



Linking dietary fiber to human malady through cumulative profiling of microbiota disturbance

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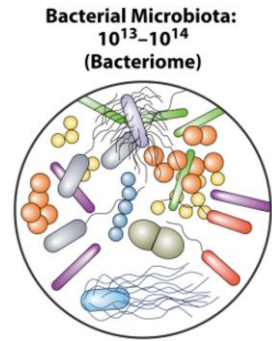
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Background

01

Numerous and diversity



02

Dynamic

Amenable to intervention

Microbiome-directed interventions

Untargeted

Targeted



Exercises Individualized nutrition Faecal microbiota transplantation



Bio-engineered commensals Drugs targeting selected microbial metabolism



Prebiotics Probiotics Synbiotics Postbiotics



Phage therapy CRISPR-Cas9-based therapy

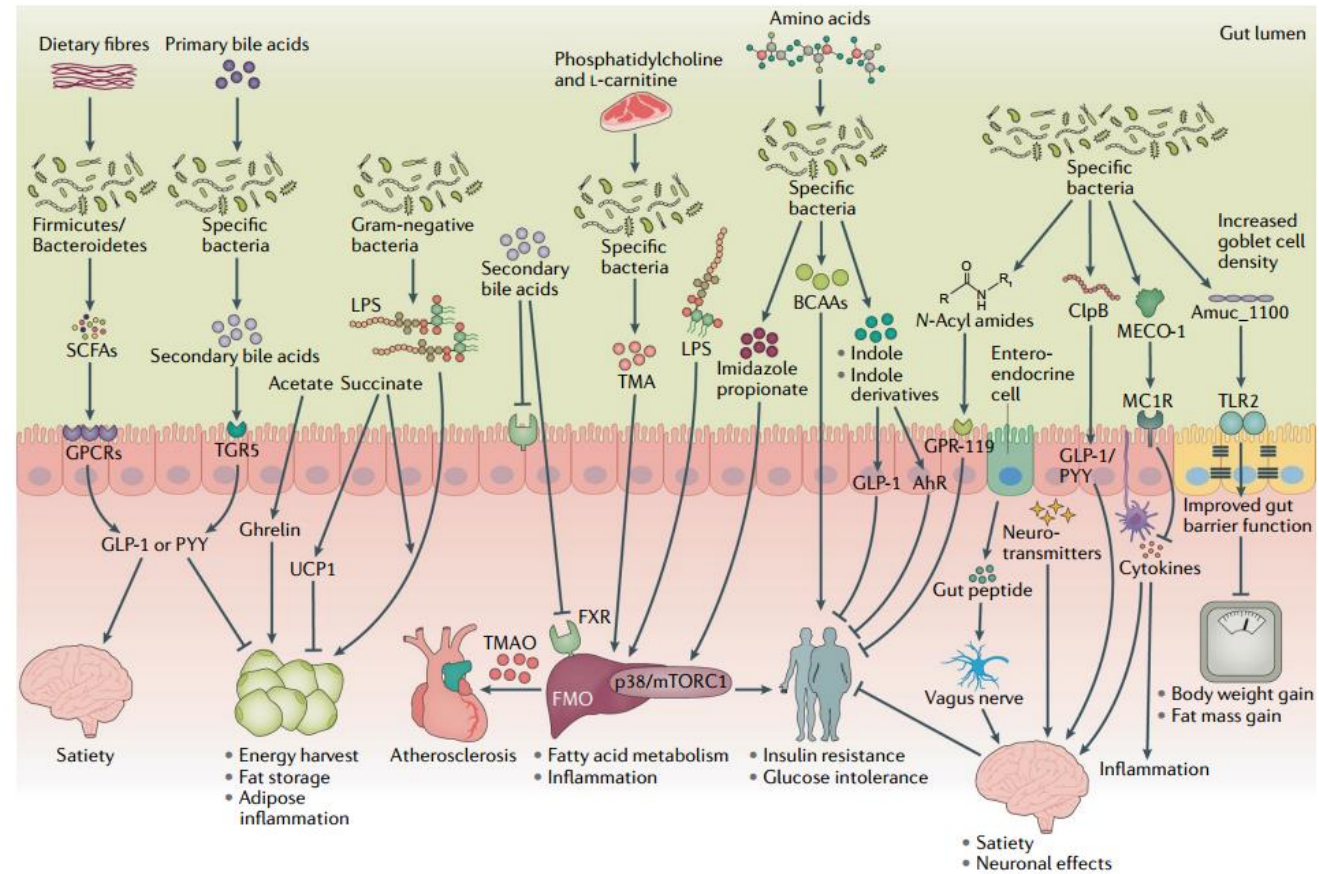
General improvement in microbial composition and functions

Specific modification in metabolism-related gut microbiota

03

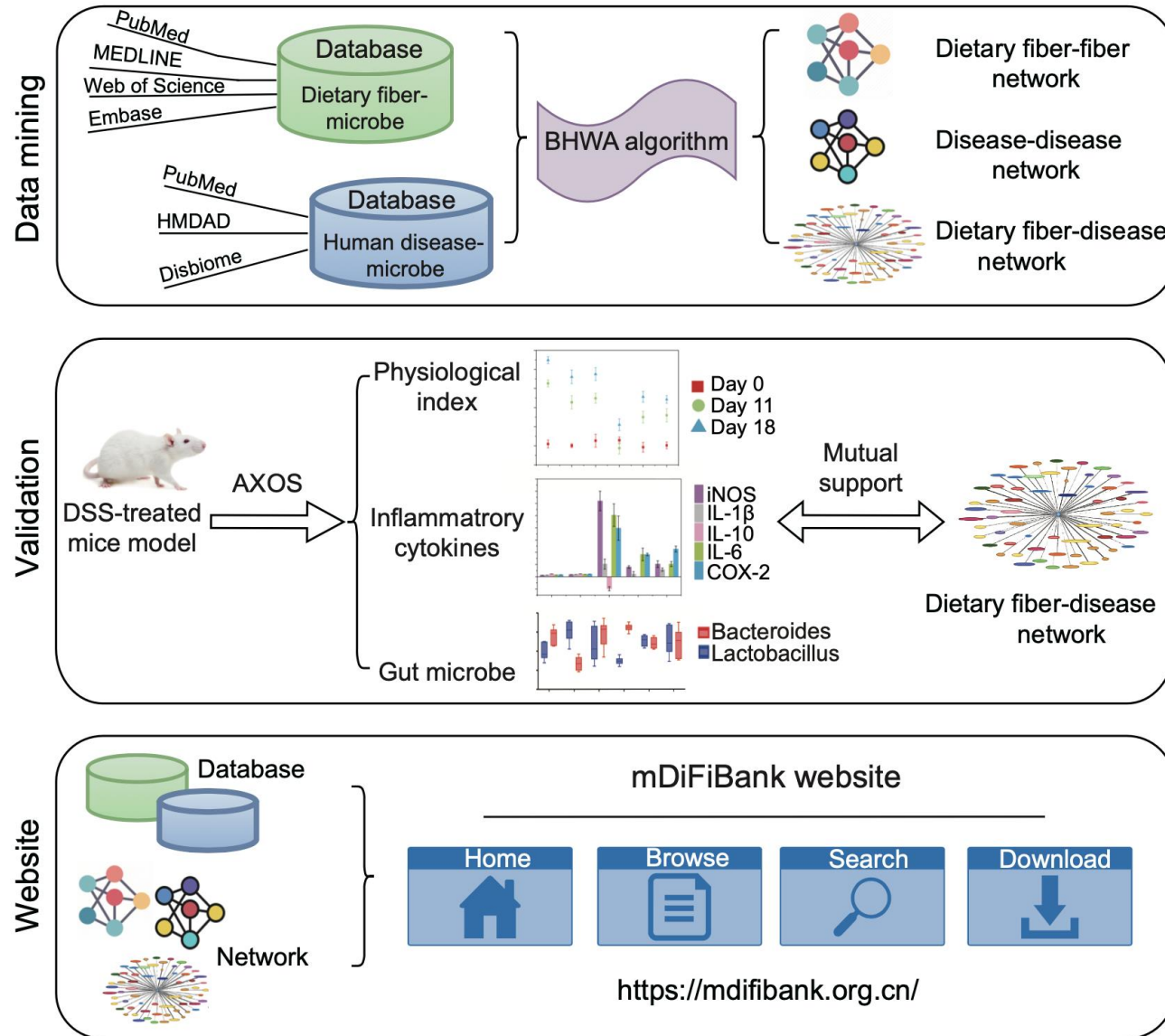
Microbiota-host interaction

Metabolism, Inflammation, Immunity, Neurotransmitters, Development





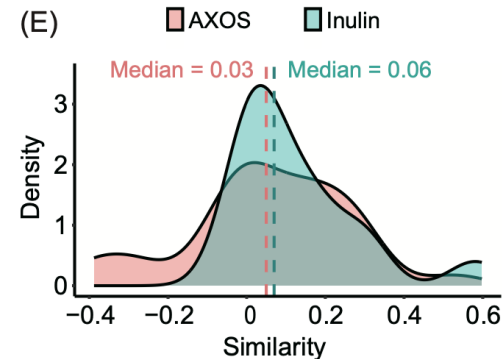
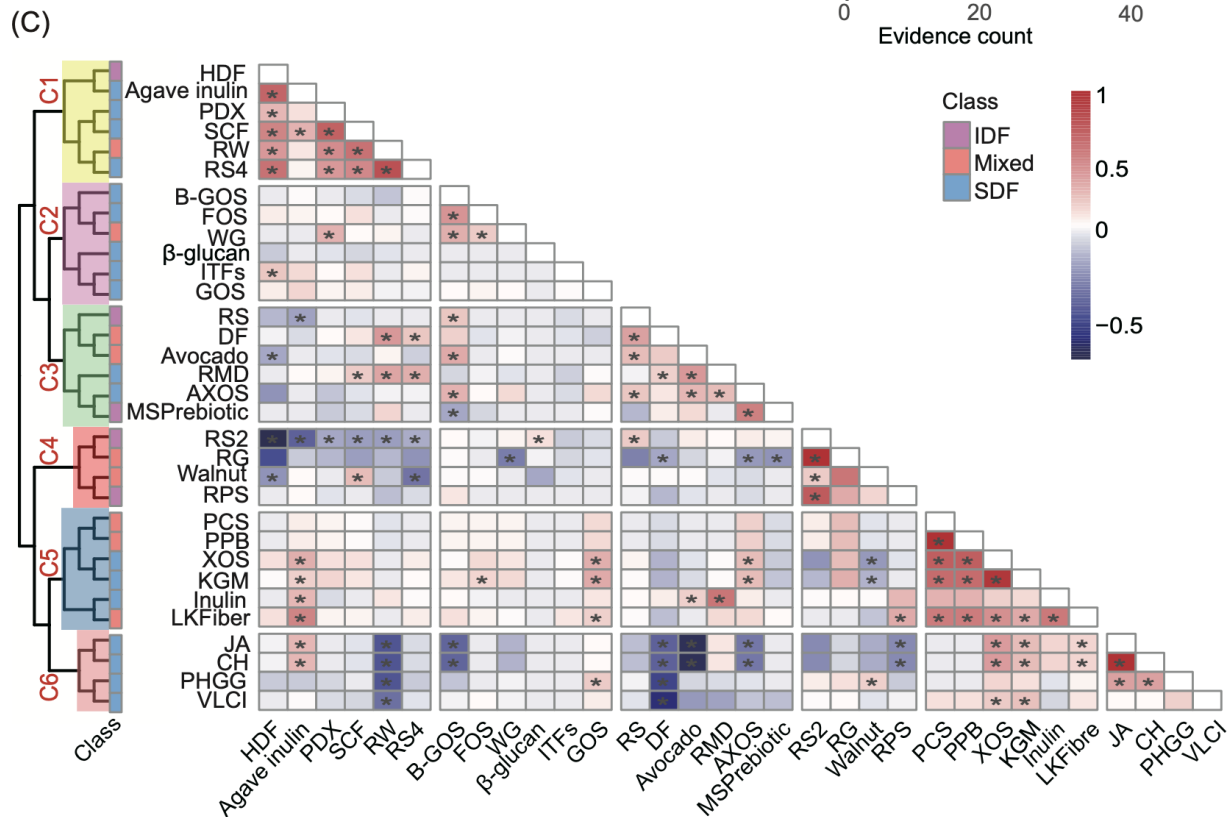
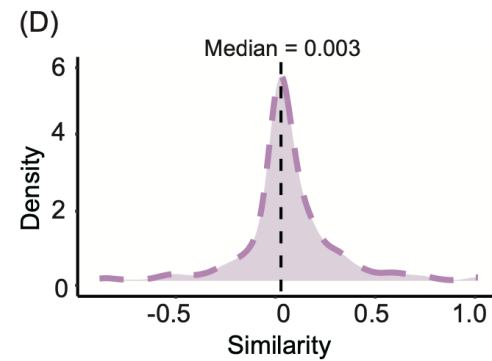
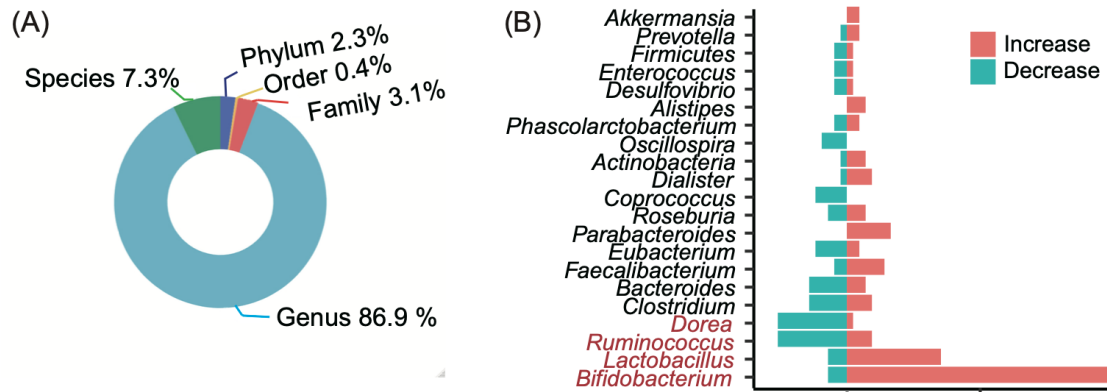
Study overview



This study is mainly divided into three parts: data mining, experimental validation, and website development.

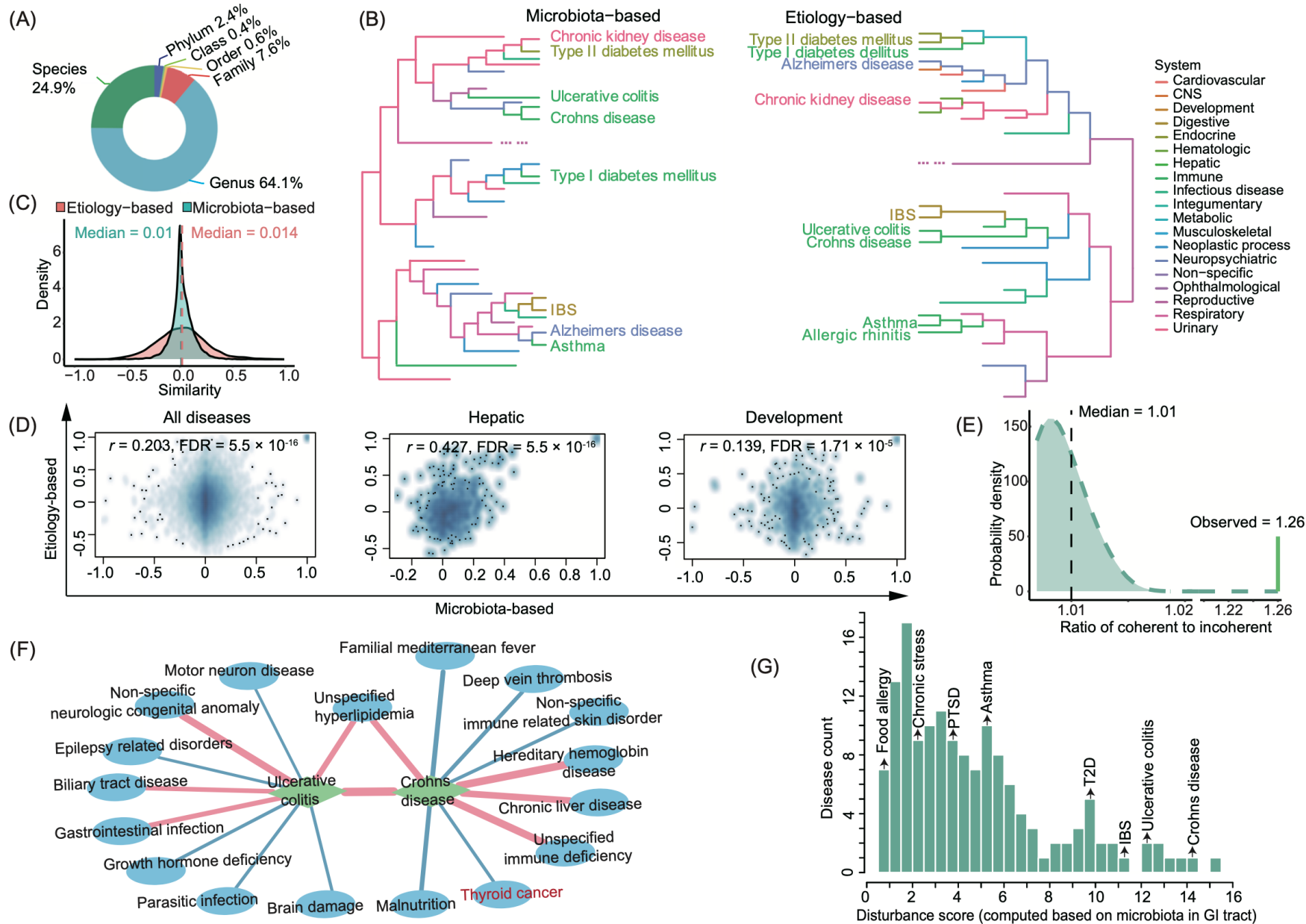


Dietary fiber-microbe database construction and fiber classification



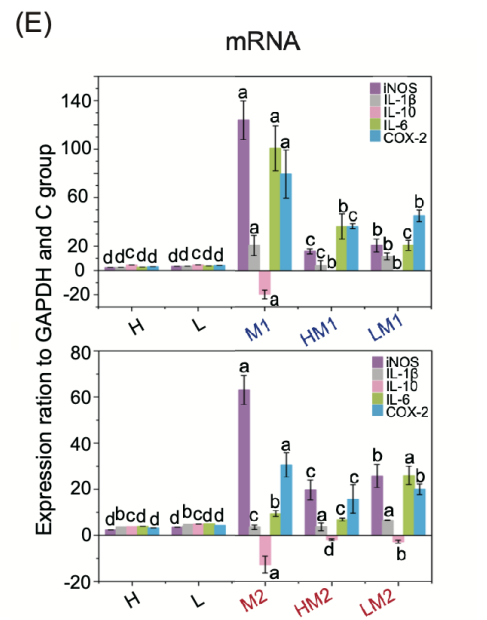
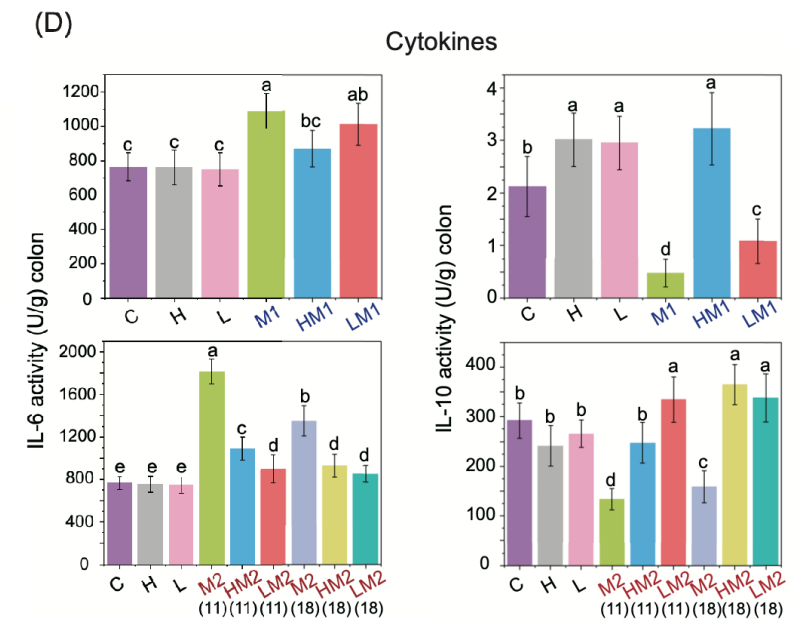
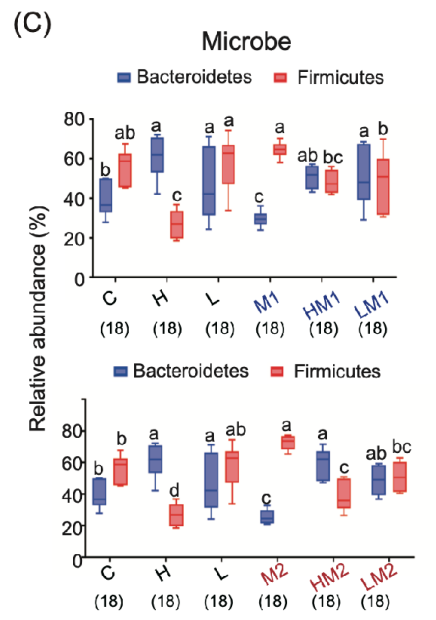
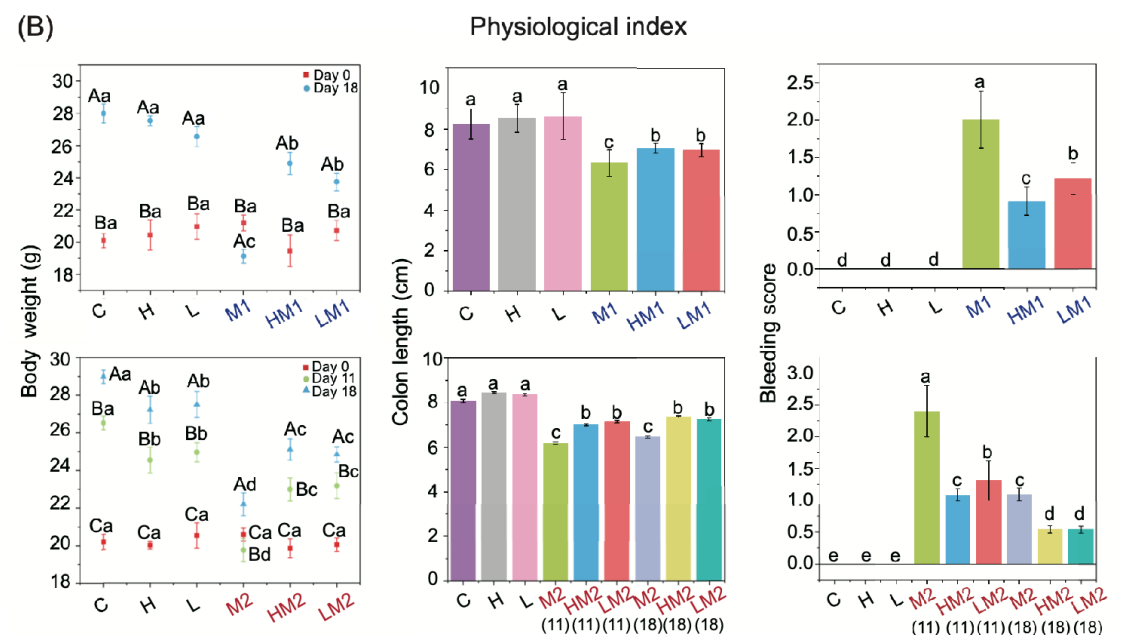
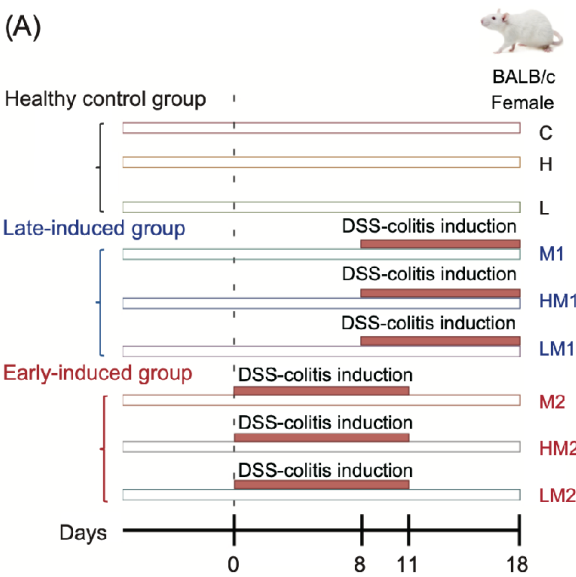
Construct a dietary fiber network using microbiota disturbance pattern similarity and perform functional classification

Establishing between-disease associations underpinned by similar microbiota



Build a disease network using microbiota disturbance pattern similarity and assess microbiota disturbance scores for diseases in different body sites

Preventive and therapeutic effects of arabinoxylan on murine models of inflammatory bowel disease



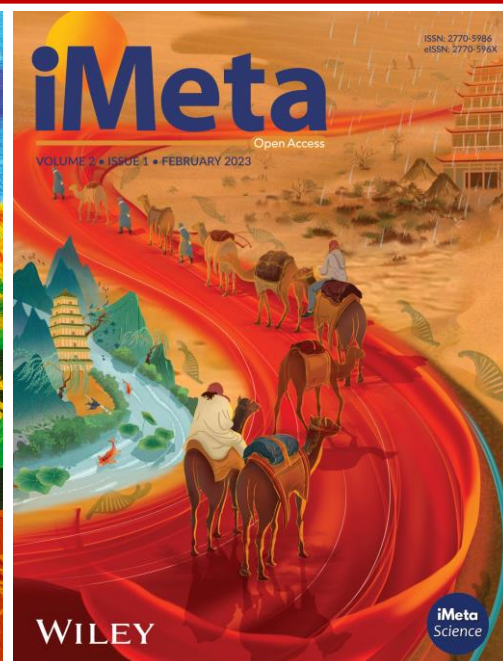
- Validate the key nodes in the network from multiple dimensions, including changes in body indicators, alterations in microbiota composition, fluctuations in inflammatory factor levels, and protein expression.
- This was done to fully demonstrate the correctness of the network construction and the rationality of the algorithm design.



Conclusion

- ❑ Our study explored the intricate relationships between dietary fibers, microbiota disturbances, and disease states, introducing Bio-taxonomic Hierarchy Weighted Aggregation (BHWA) algorithm to analyze these interactions across taxonomic levels and body sites.
- ❑ By treating microbiota disturbances as key intermediaries, we established connections between dietary fiber intake and disease outcomes, generating a candidate list of dietary fibers with therapeutic potential.
- ❑ launched an interactive webtool — mDiFiBank (<https://mdifibank.org.cn/>) — to enhance data accessibility and facilitate the development of targeted dietary interventions.

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