We assumed the final observation of each experiment represents the equilibrium densities of that community. We then used regression models to estimate the effect of each other species on the density of a given focal species (and repeated this once for each species). We can derive this approach from the standard Lotka-Volterra competition model.

**Quick derivation:**

The equation for the rate of change of species 1 in a 2-species experiment is

At equilibrium, there is no change, so is 0. This means we have

This has two possible solutions. Either

which is boring (species 1 neither reproduces or dies without competition), or

If we re-arrange terms, we can write this as

And we know N1 and N2 from Brooke’s experiments! So we’re just fitting a linear regression of the form y = mx + b, or in R

out = lm(N1 ~ N2)

With this, our intercept estimate is K, and our slope is alpha x -1. With more species, it’s exactly the same approach:

out = lm(N1 ~ N2 + N3 + N4 + N5 + N6)

We used this approach to fit models for each of our six species from the single-species and pairwise competition experiments.

**What to do with this?**

First, we estimated the alpha and K values of the standard lotka-volterra model. K represents the density we expect to see when no competing species are present, and each alpha tell us the effect of one individual of one species on the individuals of a second species, with negative alphas representing a beneficial effect, and positive alphas representing a harmful effect. We found that in many cases our estimates for alphas had very wide confidence intervals. Further, we have a negative estimated carrying capacity for JB7, because JB7 had 0 density in all of the pairwise experiments.

For these reasons, we emphasize comparing the predictions of the model (fitted from pairwise data) for the community experiment (with all species present at the initial time point). Model predictions were bad, off by an average of X-fold, and in 14 cases (2-4 replicates for 5 species), predicted negative densities when experimental densities were at least 1000.

The inability of the pairwise interaction model to predict community equilibrium indicates that pairwise interactions are influenced by the presence of additional species. [For various reasons that Brooke knows offhand], we expect that some of this mediation occurs through changes in pH. In our community experiments, pH had risen to X by the end of the experiment. To test our hypothesis, we repeated our single-species and pairwise competition experiments at pH 7. When we carried out the same fitting and prediction process using the pH 7 data, we found much better congruence both quantitatively (average error = Xfold), and qualitatively (the model gave negative population predictions for only 2 replicates each of two species). This strongly suggests

To explore which pairwise interactions are change across pH, we fit our regression models with the combined data from the experiments of both pHs, including an interaction between the density of each competitor and pH (as a categorical variable), of the form

out = lm(N1 ~ N2\*pH + N3\*pH…)

Here a significant density x pH term (e.g. N2:pH) indicates that the effect of the density of the competitor on the focal species (e.g. the effect of N2 on N1) differs significantly between the two pH treatments. Using this method, we identified X interactions that were changes with changing pH

[paragraph on each of the individual meaningful interactions, linking to the biology telling us why we expect it]