

Bo Feng

Github

bofengvn@mail.sdu.edu.cn

EDUCATION

Shandong University
MS in Marine Biology

Sep. 2022 - Jun. 2025 (Expected)

Ningbo University
BS in Aquaculture

Sep. 2018 - Jun. 2022

PUBLICATIONS

Feng, B., Yo. Li, H. Liu, J. L. Steenwyk, K. T. David, X. Tian, ... & Y. Li. (2024). **Unique trajectory of gene family evolution from genomic analysis of nearly all known species in an ancient yeast lineage.** *bioRxiv* [\[LINK\]](#)

RESEARCH EXPERIENCE

Machine Learning in Yeast Metabolism
Core Member, Shandong University

Feb. 2024 - Present

[\[Github\]](#)

- Constructed machine learning models to predict ancestral yeast carbon source utilization based on gene family presence or absence.
- Identifying key gene families for different carbon source models and comparing their amino acid sequence and structure identities across all extant yeasts.
- Predicting descendant yeast gene family presence or absence and their carbon source utilization.

Deep-Sea Shark Chromosome Synteny
Contributor, South China Sea Institute of Oceanology

May 2024 - Jun. 2024

[\[Github\]](#)

- Reconstructed ancestral shark chromosomes and compared chromosomal synteny across three superorders, utilizing karyotype evolution to help resolve shark phylogeny.
- Analyzed deep-sea sharks by identifying and comparing the genomic features of macrochromosomes and microchromosomes; screened single-copy orthologous genes to assess selective pressures.

Yeast Gene Family Evolution
Core Member, Shandong University

Sep. 2022 - Apr. 2024

[\[Github\]](#)

- Assessed gene family diversity across yeasts, filamentous fungi, animals, and plants.
- Evaluated the dynamics of gene family evolution within the yeast subphylum.
- Investigated the impact of specific gene family contractions and losses on specific yeast orders.
- Established a novel and robust thousand-genome-scale framework for studying general evolutionary trends in genomes.

Bacterial Synthetic Gene Cluster Identification
Core Member, Shandong University

Aug. 2022 - Sep. 2022

[\[Github\]](#)

- Predicted secondary metabolite biosynthesis gene clusters in bacterial genomes.

TECHNICAL SKILLS

Languages: R, Bash, Python

Libraries and Tools: ggplot2, mlr3, data.table, clusterProfiler, CAFE, BayesTraits, InParanoid, IQ-TREE, antiSMASH

ML Architectures: Random Forest, Neural Networks

AWARDS

Outstanding Award at the College Academic Forum

2024

Merit Student Scholarship

2023

First Prize in the Zhejiang College Student Science and Technology Competition

2022

Merit Student Scholarship

2020

Third Place in the Freshman Debate Competition

2018