

Dietary Predictors of the Human Gastrointestinal Microbiome

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Introduction

- Diet influences the composition of the gastrointestinal (GI) microbiota.
- The impact of specific foods and nutrients on the GI microbiota is under-investigated.
- Research utilizing modern statistical multivariate methods is needed to understand complex host-microbe interactions.

Objectives

Utilize multivariate approaches to:

- 1) Validate results generated by prototype software with previously published results, and
- 2) Identify novel associations among dietary and bacterial features.

Methods

Data generated from a clinical dietary intervention study that included:

- Daily dietary intake records
- Diet history questionnaires
- Fecal bacteria and metabolite data

Data analyses:

- Multivariate approaches that address $P \gg N$, many features but few samples, were used.
- Random Forest identified relevant microbial operational taxonomic units (OTU), bacterial metabolites, and food and nutrient data.
- Maximal Information Coefficient determined relationships among relevant features [2].

Results

Figure 1. Validation of multivariate statistical results (A,C) through comparison with previously published results (B,D).

Feature	Relevance (%)
Positive H ₂	100
Net H ₂	100
Bifidobacteriaceae	99.9
<i>Bifidobacterium</i>	99.9

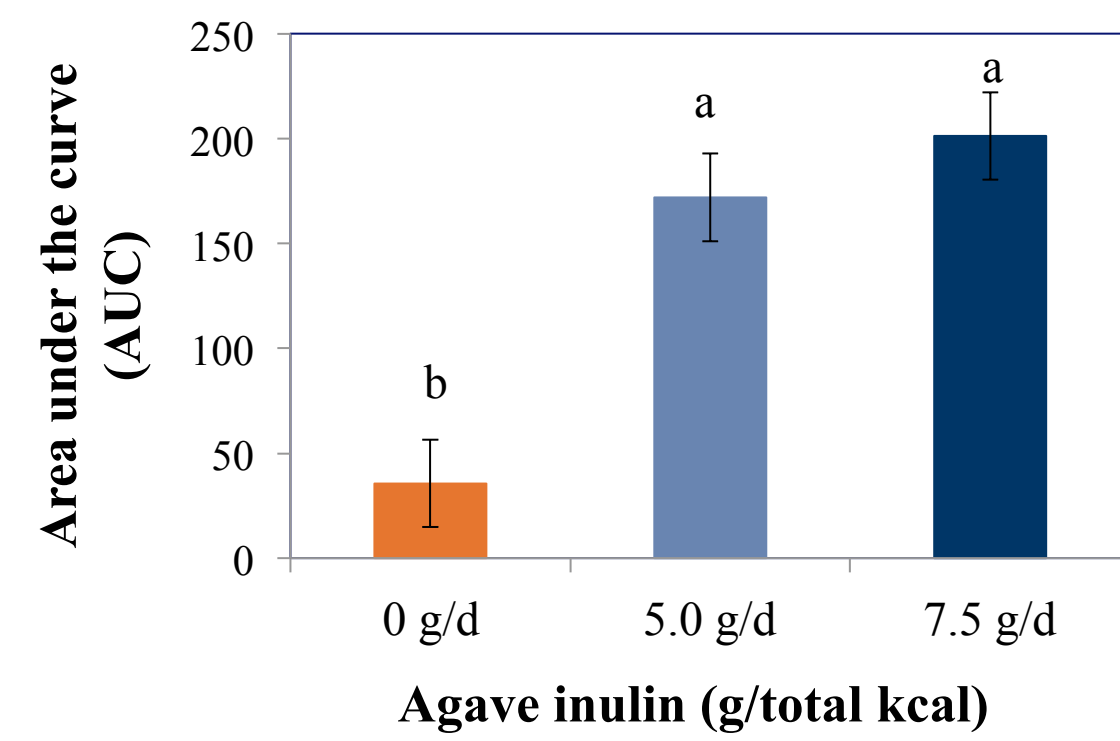


Figure 1A. Random Forest plots revealed relevant features for the prediction of participant treatment group (0,5, or 7.5 g of agave inulin).

Figure 1B. Postprandial breath H₂ response for adults consuming 0, 5 or 7.5 g of agave inulin in a crossover design. AUC was calculated using 0-8 hour breath H (ppm) values. Values are means $\pm$ SEM, n=29 [1].

Feature	Relevance (%)
Positive H ₂	100
Net H ₂	100
New Fiber	100
Agave Inulin	100

Figure 1C. Random Forest plots revealed relevant features for prediction of *Bifidobacterium* abundance.

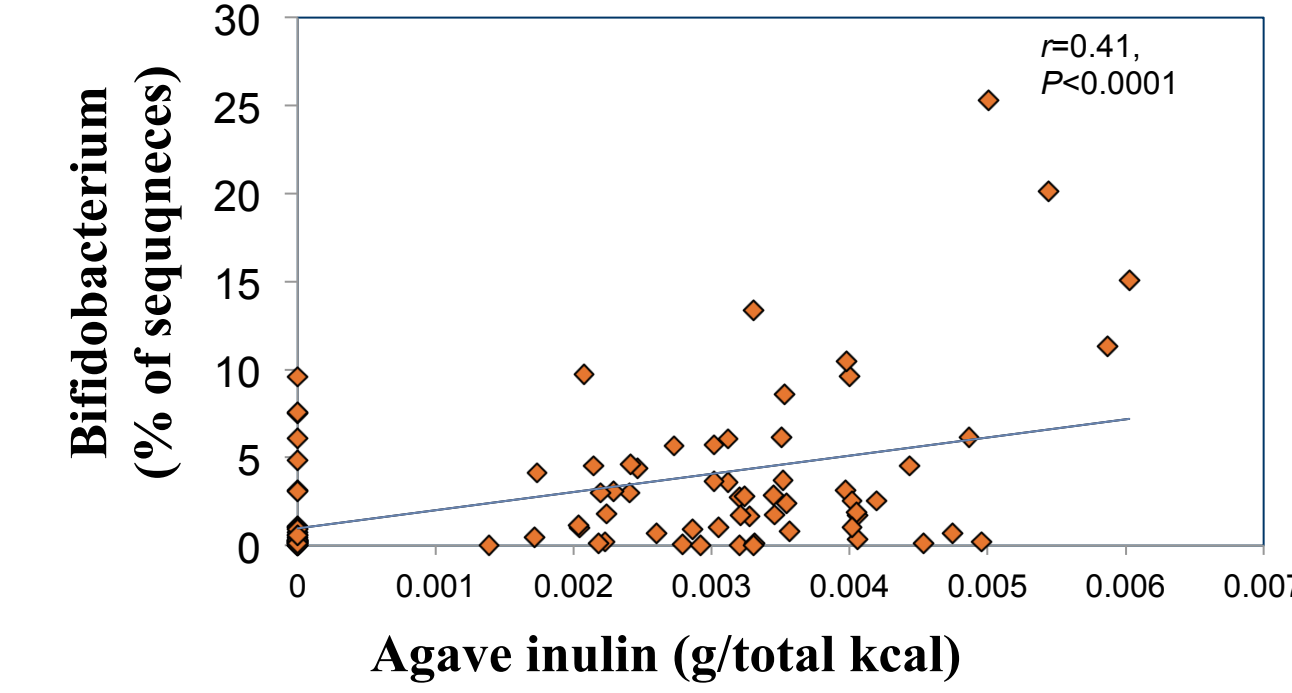


Figure 1D. Scatterplots depict relationship between fecal *Bifidobacterium* and grams of agave inulin/d in human participants consuming 0, 5.0, or 7.5 g agave inulin/d in a crossover design [1].

Figure 2. Relevant features for predicting human fecal *Faecalibacterium* abundance

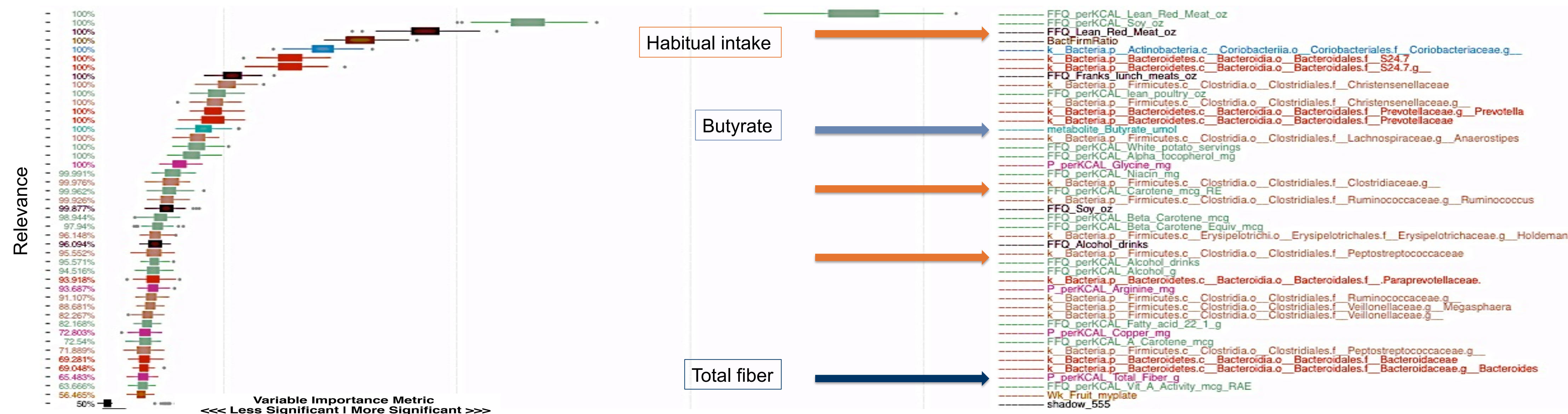
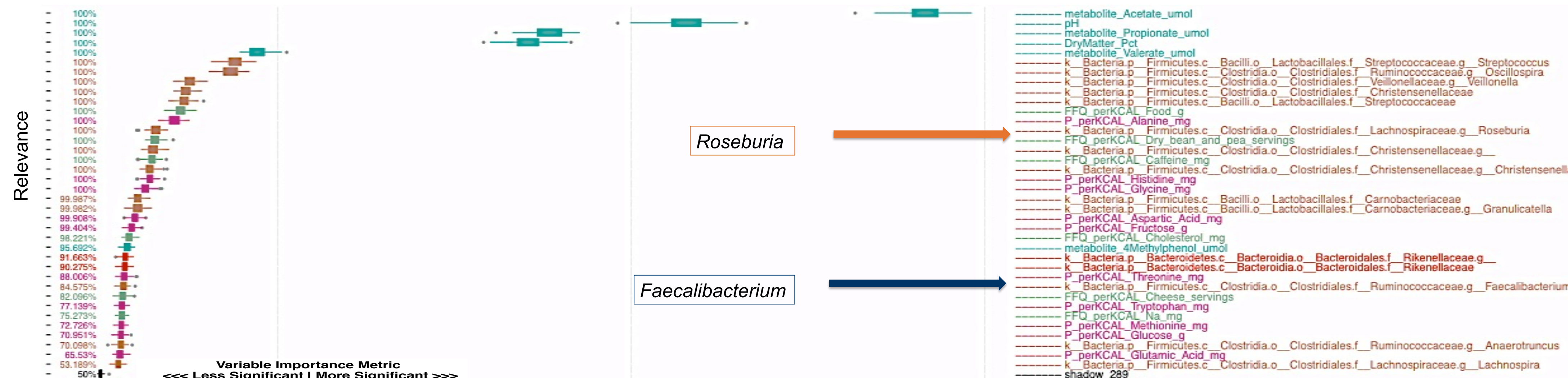
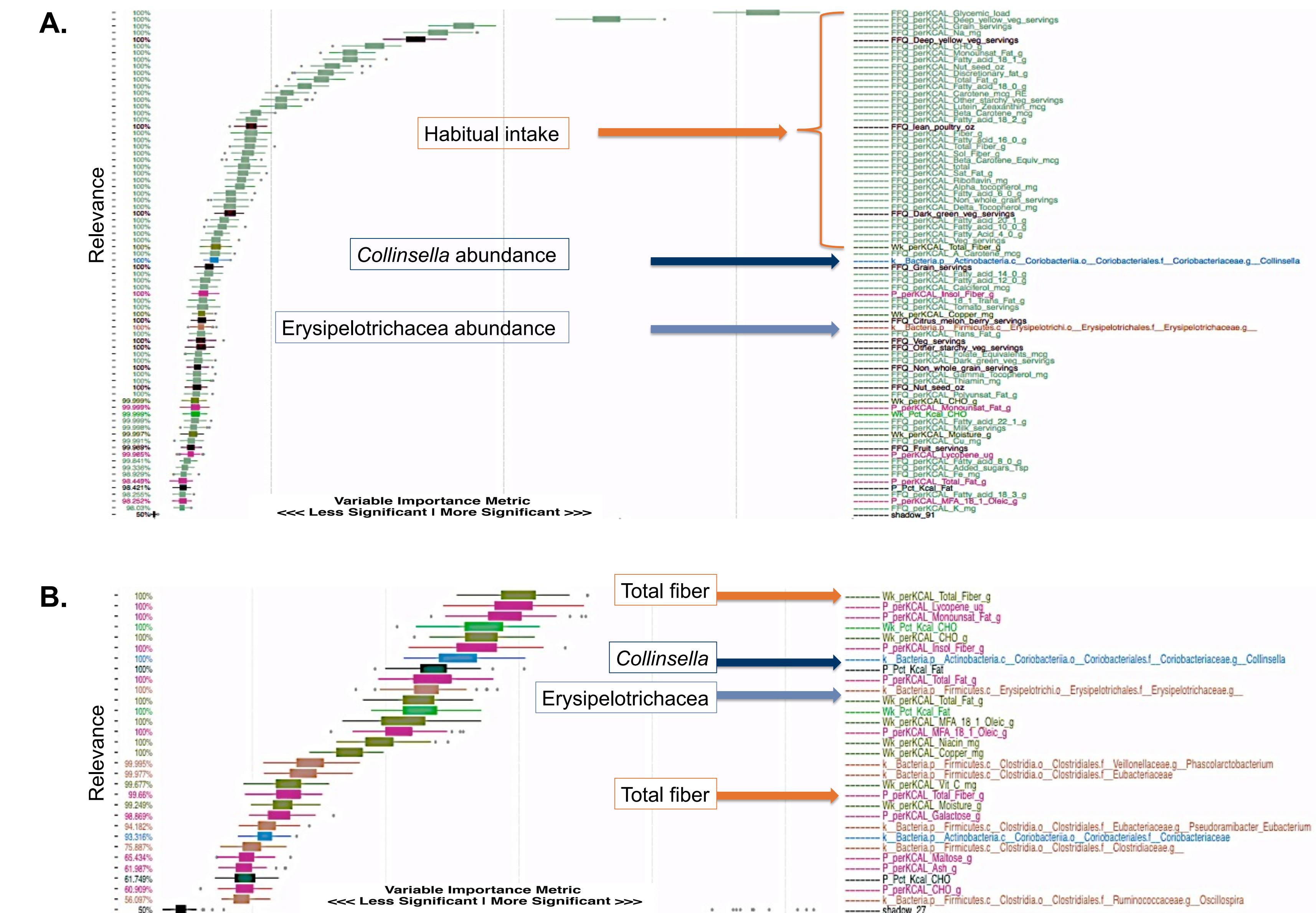


Figure 3. Relevant features for predicting human fecal butyrate concentrations



Results

Figure 4. Relevant features for predicting human BMI (A) including and (B) excluding habitual diet



Conclusions

- Findings revealed similar associations among diet, microbiota, and breath hydrogen measures as previously published results [1].
- Diet history questionnaire alone may be sufficient to characterize global diet-microbiome relationships; however, treatments aimed at modifying specific microbial communities require detailed dietary records to delineate relevant relationships.
- Further research is needed to identify an optimal set of highly relevant features for diet-microbiome studies.

References

1. Holscher HD, et al. Agave Inulin Supplementation Affects the Fecal Microbiota of Healthy Adults Participating in a Randomized, Double-Blind, Placebo-Controlled, Crossover Trial. Journal of Nutrition 2015.
2. C. B. N. R. Michael Welge, "Feature Interaction Detection with Random Forest in a High Dimensional Setting," in Individualizing Medicine Conference, Rochester, 2014.

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