Hey Björn,

I hope that you’ve been well and weathering Coronavirus without any problems! I’m sorry that this has taken so long to get to back to you; it’s been busy here, but I’ve made progress that I would like to share with you. Unfortunately, I think that we’re going to need to discuss ways to reduce the stochasticity in the succulent model, because the methods I’m using to understand its behavior are doing a poor job.

First, I’d like to invite you to look at the model fits we’ve made so far. We used Bayesian models derived with the *brms* package in R, which uses RStan. In the attached documents for each biodiversity metric (i.e. realized Shannon diversity, richness, and functional dispersion), you will find the validation process I used for each of the statistical models as well as, at the end of each document, the final model fits. You will also find a document that decomposes how traits within the succulent model translate into monoculture biomass, and how competitiveness within the community relates to both the species’ component traits and their monoculture biomass.

The predominant problem I’ve had, as I mentioned earlier, is that there is so much stochasticity in the model, and the techniques I’ve used to understand the other models’ underlying mechanisms (i.e., how the traits shape community dynamics) are insufficient. I was wondering if we could discuss together ways of mitigating this stochasticity, so that we can better understand the mechanisms driving the model’s emergent BEF patterns.

Do you have time sometime in the next week or two to discuss together, and then to execute the changes within the next month or so? Ideally Nadja, Katie, Adam and I would like to begin drafting the manuscript during May, having met with the entire subgroup in late April to discuss the results as they stand. If that isn’t enough time, let me know and we can arrange something different.

Best,

Mike