



The Microbiologist's Guide to Metaproteomics

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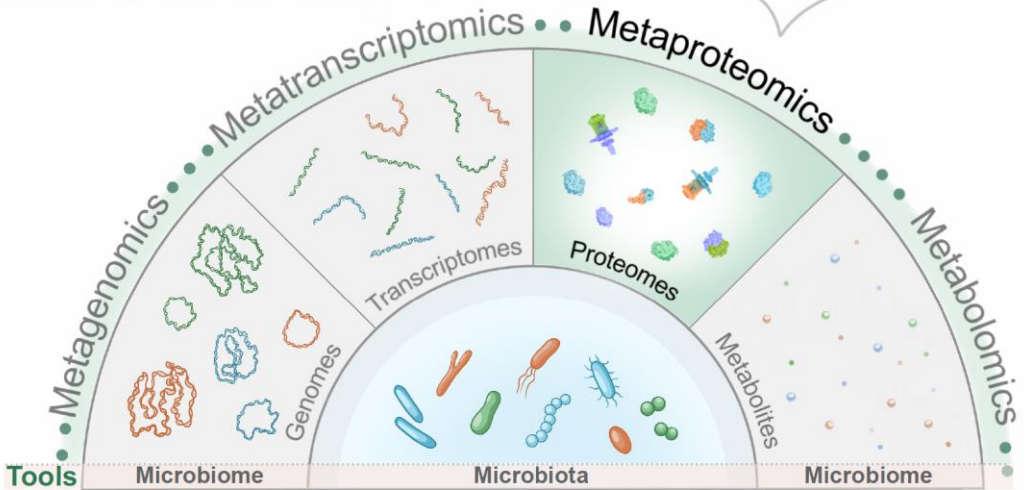
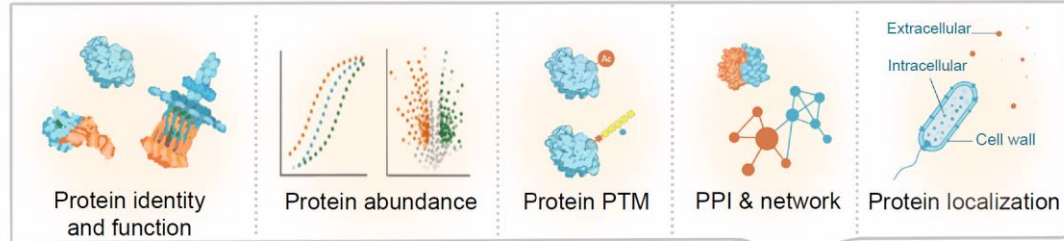


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The What and Why of Metaproteomics

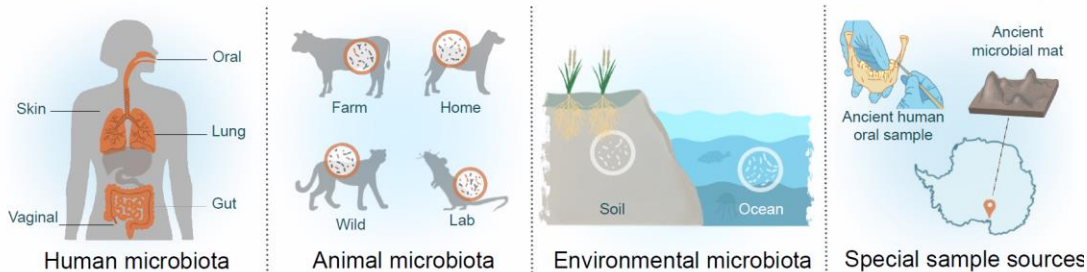


Metaproteomics...

- identifies proteins and quantifies their abundance in microbial communities
- links proteins to taxonomy and function
- can detect post-translational modifications (PTMs)

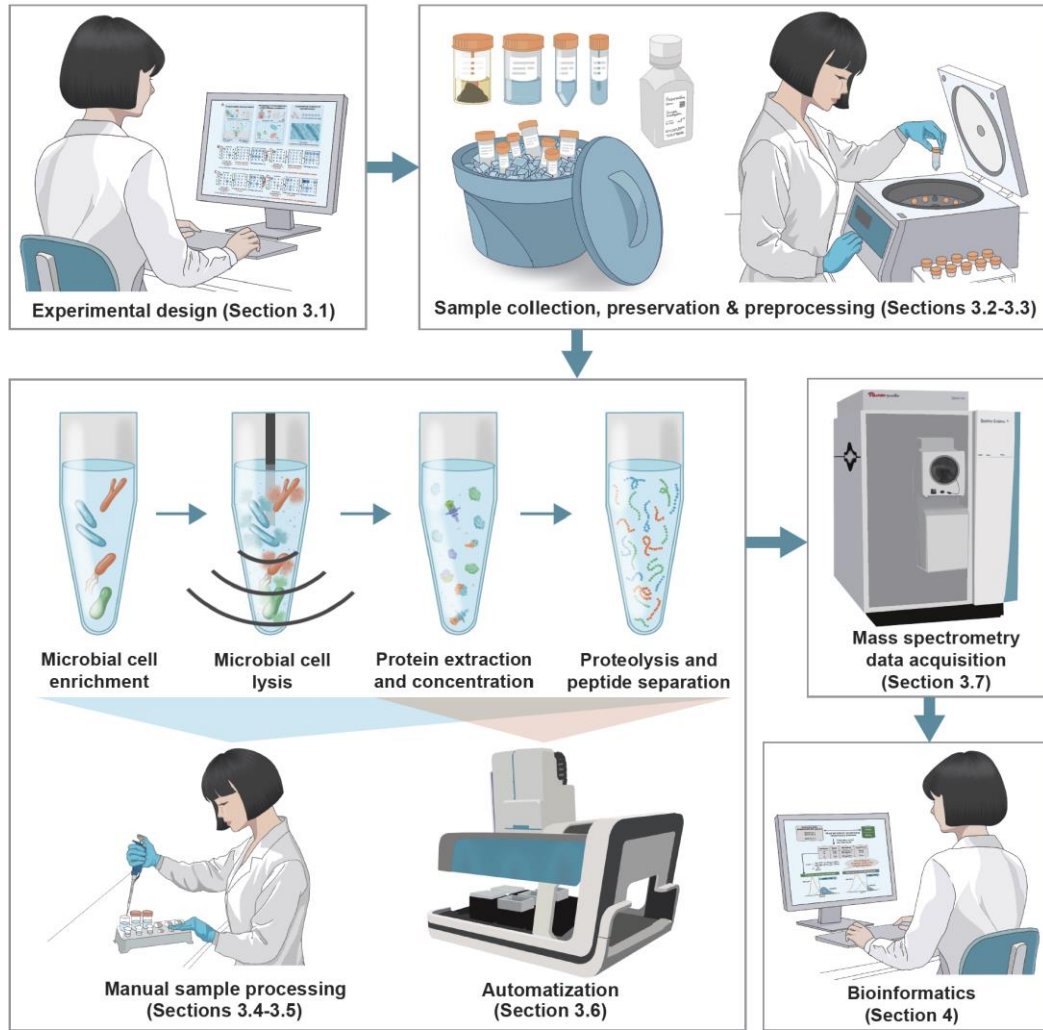
Why?

- captures active functions in microbial communities
- complements metagenomics, metatranscriptomics, and metabolomics





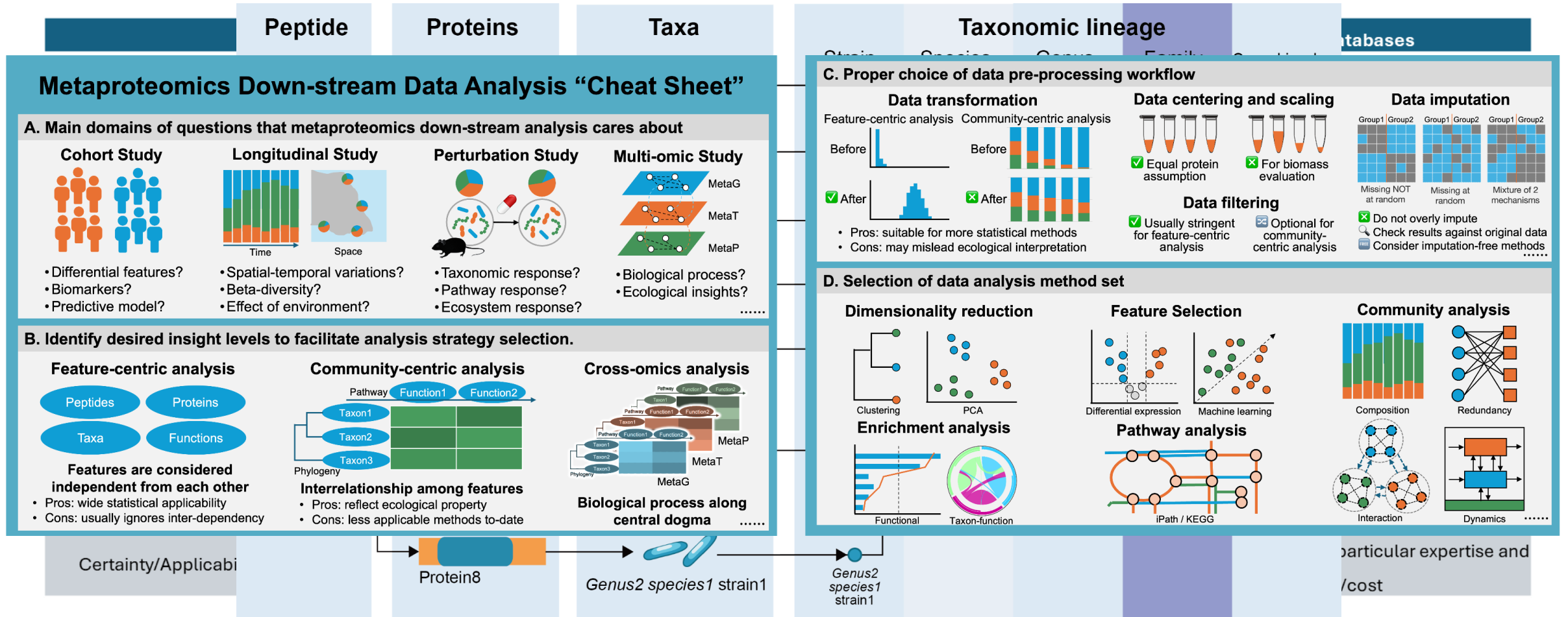
This comprehensive review covers all steps from experimental design to bioinformatics



Method	Description	Advantages	Disadvantages
Chemical Lysis	Disrupts cell membranes with chemicals like urea or guanidine hydrochloride.	Can unfold complex proteins.	If not removed or sufficiently diluted, it can interfere with protease activity. Risk of urea-induced carbamylation.
Detergent Lysis	Uses detergents (e.g., SDS, Triton X-100) to solubilize cell membranes.	Mild, preserves protein function, ideal for membrane proteins.	If a detergent is not removed or sufficiently diluted, it can interfere with protease activity.
Freeze-Thaw Cycles	Repeatedly freezes and thaws the sample to rupture cell membranes.	Simple, no special equipment needed.	Time-consuming, may not fully lyse cells, risk of protein degradation.
Bead beating	Physical force such as using bead beating to break cell walls.	Effective for bacterial cell lysis.	Requires specific instrument, sample loss due to contact with beads, can generate heat, risk of protein degradation.
Ultrasonication	Uses ultrasound waves to break cell membranes/walls and release proteins.	Fast, effective and can be non-contact for small samples, no need for harsh chemicals.	Can denature proteins if overused, heat generation requires sample cooling.



In the bioinformatics section, we'll discuss key concepts such as database design, FDR, protein grouping, LCA calculation and downstream statistics





The Metaproteomics Initiative is an international community *by and for* metaproteomics researchers

- Over 350 members in 95 labs from 23 countries
- Three pillars
 - Communication & collaboration (e.g. CAMPI, International Metaproteomics Symposium, ...)
 - Education & outreach (this *iMeta* flagship paper, organization of workshops)
 - Article | [Open access](#) | Published: 15 December 2021

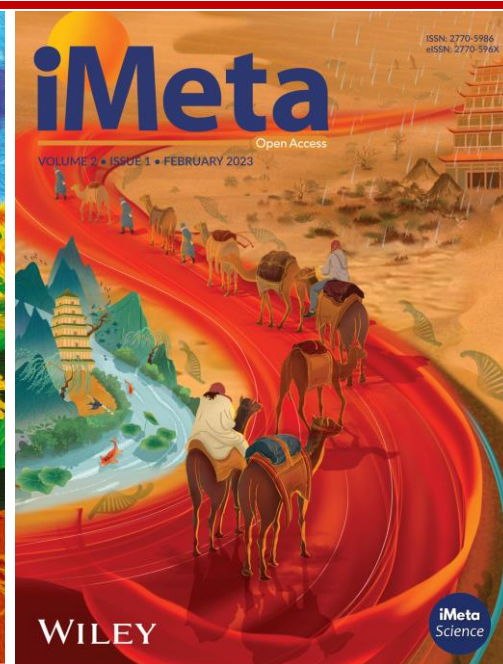
Critical Assessment of MetaProteome Investigation

lates



11k Accesses | 33 Altmetric | Metrics





“***iMeta***” is a Wiley partner journal launched by iMeta Science Society in 2022, first **impact factor (IF) 23.8 in 2024, ranking 2/161 in the microbiology**. It aims to publish innovative and high-quality papers with broad and diverse audiences. **Its scope is similar to *Nature Biotechnology, Nature Methods, Nature Microbiology, Nature Food, etc.*** Its unique features include video abstract, bilingual publication, and social media dissemination, with more than 600,000 followers. It has published 220+ papers and been cited for 5600+ times, and has been indexed by **SCIE / WOS, PubMed, Google Scholar, and Scopus**.

“***iMetaOmics***” is a sister journal of “***iMeta***” launched in 2024, with a **target IF>10, and its scope is similar to *Nature Communications, Microbiome, ISME J, Nucleic Acids Research, Briefings in Bioinformatics, etc.*** All contributes are welcome!



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