

Dietary patterns correspond with microbiome composition

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Objectives

- Previous studies have defined dietary patterns for comparison with microbiome features using factor analysis from food frequency questionnaires.
- We applied a new tree-based method to directly define dietary patterns from 24-hour food records.
- We aimed to determine if these patterns corresponded with microbial features.

Methods

Subjects

- Daily fecal samples and daily 24-hour food records (ASA24-2016) for 17 days.
- n = 32 healthy adults.

Dietary Patterns

- Foods were arranged into a tree structure (FNDDS, Fig 1).
- Tree-based weighted UniFrac food distances (QIIME 1.9.1) were used for principal coordinate analysis to define five dietary patterns.

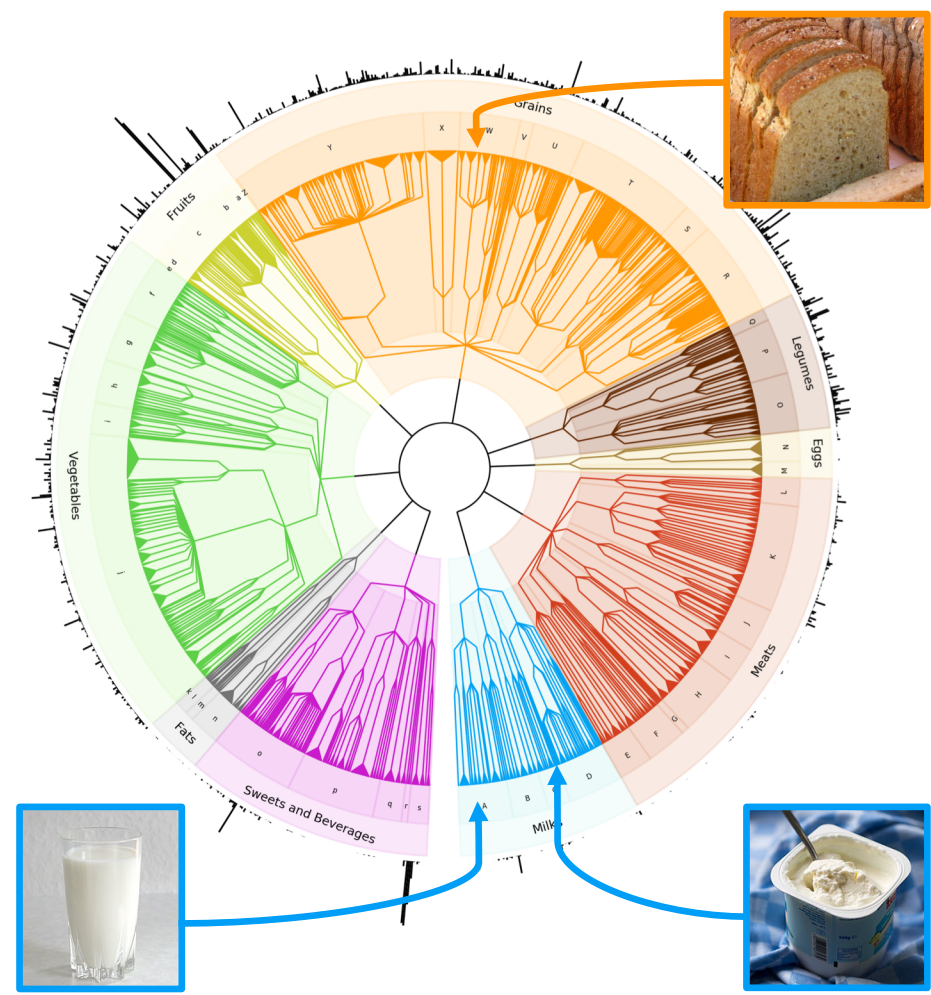
Microbiome composition

- Average microbiome composition was determined from metagenomic sequencing (Fig 2).

Statistical assessment

- Spearman correlations were calculated between dietary patterns and taxonomy and were corrected for multiple comparisons within each taxonomy level using FDR.
- Constrained redundancy analysis (RDA) was used to determine the explanatory power of dietary patterns.

Figure 1: A tree of foods for dietary analysis



The phenetic, hierarchical tree of foods is built from the Food and Nutrient Database for Dietary Studies (FNDDS) using the USDA's food codes and food grouping scheme. It can be used to apply tree-based analysis metrics of alpha and beta diversity to dietary data.

Results

- Four of the five most discriminatory dietary patterns (DPs) were associated with microbial taxa (Fig 3).
- Constrained RDA using the five dietary patterns revealed a gradient of Phylum *Bacteroidetes* along an axis driven by DP3, DP4, and DP5 (Fig 4).

Discussion

The dietary patterns derived using our tree-based method reveal relationships between diet microbial taxa. In agreement with previous studies, our tree-based patterns show that the western diet corresponds to increased *Bacteroidetes*, demonstrating the utility of this method.

Funding

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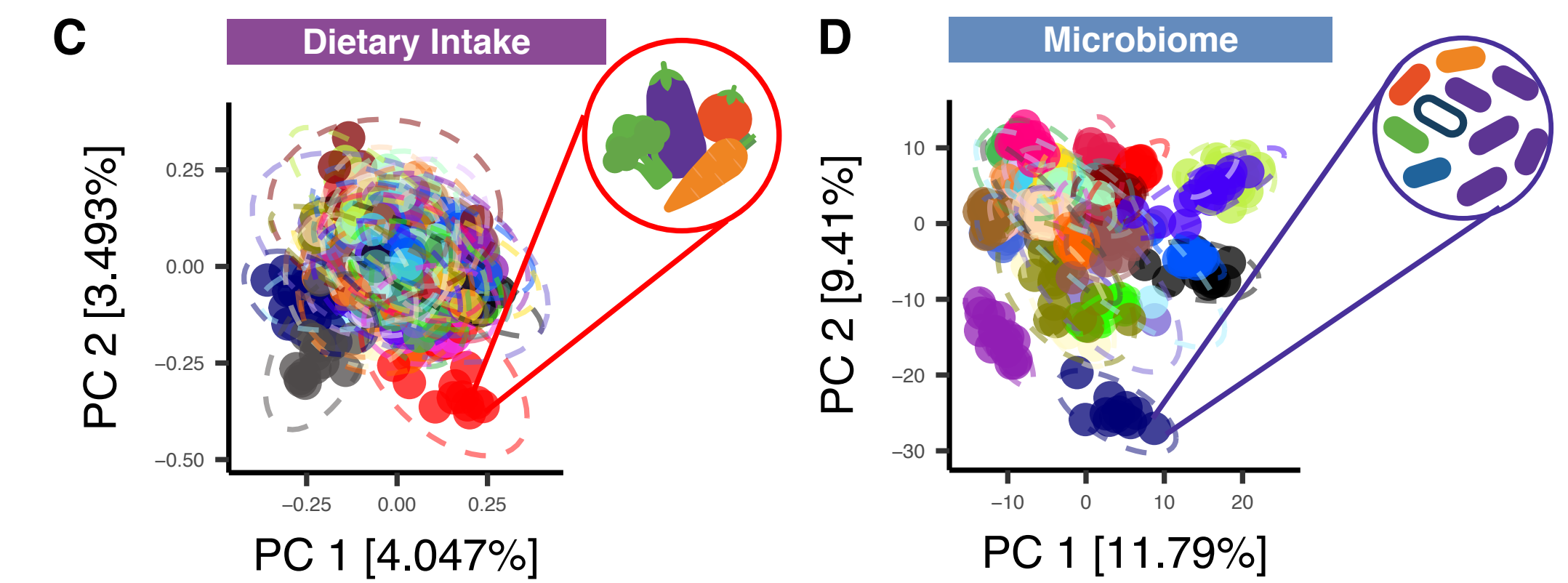
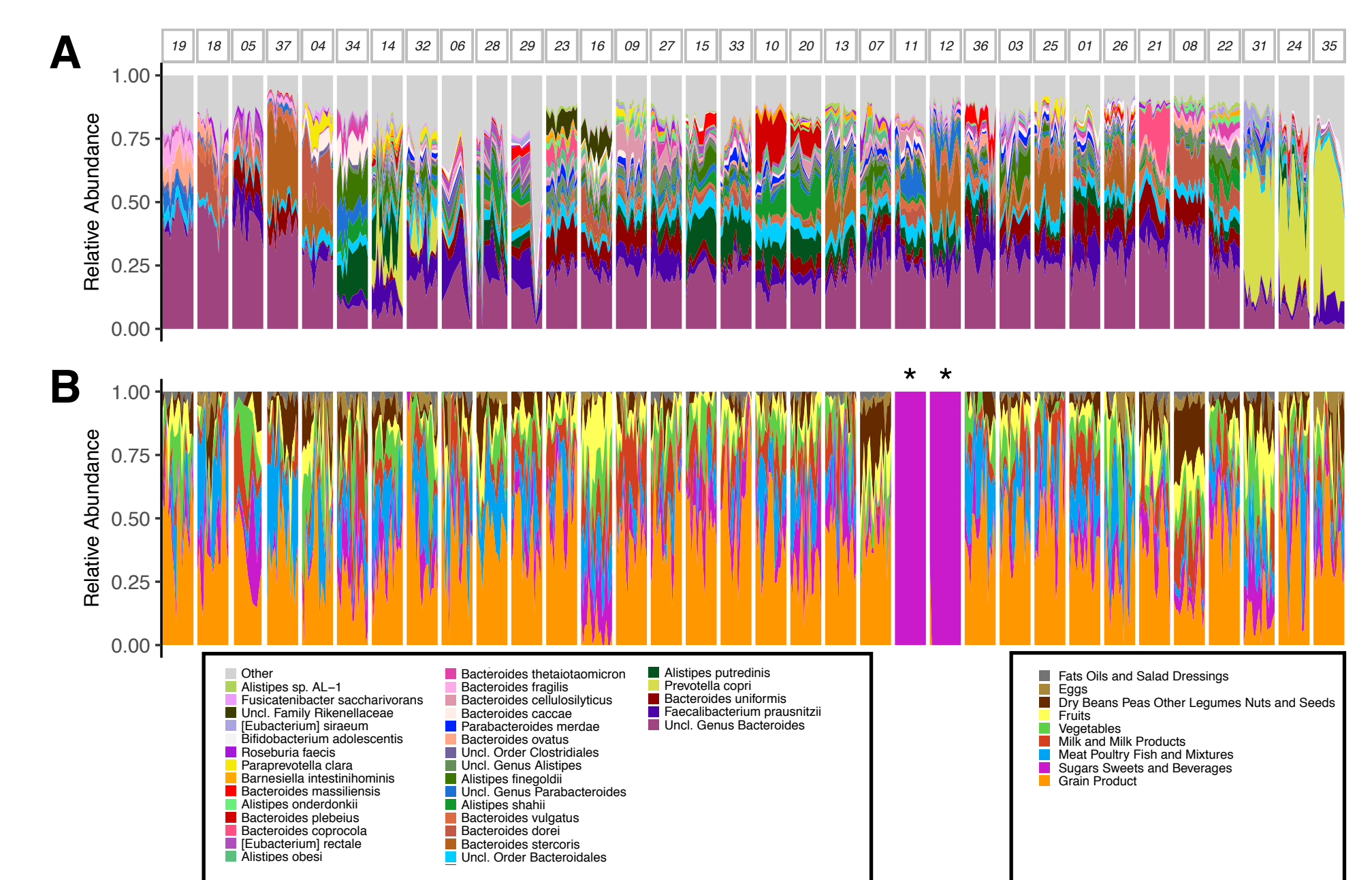
Dietary patterns are correlated with microbiome composition in humans.

This improves when dietary patterns are defined using methods that share information about food relatedness.



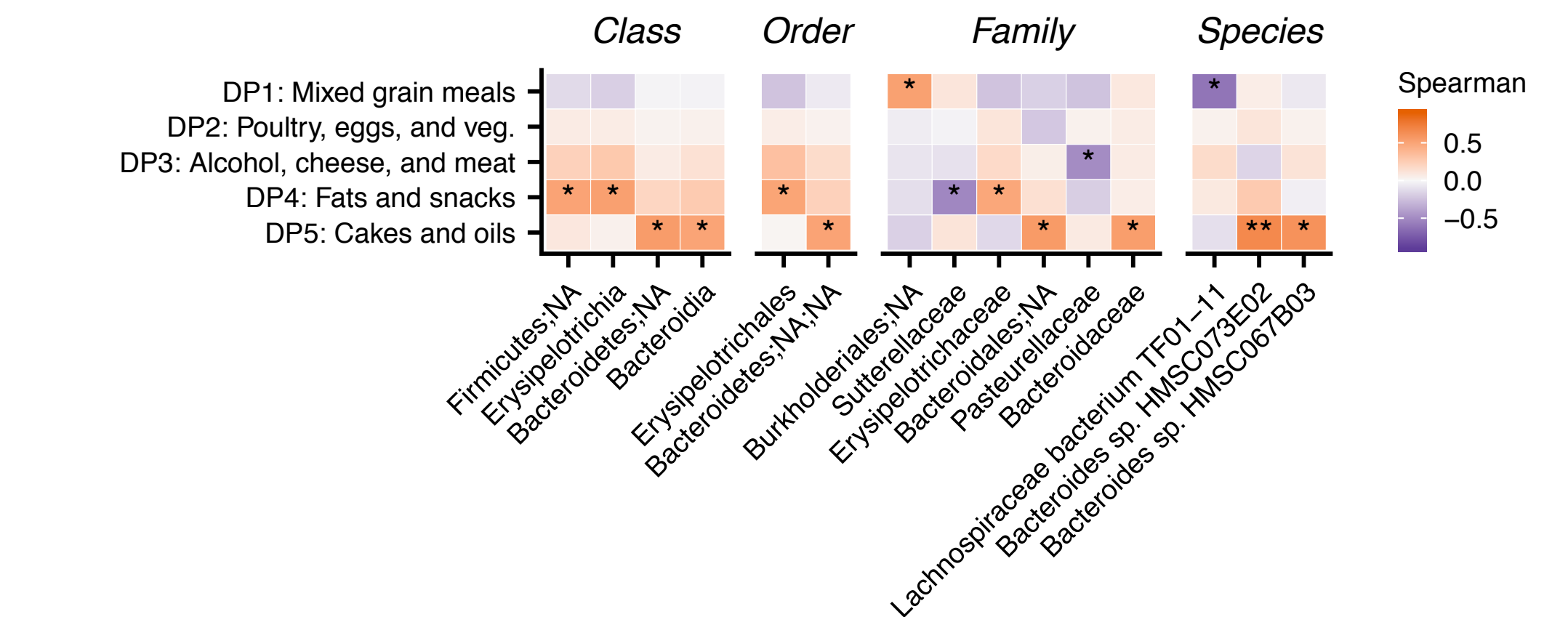
Results Figures

Figure 2: Dense, daily dietary intake and microbiome



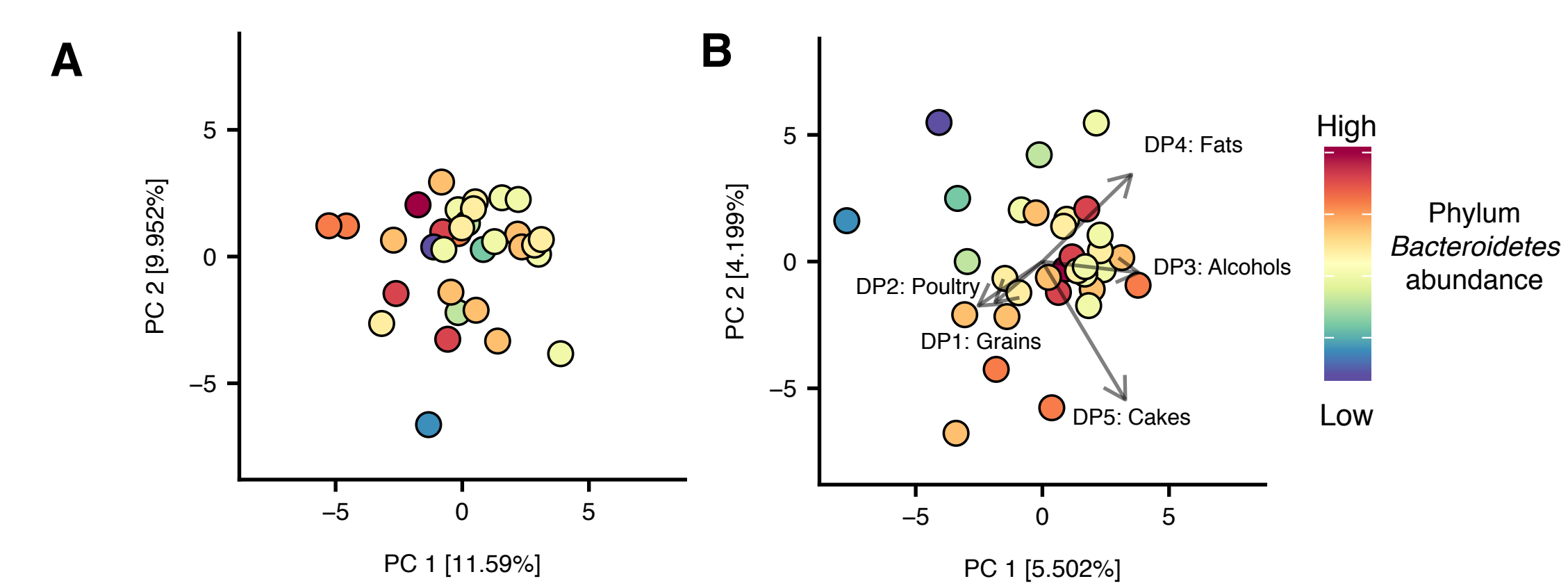
Relative abundance of (A) bacterial taxonomy and (B) food groups for 34 people over 17 days shows clustering of both diet (C) and microbiome (D) by person when using unweighted UniFrac for food beta diversity and Aitchison's distances for microbiome beta diversity. * Meal replacement beverage subjects (11 and 12) are excluded from downstream analysis.

Figure 3: Tree-based dietary patterns correlate with microbiome composition



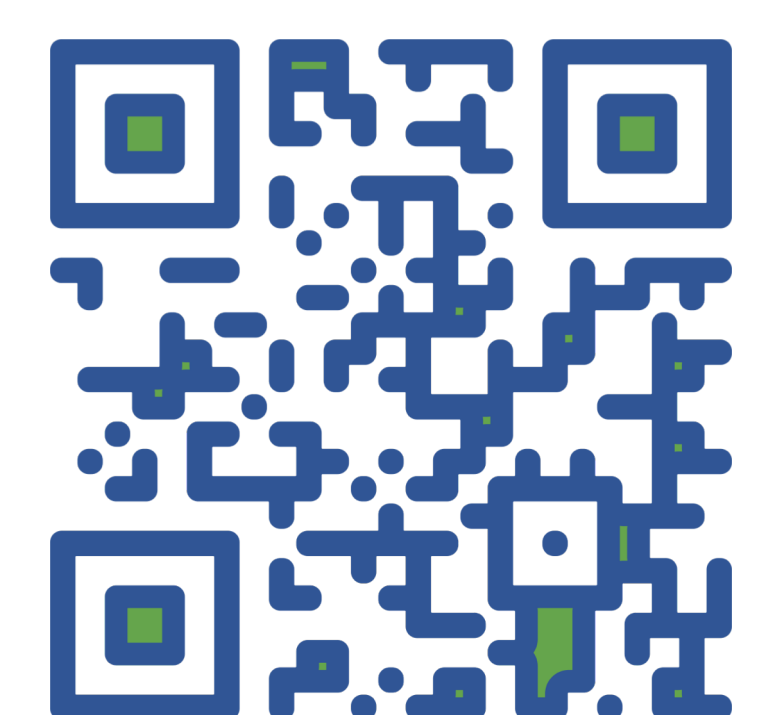
Dietary patterns defined from average dietary intake using weighted UniFrac are correlated with average microbiome composition. Spearman correlations; * denotes corrected $p < 0.2$, **corrected $p < 0.05$; adjusted for multiple comparisons within taxonomic level using FDR.

Figure 4: Dietary patterns explain ~50% of variation in microbiome composition



Average microbiome composition (A) constrained by Weighted UniFrac dietary patterns (B) show that diet explains 47% of the variation in microbiome and reveals a gradient of *Bacteroidetes* abundance.

Want to learn more?



z.umn.edu/dietstudy