

MicroEXPERT: Microbiome profiling platform with cross-study metagenome-wide association analysis functionality

Pengshuo Yang, Jialiang Yang, Haixia Long, Kaimei Huang, Lei Ji, Hanyang Lin, Xiuli Jiang, Arthur Kairui Wang, Geng Tian, Kang Ning

1 Key Laboratory of Molecular Biophysics of the Ministry of Education, College of Life Science and Technology, Huazhong University of Science and Technology, Wuhan, Hubei 430074, China

2 Geneis Beijing Co., Ltd., Beijing 100102, China

3 Qingdao Geneis Institute of Big Data Mining and Precision Medicine, Qingdao, 266000, China

4 Academician Workstation, Changsha Medical University, Changsha 410219, China

5 Sequenxe Biological Technology Co., Ltd., Xiamen 361000, China

<https://MicroEXPERT.aimicrobiome.cn/>



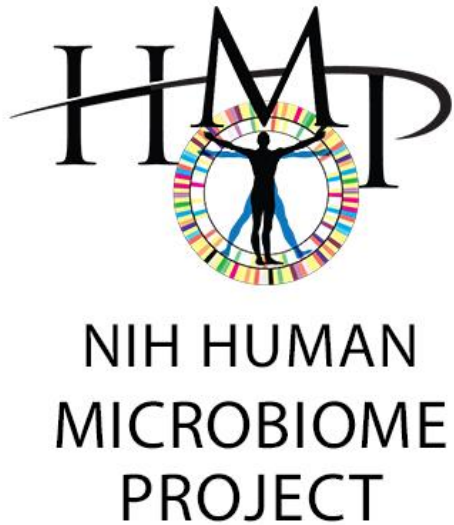
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Content

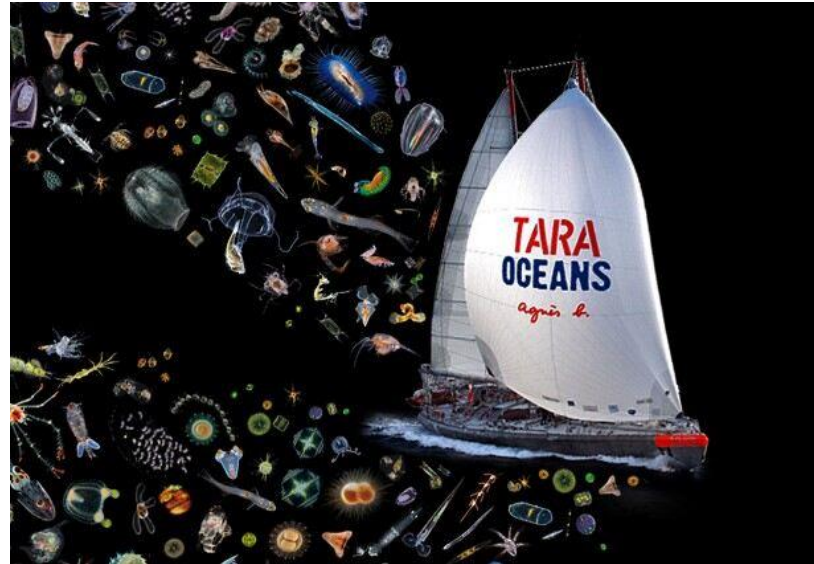
- Introduction
- Material
- Result

Introduction

Metagenomic data is growing at an extremely rapid rate



Human microbiome Project



Tara Oceans Project

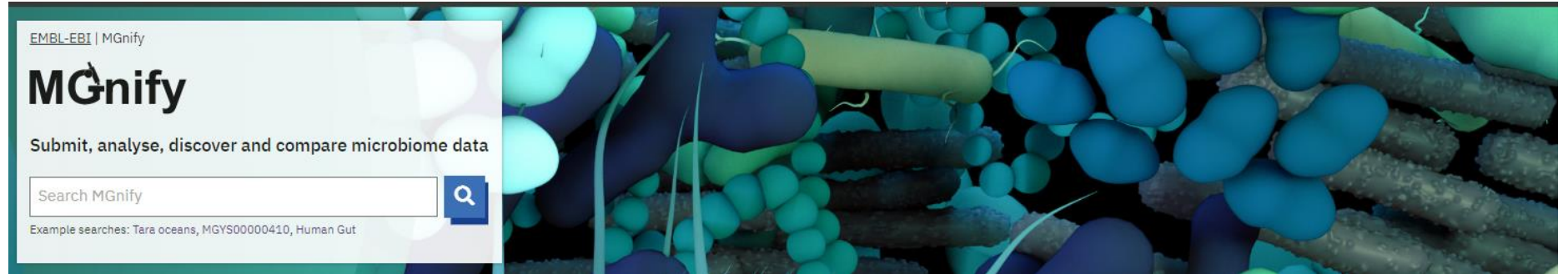


Earth Microbiome Project

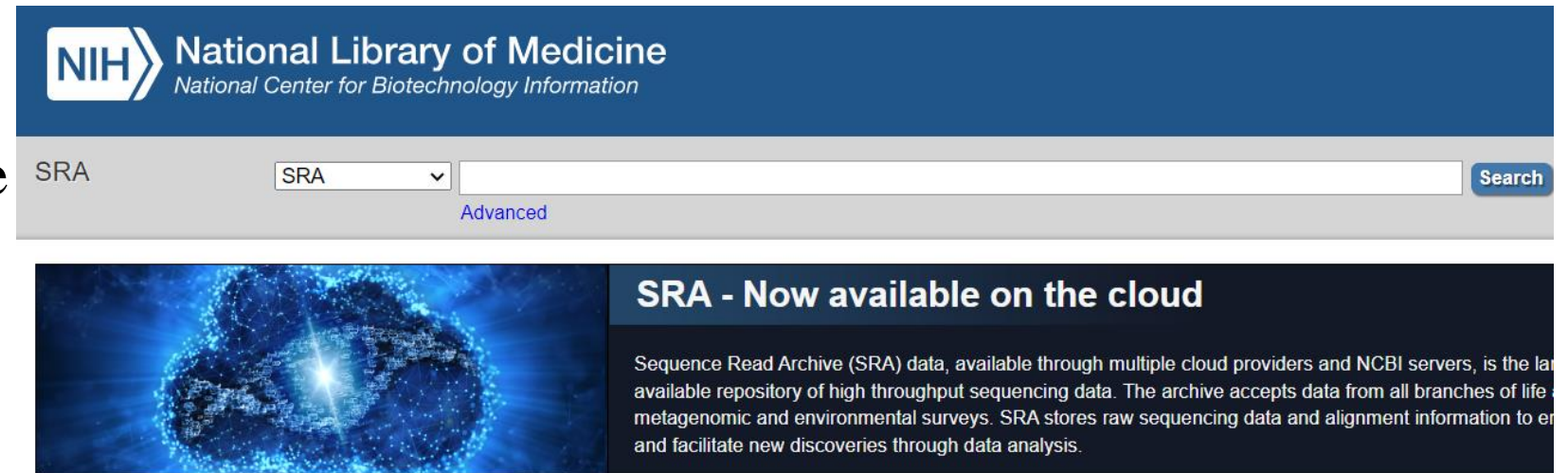
Introduction

Several databases have been constructed to maintain metagenome data and metadata such as:

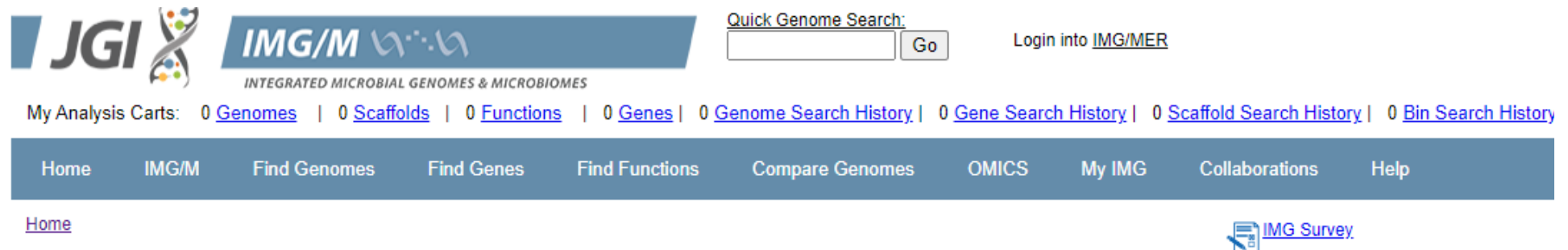
Mgnify database



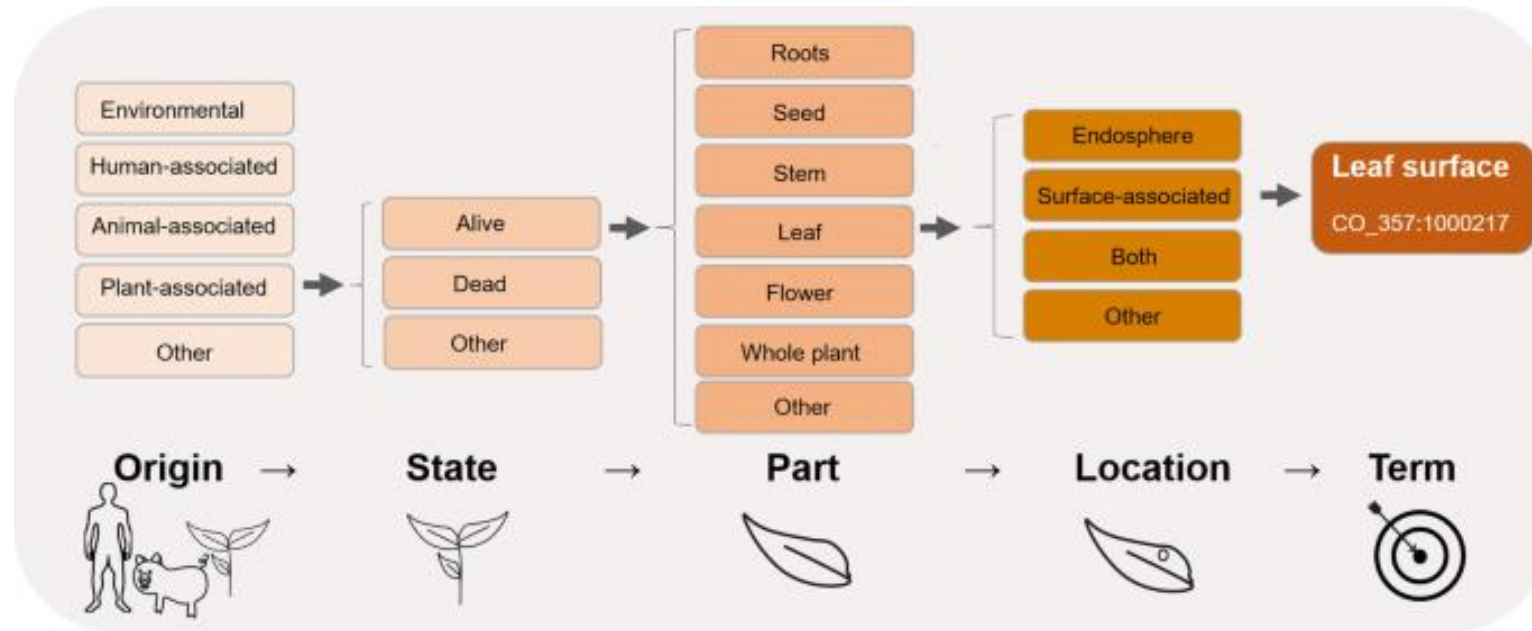
SRA database



IMG/M database

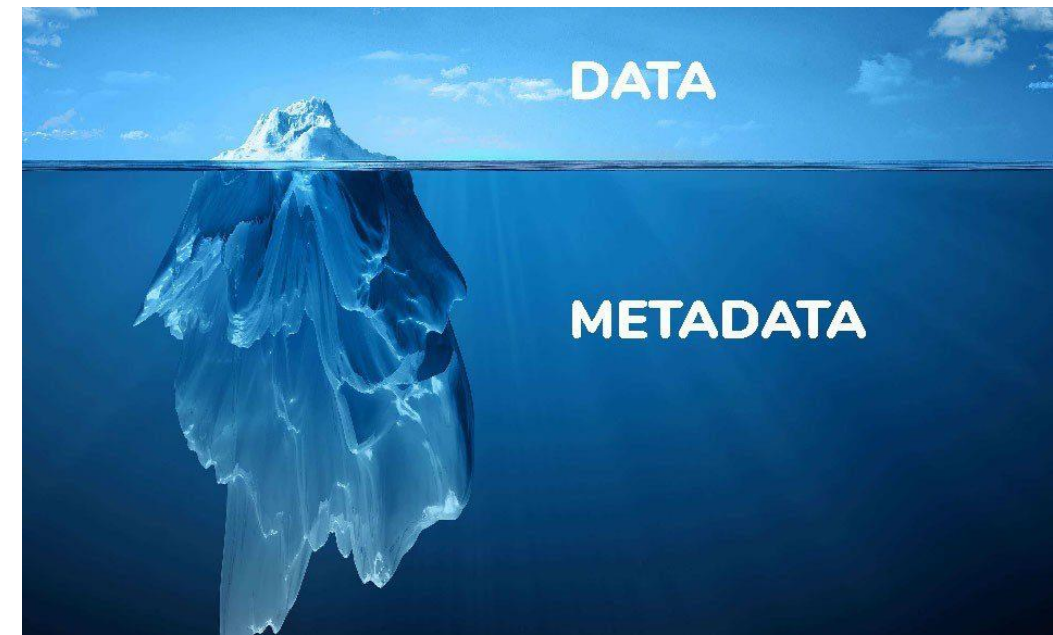


Metadata



Additional information about the samples or data collected from a microbial community.

Metadata: Massive and heterogeneous



Introduction

A platform is required to utilize the **metadata** to decipher the relationship between biomes and metagenomes



The **MicroEXPERT** platform (<https://MicroEXPERT.aimicrobiome.cn/>) for data management, data analysis, and data mining of the metagenome.

Highlight:

1. Long-term data preservation.
2. Integrate gene research tools and species identification tools.
3. A broad range of statistical tools are supplied for **Metagenome-Wide Association analysis**

Result

Results

A screenshot of the MWAS workflow

(A) 1. Sample selection

Project List

Run List (selected 8 runs)

Selected sample

(B) 2. Custom analysis selection

Run List

Sample comparison

MWAS(metadata required)

(C) 3. Custom categorization

Choose Meta

Runs Table

Project: Tara Oceans Metagenome (HUST-P-0000000067)

Choose a grouping tag: ☐ ☒ ☐ ☐ ☐ ☐

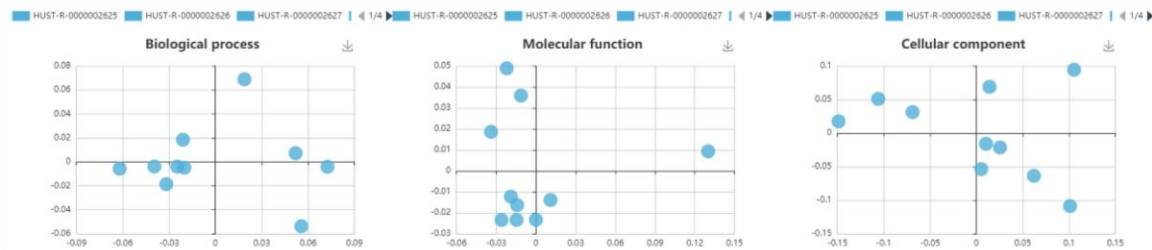
Submit Export Import

Group(Distinguish by four colors)

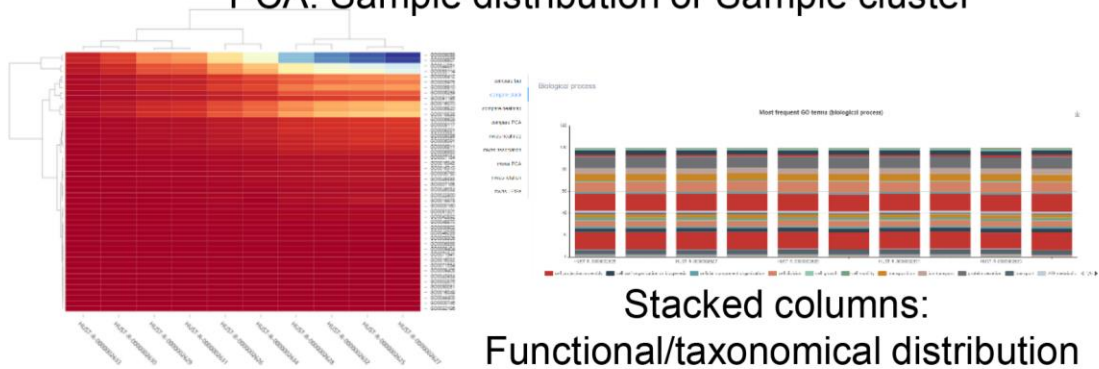
Sample ID	Run ID	temperature	depth	Oxygen Sensor	Salinity Sensor
HUST-S-0000006417	HUST-R-0000002625	22.261435	155	207.089325	35.939945
HUST-S-0000006493	HUST-R-0000002626	27.59865	5	184.061167	38.646858
HUST-S-0000006503	HUST-R-0000002627	20.5251	5	99999	36.6324
HUST-S-0000006400	HUST-R-0000002628	13.159842	45	227.686042	33.241367

Results

(D) Comparison(without metadata)



PCA: Sample distribution or Sample cluster

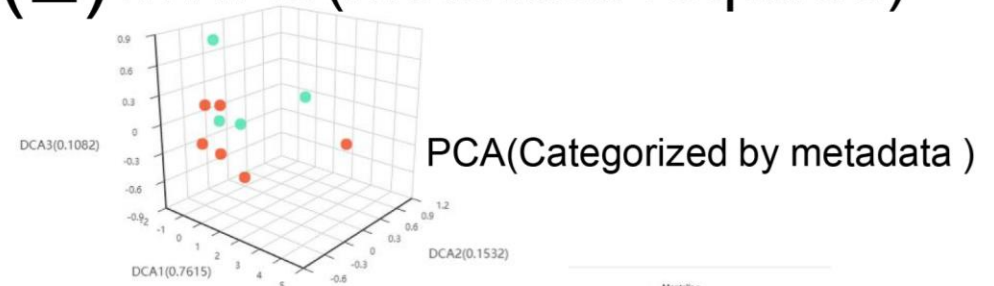


Stacked columns:

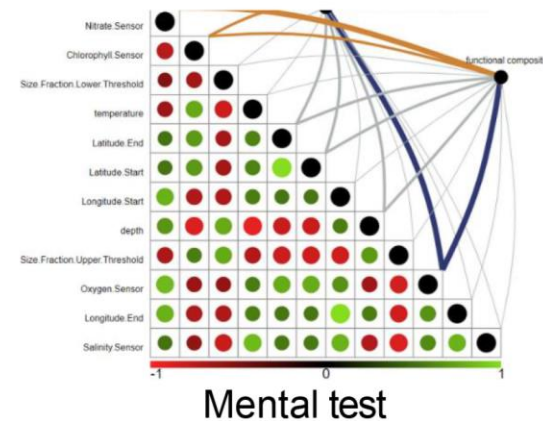
Functional/taxonomical distribution

Heatmap: Functional/taxonomical modules enrichment

(E) MWAS(metadata required)



PCA(Categorized by metadata)



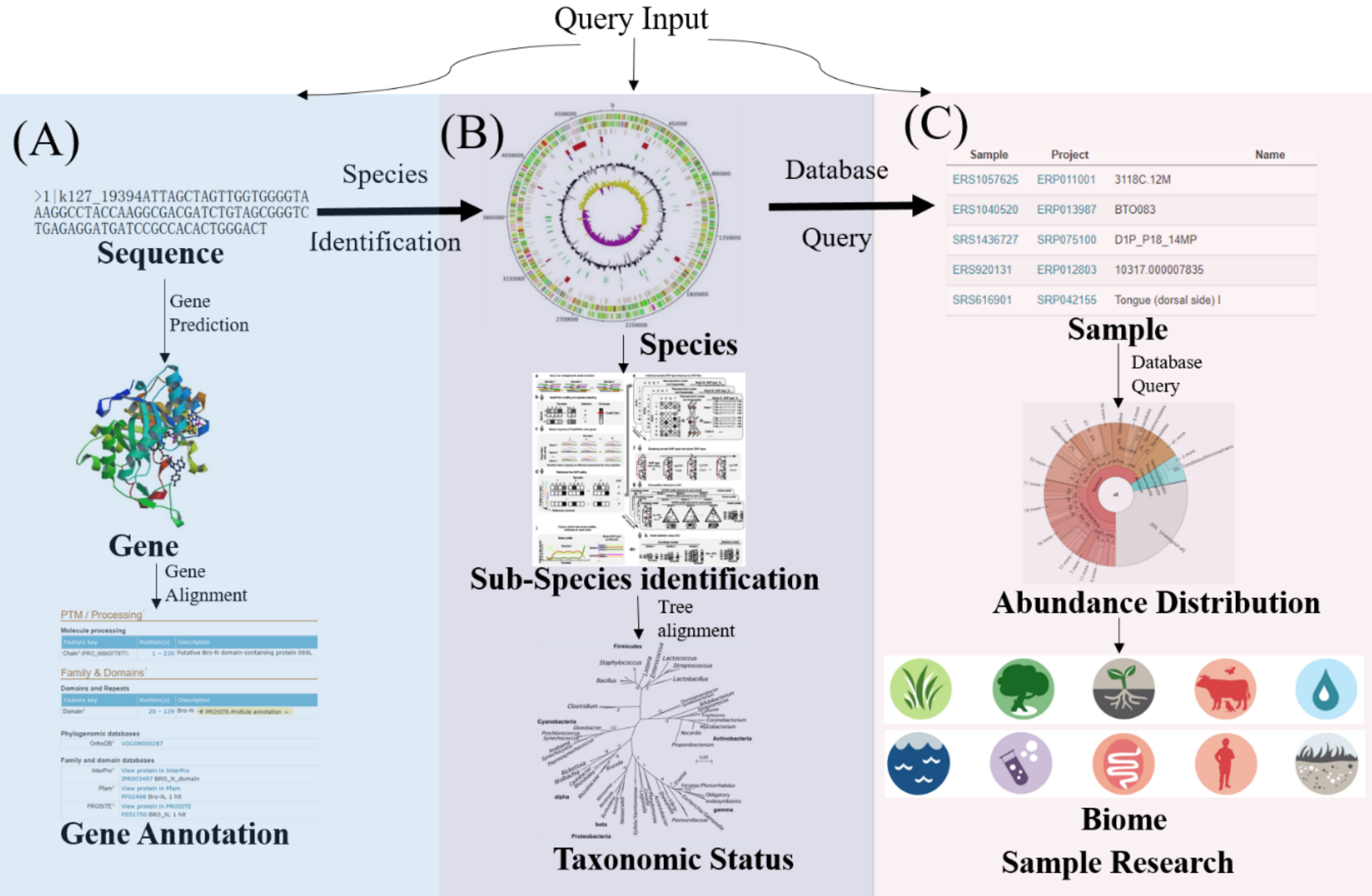
Mental test



Network: reconstruct microbial community

Results

Investigation the gene-species-sample relationship with one sequence



(A) Gene annotation
workflow

(B) Species identification
workflow

(C) Sample search
workflow

Summary

Summary

1. Retrieved 4,236 projects, covering 328,417 samples with detailed taxonomical and functional profiles.
2. Support Metagenome-Wide Association analysis and gene search module.
3. MicroEXPERT will be updated bi-annually to reflect the latest advancements in metagenome research and MWAS analysis.

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