



Majorbio Cloud 2024: update single-cell and multi-omics workflows

Chang Han ¹, Caiping Shi ¹, Linmeng Liu ¹, Jichen Han ¹,
Qianqian Yang ¹, Yan Wang ¹, Xiaodan Li ¹, Wenyao Fu ¹, Hao Gao ¹,
Huasheng Huang ¹, Xianglin Zhang ¹, Kegang Yu ¹



¹Shanghai Majorbio Bio-Pharm Technology Co., Ltd, Shanghai, China

Han, Chang, Caiping Shi, Linmeng Liu, Jichen Han, Qianqian Yang, Yan Wang, Xiaodan Li, et al. 2024. Majorbio Cloud 2024: update single-cell and multi-omics workflows. *iMeta* 3: e217. <https://doi.org/10.1002/imt2.217>



Introduction

MAJORBIO CLOUD NEW RELEASED IN 2024

Single-omics Workflows



Single-cell Transcriptome



Proteome



Metabolome

Multi-omics Workflows



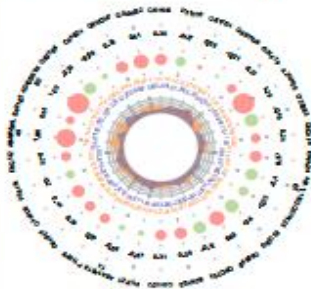
Microbiome and Metabolome Combined Analysis



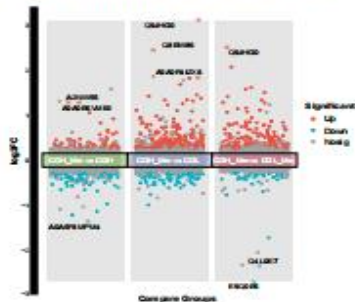
Transcriptome and Proteome Combined Analysis

Extensions

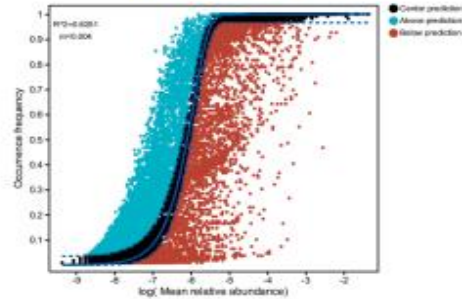
Differential Expression Radar Chart



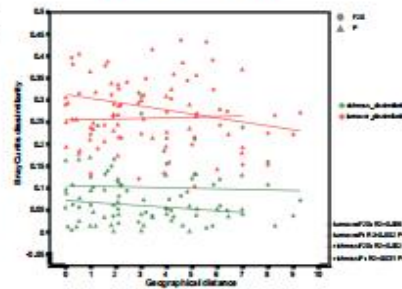
Multiple Comparison Groups Volcano Chart



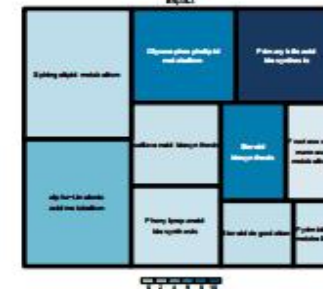
Neutral Community Model



Distance Decay Relationship



KEGG rectangular tree diagram



RNA Velocity





Workflow 1: Single-cell Transcriptomics Workflow

Single-Cell Transcriptome

01 Data Pre-processing

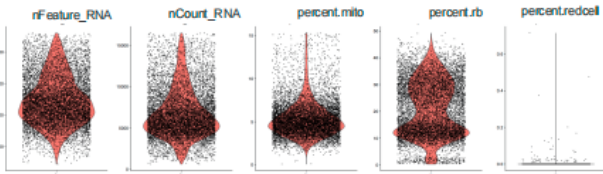
```

ATACGATAATCCGA
CATTGATATGCTAAT
GCCTTACAATCTTT
ATACGAGCAAAGGAA
GCCTTACTAATTATA
CATTGAGATTGGGTA
  
```

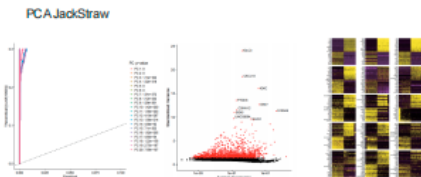
Cell Ranger

	C1	C2	C3	C4	C5	C6	C7
Gene1	3	1	2	2	5	2	5
Gene2	2	1	3	3	4	3	2
Gene3	3	2	1	1	2	3	2

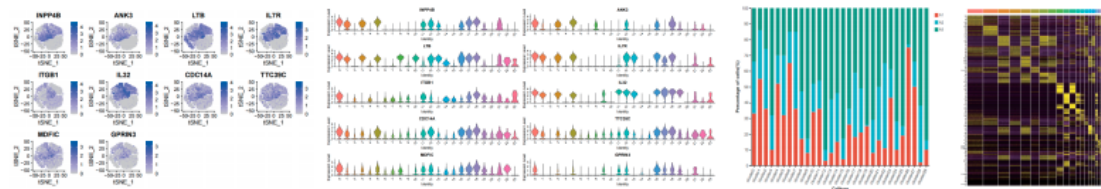
02 Cell Filtration



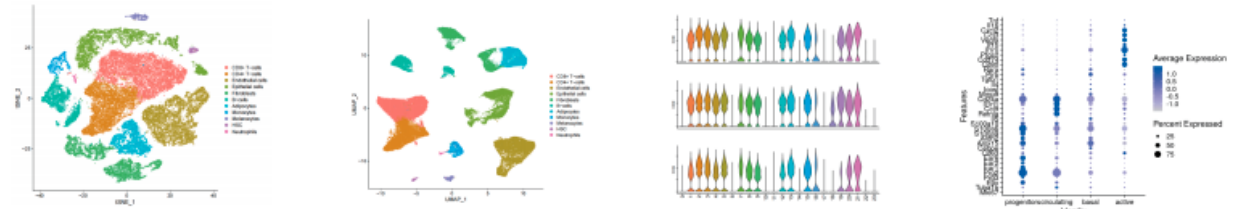
03 Batch Effect Removal & Sample Merging



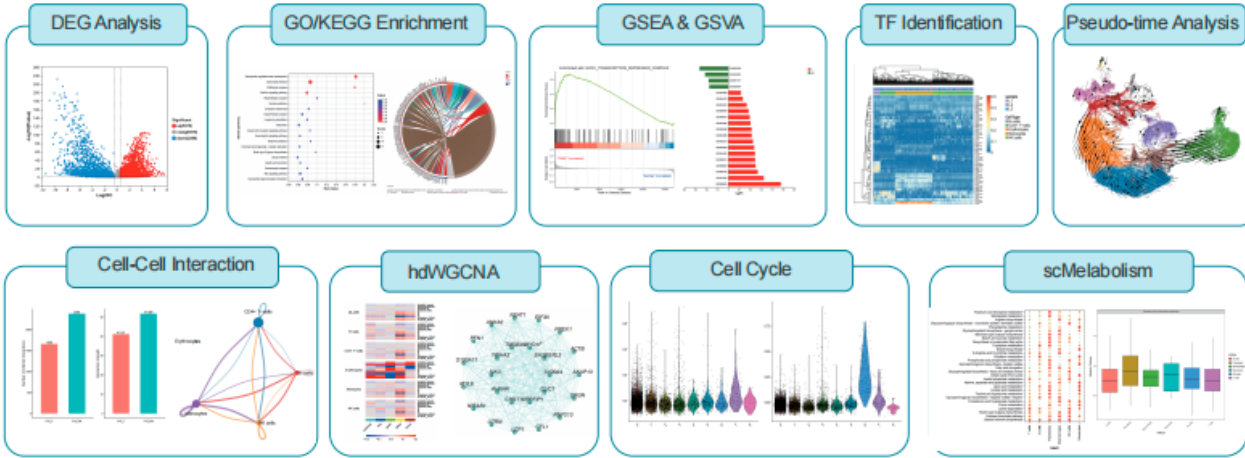
04 Clustering



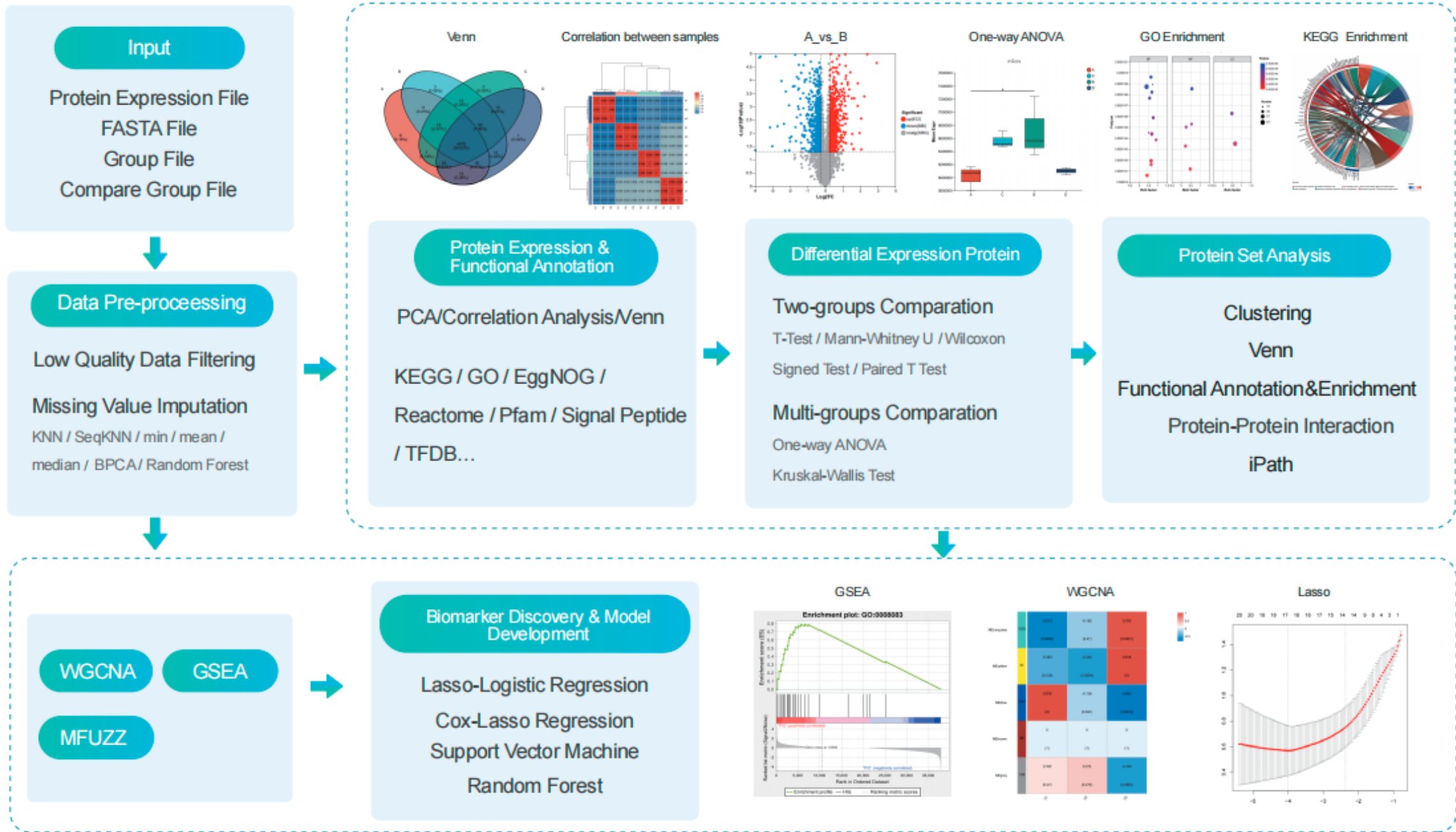
05 Marker Gene Identification



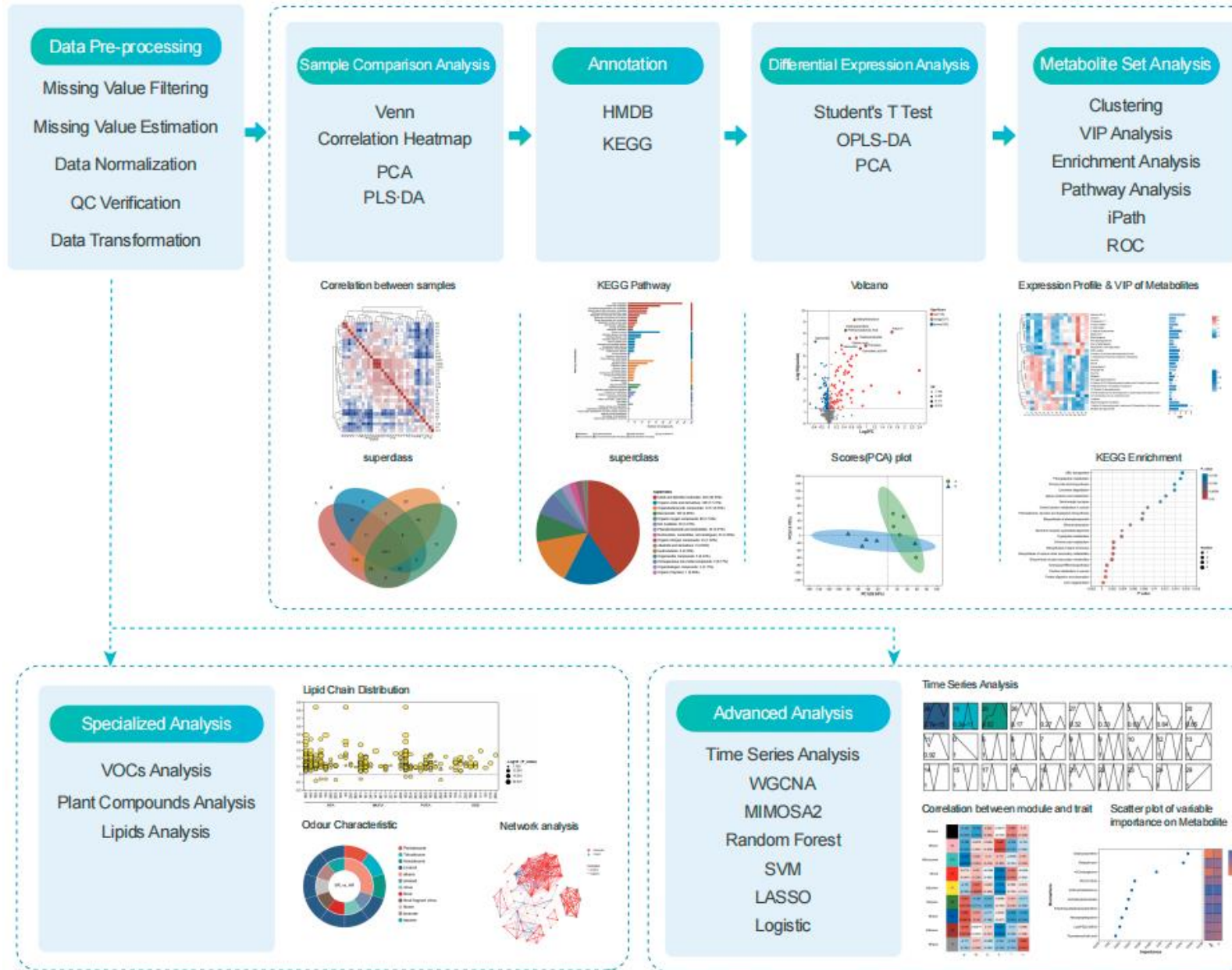
06 Downstream Analysis



Workflow 2: Proteomics workflow



Workflow 3: Metabolomics workflow



‘Pipeline+Extensions’, a new interactive analysis mode

Workflow Result → Intermediate Data Extraction & Format Processing → Set Parameters & Execute Tool Program → Generate Result

Differential Expression Hyperbolic Curve Volcano Chart

DEGs Results:

Comparison Group:

Fold Change:

Gene Label Mode:

- Show Top Genes According To $|\log_2FC|$
- Customize Gene Label
- No Label

Result

Volcano

Change

- up
- down
- none

$-\log_{10}(Pvalue)$

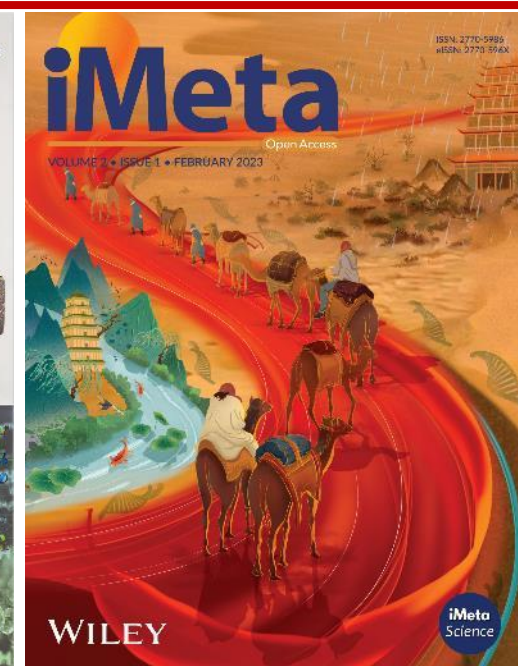
\log_2 fold-change



Summary

- ❑ Majorbio Cloud offers an easy and powerful approach to profiling the bulk transcriptome, single-cell transcriptome, proteome, metabolome, metagenome, and other omics data. It facilitates researchers to analyze complex multi-omics data and infer the biological meaning of integrated omics data.
- ❑ Since Majorbio Cloud's first publication in *iMeta*, it has attracted the attention of researchers around the world, and has been widely used by researchers who are not specialists in omics or bioinformatics.
- ❑ Website: <https://cloud.majorbio.com/>

Han, Chang, Caiping Shi, Linqing Liu, Jichen Han, Qianqian Yang, Yan Wang, Xiaodan Li, et al. 2024. Majorbio Cloud 2024: update single-cell and multi-omics workflows. *iMeta* 3: e217. <https://doi.org/10.1002/imt2.217>



“***iMeta***” is an open-access Wiley partner journal launched by iMeta Science Society consist of scientists in bioinformatics and metagenomics world-wide. iMeta aims to promote microbiome, and bioinformatics research by publishing research, methods/protocols, and reviews. The goal is to publish high-quality papers (top 10%, IF>20) targeting a broad audience. Unique features include video submission, reproducible analysis, figure polishing, bilingual, and promotion by social media with 500,000 followers. Since 2022 have been published 160 papers and cited > 2300 times. Index by [ESCI](#), [Google Scholar](#), [DOAJ](#) and [Scopus](#).



Society: <http://www.imeta.science>

Publisher: <https://wileyonlinelibrary.com/journal/imeta>

Submission: <https://wiley.atyponrex.com/journal/IMT2>



office@imeta.science



[Promotion Video](#)



[iMetaScience](#)



[iMetaScience](#)