EasyMetagenome: A user-friendly and flexible pipeline for shotgun metagenomic analysis in microbiome research

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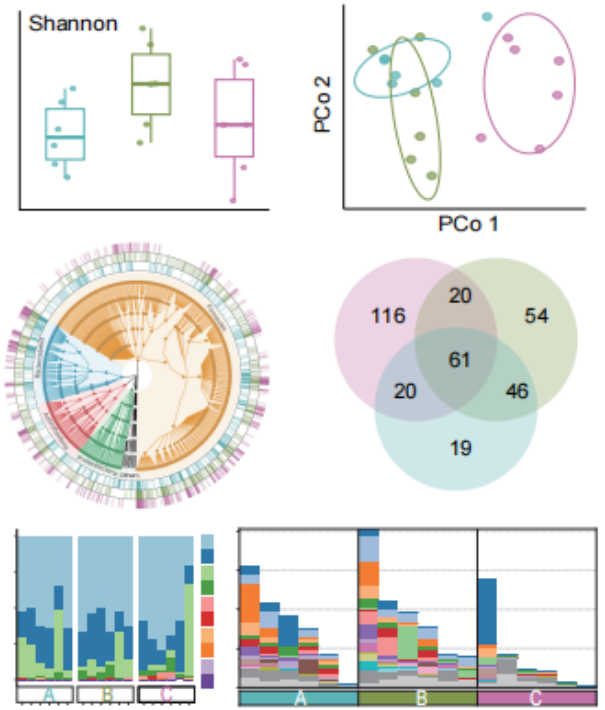
Introduction

EasyMetagenome

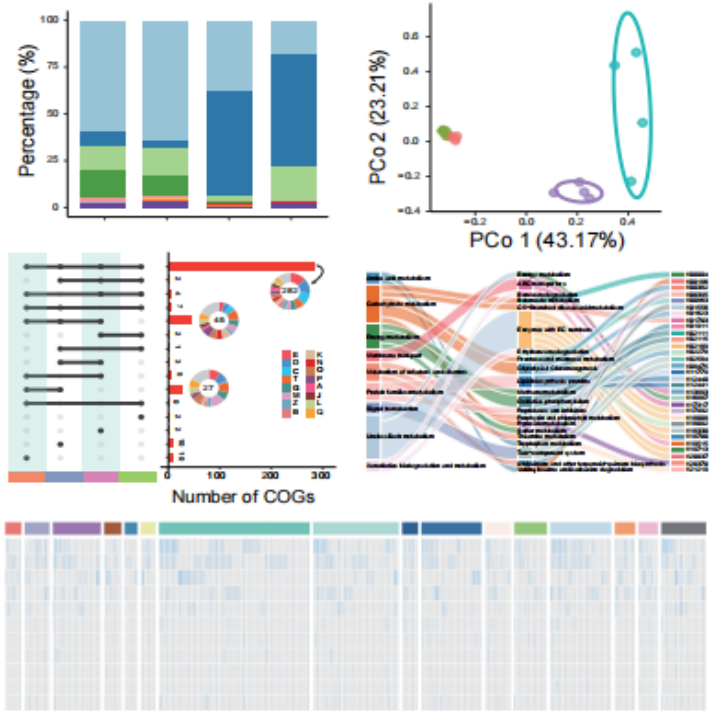
A user-friendly and flexible pipeline for shotgun metagenomic analysis in microbiome research

1 **Data preprocessing** Raw reads → Quality control & Remove host reads → Clean reads

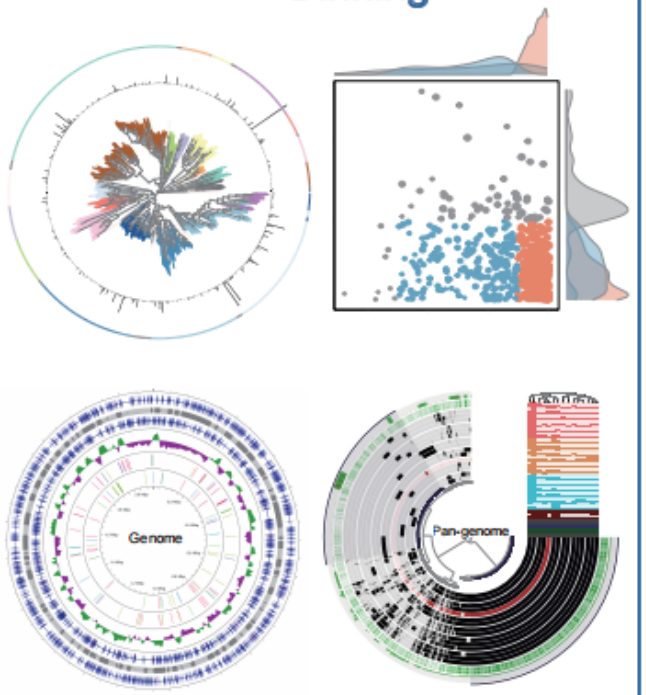
2 **Read-based analysis**



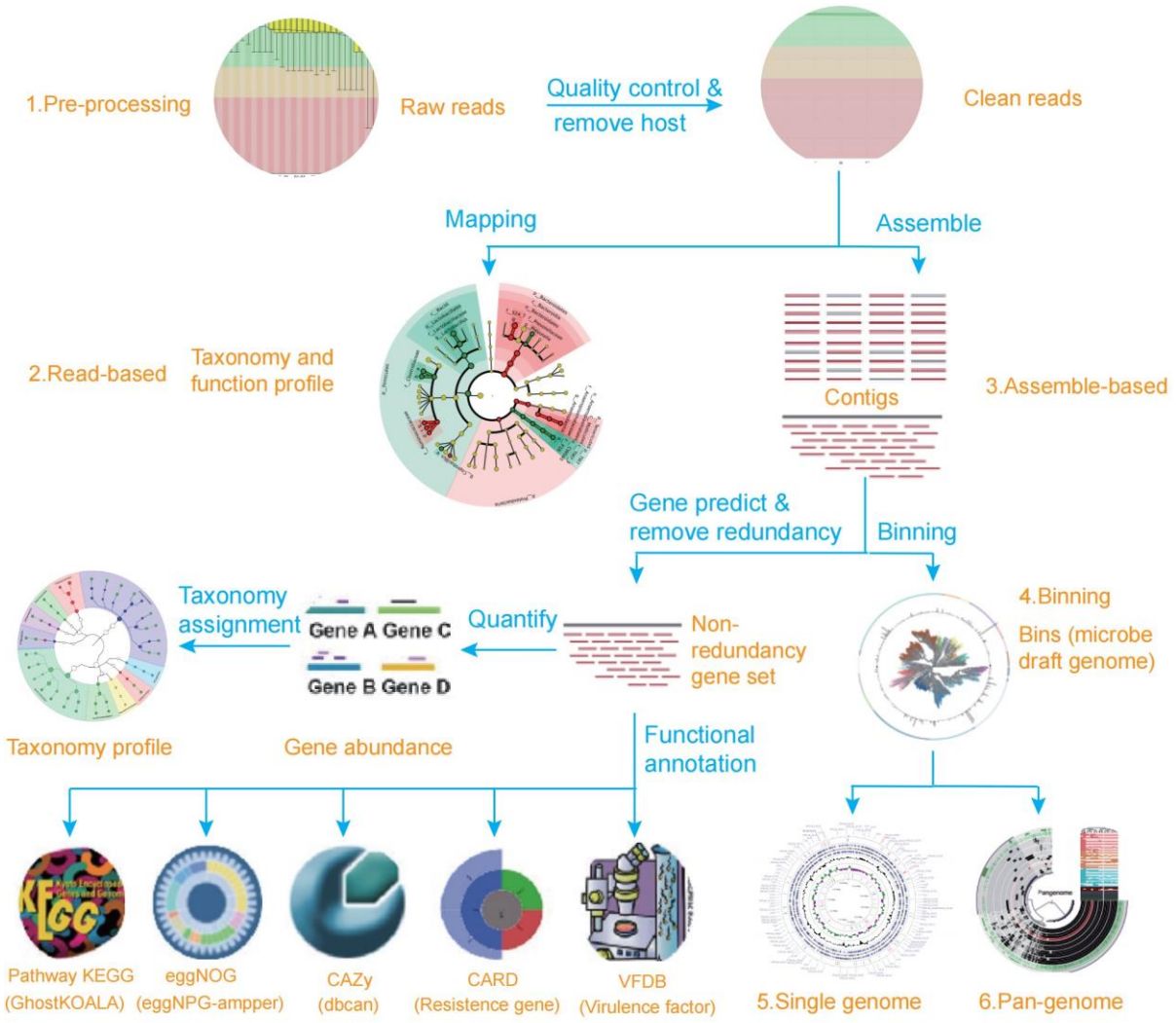
3 **Assembly-based analysis**



4 **Binning**

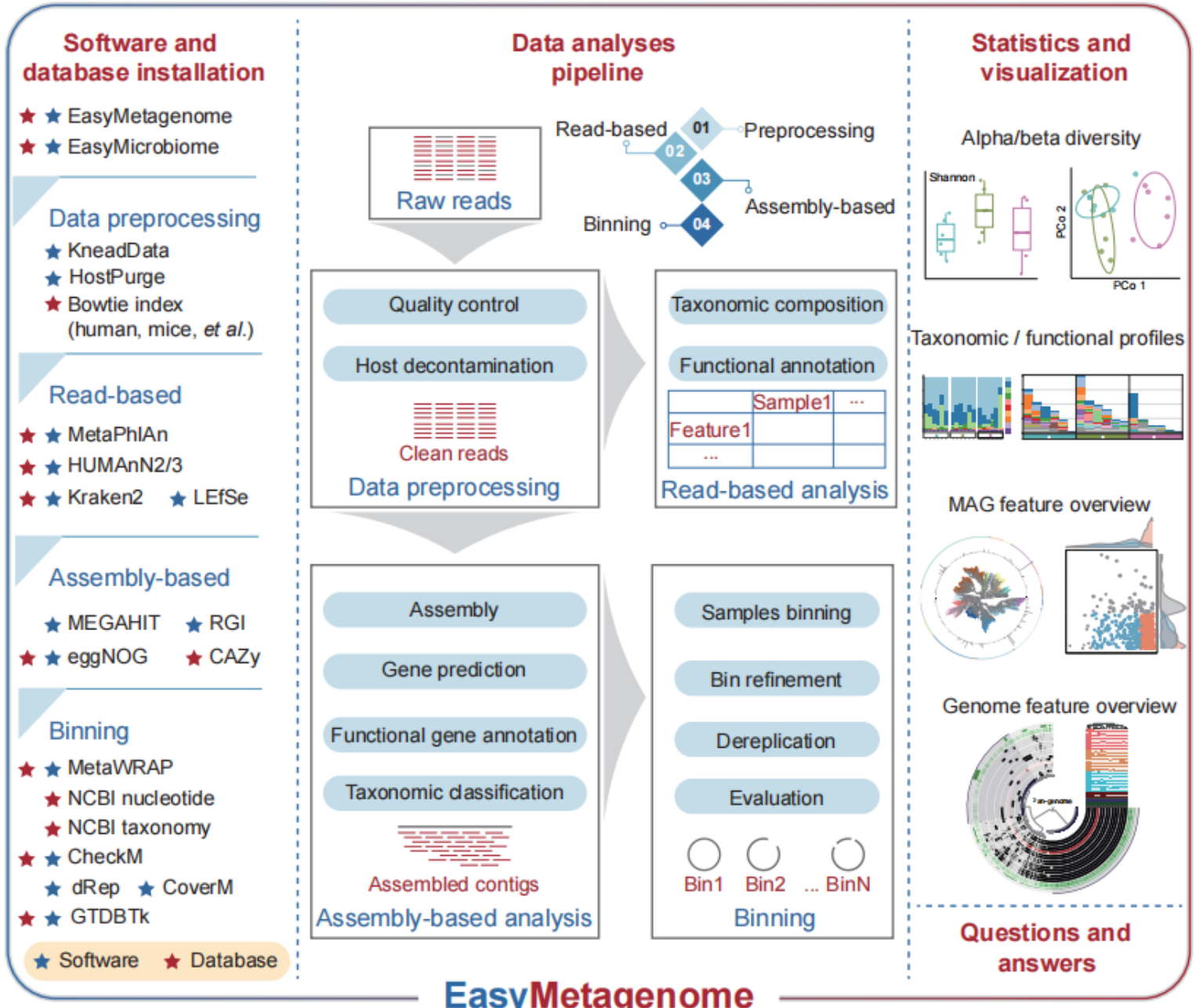


Highlights



- EasyMetagenome offers multiple installation options and detailed question and answer explanations.
- EasyMetagenome includes detailed parameter explanations to accommodate various data scenarios, ensuring flexibility and adaptability
- EasyMetagenome supports comprehensive downstream analysis from raw data, including read-based, assembly-based, binning, and genome analysis, with the ability to generate publication-ready visualizations.
- EasyMetagenome is developed as an open-source project, encouraging collaboration from the community. It's available for access and contribution at https://github.com/YongxinLiu/EasyMetagenome.

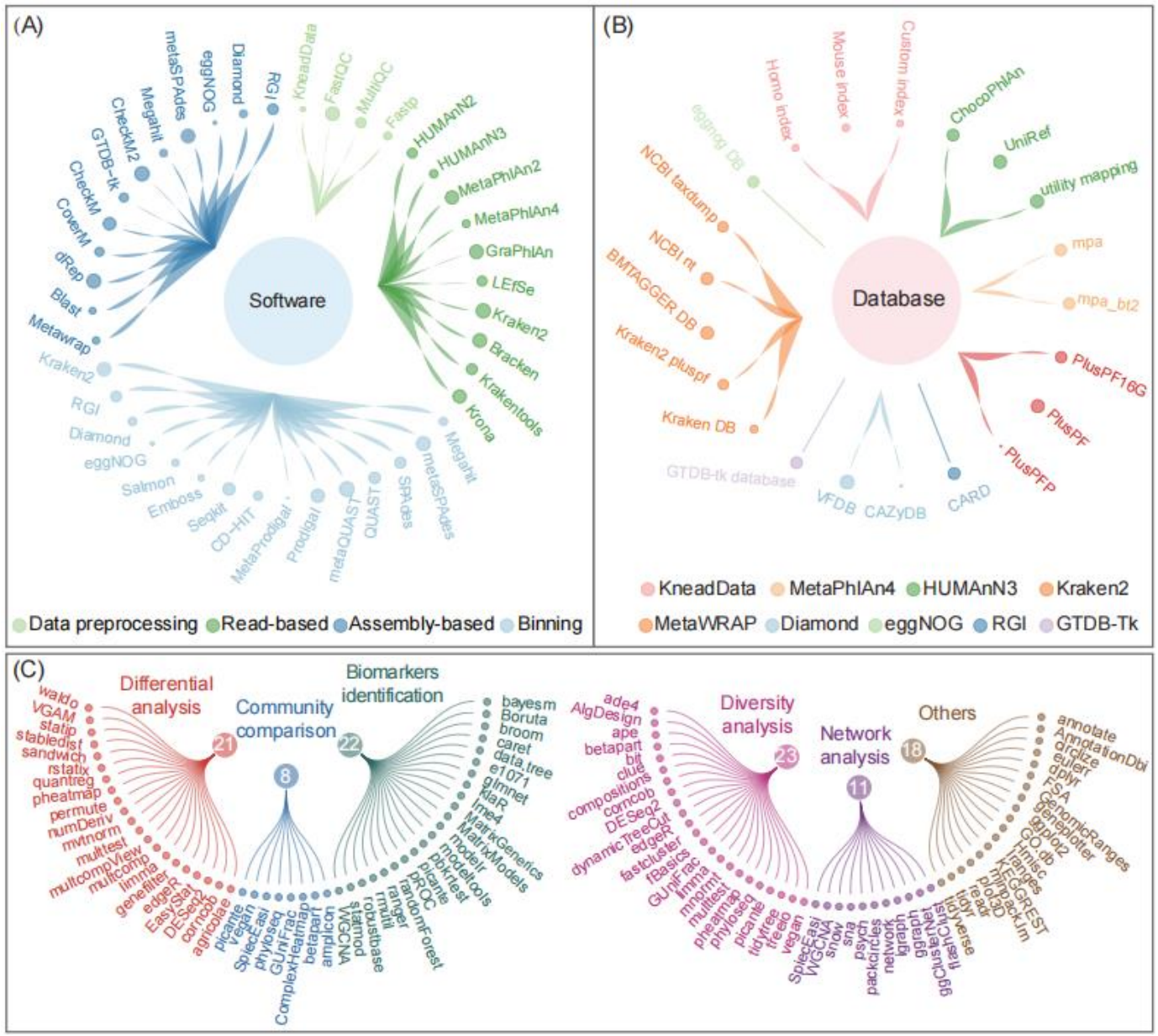
EasyMetagenome workflow



The EasyMetagenome comprises three main components: Software and database installation, data analyses pipeline, and statistics and visualization.

Figure 1 EasyMetagenome workflow

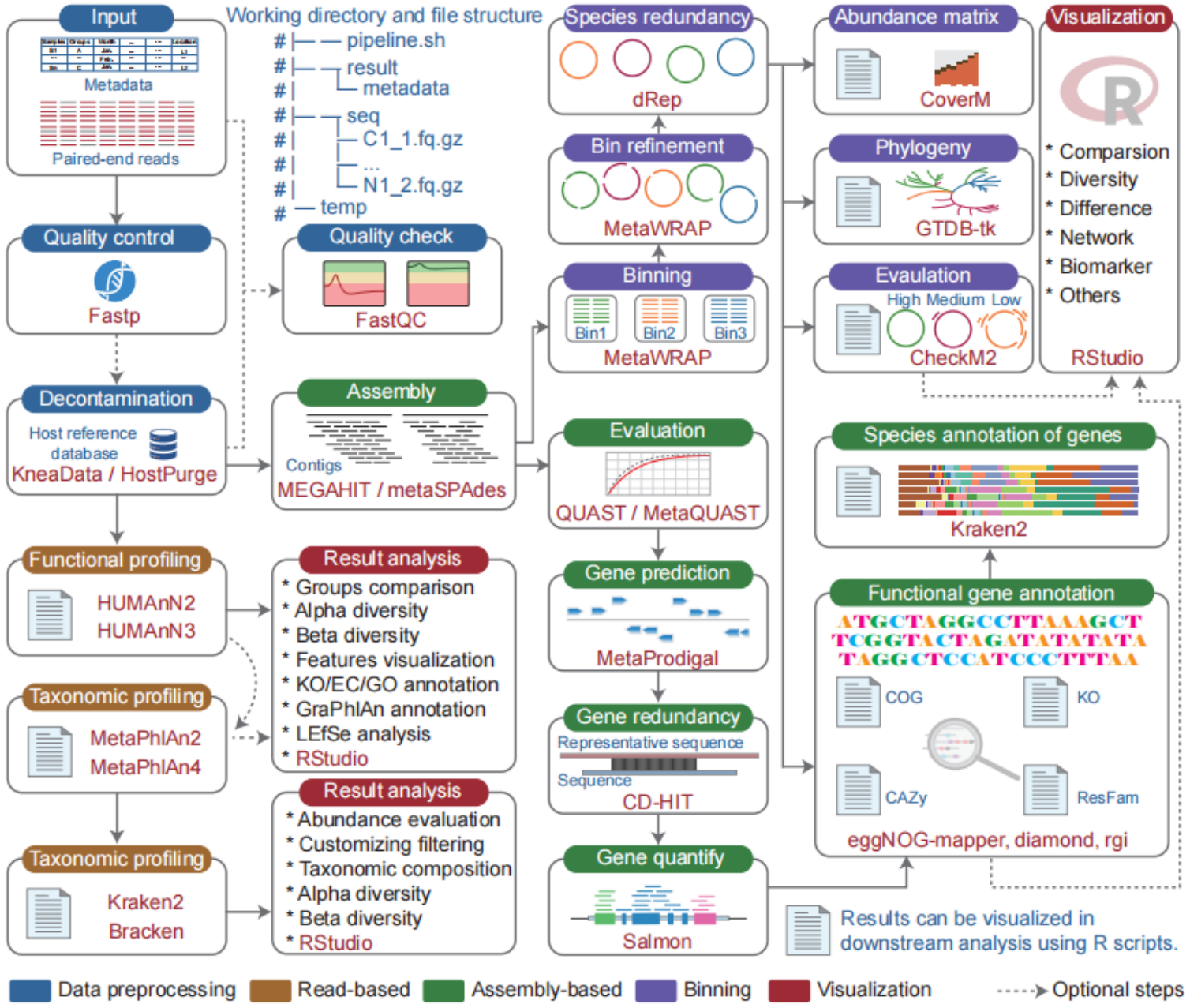
Software, databases, and R packages included in EasyMetagenome



At least 41 softwares, 21 standards or custom databases, 93 R packages utilized for differential analysis, community comparison, biomarker identification, diversity analysis, network analysis, and others.

Figure 2 Software, databases, and R packages included in EasyMetagenome

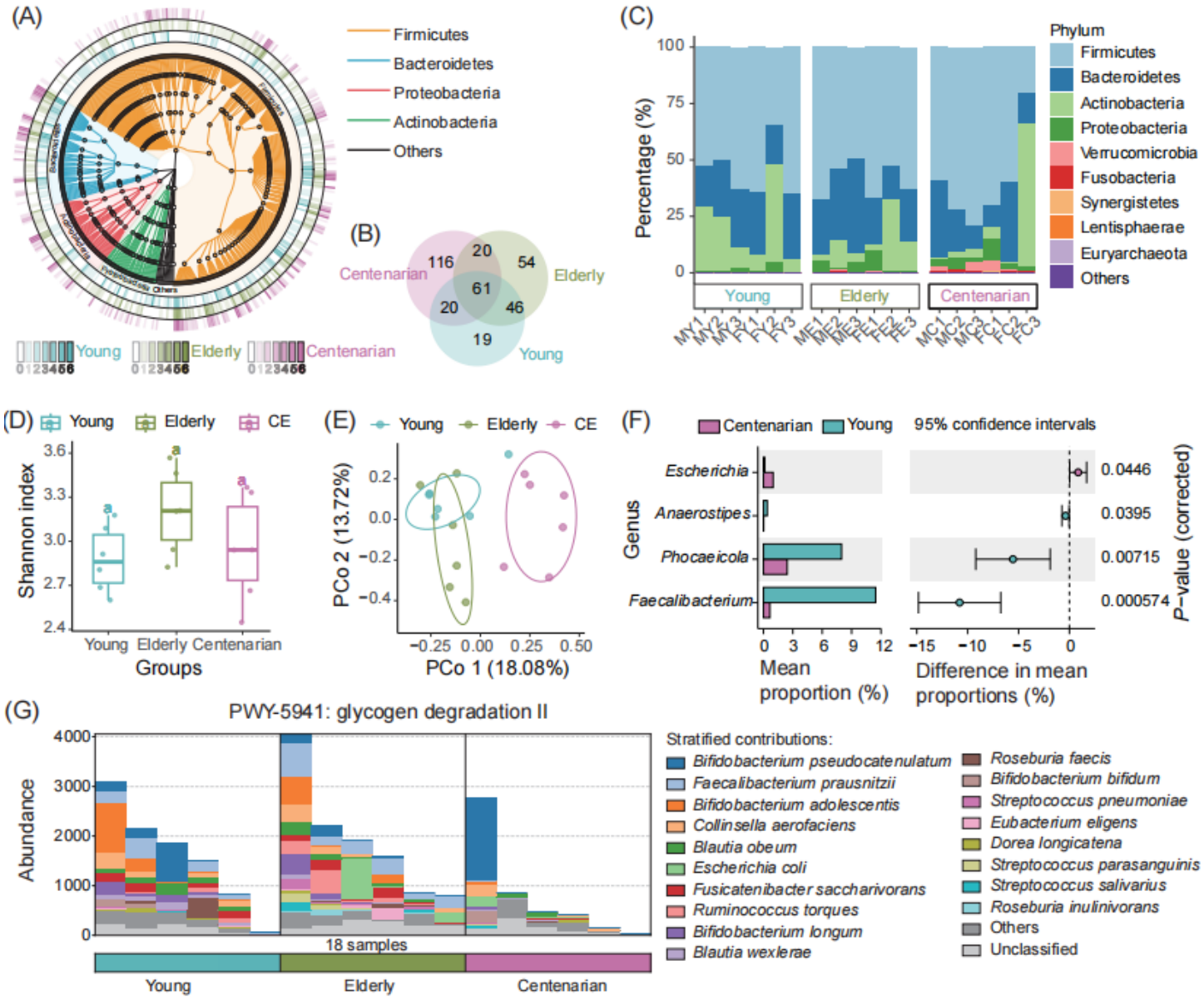
Summary of the EasyMetagenome analysis pipeline



EasyMetagenome pipeline includes data preprocessing for read-based, assembly-based, and binning analyses, with files available for data visualization.

Figure 3 Summary of the EasyMetagenome analysis pipeline

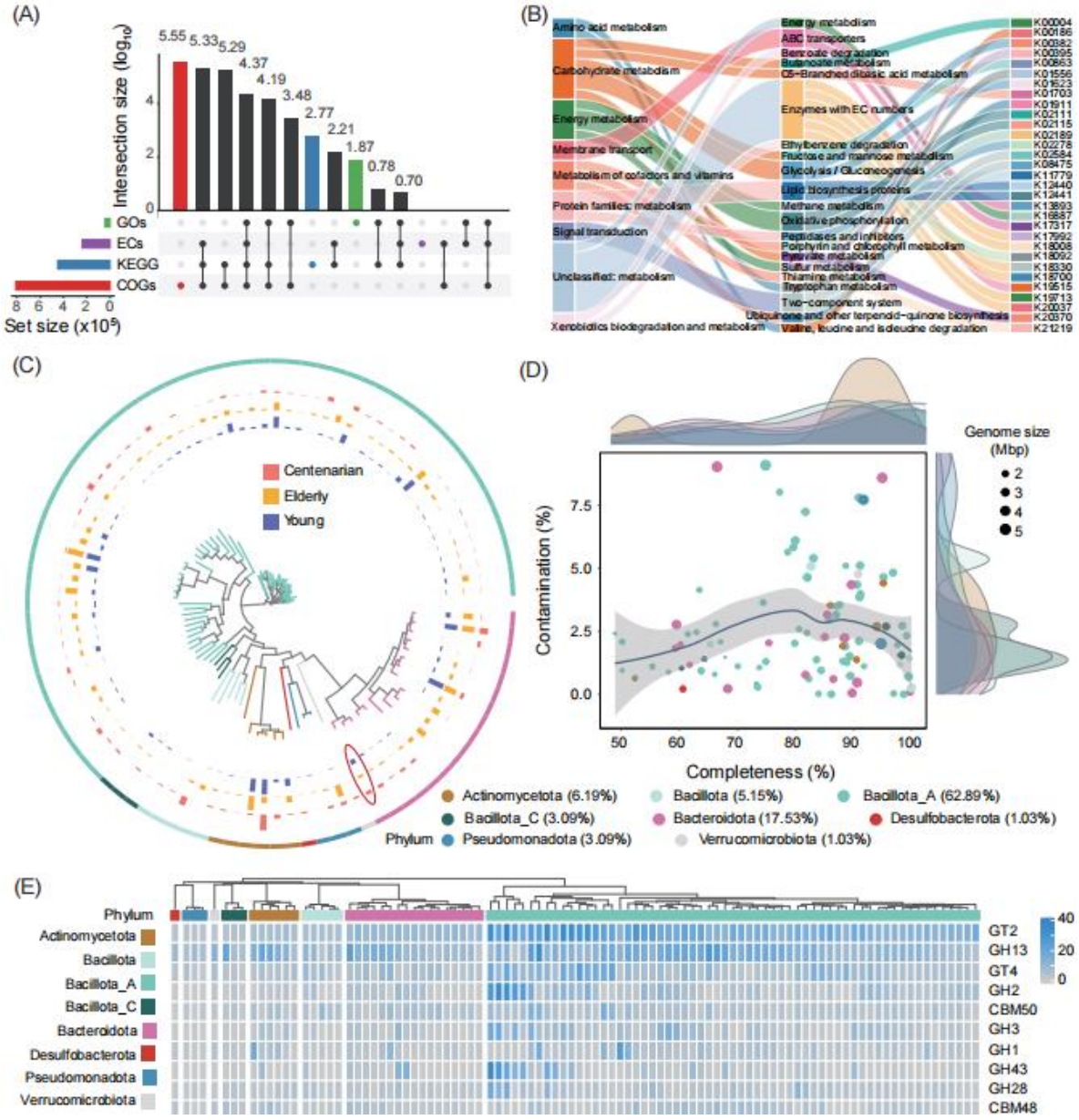
Taxonomic and functional composition from read-based analysis using EasyMetagenome in human gut microbiome samples



EasyMetagenome pipeline provides read-based analysis and visualization like microbial taxonomic composition, unique and shared taxa, Shannon diversity indices, Principal coordinates analysis (PCoA), STAMP plot, and abundance of the functional pathway.

Figure 4 Taxonomic and functional composition from read-based analysis using EasyMetagenome in human gut microbiome samples

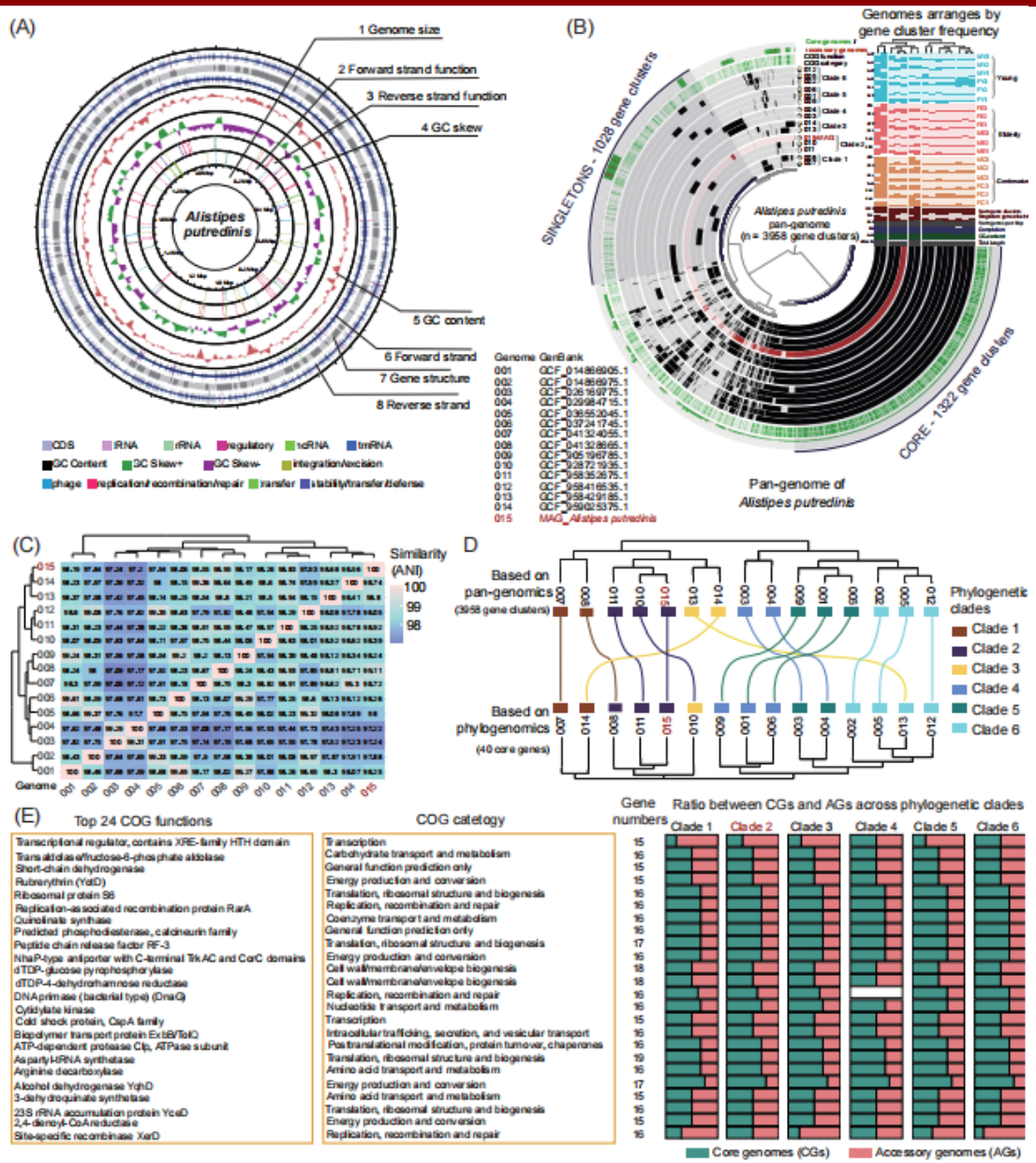
Functional annotation of assembled contigs and comparative analysis of MAGs in human gut microbiome samples



EasyMetagenome pipeline provides assembled contigs and metagenome assembled genomes (MAGs) analysis in human gut microbiome samples like functional annotations of assembled contigs, KEGG classification of annotated functional genes, phylogenetic analysis and distribution of metagenome assembled genomes (MAGs), the distribution of completeness and contamination on MAGs, and CAZy functional gene annotations within MAGs.

Figure 5 Functional annotation of assembled contigs and comparative analysis of MAGs in human gut microbiome samples.

Metagenomic assembly genome digging in example human gut microbiome



EasyMetagenome pipeline provides metagenomic assembly genome digging in human gut microbiome samples like single bacterial genome map, pan-genomic analysis of target genomes, average nucleotide identity (ANI) depicting the genomic relatedness, and pan-genome functions analysis.

Figure 6 Metagenomic assembly genome digging in example human gut microbiome

Summary

- In this study, we introduced Easymetagenome, a user-friendly shotgun metagenomics pipeline designed for comprehensive microbiome analysis.
- Currently, EasyMetagenome pipeline supports quality control, host removal, read-based, assembly-based, binning, genome and pan-genome analysis.
- EasyMetagenome pipeline offers customizable settings, data visualizations, and parameter explanations, with the ability to generate publication-ready visualizations.
- Website: https://github.com/YongxinLiu/EasyMetagenome

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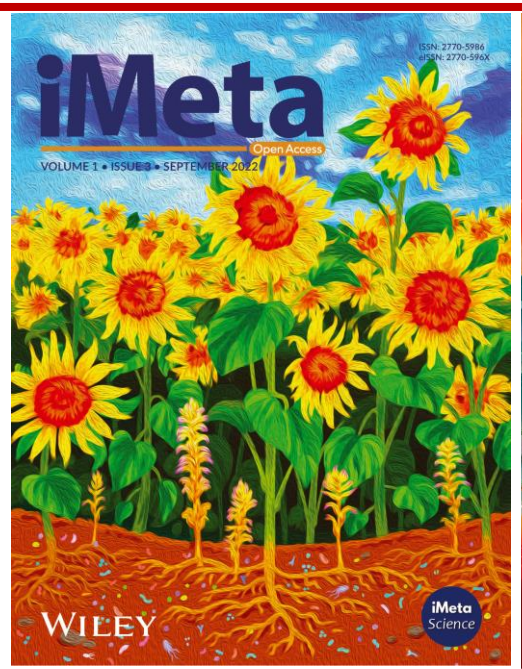

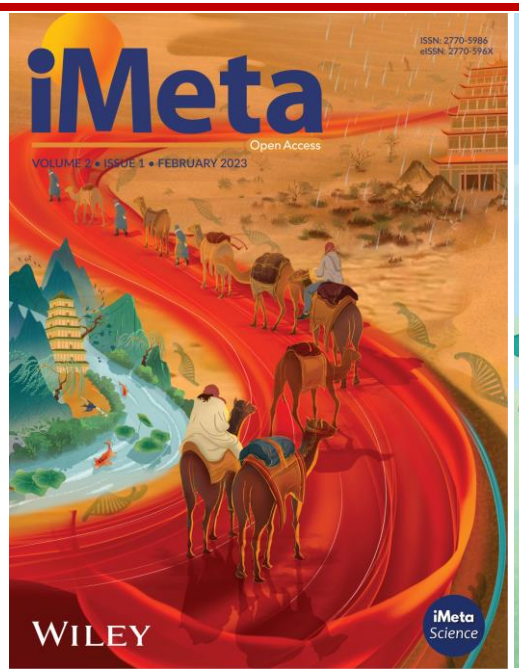

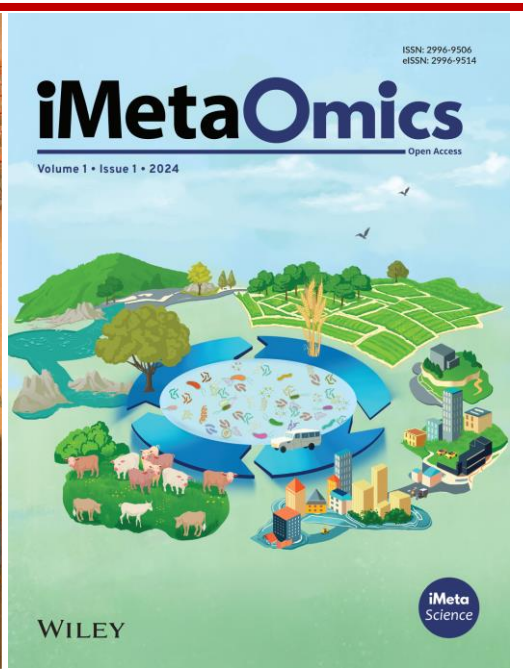

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