







# Quang Nguyen

Ph.D. Student

June 2021

 Dartmouth College  
 qpmnguyen.com  
 quangpmnguyen@gmail.com  
 quangpmnguyen  
 qpmnguyen  
 qpmnguyen

## About me

I am currently a Ph.D. candidate in the Quantitative Biomedical Sciences program at Dartmouth College. I develop statistical tool for incorporating microbial function in epidemiological microbiome-outcome analyses. Looking for any opportunities in statistics, bioinformatics and epidemiology

This is a selected list portfolio projects, including both primary research contributions and side projects

### Research

### Software

- **teaR**. An R package to perform taxonomic enrichment analysis. This package contains the primary implementation of the cILR method. Additionally, a unified interface and data structure for taxa-sets is provided, extending the existing phyloseq object commonly used in microbiome data analysis.
  - Built with: R
  - Links: GitHub
- **microbesim**. An R package to perform Monte Carlo simulations of microbiome count data. This package contains easy-to-use functions to generate synthetic counts under different distributional models. Supports predictive analysis, differential abundance analysis, and taxa-set enrichment analysis
  - Built with: R
  - Links: GitHub

### Data analysis

### Data visualization

- **TidyTuesday**. Submissions to the weekly TidyTuesday challenge in creating data visualizations using R.
  - Built with: R, ggplot, flexdashboard
  - Links: GitHub, flexdashboard

### Bioinformatics

- **Bulk RNA-seq data pipeline**: Sample bulk RNA-seq data pipeline with the Himes et al. data set(Study ID: SRP033351), taking data from raw reads to differential expression analysis.
  - Built with: snakemake, STAR, htseq-counts, salmon, sra-tools, DESeq2, R, Python.
  - Links: GitHub