Multi-Omics Service Overview

Service Description

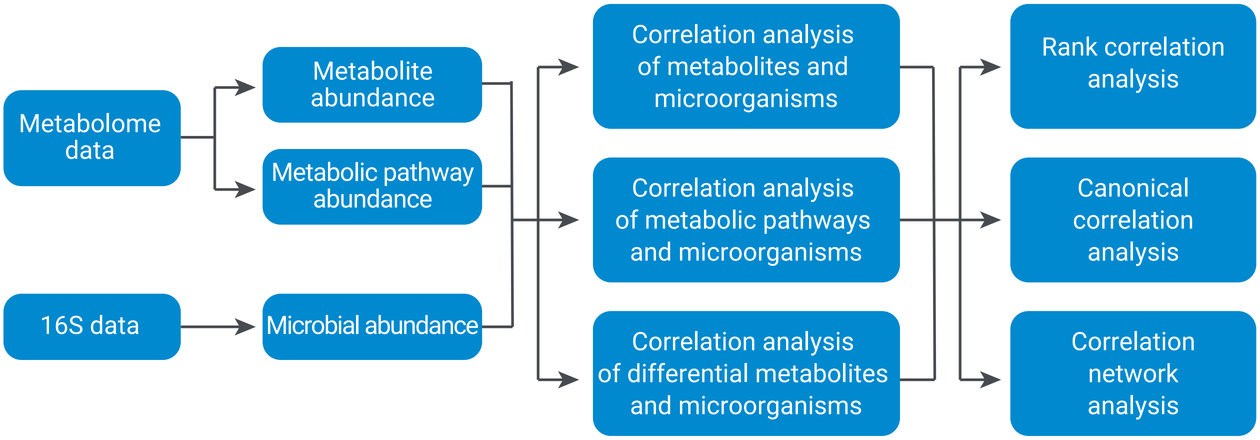
Multi-omics is the integrative biological analysis of different data sets from single omics areas for new insight. An integrated multi-omics approach to research enables a more comprehensive understanding of genotypic, phenotypic and environmental relationships and their association to disease and health of an organism.

BGI offers multi-omics services to look across genomics, transcriptomics, epigenomics, proteomics and metabolomics, with the flexibility to customize solutions that meet your specific needs. All projects are supported by a bioinformatics infrastructure that is second to none.

Metagenome / 16S + Metabolome Correlation Analysis

In recent years, research on gut related diseases has developed rapidly and it is now thought that nearly 90% of diseases may be related to gut microbiota health. Metagenome/16S + metabolome correlation analysis enables researchers to establish an association model between host metabolism and gut microbiota and explore the causal relationships between microbes and disease.

Research Approaches



Metabolome data

Metabolite abundance

Metabolic pathway abundance

16S data

Microbial abundance

Correlation analysis of metabolites and microorganisms

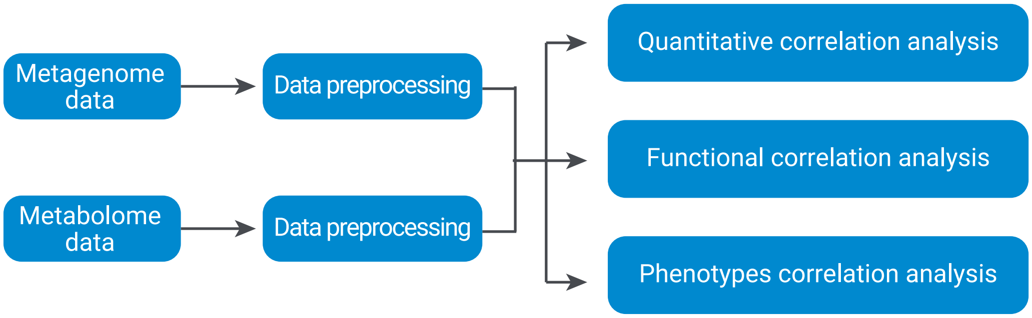
Correlation analysis of metabolic pathways and microorganisms

Correlation analysis of differential metabolites and microorganisms

Rank correlation analysis

Canonical correlation analysis

Correlation network analysis



Metagenome data

Data preprocessing

Metabolome data

Data preprocessing

Quantitative correlation analysis

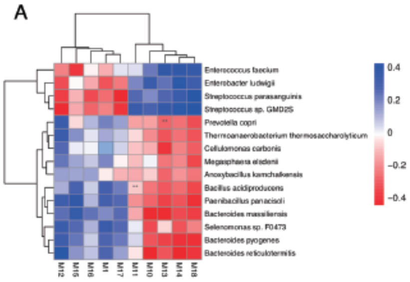
Functional correlation analysis

Phenotypes correlation analysis

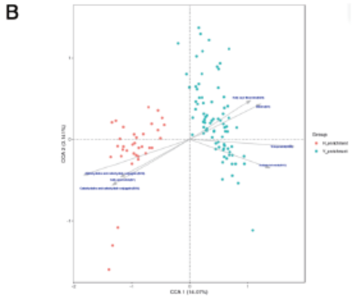
Note: Stools and intestinal contents samples are recommended for Metagenome/16S services; blood samples (serum, plasma) are recommended for Metabolome services.

Analysis Options

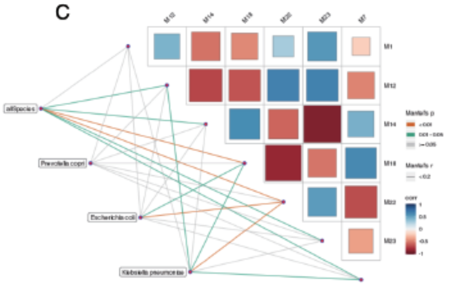
1.Quantitative correlation analysis



Spearman's correlation analysis

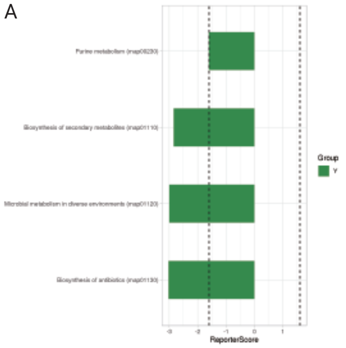


CCA

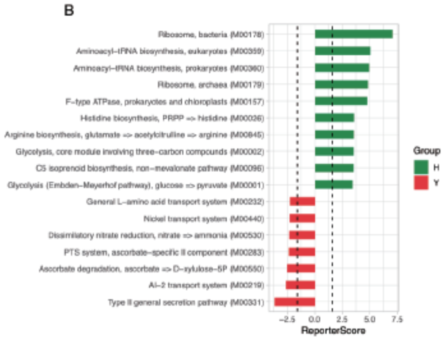


Mantel test

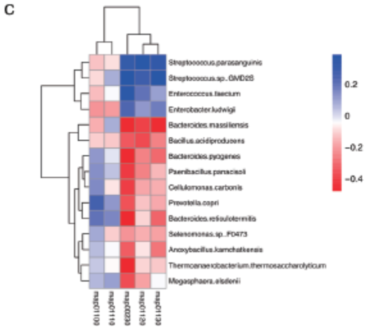
2.Functional correlation analysis



Enrichment analysis of metabolites
KEGG pathway

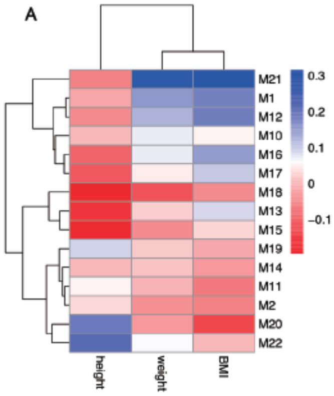


Enrichment analysis of KEGG
module of differential species

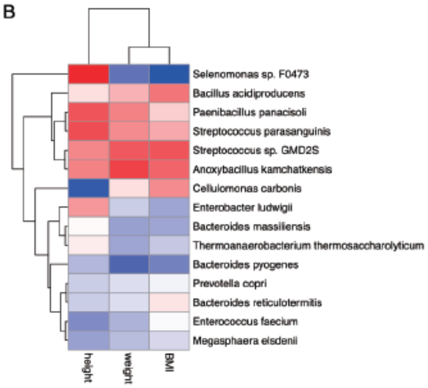


Spearman correlation heatmap
of enriched metabolites pathways
and microorganisms

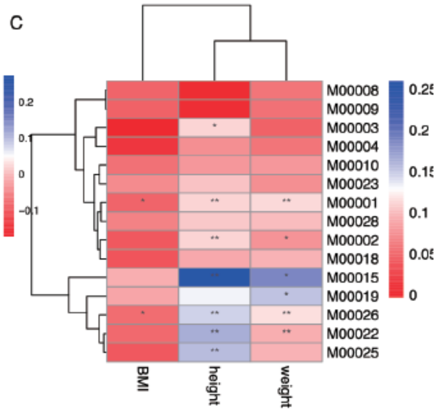
3.Phenotypes correlation analysis



Correlation heatmap between
metabolites cluster and phenotypes



Correlation heatmap between
microorganisms and phenotypes



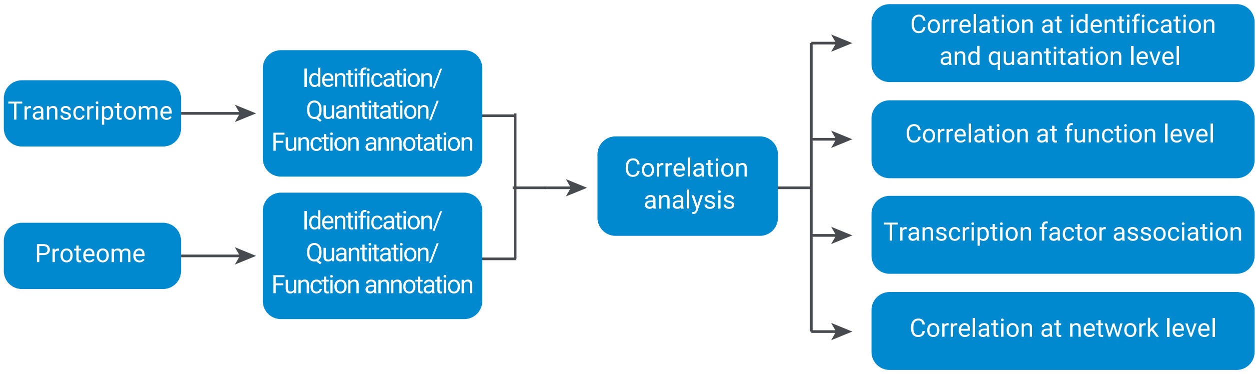
Correlation heatmap between
KEGG modules and phenotypes

Application Cases

1. Liu R, Hong J. et al. Gut microbiome and serum metabolome alterations in obesity and after weight-loss intervention (BGI's Publication). Nat Med. 2017 Jul;23(7):859-868.
2. Liu H, Chen X. et al. Alterations in the gut microbiome and metabolism with coronary artery disease severity. Microbiome. 2019 Apr 26;7(1):68.

Proteome + Transcriptome Correlation Analysis

Using a multi-omics approach to correlate transcriptomics with proteomics data provides a more comprehensive overview of expression patterns and enables researchers to interpret deeper biological implications.



Transcriptome

Proteome

Identification/ Quantitation/ Function annotation

Identification/ Quantitation/ Function annotation

Correlation analysis

Correlation at identification and quantitation level

Correlation at function level

Transcription factor association

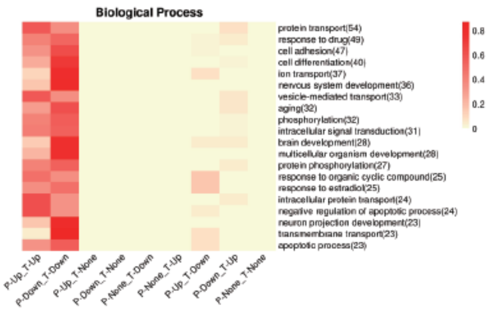
Correlation at network level

Note: Sample selection for Transcriptome and Proteome should be as consistent as possible.

Analysis Options

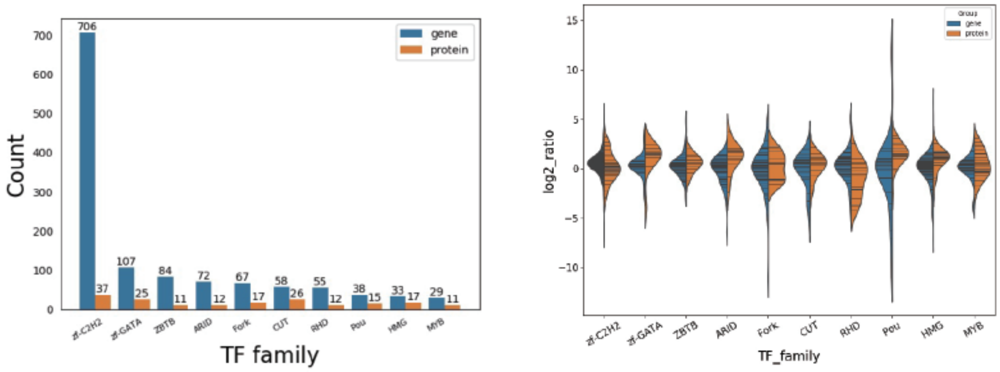
1. Four dimensional bubble diagram and heatmap make results easier to understand

Four-dimensional bubble diagram of GO/KEGG correlation analysis



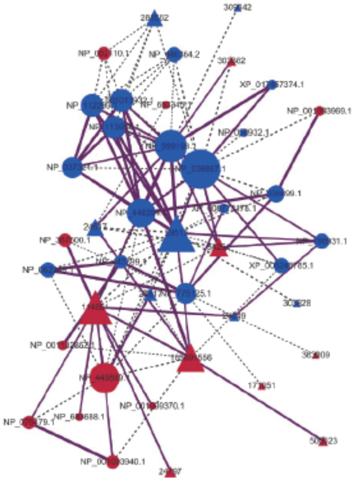
Heat map of correlated GO clusters probability

2. A new perspective - transcriptional factor two-level mining helps reveal the mechanism of transcriptional regulation



The identification number and expression distribution of transcription factors in each transcription factor family

3. Multi-Omics network analysis enables the realization of correlation integration between the co-expression networks of differential genes and differential proteins



Protein interaction network analysis of differential genes and differential proteins

Application Cases

1. Becker K, Bluhm A, Casas-Vila N. et al. Quantifying post-transcriptional regulation in the development of Drosophila melanogaster. Nat Commun. 2018 Nov 26;9(1):4970.
2. Dai F, Wang Z. et al. Transcriptomic and proteomic analyses of mulberry (Morus atropurpurea) fruit response to Ciboria carunculoides (BGI Participation). J Proteomics. 2019 Feb 20;193:142-153.

Other Multi-Omics Integrative Analysis

· Transcriptome + metabolome correlation analysis
· Proteome + metabolome correlation analysis
· Quantitative proteome + phosphoproteome correlation analysis

To Learn More

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

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DNBSEQ™ technology-based services are executed at our service laboratories in China.
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