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Integrative data analysis of genotype, microbiome and metabolomics for prediction of response to diet for improved metabolic health

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Diet is known as an important factor for metabolic health. This study investigated the impact of a whole grain-rich diet (75 g/d)/gluten-poor diet (< 2g/d) or refined grain diet (< 10g/d) on metabolic health in 102 healthy adult participants with a metabolic risk profile (40 male, 62 female). Intervention diets were consumed for 8 weeks followed by the opposite diet after an at least 6 weeks 'wash-out' period. Anthropometric measurements, biochemical blood samples, gut microbiome profiling, urine metabolites and host genetics were obtained in the beginning and end of each intervention. The whole grain-rich and gluten-poor diets induced statistically significant weight loss on the groups. However, response to diet is not universal across all individuals and is suggested to be influenced by a complex interplay between the host genome, gut microbiota and environment [1]. To further study personal response to diet, we integrated in this post hoc analysis data into machine learning models to predict weight loss from baseline markers (204 observations). The work is ongoing and identification of metagenomic species' interaction with host genotype and metabolite changes are expected to generate hypotheses of the personal response to diet using feature importance. Integration strategies are evolving and have involved use of top predictive features for each data type or pre-selecting features based on pathway information. The machine learning framework indicates that differences in the baseline gut microbiota partly explain the observed host physiological response. In addition to the weight loss, we are also examining immune markers as additional indicators of metabolic health outcome.

References
[1] Dabrowska et al, 2016. PMID: 27625642.