

Hua Zou

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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.

RESEARCH EXPERIENCE

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.

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 downloaded from TCGA by normalizing data and filtering samples or genomic features.
- Performed dimension reduction on four-omics features with autoencoder algorithm to obtain the 100 new transformed features.

- Assessed the association of the each autoencoder feature and the survival status and time to select the features associated with survival.
- Applied the k-mean clustering to samples represented by the aforementioned features to inferred survival-risk groups.
- Combined deep learning and machine learning techniques to predict the subgroups of new patients with kidney renal clear cell carcinoma.

Xbiome Company, Shenzhen, China March/2022 – Present

Integrating multiple in-house statistical approaches applied in microbiota data into user-friendly R packages (XMAS 2.0)

- Illustrated schematic figure of XMAS 2.0 for rebuilding this package.
- Created and integrated R scripts on statistical and visualized methods to build R packages.
- Provided an user-friendly tutorial for in-house users.

PUBLICATIONS

- **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 rhizoplane microbiome and its association with yield. *BMC Biology*. (Under Review).

SKILLS

Knowledge	<ul style="list-style-type: none"> • Familiar with metabolomics, metatranscriptomics and transcriptomics. • Proficient in metagenomics. • 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).

REFERENCES

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