READ ME

Data from the manuscript ´Plant-soil feedback responses to drought are species-specific and only marginally predicted by root traits´

List of data files:

**data\_conditioning.csv:**

csv file with all data from the end of the conditioning phase including metadata. One line corresponds to one pot.

Metdata:

drought = drought treatment (C = control, D = drought)

block = experimental block in time and space

species = plant species growing

FG = functional group of the plant species growing

Data:

FW = fresh weight; DW = dry weight of plant biomass

water and KCl refer to the extraction medium

**data\_feedback.csv:**

csv file with all data from the end of the feedback phase including metadata. One line corresponds to one pot.

Metdata:

drought = drought treatment of the soil in the conditioning phase (C = control, D = drought)

block = experimental block in time and space

species\_home = plant species growing

FG\_home = functional group of the plant species growing

species\_soil = plant species which conditioned the soil/ sterile soil

FG\_soil = functional group of the plant species which conditioned the soil/ sterile soil

Data:

FW = fresh weight ; DW = dry weight of plant biomass

leaves = number of leaves

**data\_feedback\_biomass.csv:**

csv file with all data from the end of the feedback phase in long format including metadata. One line corresponds to one biomass observation.

Metdata:

see data\_feedback.csv

number = identification of the plant

biomass = part of the plant that the DW refers to

soil\_treatment = origin of the soil in terms of functional group of the conditioning species or home soil or sterile soil

Data:

DW = dry weight of plant biomass

**Data\_PSF.csv:**

csv file with all data from the end of the feedback phase in long format including metadata and calculated PSF data. One line corresponds to one species pair.

Metadata:

block = experimental block in space and time

species\_home = focal species for PSF calculations

FG\_home = functional group of the focal species for PSF calculations

species\_away = conditioning species of the away soil/ sterile soil

FG\_away = functional group of the conditioning species of the away soil/ sterile soil

pair = species pair for PSF calculations (‘home’\_’away’)

Data:

‘data’\_cond\_home = plant biomass data of the home species at the end of the conditioning phase

‘data’\_cond\_away = plant biomass data of the away species at the end of the conditioning phase

‘data’\_home = root trait and soil data of the home species at the end of the conditioning phase/ plant biomass data of the home species in home soil at the end of the feedback phase

‘data’\_away = root trait and soil data of the away species at the end of the conditioning phase/ plant biomass data of the home species in away soil at the end of the feedback phase

PSF\_ = plant-soil feedback calculated between biomass in home soil vs. away soil/ sterile soil

PSF\_type = plant-soil feedback type (biotic = home vs. sterile, specific = home vs. away)