A Dynamic microbiome and metabolomics data

60 mice from 4 vendors

7 days acclimatization

+Cellulose → days: 0 1 3 5 8 13 19 25 31

+Resistant starch → days: 0 1 3 5 8 13 19 25 31

+Inulin → days: 0 1 3 5 8 13 19 25 31

16S rRNA sequencing
SCFA quantification
quantitative PCR
metagenomics sequencing
Body weight/food intake

B Systems data modeling and analysis

Ecological network inference

$$\frac{d\log(x_i(t))}{dt} = \alpha_i + \sum_j \beta_{i,j}x_j(t) + \epsilon_i u_i(t)$$

ϵ_i: diet response $\beta_{i,j}$: pairwise interaction

positive responder
no response
negative responder

0

+ 0 −

Metabolic function prediction

Machine learning model

predicted SCFA vs observed SCFA

SCFA producer

Species

C

Beijing   Guangdong

Hunan   Shanghai

Relative abundance (%)

Family level:
Muribaculaceae
Lachnospiraceae
Bacteroidaceae
Tannerellaceae
Ruminococcaceae
Deferribacteraceae
Erysipelotrichaceae
Prevotellaceae
Desulfurobacteriaceae
Rikenellaceae
unclassified Clostridia vadinBB60 group
Sutterellaceae
Oscillospiraceae
Akkermansiaceae
Helicobacteraceae
Others

D

Guangdong

Hunan

Shanghai

Beijing

$R^2 = 0.83$
$P < 0.001$

PCoA 1 (70.43%)

PCoA 2 (27.8%)