

The Microbiome Analysis Core at the Harvard T.H. Chan School of Public Health was established in response to the rapidly emerging field of microbiome research and its potential to affect studies across the biomedical sciences. The Core's goal is to aid researchers with microbiome study design and interpretation, reducing the gap between primary data and translatable biology. The Microbiome Analysis Core provides end-to-end support for microbial community and human microbiome research, from experimental design through data generation, bioinformatics, and statistics. This includes general consulting, power calculations, selection of data generation options, and analysis of data from amplicon (16S/18S/ITS), shotgun metagenomic sequencing, metatranscriptomics, metabolomics, and other molecular assays. The Microbiome Analysis Core has extensive experience with microbiome profiles in diverse populations, including taxonomic and functional profiles from large cohorts, qualitative ecology, multi'omics and meta-analysis, and microbial systems and human epidemiological analysis. By integrating microbial community profiles with host clinical and environmental information, we enable researchers to interpret molecular activities of the microbiota and assess its impact on human health.

Core services

Consultation for microbiome project development.

We provide consultation on experimental design, sample collection and sequencing, grant proposal development, study power estimation, bioinformatics, and statistical data analysis.

Validated end-to-end meta'omic analysis of microbial community data.

Using open-source analytical methods developed in the Huttenhower laboratory and by other leaders in the field, we provide cutting-edge microbiome informatics and analysis.

Fully-collaborative support for all stages of funded investigations

From preliminary data development to hypothesis formulation, grant narrative development, data analysis and inference, custom software development, and co-authored dissemination of findings.

Study Design

- Consultation
- Grant assistance
- Power analysis
- Collection methods
- Wet lab
- Dry lab

Analysis

- Bioinformatics (raw data processing, taxonomic and functional profiling)
- Downstream analysis and statistics

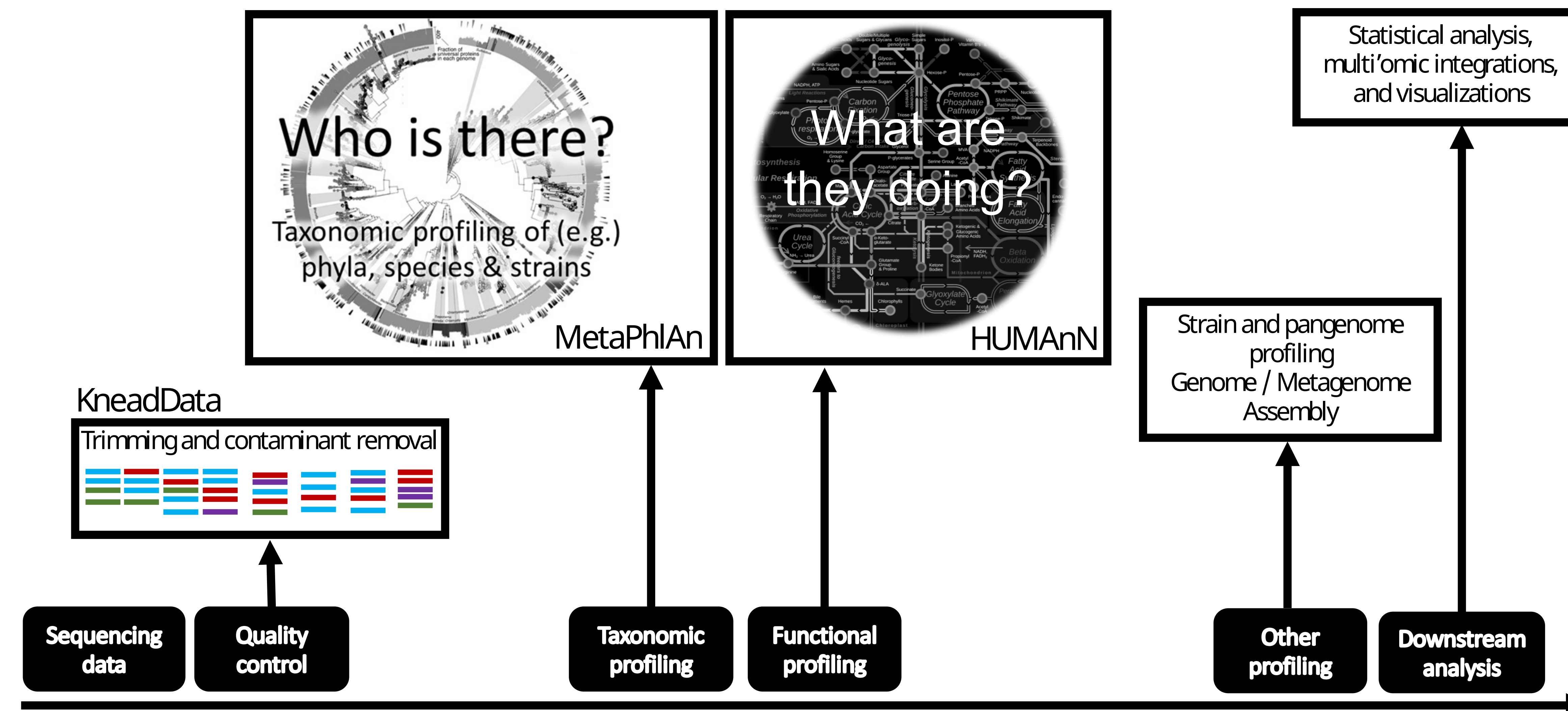
Interpretation

- Results
- Discussion
- Manuscript writing/editing
- Response to reviewers

Director: Xochitl Morgan
 Senior Software Developer: Lauren McIver
 Data Analyst: Thomas Kuntz
 Scientific Director: Curtis Huttenhower

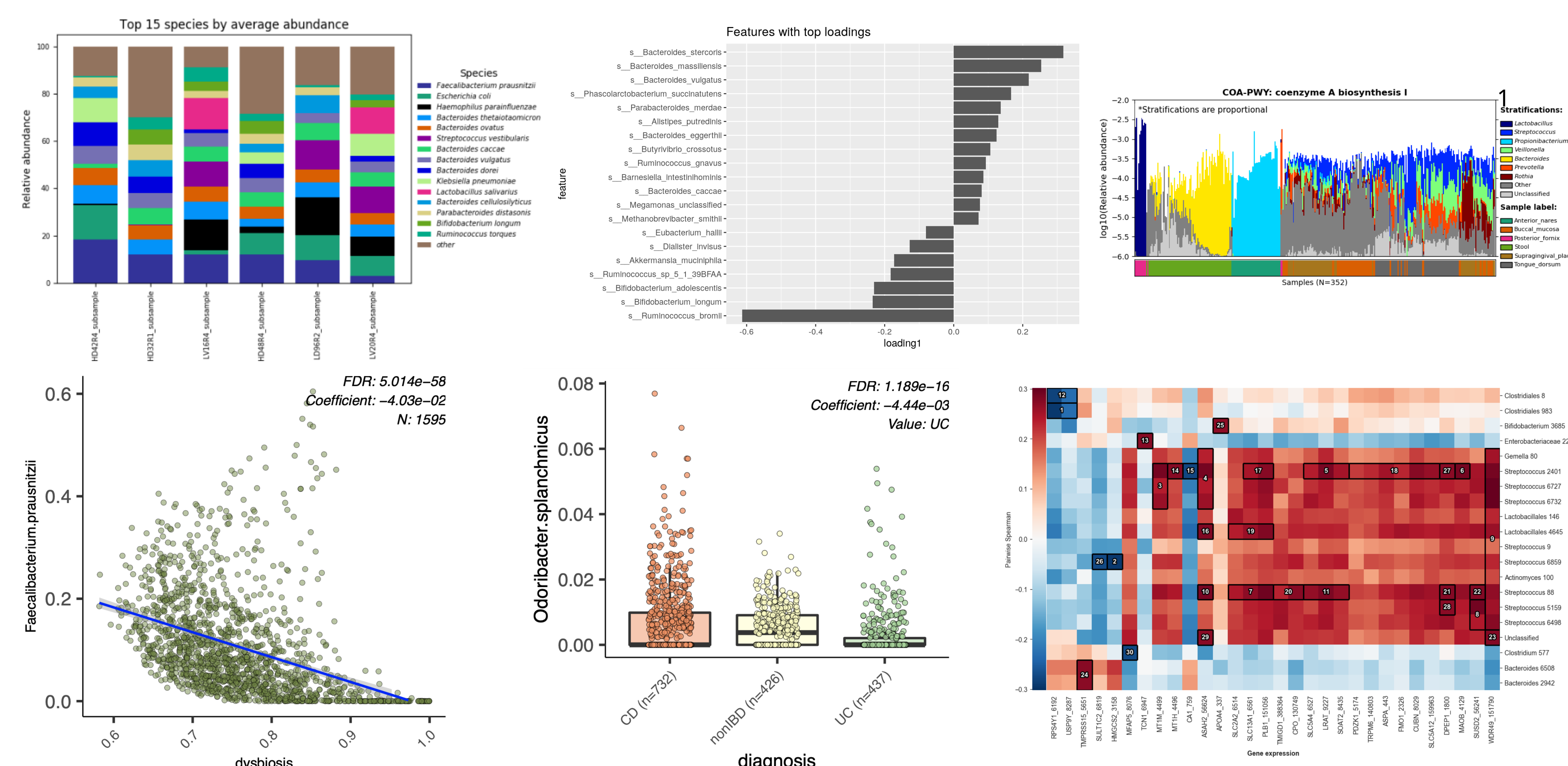
Contact us at: hcmac@hsph.harvard.edu

Microbial community profiling



The first step in microbiome molecular data analysis is quality control (KneadData) and profiling to transform raw data into biologically interpretable features using a reproducible workflow (AnADAMA/bioBakery). This includes identifying microbial species (MetaPhlAn) and strains (PanPhlAn/StrainPhlAn), characterizing their functional potential or activity (HUMANn), and integrating metagenomics with other data types.

Downstream analysis and statistics



Once profiled, microbial communities are amenable to downstream statistics and visualization much like other molecular epidemiology data such as human genetic or transcriptional profiles. Like these other data types, microbial communities often require tailored statistics for environmental, exposure, or phenotype association (MaAsLin 2.0, MMUPHIN) or for ecological interaction discovery (BANOcc). The Harvard Chan Microbiome Analysis Core provides a variety of analyses for researchers working in the microbiome space.

The Harvard Chan Microbiome Analysis Core is a part of the Harvard Chan Microbiome in Public Health Center (HCMPH). Want to learn more? Visit <https://hcmph.sph.harvard.edu>

<https://hcmph.sph.harvard.edu/hcmac>

<http://huttenhower.sph.harvard.edu>

