BRCore: An R Package Implementing Flexible Selection of Core Taxa Using Contribution to Bray-Curtis Dissimilarity and Neutral Model Fitting

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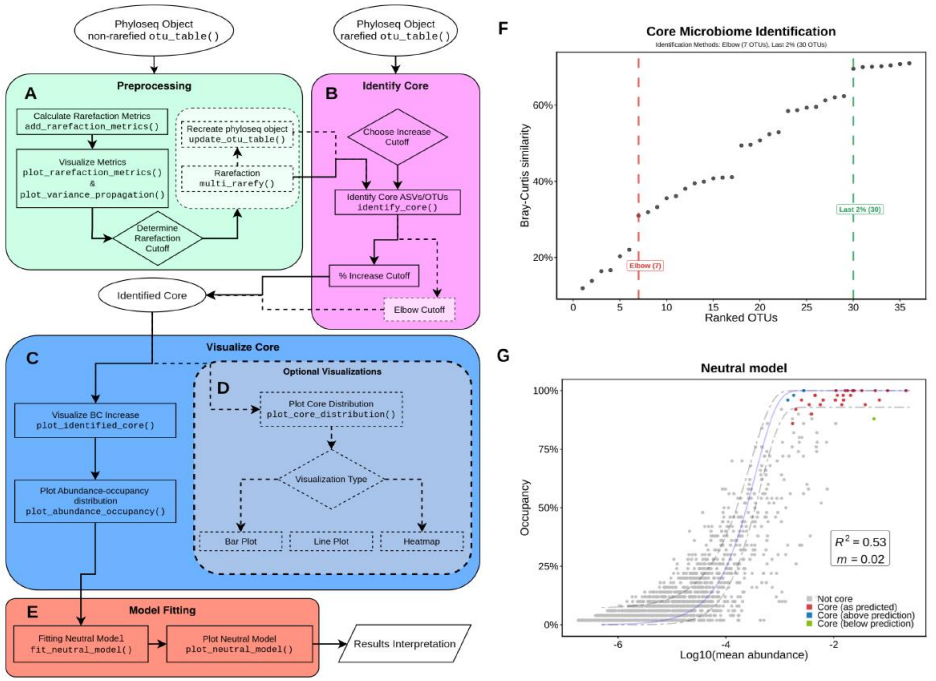
Background/Objective

Researchers define persistent microbiomes to identify abundant taxa, specifically those consistently present across samples or enriched under distinct conditions. Core taxa selection is based on relative abundance and consistent detection and tailored to the research question, data set characteristics, and study system. Researchers developed an R package aiming to identify persistent microbiomes using abundance-occupancy distributions and neutral community model fitting.

Approach

BRCore was developed as a cross-platform R package compatible with Linux, macOS, and Windows to implement a previously published proposed workflow. BRCore defines persistent taxa based on their contribution to beta-diversity, specifically Bray-Curtis dissimilarity, and provides neutral model testing while accounting for features such as crop, site, or time for detection. BRCore additionally implements rarefaction of ASV/OTUs and provides several visualization functions. As a demonstration, BRCore was applied to the built-in "bcse" dataset, comprising leaf microbiome samples collected from ten cropping systems at the Kellog Biological Station.



BRCore example pipeline

Results

Prior to the development of BRCore, a package was not publicly available that combines the ability to identify core taxa using abundance-occupancy distributions and beta-diversity contributions across ecological niches and predict stochastic and deterministic taxa.

Significance/Impacts

The BRCore R package is an example of a shared workflow that has taken a lab-specific procedure and made it a reproducible and reusable research asset. We have used in across the BRCs to demonstrate collaborative microbiome science.

Aponte Rolón et al. 2026. "BRCore: An R Package Implementing Flexible Selection of Core Taxa Using Contribution to Bray-Curtis Dissimilarity and Neutral Model Fitting." *Microbial Resource Announcements.* DOI:10.1128/mra.00251-26.