

BRYAN P. BROWN

POSTDOCTORAL FELLOW

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EDUCATION

Ph.D. Genomic and Computational Biology

July 2017

Duke University, Durham, North Carolina

Advisor: Jennifer J. Wernegreen

Dissertation: *Ecological and Evolutionary Factors Shaping Animal-Bacterial Symbioses: Insights from Insects & Gut Symbionts*

B.S. Biochemistry, Biology; Minor area of study in Spanish

December 2011

The University of Akron, Akron, Ohio

SKILLS

LANGUAGES: R, Python, Unix/Linux, Wolfram, HTML, awk

APPLICATIONS: Rstudio, GitHub, Mathematica, JMP, R Shiny, tidy, dplyr, ggplot2, phyloseq, NumPy, SciPy, Scikit-learn, sed, PAML, RAxML, MrBayes, SPAdes, MEGAHIT, Velvet, SAMtools, QIIME, mothur, distributed high-performance computing, parallelization

DATA SCIENCE: Regression (Bayesian, linear, OLS, PLS, GLM, mixed, Regularized (lasso; L1, Ridge, L2)), machine learning (decision trees, SVM, clustering (k-means, hierarchical, PAM, fuzzy, KNN)), compositional data analysis, dimensionality reduction (SVD, PCoA, NMDS, PMD, CCA, RDA), permutational multivariate analyses, ancestral state reconstruction, model selection and evaluation, maximum likelihood and Bayesian phylogenetics/phylogenomics

EXPERIENCE

POSTDOCTORAL FELLOW

October 2017 – Present

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

- Developed two R packages that enable robust statistical analysis of microbiome datasets employing contamination rate modeling, compositional data analysis, and a penalized matrix decomposition-based transformation.
- Integrated multiomics datasets (marker gene (16S/18S), proteomics, metagenomics, transcriptomics, flow cytometry, vaccine response) to delineate the effects of HIV exposure on infant morbidity and mortality.
- Lead the bioinformatics and statistical analysis of the gut associated viral and bacterial metagenome in a NIH-funded clinical trial dataset of a cohort of HIV exposed and unexposed mother-infant pairs in South Africa.
- Employed various regression models (lasso, GLM, OLS) and machine learning algorithms (supervised, dimension reduction) to identify associations between bacterial and viral species abundance from DNA sequence datasets.
- Lead the molecular, bioinformatics, and statistical analysis of the effect of hormonal contraception on the community composition of vaginal microbiota in a NIH-funded clinical trial dataset of women from South Africa and Kenya.
- Authored 3 peer-reviewed publications (1 first author) and presented research at 3 conferences.

NATIONAL SCIENCE FOUNDATION GRADUATE RESEARCH FELLOW

June 2012 – July 2017

Duke University, Durham, North Carolina

- Discovered and described a novel genus of gut-associated Proteobacteria and analyzed the associated genomics and evolutionary rates.

- Developed a high level of proficiency in R, Unix, and HPC cluster utilization and job parallelization.
- Constructed pipelines for assembling and analyzing bacterial genomes and metagenomes
- Published multiple peer-reviewed publications (2 first author, several in review/prep) and presented at multiple conferences and symposiums.
- Developed mastery with univariate and multivariate statistics, genomic and computational biology, and molecular and microbiology
- Instructed courses:
 - Advanced Data Analysis in R
 - Molecular Ecology
 - One Health
 - Genetics and Evolution

AWARDS AND HONORS

Duke University Summer Research Fellowship	June 2017 – August 2017
Duke University Graduate Fellowship	2012 – 2017
National Science Foundation Graduate Research Opportunities Worldwide Fellowship	2016 - 2017
National Science Foundation Graduate Research Fellowship	2013 - 2016
Genomic and Computational Biology Summer Research Grant	2013
The University of Akron Undergraduate Researcher of the Year	2011
The University of Akron Outstanding Undergraduate Research Award	2011
Dr. Paul Acquarone Award in Plant Sciences	2011
Placed 1st overall - The University of Akron Conference on Integrated Bioscience	2010
The University of Akron Honors Recognition Scholarship	2007 - 2008
The University of Akron Presidential Scholarship	2007 – 2008

SOFTWARE

R PACKAGES

pico: enables robust statistical analysis and modeling of compositional microbiome datasets by transforming typical microbial DNA sequence counts to Cartesian coordinates. The transformation is enabled by coupling an L1 penalized matrix decomposition to the generalized isometric log ratio transformation. *Affiliated manuscript in prep.*
github.com/itsmisterbrown/pico

microfiltR: aims to increase the accuracy of microbiome studies by identifying, modeling, and correcting for multiple sources of contamination (exogenous and cross) in compositional marker gene surveys. *Affiliated manuscript in prep.*
github.com/itsmisterbrown/microfiltR

PUBLICATIONS

Brown BP and Wernegreen JJ. Genomic erosion and rampant horizontal gene transfer in gut-associated *Acetobacteraceae*. *In review.*

Brown BP, et al. HIV exposure alters the composition of fecal microbiota and efficacy of oral polio vaccine in Nigerian infants. *In prep.*

Brown BP and Wernegreen JJ. Social interactions foster reliable bacterial transmission in Camponotus ants. *In prep.*

Brown BP and Wernegreen JJ. Ironing out a symbiosis: Host transferrin modulates interactions with beneficial microbes. *In prep.*

Ho N, Li F, Lee-Sarwar, KA, Tun, HM, **Brown BP**, et al. 2018. Meta-analysis of effects of exclusive breastfeeding on infant gut microbiota across populations. *Nature Communications*. *In Press*.

Wood LF*, **Brown BP***, et al. 2018. Feeding mode regulates gut microbial composition, peripheral T cell activation and mucosal gene expression in African infants. *Clinical Infectious Diseases*, 10.1093/cid/ciy265

*Contributed equally

Nyangahu D, Lennard, K, **Brown BP**, et al. 2018. Disruption of maternal gut microbiota during gestation alters offspring microbiota and immunity. *Microbiome*, 2018 6:124

Brown BP and Wernegreen JJ. 2016. Deep divergence and rapid evolutionary rates in gut-associated *Acetobacteraceae* of ants. *BMC Microbiology*, DOI: 10.1186/s12866-016-0721-8

Brown BP, Astrop TI, Weeks SC. 2014 Post-larval developmental dynamics of the Spinicaudatan (Branchiopoda: Diplostraca) carapace. *Journal of Crustacean Biology*

Brown BP, Brown SR and Senko JM. 2012. Microbial communities associated with wet flue gas desulfurization systems. *Frontiers in Microbiology*. 3:412. DOI: 10.3389/fmicb.2012.00412

Astrop, TI, Park, LE, **Brown, BP**, and Weeks, SC 2012. Sexual discrimination at work: Spinicaudatan 'Clam Shrimp' (Crustacea: Branchiopoda) as a model organism for the study of sexual system evolution. *Palaeontologia Electronica* Vol. 15, Issue 2;20A,15p

CONFERENCE PRESENTATIONS

Bryan P Brown, Arvind Varsani, Heather Jaspan. 2018 Altered composition and elevated diversity in the enteric virome of HIV exposed uninfected South African infants. **HIVR4P**. Madrid, Spain

Bryan P Brown, Heather Jaspan. 2018 A penalized compositional transform reveals shifts in the fecal microbiota of HIV exposed Nigerian infants. **Fred Hutch Microbiome Research Initiative Biennial Symposium**. Seattle, WA

Bryan P Brown, Heather Jaspan. 2018 HIV exposure alters the fecal microbiome and efficacy of oral Polio vaccine in Nigerian infants. **HIV Dynamics and Evolution**. Leavenworth, WA.

Bryan Brown. 2016. Genomic destabilization and rapid evolutionary rates of gut associated microbes. **Immunology and Microbiology Seminar Series**. University of Cape Town, Cape Town, South Africa.

John Senko, Bryan Brown. 2012. Microbial Communities Associated With Flue Gas Desulfurization Systems. **American Society for Microbiology: 112th General Meeting**. San Francisco, CA.

Bryan Brown and Stephen Weeks. 2011. Morphometrics and Ontogenetics: Evolutionary Dynamics of the Spinicaudatan 'Clam Shrimp'. **Evolution 2011**. The University of Oklahoma, Norman, OK.