1. **Dataset creation**

The R scripts in this section aim to assemble the data of environmental covariates, land-use intensity and community diversity for all studied years and plots.

Dataset assembly is based on the respective raw data which can be downloaded from in the project-owned information system BEXIS (<https://www.bexis.uni-jena.de/>). Most of the datasets are freely accessible, for some the data owner need to be asked for permission. The latter can be done through the BEXIS system. See the dataset description document (“dataset\_description\_GitHub.docx”) for details on the used datasets and their accessibility in BEXIS. The datasets assembled from this code build the baseline for the conducted analysis and illustrations published in Neuenkamp et al. 2025 xxx.

Steps of data creation (order of R codes with one subfolder per step):

Step 1 – Prepare environmental and land-use intensity input data plotwise & pairwise:

**Folder: 1. Prepare\_input\_data\_plotwise\_pairwise**

1. Environmental and land-use intensity information (LUI) across all plots and years are first collected into one dataset.

**Script: 1-prepare\_LUI\_covariates.R**

1. When in the next step datasets are reformatted to show spatial and temporal pairwise comparisons in environmental and LUI they are split up into a spatial and temporal dataset.

**Script: 2-create\_temporal\_spatial\_dataset\_template.R**

1. For reasons of comparability among plots, LUI is standardized per plot across years – residualling out the plot-level differences in LUI. LUI residuals are added to the pairwise-datasets (b) as new columns.

**Script: 3-LUIresid\_calculations.R**

1. Additional LUI and environmental covariate parameters used later in the analysis (linear modelling, LM) are calculated and added to the pairwise-datasets; i.e., mean and delta of compared plot pairs.

**Script: 4-add\_mean\_delta\_LUI\_and\_covariates\_to\_pairwise\_datasets.R**

**Output:** *pwise\_space.RData*, *pwise\_time.RData*

Step 2 – Prepare diversity input data for pairwise-datasets:

**Folder: 2. Alpha\_Beta\_Calculations\_Chao**

1. The community data for plants and arthropods are cleaned and assembled with relative abundances for each trophic group (plants, arthropod herbivores and secondary consumers/predators).

**Script: 0-prepare\_input\_helper\_data.R**

1. Differences in alpha and beta diversity indices are calculated each for spatial and temporal plot comparisons and added to the environmental and LUI information in the respective pairwise-datasets. Complete pairwise datasets are saved for each combination of trophic group and comparison type (time, space) separately (n= 6 datasets). in assembled data sets are split into four datasets spatial and temporal diversity responses of plants and arthropod communities respectively.

**Script: 1\_Chao Alpha Beta Calculations.R**

**Output:** *pwise\_space\_plant.RData*, *pwise\_time\_plant.RData,*

*pwise\_space\_herb.RData*, *pwise\_time\_herb.RData,*

*pwise\_space\_pred.RData*, *pwise\_herb\_pred.RData*

The already assembled data sets containing pairwise comparison of responses in plant and arthropod community diversity (alpha, beta) to spatial and temporal changes in land-use intensity and environmental covariates are archived in BExIS under the following names & IDs\*,\*\*:

1. **Spatial diversity responses of plant communities:**

Spatial pair-wise comparisons of plant-community and land-use data (all

experimental plots 2008-2018) (ID: 31924)

1. **Temporal diversity responses of plant communities:**

Temporal pair-wise comparisons of plant-community and land-use data (all

experimental plots 2008-2018) (ID: 31921)

1. **Spatial diversity responses of arthropod communities:**

Spatial pair-wise comparisons of arthropod-community and land-use data (all experimental plots 2008-2017) (ID: 31926)

1. **Temporal diversity responses of arthropod communities:**

Temporal pair-wise comparisons of arthropod-community and land-use data (all experimental plots 2008-2017) (ID: 31925)

\* Arthropod comparisons are merged for arthropod herbivores and secondary consumers/predators in the assembled datasets. In the following analysis trophic groups are addressed are separated in the script where necessary. When working with the individually assembled data (Step 2) then all needed arthropod datasets have to be uploaded separately.

\*\* Assembled data have not been created in the exact same chronological order of scripts as explained above due to consecutive decisions in the modelling process. Thus, estimates of LUI, diversity and environmental covariates of the assembled datasets archived in BEXIS and those produced in chronological order by the provided R scripts might differ slightly on some occasions. Data output has been checked for both dataset types though and differences were neglectable. For exact reproduction of the shown results the authors recommend using the archived, assembled datasets as input to the data analysis and plotting of results as provided in the following scripts.