# Appendix 1: Analysis of long-term plant community change

Code and documentation to repeat these analyses are available at XYZ, using the R packages LDATS (available X) and cvlt (available X).

**Data**

The annual plant communities on all experimental plots at Portal are censused twice annually, to capture the distinct winter and summer plant communities associated with winter and summer rainy seasons at the site. For each plot, all plants within 16 0.5x0.5m quadrats are identified to species and counted. For each season in each year, we combined all individual plants counted across the plots within each treatment used for our analysis (5 exclosure and 4 control plots) to characterize the treatment-level plant community. We analyzed summer and winter communities, and control and exclosure communities, separately. For both seasons, exclosure and control communities had qualitatively the same dynamics.

**The LDATS approach**

We used a modified version of the approach described in Christensen et al. (2018) and implemented in the R package *LDATS* (Simonis et al. 2020) to test for, and describe the timing and rapidity of, shifts in community composition of the annual plants at Portal. For a more in-depth introduction to this approach, see Christensen et al. 2018; for details on the model implementation in LDATS, see *LDATS.* Briefly, LDATS combines Latent Dirichlet Allocation (LDA) with changepoint analysis of timeseries to identify shifts in community composition over time. LDA is a technique used in text analysis to describe “topics” comprising groups of words – or, in this application, species – that occur together within a set of documents – or, in this application, census periods. Topics consist of sets of species that occur together in a fixed proportion to each other, and a single species may belong to multiple topics. Each sample in time can be characterized in terms of the proportion of *topics* that make up the sample. Applied to all of the census periods (timesteps) in a dataset, LDA reduces the high-dimensional matrix of individual species’ abundances over time into a timeseries of a handful of 2-5 topics that vary in their proportional abundance in each timestep. A change-point model fit to the *topic* proportional abundances identifies when, or if, the topic composition of the community changes over time, by breaking the timeseries into chunks characterized by different mixtures of topic proportions. If the topic proportions remain stable over time, or if they vary but without strong temporal structure, there may be little improvement in model fit to be gained by breaking the timeseries into distinct chunks, and zero changepoints are used.

We adjusted the procedure described in Christensen et al. (2018) to accommodate the relatively high species richness and low sampling frequency of the plant community (>100 species of plants compared to 21 rodent, and approximately 30 annual samples of plant community composition compared to >400 monthly samples of the rodent community). First, there is of course no seasonal dynamic in annual data, so we fit timeseries models as intercept-only models rather than with a seasonal component. Second, rather than selecting a single best-fitting LDA model and using only that model for the timeseries analysis (as in Christensen et al. 2018), we conducted a grid search of all possible combinations of numerous candidate LDA and timeseries models, and selected the model combination that achieved the best fit to the empirical data using leave-one-out crossvalidation. Applied to short, high-dimensional data such as the annual plants, the original two-stage model selection procedure is prone to fitting an LDA model with a large number of topics, often using one topic to describe each census period, which defeats the purpose of using it as a tool for dimensionality reduction. Evaluating models based on the overall performance of the LDA and timeseries models combined corrects for this tendency.

For leave-one-out crossvalidation, we evaluated each model configuration (comprising a number of LDA topics, LDA seed – as the VEM optimization used in LDA fitting can be sensitive to initial conditions - and number of changepoints) based on its performance predicting the species composition of withheld timesteps. Every timestep was used as the test timestep once, with a buffer of 2 years on either side of the test timestep withheld from the training data. First, we fit each candidate LDA model to the full dataset. We then split the timeseries of topic proportions into training and test datasets. While including the full dataset in model fitting for crossvalidation is unusual, the LDA must be fit to the full dataset, because LDA models fit to training datasets with different timesteps withheld can result in dramatically different topic compositions that cannot be re-combined into a coherent model fit. In principle, using the full dataset could result in data leakage and over-fitting the LDA, but we do not see evidence of this in this application. We fit the timeseries model to the training subset, and calculated the loglikelihood of the *observed* species proportions in the test timestep given the species proportions predicted by the combined LDA and changepoint models. We repeated this for each test timestep, and summarized the model’s fit as the mean loglikelihood over all test timesteps. Over all candidate model configurations, we selected the simplest model with a loglikelihood within one standard error of the best loglikelihood (cite Hastie). In selecting the simplest model, we first minimized the number of changepoints and then the number of LDA topics, and finally selected the LDA seed with the highest loglikelihood.

For each season and treatment, we evaluated all possible combinations of LDA models with 2-5 topics, 100 different LDA seeds, and timeseries models with 0-X changepoints. In addition to the models fit using LDA and timeseries analysis, we included as a candidate model a null hypothesis model, in which the prediction for each species in all timesteps is simply the mean proportional abundance for that species.

**Results**