Instructor* Co-taught a week-long graduate workshop on metagenomic and metatranscriptomic data analysis at the University of Costa Rica

**Seeds of Change Bioinformatics Education Program**  Spring, 2017Guest Lecturer* Presented to high-school students in Minnesota on the human gut microbiome.

**ACERA School of Science, Creativity and Leadership, Cambridge, MA** Fall, 2016Visiting Instructor* Developed microscope-based curriculum for middle school students to learn about mycorrhizal fungi.
* Visited the classroom three times: first visit, gave an introductory lecture and then took class outside to collect roots from plants in the playground; second visit, processed, cleared, and stained the roots; third visit, looked at the roots under the microscope and then gave a wrap-up lecture.

**Chief Dull Knife College, Lame Deer, MT** 2010-presentAdjunct Faculty/Visiting Instructor* Taught a molecular ecology course to undergraduate students over two semesters; designed curriculum for the classroom and the wet-lab; held office hours.
* Coordinated a 2-year student research program to characterize the microbial ecology of Tongue River sediments over a 100 km transect, which resulted in a peer-reviewed publication (i.e. [Gibbons et al. 2014](http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0097435)).
* Ran seminars and faculty trainings in wet lab techniques and data analysis.

**Marine Metagenomics Graduate Workshop, Basque Country, Spain** Spring, 2014Erasmus Fellow and Instructor* Gave a series of lectures on statistical methods for analyzing ecological data.

**Bioinformatics in Ecology Workshop, Nanjing, China** Winter, 2013Instructor* Gave a 2-day tutorial on analyzing 16S amplicon data using QIIME.

**University of Chicago, Chicago, IL** Spring 2013Bioinformatics and Microbial Ecology Graduate Course, Teaching Assistant* Served as a teaching assistant for a graduate course taught by Prof. Jack Gilbert.
* Prepared lecture materials, ran data-analysis mini-workshops, held office hours, graded coursework.
* Mentored students who wanted to submit their class projects as publications to a peer-reviewed scientific journal.

**Argonne Soil Metagenomics Conference, Lemont, IL** Fall 2012Teaching Assistant* Co-taught a bioinformatics workshop geared towards analyzing amplicon sequencing data.

**University of Chicago, Chicago, IL** Spring 2012Teaching Assistant Training Course* Took semester-long course designed to train teaching assistants in pedagogy and public speaking.
* Designed lesson plans, gave lectures that were recorded and critiqued by faculty and students, studied teaching theory.

**The University of Montana, Missoula, MT** Fall 2009Guest Lecturer* Guest lectured for an upper division undergraduate course on microbial physiology, taught by Prof. James Gannon.

**The French Ministry of Education, Voiron, France** 2004-2005Instructor* Taught an English discussion and grammar course at Lycée Ferdinand Buisson.
* Designed curriculum and taught classes 5 days a week for 1 year.
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|  |  | Peer-Reviewed Research Publications1. Pakpour, S., Bhanvadia, A., Zhu, R., Amarnani, A., Gibbons, S.M., Gurry, T., Alm, E.J., Martello, L.A. 2017. Identifying predictive features of *Clostridium difficile* infection recurrence before, during, and after primary antibiotic treatment. *Microbiome*, 5:148, doi:10.1186/s40168-017-0368-1.
2. Thompson L.R., Sanders J.G., McDonald D., Ladau J., Locey K., Navas-Molina J.A., Prill R.J., Gibbons S.M., Gonzalez A., Amir A., et al. A communal catalogue reveals Earth’s multiscale microbial diversity. *Nature,* doi:10.1038/nature24621, [rdcu.be/x0Fr](https://t.co/5aiU5T1GvK%22%20%5Co%20%22http%3A//rdcu.be/x0Fr%22%20%5Ct%20%22_blank)
* Covered by [Science Friday](https://www.sciencefriday.com/segments/today-cataloguing-the-human-microbiome-tomorrow-the-worlds/), [Wired](https://www.wired.com/story/the-crazy-ambitious-effort-to-catalogue-every-microbe-on-earth/?mbid=social_twitter_onsiteshare), and [Nature News and Views](http://www.nature.com/nature/journal/vaop/ncurrent/full/nature24756.html)
1. Duvallet, C., Gibbons, S.M., Gurry, T., Irizarry, R. and Alm, E.J., 2017. Meta-analysis of microbiome studies reveals disease-specific and shared responses. *Nature Communications, in press*
* BioRxiv Preprint <http://biorxiv.org/content/early/2017/05/08/134031>
1. Califf, K.J., Schwarzberg-Lipson, K., Garg, N., Gibbons, S.M., Caporaso, J.G., Slots, J., Cohen, C., Dorrestein, P.C., and Kelley, S.T., 2017. Multi-omics analysis of periodontal pocket microbial communities pre-and post-treatment. *mSystems*, 2(3), pp.e00017-17.
2. Gibbons, S.M., Lekberg, Y., Mummey, D.L., Sangwan, N., Ramsey, R.W., and Gilbert, J.A., 2017. Invasive plants rapidly reshape soil properties in a grassland ecosystem. *mSystems* 2.2:e00178-16.
3. Gibbons, S.M., Kearney, S.M., Smillie, C.S., and Alm, E.J., 2017. Two dynamic regimes in the human gut microbiome. *PloS Computational Biology*, http://dx.doi.org/10.1371/journal.pcbi.1005364*.*
4. Gibbons, S.M., Scholz, M., Hutchison, A.L., Dinner, A.R., Gilbert, J.A., and Coleman, M.L., 2016. Disturbance regimes predictably alter diversity in an ecologically complex bacterial system. *mBio 7*(6):e01372-16. doi:10.1128/mBio.01372-16.
5. Xiang, X., Gibbons, S.M., He, J.S., Wang, C., He, D., Li, Q., Ni, Y. and Chu, H., 2016. Rapid response of arbuscular mycorrhizal fungal communities to short-term fertilization in an alpine grassland on the Qinghai-Tibet Plateau. *PeerJ*, *4*, p.e2226.
6. O'Brien, S.L., Gibbons, S.M., Owens, S.M., Hampton‐Marcell, J., Johnston, E.R., Jastrow, J.D., Gilbert, J.A., Meyer, F. and Antonopoulos, D.A., 2016. Spatial scale drives patterns in soil bacterial diversity. *Environmental Microbiology*, *18*(6), pp.2039-2051.
7. Gibbons, S.M. and Gilbert, J.A., 2015. Microbial diversity—exploration of natural ecosystems and microbiomes. *Current Opinion in Genetics & Development*, *35*, pp.66-72.
8. Xiang, X., Gibbons, S.M., Yang, J., Kong, J., Sun, R. and Chu, H., 2015. Arbuscular mycorrhizal fungal communities show low resistance and high resilience to wildfire disturbance. *Plant and Soil*, *397*(1-2), pp.347-356.
9. Wood, M., Gibbons, S.M., Lax, S., Eshoo-Anton, T.W., Owens, S.M., Kennedy, S., Gilbert, J.A. and Hampton-Marcell, J.T., 2015. Athletic equipment microbiota are shaped by interactions with human skin. *Microbiome*, *3*(1), p.1.
10. Leone, V., Gibbons, S.M., Martinez, K., Hutchison, A.L., Huang, E.Y., Cham, C.M., Pierre, J.F., Heneghan, A.F., Nadimpalli, A., Hubert, N. and Zale, E., 2015. Effects of diurnal variation of gut microbes and high-fat feeding on host circadian clock function and metabolism. *Cell Host & Microbe*, *17*(5), pp.681-689.
* Covered by [The Scientist](http://www.the-scientist.com/?articles.view/articleNo/42715/title/Gut-Microbes-Influence-Circadian-Clock/), [The Huffington Post](http://www.huffingtonpost.com/dr-michael-j-breus/unlocking-the-sleep-gut-connection_b_8941314.html), and the [Science Life Blog](https://sciencelife.uchospitals.edu/2015/05/13/the-microbiome-and-the-midnight-snack-how-gut-microbes-influence-the-bodys-clock/).
1. Gibbons, S.M., Schwartz, T., Fouquier, J., Mitchell, M., Sangwan, N., Gilbert, J.A. and Kelley, S.T., 2015. Ecological succession and viability of human-associated microbiota on restroom surfaces. *Applied and Environmental Microbiology*, *81*(2), pp.765-773.
* Covered by the [New York Times](http://well.blogs.nytimes.com/2014/12/04/go-ahead-use-the-restroom/?_r=0), [National Public Radio](http://www.npr.org/sections/health-shots/2014/11/21/365692827/what-microbes-lurked-in-the-last-public-restroom-you-used), the [Science Life Blog](https://sciencelife.uchospitals.edu/2014/12/03/the-microbes-growing-in-a-public-restroom-and-why-thats-not-as-bad-as-it-sounds/), and featured in Ed Yong’s book [“I Contain Multitudes”](http://www.sciencefriday.com/articles/the-microbes-we-share/)
1. Fuller, M., Priyadarshini, M., Gibbons, S.M., Angueira, A.R., Brodsky, M., Hayes, M.G., Kovatcheva-Datchary, P., Bäckhed, F., Gilbert, J.A., Lowe, W.L. and Layden, B.T., 2015. The short-chain fatty acid receptor, FFA2, contributes to gestational glucose homeostasis. *American Journal of Physiology-Endocrinology and Metabolism*, *309*(10), pp.E840-E851.
2. Torres, P.J., Fletcher, E.M., Gibbons, S.M., Bouvet, M., Doran, K.S. and Kelley, S.T., 2015. Characterization of the salivary microbiome in patients with pancreatic cancer. *PeerJ*, *3*, p.e1373.
3. Van Bonn, W., LaPointe, A., Gibbons, S.M., Frazier, A., Hampton‐Marcell, J. and Gilbert, J., 2015. Aquarium microbiome response to ninety‐percent system water change: Clues to microbiome management. *Zoo Biology*, *34*(4), pp.360-367.
4. Lax, S., Hampton-Marcell, J.T., Gibbons, S.M., Colares, G.B., Smith, D., Eisen, J.A. and Gilbert, J.A., 2015. Forensic analysis of the microbiome of phones and shoes. *Microbiome*, *3*(1), p.1.
* Covered by the [Los Angeles Times](http://www.latimes.com/science/sciencenow/la-sci-sn-microbiome-analysis-fingerprint-20150512-story.html), [National Geographic](http://phenomena.nationalgeographic.com/2015/05/11/can-the-microbes-you-leave-behind-be-used-to-identify-you/), and [The Guardian](https://www.theguardian.com/science/blog/2015/may/15/bacteria-on-shoes-could-help-forensic-teams-catch-suspects).
1. Vitaglione, P., Mennella, I., Ferracane, R., Rivellese, A.A., Giacco, R., Ercolini, D., Gibbons, S.M., La Storia, A., Gilbert, J.A., Jonnalagadda, S. and Thielecke, F., 2015. Whole-grain wheat consumption reduces inflammation in a randomized controlled trial on overweight and obese subjects with unhealthy dietary and lifestyle behaviors: role of polyphenols bound to cereal dietary fiber. *The American Journal of Clinical Nutrition*, *101*(2), pp.251-261.
2. Lax, S., Smith, D.P., Hampton-Marcell, J., Owens, S.M., Handley, K.M., Scott, N.M., Gibbons, S.M., Larsen, P., Shogan, B.D., Weiss, S. and Metcalf, J.L., 2014. Longitudinal analysis of microbial interaction between humans and the indoor environment. *Science*, *345*(6200), pp.1048-1052.
* Covered in [The Washington Post](https://www.washingtonpost.com/news/speaking-of-science/wp/2014/08/28/cops-could-use-bacterial-signatures-to-catch-a-murderer/), [Slate](http://www.slate.com/articles/health_and_science/medical_examiner/2014/09/microbes_in_homes_and_on_pets_humans_inoculate_surfaces_with_own_microbiomes.html), [The Scientist](http://www.the-scientist.com/?articles.view/articleNo/42950/title/Microbiome-Fingerprints/), [New Scientist](https://www.newscientist.com/article/dn26119-moving-home-your-microbes-will-make-the-trip-too), [Nature World News](http://www.natureworldnews.com/articles/8797/20140829/microbes-invade-24-hours.htm), [Wired](http://www.wired.com/2014/12/microbe-discoveries-of-2014/), [National Public Radio](http://www.npr.org/sections/health-shots/2014/11/21/365692827/what-microbes-lurked-in-the-last-public-restroom-you-used?utm_medium=RSS&amp;utm_campaign=shotshealthnews), [Discover Magazine](http://blogs.discovermagazine.com/d-brief/2014/08/28/microbiome-bacterial-aura-follows-you/?utm_source=feedburner&utm_medium=feed&utm_campaign=Feed%3A%20DiscoverTopStories%20%28Discover%20Top%20Stories%29#.V8WLYLX7LQU), and [National Geographic](http://phenomena.nationalgeographic.com/2014/08/28/we-constantly-imprint-our-homes-with-our-microbes/)
1. Pfister, C.A., Gilbert, J.A. and Gibbons, S.M., 2014. The role of macrobiota in structuring microbial communities along rocky shores. *PeerJ*, *2*, p.e631.
2. Winston, M.E., Hampton-Marcell, J., Zarraonaindia, I., Owens, S.M., Moreau, C.S., Gilbert, J.A., Hartsel, J., Kennedy, S.J. and Gibbons, S.M., 2014. Understanding cultivar-specificity and soil determinants of the cannabis microbiome. *PloS One*, *9*(6), p.e99641.
3. Lekberg, Y., Gibbons, S.M. and Rosendahl, S., 2014. Will different OTU delineation methods change interpretation of arbuscular mycorrhizal fungal community patterns? *New Phytologist*, *202*(4), pp.1101-1104.
4. Gibbons, S.M., Jones, E., Bearquiver, A., Blackwolf, F., Roundstone, W., Scott, N., Hooker, J., Madsen, R., Coleman, M.L. and Gilbert, J.A., 2014. Human and environmental impacts on river sediment microbial communities. *PLoS One*, *9*(5), p.e97435.
5. This paper was published based on data collected during an applied molecular ecology course I taught at Chief Dull Knife College.
6. Rideout, J.R., He, Y., Navas-Molina, J.A., Walters, W.A., Ursell, L.K., Gibbons, S.M., Chase, J., McDonald, D., Gonzalez, A., Robbins-Pianka, A. and Clemente, J.C., 2014. Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. *PeerJ*, *2*, p.e545.
7. Xiong, J., Sun, H., Peng, F., Zhang, H., Xue, X., Gibbons, S.M., Gilbert, J.A. and Chu, H., 2014. Characterizing changes in soil bacterial community structure in response to short-term warming. *FEMS Microbiology Ecology*, *89*(2), pp.281-292.
8. McTee, M.R., Gibbons, S.M., Feris, K., Gordon, N.S., Gannon, J.E. and Ramsey, P.W., 2013. Heavy metal tolerance genes alter cellular thermodynamics in Pseudomonas putida and river Pseudomonas spp. and influence amebal predation. *FEMS Microbiology Letters*, *347*(2), pp.97-106.
9. Rubin, B.E., Gibbons, S.M., Kennedy, S., Hampton-Marcell, J., Owens, S. and Gilbert, J.A., 2013. Investigating the impact of storage conditions on microbial community composition in soil samples. *PloS One*, *8*(7), p.e70460.
10. Publication of a Bioinformatics and Microbial Ecology class project.
11. Lekberg, Y., Gibbons, S.M., Rosendahl, S. and Ramsey, P.W., 2013. Severe plant invasions can increase mycorrhizal fungal abundance and diversity. *The ISME Journal*, *7*(7), pp.1424-1433.
12. Gibbons, S.M., Caporaso, J.G., Pirrung, M., Field, D., Knight, R. and Gilbert, J.A., 2013. Evidence for a persistent microbial seed bank throughout the global ocean. *Proceedings of the National Academy of Sciences*, *110*(12), pp.4651-4655.
* Covered by [National Geographic](http://phenomena.nationalgeographic.com/2013/03/04/everything-everywhere-english-channel/) and the [Science Life Blog](https://sciencelife.uchospitals.edu/2013/03/26/deep-sequencing-the-english-channel-or-how-you-can-find-any-microbe-if-you-look-hard-enough/)
1. Roy, A.S., Gibbons, S.M., Schunck, H., Owens, S., Caporaso, J.G., Sperling, M., Nissimov, J.I., Romac, S., Bittner, L., Mühling, M. and Riebesell, U., 2013. Ocean acidification shows negligible impacts on high-latitude bacterial community structure in coastal pelagic mesocosms. *Biogeosciences*, *10*(1), pp.555-566.
2. Larsen, P.E., Gibbons, S.M. and Gilbert, J.A., 2012. Modeling microbial community structure and functional diversity across time and space. *FEMS Microbiology Letters*, *332*(2), pp.91-98.
3. Ramsey, P.W., Gibbons, S.M., Rice, P., Mummey, D.L., Feris, K.P., Moore, J.N., Rillig, M.C. and Gannon, J.E., 2012. Relative strengths of relationships between plant, microbial, and environmental parameters in heavy-metal contaminated floodplain soil. *Pedobiologia*, *55*(1), pp.15-23.
4. Lekberg, Y., Schnoor, T., Kjøller, R., Gibbons, S.M., Hansen, L.H., Al‐Soud, W.A., Sørensen, S.J. and Rosendahl, S., 2012. 454‐sequencing reveals stochastic local reassembly and high disturbance tolerance within arbuscular mycorrhizal fungal communities. *Journal of Ecology*, *100*(1), pp.151-160.
5. Gibbons, S.M., Feris, K., McGuirl, M.A., Morales, S.E., Hynninen, A., Ramsey, P.W. and Gannon, J.E., 2011. Use of microcalorimetry to determine the costs and benefits to Pseudomonas putida strain kt2440 of harboring cadmium efflux genes. *Applied and Environmental Microbiology*, *77*(1), pp.108-113.
6. Feris, K.P., Ramsey, P.W., Gibbons, S.M., Frazar, C., Rillig, M.C., Moore, J.N., Gannon, J.E. and Holben, W.E., 2009. Hyporheic microbial community development is a sensitive indicator of metal contamination. *Environmental Science & Technology*, *43*(16), pp.6158-6163.

**Commentaries and Book Chapters**1. Kearney, S.M., Gibbons, S.M., 2018. Designing synbiotics for improved human health. *Microbial Biotechnology*, *11*(1), 141-144.
2. Gibbons, S.M., 2017. Metapopulation theory provides new insight into microbial biogeography. *Environmental Microbiology*, doi: 10.1111/1462-2920.13702
3. Gibbons, S.M., 2017. Microbial community ecology: function over phylogeny. *Nature Ecology & Evolution*,1(1), doi:10.1038/s41559-016-0032
4. Gibbons, S.M., 2016. The Built Environment Is a Microbial Wasteland. *mSystems*, *1*(2), pp.e00033-16.
5. Gibbons, S.M., 2015*.* Statistical Tools for Data Analysis*. Hydrocarbon and Lipid Microbiology Protocols. Springer Protocols Handbooks, Humana Press.*

**Publications in Review**1. Zhao, S., Lieberman, T.D., Poyet, M., Groussin, M., Gibbons, S.M., Xavier, R.J., Alm, E.J., 2017. Adaptive evolution within the gut microbiome of individual people. *Nature, in review*
* BioRxiv Preprint <https://www.biorxiv.org/content/early/2017/10/24/208009>
1. Gibbons, S.M., Duvallet, C., Alm, E.J., 2017. Correcting for batch effects in case-control microbiome studies. *PloS Comput Biol, in review*
* BioRxiv Preprint <http://www.biorxiv.org/content/early/2017/07/24/165910>
1. Gurry, T., HST Microbiome Consortium, Gibbons, S.M., Nguyen, L.T.T., Kearney, S.M., Ananthakrishnan, A., Jiang, X., Kassam, Z., Alm, E.J. 2017. Predictability and persistence of probiotic dietary supplementation in a healthy human cohort. *Cell Reports, in review*
* BioRxiv Preprint <https://www.biorxiv.org/content/early/2017/11/21/222919>
1. Kearney, S.M., Gibbons, S.M., Poyet, M., Gurry, T., Bullock, K., Allegretti, J.R., Clish, C.B., Alm, E.J. 2017. Endospores and other lysis-resistant bacteria comprise a widely shared core community within the human microbiota. *eLife, in review*
* BioRxiv Preprint <https://www.biorxiv.org/content/early/2017/11/27/221713>
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|  |  | **Selected Presentations (Invited)**Gibbons, S.M. 2017. Determinants of resilience in microbial communities. *Invited Talk, Institute for Systems Biology, Seattle, WA*Gibbons, S.M. 2017. Individual-specific eco-evolutionary dynamics in the human gut. *Invited Talk, Center for the Study of Inflammatory Bowel Disease Annual Symposium, Massachusetts General Hospital, Boston, MA*Gibbons, S.M., Kearney, S.M., Smillie, C.S., Alm, E.J. 2017. Two dynamic regimes in the human gut microbiome? *Invited Talk, Ecological Society of America Conference, Portland, OR*Gibbons, S.M. 2017. How do we model microbial dynamics in the gut? *Invited Talk, Channing Network Division Seminar, Harvard Medical School, Cambridge, MA*Gibbons, S.M. 2017. Microbial systems as quantitative models for understanding ecological resilience. *Invited Talk, UCLA Ecology and Evolution Dept. Seminar, Los Angeles, CA*Gibbons, S.M. 2016. The ecology of the human gut microbiome in health and disease. *Invited Talk, Whitehead Institute Teacher Program Seminar, Cambridge, MA*1. Gibbons, S.M., Waldbauer, J., and Coleman, M.L. 2015. Protein expression levels constrain evolutionary trajectories during genome streamlining. *Invited Talk, Microbial Systems Seminar, MIT, Cambridge, MA*
2. Gibbons, S.M., Coleman, M.L.C., Gilbert, J.A. 2015. The search for microbes. *Invited Talk, Biological Sciences Division Graduate Student Seminar, University of Chicago*
3. Gibbons, S.M., Scholz, M., Hutchison, A.L., Dinner, A.R., Gilbert, J.A., Coleman, M.L. 2014. The Intermediate Disturbance Hypothesis: why should diversity peak at intermediate disturbance? *Invited Talk, Natural History Seminar, University of Chicago, Dept. of Ecology and Evolution, Chicago, IL*
4. Gibbons, S.M., Rideout, J., Gonzalez, A., Prestat, E., Caporaso, J.G., Knight, R., Jansson, J., and Gilbert, J.A. 2013. The Earth Microbiome Project: Planetary-scale systems ecology. *Invited talk, TDWG Biodiversity and Informatics Standards Conference, Florence, Italy*
5. Gibbons, S.M., Gilbert, J.A. 2013. The Earth Microbiome Project: Planetary-scale systems ecology*. Invited lecture, Genome Science Symposium. Tokyo, Japan*

**Selected Presentations (Contributed)**1. Gibbons, S.M., Kearney, S.M., Smillie, C.S., and Alm, E.J. 2017. Two dynamical regimes in the human gut microbiome. *Poster presentation, Simons Conference on Statistical and Algorithmic Challenges in Microbiome Data Analysis, Cambridge, MA*
2. Gibbons, S.M., Kearney, S.M., Smillie, C.S., and Alm, E.J. 2017. Two dynamical regimes in the human gut microbiome. *Poster presentation, Keystone Conference on the Human Microbiome, Keystone, CO*
3. Gibbons, S.M., Ling, X., Gurry, T., Avila, J., Roesemann, S., Rich, S., Alexander, J., Vlamakis, H., Poon, T., Burgess, J., Kim, C., Swanson, P., Smith, M., Xavier, R., and Alm, E.J. 2016. Unraveling the ecological context of the Broad Microbiome Library. *Poster presentation, Broad Institute 12th Annual Retreat, Boston, MA*
4. Gibbons, S.M., Kearney, S.M., Smillie, C.S., and Alm, E.J. 2016. Two dynamical regimes in the human gut microbiome. *Poster presentation, MIT Center for Microbial Informatics and Therapeutics 1st Annual Symposium, Cambridge, MA*
5. Gibbons, S.M., Kearney, S.M., Smillie, C.S., and Alm, E.J. 2016. Two dynamical regimes in the human gut microbiome. *Poster presentation, Boston Bacterial Meeting, Cambridge, MA*
6. Gibbons, S.M. 2016. The built enviroment is a microbial wasteland. *Oral presentation, Sloan Early Career Workshop on the Microbiology of the Built Environment, Chicago, IL*
7. Gibbons, S.M., Zhao, S., Kearney, S.M., and Alm, E.J. 2016. Phylogenetically coherent correlation modules in the human gut microbiome. *Poster presentation, Simons Foundation Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis, New York, NY*
8. Gibbons, S.M., Scholz, M., Hutchison, A.L., Dinner, A.R., Gilbert, J.A., Coleman, M.L. 2015. Combining microbial microcosms and mathematical models to enhance our quantitative understanding of diversity-disturbance relationships in ecology. *Poster presentation, 13th Symposium on Bacterial Genetics and Ecology, University of Milan, Italy*
9. Gibbons, S.M., González, A., Prestat, E., Rideout, J., Caporaso, J.G., Knight, R., Jansson, J., Lekberg, Y., Mummey, D.L., Ramsey, P.W., Coleman, M.L., and Gilbert, J.A. 2014. The Earth Microbiome Project: microbial ecology of exotic plant invasions. *Oral presentation, Argonne Soil Metagenomics Workshop, Chicago, IL*
10. Gibbons, S.M., Lekberg, Y., Mummey, D., Ramsey, P.W., Coleman, M.L., and Gilbert, J.A. 2013. Microbial Ecology of Exotic Plant Invasions. *Poster presentation, International Thünen Symposium on Soil Metagenomics, Braunschweig, Germany*
11. Gibbons, S.M., Caporaso, J.G., Knight, R., Gilbert, J.A. 2012. Microbial biogeography across the seven seas. *Poster presentation, International Society for Microbial Ecology (ISME) Meeting. Copenhagen, Denmark*
12. Gibbons, S.M., Lekberg, Y., Ramsey, P.W. 2011. Impacts of leafy spurge herbivory and disease on interactions with soil microbial communities. *Poster presentation, Soil Ecology Conference. Kelowna, Canada*
13. Gibbons, S.M., Kogan, C., Gannon, J.E., Bardsley, J. 2008. Identifying and characterizing a novel metabolic pathway involving the mineralization of sodium dimethyldithiocarbamate by a six-member bacterial consortium. *Oral presentation, University of Montana Undergraduate Research Conference. Missoula, MT*
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|  |  | **Awards and Grants**2016 Department of Energy ENIGMA Discovery Grant ($102,000)**2014 Erasmus Mundus Scholarship for Visiting Scholars (University of the Basque Country, Spain)** 2014 University of Chicago Graduate Student Council Travel Award2013 University of Chicago Biological Sciences Division Student Travel Grant2013 Travel Grant for the International Thünen Symposium on Soil Metagenomics**2012 EPA STAR Graduate Fellowship (3 years; tuition, stipend, and research expenses)** 2012 Amazon Web Services Education Grant ($1,000) **2010 Fulbright Graduate Fellowship (1 year of support to study abroad)****2008 University of Montana Top Graduating Senior in Microbiology and French Departments**2008 University of Montana Student Service Award for Distinguished Service & Achievement **2007 HHMI MILES Honors Research Fellow** 2007 Julius and Anna Wiegenstein Scholarship for Microbiology2007 Jestrab-Chaffee Scholarship for Academic Excellence 2007 Top Life Science Poster Presentation at the UM Undergraduate Research Conference2007 National SMART Grant **2006 Davidson Honors College Undergraduate Research Award** 2006 Adrian and Sally Walker Scholarship for Financial Need, Community Service, and Academics 2006 Leslie Sheridan Alumni Scholarship for Deserving Science Majors 2005 McGee, Rose Southworth Scholarship for Deserving Students Majoring in a Foreign Language2005 Robert M. Burgess Memorial Scholarship for Promising Undergraduates Majoring in the Humanities 2005 Montana Baker Grant for Low-Income Montanans 2003 Bonhomme Scholarship for Academic Excellence 2002 Fox Foundation Scholarship for Promising High School Graduates |
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|  |  | **Popular Science Writing and Science Communication**1. Gibbons, S.M. 2016. [Finding a Niche](http://microbiome.mit.edu/2016/10/19/finding-a-niche/). Blog Post, MIT Center for Microbiome Informatics & Therapeutics
2. Gibbons, S.M. 2015. [Toilet Ecology](https://www.youtube.com/watch?v=9-ETFcvgLqQ). Video Interview, ScienceVideos.org
3. Gibbons, S.M. 2015. [We contain multitudes](https://www.youtube.com/watch?v=9IknmWiT-l4). Public Lecture, Illinois Humanities Elective Studies Supper Club, bringing together artists and scientists
4. Gibbons, S.M. 2015. [Notes on the human microbiome: myriad bacteria living both in and on our bodies](http://publicradiotulsa.org/post/st-health-notes-human-microbiomes-or-myriad-bacteria-living-both-and-our-bodies#stream/0). Interview with John Schuman, National Public Radio, Tulsa, OK
5. Gibbons, S.M. 2015. [The collateral dammage of antibiotics](http://microbiome.mit.edu/2015/11/30/the-collateral-damage-of-antibiotics/). Blog Post, MIT Center for Microbiome Informatics & Therapeutics
6. Gibbons, S.M. 2015. [Protocol: 16S Amplicon Sequencing](http://www.methodquarterly.com/2015/11/protocol-16s-amplicon-sequencing/). Article, Methods Quarterly
7. Gibbons, S.M. 2015. [Gut check: the ecology of keeping time](http://microbe.net/2015/04/27/gut-check-the-ecology-of-keeping-time/). Blog Post, MicroBE.net
8. Gibbons, S.M. 2015. [Are you dirty enough?](http://www.illinoisscience.org/event/are-you-dirty-enough-microorganisms-in-you-on-you-and-around-you/) Public Lecture, Chicago Science Festival, Chicago, IL
9. Gibbons, S.M. 2014. [Toilet Ecology](http://microbe.net/2014/11/17/toilet-ecology/). Blog Post, MicroBE.net
10. Gibbons, S.M. 2014. [Rhodopseudomonas palustris](http://invisiblelife.yourwildlife.org/rhodopseudomonas-palustris/). Article, The Invisible Life Project

**Non-Scientific Publications**Gibbons, M.S. (author), Gibbons, S.M. (translator), and Held, C. (translator). 2009. Mauvaise Herbes. Propos2Editions, France. * *A book of poetry I translated from English into French as part of my undergraduate thesis.*

**Peer-Reviewer Activities** *ISME Journal; FEMS Microbiology Reviews; Environmental Microbiology; Environmental Science and Technology; PLOS One; PLOS Computational Biology; Microbiome; Applied and Environmental Microbiology; Canadian Journal of Microbiology; Frontiers in Microbiology; mSystems; Ecography; Cell Host & Microbe; Nature Biotechnology; Nature Ecology & Evolution; Nature Microbiology***Editorial Board Memberships*** *mSystems*, since 2015
* *Environmental Microbiology*, since 2017
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