

**Colonisation resistance and establishment success along gradients of functional and phylogenetic diversity in experimental plant communities.**  
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## **Galland\_et\_al\_2019\_Data\_Journal\_of\_Ecology.zip**

The files contain the community composition data from a diversity experiment designed to disentangle the role of FD and PD in plant community dynamic. Using a pool of 19 species naturally coexisting in central European mesic meadows, 40 communities of 6 species were selected to cover four independent combinations of high and low FD and PD. The 40 communities were sown on fertilised and unfertilised plots (80 plots in total). Species covers were estimated in spring and autumn over 2 growing seasons (2016 and 2017). We provide here both the sown communities' composition (designed with 6 species equally represented) and the realised communities with observed abundances of both sown and colonising species.

Remark: Another experiment running at the locality, together with marginal seed admixtures from the seed provider, provided some potential colonisers that do not belong to the local species pool (e.g. *Dianthus superbus*). Nevertheless, the vast majority of colonisers were naturally occurring species in the surrounding area.

## **File list (Galland\_et\_al\_2019\_Data\_Journal\_of\_Ecology.zip)**

Galland\_et\_al\_Sown\_communities.txt  
Galland\_et\_al\_Observed\_communities.txt

## **File Description**

Galland\_et\_al\_Sown\_communities.txt - contain the designed communities, i.e. the 6 species sown in each plot with equal proportions.

Galland\_et\_al\_Observed\_communities.txt - contain the vegetation releves for each plot at the 4 sampling time.

Both files have the same structure, with the following columns:

- **year** year of sampling, 2 levels [2016, 2017]
- **season** season of sampling, 2 levels [spring, autumn]
- **plot** plot unique identifier, 80 levels
- **treat** diversity treatment, 4 levels[HP\_HF, HP\_LF, LP\_HF, LP\_LF]. *H*=high, *L*=low, *P*=Phylogenetic diversity, *F*=Functional diversity)
- **rep** replicate number of the diversity treatment, 10 levels [1:10].
- **fert** fertilisation treatment, 2 levels [*U*, *F*]. *U*= Unfertilised, *F*=Fertilised
- **sp\_name** species names formatted as *Genus\_species*, 110 levels
- **status** whether the species was a sown or colonising species, 2 levels [sown, inva]  
*sown* = sown, *inva* =coloniser
- **cover** species percentage cover in the plot, estimated on a positively unbounded percentage scale in order to account for the different strata of vegetation [1:100]