**Model results description: Clark 2018**

**Summary:**

This model includes a simple trade-off among three traits – monoculture biomass (B\* or abmi), competitive ability for nitrogen (R\* or no3i), and tissue nitrogen concentration (q\* or pNi). Species can persist by either being a very good competitor, or by being a worse competitor, but investing in high B\* or q\*, which allows species to access resources that superior competitors may not yet have used. In general, the theoretical expectation for this model is that higher diversity should be associated with higher biomass (since species more fully utilize trait space). But, because the trade-off surface doesn’t map 1-1 with community-level biomass, and because it does not solely include combinations of traits that lead to coexistence, this relationship isn’t necessary, but is rather just expected.

In general, positive selection effects are expected, since species with high biomass that are good competitors will produce roughly their monoculture biomass in mixture, which is >> than the null expectation of B\*/N. Since the overall biodiversity effect is positive, it stands to reason that the complementarity effect should be positive as well.

**Shannon and species richness:**

Across & within planted-species richness treatments: For both Shannon and richness, we see pretty much what we would expect. For Shannon, we always have a positive relationship between biomass and diversity across levels, and a negative relationship within levels. This pattern appears to be primarily driven by a few high performing species. Higher diversity treatments have a higher probability of including these species. When they are present in a mixture, they drive up biomass substantially (i.e. the upper cluster of points), but also tend to make other species rarer, thereby dropping Shannon. For richness, the within-treatment relationships reverse, probably demonstrating that even though the high performing species perform well and reduce the abundance of other species, they are rarely able to drive them fully extinct.

**Functional diversity:**

Across planted-species richness treatments: Monoculture biomass is completely determined by the parameter B\* (i.e. abmi). Mixture biomass is also strongly correlated with monoculture biomass, especially if R\* (i.e. no3i) is low. All else being equal, species with lower R\* have higher biomass in mixture, because they are better competitors in the model and therefore lose less resource to other species, and species with lower q\* (i.e. pNi) also have higher mixture biomass, since they need less nitrogen to produce a gram of tissue. However, various intermediate combinations of traits can also lead to high biomass.

In general, if two species are “near” each other in trait space, then one or the other will likely be outcompeted (as one will necessarily be a better competitor, whereas they will both have similar total nitrogen uptake, meaning that the poorer competitor has no access to resources that the superior competitor is unable to access). Thus, higher variability in traits across species will, in general, lead to more coexistence, and thus to higher biomass production. As this model is written, poorer competitors have no effect on the biomass of better competitors, so the survival of a poorer competitor must, by definition, increase total community biomass and therefore lead to overyielding. Nevertheless, not all combinations of traits lead to high biomass, so functional dispersion does not always need to increase monotonically with mixture biomass.

**Model results description: Turnbull 2013**

**Summary:**

Species live on a 1D trade-off between r (thetai) and K (Vi). In general, high r and low K leads to fast growth, with can temporarily prevent other species from accessing resources, but does not lead to much biomass growth (i.e. we could call these “low-performing” species, or something like that). Alternatively, high K species will produce lots of biomass, but grow slowly. Over time, they may be able to displace faster growing species, but especially if seed rain is high, this process could be slow, or might not take place at all.

**Shannon and species richness:**

Across & within planted-species richness treatments: Across diversity levels, we always find positive relationships, as expected in the model. Because no species are lost, there are no richness trends within diversity treatments. For Shannon within treatments, we find negative relationships with biomass during the assembly phase, and positive during the isolation phase. This makes some sense, since during the assembly phase, we are basically forcing a bunch of low-performing species to remain abundant through propagule pressure. During the isolation phase, this propagule pressure ceases, and these poor performing species decrease in abundance and are ultimately replaced by high performing species. This outcome also partially explains the strong negative selection effect observed in some cases – i.e. low-performing species end up inhibiting high performing species.

**Functional diversity:**

Across planted-species richness treatments: Monoculture biomass is totally determined by K (i.e. Vi) in the model. And, because K is directly related to r (i.e. thetai), there is also a (negative) relationship between monoculture biomass and r. In general, higher K will also lead to higher mixture biomass, though species with very high r also seem to have somewhat higher mixture biomass, presumably because they are able to grow quickly enough to avoid being supressed as strongly by species with high K. This probably also explains the weak positive relationship between functional trait dispersion and mixture biomass – communities with high K species will always produce lots of biomass, but if they also include a few fast growing species, then these species with high r will be able to access a small amount of additional resource that the high K species were not able to access.