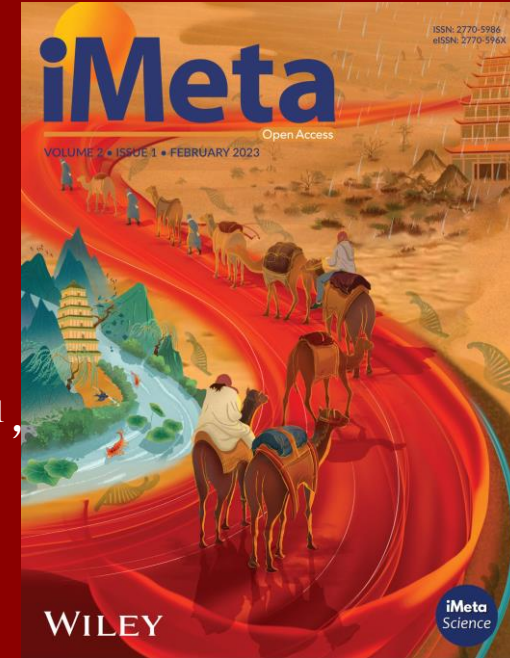


美吉生物云(Majorbio Cloud) 2024: 升级单细胞转录组和多组学 云流程

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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>

简介

MAJORBIO CLOUD NEW RELEASED IN 2024

Single-omics Workflows



Single-cell Transcriptome



Proteome



Metabolome

Multi-omics Workflows



Microbiome and Metabolome Combined Analysis



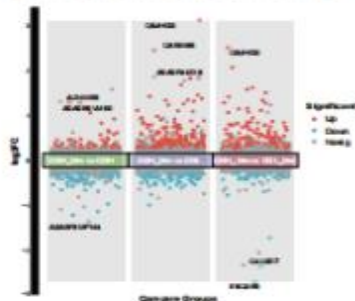
Transcriptome and Proteome Combined Analysis

Extensions

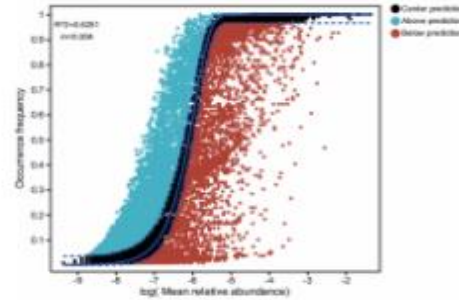
Differential Expression Radar Chart



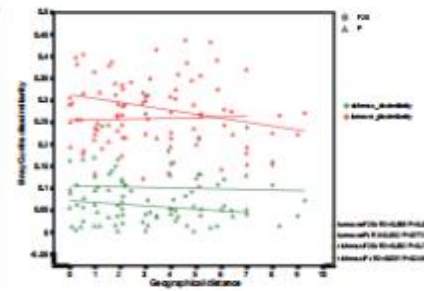
Multiple Comparison Groups Volcano Chart



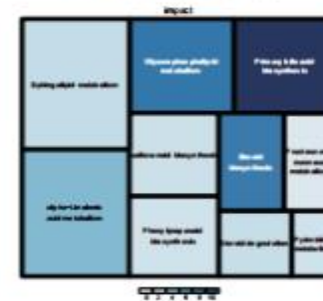
Neutral Community Model



Distance Decay Relationship



KEGG rectangular tree diagram



RNA Velocity



工作流一：单细胞转录组工作流

Single-Cell Transcriptome

01 Data Pre-processing

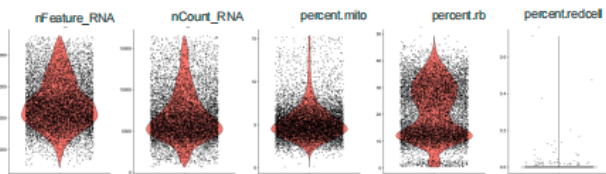
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ATACGATAATCCGA
CATTGATATGCTAAT
GCCTTACAATCTTT
ATACGAGCAAAGGAA
GCCTTACTAATTATA
CATTGAGATTGGGTA
    
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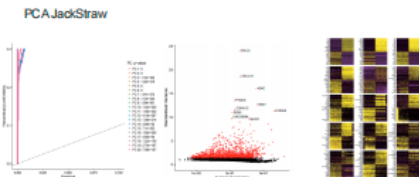
Cell Ranger

	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

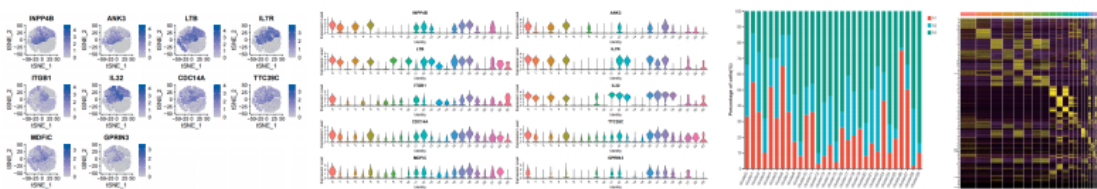
02 Cell Filtration



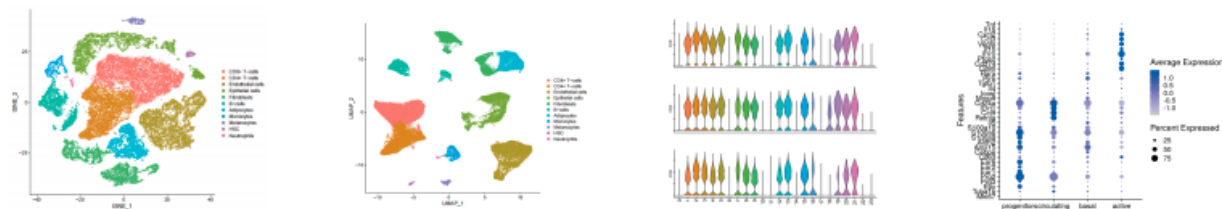
03 Batch Effect Removal & Sample Merging



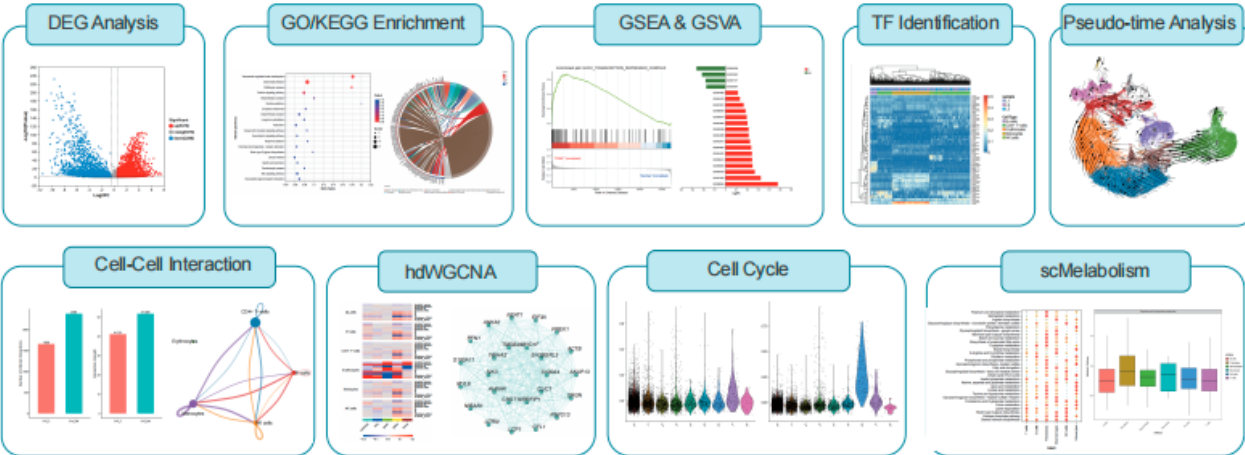
04 Clustering



05 Marker Gene Identification

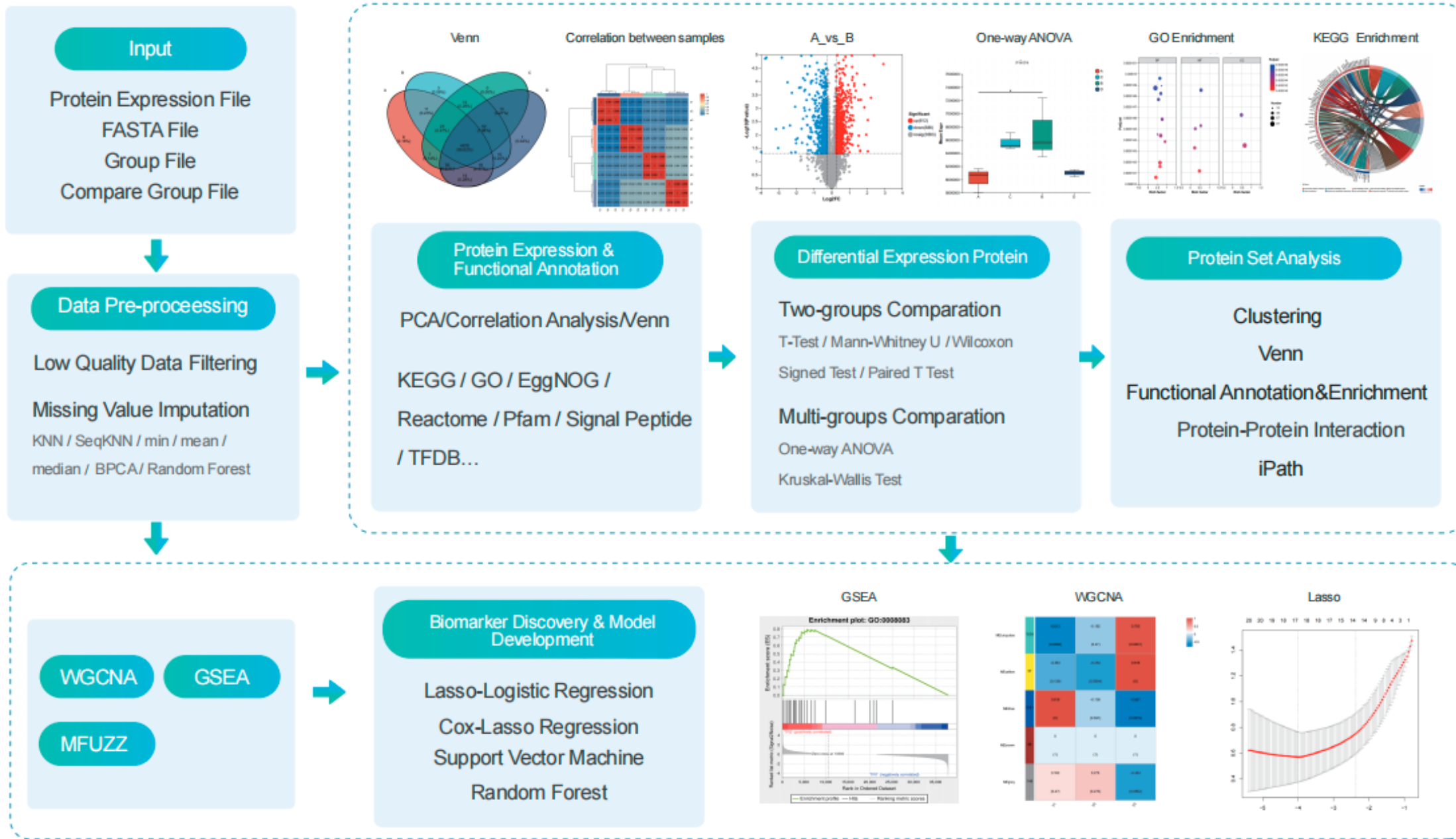


06 Downstream Analysis



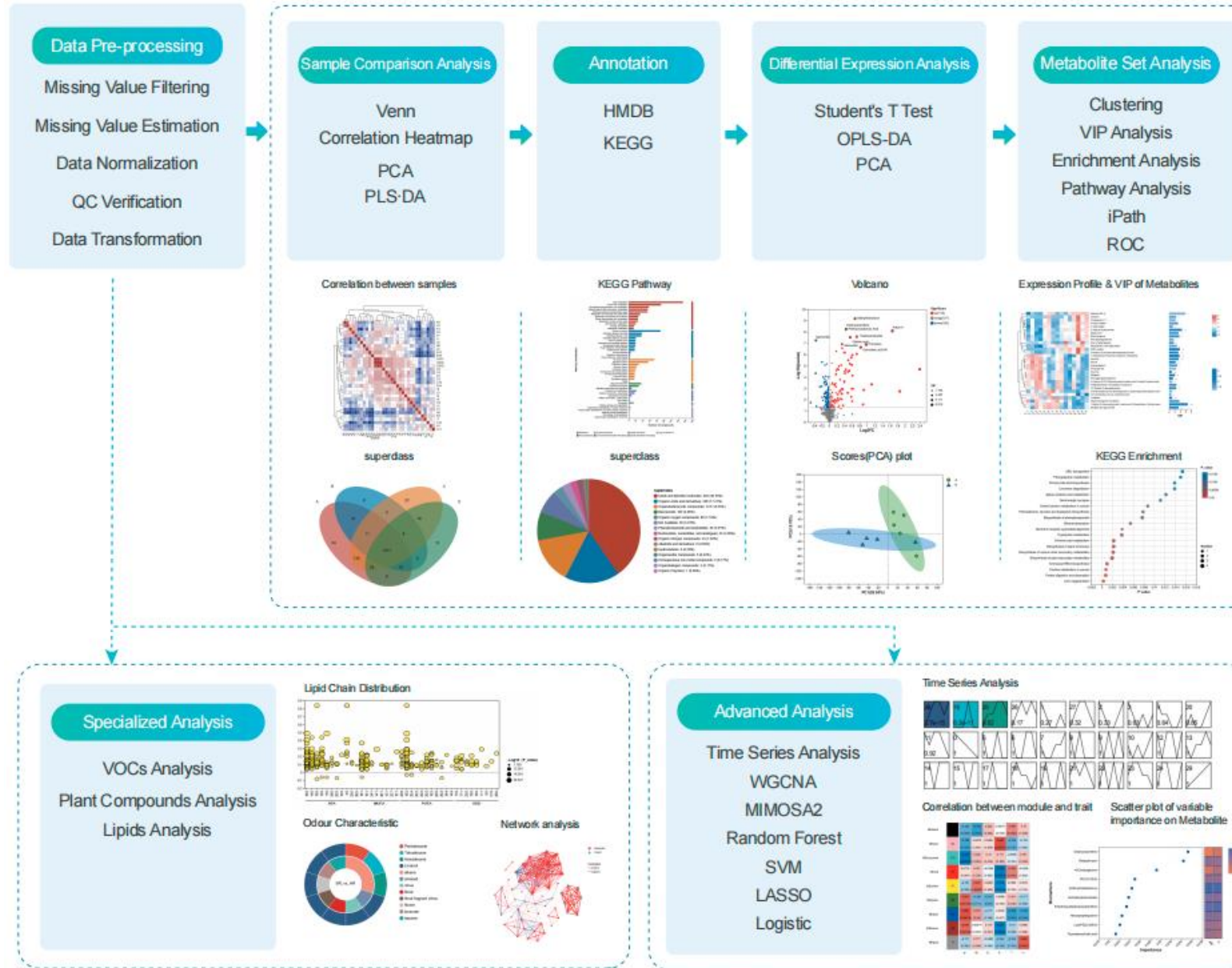


workflow二： 蛋白组学 workflow

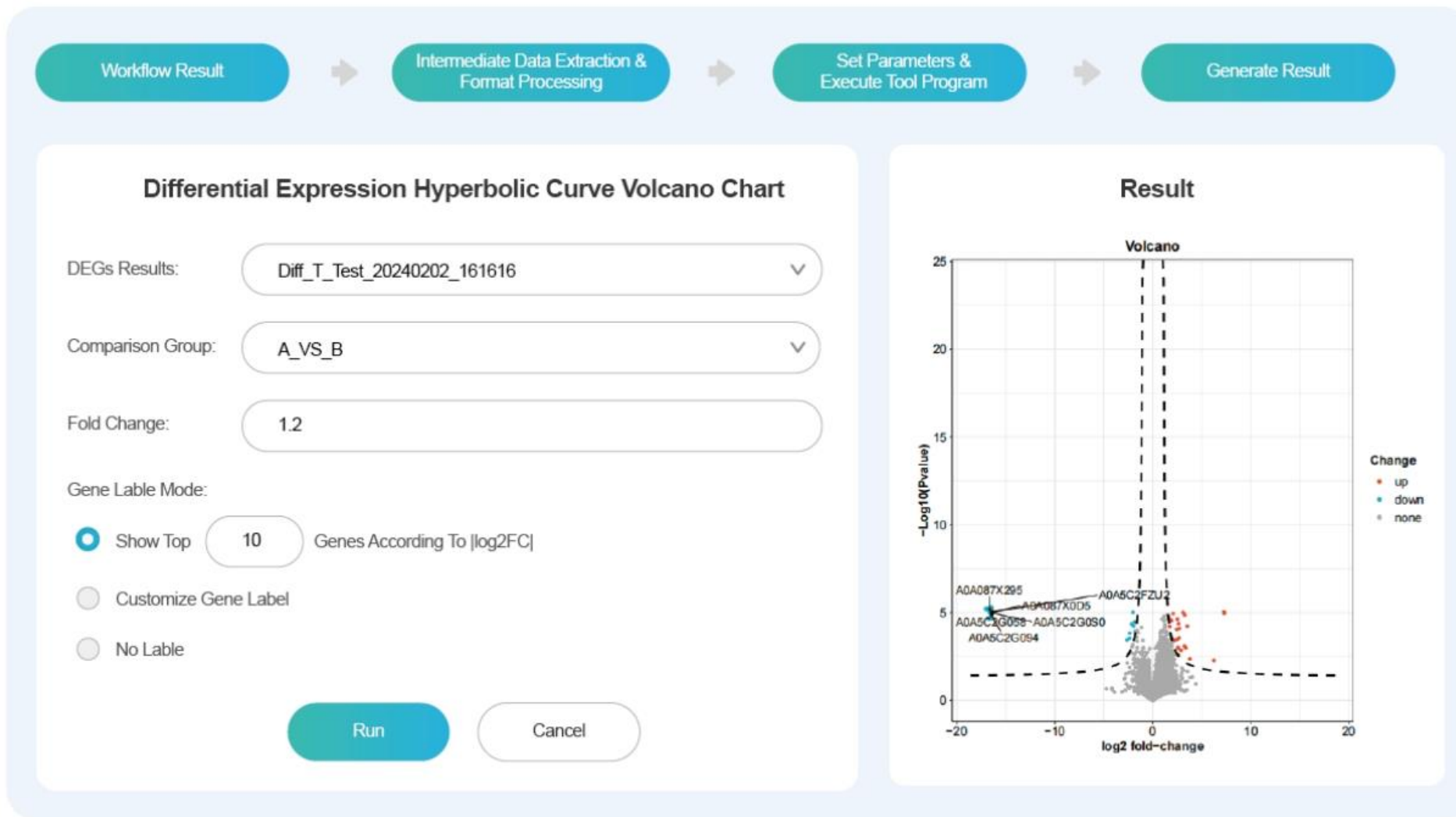




workflow三：代谢组学 workflow

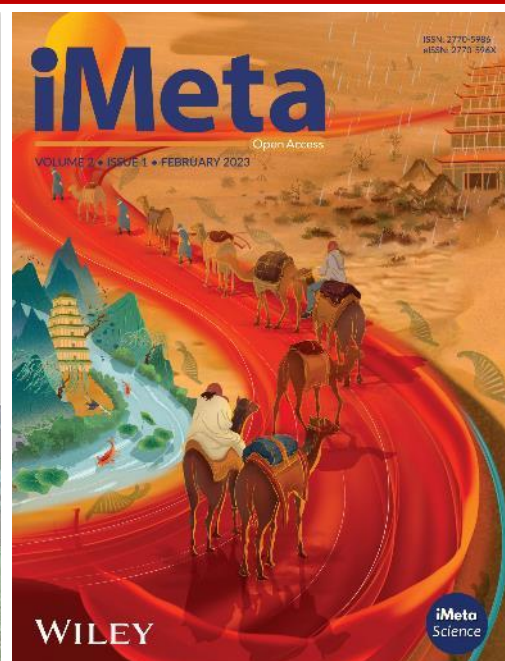
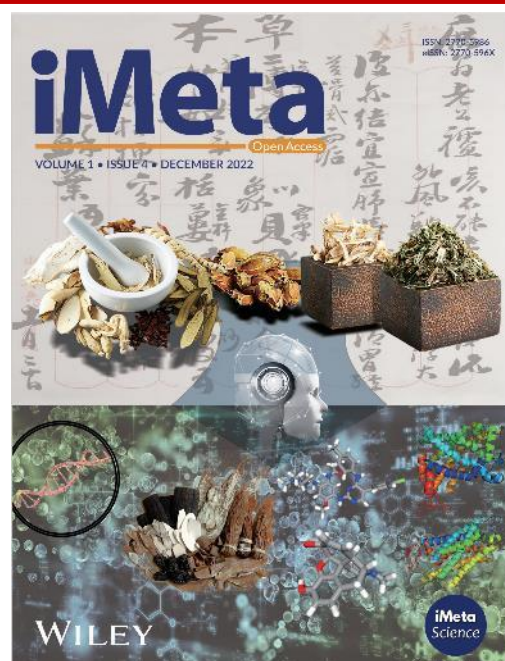
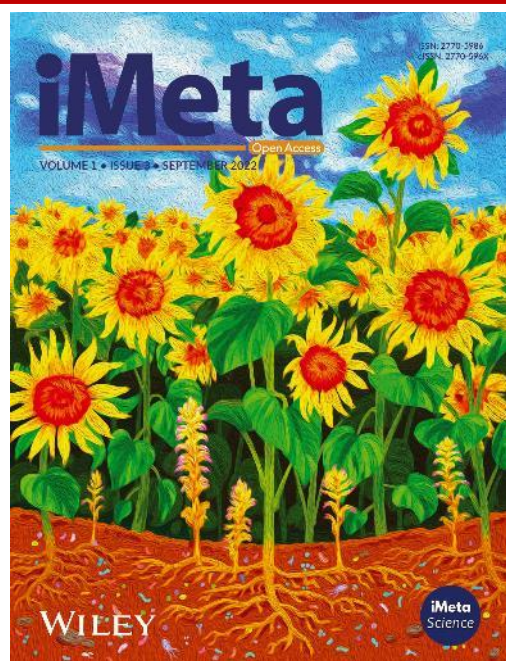


“ workflow+拓展工具”，一种新的交互式分析模式



总结

- ❑ 美吉生物云提供了简单而强大的方法来分析常规转录组、单细胞转录组、蛋白质组、代谢组、宏基因组和其他组学数据，助力研究人员分析复杂的多组学数据并推断蕴藏在组学数据背后的生物学意义。
- ❑ 自美吉生物云在iMeta上首次发表以来，吸引了全球研究人员的关注。目前，单细胞转录组学 workflow、蛋白质组学 workflow 和代谢组学 workflow 分别助力科研工作者发表了 20, 62, 393 篇学术论文。
- ❑ 平台网址：<https://cloud.majorbio.com/>



“iMeta”由威立、肠菌分会和华人科学家出版的开放获取期刊，主编由中科院微生物所刘双江和荷兰格罗宁根大学傅静远教授共同担任。目的是发表原创研究、方法和综述以促进宏基因组学、微生物组和生物信息学发展。目标是发表前10%(IF>20)的高影响力论文。期刊特色包括视频投稿、可重复分析、图片打磨、青年编委、中英双语、50万用户的社交媒体宣传等。2022年2月发行，相继被ESCI、Google Scholar、DOAJ、Scopus等数据库收录，发文161篇，被引2316次(Dimension, 2024/2/19)!



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