

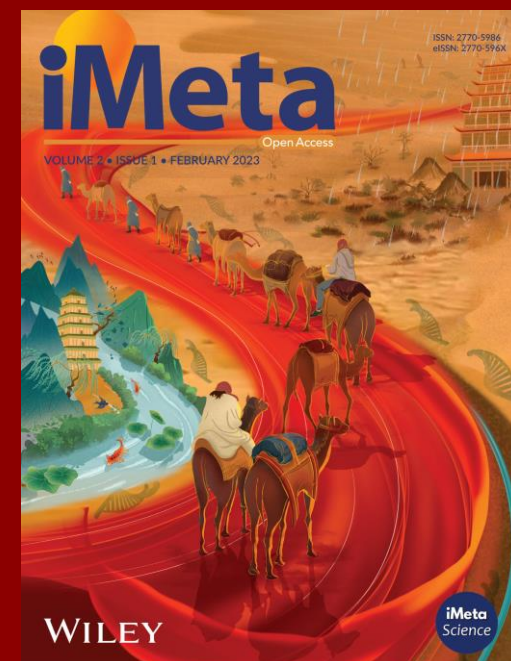


BioLadder(bioladder.cn): 专注于蛋白质组数据分析 的生物信息学平台

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Yupeng Zhang, Chunyuan Yang, Jinhao Wang, Lixin Wang, Yan Zhao, Longqing Sun, Wei Sun, Yunping Zhu, Jingli Li, Songfeng Wu. 2024. BioLadder: A bioinformatic platform primarily focused on proteomic data analysis. *iMeta* 3: e215. <https://doi.org/10.1002/imt2.215>



BioLadder云平台概述

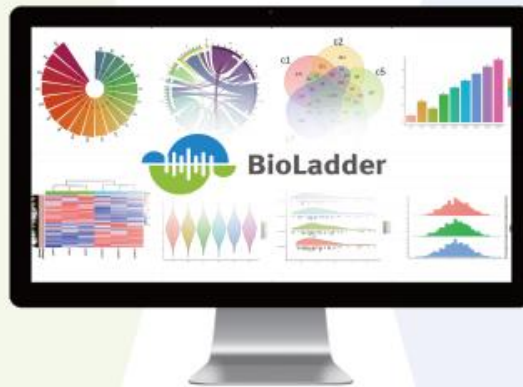
Experimental data analysis

ExpDataVisualization

DataPreProcessing

QuantitativeAnalysis

DifferenceAnalysis
QuantitativeDes
QuantitativeComp
QuantitativeCorr
QuantitativeCluster



Common data analysis

SeqAnalysis

AbundanceMap

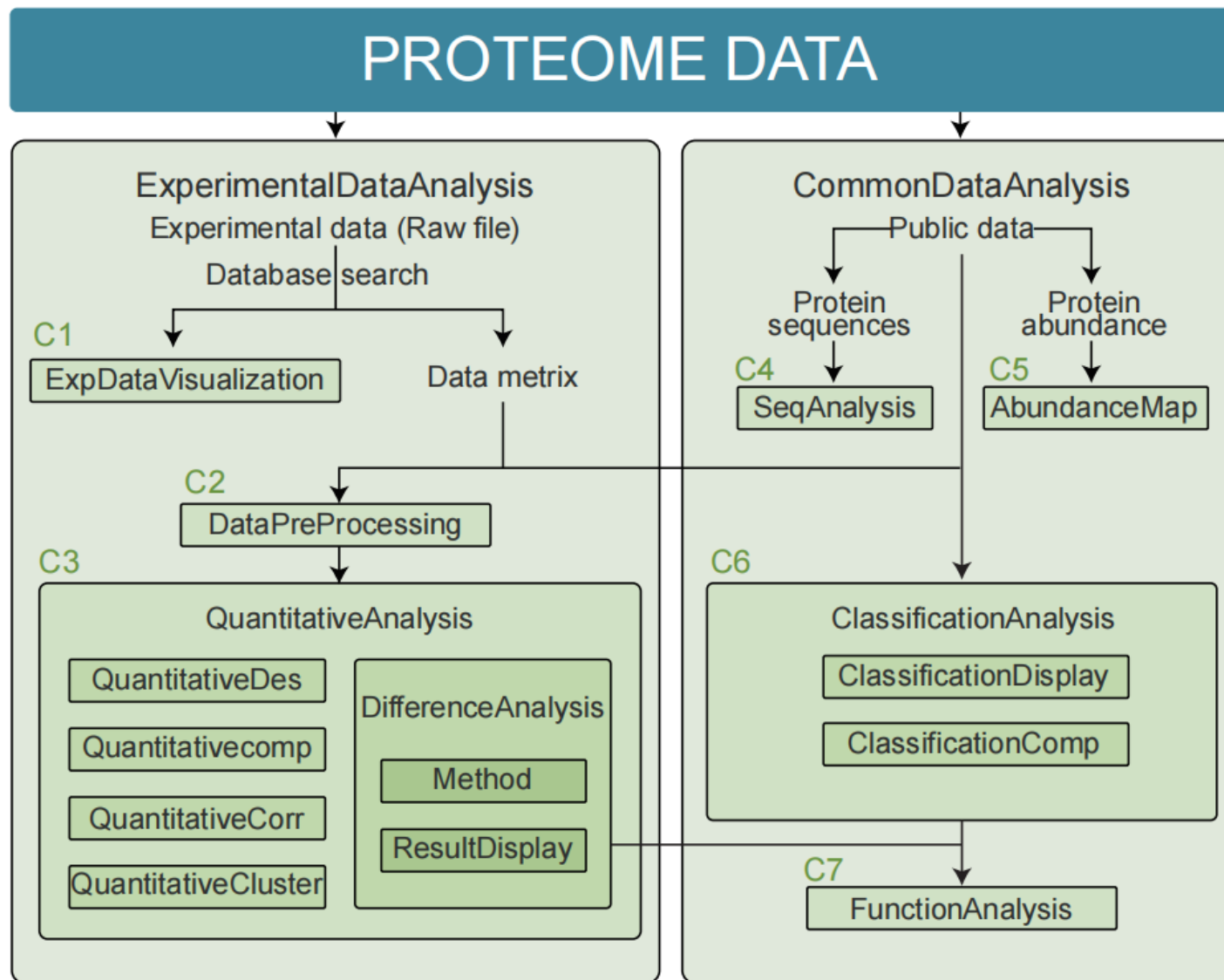
ClassificationAnalysis

ClassificationDisplay
ClassificationComp

FunctionAnalysis



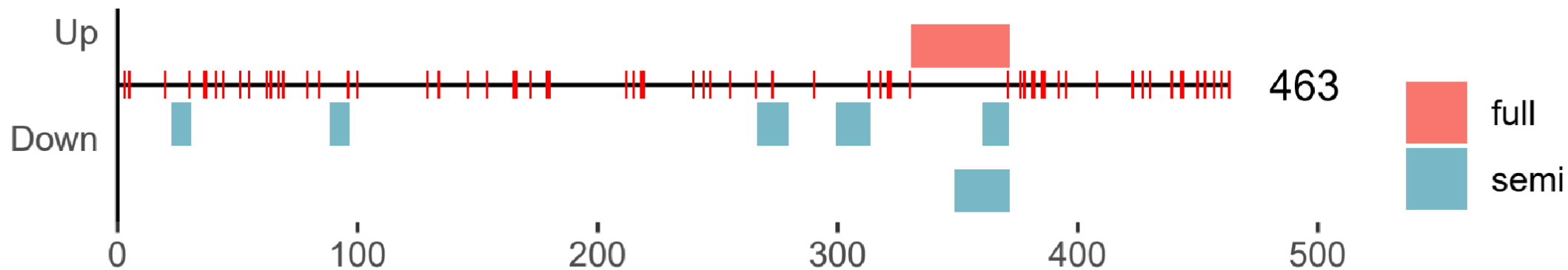
BioLadder在蛋白质组数据分析框架中的模块类别



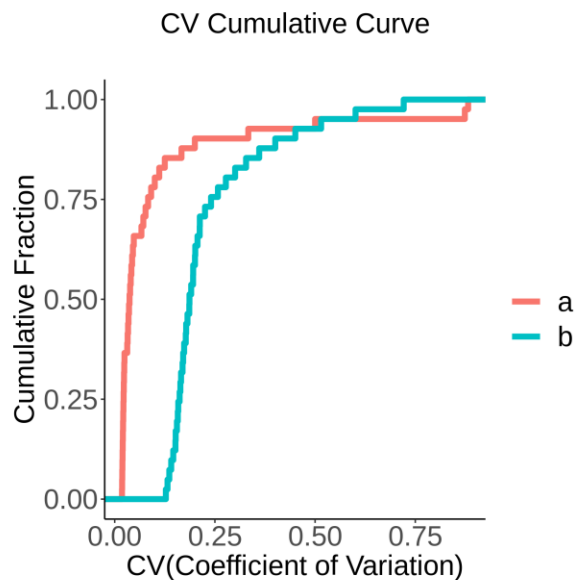


特定蛋白质组学数据分析模块

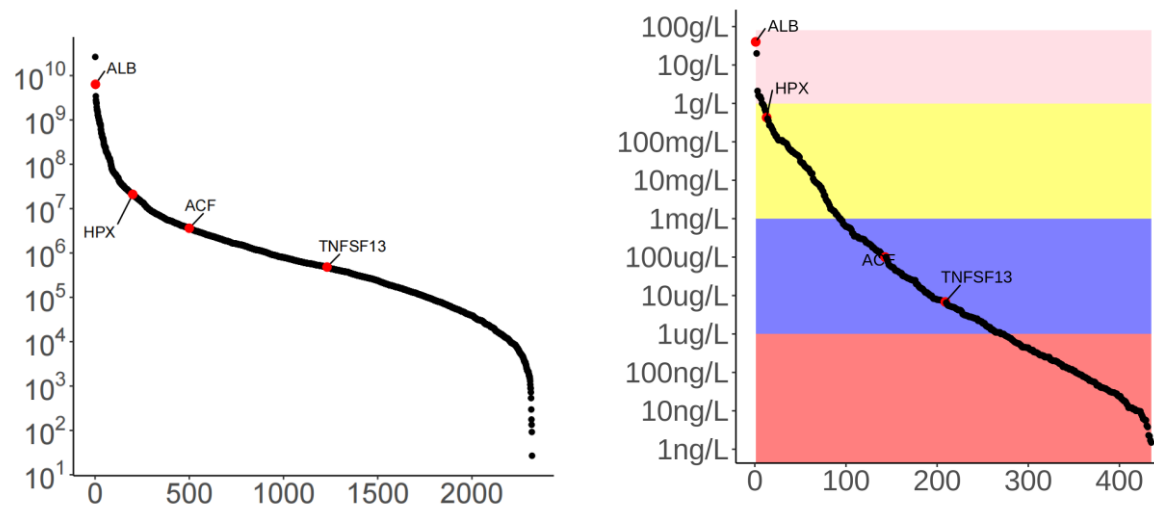
案例一：蛋白质序列中肽段的覆盖度分析



案例二：定量数据分布的分析和可视化



案例三：定量数据和标记蛋白



方便且用户友好的设计

(A)

Fileinput: Proteomics format

Default venn format

Sample1	Sample2	Sample3	Sample4
Q9H1E3	Q9H1E3	Q9H1E3	Q9H1E3
Q75970	O15400	O15400	O15400
P05166	O75970	O75970	O75970
Q9BSC4	P05166	Q9BSC4	P05166
Q9Y5P6	Q9BSC4	Q9Y5P6	Q9BSC4
Q9BUR4	Q9Y5P6	Q9BUR4	Q9BUR4
Q76L83	Q9BUR4		Q76L83
	Q76L83		

----> Common proteomic format

Accession	Sample1	Sample2	Sample3	Sample4
Q9H1E3	15800.36	24802.75	31193.56	781288.43
O15400		20304.34	143493.5	22782.97
O75970	12819.77	15533.35	222765.69	599772.29
P05166	89886.57	164294.21		907440.80
Q9BSC4	21348.71	224907.09	57276.62	23010.07
Q9Y5P6	65105.31	218851.40	167844.15	
Q9BUR4	134680.5	155411.32	152211.67	45533.31
Q76L83	56323.56	431920		40923.31

(C)

Colorscheme

Default

- Classic
- Simple
- Fresh 1
- Fresh 2
- Fresh 3
- Paper Yellow 1
- Paper Yellow 2
- Ink and wash

Excellent



Customized

- Color of Sample1 group: #66C2A5
- Color of Sample2 group: #FC8D62
- Color of Sample3 group: #8DA0CB
- Color of Sample4 group: #E78AC3

(B)

Parameter setting

✓ Omics special parameter setting

- Algorithm selection: Pearson --> Spearman
- Data Preprocessing: Logtrans formation
- Data Presentation: Heatmap gene name

✓ Easily adjustable parameters

Select the marking method

- Not marked
- Tag according to the uploaded file
- According to PValue and FC

volcano plot

Select the column where the Marker is

Marker

PValue <

0.0001

Absolute value of FC >=

100

(D)

Help information

✓ Document:

- General user guide
- Module description
- FAQ

✓ WeChat communication



✓ Real-time assistance(tooltips)

Plot explaining

Input file format

Option explaining

Download method

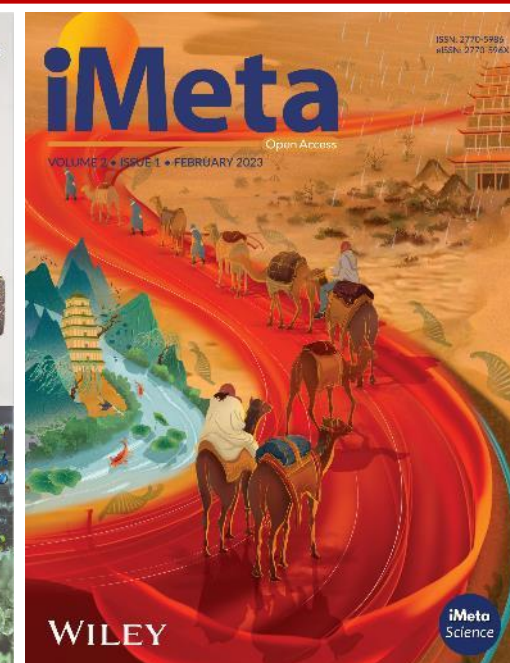


总结

- ❑ 在这项研究中，我们介绍了一个专注于蛋白质组学数据设计的用户友好型在线分析平台——BioLadder生信云；
- ❑ BioLadder由50多个分析模块组成，这些模块属于两个主要类别（实验数据分析和常规数据分析），包括了7个子类别；
- ❑ 多个蛋白质组特有的数据分析模块满足蛋白质组独特的分析需求；
- ❑ 方便且用户友好的设计，简化输入格式，针对蛋白质组学的专门默认参数，多样化和广泛的调整方法，强大的配色方案和全面便捷的帮助；
- ❑ 平台网址：<https://www.bioladder.cn/>

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<https://doi.org/10.1002/imt2.215>



“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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