

2 **Title:** Stronger connectivity of the resident gut microbiome lends resistance to invading bacteria

4 **Authors:** Cristina M. Herren^{1, 2, 3*}, Michael Baym^{3, 4}

¹Harvard Data Science Initiative, Harvard University, Cambridge, Massachusetts, USA

6 ²Freshwater and Marine Sciences Program, University of Wisconsin - Madison, Madison, Wisconsin,
USA

8 ³Department of Biomedical Informatics, Harvard Medical School, Boston, Massachusetts, USA

⁴Laboratory of Systems Pharmacology, Harvard Medical School, Boston, Massachusetts, USA

10 * To whom correspondence should be addressed: cristina_herren@hms.harvard.edu

310 Countway Medical Library, 10 Shattuck St, Boston MA 02115

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12 **Abstract:** Bacterial infection in the gut is often due to successful invasion of the host microbiome by an
introduced pathogen. Ecological theory indicates that resident community members and their interactions
14 should be strong determinants of whether an invading taxon can persist in a community. In the context of
the gut microbiome, this suggests colonization resistance against newly introduced bacteria should
16 depend on the instantaneous bacterial community composition within the gut and interactions between
these constituent members. Here we develop a mathematical model of how metabolite-dependent biotic
18 interactions between resident bacteria mediate invasion, and find that stronger biotic connectivity from
metabolite cross-feeding and competition increases colonization resistance. We then introduce a statistical
20 method for identifying invasive taxa in the human gut, and show empirically that greater connectivity of
the resident gut microbiome is related to increased resistance to invading bacteria. Finally, we examined
22 patient outcomes after fecal microbiota transplant (FMT) for recurring *Clostridium difficile* infection.
Patients with lower connectivity of the gut microbiome after treatment were more likely to relapse,
24 experiencing a later infection. Thus, simulation models and data from human subjects support the
hypothesis that stronger interactions between bacteria in the gut repel invaders. These results demonstrate
26 how ecological invasion theory can be applied to the gut microbiome, which might inform targeted
microbiome manipulations and interventions. More broadly, this study provides evidence that low
28 connectivity in gut microbial communities is a hallmark of community instability and susceptibility to
invasion.

30

30 **Introduction**

Human infection is often due to the successful invasion of harmful bacteria in the host-associated
32 microbiome (Nizet et al. 2001, Bel et al. 2017). Although the human body is frequently exposed to
harmful invaders (for example, pathogens on food [Berger et al. 2010] or household surfaces [Flores et al.
34 2013]), few introductions result in disease. However, pathogens comprise only a small subset of all
potentially invasive bacteria within the human gut microbiome (David et al. 2014). The resident
36 microbiome plays a substantial role in mediating resistance to invaders, but the mechanisms of action are
only partially understood (Baumler and Sperandio 2016).

38 Ecological invasions progress through distinct stages, beginning with transport and population
expansion, and culminating in their impact on ecosystems (Sakai et al. 2001). These same stages occur
40 when newly introduced bacteria colonize the human microbiome (Bosch et al. 2013, Kc et al. 2017). Most
ecological invasions are unsuccessful (Williamson 2006). This is also observed in invasions in the human
42 microbiome; although humans are constantly exposed to novel bacteria, the microbiomes of different
body sites retain distinct compositional profiles and display stability over time (Caporaso et al. 2011, Oh
44 et al. 2016). Thus, most bacterial populations introduced into the human-associated microbiome also fail
to establish.

46 Ecological studies have demonstrated that the success of invading taxa depends strongly on the
biotic interactions within the resident community (Lodge 1993, Fey and Herren 2014). This is also
48 observed in the context of the gut microbiome, where interactions take the form of exchanging and
competing for metabolites (Kinnunen et al. 2016, Mullineaux-Sanders et al. 2018). For example, a recent
50 study demonstrated that an alteration to the resident gut microbial community allowed invasive
Salmonella to thrive on a newly abundant metabolite (Gillis et al. 2017). Thus, the resident gut
52 community was indicative of resource availability, which mediated colonization resistance against
Salmonella. Despite the importance of metabolite-mediated bacterial interactions, few models of
54 microbial community invasion have explicitly included metabolites.

In this study, we investigate the role of the resident gut microbiome community in mediating
56 resistance to invasion. First, we developed a computational model to study how metabolite cross-feeding
and competition mediate success of an invading microbe. We then introduce a novel statistical method to
58 identify invasive taxa in empirical microbial communities, and use this approach to study the invasive
bacteria in three long-term gut time series. The gut microbiome is an ideal system to test ecological
60 invasion theory, because the gut is at constant risk of invasion from consumed bacteria and from
opportunistically invasive commensal bacteria (Benjamin et al. 2013). Finally, we evaluated whether gut
62 connectivity could predict susceptibility to invasion by the pathogen *Clostridium difficile* in patients who
received fecal microbiota transplant (FMT) therapy. We chose *C. difficile* as a test case because it is a
64 well-studied bacterial pathogen whose colonization depends on the resident gut microbiome (Schubert et
al. 2015).

66

Methods

68 *Simulation Model*

We constructed a mathematical model consisting of resident taxa, an invading taxon, and the
70 metabolites required for cell reproduction. Taxa interact through competition for metabolites in the
environment and through cross-feeding of metabolites. Of all possible metabolites in the model (m), each
72 taxon required a randomly assigned unique subset of n metabolites for growth, giving each a distinct
niche. Each taxon also excreted a non-overlapping subset of q metabolites. Excretion profiles were not
74 necessarily unique. Cross-feeding, defined as direct flow of metabolites from one taxon to another, was
possible if one taxon excreted a certain metabolite required by a different taxon. Other parameters in the
76 simulation model included the proportion of possible metabolite exchanges due to cross-feeding that are
realized (p), a competition coefficient (c), variability in competition coefficients among taxa (v), an input
78 rate for metabolites (i), a flushing rate for metabolites and cells (f), metabolite input rates (i) and the
number of taxa present in the community at the start (x). During each run, all possible combinations of m
80 choose n metabolite requirement profiles were generated, and a random subset of x requirement and

excretion profiles were assigned to the taxa. One of the x taxa had metabolic requirements matching the
82 input metabolites. From the requirement and excretion profiles, every possible one-way metabolite flow
was identified. A random subset of these possible exchanges were selected as realized cross-feeding
84 relationships. Competition coefficients for each taxon were drawn from a normal distribution with mean c
and a standard deviation of v .

86 In each time step, metabolites enter the environmental pool (Fig. 1a). Taxa then compete for these
metabolites, with uptake rates governed by their competition coefficients, which quantify scavenging
88 efficiency. Demand for each metabolite is calculated as the number of individuals lacking the metabolite
multiplied by their respective competition coefficients. If total demand is greater than the available
90 metabolites, metabolites are allocated among taxa in proportion to the demand of each taxon. We assume
for simplicity that metabolite uptake amongst individuals in a population is arranged to maximize
92 biomass production (Klitgord and Segrè 2011). Individuals that obtain one unit of each necessary
metabolite reproduce and excrete their given metabolites. If these individuals were from taxa participating
94 in cross-feeding, the excreted metabolites were preferentially available to the recipient taxon before
entering the environmental pool. If the growing taxon had more than one exchange (i.e. more than one
96 cross-feeder), an equal amount of metabolites were made available to each recipient taxon. Finally, a
proportion f of individuals and environmental metabolites were flushed from the system.

98 The invader was introduced after the community of resident taxa equilibrated (Fig 1b). The
invader had a fixed competition value (in these simulations, 0.9), and participated in no cross-feeding. We
100 reasoned that cross-feeding exchanges often need time to develop (e.g. time for proper spatial
configuration [Pathak et al. 2012], construction of nanotubes [Pande et al. 2015], or within-host
102 coevolution [Foster et al. 2017]), and that an invading taxon would therefore have no preexisting cross-
feeding relationships. The run was completed once the model reached equilibrium after the invader was
104 introduced. The outcomes recorded were persistence of the invader, standing pools of metabolites, total
number of individuals in the community, and number of taxa persisting. We evaluated these outcomes

106 while changing the strength of biotic interactions (magnitude of competition and proportion of cross-
107 feeding).

108 For simulations analyzed here, we changed the mean strength of competition (c) between 0.4 and
109 0.9 and the proportion of cross-feeding (p) between 0 and 0.5. The standard deviation of competition
110 values (v) was equal to $0.3 * c$. Any randomly generated competition values below 0.01 were set to 0.01.
111 We initialized the model with 15 taxa, 7 possible metabolites, 4 metabolites required for growth, 2
112 metabolites excreted, and an input rate of 100 units of each of 4 metabolites. The flushing rate was 0.15
113 during each time step. We used 5000 runs for each combination of competition coefficient and cross-
114 feeding proportion. The model was determined to be at equilibrium when the maximum abundance
115 change of any taxon was lower than 0.01. In a small fraction of model runs, the model resulted in a stable
116 limit cycle (see SOM). In this case, the final values were recorded at 20,000 time steps.

118 *Dynamics of invasion in healthy subjects*

119 Next, we present a technique to identify invasive taxa in three long-term time series of the human
120 gut microbiome. Invasive taxa are, by definition, newly introduced into communities during discrete
121 events. Thus, the distribution of invasive taxa over time shows clusters of presences and absences. We
122 quantified the degree of presence/absence clustering using an equation that calculates the probability that
123 a streak of successes would be observed in a series of Bernoulli trials (Feller 1968). This method of
124 identifying invasive taxa avoids problems associated with defining invasive taxa as those newly observed
125 in a community (Kinnunen et al. 2016). In that case, the taxa classified as invasive would change based
126 on the reference time frame.

127 For each taxon, we identified the longest consecutive number of days in which the taxon was
128 present (termed a “streak”). We also calculated the fraction of total samples in which was present. From
129 these two values, it is possible to calculate a p value that described the *probability that a streak equal to*
130 *or longer than the observed streak would occur if presences and absences were randomly distributed.*
This probability (q_n) is given by (see Feller 1968, p. 325 for a derivation):

132

$$q_n \sim 1 - \frac{1 - px}{(r + 1 - rx)q} \cdot \frac{1}{x^{n+1}} \quad \text{Eq. 1}$$

134

136 Where n is the number of samples, r is the length of the longest streak, p is the fraction of presences
138 across the time series, $q = 1 - p$, and x is the root nearest to 1 (but not $1/p$) of the equation:

138

$$1 - x + q p^r x^{r+1} = 0 \quad \text{Eq. 2}$$

140

142 Using this formula, a small q_n (p value) indicates that the observed streak of persistence is longer than
144 would be expected; this denotes a highly patchy presence/absence distribution. We classified invasive
146 taxa as those that were significantly patchy in their distribution ($p < 0.01$) and which were present in
148 fewer than 50% of samples. We note that a cutoff of $p < 0.05$ may not be sufficiently conservative, due to
150 expected autocorrelation in abundances. The presence threshold was necessary because common taxa that
became temporarily absent during a disturbance would also have a significantly patchy distribution.

148 Analyses were robust to changes in these cutoffs (see SOM). To account for differences in detection
limits between samples due to differing sequencing depth, we set a universal detection limit across the
entire dataset (see SOM). Any values lower than this limit were set to zero.

Data for human microbiome subjects A and B were originally published in David et al. 2014.

152

154 These data are near-daily stool samples from two unrelated male subjects. We downloaded the
operational taxonomic unit (OTU) tables generated from closed reference OTU picking from the Qiita
portal (ID 2196). We removed samples with fewer than 10000 reads and those with otherwise low
detection ability (see SOM). We removed an additional two samples from subject B (days 252 and 318)
156 because sampling became infrequent after day 242. This resulted in 321 samples from subject A and 182

158 samples from subject B. Data from subject C were obtained from the Qiita portal (ID 11052). Again, we
160 used the OTU tables generated from closed reference OTU picking. We removed samples with fewer than
162 5000 reads and further removed OTUs with fewer than 10 reads across the full dataset. We subset the data
to fecal samples from subject M03, and analyzed the longest window of consecutive fecal samples. This
window corresponded to the 511 samples taken from 14 July 2015 to 06 February 2017. Four additional
samples were removed due to poor detection limits.

164 *Calculation of connectivity using the cohesion statistics*

We quantified connectivity of the resident gut community using cohesion statistics (Herren and
166 McMahon 2017, <https://github.com/cherren8/Cohesion>), which give instantaneous measures of the degree
of interconnectedness among OTUs in a microbial sample. Connectivity is hypothesized to arise from
168 biotic interactions (see Herren and McMahon 2017 for further discussion). We operationally define
connectivity as the true network of correlations between microbes, whereas cohesion is an estimate that
170 quantifies connectivity.

In brief, cohesion statistics represent the average pairwise correlations between individuals in a
172 sample, after correcting for methodological biases. There are two cohesion values for each sample,
corresponding to connectivity from positive relationships and connectivity from negative relationships.
174 The first step in the workflow is to calculate connectedness values for each taxon. Connectedness values
are the average positive and negative correlation of the focal taxon with other taxa, after accounting for
176 bias introduced by the compositional nature of the data. Cohesion values are weighted sums of the
connectedness values multiplied by the abundances of the taxa in each sample. Taxa that are below
178 specified abundance or persistence thresholds are not included in calculating cohesion, and are given
connectedness values of zero.

180 For the long-term gut time series, we first-differenced the data before calculating cohesion values.
This is a suggested step in the cohesion workflow to handle autocorrelation in abundances due to high
182 sampling frequency (Herren and McMahon 2017). We set the persistence threshold for *inclusion* at 0.5

for the long-term gut data, which was the same cutoff for *exclusion* for defining invasive OTUs. Using the
184 same cutoff for these two analyses meant that no taxon in the invasion analyses contributed to the
cohesion values, thereby eliminating possible artificial relationships between the predictor and response
186 variables in the multilevel model (see next section). We tested two possible mean abundance cutoffs of
0.001 and 0.0001. We evaluated which cutoff yielded a better fit of the population dynamics of invasive
188 OTUs and used that cutoff value. For subjects A and B, we used a mean abundance cutoff of 0.001, while
for subject C we used 0.0001.

190

Multilevel model analysis and model selection

192 To evaluate whether connectivity could predict changes in taxon abundances, we built a
hierarchical linear mixed effects model (hereafter called a “multilevel model”). We chose a multilevel
194 model because it enables analysis of rare taxa without risk of over-parameterization. Invasive taxa are
sufficiently rare that confident parameter estimates cannot be obtained for each taxon; instead, this type of
196 analysis pools low-confidence estimates from each taxon to obtain a single overall estimate of how a
predictor variable affects all invasive taxa. A template and sensitivity analysis of this type of analysis can
198 be found in Jackson et al. 2012.

The predictors included in the multilevel models were fixed effects for the natural log-
200 transformed abundance at time t , positive cohesion values of the communities at time t , and negative
cohesion values of the communities at time t . The response variable was the natural log-transformed
202 abundances of invasive taxa at time $t + I$. We did not include time points when the OTU was absent
(abundance = 0) at time t or at time $t + I$. This was for two reasons: 1) model residuals were improved by
204 preventing zero-inflation, and 2) it was then possible to log transform the abundances without adding an
arbitrary positive value. Random effects were included to allow mean abundance (intercept) to vary by
206 OTU, for the effect of positive cohesion to vary by OTU, and for the effect of prior abundance to vary by
OTU (effectively assuming density dependence varies by OTU). We did not include a random effect to
208 allow negative cohesion to vary by OTU, because this random effect showed high collinearity with the

random effect for positive cohesion, and negative cohesion was a weaker predictor than positive cohesion.

210 We evaluated significance of random effects by comparing AIC values of models with and without the terms included.

212 In order to ensure that any significant results of our analyses of invasive OTUs were not spurious or statistical artifacts, we analyzed paired models of OTUs that were uncommon but non-invasive. We
214 expected that OTUs classified as non-invasive would have a lesser response to cohesion values. Instead of analyzing OTUs with significantly patchy distributions ($p < 0.01$), we analyzed OTUs that showed no
216 trend toward patchiness ($p > 0.3$) that were present in fewer than 50% of samples. We fit the same multilevel model for these OTUs. For subject A, highly collinear random effects caused convergence
218 problems, so we removed the random effect that allowed density dependence to vary by OTU. A full table of results from the six multilevel models can be found in SOM.

220

Relapse in patients treated with FMT

222 Finally, we tested whether the observed relationship between cohesion and resistance to invasion could be used to predict patient responses to a therapeutic microbiome intervention. We obtained data
224 from a clinical study evaluating the role of the gut microbiome during FMT for the treatment of recurring *C. difficile* (Khanna et al. 2016). We downloaded the data from the Qiita portal (id 10057), again using
226 the OTU table generated from closed reference OTU picking. As before, bacterial community composition data were obtained using 16S rRNA amplicon sequencing. We also contacted the original
228 authors to ensure accurate interpretation of the metadata. FMT is a commonly used treatment for chronic *C. difficile* infection that has a higher success rate than antibiotic treatment (van Beurden et al. 2017).
230 This study collected stool samples from 38 patients treated with FMT. Of these 38 patients, 29 had stool samples analyzed at day 28 post-FMT. The study also recorded whether patients experienced another *C.*
232 *difficile* infection within two years after FMT. We hypothesized that patients who would later relapse would have lower community connectivity after FMT. To test this hypothesis, we calculated OTU
234 connectedness values from the healthy donors, which we used to obtain cohesion values for the patients at

28 days post-FMT. The cutoffs for persistence and mean abundance of OTUs included in the cohesion
236 calculation were 0.6 and 0.001. Because of the different variances of cohesion values among relapsing
and cured patients, we used the non-parametric one-tailed Wilcoxon rank test for this analysis.

238

Software used for analyses

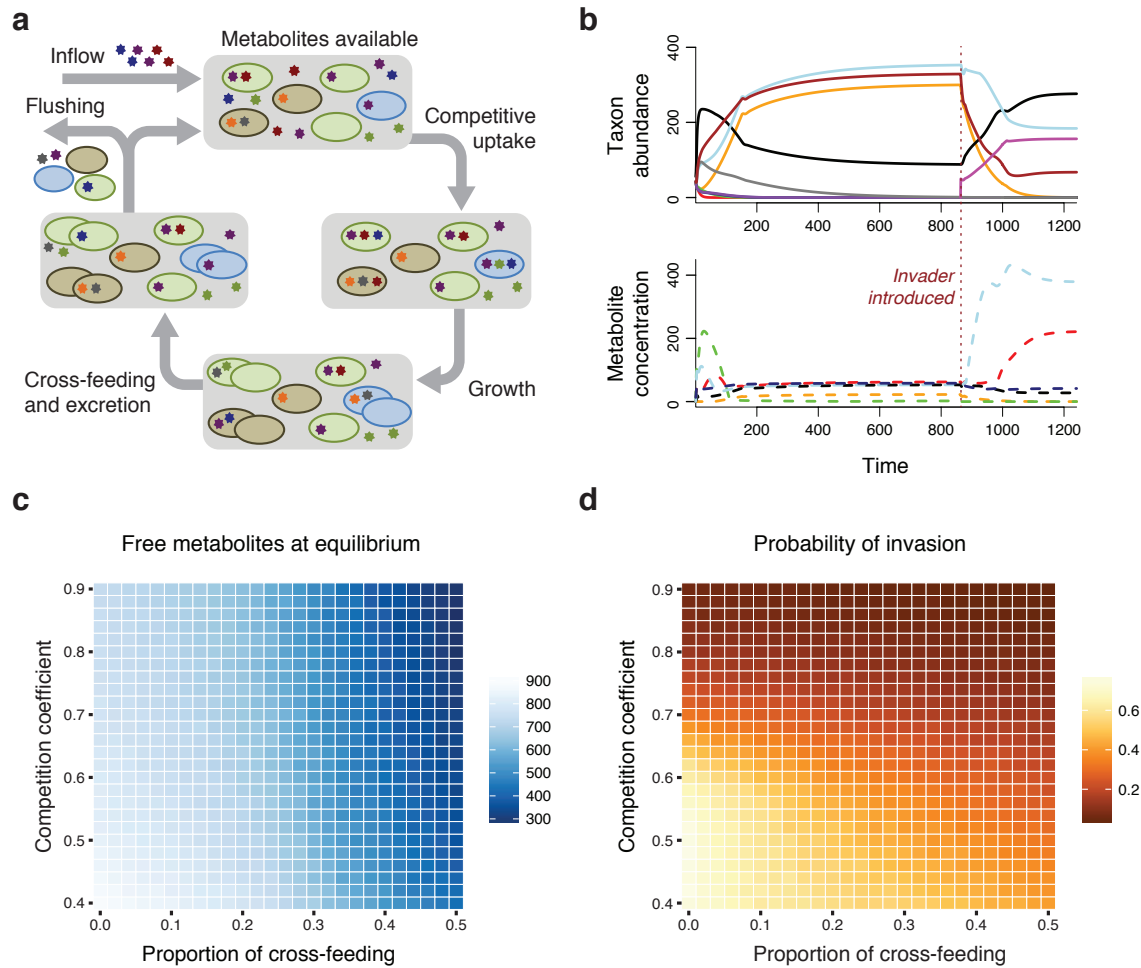
240 All analyses and simulations were conducted in R, version 3.4.0. In the metabolite exchange
simulations, taxon metabolite requirements were generated using the *combinat* package. The packages
242 *abind*, *data.table*, and *dplyr* were used to manipulate matrices. Linear mixed effects models were fit using
the *lme4* package. Conditional R^2 values were obtained using the *MuMIn* package. Significance values
244 for models were obtained using the *lmerTest* package.

246 **Results and Discussion**

Simulation model

248 Simulation results showed that the probability that an invader could persist in the community was
strongly related to the strength of biotic interactions in the resident community. As the strength of either
250 interaction (competition or cross-feeding) increased, standing metabolite pools decreased (Fig. 1c).
Similarly, invaders were less successful when interactions were stronger (Fig. 1d). The two types of
252 interactions had different mechanisms of reducing metabolites available to the invader. Stronger
competition resulted in greater metabolite scavenging from the environment by resident taxa, thereby
254 decreasing the probability that the invader could acquire metabolites. Conversely, cross-feeding decreased
the amount of excreted metabolites entering the environmental pool due to direct provisioning of
256 metabolites. Thus, stronger biotic interactions, whether originating from competition or cross-feeding,
also led to lower rates of invasion. Our model supports the hypothesis that bacterial interactions can
258 mediate invasion by inducing resource scarcity, thereby making it difficult for invaders to gain a foothold
(Kinnunen et al. 2016).

260



262 **Figure 1: Stronger biotic interactions lead to more complete metabolite uptake and a decreased chance of**
 264 **invasion.** a) A conceptual diagram showing the flux of metabolites during each step in the simulation model,
 266 the taxon abundances over time and the environmental metabolite concentrations over time. The red dashed line
 268 shows the time point where the invader (pink) was introduced. In this case, the invader persisted in the community.
 270 c) Environmental metabolite concentrations at model equilibrium decrease as either parameter of biotic interaction
 (proportion of cross-feeding or competition coefficient) becomes stronger. The figure shows median values of 5000
 runs for each parameter combination. d) The probability that an invader persisted in the community decreased when
 either parameter of biotic interaction (proportion of cross-feeding or competition coefficient) was stronger.

272

In the absence of cross-feeding, the model simplifies to the well-known result that only m taxa
274 can persist on m metabolites (Tilman 1982). When cross-feeding was introduced, one taxon for every
niche (m choose n taxa) could be present. Interestingly, this strong increase in diversity when allowing for
276 cross-feeding is another possible explanation for the paradox of the plankton (Hutchinson 1961). The
model has a carrying capacity determined by i , n , q , and f . If metabolite exchange from cross-feeding
278 were configured such that every excreted metabolite were immediately consumed, the maximum
community density (carrying capacity) is equal to

280

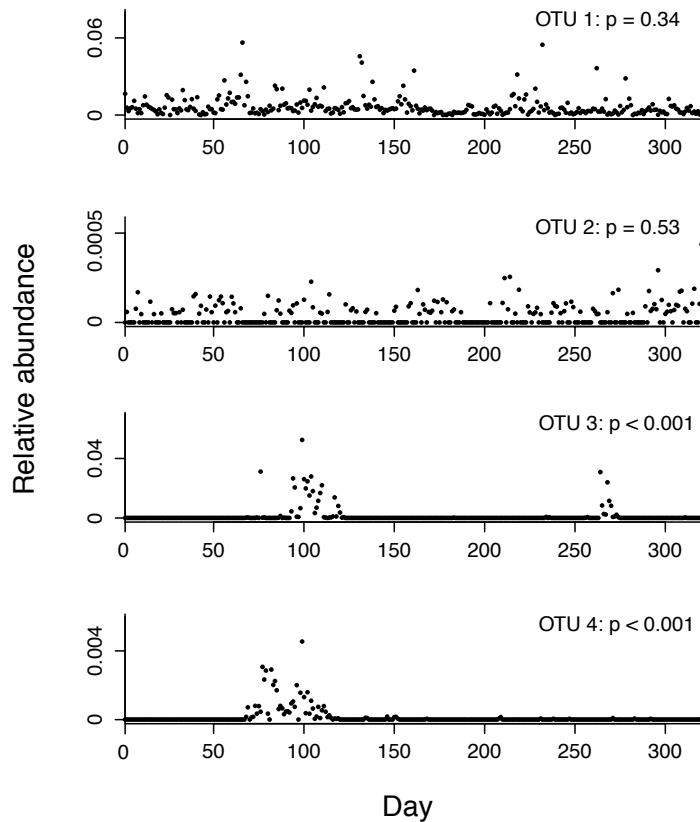
$$i \cdot \frac{(1-f)}{f} \cdot \left(\frac{1}{1-q/n} \right)$$

Eq. 3

282

Dynamics of invasion in healthy subjects

284 Next, we used our new approach for identifying invasive taxa in three long-term time series of the
human gut microbiome. We designated taxa with significantly temporally clustered presence-absence
286 profiles ($p < 0.01$) as invasive (Fig. 2).



288

Figure 2: Invasive taxa have distinct time-series signatures. We classified each OTU as invasive or non-invasive based on its presence/absence distribution across the time series. We used a formula for quantifying the temporal clustering of presence/absence data to make this classification (Feller 1968). This formula calculates the probability of observing consecutive presences of a taxon, which we call a “streak”. The p values displayed correspond to the probability that the OTU’s longest streak would occur if presences and absences were distributed independently across the time series. Taxa showing interspersed presences and absences across the time series were categorized as not significantly clustered, and therefore non-invasive (OTU 1 and OTU 2). Taxa showing highly segregated presences and absences across the time series were categorized as significantly clustered, and therefore invasive (OTU 3 and OTU 4).

298

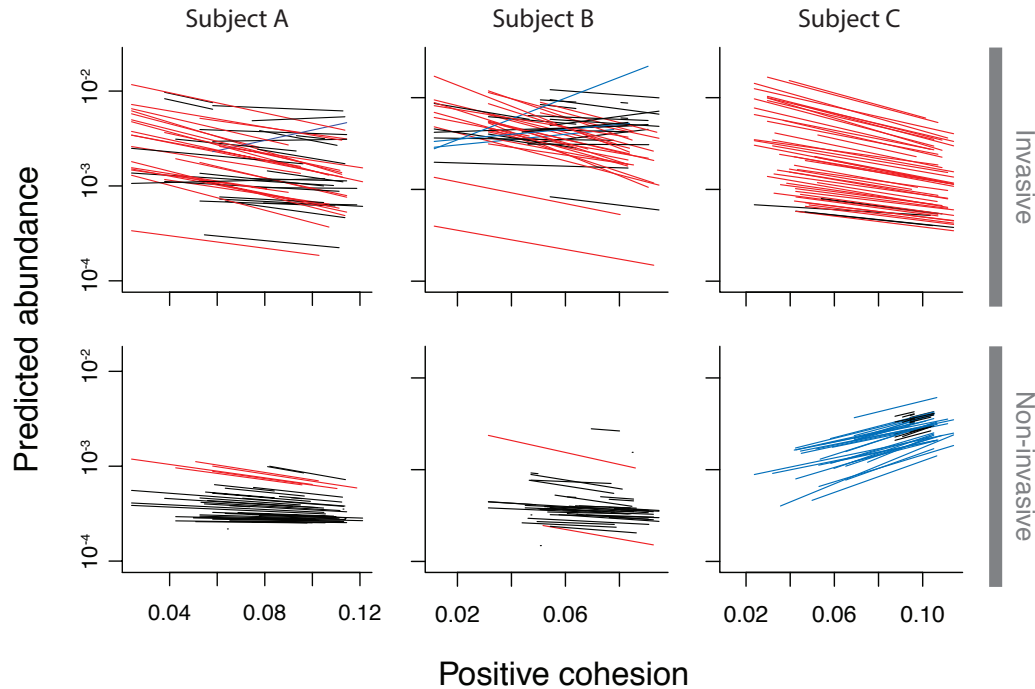
Invasive taxa were common in all three subjects. The total number of OTUs in each dataset was 1828 for subject A, 1771 in subject B, and 4918 in subject C. In subject A, we identified 250 invasive

300

OTUs (subject B: 441, subject C: 131) that comprised an average of 2.2% (subject B: 8.6%, subject C: 2.9%) of the gut bacterial community. Although invasions were common, invader abundances were low and the duration of invasions were short. Median peak invader abundance was 0.053% (subject B: 0.047%, subject C: 0.13%) of the community, with an interquartile range of 0.022-0.24% (subject B: 0.022-0.15%, subject C: 0.058 – 0.32%), and median invasion duration was 7 days with an interquartile range of 4-14 days (subject B: median 8 days, IQR of 4-15 days, subject C: median 7 days and IQR of 5-14 days). The large number of invaders in subject B is likely explained by this subject's gastrointestinal infection during the course of the sampling period.

The multilevel models showed that cohesion values were significant predictors of abundance changes for invasive OTUs, but not for non-invasive OTUs. In all subjects, invasive OTUs declined in abundance when positive cohesion in the gut community was stronger (subject A: $p < 10^{-8}$, slope 95% confidence interval = [-8.32, -4.24]; subject B: $p < 10^{-10}$, CI = [-8.32, -4.59]; subject C: $p < 10^{-5}$, CI = [-12.3, -4.98]; Fig. 2). Please see SOM for full results tables. Invasive OTUs in subjects A and B showed no response to negative cohesion, while invasive OTUs in subject C declined as negative cohesion became stronger (subject A: $p = 0.18$, CI = [-2.27, 0.45]; subject B: $p = 0.10$, CI = [-1.72, 0.16]; subject C: $p < 10^{-4}$, CI = [2.28, 6.74]). Conversely, OTUs that were not classified as invasive showed no response to changes in cohesion in subjects A (positive: $p = 0.11$, CI = [-6.07, 0.70]; negative: $p = 0.85$, CI = [-2.56, 3.08]) and B (positive: $p = 0.12$, CI = [-8.92, 1.09]; negative: $p = 0.57$, CI = [-2.66, 4.81]), and showed increases in abundance in subject C (positive: $p = 0.014$, CI = [2.56, 24.7]; negative: $p = 0.068$, CI = [-13.7, 0.63]). The range of positive cohesion values observed in communities from subject A was 0.035 to 0.148 (subject B: 0.026 to 0.121, subject C: 0.024 – 0.114). A decrease in cohesion of 0.05 was associated with an increase of the average invader's abundance by 37% (subject B: 38%, subject C: 54%) (Fig. 3). The conditional R^2 values for the hierarchical models of invasive taxa were 0.45 for subject A, 0.61 for subject B, and 0.44 for subject C.

326



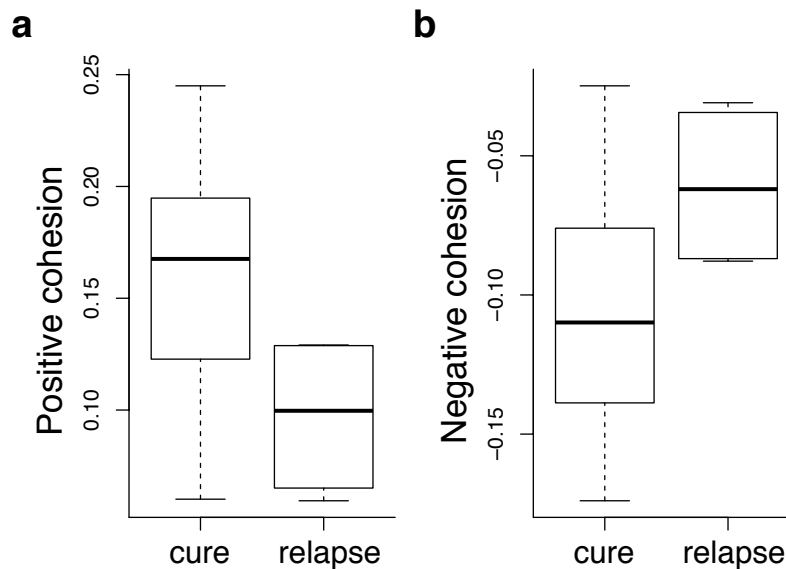
328 **Figure 3: Invasive OTUs decrease in response to stronger cohesion, whereas non-invasive OTUs do not.** Each
panel shows the predicted abundances of the 50 most abundant taxa in each multilevel model analyzing OTU
330 abundance as a function of cohesion. Each line indicates the predicted abundance of the OTU at time $t + 1$ if the
OTU were observed at a relative abundance of 0.01 at time t . Red lines indicate taxa that decreased by at least 50%
332 over the range of observed positive cohesion values. Blue lines indicate taxa that increased by at least 50%.
Although there was variability in how the OTUs responded to positive cohesion, invasive OTUs had a significant
334 overall negative response to stronger positive cohesion in all three subjects (top row). For comparison, we also
analyzed OTUs that were uncommon but non-invasive. In subjects A and B, these OTUs showed no significant
336 response to cohesion, whereas OTUs in subject C the non-invaders increased in response to positive cohesion
(bottom row).

338

Relapse in patients treated with FMT

340 Finally, we analyzed the data from a clinical study evaluating the role of the gut microbiome
during FMT for the treatment of recurring *C. difficile* (Khanna et al. 2016). Stool samples were taken
342 from patients before and after FMT, as well as from donors. We found that patients who would have a
future relapse within 2 years after FMT had weaker gut cohesion at 28 days post-FMT than patients who

344 were cured (Fig. 4). Signed Wilcoxon rank tests were significant for both positive cohesion ($p = 0.012$)
and negative cohesion ($p = 0.015$). Thus, weak connectivity of the patient gut bacterial community after
346 FMT was an indicator that the patient was more likely to relapse. Prior efforts to predict *C. difficile*
relapse from the microbiome did not find post-FMT indicators of relapse, although connectivity was not
348 previously considered (Pakpour et al. 2017).



350
Figure 4: Resident microbiome cohesion predicts *C. difficile* relapse in patients treated with FMT. Patients
352 who would later experience a relapse of *C. difficile* had lower gut bacterial cohesion values at 28 days post-FMT.
We calculated connectedness values of OTUs in healthy stool samples, which were then used to calculate cohesion
354 values for patients after they received FMT. Relapsing patients had weaker positive cohesion (Wilcoxon signed rank
test p value = 0.012) and weaker negative cohesion (Wilcoxon signed rank test p value = 0.015) after treatment.

356
We conducted similar analyses using other possible predictors of relapse to evaluate the
358 comparative explanatory power of the cohesion statistics. Other potential predictors of relapse were not
statistically significant, including post FMT gut diversity ($p = 0.92$ using a one-way ANOVA), Bray-
360 Curtis dissimilarity from the donor community ($p = 0.69$ using a one-way ANOVA), and cohesion of the
donor community ($p = 0.18$ for positive cohesion, $p = 0.14$ for negative cohesion using signed Wilcoxon

362 rank tests). The small number of relapsing patients is expected, because the success rate of FMT is high.
However, when using cohesion values as the predictor, the effect size was sufficiently large that the small
364 sample size did not impede identifying significant separation between the cured and relapsing groups.

366 *Incorporating invasion into ecological models of the gut microbiome*

The three cases considered here consistently showed that stronger connectivity of the resident
368 bacterial community led to increased colonization resistance. Agreeing with ecological invasion theory,
most bacterial invasions were short and ultimately unsuccessful. Prior studies have hypothesized that
370 antibiotics increase susceptibility to invaders by eliminating resident microbes (David et al. 2014,
Schubert et al. 2015). We further suggest that the most highly connected taxa are disproportionately
372 important to maintaining resistance against invaders, and that successful gut microbiome interventions
(such as probiotics [Johnston et al. 2016] or dietary changes [Griffin et al. 2017]) may be attributable in
374 part to restoring connectivity among resident gut microbes.

Interestingly, our results show predictive power independent of the role of the host immune
376 system, which is a substantial contributor to host susceptibility to invasion (Round and Mazmanian 2009).
Observing the responses of each invasive gut OTU (Fig. 3), it is clear that some invasive taxa had a
378 positive or neutral response to increased gut connectivity. The variability of invader response to cohesion
may be explained by factors not considered in this analysis. For example, it is possible that the taxa that
380 are largely unaffected by cohesion are instead regulated by an immune response or the synthesis of
antimicrobial compounds (Mullineaux-Sanders et al. 2018). Thus, we expect that resident community
382 connectivity is only one of several factors affecting gut invasion. Furthermore, although the empirical
results are consistent with the interpretation that pairwise correlations reflect biotic interactions, we
384 cannot exclude the possibility that other factors, such as environmental forcing, contributed to cohesion
values.

386 The mechanisms by which FMT resolves *C. difficile* infection are still poorly known (Bajaj et al.
2017, Patron et al. 2017, Zuo et al. 2017). Indeed, when announcing the FMT National Registry, the

388 American Gastronomical Society wrote that the widespread use of FMT “has advanced the practice of gut
microbiota manipulation in patients more rapidly than our scientific understanding” (Kelly et al. 2017).
390 Our results indicated that FMT is more successful when post-transplant communities have many highly
connected taxa. We therefore hypothesize that successful intervention via FMT reestablishes microbial
392 interactions, thereby creating a microbial community that can repel invaders. Taken together, our analyses
show that strong connectivity of the resident gut bacteria appears to be an important indicator of a
394 resilient microbial community.

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