

1 **Antibiotic effects on microbial communities are modulated by resource  
2 competition**

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14

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17 **ABSTRACT**

18 Antibiotic treatment significantly impacts the human gut microbiota, but quantitative  
19 understanding of how antibiotics affect community diversity is lacking. Here, we build on  
20 classical ecological models of resource competition to investigate community responses  
21 to antibiotic-induced species-specific death rates. Our analyses highlight the complex  
22 dependence of species coexistence that can arise from the interplay of resource  
23 competition and antibiotic activity, independent of other biological mechanisms. We show  
24 that resource competition can cause richness to change non-monotonically as antibiotic  
25 concentrations are increased. We identified resource competition structures that cause  
26 richness to depend on the order of sequential application of antibiotics (non-transitivity),  
27 and the emergence of synergistic and antagonistic effects under simultaneous application  
28 of multiple antibiotics (non-additivity). These complex behaviors can be prevalent,  
29 especially when generalist consumers are targeted. Communities can be prone to either  
30 synergism or antagonism, but typically not both, and antagonism is more common.  
31 Furthermore, we identify a striking overlap in competition structures that lead to non-  
32 transitivity during antibiotic sequences and those that lead to non-additivity during  
33 antibiotic combination, suggesting that our analysis is broadly applicable across a wide  
34 range of clinically relevant antibiotic treatment schemes. In sum, our results will facilitate  
35 the engineering of community dynamics via deleterious agents.

36 **INTRODUCTION**

37 Antibiotics are cornerstones of modern medicine due to their ability to inhibit the growth  
38 of pathogens during infections. Antibiotics are broadly characterized by their inhibitory  
39 mechanism as bacteriostatic (growth-halting) or bactericidal (death-causing), and by their  
40 spectrum of activity as broad or narrow (Kohanski et al., 2010). The effects of most  
41 antibiotics have been predominantly investigated in species monocultures (Andrews,  
42 2001), despite the fact that treatment in a clinical setting inevitably has unintended  
43 consequences on the multispecies communities that colonize the human gut (Cani,  
44 2018). Antibiotics can exert collateral damage on gut bacteria (Maier et al., 2021) and  
45 reduce gut microbiota diversity (Aranda-Diaz et al., 2022; Maier et al., 2018; Ng et al.,  
46 2019), the latter of which has been linked to increased propensity for *Clostridioides difficile*  
47 infection (Hromada et al., 2021; Owens Jr et al., 2008; Schubert et al., 2015) and  
48 increased mortality after cancer treatment (Taur et al., 2014). A deeper understanding of  
49 the interplay between antibiotic activity and community context could provide  
50 mechanisms to ameliorate treatment side effects and to mitigate the growing threat of  
51 antibiotic resistance (De Leenheer and Cogan, 2009; Hallinen et al., 2020).

52

53 Community dynamics during antibiotic perturbations can be challenging to predict since  
54 context can alter antibiotic effects through interspecies interactions, pH modulation, and  
55 metabolic transformation (Aranda-Diaz et al., 2022; Bottary et al., 2021; de Vos et al.,  
56 2017; Zimmermann et al., 2021). The use of a variety of treatment regimens such as  
57 variable dosage (De Leenheer and Cogan, 2009), sequential scheduling of multiple  
58 compounds (Batra et al., 2021), and concurrent treatment with cocktails (Wood and  
59 Cluzel, 2012) further complicates predictions. Moreover, concurrent application of  
60 multiple drugs can lead to synergistic or antagonistic effects (Brochado et al., 2018; Xu  
61 et al., 2018; Yeh et al., 2009), whereby the degree of killing is greater or less, respectively,  
62 than the sum of the drugs individually. Importantly, intrinsic competition for nutrients within  
63 a community is a major driver of community dynamics in the absence (Gowda et al., 2022;  
64 Ho et al., 2022a; Ho et al., 2022b; Segura Munoz et al., 2022) and presence of antibiotics  
65 (Adamowicz et al., 2018; Amor and Gore, 2022). This plethora of phenomena motivates  
66 the development of a theoretical approach to untangle the network of interspecies

67 interactions from activity of the antibiotic itself.

68

69 To interrogate the potential for emergent effects of antibiotics on community dynamics,  
70 we utilized consumer-resource (CR) models in which species growth is governed by  
71 nutrient availability (Chesson, 1990). Within CR models, species can coexist only when  
72 they occupy distinct resource niches (Marsland et al., 2019; Posfai et al., 2017;  
73 Taillefumier et al., 2017); how antibiotic perturbations affect species coexistence remains  
74 unclear. Here, we incorporate species-specific death rates into CR models to map the  
75 complex behaviors that can arise from the interplay between antibiotic activity and  
76 resource competition. We derived a general framework describing how species-specific  
77 death rates shift the resource competition landscape, and hence the criteria for  
78 coexistence and the consequences for community diversity. Using this framework, we  
79 delineated the effects of antibiotic dosage, scheduling, and combination. We found that  
80 increasing the degree of targeting of a single species, akin to varying the concentration  
81 of a narrow-spectrum antibiotic, can result in non-monotonic changes in richness. In  
82 addition, the order of sequential application of multiple antibiotics can qualitatively affect  
83 the final community architecture, and treatment with antibiotic combinations can result in  
84 synergism or antagonism at the level of community diversity. These phenomena arose  
85 solely from resource competition, independent of other biological mechanisms.  
86 Importantly, these phenomena were prevalent, suggesting that they are likely to occur in  
87 typical communities of gut commensals. Thus, our results suggest that communities can  
88 be designed to exploit resource competition for improving therapeutics.

89 **RESULTS**

90

91 **Conditions for coexistence in a CR model with antibiotic activity**

92 We explore the effects of antibiotics on community dynamics using an established  
93 formulation of a well-mixed CR model of  $m$  species competing for  $p$  supplied resources  
94 in a chemostat (Posfai *et al.*, 2017) described by the equations

95 
$$\frac{dn_i}{dt} = n_i \left( \sum_{\mu=1}^p \frac{R_{i\mu} s_{\mu}}{\sum_k n_k R_{k\mu}} - d \right), \quad (1)$$

96 where  $n_i$  is the abundance of species  $i$ ,  $R_{i\mu}$  is the rate at which species  $i$  consumes  
97 resource  $\mu$ ,  $s_{\mu}$  is the supply rate of resource  $\mu$ , and  $d$  is the dilution rate of the chemostat,  
98 which affects each species uniformly (Fig. 1A, Table 1). To model the effects of  
99 bacteriostatic antibiotics, we assumed that the consumption rates  $R_{i\mu}$  of species  $i$   
100 decrease by a factor  $b_i$ , modifying Eq. 1 as follows:

101 
$$\frac{dn_i}{dt} = n_i \left( \sum_{\mu=1}^p \frac{(R_{i\mu}/b_i)s_{\mu}}{\sum_k n_k (R_{k\mu}/b_k)} - d \right). \quad (2)$$

102 To model the effects of bactericidal antibiotics, we assumed that species  $i$  experiences  
103 death at rate  $d_i$  in addition to the effects of dilution (Fig. 1A), modifying Eq. 1 as follows:

104 
$$\frac{dn_i}{dt} = n_i \left( \sum_{\mu=1}^p \frac{R_{i\mu} s_{\mu}}{\sum_k n_k R_k} - (d + d_i) \right). \quad (3)$$

105 Importantly, when  $b_i = (d + d_i)/d$ , Eq. 2 and 3 are identical up to rescalings of time,  
106 species abundances, and resource consumption rates (Supplemental Text). Therefore,  
107 within this model, the effects of antibiotic activity on species coexistence can be  
108 understood as a reduction of the enzyme budget of species  $i$ ,  $E_i = \sum_{\mu} R_{i\mu}$ , by a species-  
109 specific factor  $b_i$  regardless of antibiotic mechanism (Fig. 1B). Steady-state species  
110 abundances are also typically similar between bactericidal and bacteriostatic antibiotic  
111 activity given the transformation described above, particularly for communities with larger  
112 overlap in consumption niche (Fig. S1A,B), suggesting that antibiotic mechanism of action  
113 may be less impactful on community composition than the nutrient niches of the targeted  
114 species.

115

116 It was previously shown that within the chemostat CR model described by Eq. 1, a set of  
117 species  $i$  with the same enzyme budgets ( $E_i = E$ ) will coexist if the convex hull of their

118 consumption rates contains the normalized resource supply rates  $(E/S)s_\mu$  (Fig. 1C),  
119 where  $S = \sum_\mu s_\mu$  is the total resource supply rate (Posfai *et al.*, 2017). Motivated by the  
120 implementation of antibiotic activity described above, we found that we could generalize  
121 this coexistence rule to species-specific enzyme budgets  $E_i$  and  $d_i = 0$  without loss of  
122 generality as follows. For a set of  $m$  species, a subset of  $m'$  species will coexist if their  
123 consumption rates lie on a hyperplane defined by  $c_\mu^*$  such that  $\sum_\mu R_{i\mu} c_\mu^* = d$  for all  
124 species  $i$  in the subset, and if the hyperplane satisfies the following requirements: 1) all  
125 axis-intercepts  $d/c_\mu^*$  are positive and finite (so that the steady state resource  
126 concentrations  $c_\mu^*$  are positive and finite); 2) no species have consumption rates that lie  
127 on the side of the hyperplane away from the origin, i.e.,  $\sum_\mu R_{i\mu} c_\mu^* \leq d$  for all species  $i$   
128 (since a species whose consumption rates lie above the hyperplane has a large enough  
129 enzyme budget that it will drive species on the hyperplane extinct); and 3) the normalized  
130 resource supply rates  $\hat{s}_\mu = s_\mu(d/S)$  lie within the convex hull of the rescaled consumption  
131 rates  $\hat{R}_{i\mu} = R_{i\mu} c_\mu^*$  of the  $m'$  species (namely, the resource supply rates must lie within a  
132 region of shared consumption niche among all coexisting species) (Supplemental Text).  
133 In an example community with three species competing for two resources, there are two  
134 hyperplanes (lines) that satisfy the first two conditions (Fig. 1D), and along each line, the  
135 species that will persist are determined according to the third condition (Fig. 1E,F). Unless  
136 otherwise specified, we will work in the space of rescaled consumption rates and  
137 normalized supply rates with no loss of generality (Supplemental Text), and we assume  
138  $d = S = 1$ . As presented in the sections below, these rules produce some intuitive  
139 behaviors as well as complex behaviors emerging from the interplay between species-  
140 specific antibiotic activity and resource competition, each of which can inform the  
141 interpretation of experiments.

142

#### 143 ***Antibiotic treatment can promote coexistence in resource competition regimes 144 involving generalists***

145 To interrogate how antibiotic activity affects species coexistence, we first applied the  
146 coexistence conditions in Fig. 1 to analyze the minimal scenario of two species competing  
147 for two resources,  $m = p = 2$ . We considered four qualitatively distinct types of

148 communities: two specialist consumers (each with only one nonzero consumption rate)  
149 with no niche overlap, one generalist (with two nonzero consumption rates) and one  
150 specialist, a pair of generalists with preference for distinct resources, and a pair of  
151 generalists with preference for the same resource (Fig. 2A). Naively, one might expect  
152 that increasing the death rate of a species would generally decrease the probability that  
153 it can persist in a community, and hence decrease the proportion of supply rates that lead  
154 to coexistence (defined by the size of the convex hull or coexistence region). For two  
155 generalists with preference for distinct resources, as the ratio of their enzyme budgets  
156 changed due to antibiotic perturbation, the coexistence region size indeed decreased  
157 (Fig. 2A, red). However, for the trivial case of two specialists, there is no competition and  
158 hence the two species coexisted regardless of death rates (Fig. 2A, purple). For a  
159 generalist and a specialist, decreasing the enzyme budget of the generalist increased the  
160 coexistence region size (Fig. 2A, green), indicating that antibiotic activity targeting a  
161 generalist can promote coexistence. For two generalists with preference for the same  
162 resource, coexistence region size can exhibit non-monotonic dependence on enzyme  
163 budgets (Fig. 2A, yellow).

164

165 These non-monotonic behaviors arise because antibiotic activity affects the shape of the  
166 coexistence region rather than simply rescaling its size (Fig. 2B). In the case of two  
167 generalists, when the more generalist of the two species (the one with more equal  
168 consumption of both resources) was targeted (Fig. 2B, i), its consumption niche was  
169 encroached upon by the non-targeted species (Fig. 2B, ii), effectively making the non-  
170 targeted species more of a generalist. As a result, the bounds of the coexistence region  
171 shifted toward the consumption niche of the targeted species since supply rates must be  
172 closer to the consumption rates of the targeted species to enable its coexistence (Fig.  
173 S2). Thus, the coexistence region size initially increased with death rate and reached its  
174 maximum when the remapped boundaries were symmetric about the point of equal  
175 supply rates (Fig. 2B, ii). When the death rate of the targeted species was increased  
176 further (Fig. 2B, iii), expansion of the consumption niche of the non-targeted species and  
177 the concomitant shrinkage of the consumption niche of the targeted species led to an  
178 overall decrease in coexistence region size (Fig. 2B, iii). Steady-state community

179 evenness in species abundance (measured as the exponential of the Shannon diversity  
180 index (Jost, 2006)) was similarly non-monotonic for this scenario (Fig. S1C), suggesting  
181 that antibiotic perturbations have similar effects on richness  $\rho$  and evenness. This  
182 analysis highlights the potential for complex behavior involving species coexistence when  
183 a generalist is targeted.

184  
185 Despite the example above, we hypothesized that antibiotic activity should generally  
186 decrease richness when averaged across communities. To test this hypothesis, we  
187 investigated communities with three species competing for three resources ( $m = p = 3$ )  
188 with consumption rates  $\vec{R}_i$  sampled uniformly from the unit simplex of equal enzyme  
189 budgets (i.e.,  $\sum_{\mu=1}^p R_{i\mu} = 1$  with equal probability of sampling all vectors that satisfy this  
190 constraint). Species-specific death rates were drawn uniformly from the unit simplex for  
191 each community, and all resources were supplied at equal rates. For communities in  
192 which all three species coexisted prior to antibiotic perturbation, the average richness  
193 across all communities indeed decreased following the implementation of species-  
194 specific death rates, and the decrease in richness was larger for communities with smaller  
195 coexistence regions (Fig. 2C, right). Consistent with this trend, mimicking an increase in  
196 antibiotic concentrations for each community by multiplying all species-specific death  
197 rates by a factor  $c$  caused average richness to decrease monotonically (Fig. 2C, left).

198  
199 For the decrease in average richness described above, all starting communities had  
200 maximal richness. To consider a scenario in which richness has more potential to rise  
201 upon antibiotic treatment, we focused on communities in which only two of the three  
202 species coexisted prior to antibiotic perturbation, and allowed for an external reservoir of  
203 species to transiently repopulate the initially extinct species during the antibiotic  
204 perturbation, as has been observed experimentally (Ng *et al.*, 2019). Now, the average  
205 richness reached a maximum  $>2$  for communities with small antibiotic concentrations or  
206 intermediate coexistence regions (Fig. 2D). Thus, non-monotonic richness behavior upon  
207 antibiotic treatment can be a prevalent feature of communities in the presence of a re-  
208 seeding pool of species.

209

210 ***Increasing death rate can lead to highly non-monotonic changes in richness***

211 Our simulations of randomly drawn communities showed that richness can increase upon  
212 antibiotic treatment in some cases (Fig. 2C). To investigate this behavior in more detail,  
213 we considered a community with  $m = p = 3$  in which only one species (blue) persisted at  
214 steady state prior to antibiotic perturbation (Fig. 3A,B). As the death rate of this species  
215 was increased, in the presence of a re-seeding reservoir of all three species, the other  
216 two species (orange and green) were able to coexist with the targeted species (blue)  
217 during low levels of antibiotic perturbation (Fig. 3B,  $d_1 = 0.5$ ), analogous to the initial  
218 increase in coexistence region size when the more generalist species was targeted in a  
219 two-member community (Fig. 2B). As the death rate of the targeted species was  
220 increased further, the rescaled consumption rates indicated that the targeted species  
221 became more specialized (i.e., moved away from the supplied resource point at the center  
222 of the simplex), whereas the other two species became more like generalists due to the  
223 relative increase in their enzyme budgets compared to that of the targeted species. The  
224 perturbed convex hull shifted toward the niche of the targeted species (Fig. 3A, S2), and  
225 in doing so, transited through six coexistence states (Fig. 3B), including two where all  
226 three species coexisted (Fig. 3B,  $d_1 = 0.5, d_1 = 8$ ), until the targeted species eventually  
227 became extinct at large enough death rates (Fig. 3B,  $d_1 = 10$  ). This example  
228 demonstrates that increasing antibiotic concentration can lead to numerous, non-  
229 monotonic richness changes representing different coexistence states.

230

231 To quantify the prevalence of non-monotonic richness changes in response to increasing  
232 antibiotic concentration, we fixed the resource consumption rates of the two non-targeted  
233 species as in Fig. 3A and varied the consumption rates of the targeted species throughout  
234 the simplex. For each set of consumption rates, we calculated the number of changes in  
235 community richness as the death rate of the targeted species was increased from zero  
236 until the targeted species went extinct. As long as the targeted species was able to coexist  
237 prior to antibiotic perturbation, which was true for almost all of the simplex in this example,  
238 there were at least two richness changes (Fig. 3C), corresponding to a non-targeted  
239 species emerging from extinction into coexistence followed by the targeted species going  
240 extinct. Moreover, when the consumption niche of the targeted species was biased

241 against the resource that was least preferred by the non-targeted species (resource 3 in  
242 Fig. 3C), indicating more competition, the number of richness changes was typically  
243 larger, with a maximum value of five occurring when the targeted species consumed its  
244 two preferred resources at approximately equal rates (Fig. 3C). Taken together, these  
245 results demonstrate that non-monotonic behavior is likely to be prevalent across resource  
246 competition landscapes.

247

248 ***Non-transitive effects during sequential antibiotic treatments typically arise from***  
249 ***promotion of antibiotic-induced extinctions by resource competition***

250 In cases involving targeting of a pathogen, antibiotics are commonly administered  
251 sequentially to reduce the emergence of antibiotic resistance in the pathogen (Batra *et*  
252 *al.*, 2021). This sequential treatment can have nonintuitive effects on commensal  
253 members of the microbiota. To predict the effects of sequential treatment in a community  
254 context, we asked whether the final richness in our model is dependent on the sequence  
255 in which two antibiotics are sequentially applied (transitivity). We first examined a  
256 community of three coexisting species and simulated the sequential application of two  
257 narrow-spectrum antibiotics that each target one of the three species (Fig. 4A). For each  
258 antibiotic, we simulated the population dynamics until steady state was reached. In this  
259 example, the blue species was driven extinct when it was targeted first (Fig. 4B, top left).  
260 Next, the antibiotic targeting the blue species was removed. The orange species was then  
261 targeted and became extinct as the green species encroached on its niche (Fig. 4B, top  
262 right). Thus, this treatment sequence eventually led to the presence of only one species  
263 (Fig. 4C, top).

264

265 However, when the antibiotic treatment sequence was reversed, the community reached  
266 a distinct state. When the orange species was targeted first, it went extinct (Fig. 4B,  
267 bottom left). Next, when the blue species was targeted, it was not outcompeted by the  
268 green species (Fig. 4B, bottom right) and the two coexisted (Fig. 4C, bottom). Thus, the  
269 reverse sequence of treatment qualitatively altered the final coexistence (Fig. 4C, bottom)  
270 and the absolute value of the richness difference between the two sequences  $\Delta\rho$  was 1  
271 (non-transitivity, Fig. 4C). For this community, the extinction of the blue species was

272 dependent on competition between the orange and blue species (Fig. 4B), hence an  
273 antibiotic that eliminated the orange species allowed the blue species to coexist with the  
274 green species even when the blue species was later targeted (Fig. 4B, bottom). That is,  
275 the mechanism leading to non-transitivity was competition promoting the action of the  
276 antibiotic that targets the blue species (Fig. 4B, top left, bottom right), while the antibiotic  
277 that targets the orange species caused the extinction of the orange species regardless of  
278 community context (Fig. 4B, top right, bottom left). Another scenario that can result in  
279 non-transitivity is competition neutralizing the action of one antibiotic but not the other. In  
280 an example of neutralization (Fig. 4D-F), the antibiotic that targets the orange species  
281 only caused extinction of the orange species when the blue species was absent (Fig. 4E,  
282 bottom left and Fig. 4E, top right). Because the antibiotic that targets the orange species  
283 was neutralized by competition while the antibiotic that targets the blue species caused  
284 the blue species to go extinct regardless of community context (Fig. 4E, top left and Fig.  
285 4E, bottom right),  $\Delta\rho = 1$  (Fig. 4F).

286

287 To explore the conditions under which the final richness depends on antibiotic  
288 sequencing, we calculated  $\Delta\rho$  for the community in Fig. 4A across a five-dimensional  
289 parameter space: the distances  $D_{T1} \in (0, \sqrt{2/3})$  and  $D_{T2} \in (0, \sqrt{2/3})$  from the supplied  
290 resource point to the consumption rates of the two targeted species, the distance between  
291 the non-targeted species and the supplied resource point  $D_N \in (0, \sqrt{2/3})$  (Fig. 4A), and  
292 the death rates of the two targeted species,  $d_1 \in (0, 1)$ ,  $d_2 \in (0, 1)$ . We varied each of  
293 these five parameters independently across their respective domains, calculating  $\Delta\rho$  for  
294 all combinations of parameter values. In all cases,  $\Delta\rho$  was 0 or 1, with  $\Delta\rho = 1$  when the  
295 final richness after an antibiotic sequence was 2 and the final richness after the reverse  
296 sequence was 1 (or vice versa); if the final richness after an antibiotic sequence is 3, then  
297 the final richness after the reverse sequence must also be 3, and thus  $\Delta\rho = 0$ . This  
298 behavior occurs when  $D_N$  is sufficiently large ( $D_N \gtrsim 0.5$ ), so that the non-targeted species  
299 is a specialist for its unique resource and hence cannot outcompete any other species in  
300 pairwise competition. As a result, the richness after any antibiotic sequence was  $\geq 2$  (Fig.  
301 S3), hence  $\Delta\rho$  was always 0.

302

303 We found that all occurrences of nonzero  $\Delta\rho$  could be classified by resource competition  
304 either promoting (Fig. 4A-C) or neutralizing (Fig. 4D-F) antibiotic action for one of the two  
305 antibiotics. Neutralization was less common than promotion, with neutralization and  
306 promotion accounting for 23.1% and 76.9%, respectively, of nonzero  $\Delta\rho$  cases. Resource  
307 competition structures strongly affected the prevalence of non-transitivity by promotion or  
308 neutralization (Fig. 4G,H). On average across all values of other parameters, promotion  
309 was most likely to occur when  $D_{T1}$  or  $D_{T2}$  was  $< 0.2$  (Fig. 4G, red), in which case one of  
310 the targeted species is a generalist and thus can outcompete the other targeted species  
311 to extinction (Fig. 4B, top left). Furthermore, promotion was more likely for intermediate  
312  $D_N \sim 0.4$  such that the non-targeted species could outcompete one of the targeted species  
313 during pairwise competition but not the other (Fig. 4B). Conversely, neutralization was  
314 most likely to occur when both  $D_{T1}$  and  $D_{T2}$  were  $> 0.4$  (Fig. 4G, blue), in which case the  
315 targeted species cannot outcompete each other during antibiotics since they are  
316 specialists with distinct niches. Instead, extinction occurred because the non-targeted  
317 species was a generalist that could outcompete one of the targeted species in pairwise  
318 competition ( $D_N \lesssim 0.3$ , Fig. 4H, blue). For both promotion and neutralization, we found  
319 that there must be a balance between  $D_N$  and the death rates such that resource  
320 competition promotes or neutralizes the action of only one of the antibiotics but not the  
321 other (Fig. 4H). In sum, these simulations show that resource competition structures can  
322 be prone to non-transitivity under sequential treatment via either promotion or  
323 neutralization of antibiotic activity (Fig. 4G,H).

324

325 ***Antagonistic effects on community richness due to antibiotic combinations are***  
326 ***more common than synergism***

327 In addition to dosage and scheduling, another common strategy for treating infections is  
328 the simultaneous use a cocktail of multiple antibiotics to avoid the emergence of  
329 resistance. An important consideration when choosing antibiotics to act on individual  
330 species is the potential for synergistic or antagonistic effects (Baym et al., 2016; Brochado  
331 et al., 2018; Torella et al., 2010). To investigate the extent of interactions among  
332 antibiotics in a community context, we considered three species with equal enzyme  
333 budgets competing for three resources (Fig. 5A), with symmetry of the community under

334 swapping of the two targeted species ( $D_{T1} = D_{T2}$ ) and the antibiotics that target them  
335 ( $d_1 = d_2$ ). When either one of the targeted species was individually subjected to a  
336 sufficiently large death rate, it was driven extinct (Fig. 5B), as expected. However, when  
337 the death rates of both targeted species were increased simultaneously, all species were  
338 able to coexist (Fig. 5C). The changes in enzyme budgets due to both antibiotics  
339 effectively nullified each other, returning the consumption rate vectors to locations near  
340 their original locations in the simplex (Fig. 5C), hence neither of the targeted species  
341 gained a competitive advantage over the other. Although the non-targeted species  
342 (green) became more of a generalist under the activity of both antibiotics, it was initially  
343 sufficiently specialized that the remapped convex hull still included the supplied resource  
344 point. Thus, for this community, the combination of antibiotics resulted in antagonism.

345

346 Next, we considered a community with larger  $D_{T1} = D_{T2}$  and with the non-targeted  
347 species (green) more of a generalist than in the example above that exhibited antagonism  
348 (Fig. 5D). When one of the species was targeted individually, it became more specialized  
349 and the non-targeted species moved toward the consumption niche of the targeted  
350 species, but the remapped convex hull still enclosed the supplied resource point, resulting  
351 in coexistence of all three species (Fig. 5E). However, when both species were  
352 simultaneously targeted, the non-targeted species became more competitive against the  
353 targeted species and its remapped consumption rates moved past the supplied resource  
354 point, allowing it to drive both targeted species extinct (Fig. 5F). The cumulative effect of  
355 targeting both species thus resulted in synergism.

356

357 To quantify the prevalence of synergism and antagonism across community structures,  
358 we varied the distance between the consumption rates of the two targeted species  $D_T$  by  
359 varying  $D_{T1} = D_{T2}$ , the distance between the non-targeted species and the supplied  
360 resource point  $D_N$ , and the death rate of both targeted species during antibiotics  $d_1 =$   
361  $d_2 \in (0,1)$ . We varied all three parameters ( $D_N, D_{T1}, d_1$ ) independently and calculated the  
362 fraction of communities that exhibited synergism or antagonism as a function of two  
363 parameters, averaging over the other parameter. Antagonism occurred most often when  
364 the niches of the targeted species were somewhat similar ( $D_T \lesssim 0.4$ ) and the non-targeted

365 species was sufficiently specialized ( $D_N \gtrsim 0.4$ ), and synergism occurred in the opposite  
366 regime (Fig. 5G). This behavior is consistent with the example communities discussed  
367 above: for antagonism, each targeted species must be driven extinct when targeted alone  
368 ( $D_T \lesssim 0.4$ ) and the non-targeted species must not outcompete the two targeted species  
369 when both are simultaneously targeted ( $D_N \gtrsim 0.4$ ), and vice versa for synergism.  
370 Increasing the death rates of the targeted species commensurately ( $d_1 = d_2$ ) increased  
371 the minimum  $D_N$  required for synergism and antagonism (Fig. 5H), as expected.  
372

373 To investigate whether these trends generalized, we generated communities with  
374 consumption rate vectors sampled uniformly across the simplex without enforcing any  
375 symmetry (Fig. 5I), sampled the two death rates independently from a uniform distribution  
376 between 0 and 1, and supplied all three resources at equal rates. Similar to the trends  
377 observed with symmetry (Fig. 5G,H), communities with smaller  $D_N$  and larger  $D_T$  were  
378 more likely to exhibit synergism (Fig. 5J, red) and communities with larger  $D_N$  and smaller  
379  $D_T$  were more likely to exhibit antagonism (Fig. 5J, blue). Moreover, to exhibit synergism,  
380 communities with larger  $D_N$  required a larger value of the smaller of the two death rates  
381  $d_{\min}$  (Fig. S4). This condition enables the non-targeted species to outcompete the  
382 targeted species, which either requires that the non-targeted species is a generalist that  
383 is close to outcompeting the other species before antibiotic perturbation or that the  
384 antibiotic perturbation is sufficiently large. Similarly, communities with larger  $d_{\min}$  required  
385 a larger  $D_N$  to exhibit antagonism (Fig. S4), generalizing the observation that increasing  
386 the death rate of the targeted species in the symmetric scenario in Fig. 5A increased the  
387 minimum  $D_N$  required for antagonism (Fig. 5H). These simulations also demonstrated  
388 that communities can be prone to synergistic and antagonistic effects due to resource  
389 competition alone during antibiotic combinations, but typically not both (Fig. 5G,H,J), and  
390 that antagonism is more common (Fig. 5J).  
391

### 392 ***Overlap in mechanisms underlying non-transitivity and non-additivity***

393 Since resource competition structures can be prone to neutralizing or promoting antibiotic  
394 action during sequential treatment (non-transitivity, Fig. 4) and to synergism or  
395 antagonism during simultaneous treatment (non-additivity, Fig. 5), we wondered to what

396 extent the underlying mechanisms were connected. For communities parametrized by  
397  $D_N$ ,  $D_{T1}$ , and  $D_{T2}$ , structures prone to neutralization and promotion (Fig. 4H) were  
398 approximate subsets of those prone to synergism and antagonism (Fig. 5H), respectively.  
399 The same trends generalized to scenarios with randomly drawn structures and death  
400 rates (Fig. 5I): Of 100,000 communities, non-transitivity due to promotion and  
401 neutralization occurred in 10,482 and 647, respectively, and non-additivity due to  
402 antagonism and synergism occurred in 37,782 and 1,156 cases, respectively. Strikingly,  
403 100% of the communities exhibiting non-transitivity due to promotion also exhibited non-  
404 additivity due to antagonism, and >97% of the scenarios exhibiting neutralization also  
405 exhibited synergism (Table 2). These findings highlight the significant overlap in  
406 mechanisms underlying non-additivity and non-transitivity.

407 **DISCUSSION**

408 The ability to predict microbial community dynamics after antibiotic treatment would be a  
409 powerful tool for minimizing unintended consequences of treatment. Motivated by growing  
410 evidence that resource competition plays a dominant role in shaping microbial community  
411 dynamics both without and during antibiotic perturbation, we introduced species-specific  
412 death rates to a CR model and analyzed community responses across a wide range of  
413 clinically relevant antibiotic treatment strategies. We found that increasing antibiotic  
414 intensity can lead to non-monotonic richness changes in the presence of a re-seeding  
415 reservoir due to changes in the competitive landscape (Fig. 3), and that the final  
416 community can differ qualitatively when the sequence of antibiotic application is reversed  
417 (Fig. 4). Furthermore, we quantified properties of resource competition landscapes that  
418 give rise to antibiotic synergism or antagonism (Fig. 5), suggesting that the effects of  
419 antibiotic perturbation are generally dependent on the metabolic properties of the  
420 exposed community. Intriguingly, we find that antagonism emerges in communities with  
421 symmetry between the consumption rates of the two targeted species when the non-  
422 targeted species is sufficiently specialized (Fig. 5A); this scenario mimics the origins of  
423 antagonism in the context of a single species, wherein simultaneous targeting of two  
424 distinct cellular processes mitigates the defects due to targeting of only one of the  
425 processes (Brochado *et al.*, 2018). Our findings reveal a wide range of phenomena  
426 explainable by resource competition alone, warranting caution when interpreting  
427 phenomena that might otherwise be attributed to chemical transformations of antibiotics  
428 or other biological mechanisms. Moreover, our results motivate quantification of the  
429 competitive landscape of communities (Ho *et al.*, 2022b), whereby the determination of  
430 generalists and specialists will help to predict treatment outcomes.

431

432 There are countless combinations of complex antibiotic cocktails (simultaneous drug  
433 administration) and treatment scheduling strategies (such as an alternating antibiotic  
434 schedule (Marrec and Bitbol, 2020)) involving broad-spectrum antibiotics. To predict  
435 microbial community dynamics in response to such complex antibiotic perturbations, we  
436 analyzed two key “building block” scenarios at the heart of antibiotic treatment regimens:  
437 the swapping of application order of two narrow-spectrum antibiotics and the

438 simultaneous application of two narrow-spectrum antibiotics. Understanding the interplay  
439 between resource competition and antibiotics in these minimal scenarios is the first step  
440 in predicting community dynamics during more complex antibiotic perturbations (and in  
441 communities with more species and nutrients) that occur in a clinical setting. For example,  
442 we can straightforwardly apply our model predictions during the simultaneous application  
443 of two narrow-spectrum antibiotics that each target a different species to a broad-  
444 spectrum antibiotic that simultaneously targets the two species.

445

446 Beyond responses of the human gut microbiota to antibiotics, our analyses can be broadly  
447 applied to other communities and to understand the effects of other environmental  
448 perturbations. Inhibition of growth is prevalent in other contexts, including soil  
449 communities, which produce numerous antimicrobials (Olanrewaju and Babalola, 2019),  
450 and wastewater communities, which can contain a wide spectrum of antibiotics  
451 (Jendrzejewska and Karwowska, 2018). In the context of our model, by allowing death  
452 rates to be both species-specific and also dependent on the presence of other species,  
453 our framework could be extended to scenarios in which antibiotics are produced and/or  
454 modified by community members. Moreover, microbial communities including the gut  
455 microbiota contain diverse bacteriophages whose deleterious effects on their bacterial  
456 host communities are not fully understood (Salmond and Fineran, 2015; Shkoporov et al.,  
457 2018). Changes in environmental parameters like temperature (Knapp and Huang, 2022),  
458 osmolarity (Tropini et al., 2018), or pH (Amor et al., 2020), likely rescale consumption  
459 rates in species-dependent manners similar qualitatively to antibiotics. *In vitro*  
460 measurements of the sensitivities of each community member to such parameters could  
461 be combined with parameterization of the competitive landscape (Ho et al., 2022b) to  
462 enable quantitative prediction of community responses.

463

464 In addition to killing, our findings suggest that deleterious agents can be used to engineer  
465 community dynamics at sublethal doses. Developing such engineering strategies will  
466 require new experiments to characterize the interplay between resource competition and  
467 antibiotic activity; these experiments include screens of communities grown *in vitro*  
468 (Aranda-Diaz et al., 2022; Goldford et al., 2018), and mouse models subject to lower than

469 usual doses of antibiotics. It will also be important to analyze model behavior out of steady  
470 state, including serial dilution protocols mimicking the periodic turnover of the gut  
471 environment that could result in fundamentally different and interesting behaviors. Other  
472 interspecies interactions such as cross-feeding, which can be incorporated into CR  
473 models (Lopez and Wingreen, 2022), may also generate the potential for community-  
474 dependent antibiotic responses. This work provides a null model for these critical future  
475 endeavors.

476 **METHODS**

477 *Simulations of population dynamics*

478 We simulated species abundances over time in Python using the SciPy function  
479 `scipy.integrate.solve_ivp`, an explicit Runge-Kutta method for solving ordinary differential  
480 equations. We integrated all species abundances  $n_i$  until they reached steady state,  
481 defined as when all species either satisfy  $\left| \frac{d^2}{dt^2} \ln(n_i) \right| < 10^{-6}$  or  $n_i$  decreases below a  
482 threshold abundance  $10^{-7}$  (signifying extinction and removal from the community). To  
483 calculate richness, we counted the number of species that satisfied the conditions  $n_i >$   
484  $10^{-7}$  and  $\frac{d}{dt} \ln(n_i) > -10^{-3}$  at steady state. For three species and three resources, the  
485 steady-state abundances of the three species can be directly calculated using a  
486 straightforward algorithm (Supplemental Text).

487

488 *Dimensionless parameters*

489 For simulating population dynamics, we introduced dimensionless parameters for time  
490  $t' \equiv td$ , for species abundance  $n'_i \equiv n_i(d/S)$ , for resource consumption rate  $R'_{i\mu} \equiv$   
491  $R_{i\mu}(S/d^2)$ , for death rate  $(d + d_i)' \equiv (d + d_i)/d$ , and for resource supply rate  $s'_\mu \equiv s_\mu/S$ .  
492 We can write Eq. 3 in terms of these dimensionless parameters as follows:

$$493 \frac{dn'_i}{dt'} = n'_i \left( \sum_{\mu=1}^p \frac{R'_{i\mu} s'_\mu}{\sum_{k=1}^m n'_k R'_{k\mu}} - (1 + d'_i) \right),$$

494 where  $s'_\mu$  is the relative supply rate of resource  $\mu$  such that  $\sum_{\mu=1}^p s'_\mu = 1$ .

495

496 *Simulations of randomly drawn communities*

497 Unless stated otherwise, we selected  $\vec{R}_i$ ,  $\vec{d}$  from a uniform distribution on the unit simplex,  
498 i.e., from the space of  $m$ -dimensional vectors such that the sum of the elements is 1. We  
499 chose  $\vec{s}$  such that all resources were supplied at equal rates.

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507 **REFERENCES**

- 508 Adamowicz, E.M., Flynn, J., Hunter, R.C., and Harcombe, W.R. (2018). Cross-feeding  
509 modulates antibiotic tolerance in bacterial communities. *ISME J* 12, 2723-2735.
- 510 Amor, D.R., and Gore, J. (2022). Fast growth can counteract antibiotic susceptibility in  
511 shaping microbial community resilience to antibiotics. *Proc Natl Acad Sci* 119,  
512 e2116954119.
- 513 Amor, D.R., Ratzke, C., and Gore, J. (2020). Transient invaders can induce shifts  
514 between alternative stable states of microbial communities. *Sci Adv* 6, eaay8676.
- 515 Andrews, J.M. (2001). Determination of minimum inhibitory concentrations. *J Antimicrob  
516 Chemother* 48 Suppl 1, 5-16.
- 517 Aranda-Diaz, A., Ng, K.M., Thomsen, T., Real-Ramirez, I., Dahan, D., Dittmar, S.,  
518 Gonzalez, C.G., Chavez, T., Vasquez, K.S., Nguyen, T.H., et al. (2022). Establishment  
519 and characterization of stable, diverse, fecal-derived in vitro microbial communities that  
520 model the intestinal microbiota. *Cell Host Microbe* 30, 260-272 e265.
- 521 Batra, A., Roemhild, R., Rousseau, E., Franzenburg, S., Niemann, S., and Schulenburg,  
522 H. (2021). High potency of sequential therapy with only beta-lactam antibiotics. *eLife* 10.
- 523 Baym, M., Stone, L.K., and Kishony, R. (2016). Multidrug evolutionary strategies to  
524 reverse antibiotic resistance. *Science* 351, aad3292.
- 525 Bottery, M.J., Pitchford, J.W., and Friman, V.-P. (2021). Ecology and evolution of  
526 antimicrobial resistance in bacterial communities. *ISME J* 15, 939-948.
- 527 Brochado, A.R., Telzerow, A., Bobonis, J., Banzhaf, M., Mateus, A., Selkirk, J., Huth, E.,  
528 Bassler, S., Zamarreno Beas, J., Zietek, M., et al. (2018). Species-specific activity of  
529 antibacterial drug combinations. *Nature* 559, 259-263.
- 530 Cani, P.D. (2018). Human gut microbiome: hopes, threats and promises. *Gut* 67, 1716-  
531 1725.
- 532 Chesson, P. (1990). MacArthur's consumer-resource model. *Theor Popul Biol* 37, 26-38.
- 533 De Leenheer, P., and Cogan, N.G. (2009). Failure of antibiotic treatment in microbial  
534 populations. *J Math Biol* 59, 563-579.
- 535 de Vos, M.G., Zagorski, M., McNally, A., and Bollenbach, T. (2017). Interaction networks,  
536 ecological stability, and collective antibiotic tolerance in polymicrobial infections. *Proc Natl  
537 Acad Sci* 114, 10666-10671.
- 538 Goldford, J.E., Lu, N., Bajic, D., Estrela, S., Tikhonov, M., Sanchez-Gorostiaga, A., Segre,  
539 D., Mehta, P., and Sanchez, A. (2018). Emergent simplicity in microbial community  
540 assembly. *Science* 361, 469-474.

- 541 Gowda, K., Ping, D., Mani, M., and Kuehn, S. (2022). Genomic structure predicts  
542 metabolite dynamics in microbial communities. *Cell* 185, 530-546.
- 543 Hallinen, K.M., Karslake, J., and Wood, K.B. (2020). Delayed antibiotic exposure induces  
544 population collapse in enterococcal communities with drug-resistant subpopulations.  
545 *eLife* 9.
- 546 Ho, P.-Y., Good, B.H., and Huang, K.C. (2022a). Competition for fluctuating resources  
547 reproduces statistics of species abundance over time across wide-ranging microbiotas.  
548 *eLife* 11, e75168.
- 549 Ho, P.-Y., Nguyen, T.H., Sanchez, J.M., DeFelice, B.C., and Huang, K.C. (2022b).  
550 Resource competition predicts assembly of in vitro gut bacterial communities. *bioRxiv*.
- 551 Hromada, S., Qian, Y., Jacobson, T.B., Clark, R.L., Watson, L., Safdar, N., Amador -  
552 Noguez, D., and Venturelli, O.S. (2021). Negative interactions determine Clostridioides  
553 difficile growth in synthetic human gut communities. *Mol Syst Biol* 17, e10355.
- 554 Jendrzejewska, N., and Karwowska, E. (2018). The influence of antibiotics on wastewater  
555 treatment processes and the development of antibiotic-resistant bacteria. *Water Sci  
556 Technol* 77, 2320-2326.
- 557 Jost, L. (2006). Entropy and diversity. *Oikos* 113, 363-375.
- 558 Knapp, B.D., and Huang, K.C. (2022). The effects of temperature on cellular physiology.  
559 *Annu Rev Biophys* 51, 499-526.
- 560 Kohanski, M.A., Dwyer, D.J., and Collins, J.J. (2010). How antibiotics kill bacteria: from  
561 targets to networks. *Nat Rev Microbiol* 8, 423-435.
- 562 Lopez, J.G., and Wingreen, N.S. (2022). Noisy metabolism can promote microbial cross-  
563 feeding. *eLife* 11.
- 564 Maier, L., Goemans, C.V., Wirbel, J., Kuhn, M., Eberl, C., Pruteanu, M., Muller, P., Garcia-  
565 Santamarina, S., Cacace, E., Zhang, B., et al. (2021). Unravelling the collateral damage  
566 of antibiotics on gut bacteria. *Nature* 599, 120-124.
- 567 Maier, L., Pruteanu, M., Kuhn, M., Zeller, G., Telzerow, A., Anderson, E.E., Brochado,  
568 A.R., Fernandez, K.C., Dose, H., Mori, H., et al. (2018). Extensive impact of non-antibiotic  
569 drugs on human gut bacteria. *Nature* 555, 623-628.
- 570 Marrec, L., and Bitbol, A.-F. (2020). Resist or perish: Fate of a microbial population  
571 subjected to a periodic presence of antimicrobial. *PLoS Comput Biol* 16, e1007798.
- 572 Marsland, R., 3rd, Cui, W., Goldford, J., Sanchez, A., Korolev, K., and Mehta, P. (2019).  
573 Available energy fluxes drive a transition in the diversity, stability, and functional structure  
574 of microbial communities. *PLoS Comput Biol* 15, e1006793.

- 575 Ng, K.M., Aranda-Diaz, A., Tropini, C., Frankel, M.R., Van Treuren, W., O'Loughlin, C.T.,  
576 Merrill, B.D., Yu, F.B., Pruss, K.M., Oliveira, R.A., et al. (2019). Recovery of the gut  
577 microbiota after antibiotics depends on host diet, community context, and environmental  
578 reservoirs. *Cell Host Microbe* 26, 650-665 e654.
- 579 Olanrewaju, O.S., and Babalola, O.O. (2019). Streptomyces: implications and  
580 interactions in plant growth promotion. *Appl Microbiol Biotechnol* 103, 1179-1188.
- 581 Owens Jr, R.C., Donskey, C.J., Gaynes, R.P., Loo, V.G., and Muto, C.A. (2008).  
582 Antimicrobial-associated risk factors for *Clostridium difficile* infection. *Clin Infect Dis* 46,  
583 S19-S31.
- 584 Posfai, A., Taillefumier, T., and Wingreen, N.S. (2017). Metabolic trade-offs promote  
585 diversity in a model ecosystem. *Phys Rev Lett* 118, 028103.
- 586 Salmond, G.P., and Fineran, P.C. (2015). A century of the phage: past, present and  
587 future. *Nat Rev Microbiol* 13, 777-786.
- 588 Schubert, A.M., Sinani, H., and Schloss, P.D. (2015). Antibiotic-induced alterations of the  
589 murine gut microbiota and subsequent effects on colonization resistance against  
590 *Clostridium difficile*. *mBio* 6, e00974-00915.
- 591 Segura Munoz, R.R., Mantz, S., Martinez, I., Li, F., Schmaltz, R.J., Pudlo, N.A., Urs, K.,  
592 Martens, E.C., Walter, J., and Ramer-Tait, A.E. (2022). Experimental evaluation of  
593 ecological principles to understand and modulate the outcome of bacterial strain  
594 competition in gut microbiomes. *ISME J* 16, 1594-1604.
- 595 Shkorporov, A.N., Khokhlova, E.V., Fitzgerald, C.B., Stockdale, S.R., Draper, L.A., Ross,  
596 R.P., and Hill, C. (2018). PhiCrAss001 represents the most abundant bacteriophage  
597 family in the human gut and infects *Bacteroides intestinalis*. *Nat Commun* 9, 4781.
- 598 Taillefumier, T., Posfai, A., Meir, Y., and Wingreen, N.S. (2017). Microbial consortia at  
599 steady supply. *eLife* 6.
- 600 Taur, Y., Jenq, R.R., Perales, M.A., Littmann, E.R., Morjaria, S., Ling, L., No, D.,  
601 Gobourne, A., Viale, A., Dahi, P.B., et al. (2014). The effects of intestinal tract bacterial  
602 diversity on mortality following allogeneic hematopoietic stem cell transplantation. *Blood*  
603 124, 1174-1182.
- 604 Torella, J.P., Chait, R., and Kishony, R. (2010). Optimal drug synergy in antimicrobial  
605 treatments. *PLoS Comput Biol* 6, e1000796.
- 606 Tropini, C., Moss, E.L., Merrill, B.D., Ng, K.M., Higginbottom, S.K., Casavant, E.P.,  
607 Gonzalez, C.G., Fremin, B., Bouley, D.M., Elias, J.E., et al. (2018). Transient osmotic  
608 perturbation causes long-term alteration to the gut microbiota. *Cell* 173, 1742-1754.
- 609 Wood, K.B., and Cluzel, P. (2012). Trade-offs between drug toxicity and benefit in the  
610 multi-antibiotic resistance system underlie optimal growth of *E. coli*. *BMC Syst Biol* 6, 48.

611 Xu, X., Xu, L., Yuan, G., Wang, Y., Qu, Y., and Zhou, M. (2018). Synergistic combination  
612 of two antimicrobial agents closing each other's mutant selection windows to prevent  
613 antimicrobial resistance. *Sci Rep* 8, 1-7.

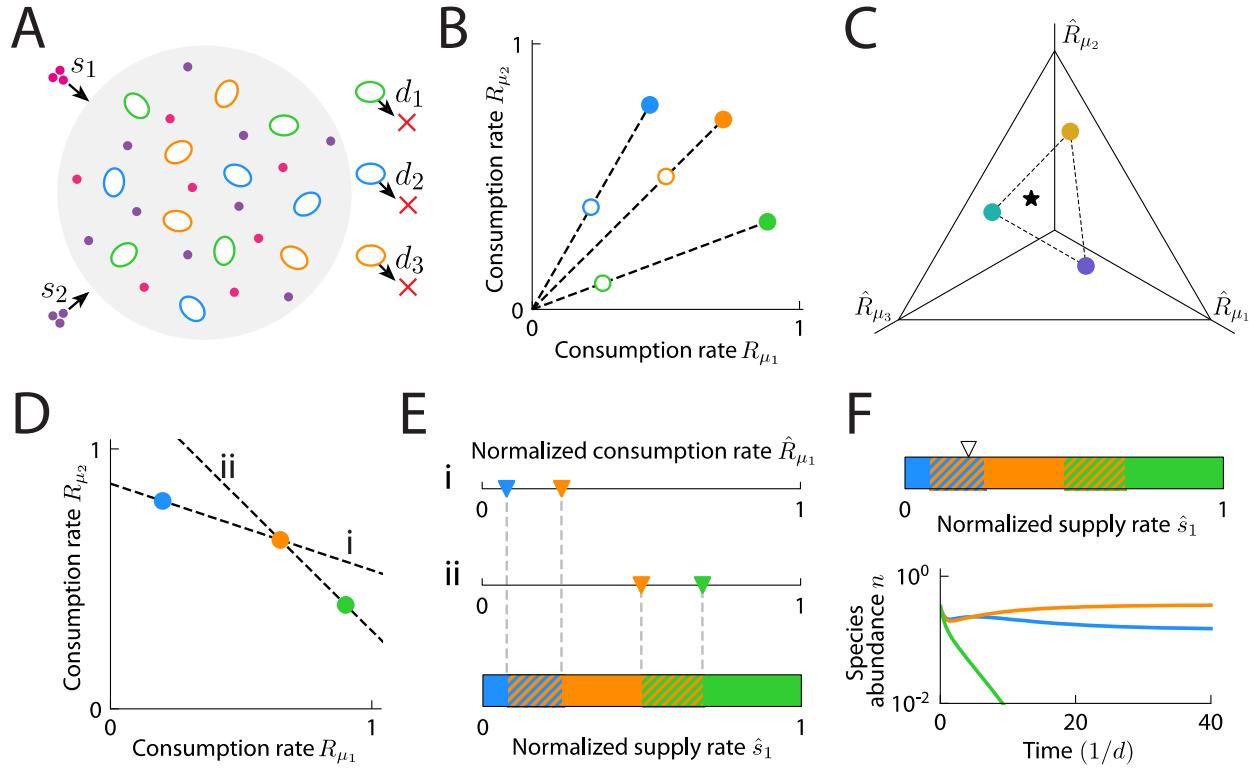
614 Yeh, P.J., Hegreness, M.J., Aiden, A.P., and Kishony, R. (2009). Drug interactions and  
615 the evolution of antibiotic resistance. *Nat Rev Microbiol* 7, 460-466.

616 Zimmermann, M., Patil, K.R., Typas, A., and Maier, L. (2021). Towards a mechanistic  
617 understanding of reciprocal drug-microbiome interactions. *Mol Syst Biol* 17,  
618 e10116.

619

620 **FIGURES**

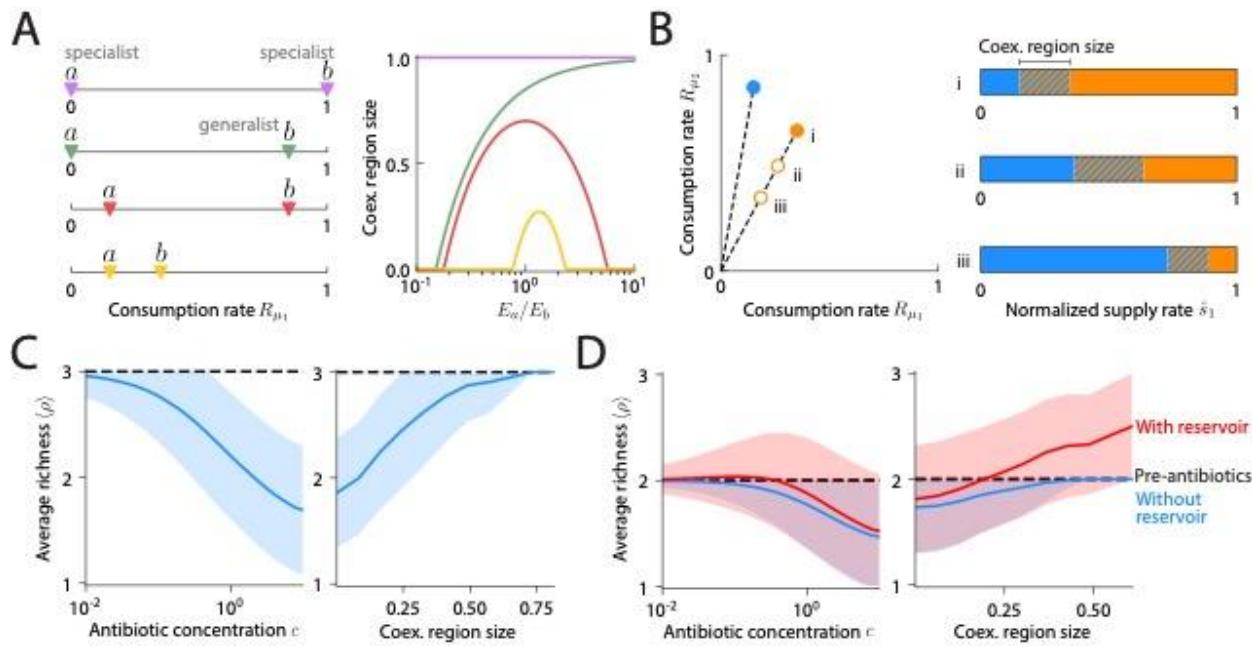
621



622 **Figure 1: Implementation of antibiotic activity in a CR model.**

- 623
- A) Schematic of a well-mixed CR model (Posfai *et al.*, 2017) with species-specific death rates  $d_i$ . Depicted are cells (colored ovals) from three species competing for two resources (small circles) supplied at rates  $s_\mu$ .
  - B) The effects of species-specific death rates on coexistence can be determined by reducing the consumption rates  $R_{i\mu}$  by  $b_i = (d + d_i)/d$ . The transformed consumption rates (open circles) have reduced enzyme budgets compared to the original consumption rates (filled circles).
  - C) When a community of three species competes for three resources, the consumption rates can be visualized on a simplex representing the hyperplane containing the consumption niches of the three species in the space of rescaled consumption rates. In the case shown, the convex hull of the species consumption rate vectors (dashed line) encloses the point representing the normalized resource supply rates (star), hence all species coexist (Posfai *et al.*, 2017).

- 637 D) Example in which two possible hyperplanes (dashed lines, i and ii) dictate the  
638 conditions for coexistence of three species (colored circles) competing for two  
639 resources.
- 640 E) Along each hyperplane, a pair of species coexists if the normalized resource  
641 supply rates  $\hat{s}_\mu$  lie between the rescaled consumption rates (colored triangles) of  
642 the species pair (hatched multicolored regions). Otherwise, only the species with  
643  $\hat{R}_{i\mu}$  closest to  $\hat{s}_\mu$  persists (solid regions).
- 644 F) Species dynamics (bottom) for the community shown in (D) for one case of supply  
645 rates (triangle, top).



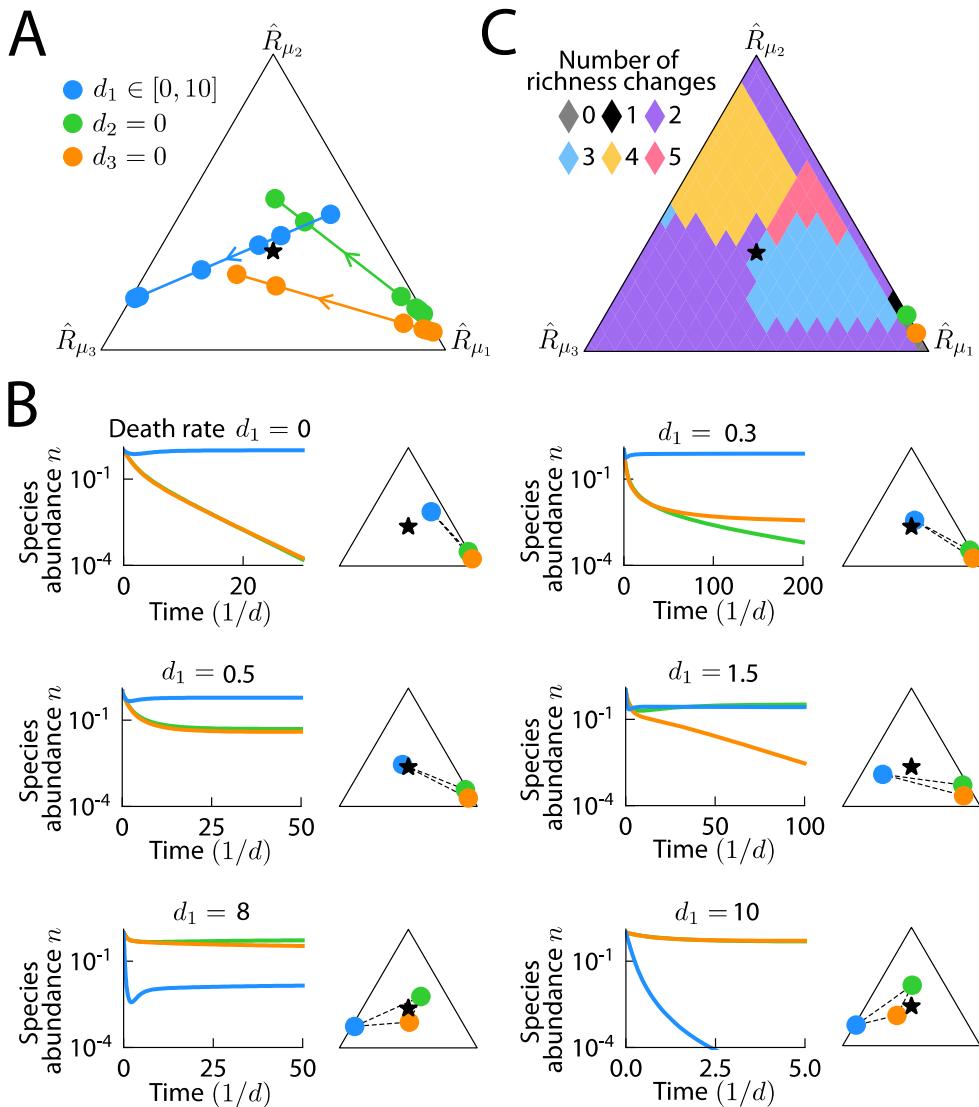
646

647 **Figure 2: Resource competition results in complex dependence of species**  
 648 **coexistence on antibiotic activity.**

- 649 A) Effect of antibiotic activity on two species (*a* and *b*) competing for two resources.  
 650 (Left) Four types of communities with qualitatively different consumption niches  
 651 were considered, including a specialist and a generalist (green), two specialists  
 652 (purple), two symmetrically distributed generalists (red), and two asymmetrically  
 653 distributed generalists (yellow). (Right) The fraction of supply rates that lead to  
 654 coexistence (coexistence region size) can depend non-monotonically on the  
 655 relative enzyme budget ( $E_a/E_b$  of species *a* and *b* on the left).
- 656 B) Example community consisting of a non-targeted species (blue) and a targeted  
 657 species (orange) that was initially more of a generalist (more equal consumption  
 658 of both resources). (Left) Antibiotic activity resulted in decreased enzyme budget  
 659 (empty circles). (Right) Map of coexistence regions as in Fig. 1E for the scenarios  
 660 on the left.
- 661 C) Average richness decreases with increasing antibiotic concentration  $c$  (left) and  
 662 decreases with decreasing coexistence region size (right). Simulations of randomly drawn  
 663 communities of three species competing for three resources ( $m = p = 3$ ) with  
 664 consumption rates  $\vec{R}_i$  sampled uniformly from the unit simplex and all resources  
 665 supplied at equal rates. Average richness calculated across all communities with

666 richness of 3 before antibiotic perturbation. Antibiotic concentration  $c$  scales the  
667 death rates, i.e.,  $d_i \rightarrow cd_i$ .

668 D) A reservoir of species can lead to an increase in average richness during antibiotic  
669 perturbation. As in (C), but for communities with richness of 2 before antibiotic  
670 perturbation without (blue) or with a re-seeding pool of species to transiently  
671 repopulate the initially distinct species during antibiotic perturbation (red).

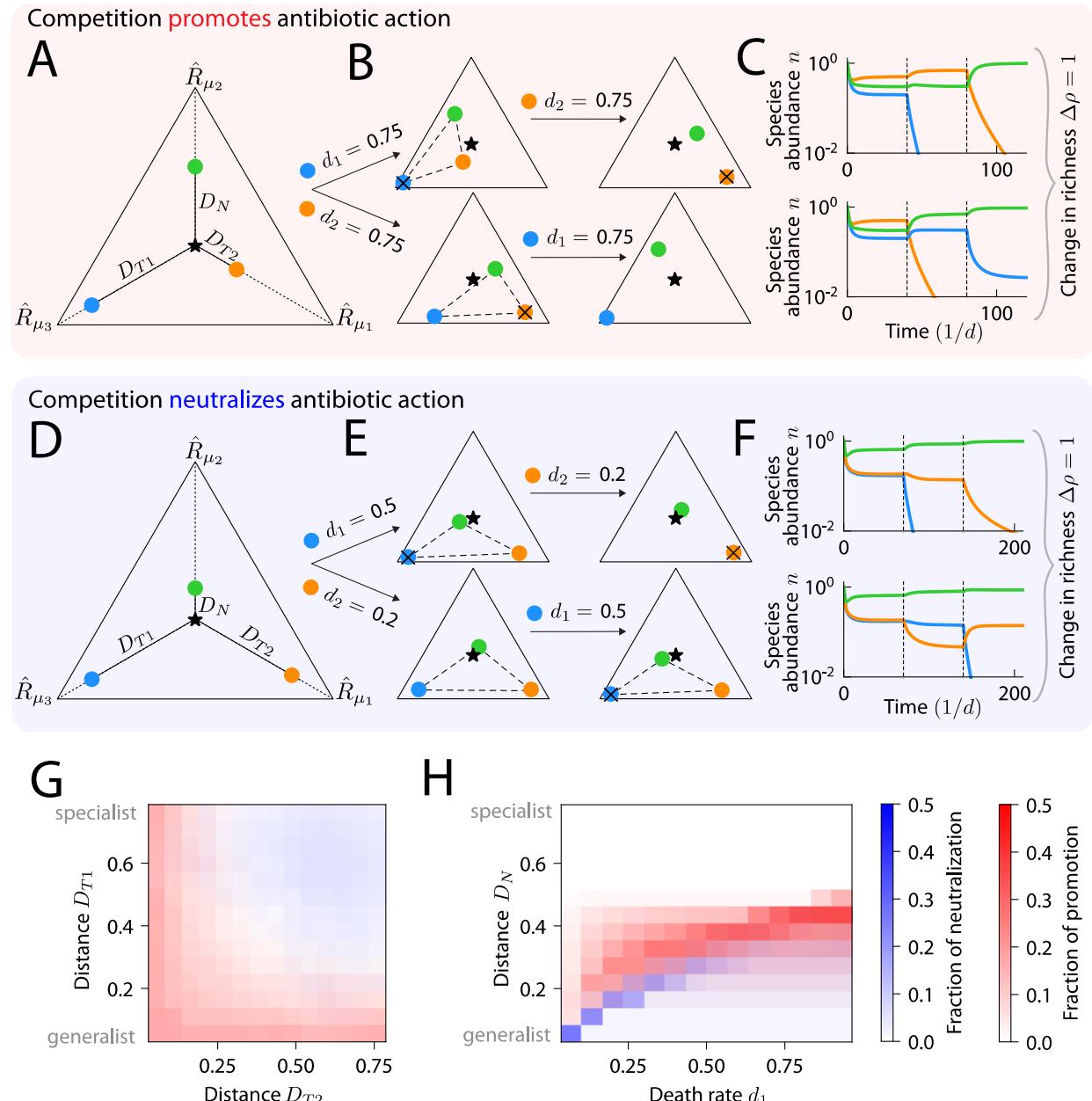


672

673 **Figure 3: Richness can change non-monotonically with increasing death rate.**

- 674 A) Trajectories of rescaled consumption rates as the death rate of the targeted  
 675 species (blue) is increased. Arrow denotes the direction of increasing death rate.  
 676 Circles mark the six death rates shown in (B). With increasing death rate, the  
 677 targeted species became more specialized, while the non-targeted species  
 678 became more of a generalist and closer to the supplied resource point at the center  
 679 of the simplex.
- 680 B) Population dynamics at the six death rates marked in (A). ( $d_1 = 0$ ) In the absence  
 681 of antibiotic targeting, only the blue species persisted. ( $d_1 = 0.3$ ) For low death  
 682 rates of the blue species, the orange species was able to coexist. ( $d_1 = 0.5$ ) There  
 683 was a range of death rates that allowed for coexistence of all three species. ( $d_1 =$

- 684 1.5) As the death rate was increased further, the orange species went extinct. ( $d_1 =$   
685 8) As the death rate increased even further, coexistence of all three species was  
686 again realized. ( $d_1 = 10$ ) Finally, at sufficiently high death rate the blue species  
687 went extinct.
- 688 C) Number of richness changes until the extinction of the targeted species as its  
689 consumption niche was varied across the simplex, while the consumption niches  
690 of the non-targeted species were fixed as in (A).

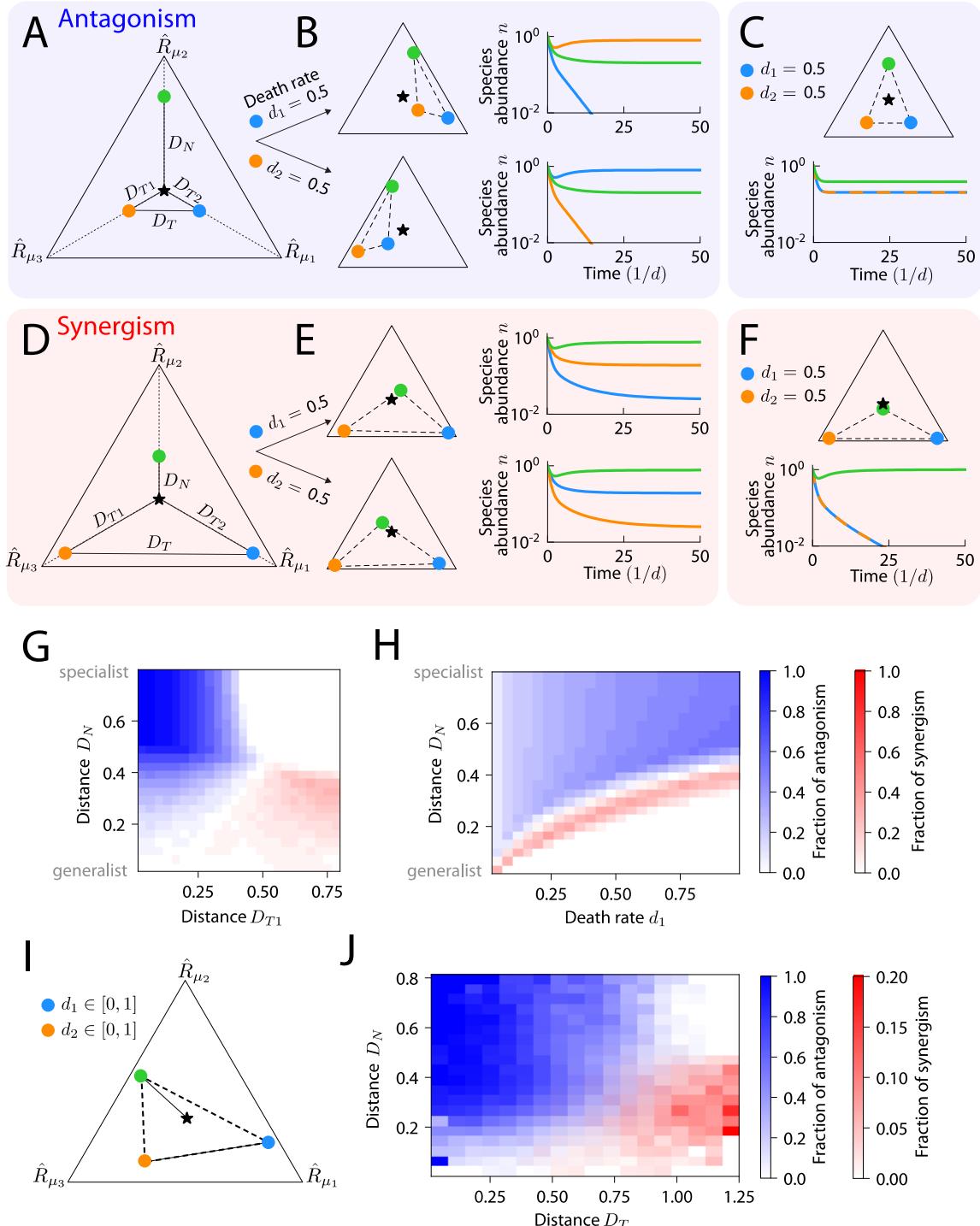


691

692 **Figure 4: Final coexistence is dependent on the sequence of antibiotic treatment.**

- 693 A) An example community of three species (colored circles) for which the sequence  
 694 of narrow-spectrum antibiotics can affect the final richness. The orange species  
 695 promoted the action of the antibiotic that targets the blue species, causing the final  
 696 richness to be non-transitive to the sequence of antibiotic treatment.
- 697 B) (Top left) Remapping of the consumption niche of all species when the death rate  
 698 of the blue species was increased. The blue species went extinct, as the remapped  
 699 convex hull does not enclose the supplied resource point. (Top right) Increasing

- 700 the death rate of the orange species after the extinction of the blue species led to  
701 its extinction. (Bottom row) Same as top row, but the sequence of sequential  
702 antibiotics was reversed. Now, the blue and green species coexisted after the two  
703 treatments, thus  $\Delta\rho = 1$ .
- 704 C) Population dynamics were simulated until steady state for the scenarios in (B):  
705 (top) first with zero death rates, then with nonzero death rate for the blue species,  
706 then with nonzero death rate for the orange species (and zero death rate for the  
707 now extinct blue species); (bottom) with the reversed sequence of death rates.
- 708 D) An example community with nonzero  $\Delta\rho$  due to the blue species neutralizing the  
709 action of the antibiotic that targets the orange species.
- 710 E) Like (B) but for the community in (D).
- 711 F) Like (C) but for the community in (D).
- 712 G) Prevalence of non-transitivity via promotion (red) or neutralization (blue) (or some  
713 combination of the two shown by overlapping red and blue) as a function of the  
714 resource competition structure.  $\Delta\rho$  was calculated and the mechanism of non-  
715 transitivity was determined for communities of the form in (A) and (D) across  
716 parameters  $(D_{T1}, D_{T2}, D_N, d_1, d_2)$ , for death rates  $d_1 \in (0, 1)$ ,  $d_2 \in (0, 1)$  and  $D_{T1},$   
717  $D_{T2}$ , and  $D_N$  across their entire domains. The fraction of promotion and  
718 neutralization were averaged across all combinations  $D_N$ ,  $d_1$ , and  $d_2$ . Non-  
719 transitivity due to promotion (neutralization) was more likely for low (high)  $D_{T1}$  and  
720 low (high)  $D_{T2}$ .
- 721 H) Same as (G) but averaged across all  $D_{T1}$ ,  $D_{T2}$ , and  $d_2$  (or equivalently,  $d_1$  if  $d_2$  was  
722 shown on the x-axis). The fraction of neutralization was large when  $D_N$  and  $d_1$   
723 were small, and the fraction of promotion was largest when  $D_N$  and  $d_1$  were  
724 increased.



725

726 **Figure 5: Resource competition can lead to non-additive effects during**  
 727 **simultaneous application of two antibiotics, with antagonism more likely than**  
 728 **synergism.**

- 729 A) A community for which antibiotic targeting leads to antagonism. Before antibiotic  
730 treatment, all three species coexisted, as shown by the simplex of the resource  
731 consumption rates of three species (colored circles) along with the supply rates of  
732 three resources (star) with distances  $D_N$ ,  $D_{T1}$ ,  $D_{T2}$  as in Fig. 4A, as well as the  
733 distance between the two targeted species  $D_T$ .
- 734 B) (Top) When the death rate of the blue species in (A) was increased, remapping of  
735 the convex hull resulted in extinction of the blue species. (Bottom) When the death  
736 rate of the orange species was increased, the orange species similarly went  
737 extinct.
- 738 C) When both species in (A) were targeted simultaneously, competition between the  
739 targeted species was relieved. (Top) Remapping due to both antibiotics led to only  
740 small changes in the consumption rate vectors compared with each antibiotic  
741 alone, as compared to unperturbed community in (A). (Bottom) Coexistence of all  
742 three species was restored, representing antagonism.
- 743 D) Like (A), but showing a community for which antibiotic targeting led to synergism.
- 744 E) Targeting of the blue (top) or orange (bottom) species in (D) alone preserved  
745 coexistence of all three species.
- 746 F) When both species in (D) were targeted simultaneously, the non-targeted species  
747 (green) outcompeted the targeted species, since the remapped convex hull no  
748 longer contained the supplied resource point. The targeted species became  
749 extinct, representing synergism.
- 750 G) The fraction of synergism (red) and antagonism (blue) for communities of the form  
751 in (A) and (D) (i.e.,  $D_{T1} = D_{T2}$  and  $d_1 = d_2 \in (0,1)$  ), averaged across all  
752 combinations of  $D_{T2}$ ,  $D_N$ , and  $d_2$ . Synergism was more likely for high  $D_{T1}$  and low  
753  $D_N$ , and vice versa for antagonism.
- 754 H) Same as (G) but averaged across all values of  $D_{T1}$ ,  $D_{T2}$ , and  $d_2$ . The value of  $D_N$   
755 at which the fraction of synergism peaked increased as a function of  $d_1$ , and  
756 antagonism was likely for  $D_N$  above this value.
- 757 I) Schematic of communities with consumption rate vectors drawn uniformly from the  
758 simplex, both death rates drawn independently from a uniform distribution between

759 0 and 1, and resources supplied at equal rates.  $D_N$  and  $D_T$  are labeled for a  
760 random community.

761 J) Of the communities in (I) without symmetry in the consumption rates of the targeted  
762 species, a smaller fraction exhibited synergism than antagonism, and the likelihood  
763 of either form of non-additivity depended strongly on  $D_N$  and  $D_T$ , analogous to  
764 communities with symmetry as in (G).

765 **TABLES**

766

767 **Table 1: Definitions of key variables and terms.**

Symbol	Definition
$m$	Number of species initially present
$p$	Number of types of supplied resources
$n_i(t)$	Abundance of species $i$ at time $t$
$n_i^*$	Steady state abundance of species $i$
$\rho$	Richness, or number of species with nonzero abundance at steady state
$R_{i\mu}$	Rate at which species $i$ consumes resource $\mu$
$s_\mu$	Supply rate of resource $\mu$
$d$	Dilution rate of the chemostat
$b_i$	Species-specific reduction factor of $R_{i\mu}$ values corresponding to species $i$ , interpreted as the susceptibility of species $i$ to antibiotics
$d_i$	Death rate of species $i$
$E_i$	Enzyme budget of species $i$ , where $E_i = \sum_\mu^p s_\mu$
$S$	Total resource supply rate (in general, assumed to be $S = 1$ )
$c_\mu^*$	Steady-state concentration of resource $\mu$
$\hat{s}_\mu$	Normalized supply rate of resource $\mu$ , where $\hat{s}_\mu = (d/S)s_\mu$
$\hat{R}_{i\mu}$	Rescaled rate at which species $i$ consumes resource $\mu$ , where $\hat{R}_{i\mu} = c_\mu^* R_{i\mu}$
coexistence region size or size of convex hull	Fraction of supply rates that lead to coexistence
specialist/generalist consumer	Species that consumes one/all resources at nonzero rates

“more” specialist/generalist consumer	Species that has a more/less even distribution of consumption rates
$c$	Factor that scales all values of $d_i$ equally to mimic the concentration of an antibiotic
$D_{Ti}$	Magnitude of the difference between $\hat{R}_i$ and $\hat{s}$ , where species $i$ is targeted by antibiotics
$D_T$	Magnitude of the difference between $\hat{R}_i$ and $\hat{R}_j$ , where $i$ and $j$ are the two species targeted by antibiotics
$D_N$	Magnitude of the difference between $\hat{R}_i$ and $\hat{s}$ , where $i$ is the non-targeted species
$d_{\min}$	Minimum value of $d_i$ among all nonzero species-specific death rates $d_i$ during antibiotic perturbation
$r_i^*$	Relative abundance of species $i$ at steady state
$N_{\text{eff}}$	Effective number of species at steady state ( $N_{\text{eff}} = \exp(-\sum_i r_i^* \ln(r_i^*))$ ), where $r_i^*$ is the relative abundance of species $i$ at steady state

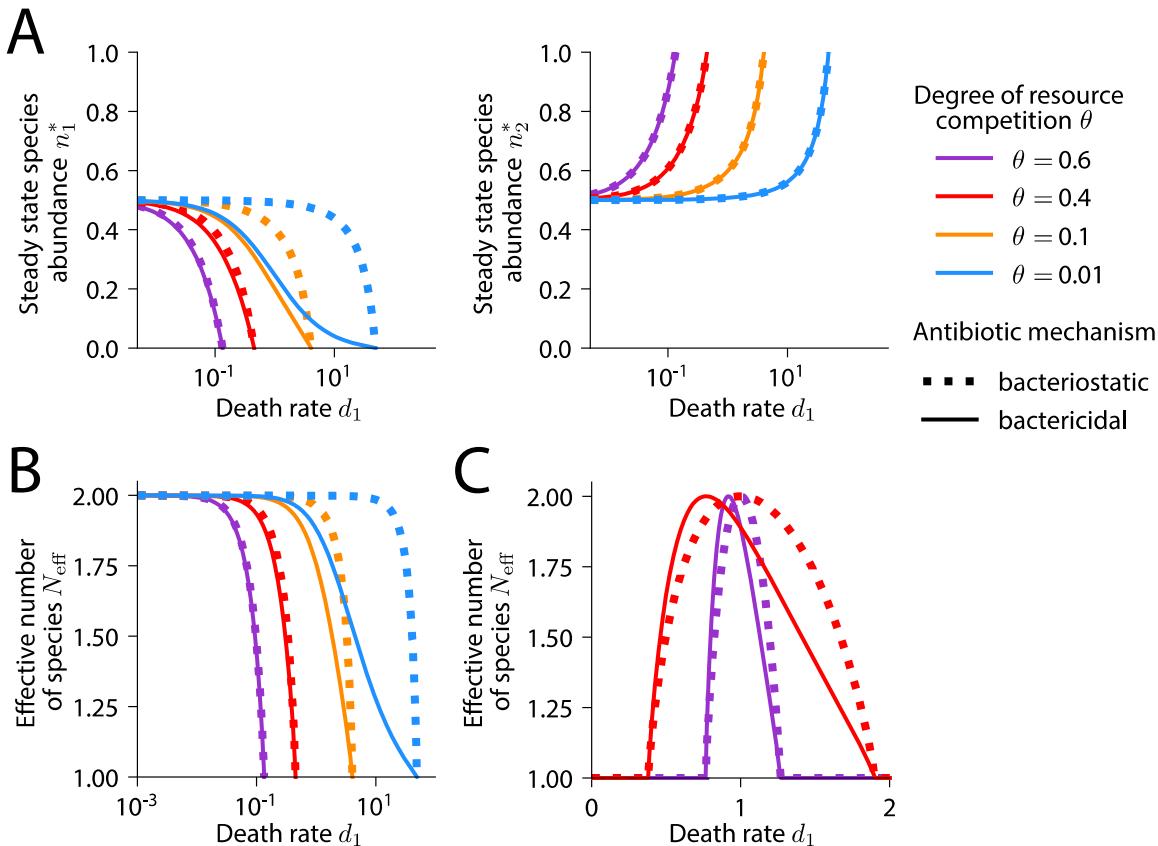
769 **Table 2: Cross-occurrences of non-transitivity during antibiotic sequences and**  
770 **non-additivity during antibiotic combinations in 100,000 random communities.**

Behavior	Additivity	Antagonism	Synergism	Total
Transitivity (i.e., $\Delta\rho = 0$ )	61,050	27,293	528	88,871
Nonzero $\Delta\rho$ due to <i>promotion</i>	0	10,482	0	10,482
Nonzero $\Delta\rho$ due to <i>neutralization</i>	12	7	628	647
<b>Total</b>	<b>61,062</b>	<b>37,782</b>	<b>1,156</b>	<b>100,000</b>

771

772 **SUPPLEMENTAL FIGURES**

773

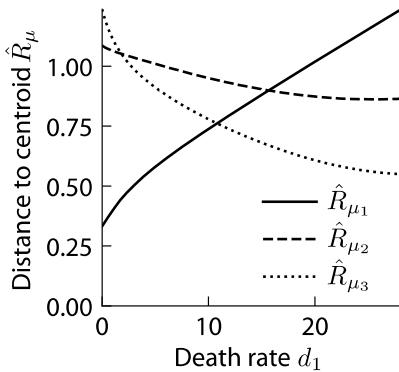


774

775 **Figure S1: Bactericidal and bacteriostatic antibiotics have similar effects on**  
776 **species abundances.**

- 777 A) Simulations of a community with  $m = p = 2$  defined by the resource  
778 consumption rate matrix  $R = ((1, \theta), (\theta, 1))$ , where  $\theta$  parametrizes the niche  
779 overlap between the two species. Species 1 was targeted with increasing death  
780 rate  $d_1$ . (Left) The steady state abundance of species 1 ( $n_1^*$ ) during treatment with  
781 a bactericidal antibiotic was always lower in comparison with the corresponding  
782 perturbation with a bacteriostatic antibiotic, given by  $b_1 = (d + d_1)/d$   
783 (Supplemental Text). (Right) The steady-state abundance of species 2 ( $n_2^*$ ) was  
784 independent of the antibiotic mechanism.
- 785 B) For the community in (A),  $N_{\text{eff}}$  was generally higher at steady state for  
786 bacteriostatic versus bactericidal antibiotics.

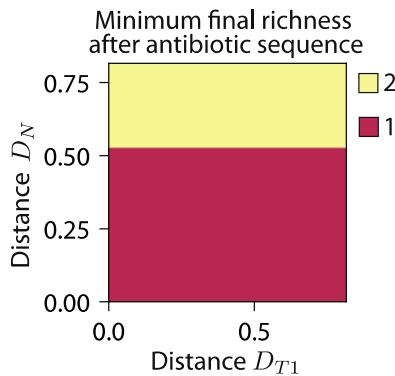
787 C) For a community defined by the resource consumption rate matrix  $R =$   
788  $((2, 2\theta), (\theta, 1))$ , steady-state evenness  $N_{\text{eff}}$  was non-monotonic (Supplemental  
789 Text), analogous to the richness in Fig. 2A. The difference in  $N_{\text{eff}}$  between a  
790 bacteriostatic and bactericidal antibiotic was greater when there was less niche  
791 overlap ( $\theta = 0.4$ ).



792

793 **Figure S2: The centroid of the coexistence region shifts towards the niche of the**  
794 **targeted species during antibiotic treatment.**

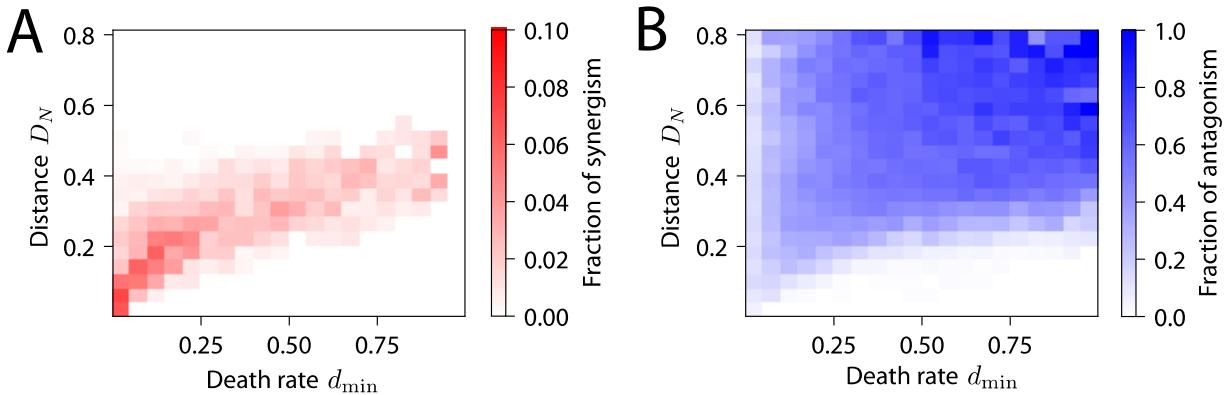
795 For the community in Fig. 3A, we plotted the distance between the centroid of the  
796 coexistence region and each corner of the simplex, corresponding to each consumption  
797 niche. The niche of the targeted species (blue) is resources 2 and 3, so targeting the blue  
798 species caused the non-targeted species to encroach on the niche of the targeted  
799 species, as indicated by the centroid of the coexistence region moving closer to the  
800 corners of the simplex corresponding to resources 2 and 3, and farther from resource 1.



801

802 **Figure S3: Final richness after antibiotic sequencing is always  $\geq 2$  when  $D_N \gtrsim 0.5$ ,**  
803 **precluding non-transitivity.**

804 We calculated the final richness after all antibiotic sequences (and reverse sequences)  
805 across the parameters ( $D_{T1}$ ,  $D_{T2}$ ,  $D_N$ ,  $d_1$ ,  $d_2$ ). The minimum final richness after all  
806 antibiotic sequences with  $D_N \gtrsim 0.5$  was 2. For  $\Delta\rho$  to be nonzero (non-transitivity), the final  
807 richness after an antibiotic sequence must be 1, indicating that non-transitivity is not  
808 possible when  $D_N \gtrsim 0.5$ .



809

810 **Figure S4: Non-additivity requires a balance between  $D_N$  and death rates.**

811 A) For communities with higher  $D_N$ , representing a more specialized non-targeted  
812 species, the fraction exhibiting synergism was maximal at larger values of  $d_{\min}$  (the  
813 smaller of the two death rates).

814 B) Communities with higher  $d_{\min}$ , the fraction exhibiting antagonism increased with  
815 increasing  $D_N$ .

816 These simulations generalize the results in Fig. 5H in the main text to communities without  
817 symmetry in consumption rates.