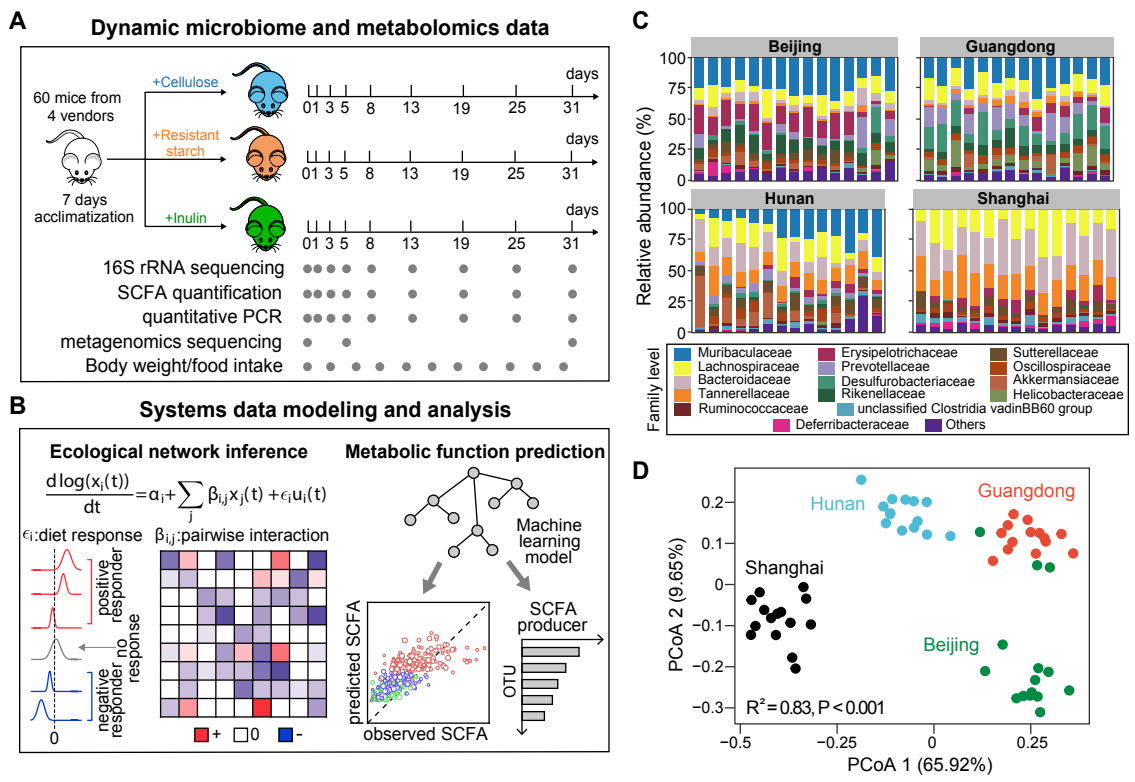
A
Dynamic microbiome and metabolomics data
60 mice from 4 vendors
7 days acclimatization
+Cellulose
+Resistant starch
+Inulin
days
01 3 5 8 13 19 25 31
16S rRNA sequencing
SCFA quantification
quantitative PCR
metagenomics sequencing
Body weight/food intake
B
Systems data modeling and analysis
Ecological 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
SCFA producer
OTU
predicted SCFA
observed SCFA
C
Beijing
Guangdong
Hunan
Shanghai
Relative abundance (%)
100
75
50
25
0
Family level
Muribaculaceae
Lachnospiraceae
Bacteroidaceae
Tannerellaceae
Ruminococcaceae
Erysipelotrichaceae
Prevotellaceae
Desulfurobacteriaceae
Rikenellaceae
unclassified Clostridia vadinBB60 group
Deferribacteraceae
Others
Sutterellaceae
Oscillospiraceae
Akkermansiaceae
Helicobacteraceae
D
Hunan
Guangdong
Shanghai
Beijing
PCoA 2 (9.65%)
PCoA 1 (65.92%)
0.2
0.1
0
−0.1
−0.2
−0.3
−0.5
−0.25
0
0.25
$R^2 = 0.83, P < 0.001$