

Bryan P. Brown, PhD

Acting Assistant Professor

Department of Pediatrics, Division of Infectious Disease, University of Washington School of Medicine

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EDUCATION

- 2017 Doctor of Philosophy, Duke University, Durham, NC
Center for Genomic and Computational Biology; Nicholas School of the Environment
Dissertation: *Ecological and Evolutionary Factors Shaping Animal-Bacterial Symbioses: Insights from Insects & Gut Symbionts*
Advisor: Jennifer J. Wernegreen, PhD
- 2011 Bachelor of Science, The University of Akron, Akron, OH
Majors: Biochemistry, Biology; Minor: Spanish
Advisors: Stephen C. Weeks, PhD and John M. Senko, PhD

RESEARCH EXPERIENCE

- 2022 – Present **Acting Assistant Professor, University of Washington**
University of Washington School of Medicine, Department of Pediatrics, Division of Infectious Disease, Seattle, WA
- Investigating the effect of maternal HIV infection on the development of the enteric microbiome and immune response of related infants. Developed a methodology for bias-free whole genome amplification to sequence viral and bacterial metagenomes from maternal and infant stool and breastmilk samples. Developing supervised learning tools to identify microbial taxa associated with discrete or continuous variables, such as vaccine responsiveness in infants.
 - Identifying viruses and prophages in the female genital tract that are associated with adverse birth outcomes in a cohort of South African women using short and long read metagenomics.
- 2017 - 2022 **Research Scientist III/ Postdoctoral Fellow, Seattle Children's**
Seattle Children's Research Institute, Center for Global Infectious Disease Research, Seattle, WA (PIs: Heather Jaspan, MD, PhD; Rhea Coler, PhD)
- Integrated multiomic datasets (next generation sequencing and multiplexed cytokine assays) to assess shifts in vaginal microbiota and immune activation induced by contraceptive initiation and use in a cohort of African women. Conducted as part of the ECHO clinical trial (NCT02550067). Simultaneously, identified vaginal microbial and inflammatory predictors of Bacterial Vaginosis and HIV seroconversion. First author article in *Nature Communications*.
 - Used next-generation sequencing and comparative genomic analyses to identify single nucleotide variants arising from positive selective pressure across several human crAssphage genomes. First author article in *Virus Research*.
 - Used unsupervised learning approaches to identify interactions between bacterial microbiota and neonatal mucosal transcriptional responses elicited by alterations in feeding modality during the first year of life. First author articles in *Clinical Infectious Diseases* and *Gut Microbes*.
 - Developed two R packages to enable robust statistical analysis of multiomic (transcriptome, proteome, metabolome) datasets.
 - Performed the statistical qualification of a SARS-CoV-2 Spike-antigen ELISA and ELISPOT endpoint assay. Estimated survival and hazard ratios for several formulations of preclinical models of Mycobacterium tuberculosis vaccines. Co-author articles in the *Journal of Immunological Methods* and *Frontiers in Microbiology*.
- 2012 - 2017 **Predocctoral Fellow, Duke University**

Nicholas School of the Environment, Durham, NC (PI: Jennifer Wernegreen, PhD)

- Discovered novel, insect gut associated species of Acetobacteraceae bacteria and characterized their genomes using isolate culturing and PacBio sequencing. First author article in *BMC Microbiology*.
- Isolated and characterized fastidious gut microbes under diverse conditions using a multistage bioreactor.
- Performed bacterial metagenome sequencing on an Illumina platform to identify sources of horizontal gene transfer in specific strains of gut bacteria. Employed phylogenomics to reconstruct evolutionary histories of various gut associated bacteria. First author article in *BMC Genomics*.

2009 – 2011 **Research Assistant, The University of Akron**

Department of Biology, Akron, OH

- Modeled crustacean development using geometric morphometric analyses.
- Employed various unsupervised learning approaches to infer population gender ratios and sexual system evolution through deep time via the fossil record. First author article in the *Journal of Crustacean Biology*

2010 – 2011 **Research Assistant, The University of Akron**

Department of Geosciences, Akron, OH

- Performed 16S rRNA gene pyrosequencing to identify bacterial communities with high corrosive potential in engineered environments. First author article in *Frontiers in Microbiology*.
- Used aerobic and anaerobic culturing to isolate thermophilic bacteria from flue gas desulfurization systems.

AWARDS AND HONORS

2021 – 2026	Pathway to Independence Award, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health, Department of Health and Human Services
2021 – 2022	Loan Repayment Program Renewal Award, Pediatric Research, National Institute of Allergy and Infectious Disease, National Institutes of Health, Department of Health and Human Services
2020	Research Scholarship, 4th HIV Research for Prevention Conference (HIVR4P), International AIDS Society
2020 - 2021	Ruth L. Kirschstein National Research Service Award Individual Postdoctoral Fellowship, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health, Department of Health and Human Services
2019	New Investigator Scholarship, 2020 Conference on Retroviruses and Opportunistic Infections (CROI), International Antiviral Society-USA
2019 - 2021	Loan Repayment Program, Pediatric Research, National Institute of Allergy and Infectious Disease, National Institutes of Health, Department of Health and Human Services
2019	International Scholarship, 10th International AIDS Society Conference on HIV Science, International AIDS Society
2018	Travel award, 4 th International Workshop on Microbiome in HIV, National Institutes of Allergy and Infectious Diseases, National Institutes of Health
2015 - 2016	Graduate Research Opportunities Worldwide Travel Award, National Science Foundation
2013 - 2016	Graduate Research Fellowship, National Science Foundation
2011	Undergraduate Researcher of the Year, The University of Akron
2011	Outstanding Undergraduate Research Award, The University of Akron
2011	Dr. Paul Acquarone Award in Plant Sciences, The University of Akron
2010	Placed 1st overall, Conference on Integrated Bioscience, The University of Akron
2007 - 2008	Honors Recognition Scholarship, The University of Akron

RESEARCH FUNDING

Pending funding

R00HD106861 9/1/2023 – 8/31/2026
Eunice Kennedy Shriver National Institute of Child Health and Human Development
National Institutes of Health
PI: Brown
NIH Pathway to Independence Award
Title: Identifying inter-kingdom microbial determinants of altered immunity in HIV exposed infants
Description: The project utilizes integrative multiomic techniques and gnotobiotic mouse models to characterize the effects of the expanded gut virome of HIV-exposed infants on their bacterial microbiota and responses to vaccination. Role: Principal Investigator

Active funding

K99HD106861 9/1/2021 – 8/31/2023
Eunice Kennedy Shriver National Institute of Child Health and Human Development
National Institutes of Health
PI: Brown
NIH Pathway to Independence Award
Title: Identifying inter-kingdom microbial determinants of altered immunity in HIV exposed infants
Description: The project utilizes integrative multiomic techniques and gnotobiotic mouse models to characterize the effects of the expanded gut virome of HIV-exposed infants on their bacterial microbiota and responses to vaccination. Role: Principal Investigator

Completed research funding

L40A1147257 7/1/2019 – 6/30/2022
National Institute of Allergy and Infectious Diseases
National Institutes of Health
PI: Brown
Extramural Loan Repayment Program for Pediatric Research
Title: Influence of gut virome on bacterial microbiota and vaccine responsiveness in HIV-exposed infants
Description: The project aims to characterize the effects of maternal HIV infection on infant endogenous microbial communities and their responses to vaccination. Role: Principal Investigator

F32HD102290 4/1/2020 – 3/31/2023
Eunice Kennedy Shriver National Institute of Child Health and Human Development
National Institutes of Health
PI: Brown
Ruth L. Kirschstein National Research Service Award Individual Postdoctoral Fellowship
Title: Influence of gut virome on bacterial microbiota and vaccine responsiveness in HIV-exposed infants
Description: The project aims to characterize the effects of maternal HIV infection on infant endogenous microbial communities and their responses to vaccination. Role: Principal Investigator

NSF1106401 9/1/2013 – 8/31/2016
National Science Foundation
PI: Brown
NSF Graduate Research Fellowship
Title: Ecological and evolutionary forces shaping animal-bacterial interactions
Description: The project aims to identify mechanisms underlying genomic adaptation of bacterial mutualists living inside of animal hosts. Role: Principal Investigator

NSF1106401

8/1/2015 – 4/30/2016

National Science Foundation, United States Agency for International Development

PI: Brown

NSF Graduate Research Opportunities Worldwide, and USAID Research and Innovation Fellowship

Title: Structural and functional dynamics of vaginal microbiota associated with altered HIV susceptibility

Description: The goal of this study is to identify shifts in vaginal bacterial microbiota that are associated with elevated HIV susceptibility in adolescent South African women. Role: Principal Investigator

DUSOM1075

2/1/2016 – 1/31/2017

Duke University

PI: Wernegreen

Research Grant, Duke University School of Medicine

Title: A world within: Diversity and dynamics of bacterial communities inhabiting ants

Description: The purpose of this study is to identify mechanisms and dynamics of bacterial transmission between interacting hosts and across developmental stages. Role: Co-Investigator

DUNSOE0789

1/1/2016 – 4/30/2017

Duke University

PI: Wernegreen

SEED grant, Duke University Nicholas School of the Environment

Title: Evolutionary dynamics across the genomes of persistent gut bacterial associates

Description: This project aims to characterize the genomes of persistent gut bacteria and to identify selective pressures acting on these associates via adaptation to the gastrointestinal tract. Role: Co-Investigator.

BIBLIOGRAPHYPeer-Reviewed Publications

19. Brown BP, Feng C, Tanko RF, Jaumdally SZ, Bunjun R, Dabee S, Happel AU, Gasper M, Nyangahu DD, Onono M, Nair G, Palanee-Phillips T, Scoville CW, Heller K, Baeten JM, Bosinger SE, Burgener A, Passmore JS, Heffron R, Jaspan HB. Copper intrauterine device increases vaginal concentrations of inflammatory anaerobes and depletes lactobacilli compared to hormonal options in a randomized trial. **Nat Commun**. 2023 Jan 30;14(1):499. doi: 10.1038/s41467-023-36002-4. PMID36717556
18. Happel AU, Balle C, Havyarimana E, Brown BP, Maust BS, Feng C, Yi BH, Gill K, Bekker LG, Passmore JA, Jaspan HB. Cervicovaginal Human Papillomavirus Genomes, Microbiota Composition and Cytokine Concentrations in South African Adolescents. **Viruses**. 2023 Mar 15;15(3):758.
17. Jimoh AO, Balle C, Brown BP, Feng C, Havyarimana E, Konstantinus IN, Gill K, Bekker LG, Passmore JS, Jaspan HB, Varsani A, Happel AU. Genome Sequences of Anelloviruses, a Genomovirus, Microviruses, Polyomaviruses, and an Unclassified Caudovirus Identified in Vaginal Secretions from South African Adolescents. **Microbiol Resour Announc**. 2023 Jan 24;12(1):e0114322. doi: 10.1128/mra.01143-22. Epub 2022 Dec 19. PMID36533922
16. Nyangahu DD, Courtney P, Brown BP, Feng C, Havyarimana E, Cohen S, Urdahl K, Jaspan HB. Antibiotic treatment during gestation enhances susceptibility to Mycobacterium tuberculosis in infant mice. **Microbiol Spectr**. 2022 Oct 31:e0249122. doi: 10.1128/spectrum.02491-22. PMID36314979.
15. Baldwin SL, Reese VA, Larsen SE, Pecor T, Brown BP, Granger B, Podell BK, Fox CB, Reed SG, Coler RN. Therapeutic efficacy against Mycobacterium tuberculosis using ID93 and liposomal adjuvant formulations. **Frontiers in Microbiology**. 2022:3063. PMID36090093
14. Bunjun R, Tanko RF, Jaumdally SZ, Noel-Romas L, Ayele H, Brown BP, Gamielien H, Harryparsad R, Nair G, Onono M, Palanee-Phillips T, Scoville C, Heller KB, Baeten JM, Bosinger SE, Burgener A, Passmore JS, Jaspan HB, Heffron R. Initiating intramuscular depot medroxyprogesterone acetate (DMPA-IM) increases frequencies of Th17-like HIV target cells in the genital tract of women in South Africa: a randomised trial. **Clin Infect Dis**. 2022 Aug 9. PMID35941737
13. Dabee S, Tanko RF, Brown BP, Bunjun R, Balle C, Feng C, Konstantinus I, Jaumdally SZ, Onono M, Nair G, Palanee-Phillips T, Gill K, Baeten JM, Bekker LG, Passmore JS, Heffron R, Jaspan HB, Happel A. Comparison of Female Genital Tract Cytokine and Microbiota Signatures Induced by Initiation of

Intramuscular DMPA and NET-EN Hormonal Contraceptives-a Prospective Cohort Analysis. **Frontiers in Immunology**. 2021: 5296. PMID34956191

12. Larsen S, Berube B, Pecor T, Cross E, Brown BP, Williams B, Johnson E, Qu P, Baldwin SL, Coler RN. Qualification of ELISA and neutralization methodologies to measure SARS-CoV-2 humoral immunity in human clinical samples. **Journal of immunological methods** 2021 Dec 1;499:113160. PMID34599915
11. Brown BP, Wendoh J, Chopera D, Havyarimana E, Jaumdally S, Nyangahu DD, Gray CM, Martin DP, Varsani A, Jaspan HB. crAssphage genomes identified in fecal samples of an adult and infants with evidence of positive genomic selective pressure within tail protein genes. **Virus Res**. 2020 Oct 30;198219. PMID33137401
10. Nyangahu DD, Darby M, Havyarimana E, Brown BP, Horsnell W, Jaspan HB. Preconception helminth infection alters offspring microbiota and immune subsets in a mouse model. **Parasite Immunology**. 2020 Apr 11:e12721. PMID32277499
9. Brown BP, Jaspan HB. Compositional analyses reveal correlations between taxon-level gut bacterial abundance and peripheral T cell marker expression in African infants. **Gut microbes**. 2019 Jul 28:1-8. PMID31347944
8. Brown BP, Wernegreen JJ. Genomic erosion and extensive horizontal gene transfer in gut-associated Acetobacteraceae. **BMC genomics**. 2019 Dec;20(1):472. PMID31182035.
7. Wood LF*, Brown BP*, Lennard K, Karaoz U, Passmore JS, Hesselting AC, Edlefsen PT, Mulder N, Brodie EL, Sodora DL, Jaspan HB. Feeding related gut microbial composition associates with peripheral T cell activation and mucosal gene expression in African infants. **Clin Infect Dis** 2018 Sep 28;67(8):1237-1246. PMID29659737. *co-first authors.
6. Nyangahu D, Lennard KS, Brown BP, Darby MG, Wendoh JM, Havyarimana H, Smith P, Butcher J, Stintzi A, Mulder N, Horsnell W, Jaspan HB. Disruption of maternal gut microbiota during gestation alters offspring immunity. **Microbiome** 2018 Jul 7;6(1):124. PMID29981583. PMC6035804.
5. Ho NT, Li F, Lee-Sarwar KA, Tun HM, Brown BP, Pannaraj PS, Bender JM, Azad MB, Thompson AL, Weiss ST, Azcarate-Peril MA, Litonjua AA, Kozyrskyj AL, Jaspan HB, Aldrovandi GM, Kuhn L. Meta-analysis of effects of exclusive breastfeeding on infant gut microbiota across populations. **Nat Commun** 2018 Oct 9;9(1):4169. PMID30301893. PMC6177445.
4. Brown BP and Wernegreen JJ. Deep divergence and rapid evolutionary rates in gut-associated Acetobacteraceae of ants. **BMC Microbiol** 2016 Jul 11;16(1):140. PMID27400652. PMC4939635.
3. Brown BP, Astrop TI, Weeks SC. Post-larval developmental dynamics of the Spinicaudatan (Branchiopoda: Diplostraca) carapace. **Journal of Crustacean Biology** 2014 34 (5), 611-617.
2. Astrop, TI, Park, LE, Brown BP, and Weeks, SC. Sexual discrimination at work: Spinicaudatan 'Clam Shrimp' (Crustacea: Branchiopoda) as a model organism for the study of sexual system evolution. **Palaeontologia Electronica** 2012 Vol. 15, Issue 2;20A,15p.
1. Brown BP, Brown SR and Senko JM. Microbial communities associated with wet flue gas desulfurization systems. **Front Microbiol** 2012 3:412. PMID23226147. PMC3510643.

Submitted Manuscripts and Cited Preprints

3. Donald D Nyangahu, Anna-Ursula Happel, Jerome Wendoh, Agano Kiravu, Colin Feng, Courtney Plumlee, Sara Cohen, Bryan P Brown, Danijel Djukovic, Tariq Ganief, Melanie Gasper, Daniel Raftery, Jonathan M Blackburn, Clive M. Gray, Jisun Paik, Kevin B Urdahl and Heather B Jaspan. Bifidobacterium infantis associates with T cell immunity in human infants and is sufficient to enhance antigen specific T cells in mice. Under revision at Science Advances
2. Maust BS, Petkov S, Herrera C, Feng C, Brown BP, Lebina L, Opoka D, Ssemata A, Pillay N, Serwanga J, Seattholo P. Bacterial Microbiome of Foreskin Tissue: Impact of Short-course PrEP and Host Inflammation. **bioRxiv**. 2022 Jan 1.
1. Brown BP, Wendoh J, Chopera D, Havyarimana E, Jaumdally SZ, Nyangahu DD, Gray C, Martin DP, Varsani A, Jaspan HB. crAssphage abundance and genomic selective pressure correlate with altered bacterial abundance in the fecal microbiota of South African mother-infant dyads. **bioRxiv**. 2019 Jan 1:582015.

Invited presentations

4. Brown BP, Feng C, Tanko RF, Jaumdally SZ, Bunjun R, Dabee S, Heffron, RH, Jaspan HB. (2023, March). Contraceptive induced alterations to the cervicovaginal environment: insights from the ECHO Trial. **Institute of Infectious Disease and Molecular Medicine Seminar Series**, University of Cape Town. Cape Town, South Africa
3. Brown BP, Feng C, Maust BM, Happel AU, Varsani A, Jaspan HB. (2023, March). Defining the Vaginal Virome. **Vaginal Microbiome Research Consortium 2023 Annual Meeting**. Durban, South Africa
2. Brown BP, Maust BM, Happel AU, Havyarimana E, Jaumdally SZ, Varsani A, Coler, RN, Jaspan HB. (2022, November). Inter-kingdom microbial determinants of altered immunity in HIV-exposed infants. **7th International Conference on Vaccines Research and Development**. Boston, MA, USA.
1. Brown BP, Maust BM, Happel AU, Havyarimana E, Jaumdally SZ, Varsani A, Jaspan HB. (2022, April). Multi-omic insights into endogenous microbiota and immunity in African women and infants. **Pacific Northwest Research Institute Seminar Series**, Seattle, WA, USA.

Platform presentations

4. Brown BP, Wendoh J, Chopera D, Havyarimana E, Jaumdally SZ, Martin DP, Varsani A, Jaspan HB. (2019, July). Maternal HIV infection alters the community composition and dynamics of the enteric microbiome of associated infants. **10th International AIDS Society Conference on HIV Science**, Mexico City, Mexico.
3. Balle C, Lennard K, Konstantinus I, Jaumdally S, Esra R, Gasper M, Brown BP, Karaoz U, Gill K, Myer L. (2018, October). Hormonal Contraception Induced Changes to the Female Genital Microbiota in South African Adolescents: A Randomized, Crossover Trial. **HIV Research for Prevention**. Madrid, Spain.
2. Brown BP, Jaspan HB, Study Team I. (2018, October). A compositional transform reveals HIV exposure induced shifts in the fecal microbiota and vaccine responsiveness of Nigerian infants. **4th International Workshop on Microbiome in HIV Pathogenesis, Prevention and Treatment**. Washington, DC, USA.
1. Brown BP, Jaspan HB. (2018, September). A penalized compositional transform reveals shifts in the fecal microbiota of HIV exposed Nigerian infants. **Fred Hutchinson Microbiome Research Initiative Biennial Symposium**. Seattle, WA, USA.

Poster presentations

7. Brown BP, et al. (2021, January). HIV exposure alters the fecal microbiome in Nigerian infants. **4th HIV Research for Prevention Conference (HIVR4P)**. Virtual.
6. Brown BP, et al. (2020, March). Contraceptive use induces durable shifts in the female genital-tract microbiota. **2020 Conference on Retroviruses and Opportunistic Infections (CROI)**. Boston, MA, USA.
5. Brown BP, Jaspan HB. (2018, October). A compositional transform reveals HIV exposure induced shifts in the fecal microbiota and vaccine responsiveness in Nigerian infants. **3rd HIV Research for Prevention**. Madrid, Spain.
4. Brown BP, Varsani A, Jaspan HB. (2018, October). Altered composition and elevated diversity in the enteric virome of HIV exposed uninfected South African infants. **3rd HIV Research for Prevention**. Madrid, Spain.
3. Brown BP, Jaspan HB, Study Team I. (2018, April). HIV exposure alters the fecal microbiome and efficacy of oral polio vaccine in Nigerian infants. **25th International HIV Dynamics & Evolution**. Leavenworth, WA, USA.
2. Brown BP, Senko J. (2012, June). Microbial Communities Associated With Flue Gas Desulfurization Systems. **American Society for Microbiology: 112th General Meeting**. San Francisco, CA, USA.
1. Brown BP, Weeks S. (2011, June). Morphometrics and Ontogenetics: Evolutionary Dynamics of the Spinicaudatan 'Clam Shrimp'. **The Evolution Conference**. Norman, OK, USA.

TEACHING AND MENTORING

Courses taught

One Health: Philosophy to Practical Integration of Human, Animal, and Environmental Health

Duke University, Global Health Institute

Role: Teaching Assistant, Co-Instructor

Description: This graduate-level, interdisciplinary course will introduce the concept of One Health as an increasingly important approach to a holistic understanding of the promotion and maintenance of human, animal, and environmental health.

Applied Data Analysis for Environmental Sciences

Duke University, Nicholas School of the Environment

Role: Teaching Assistant, Laboratory Instructor

Description: This graduate-level course provides an introduction to statistical analysis and modeling for applied problems in the environmental sciences. All labs are instructed using the R statistical framework.

Molecular Ecology

Duke University, Department of Biology

Role: Teaching Assistant, Co-Instructor

Description: This graduate-level course explores key questions in molecular ecology, a field that employs molecular tools to investigate ecological processes within natural populations and communities. While genetic techniques are central to this discipline, the course is not a methods class per se. Rather, emphasis is placed on fundamental principles and predictions from ecological and evolutionary theory, as well as historical approaches and precedents.

Genetics and Evolution

Duke University, Department of Biology

Role: Teaching Assistant, Laboratory Instructor

Description: This undergraduate-level course provides an introduction to principles of genetics and evolution. Includes Mendelian and non-Mendelian inheritance, quantitative genetics, genetic mapping, evidence for evolution, natural selection, genetic drift, kin selection, speciation, molecular evolution, and phylogenetic analysis.

Lectures

Molecular techniques in viral metagenomics (2023, February)

Seattle Children's Research Institute, Center for Global Infectious Disease Research

Role: Instructor

Description: This workshop focused on methods for extracting, preparing, amplifying, and sequencing viral nucleic acid for metagenomics studies.

Computational approaches for viral metagenomics (2023, March)

Seattle Children's Research Institute, Center for Global Infectious Disease Research

Role: Instructor

Description: This workshop focused on methods for quality trimming and filtering raw sequencing reads used in viral and bacterial metagenomic studies. Additionally, students were provided hands-on instruction for best practices in viral metagenomics including assembly into contigs, dereplication into operational taxonomic units (OTUs), genome binning, identification of viral OTUs, read alignment for quantification, and community ecology analyses.

Mentoring

Advising: Research

Current:

1 PhD student:

1. Adijat Jimoh, PhD student, University of Cape Town

Past:

5 undergraduate researchers; Representative trainees:

1. Carlton Adams, Undergraduate trainee, Duke University; Currently, PhD Candidate, The Feinberg School of Medicine, Northwestern University
2. Eric Song, Undergraduate trainee, Duke University; Currently, Software Development Manager, Amazon Web Services
3. Aubrey Brown, Undergraduate trainee, Seattle Children's; Currently, Medical student, School of Medicine, University of Washington
4. Celeste Coler, Research intern, Seattle Children's; Currently, recent graduate from Claremont McKenna College

OTHER

Editorial boards

Review Editor, HIV and STIs section, *Frontiers in Reproductive Health*

Reviewing activities

Journals:

Clinical and Translational Medicine

Gut Microbes

Microbiology Spectrum

Microbiome

mSystems

PLOS ONE

Symbiosis

Outreach

2012 Environmental Science Instructor, Lakewood Elementary School, Durham, NC

R packages developed

pico: a suite of compositional data analysis functions targeted for marker gene (16S/18S/ITS) and metagenomic microbiome datasets, including a novel transformation that couples an L1 penalized matrix decomposition to the isometric log ratio transformation.

microfiltR: identifies and corrects for multiple sources of contamination (exogenous and cross) in compositional marker gene surveys. Available at <https://github.com/itsmisterbrown/microfiltR>