

Hua Zou

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PROFILE

A joint master from BGI and University of Chinese Academy of Sciences currently, majoring in genomics. I am currently working as a senior bioinformatic analyst in Xbiome company, Shenzhen, China, mainly focusing on host-microbiota interactions and therapeutic effects of human gut microbiota on immune checkpoint inhibitors in cancer patients through next-generation sequencing. I am proficient with multi-omics data analysis, including amplicon sequencing data, metagenomic data and metabolomic data.

EDUCATION

2016 - 2020	Master of Science	Genomics, BGI-Shenzhen and the University of the Chinese Academy of Sciences, Shenzhen and Beijing, China.
2011 - 2016	Bachelor of Science	Biotechnology, College of Bioinformatics Science and Technology, Harbin Medicine University, Harbin, Heilongjiang, China.

SKILLS

Knowledge	<ul style="list-style-type: none">• Proficient in metagenomics.• Familiar with metabolomics, metatranscriptomics and transcriptomics.• Familiar with statistical analysis.
Coding	<ul style="list-style-type: none">• Proficient in pipeline development via snakemake.• Proficient in Perl and R.• Familiar with git.• Experienced in Shell.• Experienced in Python.• Experienced in managing Linux server.
Database	<ul style="list-style-type: none">• Familiar with EBI, NCBI and KEGG databases.• Familiar with ClinicalTrials for registering clinical trial.
Visualization	<ul style="list-style-type: none">• Comfortable in visualization with R and Adobe Illustrator.
English	<ul style="list-style-type: none">• Comfortable with reading and writing (IELTS score: 6.5).

RESEARCH EXPERIENCE

Xbiome Company, Shenzhen, China March/2022 – Present

Integrating multiple in-house statistical approaches applied in microbiota data into user-friendly R package (XMAS 2.0 : https://xbiomeanalysis.github.io/XMAS_tutorial/)

- Illustrated the schematic figure of XMAS 2.0 for rebuilding this package.
- Created and integrated R scripts on statistical and visualizing methods into the R package.
- Provided a user-friendly tutorial for in-house users.

Building metabolomic data analysis pipeline ([metabolomic workflow: https://xbiomeanalysis.github.io/Metabolomics_Analysis/](https://xbiomeanalysis.github.io/Metabolomics_Analysis/))

- Integrated data processing, statistical methods and functional analysis into a comprehensive workflow.

Association of gut microbiota and immune-related adverse events (irAEs) in gastrointestinal cancer

- Participated in the project as an analyst.
- Performed the primary analysis by:
 - Screening volunteers according to the criterions.
 - Collecting and checking the phenotypic information.
 - Profiling of gut microbiota taxonomical and functional annotation.
- Explored the relationship between irAEs and the gut microbiota when treated with immune checkpoint inhibitors.

Bioland Laboratory, Guangzhou, China June/2020 – February/2022

Deep learning-based multi-omics integration robustly predicts survival in kidney renal clear cell carcinoma

- Preprocessed more than 250 published samples with multi-omics sequencing data.
- Obtained 100 new transformed features using autoencoder algorithm.
- Selected the features associated with survival.
- Inferred survival-risk groups based on the aforementioned features.
- Combined deep learning and machine learning techniques to predict the subgroups of new patients with kidney renal clear cell carcinoma.

The Institute of Metagenomics, BGI Research, Shenzhen, China March/2017 – June/2020

Dietary intervention on human gut microbiota

- Participated in the project as a project leader.
- Performed the primary analysis by:
 - Screening volunteers according to the criterions.
 - Collecting and checking the phenotypic information, blood samples, and stool samples.
 - Profiling of gut microbiota taxonomical and functional annotation.
- Evaluated the effects of dietary intervention on BMI, amino acids, and gut microbiota.
- Analyzed the relationship among the BMI, amino acids, and gut microbiota during dietary interventions.

Association between the PD-1 efficacy and human gut microbiota in NCLC

- Performed quality control and statistical analysis on phenotypic data.
- Profiled of gut microbiota taxonomical and functional annotation.
- Investigated the association between gut microbiota and phenotypic information.

Distinct gut potential biomarkers on metagenomics and metaproteomics in T2D

- Identified the potential biomarkers associated with T2D from metagenomes and metaproteomes.
- Visualized the statistical results.

Construction of the microbial gene catalog for plant-associated microbiome

- Constructed the plant-root microbial gene catalog by retrieving the publicly available shotgun metagenomic and metatranscriptomic sequencing data of plant samples from NCBI.

- Performed raw reads filtering, reads mapping, and contig assembly.
- Reconstructed genome-resolved microbes with metagenomic binning approaches.
- Inferred the efficacy of 515F-806R/515F-926R primers in amplifying metagenome-assembled 16S rRNA sequences.

PUBLICATIONS

- Zhang Yifan, Cheng Siyuan, **Zou Hua**, ... & Peng Zhi. (2023). Correlation of the gut microbiota and immune-related adverse events in gastrointestinal cancer treated with immune checkpoint inhibitors. *Frontiers Cellular and Infection Microbiology*, 13, 192.
- Fang, C., Fang, W., Xu, L., Gao, F., Hou, Y., **Zou, H.**, ... & Zhang, L. (2022). Distinct Functional Metagenomic Markers Predict the Responsiveness to Anti-PD-1 Therapy in Chinese Non-Small Cell Lung Cancer Patients. *Frontiers in oncology*, 12.
- **Zou, H.**, Wang, D., Ren, H., Cai, K., Chen, P., Fang, C., ... & Zhong, H. (2020). Effect of caloric restriction on BMI, gut microbiota, and blood amino acid levels in non-obese adults. *Nutrients*, 12(3), 631.
- Zhong, H., Ren, H., Lu, Y., Fang, C., Hou, G., Yang, Z., ... **Zou, H.** ... & Li, J. (2019). Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. *EBioMedicine*, 47, 373-383.
- Pengfan Z., Yayu W., Huan L., Shuilin L., Shanshan L., Jin X., Sunil Kumar Sahu., **Hua Z.**, Nian W., Guangyi F., Yunzeng Z., Xun X., Tao J., Xin L. The functional structure of foxtail millet rhizosphere microbiome and its association with yield. *BMC Biology*. (Under Review).

REFERENCES

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 Professor in University of Chinese
 Academy of Sciences
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