Strength of species interactions determines biodiversity and stability in microbial communities

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Organisms—especially microbes—tend to live together in ecosystems. While some of these ecosystems are very biodiverse, others are not, and while some are very stable over time, others undergo strong temporal fluctuations. Despite a long history of research and a plethora of data, it is not fully understood what determines the biodiversity and stability of ecosystems. Theory and experiments suggest a connection between species interaction, biodiversity and the stability of ecosystems, where an increase in ecosystem stability with biodiversity could be observed in several cases. However, what causes these connections remains unclear. Here, we show in microbial ecosystems in the laboratory that the concentrations of available nutrients can set the strength of interactions between bacteria. High nutrient concentrations allowed the bacteria to strongly alter the chemical environment, causing on average more negative interactions between species. These stronger interactions excluded more species from the community, resulting in a loss of biodiversity. At the same time, the stronger interactions also decreased the stability of the microbial communities, providing a mechanistic link between species interaction, biodiversity and stability in microbial ecosystems.

Microbes do not usually live in isolation. Instead, they reside with myriad other microbes in complex communities2–4. The interactions between microbes strongly influence the presence or absence of other organisms in the community and therefore set the overall composition, stability and biodiversity of microbial ecosystems (Fig. 1a)2–4,17–20. Accordingly, it should be possible to understand microbial communities from the interactions within them5. However, how all of these microbial interactions work together remains unresolved, which makes us wonder whether we can gain insight into complex communities from studying simple microbial interactions at all41. Here, we show that we can indeed transfer basic properties of simple interactions to large microbial assemblages and in this way mechanistically understand what determines biodiversity and stability in several complex microbial communities.

Microbes interact in many ways; they can compete for resources18, inhibit each other by the production of antibiotics19 or support each other via cross-feeding20–23. Most of these interactions are mediated by the environment: bacteria chemically modify their surroundings, which directly influences them as well as other members of the community. We and others recently showed that interactions between microbes can be understood and even predicted by understanding how they modify and react to their environment17,24–26. The higher the nutrient concentrations to which microbes have access, the more they grow and the more substrate they metabolize, and hence the more they can modify the environment22. Accordingly, we expect that higher nutrient concentrations lead to stronger interactions, which may have a strong impact on essential ecosystem properties, such as biodiversity and stability27,28.

Results

We began by exploring how interaction strength is influenced by nutrient concentrations in the context of pairwise interactions. An important environmental parameter that all microbes influence and are influenced by is pH. pH is altered by the uptake and production of many different substances and is therefore an integral metric of how bacteria change their environment. Since different bacteria reach maximum growth at different pH values (Extended Data Fig. 1), by changing the pH, they can directly impact their own and others’ growth. We measured the change in environmental pH by 92 soil bacteria (Extended Data Fig. 2a) in media with 0.1% yeast extract and 0.1% soyton with or without an additional 1% glucose and 0.8% urea. We refer to these two conditions as high and low nutrient concentrations, respectively. When grown at low nutrient concentrations with an initial pH of 7, bacteria slightly shifted the pH of the media towards alkaline, whereas at high nutrient concentrations they either strongly increased or decreased the pH (Fig. 1b). As expected, stronger buffering or intermediate nutrient concentrations led to intermediate pH change (Extended Data Fig. 2).

To test how this stronger environmental change at high nutrient concentrations affects bacterial interactions, we grew eight different soil bacteria (Extended Data Fig. 3) at low and high nutrient concentrations, then took their spent media and re-grew each of the species in the spent media of the others (Fig. 1c, top). Bacteria grown on spent media from low-nutrient media usually exhibited lowered but not completely inhibited growth. This growth effect could be attenuated by adding fresh nutrients to the spent media, showing that the growth inhibition was largely driven by resource competition. In contrast, spent media from high nutrient concentrations led to even more pronounced negative interactions and repressed bacterial growth completely in many cases. Therefore, the higher nutrient concentrations caused effectively stronger negative interactions. This does not exclude the presence of positive interactions in the microbial community. Indeed, in ten out of 64 cases, relative facilitation of growth at high compared with low nutrient concentrations was observed (Extended Data Fig. 4). Unlike our observation for low nutrient concentrations, the growth inhibition at high nutrient concentrations could not be overcome by the addition of...
Higher nutrient concentrations lead to more negative interactions between microbes. a, Can we understand the biodiversity and stability of complex microbial communities from simple bacterial interactions? b, Bacteria change the environmental pH more strongly at higher nutrient concentrations. c, At higher nutrient concentrations, bacteria produce a more growth-inhibiting environment. Spent media of different bacteria were used either directly (purple) or after replenishing the resources (green) to re-grow the bacteria (all 64 pairs are shown separately in Extended Data Fig. 4). Relative growth for every interaction pair is shown as a scatter plot. Central lines and shading represent means ± s.e.m. OD, optical density at 600 nm.
d, High nutrient concentrations decrease coexistence between interacting pairs. Low nutrient included 0.1% yeast extract and 0.1% soytone. High nutrient was the same medium with an additional 1% glucose and 0.8% urea. All 28 co-culture outcomes are shown as a swarm plot. Central lines and shading represent means ± s.e.m. For more detailed information, see the Methods. Diversity was calculated with the equation $D = \exp \left(-\sum_{i=1}^{S} p_i \ln p_i \right)$, where $p_i$ is the relative abundance of species $i$ and $S$ is the total number of species. If both species went extinct $D$ was set to 0. $P$ values were calculated using one-sided t-tests. PO_4, phosphate.

fresh nutrients (Fig. 1c, bottom). Therefore, these negative interactions are mostly driven by the production of toxic metabolites and not by competition for resources. Buffering the media removed a large fraction of the inhibitory effect of the supernatant, suggesting that pH was a major factor causing this toxicity (Extended Data Fig. 5). Our bacteria tend to produce a more harmful environment when grown at higher nutrient concentrations.

To determine the consequence of these environmental modifications on the coexistence of bacterial pairs, we co-cultured all pairwise combinations of the eight species in batch culture with daily dilution in both low and high nutrient concentrations (Fig. 1d). After 5 d, the composition of the cultures was assayed by plating the bacteria and counting the different colonies (see Methods for details). At low nutrient concentrations, there was a high amount of coexistence in pairwise co-culture. For the same interaction partners at high nutrient concentrations, we observed a striking loss of coexistence, where either one species outcompeted the other or, in many cases, both went extinct by ecological suicide—an effect we described recently. Intermediate nutrient concentrations led to intermediate loss of coexistence (Extended Data Fig. 6). Higher buffer concentrations prevented the loss of coexistence at high nutrient concentrations, showing once more that pH is a major driver of the species interactions in this system (Fig. 1d, middle). In addition to pH, other drivers of interaction may exist that work independent of, or even together with, pH. However, since adding buffer strongly reduces mutual exclusion at high nutrient concentrations, pH change is sufficient to explain most of the observed difference in interactions between high and low nutrient concentrations. A similar but weaker loss of coexistence at high nutrient concentrations was also observed when increasing the concentrations of complex nutrients (Extended Data Fig. 7). Therefore, an increase in nutrient concentrations led to stronger, effectively more negative interactions, resulting in a loss of coexistence.

To explore how these observations play out in complex communities, we sampled several soil microbiotas: compost, soil from an indoor flower pot and soil from a local backyard. These samples were cultivated in low and high nutrient concentrations as described above, with daily dilutions into fresh media (see Methods for details). The composition of the communities was followed over time by taking samples every day and performing 16S ribosomal RNA amplicon sequencing (Fig. 2 and Extended Data Figs. 8–10).

These time courses reveal striking differences between the low and high nutrient concentrations; at low nutrient concentrations, there were more species present and the temporal change of the
system was smooth (compost community shown in Fig. 2; others shown in Extended Data Fig. 10). In contrast, at high nutrient concentrations, the community exhibited sudden jumps between several low-diversity states.

To gain intuition into whether the properties of the microbial interactions found in mono- and co-culture (Fig. 1) may explain the observed behaviour of complex communities (Fig. 2), we developed a mathematical model in which bacteria interact by changing the environment and are at the same time affected by these environmental changes. The model is a multi-species extension of a model we previously used to understand homogeneous populations and pairwise interaction outcomes:

\[
\frac{\partial n_i}{\partial t} = \left\{ \begin{array}{ll}
    -k_{\text{growth}} n_i (1 - n_i) & \text{for } p \in [p_{ao} - p_c, p_{ao} + p_c] \\
    -k_{\text{death}} n_i (1 - n_i) & \text{for } p \notin [p_{ao} - p_c, p_{ao} + p_c]
\end{array} \right.
\]

(1)

\[
\frac{\partial p}{\partial t} = \sum_i c_i n_i
\]

(2)

The bacterial species \( n_i \) grow logistically with growth rate \( k_{\text{growth}} \) but only if the environmental parameter \( p \) lies within the suitable range \( [p_{ao} - p_c, p_{ao} + p_c] \), where \( p_{ao} \) and \( p_c \) define the suitable range within the bacteria can grow. Although our system is strongly driven by pH, the parameter \( p \) could be any (or a combination) of several chemical compounds in the environment that the bacteria modify and are impacted by. Outside that range, the bacteria die with rate \( k_{\text{death}} \). Additionally, bacteria change the environmental parameter \( p \) with rate \( c_i \), which is taken from a uniform distribution in the interval \((-c_j, c_j)\). Accordingly, \( c_j \) is the maximum amplitude of the environmental change. At the end of every growth cycle, the system is diluted by a constant factor (see Supplementary Methods for details).

Simulating 40 interacting pairs with this model and varying the extent to which they changed the environment, and thus the interaction strength, led to results similar to what we observed experimentally (Fig. 3a, purple; for more values of \( c_j \) see also Supplementary Fig. 8). Increasing the modification of the environment \( c_j \) led to a loss of coexistence in co-culture, as seen in the experiments (Figs. 1d and 3b, purple). Since this model recapitulated the findings for pairwise interactions, we were curious what it could tell us about complex communities. For this purpose, the above simulations were repeated with communities containing 20 species. Increasing the environmental modification by the bacteria caused a decrease in biodiversity (Fig. 3a), in line with similar findings in Lotka–Volterra models.

To test whether this predicted decrease in biodiversity could also be observed in the experiments where we propagated complex communities in low and high nutrient concentrations, we calculated the diversity of the communities at the end of the experiment. Indeed, we observed a loss of biodiversity when the nutrient concentrations and thus the interaction strength were increased, as predicted by the model (Fig. 3b and Extended Data Fig. 8). pH modification could be identified as an important driver for the pairwise interactions in Fig. 1 (Extended Data Figs. 1, 2 and 5). Accordingly, adding buffer to the complex communities also reduced the loss of biodiversity in high nutrient concentrations. Therefore, the loss of biodiversity was largely driven by modifications of the environmental pH, not by the loss of limiting resources upon adding nutrients. Overall, high nutrient concentrations caused stronger environmental modifications and stronger, more negative interactions, leading to a loss of biodiversity in the microbial communities, as predicted by our simple model.

Another important property of ecosystems that seems to be linked to biodiversity is their stability (for example, how unchanged an ecosystem remains over time). We show and discuss below how interaction strength impacts the stability of complex microcosms (the effects on pairwise interactions are similar and can be seen in Supplementary Fig. 2). To get an impression of how interaction strength might affect the stability of microbial communities, we performed simulations with the above model to obtain the total bacterial density \( \sum n_i \) over time for weak and strong interactions (for example, weak and strong modifications of the environment by tuning \( c_j \)). Our model predicts that the fluctuations of the total bacterial density were much higher at stronger interactions (Fig. 4a, top).

To determine whether this predicted loss of stability was present in our experimental communities, we analysed the total biomass over time (as quantified by optical density). Consistent with our model predictions, we found that high nutrient concentrations caused stronger temporal fluctuations in all samples (Fig. 4a, bottom). In addition to increased fluctuations of the total bacterial density, the model predicted an increase in fluctuations of the environmental parameter \( p \) at stronger change of the environment and thus higher nutrient concentrations (Fig. 4b, top). Consistent with this prediction, we found the same effect in the experiments when
Interaction strength, more pronounced changes in composition over time were observed (top middle: simulation; bottom middle: measurement). The left panels, example curves are shown, whereas the bar plots on the right show the mean of the standard deviations for all obtained time curves. The environment also fluctuates more strongly for stronger interactions in the model (top) and the experiments (bottom). On the one hand, total bacterial density fluctuates more over time for stronger interactions in both the simulation (top) and experiment (bottom). OD, optical density.

The hypothesis has been the difficulty of measuring and experimentally manipulating interspecies interactions37,38. We showed here a way to tune the interaction strength between bacteria, which allowed us to understand how interactions affect the biodiversity of microbial communities. High nutrient concentrations caused more negative microbial interactions, which led to less diverse communities. In contrast with microbial systems, interactions in other ecosystems may not be primarily mediated by the environment, and it remains to be seen how far our findings can be transferred outside the microbial world. In a plant community, a similar mechanism for biodiversity loss was described. High nutrients led to shading of light (that is, a change of the environment), which caused a loss of biodiversity39. Moreover, at least in theory, a loss of biodiversity was also described for stronger direct interactions40.

This mechanism for diversity loss is reminiscent of eutrophication, an over-enrichment of nutrients in ecosystems that often leads to blooms of microbial algae that exclude other species40–42. In the case of eutrophication, stronger negative interactions are also mediated by the environment (for example, by limiting light or oxygen) and were suspected to contribute to biodiversity loss40,41,44. Our findings suggest that the idea of eutrophication can be extended to other microbial systems, such as soil microbiota.

Such eutrophication in microbial systems may even be medically relevant. In the human gut microbiome, a loss of biodiversity was associated with western, high-caloric and low-complexity diets compared with fibre-rich, low-caloric nutrition43–45. We speculate that such a loss of biodiversity upon easily accessible nutrients may be driven by an increased interaction strength between the gut microbes.

There exists a variety of evidence for the connection between biodiversity and stability. Higher biodiversity often, but not always, comes with higher stability in ecosystems21,25,32–34. In our experiments, an increase in interaction strength decreased the stability in pairwise co-cultures as well as in complex communities, indicating that the loss of stability was independent of the initial biodiversity of the microbial system. The loss of stability seems therefore not to be directly caused by the biodiversity itself; instead, the interaction...
strength between the organisms negatively affects both biodiversity and stability at the same time.

Using simple microbial systems in the laboratory with the goal of investigating basic principles of ecology and evolution has led to many fundamental insights\(^{57-59}\). However, because of the simplicity of these systems, it is often unclear how far the obtained findings can be transferred to natural, more complex communities. We show here that at least the biodiversity and stability of complex systems can be understood from properties of simple pairwise interactions. For these ecosystem properties, the average species interaction...
seems to be more important than the mechanistic details of the interactions and how the specific interactions sum up to build the community. This surprising simplicity suggests that it is possible not only to understand properties of complex microbial communities, but also ultimately to engineer them.

Methods

**Media, buffer and bacterial culture.** All of the chemicals were purchased from Sigma–Aldrich unless otherwise stated.

Pre-cultural bacteria were made in 1× nutrient medium (10 g l\(^{-1}\) yeast extract and 10 g l\(^{-1}\) soytryptone (both Becton Dickinson), 100 mM sodium phosphate, pH 7) or Tryptic Soy Broth (TSB; Teknok). The experiments were performed in base medium, which contained 1 g l\(^{-1}\) yeast extract, 1 g l\(^{-1}\) soytryptone, 0.1 mM CaCl\(_2\), 2 mM MgCl\(_2\), 4 mM NiSO\(_4\), and 30 g l\(^{-1}\) MnCl\(_2\). Different amounts of phosphate (added as sodium dihydrogen phosphate), glucose and urea were added depending on the experimental conditions, as outlined below. The initial pH was adjusted to 7 unless otherwise stated. All media were filter sterilized using Bottle Top Filtration Units (WVR). For plating of bacteria, the cultures were diluted in phosphate buffered saline (PBS; Corning). Plating was done on TSB agar, with 2.5% agar (Becton Dickinson).

For the experiments, the bacteria were grown in 96-deepwell plates (Deepwell plate 96/500 µl; Eppendorf) covered with AeraSeal adhesive sealing films (Excel Scientific). The growth temperature was 30 °C for the isolates and 25 °C for the American Type Culture Collection (ATCC) (12633), Pseudomonas aurantiaca (ATCC: 33663), Pseudomonas citronellolis (ATCC: 13674), Micrococcus luteus (Ward’s Science), Sporosarcina ureae (Ward’s Science), Bacillus subtilis (strain 168), Escherichia coli (strain 168), Enterobacter aerogenes (ATCC: 13048) and Serratia marcescens (ATCC: 13880). These species can be differentiated by colony morphology (Extended Data Fig. 3) and have been used for interaction studies before\(^{58}\). The bacteria were grown in 5 ml TSB (Teknova) overnight at 30 °C. The bacteria were spun down (15 min; 3,220 g; Eppendorf Centrifuge 5810) and re-suspended in 5 ml base medium. The re-suspended bacteria were diluted 1/100-fold into 2× 5 ml base media (Fig. 1). The different media used were either 10 or 100 mM phosphate (pH 7) (spent media cultures). At the same time, a new pre-culture was set up in TSB, as described above. Both cultures were grown for 24 h at 30 °C. The spent media cultures were spun down (15 min; 3,220 g; Eppendorf Centrifuge 5810) and the supernatant filter was sterilized with a 0.2-µm Sterilfilter Unit (SCG00525; Millipore Sigma/Aldrich). Then, 5% of this spent media was spotted onto TSB plates to verify sterility. The spent media were either used directly or supplemented with 1/20 of 2× original media without PBS to re-plenish the nutrients. The second pre-culture was spun down as well after 24 h (15 min; 3,220 g; Eppendorf Centrifuge 5810) and re-suspended with base medium as described above. Those bacteria were then diluted 1/100× into the spent media and also into the corresponding fresh media described above. The cultures were grown for 24 h at 30 °C in 96-deepwell plates (Deepwell Plate 96/500 µl; Eppendorf), 200 µl per well in a shaker culture (1,350 r.p.m. shaking speed on a Heidolph Titramax shaker). After 24 h the OD\(_{600}\) of the cultures (100 µl in 96-well flat-bottomed plates (Falcon)) in the different spent media was measured and the OD\(_{600}\) was obtained from fresh media. The resulting data are shown in Fig. 1c and Extended Data Figures 4 and 5.

**Pairwise interactions.** The eight soil strains described above were grown in TSB overnight at 30 °C. The bacteria were spun down for 5 min at 3,220 g in an Eppendorf Centrifuge 5810 and re-suspended in 2× 5 ml base medium (pH 7). For each of the 28 pairwise combinations, 10 µl of each strain was diluted in 200 µl base and 10 mM 100 mM phosphate ± 1% glucose and 0.8% urea. The co-cultures were incubated at 30 °C and a shaking speed of 1,350 r.p.m. on a Heidolph Titramax shaker in 96-deepwell plates. Every 24 h, the co-cultures were diluted 1/10× into fresh media. The pH and OD\(_{600}\) were measured at the end of every incubation cycle (every 24 h). After 5 d, the co-cultures were plated by droplet plating as described above. The agar plates were incubated at 30 °C for around 2 d until colonies were clearly visible. The colonies were then counted. The \(\Delta D\) diversity was calculated according to \(\Delta D = \exp\left(-\sum_{i=1}^{n} p_i p_{hi}\right)\) , where \(D\) was set to 0 if both species went extinct. The results are shown in Fig. 1d and Extended Data Fig. 5.

**Obtaining environmental samples.** The compost used for the experiments was purchased from Bootstrap Compost in Boston, Massachusetts. The soil was sampled in Cambridge, Massachusetts, at a depth of ~30 cm. The soil was kept at 4 °C until the experiments were performed. Flower pot soil was sampled the day of the experiment by taking soil from a large indoor plant pot at a depth of 10 cm.

**Temporal dynamics of soil microcosms.** For the compost and flower pot experiments, 4 g of sample was diluted in 20 ml PBS, then vortexed at an intermediate speed for 30 s and iced incubated on a platform shaker (Innova 2000; Eppendorf) at 250 r.p.m. and room temperature. After 30 min, the samples were allowed to settle for 5 min and the supernatant was transferred to a new clean tube. The sample was then diluted 1/10 before inoculation of the experiments. For the soil experiment, four grains of soils (~0.1 g) were diluted in 40 ml PBS, vortexed and inoculated with 100 µl of recombinant samples. The supernatant collected after settling was directly used for inoculation without further dilution. Experiments were inoculated by mixing 170 µl of these obtained liquids into 1,530 µl of the appropriate media, as indicated below.

**Experiments were performed in 2,000-µl 96-deepwell plates (Deepwell Plate 96/2000 µl; Eppendorf) using base media at pH 7, to which either 10 mM (referred to as low buffer) or 100 mM (referred to as high buffer) phosphate was added. Glucose/urea ratios of 0/0.5, 0.5/0.4, 1/0.8, 2/1.6, 3.2/4 and 5/4% (mV\(^{-1}\)) were added to the high- and low-buffer media, respectively. Plates were covered with two sterile AeraSeal adhesive sealing films (Excel Scientific) and incubated at 25 °C on a VWR Microplate Shaker at 500 r.p.m. After 24 h, the cultures were thoroughly mixed by pipetting up and down 30 times using the VIALFO 96-well pipette (mixing volume: 300 µl; speed: 10 cycles: 30). Then, the cultures were diluted 1/10 into fresh media. At the end of every cultivation day, 170 µl of culture was transferred into flat-bottomed 96-well plates (Falcon) and the optical density (OD\(_{600}\)) was measured with a Varioskan Flash (Thermo Fisher Scientific) plate reader. The pH was measured as described above. The remaining bacterial culture was stored at −80°C for subsequent DNA extraction. The DNA extractions were performed using an Agencourt DNA/vesure A48705 extraction kit (Beckman Coulter) following the provided protocol. The obtained DNA was used for 16S ampiclon sequencing of the V4–V5 region. Some amount of the samples was also checked for eukaryotes by sequencing the 18S V4 region. The sequencing was done on an Illumina MiSeq by the Comparative Genomics and Evolutionary Bioinformatics–Integrated Microbiome Resource at Dalhousie University (Halifax, Nova Scotia, Canada).

**Data analysis.** We analysed the obtained 165 reads as described elsewhere\(^{59}\). From the 165 reads, the amplicon sequence variants were obtained with the dada2
package in R. Taxonomic identities were assigned to the amplicon sequence variants using the GreenGenes Database Consortium (version 13.8) as a reference database. The principle component analysis shown in Fig. 4 was performed with the scikit-learn package in Python.

**Reporting Summary.** Further information on research design is available in the Nature Research Reporting Summary linked to this article.

**Data availability**
The data and sequencing raw data are available at https://doi.org/10.5061/dryad.vdnjcsajq.

**Code availability**
The code for the simulations is available at https://github.com/cratzke/Interaction-biodiversity-stability.

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Author contributions

C.R., J.B. and J.G. designed the research. J.B. and C.R. carried out the experiments and performed the mathematical analysis. C.R., J.B. and J.G. discussed and interpreted the results, and wrote the manuscript.

Competing interests

The authors declare no competing interests.

Additional information

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Extended Data Fig. 1 | Different soil strains have different suitable pH ranges. We tested the optimal growth pH of 81 isolated soil species. It is a subset of the species shown in Extended Data Fig. 2B. All isolates were pre-cultured in 200µL of 1xNutrient medium for 24h at 25°C with 1350 rpm shaking speed in 500-µl 96-deepwell plates (Eppendorf, Hauppauge, USA). After 24h of growth the cultures were diluted 1:100 into 500-µl 96-deepwell plates and a final volume of 200µl of Base media with 100mM phosphate with pH values of 3–11. Cultures were incubated for 24h at 25°C at 1350 rpm on a Heidolph Titramax shaker. Population densities were estimated by CFU counting at the start of the experiment and after 24h, which allows to estimate the fold growth in 24h that is shown in the figure. Several example curves are shown in the upper panel. As can be seen those curves can have several shapes. For simplification, we decided to describe the shape of those curves with a heaviside function in our simulations (see below).
Extended Data Fig. 2 | Nutrient concentrations and buffering determine pH change of growth media. (a) The top and bottom panels show the same data as Fig. 1b. Using intermediate nutrient concentrations also causes intermediate pH shifts (green) compared to high (blue) and low (yellow) nutrient concentrations. Also adding higher concentrations of buffer lowers pH shifts (red) compared to the situation with low buffer (blue). (b) List of soil isolates that were used to measure the data in main text Fig. 1b and Extended Data Fig 1A and 2B. Strains were identified down to genus level by sequencing their 16S rRNA gene and comparing it to the RDP database. The strains belong to a collection of soil strains that we used before for interaction studies. As can be seen many of those strains belong to the genus Bacillus, nevertheless they can change the pH into alkaline or acidic directions. For some cases the sequencing failed which lead to empty entries. PO₄ means phosphate.
**Extended Data Fig. 3** | **Bacteria for the pairwise interaction experiments.** The different colony morphologies allowed to distinguish them after plating on agar plates.
Extended Data Fig. 4 | High nutrient concentrations lead to stronger negative interactions between bacteria. The figure shows all the data of main text Fig. 1c for low nutrient concentrations (top) and high nutrient concentrations (middle). The bottom panel shows the difference between the top and middle one. As can be seen in most cases (84%, for spent media without replenishment) increasing nutrient concentrations lead to a stronger inhibition of the interaction partner (values below zero), however in the remaining cases it leads to a relative facilitation (values above zero). Spec_X_Sn_Y means species X was grown in supernatant of species Y.
Extended Data Fig. 5 | Growth inhibition caused by high nutrient spent media is partially caused by pH and can be removed by buffering. The scatter plots show the ratio of final OD in spent and final OD in fresh media for all 64 interaction pairs in buffered media at low (left) and high (right) nutrient concentrations. The solid lines and boxes show the corresponding mean and SEM. This figure is thus equivalent to Fig. 1c in the main text with higher buffer concentrations (100mM phosphate). The black circles show the data of Fig. 1c eg with lower buffer concentrations (10mM phosphate). As can be seen the presence of higher buffer concentrations slightly facilitates growth in spent, but not replenished media, possibly because adding phosphate avoids phosphor to be a limiting resource. However, the strongest effect of buffering can be seen in the replenished supernatant. Whereas there is no effect upon the low nutrient replenished supernatant, bacteria grow much better in high nutrient replenished media with higher buffer concentration compared to lower phosphate (one-sided t-test p-value = 0.006). Since in the replenished media nutrient competition as a mode of interaction does not matter, this shows that the growth hindering and thus toxic effect of replenished high nutrient media can partially be diminished by buffering. Thus, at least a part of the toxic effect of high nutrient supernatant is caused by pH.
Extended Data Fig. 6 | Nutrient levels determine interaction strength. The first three columns correspond to Fig. 1d. The fourth column shows the interaction outcomes for a medium nutrient concentration of 0.4% glucose and 0.32% urea e.g. 0.4x the high nutrient condition. As expected the results fall in between the results for the low (no Glucose and Urea) and high (1% Glucose and 0.8% Urea) nutrient outcomes. PO₄ means phosphate.
Extended Data Fig. 7 | Complex nutrients weakly effect interaction. Increasing the amount of yeast extract and soytone from 1g/L each to 20g/L leads to a slight decrease in overall diversity (p-value: 0.112). However, the effect of glucose and urea is much stronger. One reason for that may be that yeast extract and soytone also work as buffers, which stabilize pH at high nutrient concentrations. PO₄ means phosphate.
Extended Data Fig. 8 | Rarefaction curves for data of last day of complex community cultivation in high and low nutrient concentrations and alternative diversity metrics for complex communities. (a) The curves become flat at the read depth of the samples (= end of curves) which shows that the read depth is sufficient to capture the species richness in the sample. The diversity for $q=2$ (2D diversity) (b) and richness (c), which puts more emphasis on common species shows the same effect of nutrients and buffering in the diversity as shown for the 1D diversity in Fig. 3.
Extended Data Fig. 9 | Initial community compositions. Shown are the ASVs with more than 0.05 abundance. The corresponding 1D diversity and richness are much higher than at the end of the experiments (Fig. 3), e.g. those communities collapsed to communities with lower diversity during the experiments. The sequencing of the initial soil community failed.
Extended Data Fig. 10 | See next page for caption.
Extended Data Fig. 10 | Community composition over time for different samples sites, replicates and nutrient conditions. The colors that represent the different species are consistent for a specific sample (compost, flowerpot, soil), but may vary between them. In a few cases different ASVs were identified as the same species, which causes a connection of the same species name with different colors within the same sample site. The white columns indicate days for which the sequencing failed.
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Software and code

Policy information about availability of computer code

Data collection

16S amplicon sequencing raw data was processed with dada2 package in R, as described in Callahan, B. J., Sankaran, K., Fukuyama, J. A., McMurdie, P. J. & Holmes, S. P. Bioconductor Workflow for Microbiome Data Analysis: from raw reads to community analyses. F1000Res 5, (2016).

Data analysis

Data analysis was done in Python3, which SciPy and NumPy packages. Plotting was done with matplotlib package.

Simulations were run by integrating the given equations with Odeint in SciPy, as described in the Supplementary Methods.

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Life sciences study design

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Sample size
We did several test runs of both the pairwise interaction experiments as well as the experiments on complex communities. In both cases we could see that the expected effects are rather large and thus 8 species (and thus all their combinations) for the pairwise competition and 3x3 (three different sample sites with three technical replicates each) samples for complex communities should be more than sufficient.

Data exclusions
For the bacterial co-culture at high nutrient, high buffer one community showed cross contamination and was removed from further analysis. Few of the 16S sequencing reactions failed and therefore excluded themselves as shown in Supplementary Fig. 9.

Replication
All the pairwise interactions experiments were at least repeated twice, in all cases successfully. The experiments with complex communities were done few times without sequencing (just measuring OD, pH and plating on agar to get rough estimates for the biodiversity) with the same outcomes as shown in the paper. We chose three different sampling sites for the complex communities with 3 technical replicates each, that all showed similar outcomes as shown in the paper.

Randomization
We used the same species/soil samples and just varied the environmental conditions under which they grew in the lab.

Blinding
For the pairwise interactions there was no blinding. However, the data was obtained by counting colonies of bacteria with different colony morphologies. Since this is a very digital process (colony is there or not) we do not expect that a bias is introduced by the investigator. For the complex communities the experiments were blinded since sequencing and analysis were done by a different person (CR) then the experiments (JB).

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