OMB No. 0925-0001 and 0925-0002 (Rev. 03/2020 Approved Through 02/28/2023)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.  
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Schloss, Patrick

eRA COMMONS USER NAME (credential, e.g., agency login): PSCHLOSS

POSITION TITLE: Professor

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

| INSTITUTION AND LOCATION | DEGREE  (if applicable) | Completion Date  MM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- |
| Cornell University, Ithaca, NY | BS | 05/1997 | Agricultural & Biological Engineering |
| Cornell University, Ithaca, NY | PHD | 12/2001 | Biological & Environmental Eng |
| University of Wisconsin, Madison, WI | Postdoctoral Fellow | 05/2006 | Microbial ecology |

**A. Personal Statement**

My research group is broadly interested in beneficial and pathogenic host-microbiome interactions with the goal of improving our understanding of how the microbiome can be used to reach translational outcomes in the prevention, detection, and treatment of colorectal cancer and *Clostridium difficile* infection. To support these efforts, we develop and apply bioinformatic tools to facilitate our analysis. This has made us leaders in the field of host-microbiome research. Leveraging this expertise, we have become highly involved in training others to use the same types of tools that we use to ensure that our research is computationally reproducible. Toward this goal, I direct the University of Michigan’s local chapter of The Carpentries for whom I teach several workshops each year. I also teach reproducible research practices as a class at the University of Michigan and in off campus workshops. Through these activities, I have taught more than 1200 individuals. Beyond these traditional forms of teaching, I have also been a leader within the biomedical sciences for developing instructional materials for improving the reproducibility of data science. The rich history of practice and teaching reproducible data science in the environment of an active research laboratory and my past oversight of numerous federally-funded projects makes it an ideal environment to conduct the proposed research. My h-index is 51 and our microbiome-focused research spanning more than 100 peer reviewed publications has been cited more than 29,000 times (Web of Science; accessed 6/4/2020).

**B. Positions and Honors**

Positions and Employment

|  |  |
| --- | --- |
| 1997 - 2002 | Graduate Research Assistant, Dept of Biological and Environmental Engineering, Cornell University, Ithaca, NY |
| 2002 - 2006 | Associate Researcher, Dept of Plant Pathology, U of Wisconsin, Madison |
| 2006 - 2009 | Assistant Professor, Dept of Microbiology, U of Massachusetts, Amherst |
| 2009 - 2016 | Associate Faculty, Center for Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor |
| 2009 - 2013 | Assistant Professor, Dept of Microbiology & Immunology, U of Michigan, Ann Arbor |
| 2012 - 2013 | Assistant Professor, Dept of Civil & Environmental Engineering, U of Michigan, Ann Arbor |
| 2013 - 2017 | Associate Professor, Dept of Microbiology & Immunology, U of Michigan, Ann Arbor |
| 2013 - 2015 | Associate Professor, Dept of Civil and Environmental Engineering, U of Michigan, Ann Arbor |
| 2014 - 2017 | Editor, Applied & Environmental Microbiology, Washington, DC |
| 2017 - | Chair of American Society for Microbiology Journals Board, Washington, DC |
| 2017 - | Professor, Dept of Microbiology & Immunology, U of Michigan, Ann Arbor |

Other Experience and Professional Memberships

|  |  |
| --- | --- |
| 2004 - | Member, American Society for Microbiology |
| 2005 - | Member, International Society for Microbial Ecology |
| 2017- | Member, American Association for the Advancement of Science |

Honors

|  |  |
| --- | --- |
| 2003 | Soil Biology Postdoctoral Fellow, United States Department of Agriculture |
| 2003 | University of Wisconsin Teaching Fellowship, Howard Hughes Medical Institute |
| 2008 | Chancellor's Junior Faculty Fellow, University of Massachusetts |
| 2013 | Distinguished Alumnus, University of Wisconsin Department of Bacteriology |
| 2014 | League of Research Excellence, University of Michigan Medical School |
| 2016 | Frederick Novy Collegiate Professorship in Microbiome Research |
| 2016 | Elected to American Academy for Microbiology |

**C. Contributions to Science**

1. A critical aspect of the scientific method is the ability to reproduce the research performed by others so that the field can correct itself as well as build upon previous work and methods to move forward. My lab’s efforts in this area have included implementing these materials in our own research, carrying out meta-analyses to validate and synthesize the work of others, and developing instructional materials to disseminate best practices for ensuring that microbiome research is reproducible. Believing that the best way to lead is through our own example, in each of the manuscripts published by the Schloss lab since 2014, our lab has posted the code and literate programming documents for each of our papers to a GitHub repository to insure transparency to better demonstrate the methods behind each of the numbers and figures in our papers. This has led to numerous other research groups being able to build off of our own research. As the Chair of the American Society for Microbiology Journals Board, I am committed to developing protocols to improve the reproducibility of the research reported in our society’s journals. To make it easier for others to develop the skills to implement these methods that focus on transparency, automation, version control, and literate programming, we have leveraged funding from an NIH grant to develop instructional materials that others can use to implement the practices used in our lab in their own research. This effort builds upon a tradition in other areas of our laboratory known for producing an open source software package, mothur, which has formalized much microbiome research making it more reproducible. These resources have been posted at <https://www.riffomonas.org> and their accompanying videos have been posted on YouTube at <https://www.youtube.com/channel/UCGuktEl5InrcxPfCjmPWxsA>.
   1. Schloss PD. The Riffomonas Reproducible Research Tutorial Series. Journal of Open Source Education. 2018. 1(3), 13. https://doi.org/10.21105/jose.00013. [Not indexed in PubMed]
   2. Schloss PD. Identifying and Overcoming Threats to Reproducibility, Replicability, Robustness, and Generalizability in Microbiome Research. mBio. 2018 Jun 5;9(3). doi: 10.1128/mBio.00525-18. PubMed PMID: 29871915; PubMed Central PMCID: PMC5989067.
   3. Schloss PD. Preprinting Microbiology. MBio. 2017 May 23;8(3). e00438-17. PMID: 28536284; PMCID: PMC5442452
2. Sequencing 16S rRNA genes and clustering those sequences into operational taxonomic units (OTUs) is the primary analysis method that underlies most microbiome research projects. When I began developing software to analyzing 16S rRNA gene sequences, researchers either assigned sequences to OTUs manually or they used private scripts. Our tool, DOTUR, automated and standardized the process and made the source code publicly available. DOTUR has gone on to be cited 1,900 times since it was published in 2005 (Web of Science, 1/23/2020). Noticing that a growing number of tools were being published without providing their source code, we resolved to create a fully open source software package that any researcher could use to perform a broader set of analyses. The result was mothur. In the ten years since it was published, mothur has been cited more than 9,300 times. We are able to keep mothur relevant through regular feature releases and by publishing articles that describe and test new algorithms. The long list of co-authors attests to our mission of serving the research community. While the first three authors wrote the source code, the rest provided documentation and a diverse array of use cases. We are frequently commended for supporting the diverse community of researchers who frequently have limited bioinformatics skills. We are proud of the broad adoption of mothur by users across the microbiome field and around the world. The citations alone are a measure of the significance of this paper. More importantly, mothur has resulted in the standardization of methods and increased the bioinformatics literacy within the field. Sequencing of 16S rRNA genes will continue to be part of microbiome research and mothur will remain a significant part of that effort.
   1. Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, Lesniewski RA, Oakley BB, Parks DH, Robinson CJ, Sahl JW, Stres B, Thallinger GG, Van Horn DJ, Weber CF. Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. Appl Environ Microbiol. 2009 Dec;75(23):7537-41. PubMed PMID: 19801464; PubMed Central PMCID: PMC2786419.
   2. Kozich JJ, Westcott SL, Baxter NT, Highlander SK, Schloss PD. Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq Illumina sequencing platform. Appl Environ Microbiol. 2013 Sep;79(17):5112-20. PubMed PMID: [23793624](http://www.ncbi.nlm.nih.gov/pubmed/23793624/); PubMed Central PMCID: [PMC3753973](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3753973/).
   3. Westcott SL, Schloss PD. OptiClust, an Improved Method for Assigning Amplicon-Based Sequence Data to Operational Taxonomic Units. mSphere. 2017 Mar-Apr;2(2): e00073-17.. PubMed PMID: [28289728](https://www.ncbi.nlm.nih.gov/pubmed/28289728/); PubMed Central PMCID: [PMC5343174](https://www.ncbi.nlm.nih.gov/pubmed/28289728/).
   4. Schloss PD. Reintroducing mothur: 10 Years Later. Appl Environ Microbiol. 2020. Jan 7;86(2):e02343-19. PubMed PMID: 31704678; PubMed Central PMCID: PMC6952234.
3. The standard microbiome analysis will determine whether the communities from healthy and diseased individuals have the same diversity or composition. By analogy, these studies are similar to genome-wide association studies that seek to identify single alleles that can be associated with the disease. Just as geneticists sought out the gene responsible for Huntington’s Disease, there are microbiome researchers searching for the “obesity bug”. It is far more likely that the microbiome involvement for many diseases is analogous to polygenic traits. Geneticists are also looking for the combination of alleles that result in diabetes and so microbiome researchers need to seek out the consortia within the broader microbiome that is responsible for colon cancer. Another difficulty with the standard microbiome study is that they rarely incorporate clinical data; even if the clinical data are reported it only serves a descriptive role and is not incorporated into the overall analysis. In this study we overcame these limitations to identify the subsets of microbiome found in patients’ microbiomes that were associated with *Clostridium difficile* colonization. *C. difficile* infections have emerged as the leading nosocomial infection in the US. Through animal models and epidemiological studies, it has been determined that antibiotic perturbations alter the composition of the gut microbiome to allow colonization by *C. difficile*. We sequenced the microbiome of individuals with and without diarrhea and used their microbiome and clinical data to identify collections of bacteria and clinical data that were associated with *C. difficile* infection. This was a significant result demonstrating that incorporating the microbiome into diagnostic and risk models improve models based on clinical data alone. In subsequent work in my laboratory, we are using multi-omics approaches in animal models of *C. difficile* infection.
4. Schubert AM, Rogers MA, Ring C, Mogle J, Petrosino JP, Young VB, Aronoff DM, Schloss PD. Microbiome data distinguish patients with Clostridium difficile infection and non-*C. difficile*-associated diarrhea from healthy controls. MBio. 2014 May 6;5(3):e01021-14. PubMed PMID: 24803517; PubMed Central PMCID: PMC4010826.
5. Schubert AM, Sinani H, Schloss PD. 2015. Antibiotic-induced alterations of the murine gut microbiota and subsequent effects on colonization resistance against *Clostridium difficile*. mBio. 6: e00974-15. PubMed PMID: 26173701; PubMed Central PMCID: PMC4502226.
6. Jenior ML, Leslie JL, Young VB, Schloss PD. *Clostridium difficile* Colonizes Alternative Nutrient Niches during Infection across Distinct Murine Gut Microbiomes. mSystems. 2017. 2(4). PubMed PMID: 28761936; PubMed Central PMCID: PMC5527303.
7. Jenior ML, Leslie JL, Young VB, Schloss PD. *Clostridium difficile* Alters the Structure and Metabolism of Distinct Cecal Microbiomes during Initial Infection to Promote Sustained Colonization. mSphere. 2018. 3(3). PubMed PMID: 29950381; PubMed Central PMCID: PMC6021602.
8. Whether changes in the microbiome induce tumorigenesis or does the microbiome change as a result of tumorigenesis is the heart of our research into the role of the microbiome in colorectal cancer. Our studies in this area have been significant because they demonstrated an experimental framework for establishing causation in microbiome research and the use of machine learning algorithms to identify biomarkers that are diagnostic of tumors. Through a series of studies using a mouse model of colorectal cancer, we used 16S rRNA gene sequencing to identify changes in the microbiome in a murine model of colon cancer, demonstrated that altering the gut community with antibiotics suppressed tumor formation, and showed that transferring the original tumor-associated microbiome into germ free mice and applied the tumorigenesis-inducing treatment increased the number and size of tumors. Overall, our results point to the microbiome as a necessary component to the process of tumorigenesis. With these results, we then proceeded to apply sequencing and metabolomics techniques to identify biomarkers of disease in human populations. The first wave of microbiome research has been limited to the characterization of the composition of the microbiome under a variety of conditions. Our works is significant because it moves beyond this threshold and delves into designing experiments that manipulate the communities to test predictions about the role of the microbiome and translate those results into results into a potential diagnostic tool for the clinic. Furthermore, it demonstrates an extreme level of rigor that my lab is working at to understand the role of the microbiome in health and disease.
   1. Zackular JP, Baxter NT, Iverson KD, Sadler WD, Petrosino JF, Chen GY, Schloss PD. The gut microbiome modulates colon tumorigenesis. MBio. 2013 Nov 5;4(6):e00692-13. PubMed PMID: [24194538](http://www.ncbi.nlm.nih.gov/pubmed/24194538/); PubMed Central PMCID: [PMC3892781](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3892781/).
   2. Zackular JP, Baxter NT, Chen GH, Schloss PD. Manipulation of the gut microbiota reveals role in colon tumorigenesis. *mSphere*. 2015 Nov;1(1):e00001-15. PubMed PMID: [27303681](https://www.ncbi.nlm.nih.gov/pubmed/27303681); PubMed Central PMCID: [PMC4863627](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4863627/).
   3. Baxter NT, Ruffin MT IV, Rogers MAM, Schloss PD. Microbiota-based model improves the sensitivity of fecal immunochemical test for detecting colonic lesions. *Genome Medicine*. 2016: Apr;8:37. PubMed PMID: [27056827](https://www.ncbi.nlm.nih.gov/pubmed/27056827); PubMed Central PMCID: [PMC4823848](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4823848/).
   4. Sze MA, Topçuoğlu BD, Lesniak NA, Ruffin MT 4th, Schloss PD. Fecal Short-Chain Fatty Acids Are Not Predictive of Colonic Tumor Status and Cannot Be Predicted Based on Bacterial Community Structure. MBio. 2019.10(4). PubMed PMID: 31266879; PubMed Central PMCID: PMC6606814.
9. My research group participated in the first phase of the Human Microbiome Project (HMP) as a member of the Data Analysis Working Group. We developed the data curation pipeline that was used to process the data that was ultimately used in publications from the first phase of the project. This series of papers has symbolic significance indicating my overall service to the community of microbiome researchers. Several dozen papers were published from the HMP in the initial phase that were based on a single time point, including several involving my lab. The HMP has since released data collected from additional time points. The final dataset included sampling 300 individuals at up to 18 body sites on two or three occasions. In Ding & Schloss (2014), we asked whether there were enterotypes, or more broadly, community types, that could be identified at the 18 body sites across the body. Previous analyses were limited to single time points and were unable to quantify the stability of community types through time. To address these questions, we characterized the stability of the community types at each body site, identified associations between the community types found at each body site, and quantified the association between each community type and the subjects’ metadata. Overall, we showed that the interpersonal variation of the microbiome sampled from healthy individuals is considerable and that we still do not understand which factors drive differences in the structure of the microbiome. This study was significant because it demonstrated that “healthy” does not represent matching some ideal microbiome composition. Furthermore, it established a framework to connect clinical data with community types that will prove useful in developing diagnostics and assessing risks for developing diseases.
   1. A framework for human microbiome research. Nature. 2012 Jun 13;486(7402):215-21. PubMed PMID: [22699610](http://www.ncbi.nlm.nih.gov/pubmed/22699610/); PubMed Central PMCID: [PMC3377744](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3377744/).
   2. Structure, function and diversity of the healthy human microbiome. Nature. 2012 Jun 13;486(7402):207-14. PubMed PMID: [22699609](http://www.ncbi.nlm.nih.gov/pubmed/22699609/); PubMed Central PMCID: [PMC3564958](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3564958/).
   3. Ding T, Schloss PD. Dynamics and associations of microbial community types across the human body. Nature. 2014 May 15;509(7500):357-60. PubMed PMID: [24739969](http://www.ncbi.nlm.nih.gov/pubmed/24739969/); PubMed Central PMCID: [PMC4139711](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4139711/).

***Additional publications:***

<https://www.ncbi.nlm.nih.gov/myncbi/patrick.schloss.1/bibliography/public/>

**D. Additional Information: Research Support and/or Scholastic Performance**

Ongoing Research Support

2018/01/15-2020/12/31

R01 CA215574-01, National Cancer Institute (NCI)

Schloss, Patrick David (contact-PI) & Ruffin IV, Mack (multi-PI)

Identification of Microbiome Based Markers to Improve Colorectal Cancer Detection

Identify and validate microbiome-based biomarkers for a non-invasive diagnostic of colorectal cancer

Role: dual-PI

2016/03/01-2021/02/28

U01 AI124255-01, National Institute of Allergy and Infectious Diseases (NIAID)

Young, Vincent B (contact-PI) & Schloss, Patrick David (multi-PI)

Systems biology of *Clostridium difficile* infection

Model the infection and severity of Clostridium difficile in hospital and long-term care facilities

Role: dual-PI

Completed Research Support

2010/09/27-2014/06/30

R01 HG005975-03, National Human Genome Research Institute (NHGRI)

Schloss, Patrick David (PI)

Identifying population-level variation in cross-sectional and longitudinal HMP studies

Develop the mothur software package to accommodate the rapidly changing sequencing technologies and enable human microbiome research.

Role: PI

2012/02/01-2016/01/31

R01 GM099514-01, National Institute of General Medical Sciences (NIGMS)

Schloss, Patrick David (PI)

Diversity and stability relationships in the murine microbiome

Characterize the succession of the gut microbiota in colonized germ-free mice and following antibiotic perturbations.

Role: PI

2015/09/01-2017/08/31

R25GM116149-01, National Institute of General Medical Sciences (NIGMS)

Schloss, Patrick David (PI)

Development of reproducible informatics skills among microbiome researchers

Developing instructional materials to improve reproducible informatics skills among microbiome researchers

Role: PI