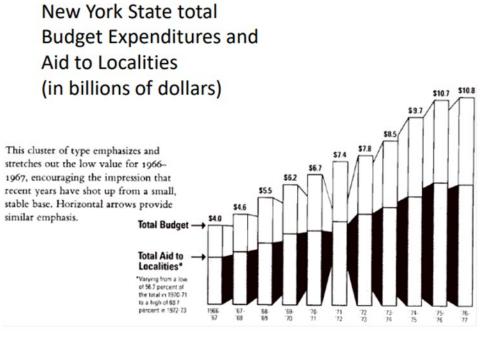
THE SHRINKING FAMILY DOCTOR In California Percentage of Doctors Devoted Solely to Family Practice 1975 1990 1964 12.0% 16.0% 27% 6,212 1: 3,167 1: 2,247 RATIO TO POPULATION 8,023 Doctors



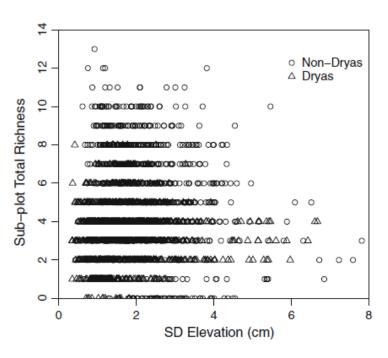


Fig. 1 Scatter diagram of sub-plot total richness vs. SD elevation for all plots. Non-Dryas plots are represented by circles, while Dryas plots are represented as triangles. N = 2048

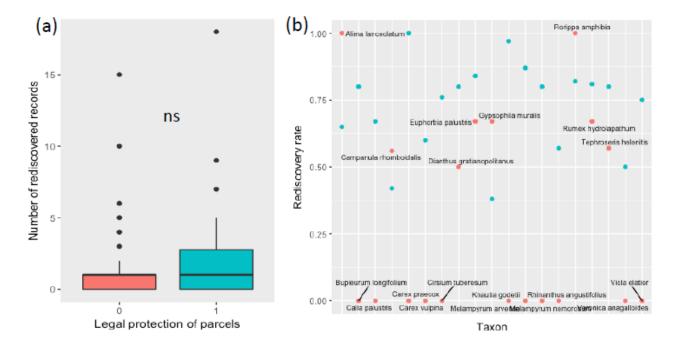


Figure 7. (a) Comparison between the number of rediscovered records of priority plant species within legally protected and outside protected parcels (1=inside, 0=outside; "ns" corresponds to nonsignificant); (b) Rediscovery rates of the same rediscovered priority plant species within this study (indicated in red) and a study conducted by Kempel et al. (in preparation, indicated in blue), which are significantly different (Welch's two sample t-test, p = 0.00028).

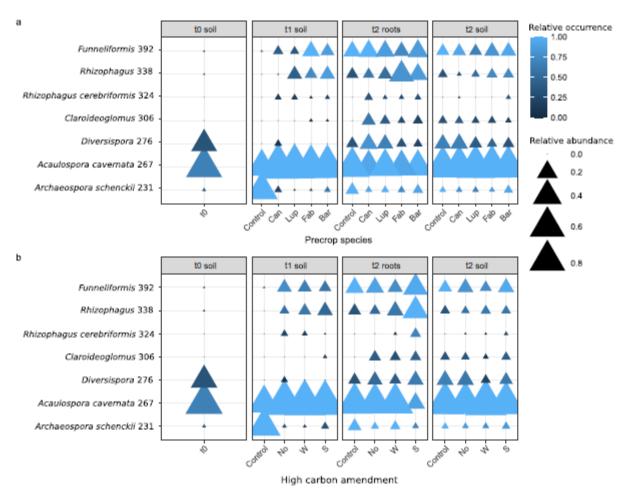
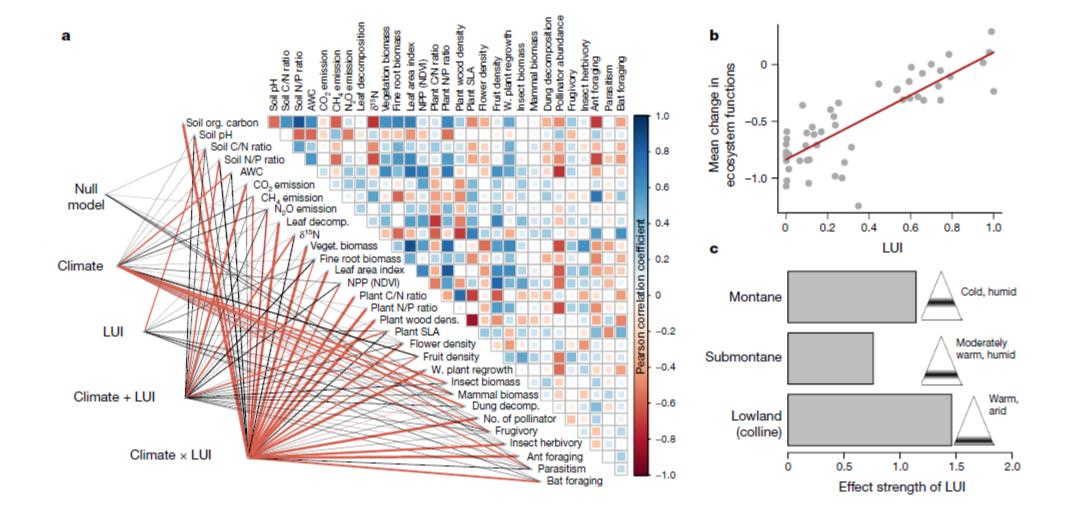


Fig. 3. Distribution of AM fungal clades across rotation phases, pre-crops, high carbon amendment, and plant compartment. Distribution across (a) pre-crop species and (b) high carbon amendment treatments is emphasized. The size of the point represents clade relative read abundance. The color of the points represents clade relative occurrence. Communities are t0, original soil communities; t1, soil communities after pre-crop conditioning phase; and t2, root communities at crop harvest. Abbreviations are Can, canola; Lup, white lupine; Bar, spring barley; Fab, faba bean; Control, control; No, no amendment; W, wheat straw; S, sawdust.



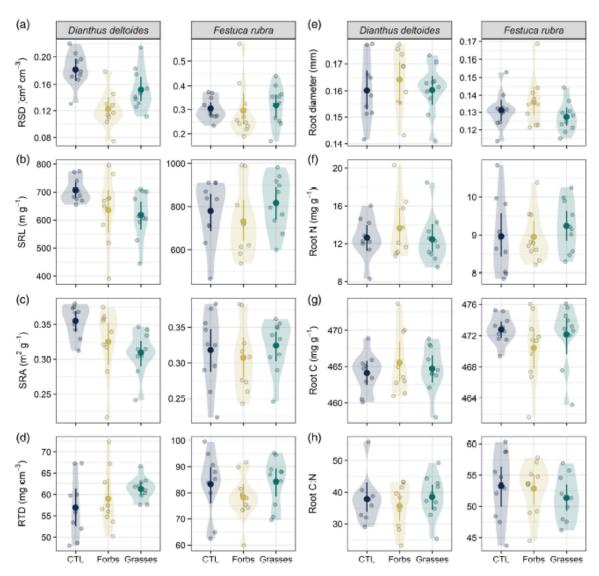


FIGURE 5 Root functional traits of *D. deltoides* and *F. rubra* when exposed to the metabolome found in the soil solution of plant communities differing in species composition. Soil solution was collected from mesocosms in which a forb (Forbs) or a grass (Grasses) community was sown, as well as from unsown mesocosms containing only soil (CTL). The following root traits were measured: (a) root surface density (RSD), (b) specific root length (SRL), (c) specific root area (SRA), (d) root tissue density (RTD), (e) root diameter, (f) root N concentration, (g) root C concentration, and (h) root C:N ratio. For each treatment, mean values and compatibility intervals are shown (n = 9-10). Individual observations and data distributions are displayed at the back of each graph as dots and density plots, respectively. For each response variable, effect sizes and compatibility intervals can be found in Figure S8 [Colour figure can be viewed at wileyonlinelibrary.com]

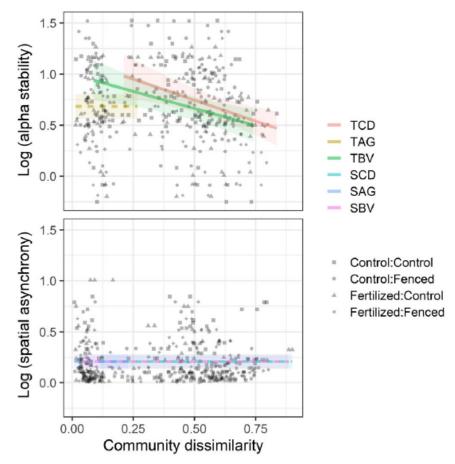
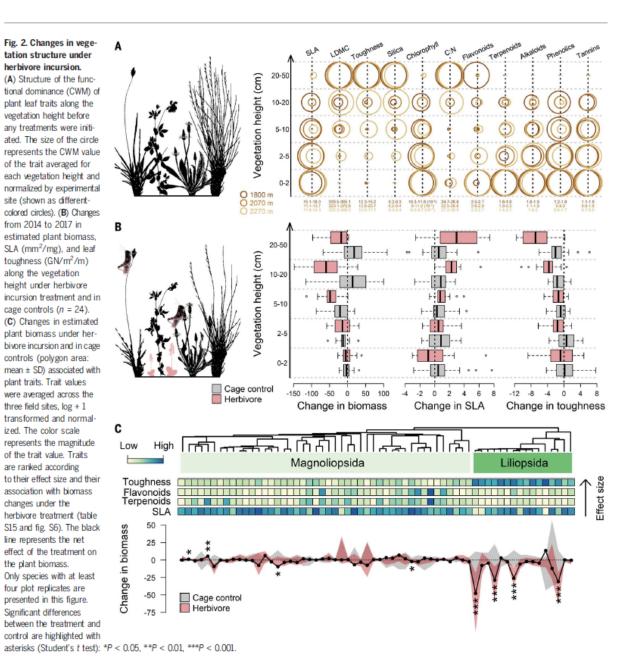
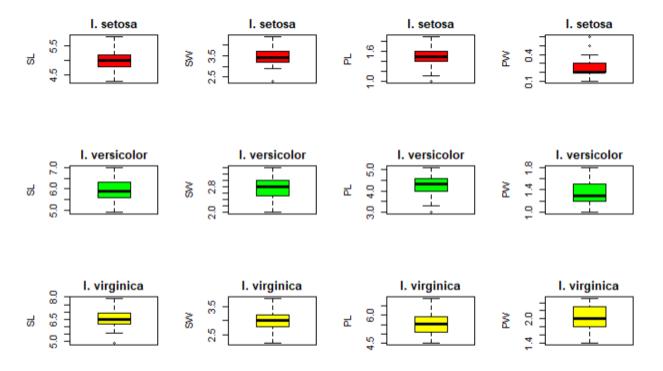


FIGURE 3 Relationships between community dissimilarity, its components, and alpha stability and spatial asynchrony. Lines are fitted with linear mixed-effect models; shades are 95% confidence bands. Solid lines show significant relationships; dashed lines show nonsignificant relationships. Note, three regression lines overlapped with each other in the lower panel. SAG, spatial abundance gradients; SBV, spatial balanced variation; SCD, spatial community dissimilarity; TAG, temporal abundance gradients; TBV, temporal balanced variation; TCD, temporal community dissimilarity. See Table S5 for model specifications and test statistics

What about this one?





Exercise 1: improve this graph (base R or ggplot2)

get data in R: data("iris")

Exercise 2: create a graph with your own data

• What do you want to show? How?