# iMetaLab Suite宏蛋白质组学一站式工具集

## iMetaLab Suite: A One-stop Toolset for Metaproteomics

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Li, Leyuan, Zhibin Ning, Kai Cheng, Xu Zhang, Caitlin M. A. Simopoulos, and Daniel Figeys. 2022. iMetaLab Suite: A one-stop toolset for metaproteomics. *iMeta* e25. https://doi.org/10.1002/imt2.25


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# iMetaLab Suite: A one-stop toolset for metaproteomics

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First published: 21 May 2022 | https://doi.org/10.1002/imt2.25

Leyuan Li and Zhibin Ning contributed equally to the manuscript.



## Abstract

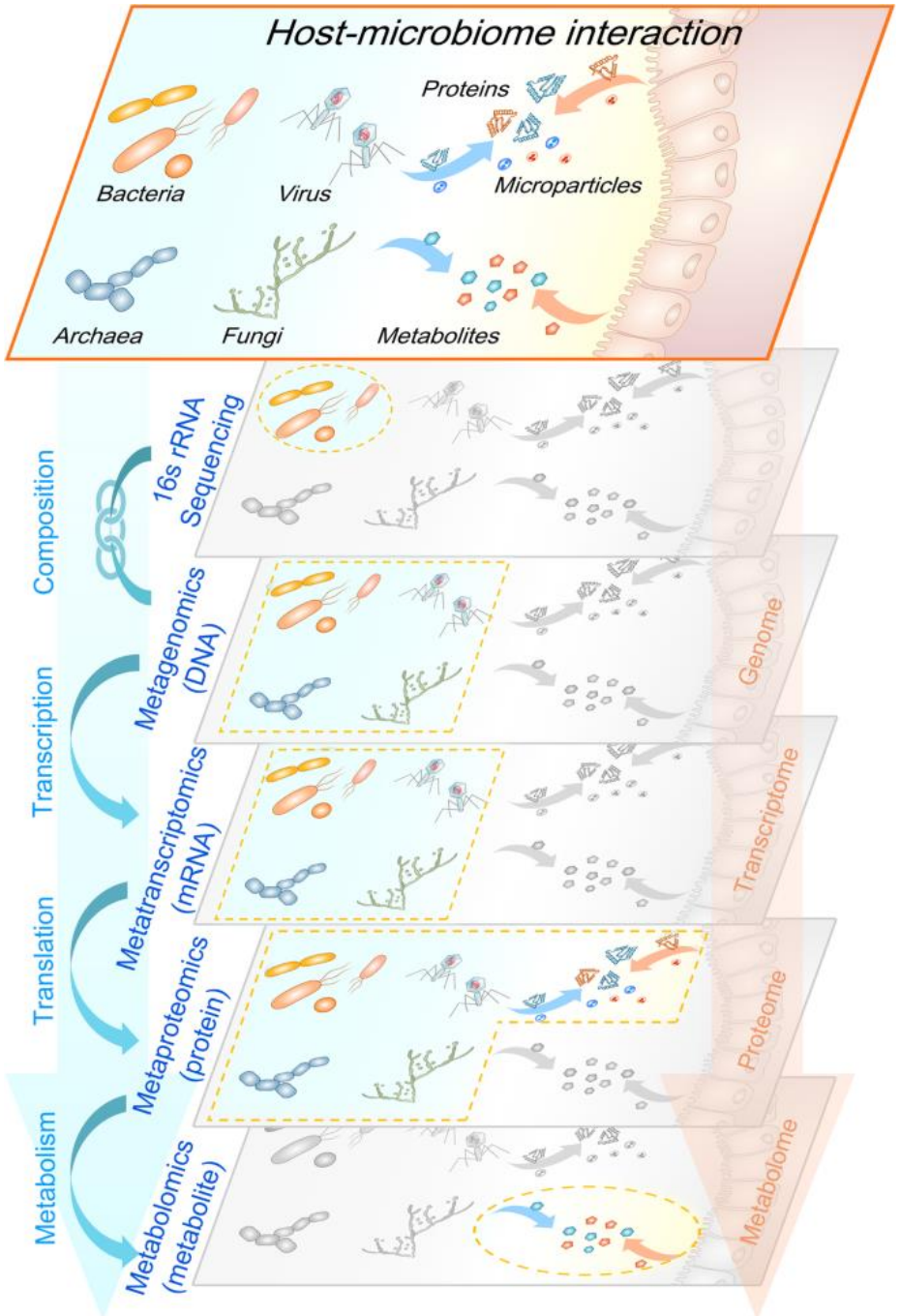
Metaproteomics is a recently thriving technique that studies the collection of proteins in complex microbiomes of the human, animal, plant, and environment. The bioinformatics workflow required for metaproteomics research, from the database search and protein quantification to downstream functional and taxonomic analysis has been challenging and thus limiting the accessibility of metaproteomics to microbiome researchers. To overcome these challenges, we have developed a set of tools named iMetaLab Suite. iMetaLab Suite includes the following components: (1) MetaLab Desktop, an automated database search software that facilities proteins identification and quantitation from microbiomes; (2) the automated iMetaReport that allows users to quickly access database search results and data set profiles; and (3) an interactive online toolset, iMetaShiny, covering most frequently used functional, taxonomic, and statistical analysis in metaproteomics. iMetaLab Suite is a free, easily accessible, and actively updated toolset available to assist researchers to explore metaproteomic data.

## Highlights

- A one-stop solution for metaproteomics data analysis for nonexpert.
- Database search and result reports that include taxonomy and function.
- Interactive tools for frequently used metaproteomics data analysis tools.

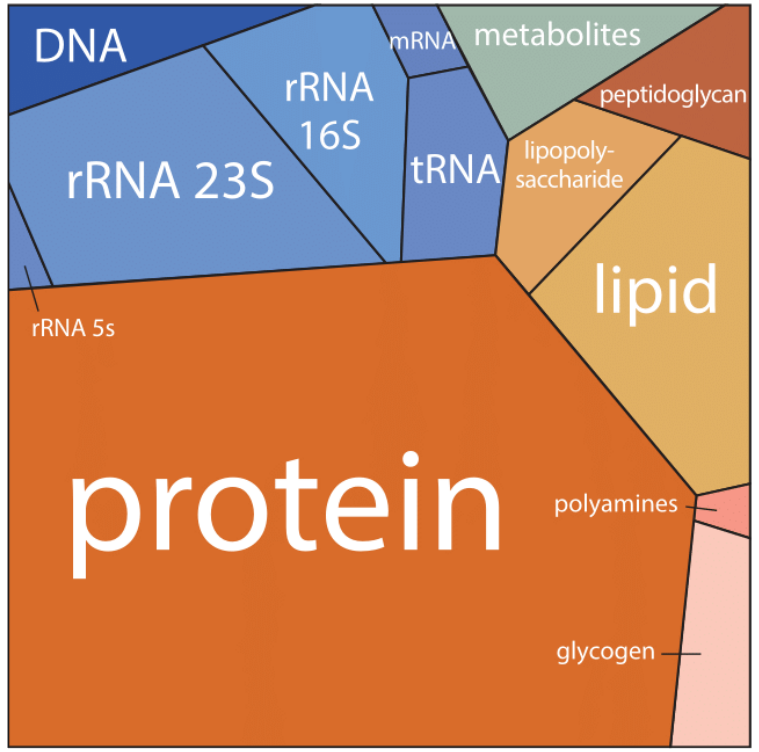

一、宏蛋白质组学
技术简介

# 宏蛋白质组学：宏多组学中经常缺席的成员




Zhang et al., *Microbiome*, 7:154, 2019

- 微生物组学研究中，不同宏组学技术提供不同层面的解析

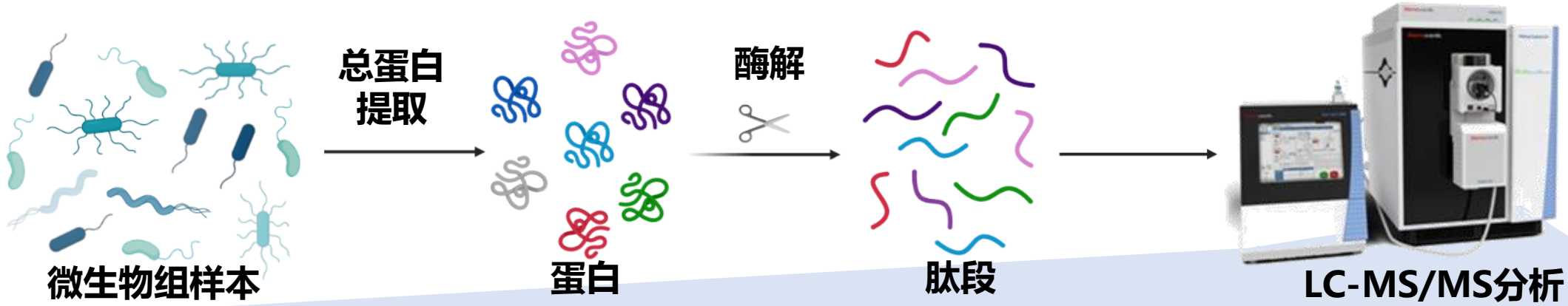


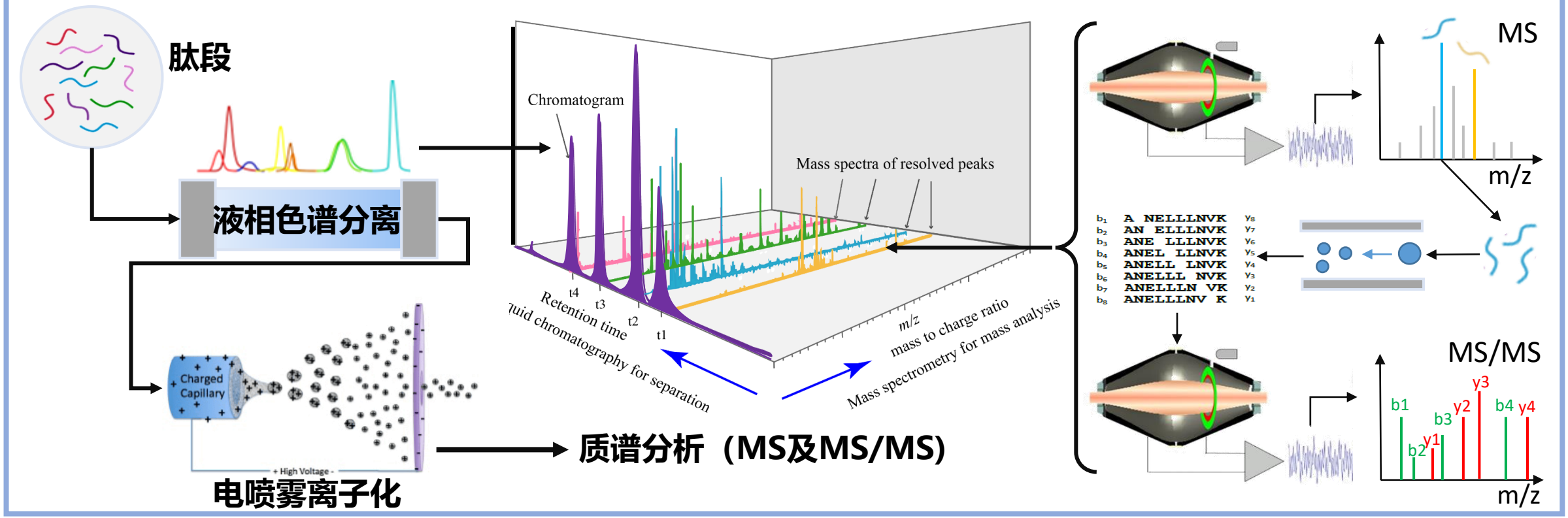

图片来源https://bionumbers.hms.harvard.edu

- 宏蛋白质组学：
  - 在微生物细胞中，蛋白质大约占细胞干重的50%。这些蛋白质是细胞生物过程的基本功能单元
  - 宏蛋白质组学分析复杂微生物组的蛋白质组成，对理解其功能非常重要

- **然而在目前的宏多组学研究中，宏蛋白质组学普遍缺席**

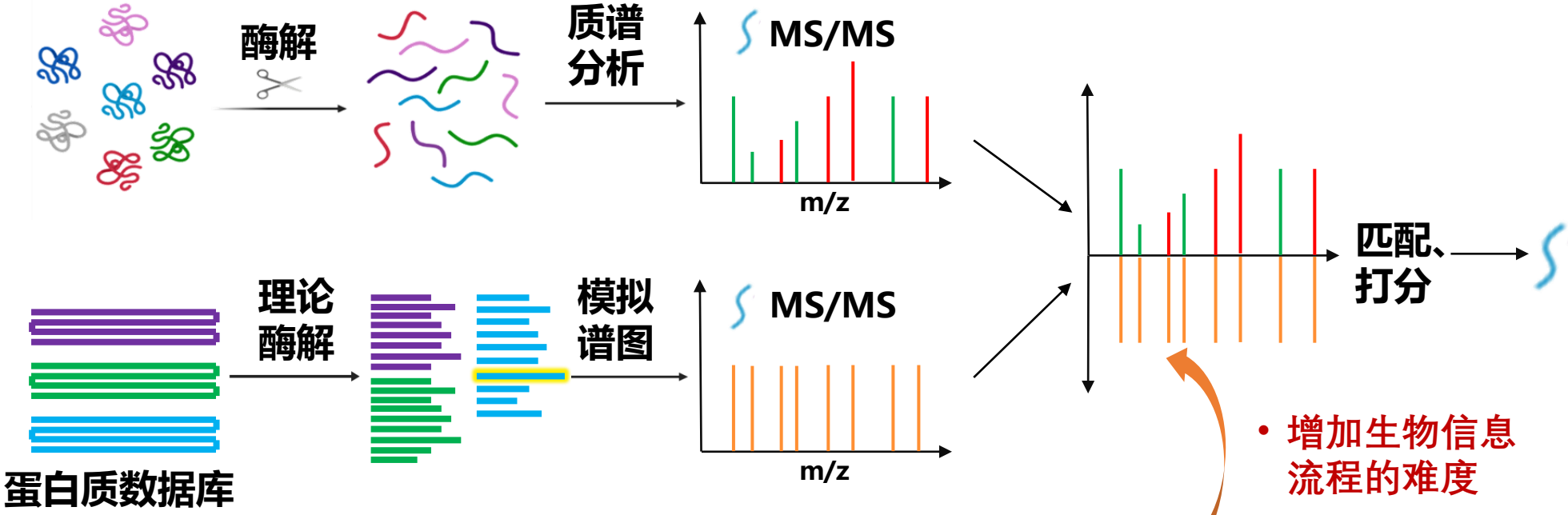
# 宏蛋白质组学：基于液相色谱-串联质谱的测序技术



# 宏蛋白质组学生物信息流程比传统蛋白质组学更具挑战

## 传统蛋白质组学生物信息流程：



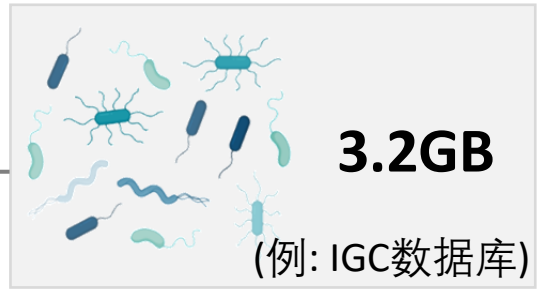

- 增加生物信息流程的难度

**宏蛋白质组学搜库面临挑战：**

**单个微生物物种蛋白质数据库**


**~2,000倍**

**微生物组蛋白质数据库**



# 本团队的宏蛋白质组学技术发展

**MetaPro-IQ搜库流程**
Zhang et al. *Microbiome* 2016, 4:31

**MetaLab软件**
Cheng et al., *Microbiome* 2017, 5:157

**iMetaLab 云端搜库**
Liao et al. *Bioinformatics*. 2018, 34(22)

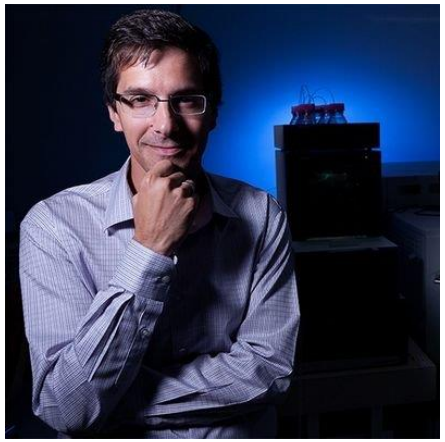
**MetaLab 2.0**
Cheng et al., *J. Am. Soc. Mass Spectrom*. 2020, 31:7

**iMetaLab Suite**
Li and Ning et al, *iMeta*, 2022, e25

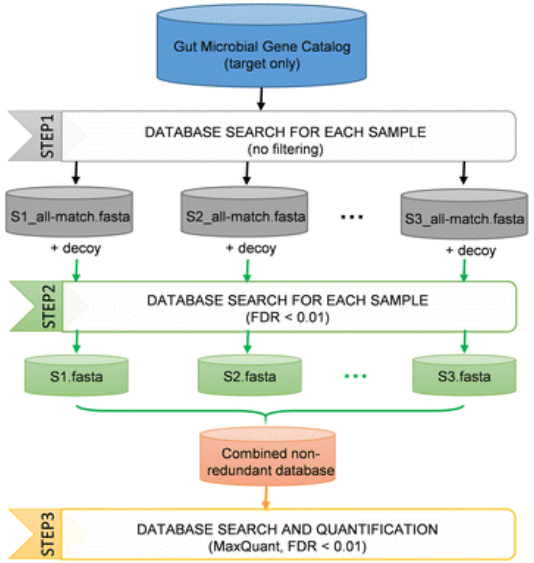
蛋白质组学

宏蛋白质组学

2015 2016 2017 2018 2019 2020 2021 2022



渥太华大学
Daniel Figeys教授团队

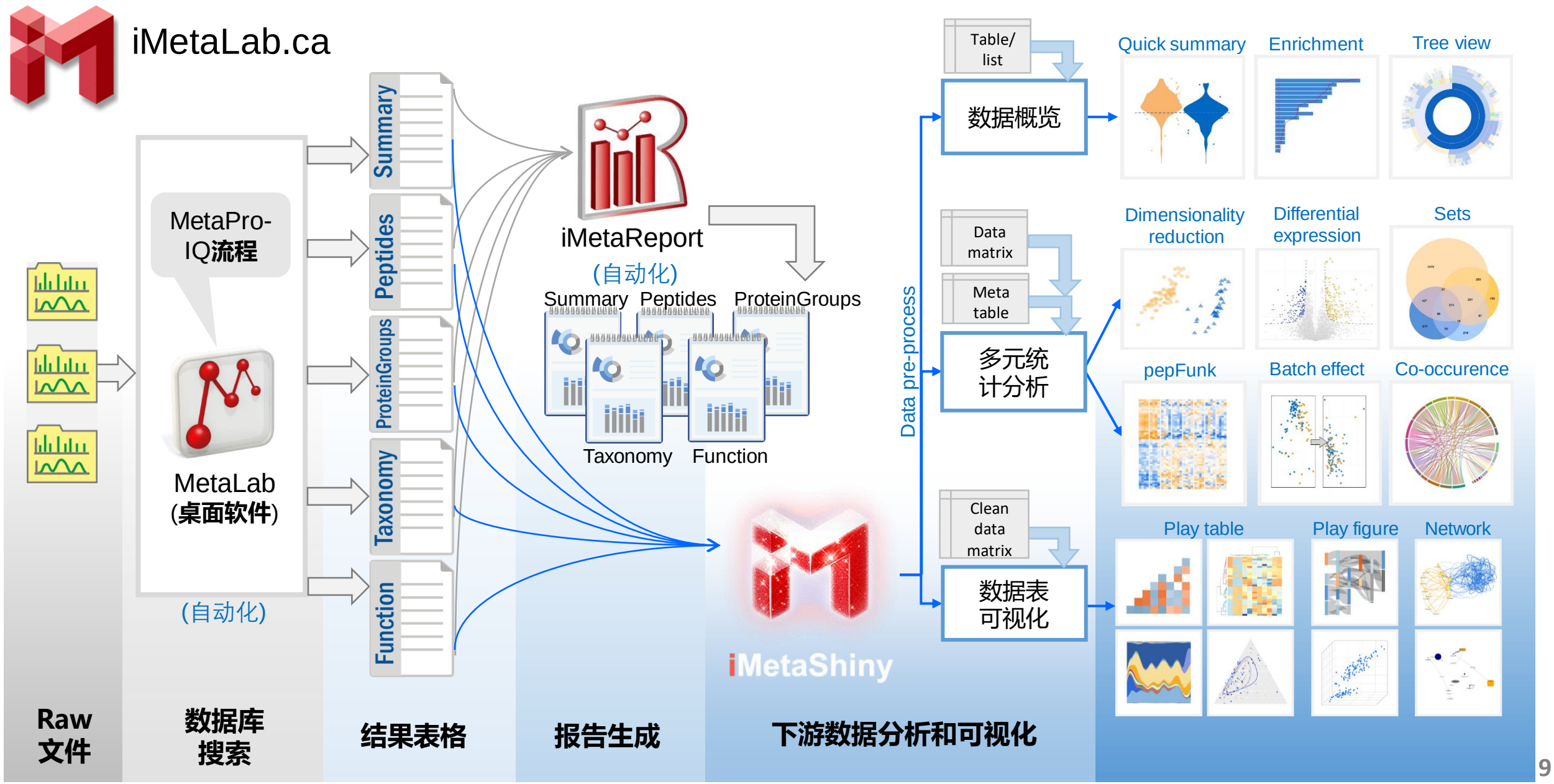


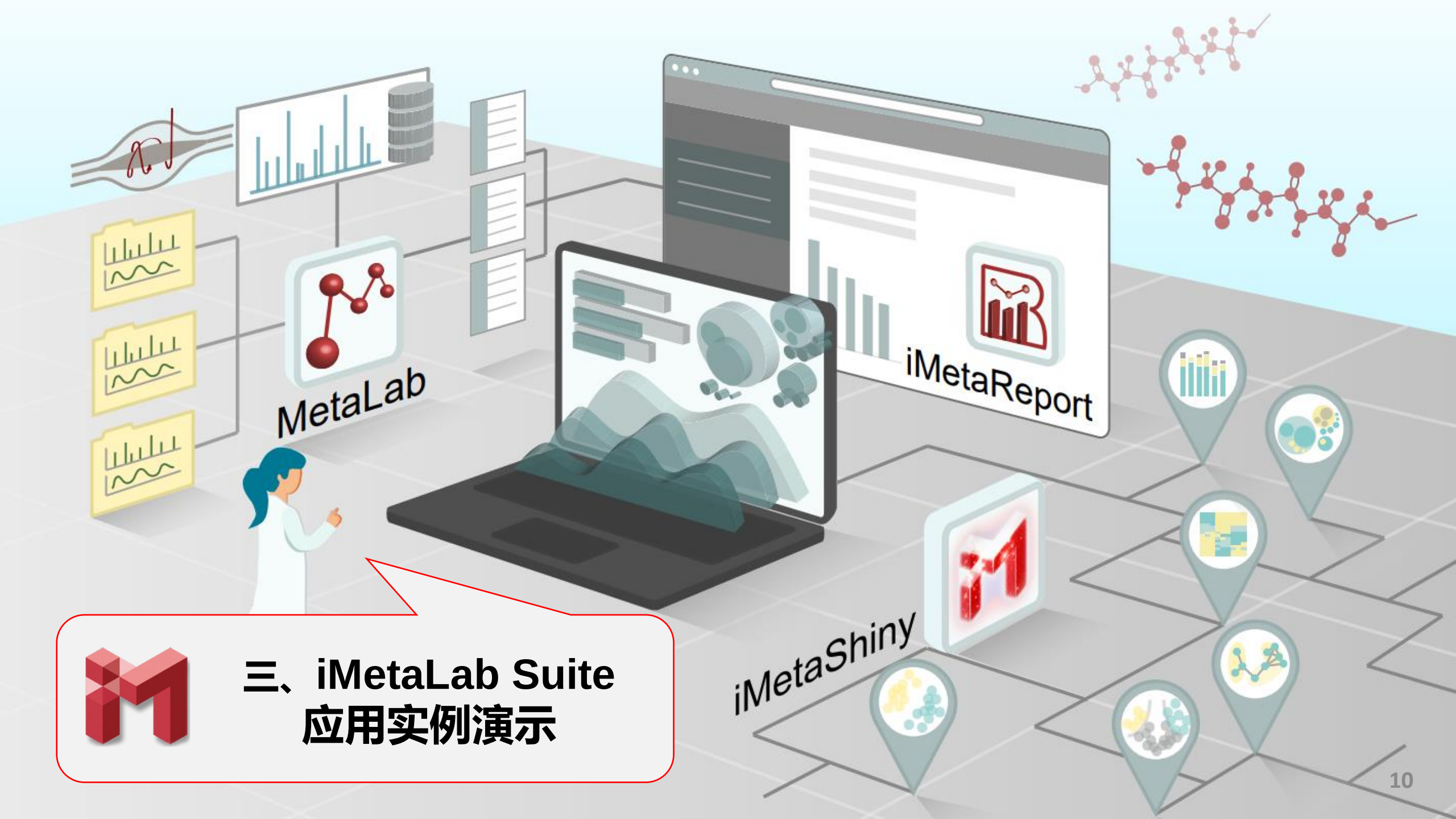

MetaPro-IQ搜库流程


iMetaLab Suite


# 二、iMetaLab Suite：宏蛋白质组学一站式工具集

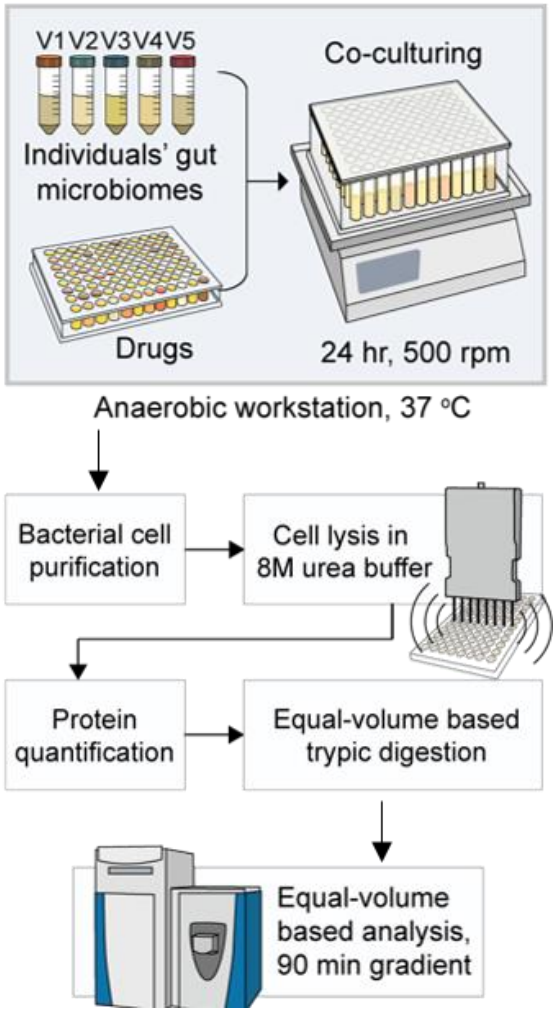
# MetaLab自动化搜库、iMetaReport自动报告、iMetaShiny交互式数据分析应用






# 三、iMetaLab Suite 应用实例演示

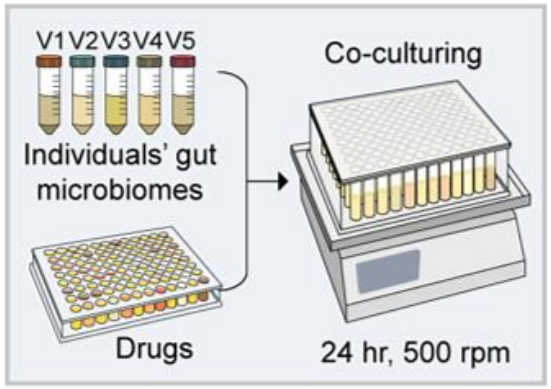
# iMetaLab Suite应用实例



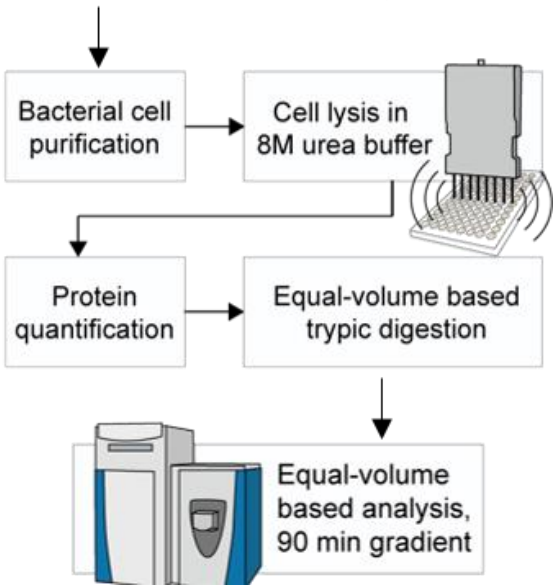

以双氯芬酸vs对照为例
（Diclofenac vs DMSO）

Li et al., *Microbiome* 8:33, 2020

# iMetaLab Suite应用实例




Anaerobic workstation, 37 °C

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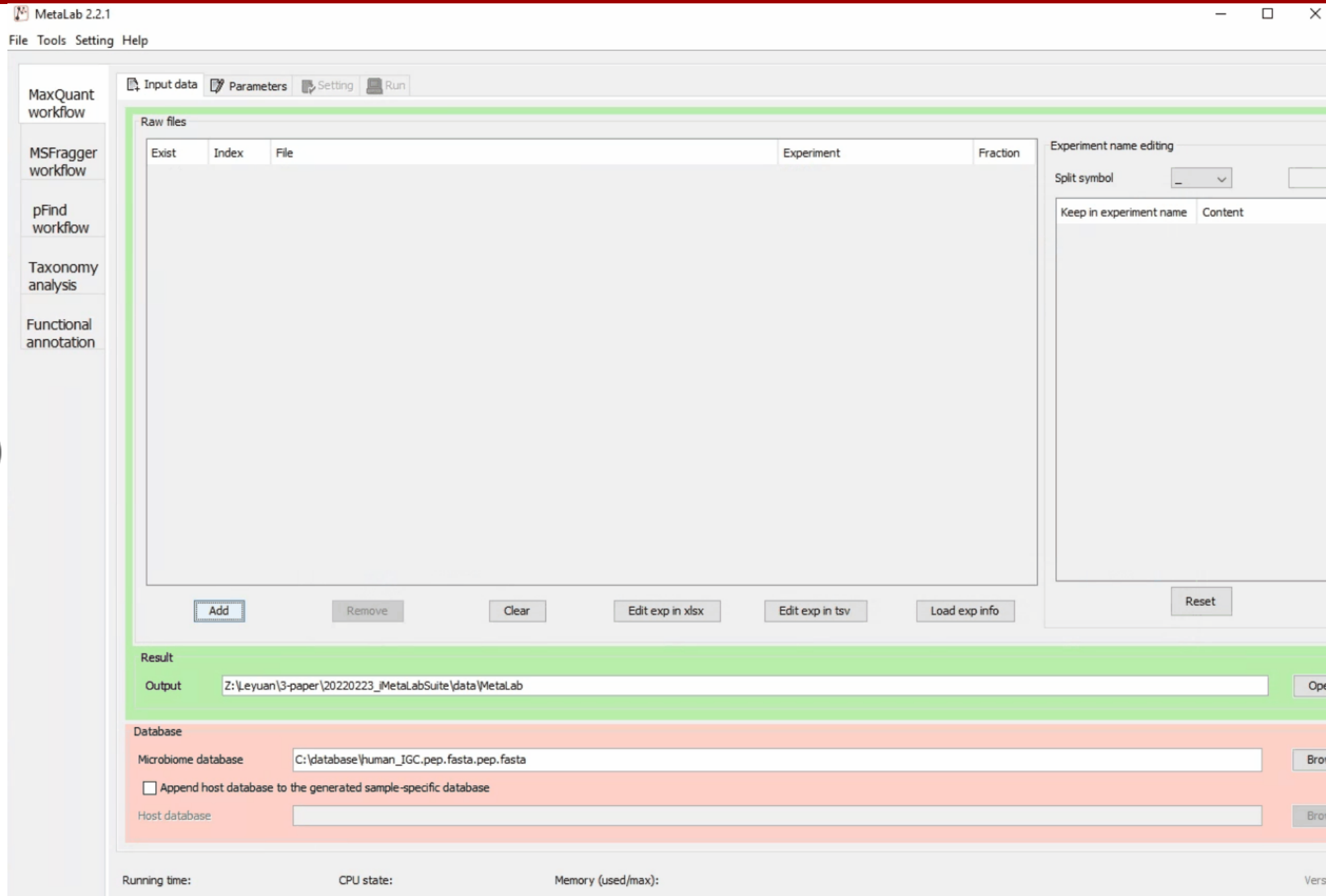
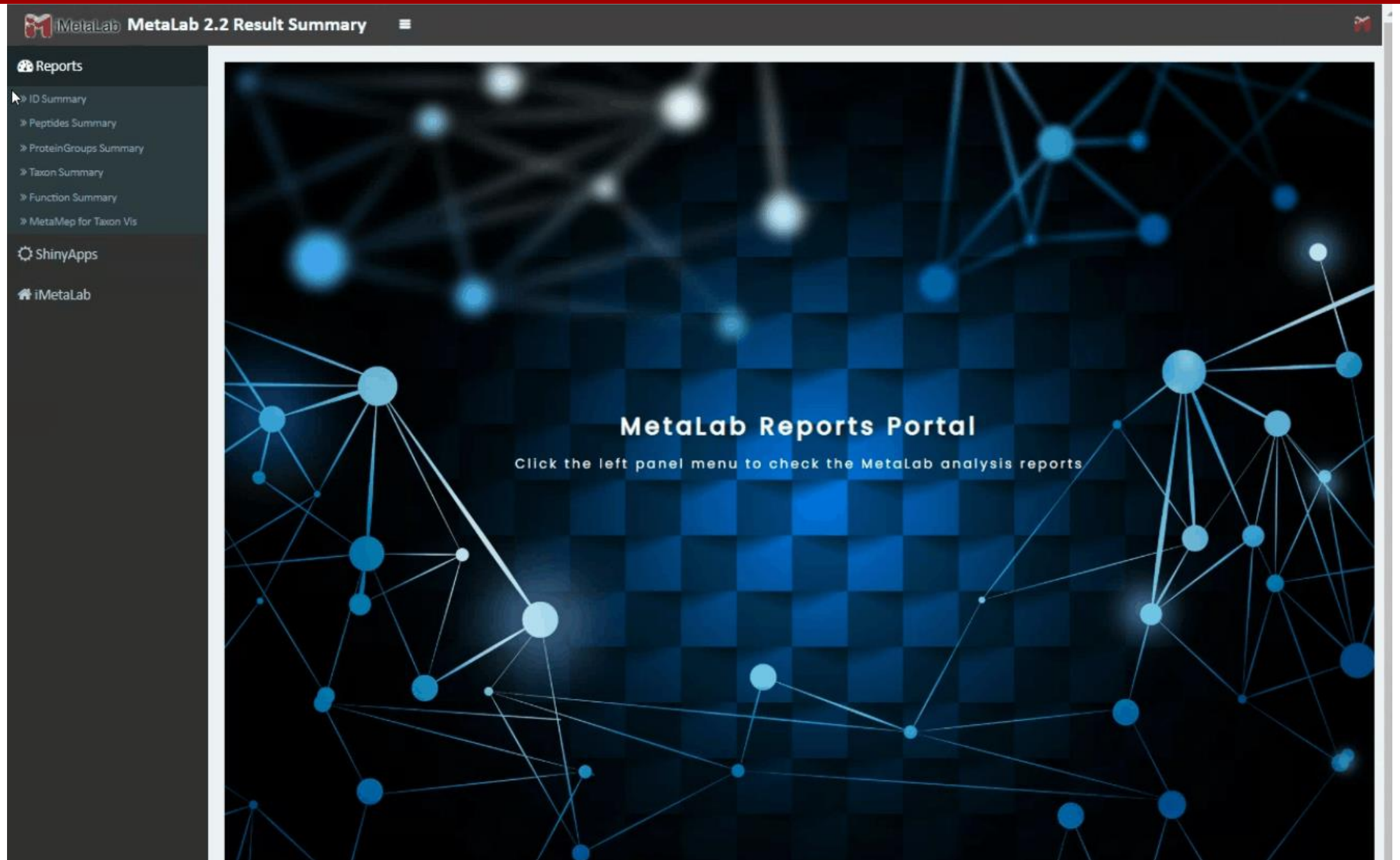


# iMetaReport自动报告



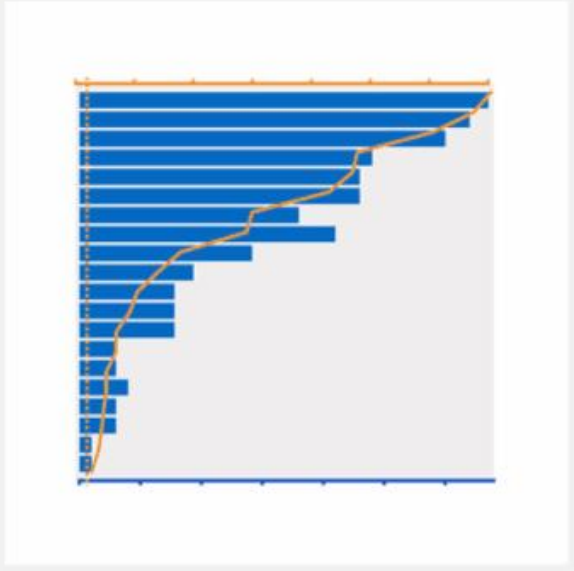
iMetaLab

# iMetaShiny Apps

Analyze your metaproteomic data and generate publishable scientific figures

All Metaproteomics Statistics Simply plotting Special analysis

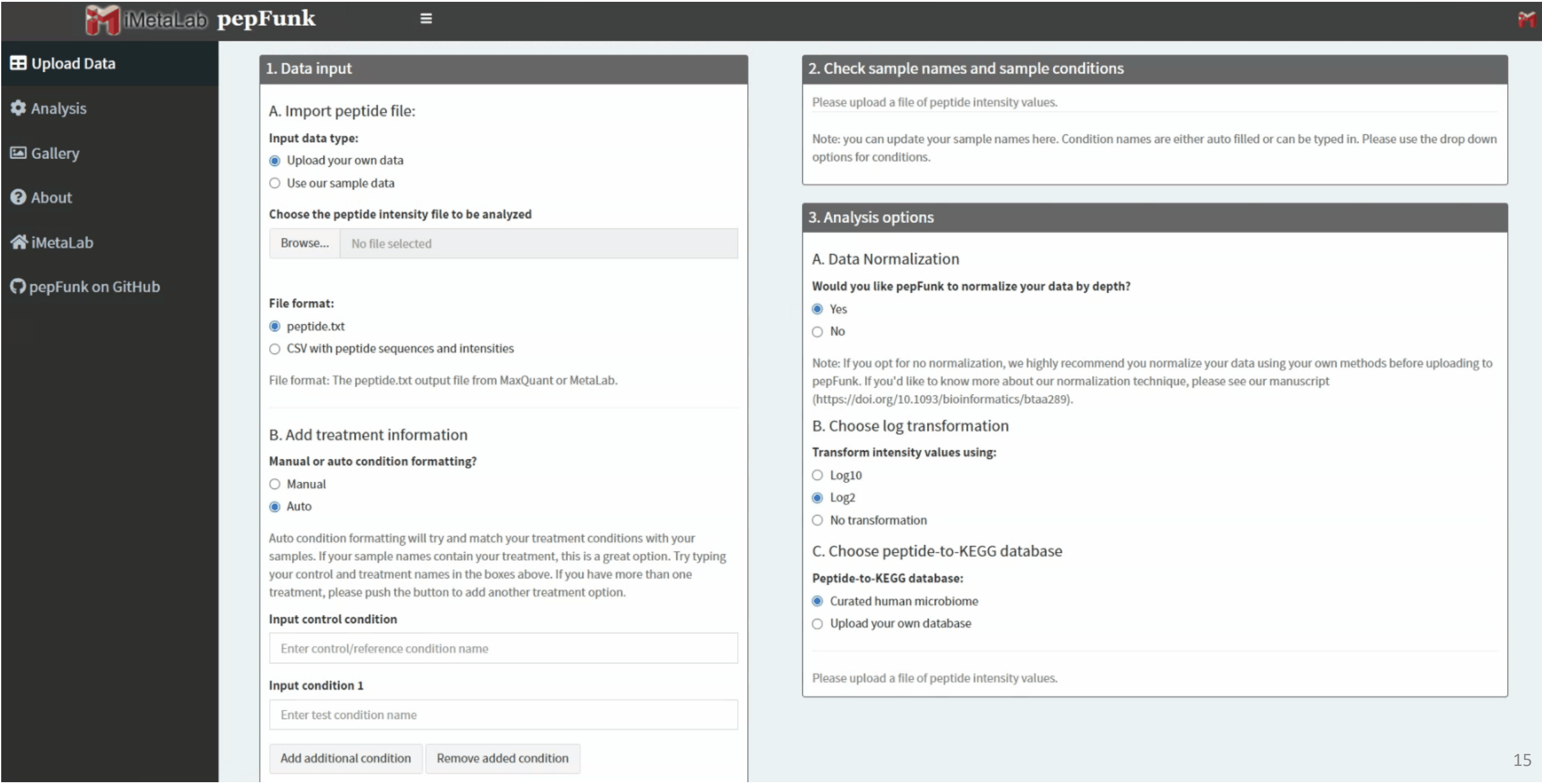
Quick MQ summary



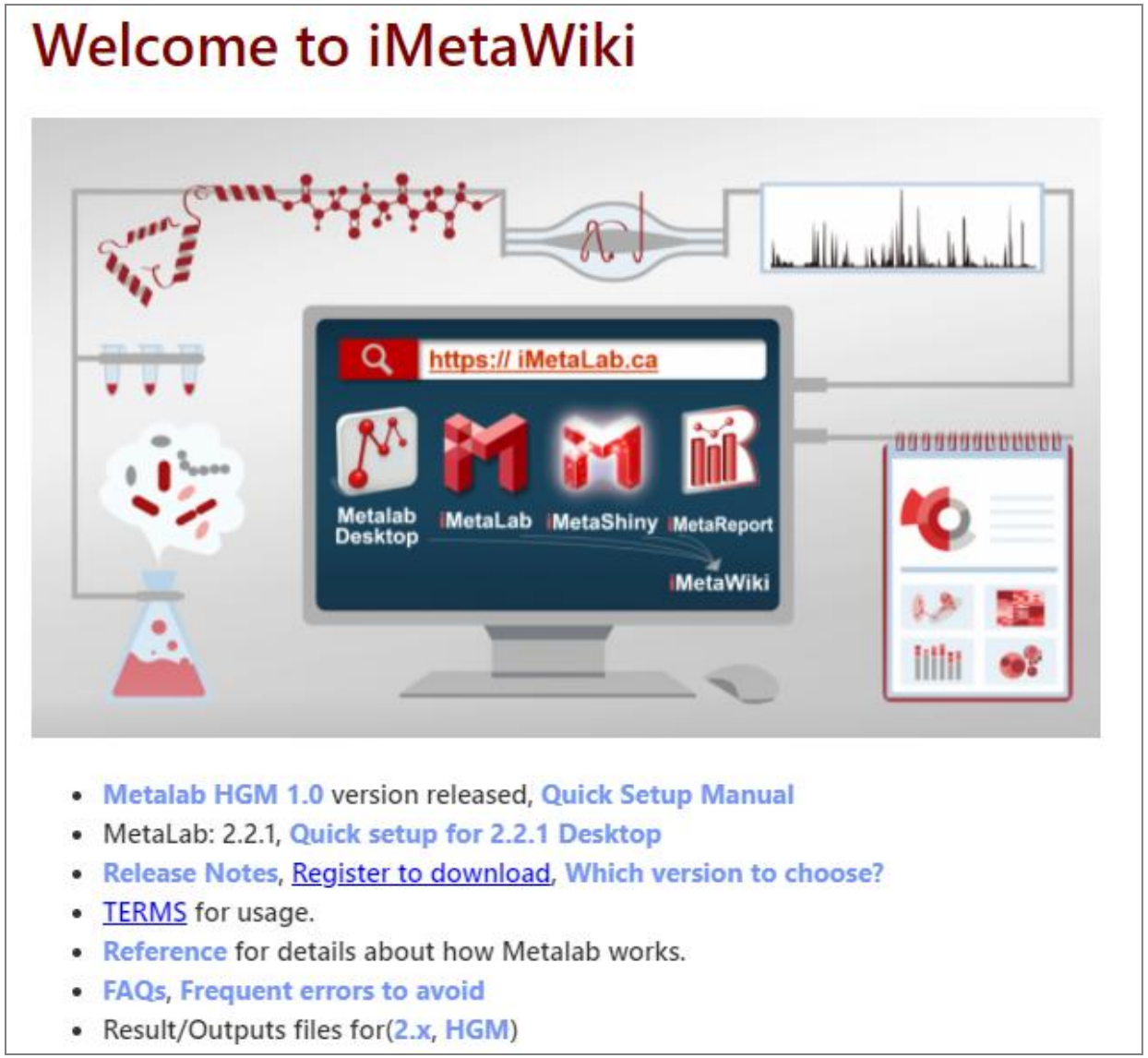
Enrichment analysis

Phylo explorer

# iMetaShiny数据分析和可视化应用



# 使用教程和技术支持




**使用教程网站：**

**wiki.imetalab.ca**

**技术支持团队：**

**techteam.metalab@gmail.com**

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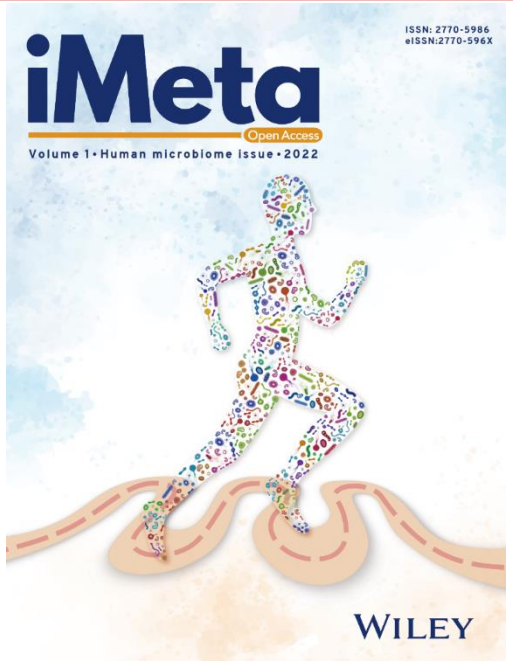
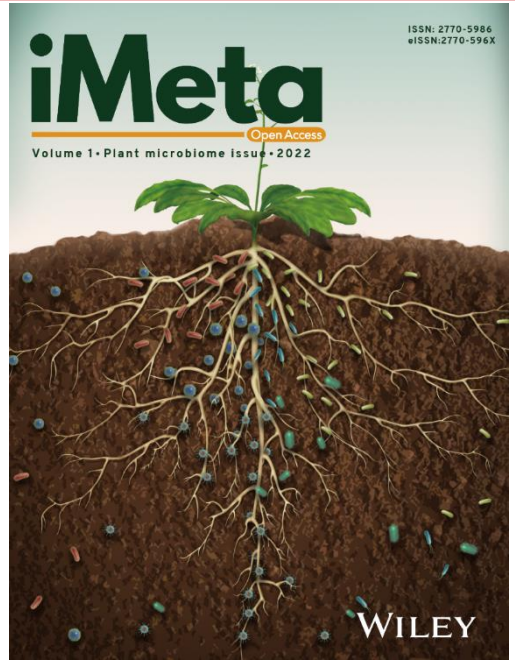
# *iMeta*: 整合宏组学重新认识生命和环境科学

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