

# John Christian Gaby

## Research Microbiologist



chrisgaby.github.io



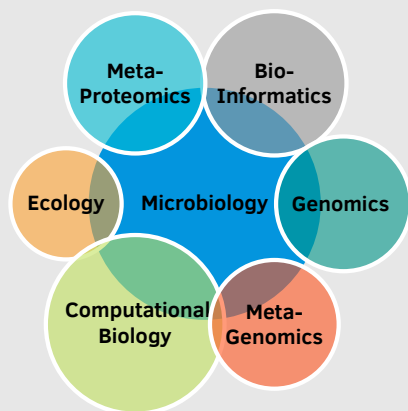
/in/john-gaby-56525410b/



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., Biology

The 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 - 2016

### Postdoctoral Researcher

The Georgia Institute of Technology

- **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,  $^{15}\text{N}_2$  Stable Isotope Assays of  $\text{N}_2$ -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

**925 citations** in Google Scholar as of August 5, 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** and D. H. Buckley. A global census of nitrogenase diversity. *Environmental Microbiology*, 13(7):1790–1799, jul 2011.
- [3] 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, jan 2012.
- [4] 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, jan 2014.
- [5] 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.