

環境中の微生物群集構造および機能的多様性の解析

Analysis of environmental microbial community structure and functional diversity

京都大学 化学研究所 数理生物情報研究領域 Zai Yinghan

研究成果概要

This study investigated soil microbial community structure and interaction patterns using high throughput 16S rRNA sequencing combined with comprehensive bioinformatics analyses. Raw sequencing data were processed in QIIME 2, including quality filtering, DADA2 denoising, ASV table construction, and taxonomic assignment using the SILVA database. Alpha and beta diversity analyses, along with PCoA visualization, were performed to assess community composition and structural differences under varying environmental conditions. To further explore potential ecological relationships, co-occurrence networks were constructed using both Spearman correlation and SparCC methods, accounting for compositional effects. Positive and negative correlation networks were analyzed separately to distinguish potential cooperative and competitive interactions. Network topology metrics and Louvain community detection were applied to identify modular structures and key nodes. Sensitivity analyses across correlation thresholds demonstrated that network architecture is highly parameter-dependent, providing deeper insights into microbial community organization and stability.

Through supercomputing-based analysis, large-scale network inference and modularity detection were achieved, generating high-resolution interaction networks and quantitative topology metrics that revealed the structural complexity and potential functional organization of microbial communities under different environmental conditions.