# The function-dominance correlation drives the direction and strength of biodiversity-ecosystem functioning relationships

# Appendix S1 – Extended Methods

# Model preparation

In the case of Dryland, our experimental design necessitated a modification to the species pool of the original model, to increase chances of simulating high-diversity communities. First, one level of maximum plant size (4 g) was added to the trade-off surface relative to the original publication (1, 10, 100 g). A value of 4 g was chosen because smaller plants use the limiting resource (water) more efficiently in the model, and thus tend to have higher chances of survival. For each maximum size level, 16 allocation strategies to root, leaves, and water storage were selected. All chosen strategies were among the 91 root-leaf-water storage allocation strategies in the original publication that produced the highest biomass in monoculture.

# Experimental design

## Simulation duration

We fixed the duration of each simulation to the amount of time it took for the Shannon diversity of the 64-species treatment to stabilise with a high level of seed addition (10 times the one used for the seed rain stage).

# Statistical methodology

We used two Bayesian linear regressions for each plant community model to fit the overall, “*across communities*” effect of the BEF relationship and its “*within communities*” effect separately. This analysis mirrors that of Leibold et al. (2017, Rychtecká et al. 2014), except that both statistical models also include the presence or absence of seed rain as an explanatory variable (Stage).

Regressions were fit using the Hamiltonian Monte Carlo (HMC) sampler Stan (Carpenter et al. 2017) through the ‘brms’ package (Bürkner 2018) in R (version 4.0.0, R Core Development Team 2019). See the main manuscript for further information on running the regressions, and Appendix S5 for model validation.

## Across-community model

For the across-community statistical model, we used the formula:

where represents the total biomass of a community *i*, represents the seed rain stage (*with* or *without* seed rain), and represents the Shannon diversity of the community.

## Within-community model

For the within-community statistical model, we used the formula:

where represents the total biomass of a community *i*, represents the seed rain stage (*with* or *without* seed rain), represents the categorical variable of planted species richness, and represents the emergent Shannon diversity of the community.