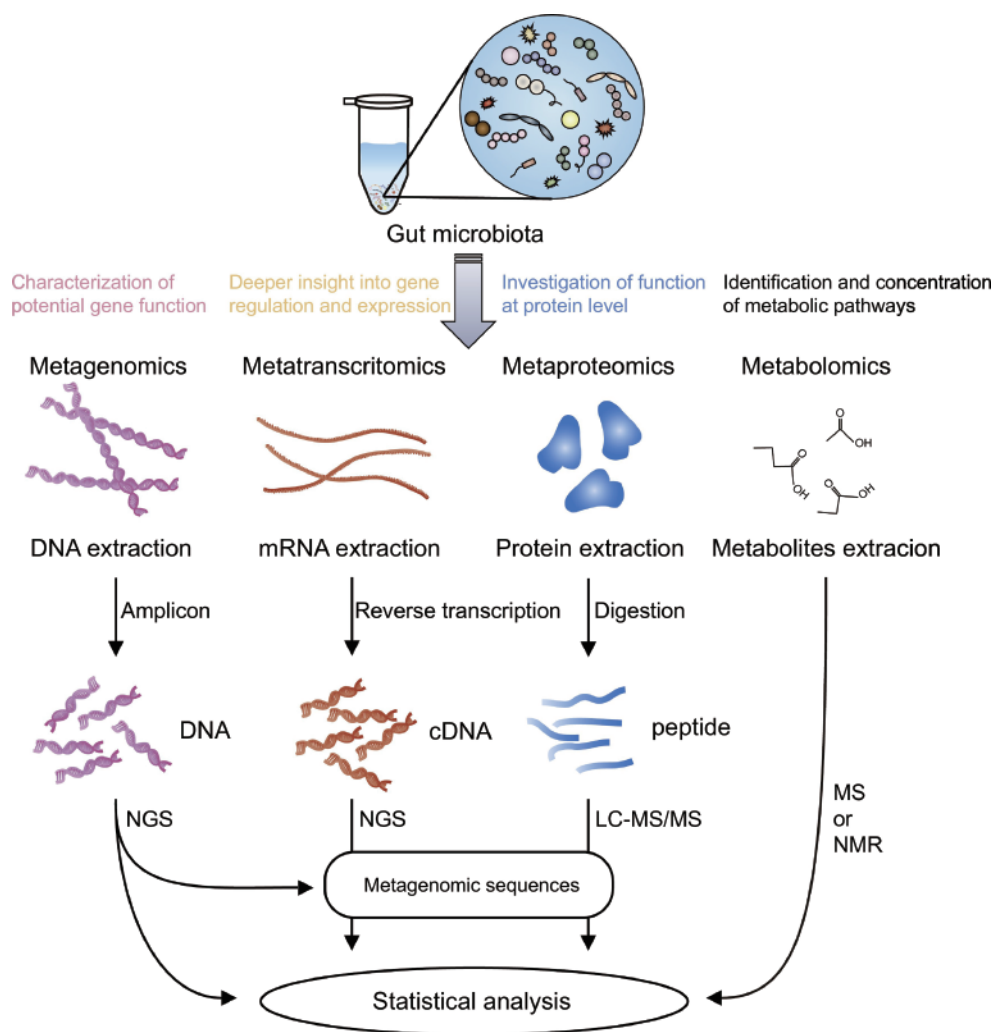


Service Description

Metagenomics takes microbial populations from human or environmental samples as the research object and utilizes whole genome sequencing and big data analysis to understand the complex relationships within microbial diversity, including population structure, evolutionary relationships, functional activity, population interaction and interaction with the living environment.



Metagenomics, metatranscriptomics, metaproteomics and metabolomics for human gut microbiota studies

Wang Y Q, et al., Metaproteomics: A strategy to study the taxonomy and functionality of the gut microbiota, (2020)

The metabolism of microbial communities is determined by the proteome, which is defined as the total set of proteins of the microbial cells, including enzymes for growth and maintenance. Since its inception in 2004, metaproteomics aims at the large-scale characterization of all proteins expressed by environmental microbiota at a given point in time. Metaproteomics enables an in-depth study of the diversity, structure and potential gene function of a microbial community.

BGI has extensive experience in the field of metaproteomics spanning microorganism research across human fecal samples, water samples, and fermentation processes within the beverage industry.

Common Challenges with Metaproteomics Studies

Abundance

- A lot of impurities
- Complex microbial composition

Database Limitations

- Few microbial protein specific sequences
- No microbial protein database

Function Annotation

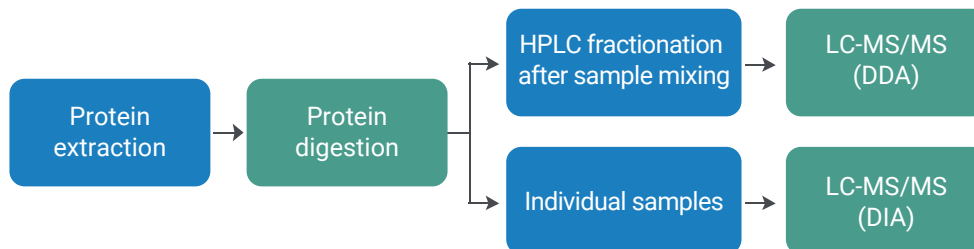
- Many uncharacterized proteins with unknown functions

Research Applications



- Microorganisms in activated sludge and sewage
- Energy metabolism and material metabolism of marine microorganisms
- Microorganisms in soil
- Intestinal microflora research
- Microbial community analysis in fermented food

Metaproteomics Analysis Workflow



BGI Service Advantages

Unique and Effective Extraction

We provide professional protein extraction solutions for various types of environmental samples

Market Leading MS Platform

We participate in quantitative performance assessment and standardization of Multi-National DIA proteomics analysis

Second to None Information Analysis

We provide professional and comprehensive analysis results based on years of experience

Bioinformatics Analysis Workflow

Standard:

Protein Analysis

- 01 DDA spectra library analysis
- 02 QC of peptides and proteins
- 03 Quantification of peptides and proteins
- 04 Differential protein analysis

Species Analysis

- 01 Species annotation
- 02 Species accumulation curve
- 03 Species composition
- 04 Differential species analysis

Diversity Analysis

- 01 Alpha diversity
- 02 Beta diversity
- 03 PCA/PCoA
- 04 NMDS

Correlation Analysis (with phenotype)

- 01 Species correlation network
- 02 Species and function correlations
- 03 CCA
- 04 Mantel

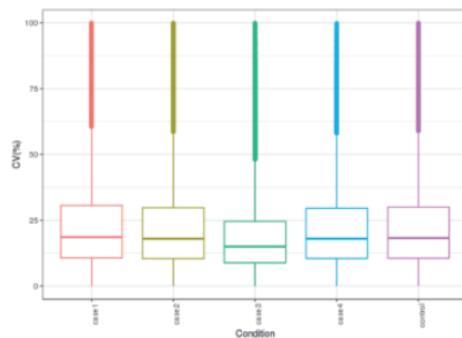
Function Analysis

- 01 Function annotation
- 02 Function enrichment
- 03 Function composition
- 04 Differential function analysis

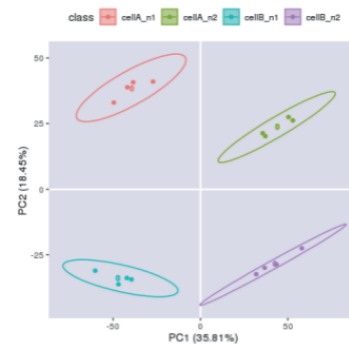
Correlation Analysis (without phenotype)

- 01 Species correlation network
- 02 Species and function correlations

Examples of Data QC Analysis - Stability and Repeatability

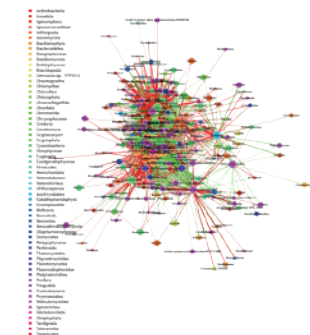


CV Distribution



PCA Analysis

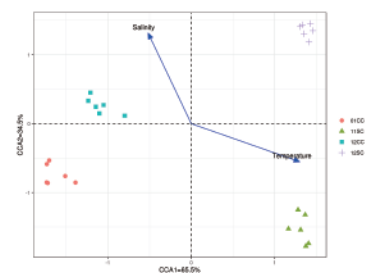
Examples of Correlation Analysis



Species Correlation Network



Species and Function Correlations



CCA

Turn Around Time

Sample size: 1-20, 4-5 weeks



To Learn More

To learn how your research can benefit from BGI's extensive experience in Metaproteomics, visit www.bgi.com, write to us via info@bgi.com or contact your local BGI office.

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BGI Genomics



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