Microbiome and Metabolome Research Solutions

Microbiome and metabolome research can help discover microorganisms and their key roles in the physiological and disease development processes and reveal related mechanisms.

Analysis Process

**Microbiome**
- Microbial composition analysis
- Microbial community correlation analysis

**Drug metabolism analysis**
- Correlation analysis
- Relationships between microbial functions and metabolism

**Disease marker research**
- Combined analysis of multi-omics data

**Phenotypic correlation analysis**
- Metabolic pathway analysis

**Integration analysis of multi-omics data**

**Bioinformatics Analysis**

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

1. **Microbial and metabolite correlation analysis**
2. **Microbial and metabolite correlated network construction**
3. **Integration analysis of multi-omics data**

The simplest approach for cross integration involves univariate correlation analysis. In determining the relationship between microbial metabolites or metabolite interactions (Pearson’s correlation) or ecosystem relations (Daeum’s correlation) between microbial metabolites and genes or tissue (microbiome).

Although univariate correlations are intuitive and straightforward, these methods suffer from high false positive rates and require multiple true corrections to minimize the type I error rate. In addition, while associations between metabolites and microbiome can be identified, these associations lack the necessary context in terms of biological plausibility and mechanistic insight. Methods based on univariate correlation are often useless 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 sets.

- **Dimensionality reduction** has become the primary strategy in performing data integration, with the goal to reduce a large number of variables to a small number of new components or principal components with minimal loss of information.

- **Multivariate historical integration methods** are often extensions of commonly used dimensionality reduction techniques, including principal component analysis (PCA) and partial least squares (PLS). PLS is a data reduction technique that identifies linear combinations of variables that maximize variance within one data matrix. PCA is a supervised method aimed to maxi-

Typical correlation analysis (CCA) and covariance analysis (CA) are two such multivariate correlation methods commonly used for biological integration. CCA is a feature analysis method that identifies the most correlated linear combinations of variables that maximize variance within one data matrix. CA is a supervised method aimed to maxim-

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

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