

# Microbiome and Metabolome Research Solutions

Gut microbes provide energy to the microbiota by digesting food residues and releasing metabolites for the gut, affecting the host if they enter the host's circulatory system. Conversely, intestinal metabolites can influence the composition, gene expression, and gut microbiota-derived metabolites. Structural changes and metabolic changes in the gut microbial community, as well as metabolic changes in the host's blood or tissues, tend to cause a variety of diseases. The joint study of microbiome and metabolome can help discover microorganisms and metabolites that play key roles in the physiological and disease development processes and reveal related mechanisms.

Disease marker research

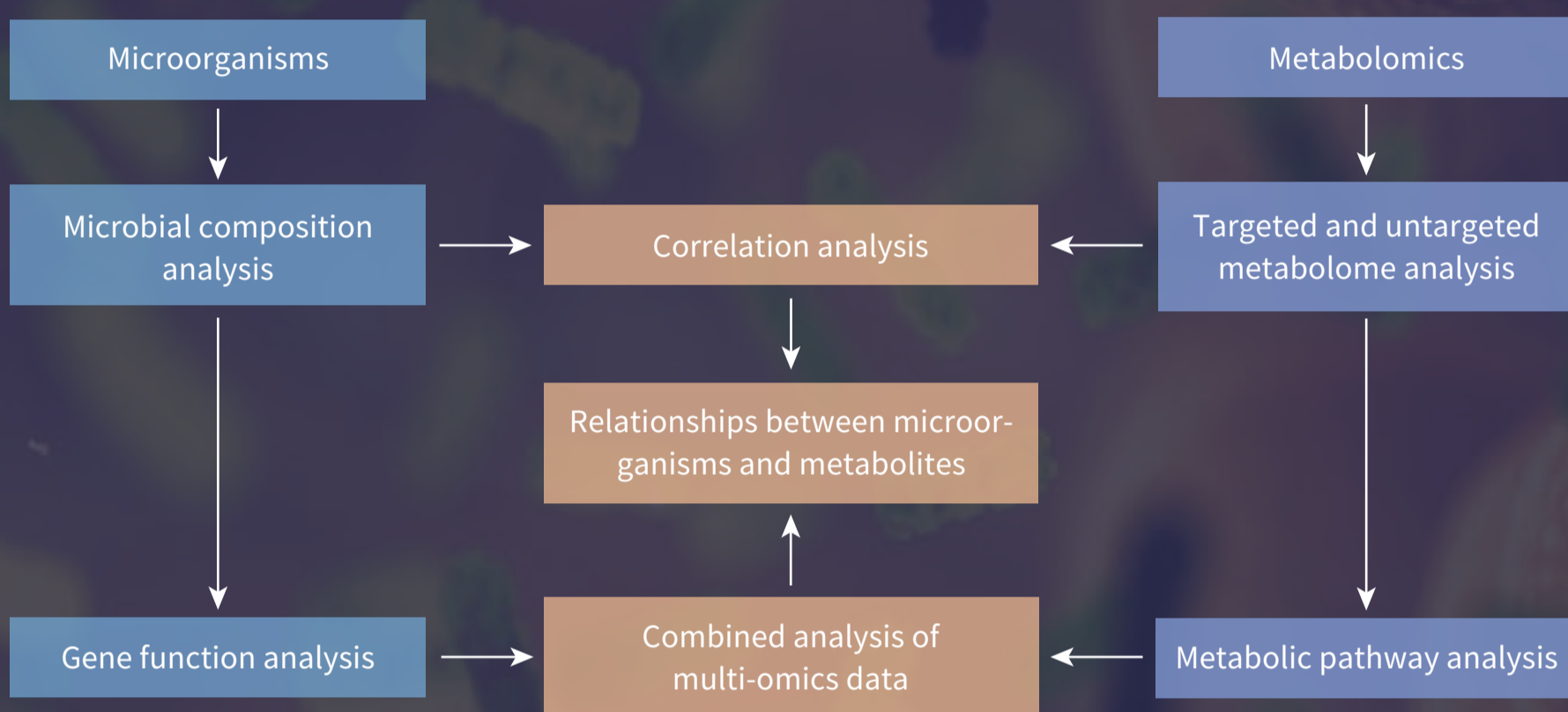
Drug metabolism analysis

Disease mechanism research

Phenotypic correlation analysis

Disease treatment research

## Analysis Process



## Bioinformatics Analysis

We will visualize the data and gain a comprehensive understanding of the relationship between the microbiome and the metabolome through the following methods:

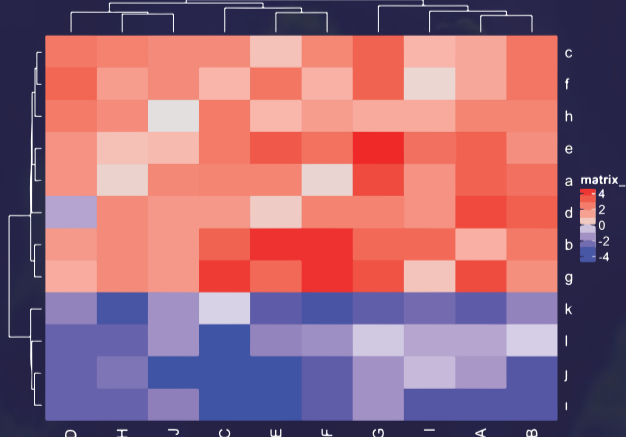
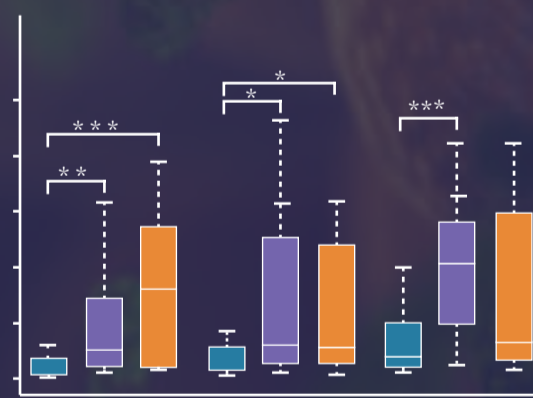
Microbial and metabolite correlation analysis

Microbial and metabolite correlation network construction

Integrative analysis of multi-omics data

The simplest approach for omics integration involved univariate correlation analysis in determining the presentation of strong linear relationships (Pearson's correlation) or monotonic relationships (Spearman's correlation) between individual metabolites (metabolome) and genes or taxa (microbiome).

Although univariate correlations are relatively straightforward, these methods suffer from high false-positive rates and require multiple test corrections to minimize the type I error rates. In addition, while associations between metabolites and microbiomes can be inferred, these associations often lack explanatory context in terms of biological plausibility and mechanistic insight. Methods based on univariate correlations are often used in conjunction with other knowledge-based methods to aid in data interpretation.



Multivariate analysis methods allow for simultaneous consideration of interactions between and within the data matrices. Dimensionality reduction has become the primary strategy in performing statistical integration, with the aim to reduce a large number of variables to a small number of new components or principal variables with minimal loss of information.

Multivariate histological integration methods are often extensions of commonly used dimensionality reduction techniques, including principal component analysis (PCA) and partial least squares (PLS). PCA is a data-reduction technique that identifies linear combinations of variables that maximize variance within one data matrix (X). PLS is a supervised method aiming to maximize the covariance between extracted components of X and Y.

Typical correlation analysis (CCA) and covariance analysis (CIA) are two other multivariate correlation methods commonly used for histological integration. CCA is a feature extraction method that identifies the most correlated linear combination of X and Y to maximize the correlation between components. CIA describes the synergistic structure between two data sets by maximizing the covariance between components.

Procrustes Analysis (PA) is a statistical technique that visually integrates histological data using data reduction methods, such as PCA and CCA. PA superimposes the main components of two datasets in a low-dimensional space and allows researchers to quickly check the consistency of multi-omics datasets.

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