John Christian Gaby

Research Microbiologist

Resume Last Updated:
28 August 2021

Gainesville, Florida, USA

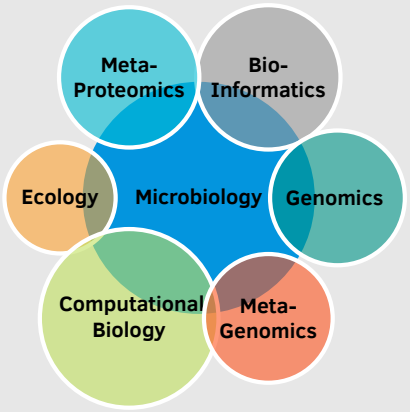
chrisgaby.github.io

/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., 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, $^{15}N_2$ Stable Isotope Assays of 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

941 citations in Google Scholar 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** and D. H. Buckley. A global census of nitrogenase diversity. *Environmental Microbiology*, 13(7):1790–1799, 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, 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, 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.