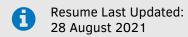
John Christian Gaby

Research Microbiologist



Gainesville, Florida, USA

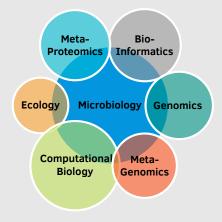
chrisgaby.github.io

/in/john-gaby-56525410b/

chrisgaby

Knowledge -

Domains



About Me —

John Christian Gaby is a Research Microbiologist with the Genomics and Bioinformatics Research Unit (GBRU) of the United States Department of Agriculture (USDA) Agricultural Research Service (ARS). His research interests include microbial ecology, biological nitrogen fixation, the nitrogen cycle, biogas production, genomics, metagenomics, metaproteomics, bioinformatics, and computational biology. He currently works on the development of machine learning models to predict prokaryotic phenotype from genome sequence data.

Education –

Ph.D., Microbiology

Minors: Genomics and Ecology Cornell University 2013 Ithaca, NY

B.S., BiologyThe University of Tennessee
2002 Knoxville, TN

Experience

2020 -Present

Research Microbiologist Research Associate

USDA ARS GBRU

- Topic: Machine Learning Prediction using Genomic Data
- Tools: Python, Pandas, NumPy, Matplotlib, R, SQL, Jupyter, Docker, NextFlow, Git, MASH, Dashing, GitHub, Sequence Read Archive (SRA), NCBI Assembly Database, Google Cloud, UNIX Shell

2016 -2020

Postdoctoral Researcher The Norwegian University of Life Sciences (NMBU)

• Topic: Multi-omics Analysis of Microbial Function in Digestive

- Ecosystems (Biogas Reactors and Intestinal Microbiomes)

 Methods: MetaGenomics, MetaProteomics, Amplicon Sequencing
- Tools: R, R Markdown, DADA2, PhyloSeq, VEGAN, ggplot2, cowplot, GitHub, MaxQuant, Perseus, MetaSPAdes, MegaHIT, MetaBAT, MaxBin, InterProScan, Prokka, Prodigal, HMMer, MetaGeneMark, GTDB-Tk, CheckM, fastANI, fastQC, MASH, Trimmomatic, metaQUAST, HPC Cluster, Slurm, UNIX Shell

2013 - Postdoctoral Researcher

The Georgia Institute of Technology

2013

- Topic: Nitrogen Fixation in Terrestrial and Marine Ecosystems
- Methods: Amplicon Sequencing, qPCR, Acetylene Reduction, Selective Enrichment and Isolation, Ribosomal RNA Intergenic Spacer Analysis (RISA)
- Tools: R, Plymouth Routines In Multivariate Ecological Research

2011 -2012

Fulbright US Student Fellow

Corporacion Corpogen

- Topic: Nitrogen Cycling in the Colombian Paramo
 - Methods: DNA Extraction, qPCR
 - Tools: NCBI Genbank Database, Arb

2005 -2011

Graduate Research Assistant

Cornell University

- Topic: The Diversity and Ecology of Nitrogen-fixing Bacteria
- Methods: PCR, qPCR, Sangar Sequencing, ¹⁵N₂ Stable Isotope Assays of N₂-fixation Rate, Nitrogen Mineralization Rate Assays, Soil Bulk Density Analysis, Soil Carbon Content Analysis by Loss on Ignition, Soil Moisture Analysis
- Tools: NCBI Genbank Database, Arb, R, EMBOSS, UNIX Shell

Publications, 5 Selected of 17 Total

941 citations according to my Google Scholar page as of August 28, 2021 Peer reviewed articles: 6 first author, 9 co-author, 1 corresponding author

- [1] L. Michalak, J. C. Gaby, L. Lagos, S. L. La Rosa, T. R. Hvidsten, C. Tétard-Jones, W. G. Willats, N. Terrapon, V. Lombard, B. Henrissat, J. Dröge, M. Ø. Arntzen, L. H. Hagen, M. Øverland, P. B. Pope, and B. Westereng. Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. *Nature Communications*, 11(1), 2020.
- [2] J. C. **Gaby**, M. Zamanzadeh, and S. J. Horn. The effect of temperature and retention time on methane production and microbial community composition in staged anaerobic digesters fed with food waste. *Biotechnology for Biofuels*, 10(1):302, 2017.
- [3] J. C. **Gaby** and D. H. Buckley. A comprehensive aligned *nifH* gene database: A multipurpose tool for studies of nitrogen-fixing bacteria. *Database: The Journal of Biological Databases and Curation*, 2014:bau001, 2014.
- [4] J. C. **Gaby** and D. H. Buckley. A comprehensive evaluation of PCR primers to amplify the *nifH* gene of nitrogenase. *PLoS ONE*, 7(7):e42149, 2012.
- [5] J. C. **Gaby** and D. H. Buckley. A global census of nitrogenase diversity. *Environmental Microbiology*, 13(7):1790–1799, 2011.