**Baseline microbiota modulates prebiotics-mediated ecological dynamics of gut microbiota and SCFA metabolism**

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**Abstract**

Fiber intake indirectly promotes human health via gut microbiome and associated metabolism but the effects are highly personalized. While many factors are possibly at play, the well-documented individuality has been mostly associated with baseline microbiota before dietary intervention. However, little is known about the fiber-induced ecological dynamics of gut community and its baseline dependence, thus precluding in-depth understanding of the end-point response heterogeneity. Here we supplied inulin to isogenic mice that carry 4 distinct baseline microbiota for 4 weeks and longitudinally profiled microbiome and short-chain fatty acids (SCFAs) in absolute abundance. Despite the microbiota and SCFAs share consensus two-phase responses—short-term rapid stimulation and long-term partial recovery, we confirmed that the dynamical shifts in the total bacterial load, butyrate and propionate concentrations are indeed baseline-dependent. By combining statistical inference and ecological modeling, we revealed a subcommunity of 7 bacterial responders that almost fully determines the dynamics of microbiota and the relative profiles of these taxa were largely controlled by their baseline abundances and interspecies competition. Despite a challenge in accurate prediction of SCFAs from gut microbiota, we provided statistical evidences that the previously found correlations of baseline microbiota or total bacterial load with propionate may be mediated by these key respnders. Finally, we demonstrated that the major findings from inulin can be generalized to resistant starch. Our study emphasizes the importance of ecology and quantitative modeling in mechanistic understanding of the personalized human responses to dietary fiber.

~~Gut microbiome is a complex ecosystem. Prebiotics such as dietary fibers can lead to system-wide shifts in microbiota composition and metabolic capacity. There is growing evidence that the response to prebiotics intervention is dependent on the baseline gut microbiota, yet the underlying dynamical process remains largely unclear. To understand the dynamical response of gut microbiota to prebiotics, we treated isogenic mice of distinct baseline gut microbiota with dietary fibers (inulin, resistant starch) and tracked the dynamics of fecal microbiome and short-chain fatty acids (SCFAs) over four weeks. Across different baseline microbiota, inulin induced a larger increase in SCFAs than resistant starch. Moreover, we observed a general pattern of bi-phasic response in microbiota diversity and SCFAs, which changed rapidly in the short term and then returned to the steady-state level. Using the generalized Lotka-Volterra model, we identified a small group of bacterial taxa as inulin responders, which collectively shaped the ecological dynamics in response to dietary shifts. We found that the dynamics of ~20% bacterial taxa was dependent on the baseline microbiota composition. Finally, we showed that the strong heterogeneity in baseline gut microbiome posed a great challenge to the prediction of SCFA profiles from gut microbiota, in accordance with previous studies in human. Our study reveals that the baseline microbiota composition modulates the dynamical response to prebiotics, calling for further studies on the role of gut microbiome in personalized nutrition.~~

**Keywords:** gut microbiome, dietary fiber, ecological dynamics, short-chain fatty acids, baseline-dependent dependence, generalized Lotka-Volterra

**Introduction**

Fermentable dietary fibers such as inulin and resistant starch are edible carbohydrate polymers that can escape colonic digestions in the small intestine but are fermented by gut microbiota in the large intestine. Human gut microbiome harbors hundreds of trillions of microbes and their associated metabolism that co-evolve with us. The major anaerobic fermentation products of gut bacteria in the large intestine are short-chain fatty acids (SCFAs). SCFAs, mainly acetate, propionate and butyrate, have broad impacts on human host physiology (e.g., stimulate glucagon-like peptide-1 secretion), immune system (e.g., regulate expression of pro-inflammatory cytokines) and intestinal homeostasis (e.g., serve as energy sources for colonocytes) [1]. Converely, impaired SCFAs production has been associated with gut microbiota dysbiosis and a wide range of dieseases [2][3][4]. To increase intestinal levels of SCFAs and eventually improve overall digestive health, some fiber molecules have been considered as “prebiotics” and made commercially available based on the premise that they can selectively enrich beneficial SCFA-producing bacteria. To test this hypothesis, diets supplemented with prebiotics have been administered as a therapeutic strategy to modulate and restore intestinal gut microbiota and SCFA levels in clinical trials.

To date, it has been well established that prebiotics can rapidly alter gut microbiota composition, including both relative abundance of individual bacteria and their total load. However, their efficacy in stimulating SCFAs remains unclear yet. Several clinical trials of healthy adults have collectively revealed that the ability of prebiotic fibers to produce SCFAs varies among individuals [9-12]. For example, Baxter et al. shows that resistant starch was able to promote butyrate production in only 63% participants [10]. Although the individualized response can arise from a combination of factors such as genetics and diet history, there is growing evidence that baseline gut microbiota is a critical factor in explaning the observed heterogeneity at multiple levels [12, 13]. The reason for the inter-individual variation in fiber consumption can be explained by the presence and absence of key fiber-degrading bacteria. One famous example is the degradation of resistant starch by *Ruminococcus brommi* and the impaired ability of healthy human donors’ fecal samples to ferment resistant starch can be *in vitro* restored by their co-incubation with *R. brommi*. The baseline dependence of microbiome and metabolome variations was much less understood, though a few studies have attributed this individuality to the lack of specific keystone species (e.g., SCFAs producers) or the overal structural differences in the baseline community. The variations in gut multi-omics can further propogate to human host, resulting in heterogenous clinical outcomes such as body mass index and glucose tolerance.

As externally provided substrates, intake of dietary fibers perturbs ecological niche of substrate utilization in the gut and thus selects for specific shifts away from the baseline composition. We propose that the compositional shift in time can be abstracted by the dynamics of a baseline-specific ecological network selected by the environmental change and its infleunces on bacterial fitness and interactions (Fig. 1A). Several robust characteristics of ecological responses of gut microbiota to dietary fiber have been found so far. First, consumption of fibers selectively enriches a limited number of bacteria which rapidly expand and dominate the biomass of gut microbiota after substantial induction. In healthy people, *Bifidobacterium* species are one of few bacteria whose abundance consistently increases following intake of diverse fibers. Second, competitative interactions shape the relative profiles of these key bacteria. By administering multiple fibers to the murine gut, Patnode *et al.* identified competitive inhibition as the ecological mechanism for consistent dominance of *Bacteroides cellulosilyticus* over *Bacteroids vulgatus* even though both species contain fiber-processing polysaccharide utilization loci (PULs). Third, production of SCFAs, especially butyrate, involves cross-feeding cooperations among specialized gut bacteria (Fig. 1A). By hydrolyzing complex polysaccharide fibers, primary degraders release into the gut environment the breakdown products (e.g., mono- and oligo-saccharides) and fermentation metabolites (e.g., pyruvate), which can respectively benefit the secondary fiber degraders and SCFAs producers [5, 6, 7, 8]. Despite these invaluable insights, our knowledge about the fiber-induced ecological dyanmics and its dependence on baseline microbiota composition remains limited.

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n this study, we used age- and gender-matched isogenic mice that harbor distinct baseline gut microbiota composition to study its ecological dynamics in response to dietary interventions and the inter-individual variation within these dynamical trajectories [19]. Murine models, as a complimentary alternative to clinical trials on humans, has better controls over confounding variations between individuals driven by genetic, environmental and other host differences. We monitored temporal shifts in the absolute abundance of gut bacteria and genes (quantitative PCR, 16S rRNA amplicon sequencing, metagenomics sequencing), SCFAs concentration (targeted metabolome) as well as physiological changes following the intervention of two fermentable fibers (inulin, resistant starch from maize) and cellulose (control group) (Fig. 1B). Both inulin and resistant starch are degraded by gut bacteria in the cecum and colon [20, 21], and thus have been harnessed to stimulate the production of SCFAs [10, 22]. Motivated by the hypothesis that individualized dynamics of gut microbiota and SCFAs are primed by the baseline microbial community (Fig. 1A), we developed two computational approaches that employed time series data to analyze the heterogeneity in dietary responses and study its relationships with baseline composition. As the major findings, we showed that the total bacterial load and propionate concentration exihibit baseline-dependent responses which can be linked to the abudnances of a few fiber-responsive bacteria in the baseline community. The abundances of these key bacterial responders constitute the majority of total bacterial load and their short-term responses are controlled by the individual’s ability of fiber degradation and fiber-induced interspecific competition. Our study indicated that ecological inference of keystone bacteria from longitudinal data is critical for understanding the differential responses of gut microbiota to dietary fiber and other perturbations.

**Results**

**Heterogenous baseline gut microbiota composition across different vendors**. Age- and gender-matched isogenic mice were purchased from four commercial vendors (Beijing, Guangdong, Hunan, Shanghai), i.e. independent breeder sources. All mice were fed with cellulose-based diet 7 days prior to dietary fiber intervention. Consistent with previous studies [23, 24], these mice can be naturally divided by vendor sources into groups with distinct microbiota composition. Beta-diversity (between-sample distance) calculated by Aitchison distance shows that the baseline compositions of our mice cluster by vendor (Adonis, *P* < 0.001) and are characterized by distinct bacterial taxa (Fig. 1B). For example, Shanghai mice have low relative abundances of several commensal polysaccharide-degrading bacteria such as *Muribaculaceae* and *Rikenellaceae* [25, 26]. The profound inter-vendor difference (Adonis, *P* < 0.001) was also observed at the family level (Fig. S1). all 58 , (Fig. 1C). Due to the high between-vendor variation, mice from the same vendor can be effectively considered as independent biological replicates for each baseline microbiota composition.

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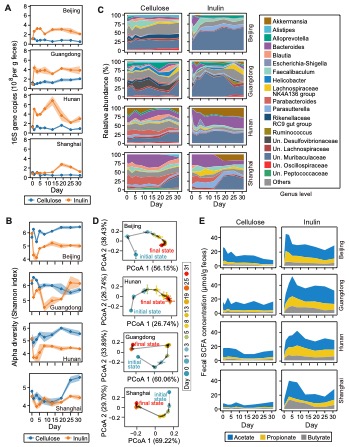
**Figure 1. High-resolution temporal profiling of murine gut microbiota and metabolome to study their individualized responses during dietary fiber intervention.** **A**. An ecological perspective of baseline-dependent dynamical responses of gut microbiota and SCFAs. Administration of dietary fibers alters ecological substrate niche in the gut and selects for an unique ecological network for each baseline microbiota type. Within the network, a few gut bacteria playing key metabolic roles as primary/secondary degraders and SCFAs fermenters drives heterogenous responses of bacteria and SCFAs via diverse ecological interactions (e.g., resource compeitition and cross-feeding). **B**. Experimental design. All mice from the four vendors were continuously fed with either dietary fiber (inulin or resistant starch)- or cellulose-supplemented diets for 4 weeks. Gray dots indicate the days on which data were collected from fecal samples. **C**. Baseline microbiota composition shown in robust PCoA (principal coordinate analysis) biplot. Isogenic age- and gender-matced mice were purchased from four different vendors (Beijing, Guangdong, Hunan, Shanghai). Gray arrows represent the dominant bacterial taxa in these samples. Adonis analysis was performed to test for differences in baseline gut microbiota composition across four vendors (P<0.001). Un.: unclassified/uncultured. **D**. Top 4 panels: pwhite boxes indicates absence and abundance (colored boxes) the same samples. Bottom panel: tall ) or ).

**Two-phase dynamics of gut microbiome and SCFA metabolism**. Dietary intake of inulin increases mice body weight gradually over time, but the amount of body weight gain is generally insignificant compared to mice treated with the cellulose control (Fig. S2A). Although there were no obvious temporal patterns in the inulin intake (Fig. S2B, C) and fecal weight (Fig. S2D), the fecal weight was dramatically lower in inulin-fed mice, suggesting that intestinal absorption of inulin may cause increased colonic transit time and decreased defecation frequency. Except for Shanghai mice, the inulin absorption nourished gut microbes by rapidly (in a day) boosting their density to more than 70% of maximum load (Fig. 2A). More interestingly, inulin induced a qualitatively consistent two-phase dynamics of microbiota (Fig. 2B)rapidly in the short-terma in the long-term (i.e., undershoot)CTinitial loss of it (largely) Notably, the long-term recovery is only partial for Beijing and Hunan mice with much lower gut microbiota diversity at day 31 compared to day 0.

In addition to phase-dependent responses, we also found strong tendency of gut microbiota composition to stabilize under sustained stimulation of inulin (Fig. 2D). Regardless of the baseline microbiota, the steady-state compositions are distinct from their baselines and thus represent new equilibria sustained by inulin intake. Specifically, the gut microbiota in Guangdong mice was highly resilient to inulin intervention and almost returned to its baseline composition at day 31. In addition, inulin, and even cellulose, reduced baseline microbiota differences by ~35% at day 31 (Fig. S4B), suggesting that long-term dietary fiber intervention promotes adaptative convergence of baseline microbiota towards similar composition between different vendors. The adaptation is also evident in the dynamics of the dominant bacterial taxa. For example, the relative abundance of unclassified *Muribaculaceae* in Shanghai mice was initially much lower at day 0 but finally reached similar levels as in the mice from the other three vendors at day 31 (Fig. 2C).

To quantify the rate of stabilization, we fit a harmonic oscillator model (Eq. 1-2) from physics to time series of biodiversity and calculated damping ratio—a dimensionless measure of whether and how dynamical systems approach new steady states upon perturbations—from the best-fit parameters (see Methods, Table S1). The model fits the data reasonably well with mean R2 of 73% (Table S1, Fig. SX). The damping ratios are all equal or greater than 1, meaning that their responses were critically or overdamped and no oscillations were involved in the adaptive responses. The oscillation-free property is critical for ecosystems to maintain dynamic stability and integrity during adaptation. Although the damping ratio varies among individual mice and treatment, the dynamical responses of 42% of our mice were critical damping which leads to the fastest non-oscillatory convergence towards stationary equilibria. Interestingly, the critical damping behavior was also found in human gut microbiome recovery after transient antibiotic exposure [31].

Supporting the biphasic responses of gut microbiota composition, metagenomic sequencing also revealed that the initial (day 0), short (day 5)- and long (day 31)-term microbiomes have distinct gene family profiles and functions (Fig. SXA). Particularly, for inulin hydrolysisSXB Consistently, we observed a strong stimulating effects of inulin on SCFAs production. The averaged peak concentraitons of total SCFAs are as high as 3x, 1x, 2x and 5x of their baseline levels for Beijing, Guangdong, Hunan and Shanghai mice respectively. Since SCFAs are metabolites produced by colonic bacterial fermentation of inulin, we expect a similar biphiasic dynamics of fecal SCFAs concentration. Indeed, the inulin-induced changes in fecal concentrations of both total and the three major SCFAs also show two temproal phases (Fig. 2E): their levels peaked in short-term before gradually decreasing until steady states (i.e., overshoot), with an exception of Shanghai mice whose propionate production was notably delayed and compromised. Despite reduced SCFAs in the second phase, the mean endpoint level of total SCFAs at day 31 still remains 60%-65% of its peak and 2.0-3.5 times as high as its baseline level at day 0. We confirmed that the long-term decrease in fecal SCFA concentration was not a result of reduced diet intake as the intake rate remains largely unchanged over time (Fig. S2B, C).

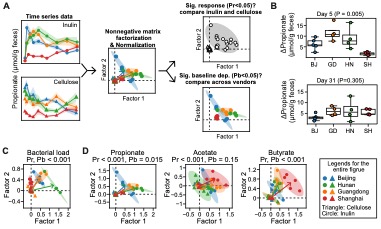


**Figure 2.** **Inulin-induced temporal changes in murine gut microbiota and SCFA metabolism. A.** Tload. **B.** Alpha diversity. **C.** Bacterial composition at the genus level. **D.** Bacterial composition represented by robust PCoA (principal coordinate analysis) plot. Initial and final state represent **E.** Fecal concentration of three major SCFAs. Beijing, Guangdong, Hunan, Shanghai are four different mice vendors. The heights of stacked bands (panels A, C), lines (panel B) and dots (panel E) represent the mean values across mice within the same vendor. Shading areas (panel B) and error bars (panel E) represent standard error of the mean. E. Un.: unclassified.

**total bacterial load and two major SCFAs** had delayed increase in bacterial load2A and produced low levels of propionate (Fig. 2E) in response to inulinThe distinct behavior of Shanghai mice indicated that the responses of total bacterial load and SCFAs may depend on the vendor, i.e., baseline microbiota. test if they (and any measured quantity) exihibit baseline-dependent responsesdeveloped a novel framework that separately tests for the significance of two orthogonal concepts, “baseline dependence” and “responsiveness”, based on the longitudinal data from intervention and control group (see Methods). As shown in a schematic diagram (Fig. 3A), both groups of time series are first transformed into a 2-dimensional space by non-negative matrix factorization. Using the low-dimensional data representation, we then obtained two *P*-values by comparing the differential responses between the intervention and control group (“responsiveness”, *Pr*) as well as those between the four vendors (“baseline dependence”, *Pb*). We concluded a quantity has a baseline-dependent temporal response if both *P*-valus are smaller than 0.05.

Our approach has three advantages. First, the use of time series data improves our ability to distinguish responses that have different temporal trends but similar endpoint values. For example, the changes in total bacterial load (Fig. SX) and propionate concentration (Fig. 3B) from their baseline levels differ significantly among the four vendors in the short-term (day 5) but not at the endpoint (day 31). Second, the use of control group data to assess the intervention effects, compared to the pre-to-post changes in the intervention group alone, avoids the caveat that the latter may be entirely attributed to random variations [43]. Third, the use of dimensionality reduction in our approach facilitates visualization of the variations across different baseline microbiota. For each vendor, the mean response difference between the intervention and control group is represented by an arrow in a specific color. Therefore, any differences in the magnitude and direction of these vendor-specific arrows indicate baseline effects.

Using this approach, wced that temporal responsesload (Fig. 3C) and propionate (Fig. 3D) are indeed baseline-dependent. We further applied it to acetate and butyrate: only the latter metabolite shows significant baseline dependence3D



**3**A schematic diagram of our quantitative framework to test for the significance of baseline-dependent response. The framework involves two steps: (1) projecting all time series from both intervention and control groups onto the same low-dimensional space and (2) performing two separate statistical tests based on the projected data. **B**. comparison of propionate changes at day 5 (upper panel) and day 31 (bottom panel) from day 0 across four different vendors.

C,D. The simplified representation of the inulin-induced responses in the bacterial load and three major SCFAs. diagram For A,C,D, each symbol in the 2-dimensional space represents a mouse (dots: cellulose group, crosses: inulin group) and all mice data from the same vendor under the same dietary fiber treatment was used to fit an eclipse (ellipse’s radius was determined by 2 standard deviations). For each vendor, an arrow was drawn from the eclipse center of the vendor under cellulose treatment (standardized to the origin) to that under the dietary fiber treatment.

**Inference of inulin responders and putative degraders.** The computational assay we described in the proceeding section provides a statistical definition for “responders” based on *Pb*, i.e, the *P*-value for the test of “responsiveness”. We found a total of 37 bacterial taxa whose adjusted *Pb* < 0.05 after Benjamini-Hochberg correction. These responders include different taxa well known for inulin degradation, such as multiple Bacteroides species. However, the *in vivo* selectivity of fiber-induced bacterial expansion cannot be predicted from *in vitro* growth experiment and the selected bacteria must outcompete other community members in addition to being able to ferment fibers. Instead of isolating and testing the growth of these responders *in vitro*, we therefore employed a data-driven approach based on the generalized Lotka–Volterra (gLV) equation to identify putative degraders that initialize the utilization of inulin (Fig. 4A, see Methods). The gLV model assumes that fiber degradation/utilization boosts bacterial growth by an increment after controlling for the indirect growth benefits from other bacteria via interspecies interactions. To estimate the uncertainty associated with model parameters, we further formulated the gLV-based inference problem in a rigorous Bayesian framework and their posterior distributions, rather than point estimates, were obtained. Therefore, any bacteria whose 95% credible interval of its posterior distribution of is completely to the right of 0 is considered a candidate of inulin degrader.

The gLV-based ecological model identified five taxonomically heterogenous candidates for inulin degradation and all were previously inferred as the responders by our statistical approach (Fig. 3B): (from highest to lowest signal strength) *Bacteroides acidifaciens* (species), unclassified *Muribaculaceae* (family), unclassified *Faecalibaculum* (genus), unclassified *Parasutterella* (genus), and unclassified *Bacteroides* (genus). Genetic or *in vitro* evidences have been found, except for unclassified *Parasutterella*, to support the their potential role in degrading inulin (Table S2). For example, members from *Bacteroides* and *Muribaculaceae* harbor gene clusters known as polysaccharide utilization loci (PULs), which contain *susC/susD* homologous gene pair that facilitates sensing and import of inulin [35, 36]. Putative inulin PULs were also detected in the metagenome-assembled genomes of *B. acidifaciens* and unclassified *Muribaculaceae* (Table S3). *Akkermancia muciniphila* and *Bacteroides uniformis*—two bacterial species whose sthe /or—were inferred as responders but not degraders. In addition to inulin-induced growth, our ecologicall approach also predicts intense competitions among the five degraders, which agrees with the well-accepted notion that fiber-induced selective growth is due to competitivie interactions. The only significant positive interaction occurs between *B .acidifaciens* and *A. muciniphila*.Considering *A. muciniphil* does not grow well *in vitro* by supplementing inulin [38], its strong response to inulin may be indirectly mediated by cross-feeding metabolites with the inferred inulin-degader *B. acidifaciens*.

**Inulin responders drive the baseline-dependent termporal responses of gut microbiota.** Compared to taxonomic groups, ecological guilds (groups of bacteria that perform similar ecological functions) are more fundamental units for microbiome data analysis [39, 40]. In line with the guild-based concept, we divided the entire community into three ecological groups (eco-group): (1) the five putative inulin degraders; (2) the 37 inulin responders excluding the degraders (referred as generic responders below); (3) the non-responders. As shown by the individual dynamics of each eco-group (Fig. 4D), the eco-group abundance of the inulin degraders dominates the total bacterial load in short-term (Guangdong, Hunan), long-term (Shanghai), or even the entire period of observation (Beijing). Interestingly, the eco-group of generic responders in Hunan mice has a delayed response caused by a subgroup of *A. municipila* and *B. unifomis*. The dynamics of the two-species subgroup and inulin degraders co-oscillated after the delay, suggesting intimate interactions between each other.

Both Hunan and Shanghai mice showed individualized responses of gut microbiota. The delayed responses of *A. municiphila* and *B. unifomis* in Hunan mice, compared to mice from other three vendors where responses are minimal and negligible, are significantly associated with their baseline abundances (P-value of Spearman correlation: xx and xx). Notably, Hunan mice also have the highest baseline abundance of *B. acidifaciens*, which may also contribute to the delayed but substantial growth of *A. municiphila* via a positive interaction (Fig. 4C). More interestingly, the lack of short-term responses in Shanghai mice can be explained by the extremely low abundance of the top inulin degraders, *B. acidifaciens* and unclassified *Muribaculaceae*, in their baseline microbiota (Fig. 3F, S7B, S8B). This remarkable association suggests that the overall inulin-induced gut microbiota response may be quantitatively predicted by the baseline abundance of the inulin degraders. However, we found that not all degrraders are equally predictive and positive correlations were only found in *B. acidifaciens* and *unclassified Muribaculaceae* (Fig. S14A), which together explains 56% of the variability (Spearman correlation) in the.

The inequality among the inulin degraders was also reflected in the heterogeneity of ther termporal dynamics (Fig. 3F, S7B,C). *B. acidifaciens* and unclassified *Facelibaculum* showed transient dynamics with quick rise and drop in their relative and absolute abundances, which correspond to and may explain the initial drop of the gut microbiota diversity (Fig. 2B). By contrast, the abundance of unclassified *Muribaculaceae* increased continuously and remained high throughout the entire period of study. Except for Shanghai mice, the total bacterial density reached local maximum rapidly within 1-3 days (Fig. 2A), suggesting that these degraders may compete for inulin after the gut microbiota has reached its temporary maximum load (i.e., carrying capacity). The competition for inulin among the degraders was supported by the gLV-based inference of bacterial interactions (Fig. 4C), where unclassified *Muribaculaceae* negatively impact growth of *B. acidifaciens* and unclassified *Facaelibaculum* (highlighted in red). This stimulation-then-competition mechanism found *in vivo* was also observed in a synthetic community of two auxotrophic yeast strains under high amino acid supplementation [42].

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**Figure 4. The inference of inulin** **responders** **and ecological interactions by generalized Lokta-Volterra model. A.** Increased abundance of inulinase in gut metagenome following the inulin intervention. Each dotted line represents an individual mouse. Wilcoxon matched-pair signed-rank tests (two-tailed) followed by FDR corrections, \* *P* < 0.05; \*\* *P* < 0.01; \*\*\* *P* < 0.001. **B**. Generalized Lotka-Volterra model combined with Bayesian statistics to infer inulin responders and bacterial interactions, see Methods for more details. The gLV model summarizes the underlying ecology by three terms that additively determine bacterial growth rates: the basal growth rates (), the influences from other bacteria (), and the impacts of dietary fiber (). **C**. **D.** Posterior distribution of five bacterial taxa with a significant increase in the growth rate (i.e. inulin responders). **E**,**F**. The absolute abundance of total (E) and individual (F) inulin responders shown in panel D. **G.** The inferred ecological interaction network. Inulin responders (bold font) and key inhibitions (red arrows) are highlighted. Point and blunt arrows represent positive and negative interactions respectively. The arrow thickness is proportional to the posterior mean of the corresponding interaction coefficient; only interaction coefficients significantly different from 0 (95% credible interval) are shown. For panels D, F, G, taxonomic labels w/ “Un.” group bacteria that are unclassified or uncultured at lower taxonomic ranks**.**

**Inulin degraders mediate the baseline-dependent propionate production.** Positive correlations were previously reported between total bacterial load and the three major SCFAs in obese males consuming resistant starch?. Here we confirmed the positive associations in the murine gut microbiota stimulated by inulin and all associations are significant. Among the three major SCFAs, propionate is mostly correlated with total bacterial load with Spearman coefficient as high as XX. By dividing the gut community into the same three eco-groups as we described above, we further found the significant associaitions resulted from the inulin degraders and generic responders with more or less equal contribution (Fig. 5B-D). Interestingly, the top four individual bacteria taxa mostly associated the propionate concentration (*B. acidifaciens* and *un. Muribaculaceae* *A. municipila* and *B. unifomis*) are the exactly the same taxa linking baseline composition and gut microbiota response (Fig. SX). The baselinelve of Two out of fpour taxa are significant with the propionate Spearman coefficient 0.XX for Muri and XX for Bac. Uniformic. Based on these statistical analysis, we came up with a coneptutal model that reconcile fthe ifnidng isn the literature. The baseline composition determines total bacterial load based on the initial abundance of fiber degraders. Since these degraders can also produce propionate (i.e., baseline-depednent effect of propionate production), the correlations between total bacterial load and propionate elvele turn out to be indirect (Fig. 5E).

Predicting SCFAs from microbiota has been of long-standing interest but controversies regarding the predictability has not been resolved [44-46]. We evaluated the performance of machine learning models to predict the fecal SCFA concentrations using absolute abundance of bacterial taxa as predictors. All mice were split into training and test sets using two data-split approaches (Fig. 5A). The “interpolation” strategy generated balanced distribution of baseline microbiota composition between the training and test sets by randomly selecting a single mouse from each vendor as test data and leaving the other mice of the same vendor for training. By contrast, the “extrapolation” strategy produced highly unbalanced microbiota distribution by randomly selecting all mice from a vendor as test data and leaving the other vendors for training. Using Random Forest classifiers (see Methods), we confirmed that Despite a good R2 score on the training data, a Random Forest (RF) regression model generalizes poorly to the test data, especially in the “extrapolation” scenario (negative R2 means our model generalizes worse than training data average). or adding weights to training samples (Fig. 10C).

the training accuracy in terms of R2 is at least 66% regardless of SCFAs and data-split strategy. In the scenario of “interpolation”, the prediction accuracy of the three SCFAs varies from 10% to 45%, where butyrate is the most predictable SCFA probably due to its main production pathway is retained to limited bacterial species [47].

We hypothesized that the poorer performance of RF model in “extrapolation” strategy was caused by the larger microbial dissimilarity between the training and test group compared to the “interpolation”, which largely stemmed from the substantial different baseline gut microbiota composition. Some of these bacteria that are missing in at least one vendor have been inferred as SCFAs producers (Fig. S12A). Formally, we quantified the

The top porpioant predictor is un B. acidificance. The R2 for propioant in the “intraplaito” data soplit is as low as 10%, which seems to contradict the high associations between inulin degraders (either as a whole or individually() and porpinoat concentration. To find out the reason, we trained multioples RF model on different predictors using the same hyperparameter-tuning procedure. We found that the RF model is most predictivly when trained with only the five degraders, better than the model trained with all bacterial taxa. This knowledge-informed feature selection also outcompetes automatic eature selection algorithms suych as Lasso when combined with RF. Despite promising, we found that this boost is specific to propionate and the model with all bacterial taxa wins over the model with only inulin degraders for acetate and propionate. This in silico case/control eexperiment suggests that the knowledge of fiber degraders can aid feature selection and improves model prediction.

**.**

**Graphical user interface

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**Figure 5.** **Prediction of short-chain fatty acids concentrations from gut microbiota composition using machine learning models has limited prediction power. A**. Two data-split strategies for testing model performance. Mice in the test sets were randomly selected on a one-per-vendor basis for “interpolation” and exclusively selected from a single vendor for “extrapolation”. Data before intervention (i.e., day 0) was not included. **B**.Performances of Random Forest regression models on the training and test datasets. **D**. Receiver operating characteristic (ROC) curve analysis of the similarity between training and test datasets. A Random Forest classifier trained to discriminate the two datasets outputs area under the ROC curve (auc) as a dissimilarity metric.

**Our major findings are reproducible and generalizable.** degrader gLV-basedthe onlydegrader, probably due to the lack of quantitative dataNonetheless, t

Using the same experimental setup (Fig. 1B), we administered resistant starch to mice from the same four vendors. Consistent with previous human studies [10, 28], inulin stimulated higher production of total and three major individual SCFAs (acetate, propionate, and butyrate) than resistant starch regardless of baseline microbiota (Fig. S2B). Still, the quantitative differences in the stimulating effects of inulin and resistant starch are SCFA- and baseline-dependent. On

For resistant starch, three bacterial taxa were inferred as responders: (from highest to lowest signal strength) unclassified *Faecalibaculum* (genus), unclassised *Muribaculaceae* (family), and unclassified *Desulfovibrionaceae* (family). Some indirect evidences have been shown for the first two responders in utilizing resistant starch (Table S2). Similarly, the total relative abundance of unclassified *Muribaculaceae* and *Desulfovibrionaceae* in the baseline community explains 74% of heterogeneity in microbiota response induced by resistant starch (Fig. S14B).

In both data-split scenarios, the RF predictions are even more inaccurate using data from resistant starch intervention (Fig. S11A).

Compared to inulin, the guild of resistant starch responders plays much less dominant role in shaping the overall response of gut microbiota (Fig. S8A). In Hunan and Shanghai mice, the total density of other bacteria, despite not inferred as responders, increased sharply to higher levels than that of the responders. One possibility of this seemingly counterintuitive result might associated with the character of resistant starch, a fiber that many bacteria have the ability to utilize [12], such that no specific starch-degrading bacteria could be universally detected among four vendors. Nonetheless, we found similar trends, as observed in the inulin-group mice, for the dynamics of unclassified *Muribaculaceae* and unclassified *Faecalibaculum* (Fig. S8B): the absolute abundance of the former bacteria showed gradual but continued increase, while that of the latter bacteria showed a quick rise-and-drop pattern. GLV-based inference further suggests that the observed dynamics may be driven by mutual inhibition between the two taxa (Fig. S8C).

**Discussion**

# Discuss how our study shows that dynamics is important for understanding individualized responses

In summary, our results indicated paramount importance of dynamics for understanding inter-individual differences in dietary responses. The significance of dynamics is two-fold. Firstly, Secondly, dynamics can bridge the gap between the baseline state and the endpoint state and help identify the sources of heterogeneity. For instance, we found that the variability in bacterial load was correlated to the baseline abundance of inulin responders (*Bacteroides acidifaciens* and unclassified *Muribaculaceae)*. Taken together, characterizing dynamic responses to dietary fiber intervention across individuals, with integrated longitudinal analysis of 16S rRNA sequencing, metagenomics and metabolomics, is an important priority for microbiome research to further understanding of diet-induced responses [51]. Such studies thus have great potential to improve human health and treat gut microbiome-associated disease via microbiome engineering.

# Discuss the relevance of biphasic SCFAs dynamics to the literature

Diet-induced changes in SCFAs are often transient and vanish shortly after cessation of dietary intervention [52-55]. Our experiments add to the literature by further showing that SCFA concentrations cannot be maintained at its peak and drop by 35%-40% even under continuous inulin intake until 4 weeks. The transient responses under sustained dietary fiber intake were also observed in colorectal cancer patients [56]. Despite the drop, our data demonstrates that a continuous intervention that lasts for 31 days is sufficient to elevate and stabilize the SCFAs concentration, but it is not clear yet whether the elevated level persists after the intervention discontinues. We envision two possibilities that may explain the after-peak decrease of SCFA concentration. First, some bacteria are known to consume SCFAs and a net consumption of SCFAs may occur when SCFAs consumers dominate over producers [57]. The other possibility is increased absorption of SCFAs by host cells, leaving less produced SCFAs excreted to feces. In healthy individuals, quantification of fecal SCFAs only provides steady state levels and may not accurately reflect the level of bacterial production as most SCFAs produced in the colonic lumen (90–95%) are absorbed by the gut mucosa [58]. Nevertheless, the analysis of SCFAs in fecal samples is used as an approximation of gut levels, since excreted SCFA concentrations are associated with RS enriched diets (substrates of SCFAs-producing bacteria), inferring the relationship between intestinal SCFAs production and fecal levels [10, 59, 60].

# Discuss how our inference approach helps tackle the replicability issue

Using public datasets, we demonstrate that our approach for inferring dietary fiber responders helps tackle replicability issue in microbiome science [61]. The structure of gLV allows for modeling bacterial interactions as covariates and accounting for confounding variables reduces the risk of producing biased estimates of indirect effects. Controlling for confounding variables is highly important for replicability between results of similar microbiome studies, as the underlying mechanisms driving microbiota dynamics is, to a great extent, shared and should play consistent roles [34], while these true microbial dynamic signatures could be largely masked by uncontrolled confounding variables [62].

Since gLV is a differential-equation model, it is naturally more amenable to analyzing longitudinal data compared to traditional cross-sectional statistical tests that based on pre-to-post changes [10, 11, 13]. Indeed, bacteria whose relative abundances were significantly altered by inulin vary depending on the day of sample collection (Fig. S5).

In fact, any scientific field that heavily relies on complex statistical analysis of large datasets may encounter challenges in replicability. Remarkably, our inference approach applied to different mouse or human gut microbiome datasets produced highly compatible results regarding inulin responders. In the mouse gut, both our data and data from Chijiiwa et al.[33] agree that the strongest inulin responder is *Bacteroides acidifaciens*, which was also reported by a third study that treated mice with inulin (data not reanalzyed) [63]. On the other hand, reanalysis of four human datasets that all administered inulin revealed that unclassified *Bifidobacterium* (in three studies) and *Anaerostipes* (in all four studies) exhibit significant responses to inulin, despite the huge differences in the pretreatment microbiota composition among human subjects in these studies (Fig. S13). Hence, consistent with a recent review that focus on the impact of inulin on human gut microbiome [64], our model further confirms the bifidogenic nature of inulin, which has been attributed to the ability of genus to efficiently take up and intracellularly degrade larger inulin. By contrast, another three inulin responders that previously associated with polysaccharide-degrading, *Faecalibacterium*, *Prevotella*, and *Lachnospiraceae*, were individually identified, suggesting that the enrichment and responses of these three bacteria might depends on the gut microbial community structure.

# Can we predict microbiota responses from baseline abundance of responders?

By combining gLV model and Bayesian regression, we identified multiple inulin and resistant starch responders from the complex microbial community of the murine intestine, which we believe play critical roles in bridging the variability in baseline microbiota to the variability in microbiota responses.

# Discuss the major reason for the failure of predicting SCFAs from microbiota composition

Considerable debates have been raised over the feasibility of predicting metabolite profiles solely based on microbiome sequencing data. For example, the MelonnPan algorithm based on linear regression accurately predicted relative abundances of >50% metabolites from metagenomes in patients with inflammatory bowel disease and healthy controls [45]. Oppositely, it was also reported that only 14% of the observed variation in the SCFAs concentration can be explained by RF regression models trained on 16S rRNA or metagenomic gene sequences in colorectal cancer patients and healthy controls [46]. While the possibility of using different regression models and patient cohorts between these controveral studies cannot be excluded, our study points out that the similarity of data distribution between training and test sets, which is strongly affected by the degree of inter-individual variability of gut microbiota, may contribute to the disagreement. Using mouse models, we showed that the predictability was completely lost when extrapolating models to predict SCFAs from gut microbiota compositions that were unseen during training (Fig. 5). In studies with humans, inconsistent model performances may be partially attributed to the neglection of stratified train-test split, leading to an undesired consequence that training and test set data are not independent and identically distributed (i.i.d.). Even though data split is stratified based on microbiome characteristics, regression models may still perform poorly in cases when inter-individual variability is too large to fulfill the i.i.d. assumption, the violation of which would cause covariate shift and machine learning to fail. To improve model predictability, large-scale human cohorts are therefore needed to cover the substantial inter-individual variation of human gut microbiome.

# Complex microbiome-metabolome relationship brings additional challenge for predicting SCFAs

Other than covariant shifts, the complex relationship between SCFAs and gut microbiota composition poses an additional challenge for predictive model development. By regressing SCFAs concentration on absolute abundance of microbes, we implicitly assume that SCFAs concentration remains unchanged if gut microbiota has a steady composition. However, this assumption does not always hold and here we provided two pieces of evidence proving that it can be violated. First, Shanghai mice showed delayed changes in total biomass (Fig. 3C) following inulin intervention, but their acetate and butyrate concentrations were neither delayed nor compromised (Fig. 2A). Second, SCFAs were highly produced by gut microbiota that maintains relatively stable composition between day 0 and day 1, regardless of vendors (Fig. S15A). It is likely the mouse gut resembles an *in vitro* culturing system at the beginning of intervention when the microbiome-metabolome relationship follows a rate model [65], i.e., gut microbiota composition determines the change in SCFAs concentration. This issue is more severe for densely sampled longitudinal data than cross-sectional data as the possibility of sampling very similar microbiota composition at two timepoints far from each other is quite low. This is consistent with previous human studies showing that short‐term diet interventions could rapidly and significantly alter gene expression of the gut microbiome, without changing the community structure [54, 66, 67]. Taken together, the decoupling of changes in SCFAs from gut microbiota responses suggests that SCFAs production may be additionally regulated at transcriptional (gene expression) and metabolically (enzyme activity) levels. Our evidence for potential molecular-level regulations justifies the emerging essentiality of integrating transcriptomics and metabolomics data in dietary response analysis.

The problem of the changed distribution between training and test dataset is formally known as covariate shift and the distribution gap can be sometimes counteracted by assigning weights to the training sets (see Methods) [48]. Unfortunately, the baseline gut microbiota between vendors seems to be too different and adding weights does not improve the prediction accuracy (Fig. S10C).

# Discuss the challenge of finding SCFAs producers

The challenges of predicting SCFAs from gut microbiota composition, as discussed above, brings similar difficulties in robust inference of SCFAs producers. Using three different approaches, we showed that the inferred top producers do not agree with each other. Taking propionate producers as an example. Using the RF model developed in Fig. 5, we ranked propionate producers based on their Gini importance scores and the top three bacterial taxa are *Bacteroides acidifaciens*, unclassified *Alloprevottella* and *Akkermansia muciniphila* (Fig. S12A). The second approach is repeated correlation [50], and we identified *Parabacteroides distasonis* as the sole significant producer (Fig. S12B), which ranked the 5th in the RF model. The third approach also trained a RF model but different variables and only subset of data were used. As discussed above, SCFAs production may follow a rate model within the first day (Fig. S15A) and we threrefore regressed the first-day changes in propionate concentration on absolute abundances of bacterial taxa. Based on Gini importance, the top three propionate producers are unclassified *Parabacteroides*, an unknown species from mouse gut metagenome, and *Parabacteroides merdae*. As shown in Fig. S15B, the absolute abundance of unclassified *Parabacteroides* showed a linear association (Pearson r: 0.71) with first-day propioinate change, while this association fades away with data after day 1 (Pearson r: 0.21). Despite the results of these three approaches have little overlap, the genus *Parabacateroides* as known propionate producers seems to regulate the proprionate level in our dataset [68].

# Limitations in translating knowledge from mice experiments to human

Studying dietary effects on gut microbiota using mouse models, as a complimentary alternative to clinical trials, has better controls over confounding variations between individuals driven by environmental and other host differences. However, we note two major limitations that may hinder translating the insights provided from our mouse experiments to humans. First, mice have much less inter-individual variability than humans [70]. Since individual mice in our study can be stratified into four distinct microbiota compositions based on vendor sources, the major conclusions we draw were essentially based comparative analysis of dietary responses among the four microbial communities each with several replicates. Whether and how well the four community types correspond to the enterotypes—distinct microbiome configurations [71] —in humans are worth further study. To soften this limitation, we have made efforts to augment the microbiome diversity by reanalyzing public dataset from a similar study. Second, the murine gut microbiota has distinct compositions from humans [72]. Although Bacteroidetes and firmicutes are two major phyla shared between mice and human, 85% genera found in the mouse gut are not detectable in the human gut [73]. For example, the family *Muribaculaceae*—a major inulin responder inferred by this study—was specific to the mouse gut [74]. Moreover, the differences in microbiota composition between mice and human diversify the gut environment at functional levels, resulting in differential dietary responses of the same microbes between the two ecosystems. For instance, the two human inulin responders—*Bifidobacterium* and *Anaerostipes*—were present in the mice gut but their relative abundances remain low and unresponsive to inulin intervention throughout the entire period of observation (Fig. S13B). This example shows that bacteria responding to dietary fiber in one of the two mammalian systems may not consistently respond in the other, suggesting that community ecology may play a selective role in the activation of fiber degraders depending on the surrounding environment.

**Methods**

**Animal experiments.** Specific-pathogen-free (SPF) female C57BL/6J mice were obtained at 6 weeks of age from four different vendors, including Beijing (A Charles River Company, Beijing, China), Hunan (Hunan Slac Jingda Laboratory Animal Company, Ltd., Changsha, China), Guangdong (Guangdong Medical Laboratory Animal Center, Foshan, China)) and Shanghai (SLAC Laboratory Animal Co., Ltd., Shanghai, China). Mice were maintained in 12-h light/dark cycle and allowed ad libitum access to food and water throughout the experiment. After acclimatizing to the diet and housing environment for 1 week, mice from each vendor were randomly separated into three groups: cellulose group (n = 5), resistant starch group (n = 5), and inulin group (n = 5). Composition of all diets including the source of dietary fibers cellulose, resistant starch, and inulin are provided in supplementary table 1 (Table S7). Fecal pellets from each mouse were freshly collected over multiple time points: day 0 (before diet change), day 1, 3, 5, 8, 13, 19, 25, and 31 (Figure 1A). Fecal samples were snap-frozen in liquid nitrogen and stored at −80 °C until further processing. At every cage change (moving the mice to a new clean cage with fresh bedding twice in one week), body weight was individually measured, and food intake and fecal output of each cage mice during the past three days per cage were measured. This study was approved by the Institutional Animal Care and Use Committee (IACUC) of the Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences.

**Quantification of fecal SCFA concentration by GC-MS.** The SCFAs of mice fecal samples were analyzed by GC-MS [75]. For the sample extraction, 0.05 g of frozen feces were mixed with 300 µL of pure water containing caproic acid-6,6,6-d3 (CDN Isotopes, Quebec, Canada) as internal standard (IS, final concentration 20 µg/mL). After adding 1.0 mm diameter zirconia/silica beads (BioSpec, Bartlesville, OK), feces were homogenized for 20 s under 6500 rpm for three times, then incubated at 4 °C with shaking for 30 min, followed by centrifugation for 30 min at 13,000×g. Following extraction with anhydrous diethyl ether, the SCFA extract accurately transferred into a glass insert in a GC vial and capped tightly after added 5 µl of N, O-bis(trimethyl-silyl)-trifluoroacetamide and vortexed for 5 s. The mixture was kept in the GC vial and incubated at room temperature (22 °C) overnight (or over 8 h) before loading to GC/MS. The analysis of acetic, propionic and butyric acids was performed by Agilent 8890/7000D triple quadrupole GC/MS equipped with a capillary HP-5 ms capillary column (30 m × 0.25 mm × 0.25 µm film thickness) (Agilent Technologies). The analytes were quantified in the selected ion monitoring (SIM) mode using the target ion and confirmed by confirmative ions. The concentration was determined with reference to the peak side of IS.

**DNA extraction and quantification of bacterial load.** DNA of mice fecal samples was extracted using the QIAmp PowerFecal DNA kit (Qiagen, #12830–50) following standard manufacturer procedures. DNA samples were resuspended in Buffer C6 and quantitated using the Qubit fluorometer (ThermoFisher Scientific). To quantitatively assess bacterial load, total bacteria density were determined using qPCR as described recently [76]. The absolute abundance of a bacterial taxon was estimated by multiplication of its relative abundance and the total bacterial load.

**16S rRNA amplicon sequencing and shotgun metagenomic sequencing.** 16S rRNA gene sequencing was performed as previously described with modifications [77]. Library preparation was done using a two-step PCR method. During the first step of PCR, primers S-D-Bact-0341-b-S-17 (forward) and S-D-Bact-0785-a-A-21 (reverse) were used to target and amplify the v3-4 region [78], as well as to add second-step priming sites. Dual index codes were added to each sample at the second PCR step. The PCR products were purified with Agencourt AMPure XP magnetic beads (Beckman Coulter, Brea, CA, USA) and quality controlled with TapeStation (Agilent Technologies, Santa Clara, CA, USA). The final DNA concentrations of the purified products were measured with Qubit 2.0 fluorometer (Thermo Fisher Scientific). The purified products were pooled in equal molar concentrations, and denatured following the Illumina protocol. All sequencing was done in a single run, which was performed with a 250-cycle SP kit on the NovaSeq 6000 following the NovaSeq XP workflow (Illumina, USA). Blank controls (no sample added, processed routinely, n = 4) were included in the extraction process to control for contamination throughout processing.

Metagenomic sequencing was performed using fecal samples from the inulin diet group at day 0, 5 and 31. Extracted DNA sample was purified using silica-based columns. Metagenomics sequencing libraries were prepared with at least 2 μg of total DNA using the Nextera XT DNA sample Prep Kit (Illumina, San Diego, USA) with an equimolar pool of libraries achieved independently based on Qubit 2.0 fluorometer results combined with SYBR Green quantification (Thermo Fisher Scientific, Massachusetts, USA). The indexed libraries were sequenced with a 150-cycle S4 kit on the NovaSeq 6000 following the NovaSeq XP workflow (Illumina, USA).

**Bioinformatics analysis**. The 16S rRNA sequencing reads were analyzed by QIIME 2-2020.2 software [79]. Demultiplexed paired-end reads were trimmed to remove primers and low-quality bases with q2-cutadapt plugin. The trimmed sequences were denoised and joined with q2-dada2 plugin. Potential reagent contaminants were identified using decontam package based on either the frequency of the ASV in the blank control or the negative correlation with DNA concentration [80]. The generated feature table was filtered to remove ASVs present in only a single sample and remaining ASVs were used to construct a rooted phylogenetic tree via q2-phylogeny. Rarefaction curve analysis of the data obtained was used to estimate the completeness of microbial communities sampling and performed using the iNEXT R package [81]. Subsequently, in order to avoid sample-to-sample bias due to variable sequencing depth (different number of reads per sample), samples were rarefied to 38,980 sequences per sample. Rarefaction analysis showed that great majority of the bacteria species diversity and richness that could be sampled was captured by our sequencing depth (Fig. S18), indicated sufficient sequencing depth for majority of the analyzed samples. Estimated alpha diversity metrics, beta diversity metrics (Aitchison distance [27]) and Principle Coordinate Analysis (PCoA) using q2-diversity. Group significance between alpha and beta diversity indexes was calculated with QIIME2 plugins using the Kruskal–Wallis test and permutational multivariate analysis of variance (PERMANOVA), respectively. To assign taxonomy to the amplicon sequence variants (ASVs), the q2-feature-classifier basing on the classify-sklearn naïve Bayes taxonomy classifier was used with the SILVA (v.138) as reference database.

Indicate that PCOA plot used using DEICODE [27]

For metagenome analysis, raw sequencing reads were subjected to quality filtering and barcode trimming using KneadData (v0.5.4) by employing trimmomatic settings of 4-base wide sliding window, with average quality per base >20 and minimum length 90 bp. Reads mapping to the mouse genome were removed. Kraken2 was run against genome taxonomy database (GTDB\_r89\_54k) with default parameters [82]. Following classification by Kraken2, Bracken was used to re-estimate bacterial abundances at taxonomic levels from species to phylum using a read length parameter of 150. Next, the filtered sequences were assembled into contigs using metaSPAdes with default settings [83]. The gene abundance was analyzed and calculated as previously described with modifications [84]. Putative genes were then predicted on contigs longer than 200 base pairs using Prodigal under metagenome mode (-p meta) [85]. A non-redundant gene catalogue was constructed with CD-HIT using the parameters “-c 0.95 –aS 0.9” [86]. The abundance of each predicted gene was evaluated by mapping reads back with KMA algorithm and then normalized with the following equation: RPM = 1M × (mapped reads/gene length)/(sum of mapped reads/gene length) [87]. For all the predicted genes, CAZymes were annotated using hmmsearch against the dbCAN2 database V9 (e value <1 × 10−10; coverage >0.3) [88]. The domain with the highest coverage was selected for sequences overlapping multiple CAZyme domains. For all samples, short genomic assemblies (<2,000 bp) that could have biased the subsequent analysis were first excluded. Genomes were then binned using VAMB [89]. The binning results were refined based on the bin quality assessment (completeness >75, and contamination <15) of different binners from CheckM [90]. Taxonomic classification of each bin was determined by GTDB-tk [91], and subjected to prediction of polysaccharide utilization loci (PULz) using pipeline PULpy [92].

**Harmonic oscillation model.** The dynamic behavior of a damped harmonic oscillator is modeled by the following second-order differential equation

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| --- | --- |
|  | Eq. (1) |

where is the displacement from its equilibrium position in the absence of external force , is the frictional force constant and is the spring constant. Given the initial position (fixed to data) and initial velocity (free parameter), the model can be solved analytically

|  |  |
| --- | --- |
|  | Eq. (2) |
|  |  |

where and . Parameters () were optimized using modified Powell algorithm with constraints . The best-fit values of and were then used to calculate the damping ratio .

**Ecological inference of dietary fiber responses.** The generalized Lotka-Volterra (gLV) model describes how the absolute abundance of bacterial species change over time

|  |  |  |
| --- | --- | --- |
|  |  | Eq. (3) |

where is the number of bacterial taxa, is the absolute abundance of taxon () , is the basal growth rate, represents the influence of taxon () on the growth of taxon , is the susceptibility coefficient that represents growth response to any given fiber, is a binary variable that indicates whether the fiber is administed at time . Bayesian regression techniques were used to parameterize the generalized Lotka-Volterra (gLV) model, as similarly used in Morjaria et al [93]. For each mice (), Eq. (1) can be transformed into a matrix form that incorporates all discrete time points of measurements (, )

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| --- | --- | --- |
|  |  | Eq. (4) |

where and . The log-derivatives of on the left-hand side of Eq. (2) were estimated from a cubic spline interpolation. Using a simplified notation for Eq. (2), i.e., , we can incorpates data from all mice into a single regression model

|  |  |
| --- | --- |
|  | Eq. (5) |

The linear regression as described in Eq. (3) (for brevity ) can be further transformed into a Bayesian regression where and are normal distribution and standard deviation respectively. We used uninformative priors for all gLV parameters and Stan program [94] to produce posterior distributions for each parameter after “no U-turn” sampling of 10,000 samples from at least 3 independent Markov chain Monte Carlo traces. Since Stan is computationally expensive, we limited the inferences of dietary fiber responders to the top 20 bacterial species with the highest absolute abundances.

Since gLV models the absolute abundance of bacterial taxa, we (Fig. 3C) and then multiplied the density by their relative abundance to calculate absolute abundance. Considering ecological forces driving microbiome dynamics are largely host-independent [34], the time-series data from all mice were simultaneously fed into the gLV model after grouping bacteria according to their lowest classified taxonomic ranks.

**Significance test of baseline-dependent responses.** Sequential non-negative matrix factorization [95] was applied to transform all high-dimensional time series data from both intervention (inulin and resistant starch) and control group into two-dimensional space. We chose two factors because (1) reconstructed time series from the two latent factors preserve the quantitative trends of the untransformed time series sufficiently well (Fig. S17) and (2) two-dimensional data can be easily visualized. Suppose the reduced representation for the intervention group and control group are vectors and respectively, where () refers to the index of vendor and ( and ) refers to the index of mouse. For each vendor , both vectors were then standardized by subtracting the mean vector of the vendor in the control group, i.e., and . The significance test of the responsiveness (i.e., whether time series in the intervention group differs from that in the control group regardless of vendor) and baseline dependence (i.e., whether time series in the intervention group varies among vendors ) were performed separately using Permutational Multivariate Analaysis of Variance (PERMANOVA) with Minkowski distance as the distance metric. The Benjamini-Hochberg procedure [96] was used for controlling the false discovery rate in multiple test correction. The same PERMANOVA and muitiple test correction methods were used to test the baseline dependence based on pre-to-post changes (different of absolute abundance between day 0 and day 31).

**Random forest (RF) model.** Model development was run in a pipeline by combining normalization for data transformation, LASSO (least absolute shrinkage and selection operator) for feature selection, and RF regression for data fitting and prediction. The tolerance used in LASSO is 1e-5 and features whose coefficients below this threshold were discarded and not used to build RF regression model. Regarding model training, five hyperparameters were tuned using 5-fold cross validation and R2 as the scoring metric: constant that multiplies the L1 term in LASSO (1e-4, 1e-3, 1e-2, 1e-1, 1), the number of features to consider when looking for the best split in RF (square root, log2, 16%, 32%, 64%, 100% of all features), the maximum depth of the tree in RF (2, 4, 8, 16), the minium number of samples required to split an internal node in RF (2, 4, 8, 16), and the minimum number of samples required to be at a leaf node (1, 2, 4). We fixed the number of trees in RF model to 2,000.

ROC (Receiver Operating Characteristic) curves in Fig. 5D were obtained for RF classifiers that compute the probability of samples in the full datasets (both training and test sets) predicted as being taken from the training distribution. Specificially, we first concatenated the training and test sets and assign labels 1 and 0 respectively. The new dataset was stratified into 20 folds and each time, a RF classifier was trainined on 19 folds and the used to predict the probability of the remaining fold being sampled from the training set. Suppose the probabilities of sample taken from the training and test set are and respectively. The weight assigned to sample was given by , which makes intuitive sense: the higher the numerator and the lower the denominator, the closer the sample gets to the high-density regions of the test data.

**Data availability**

Sequencing data, desposit to SRA

SCFA and other data: supplementary tables

**Code availability**

All scripts will be available on Github.

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