**README**

*Species contributions to stability in perturbed communities*

There are two folders containing analyses and data creation for model simulations (BEFD\_Analysis) and empirical data (SITES\_Analysis).

**R version 4.1.3 (2022-03-10)**

**Platform**: x86\_64-apple-darwin17.0 (64-bit)

**Running under:** macOS 13.4

**Package versions:**

sjPlot\_2.8.10

lme4\_1.1-28

Matrix\_1.4-0

ggpmisc\_0.4.5

ggpp\_0.4.3

cowplot\_1.1.1

ggpubr\_0.4.0

MESS\_0.5.9

here\_1.0.1

lubridate\_1.9.2

forcats\_1.0.0

stringr\_1.5.0

dplyr\_1.1.2

purrr\_1.0.1

readr\_2.1.4

tidyr\_1.3.0

tibble\_3.2.1

ggplot2\_3.4.2

tidyverse\_2.0.0

**Model simulations – BEFD\_Analysis**

**List of R scripts:**

* 05BEFDcreateData
* 06BEFDcalculateAUC
* 07BEFDanalyseAUC
* 08BEFDdominance

**List of data:**

* LRRdata1.csv
* StabAlphaAUC.csv

**Description of data:**

LRRdata1.csv: simulated species responses with and without disturbances

* timepoint: time information, time step 0.5
* runNumber: run number, 1-50
* survivingSpecies: amount of species that survived the disturbance
* species: species information, each run contains 5 species named species1, species2, etc.
* growth: simulated biomass production of species
* competition: competition term alpha of each species
* sensitivity: sensitivity values of species to the perturbation
* Limit: sensitivity scenario, i.e. Limit1 = all equally sensitive, Limit2 = one tolerant species, Limit3 = one sensitive species
* Model: information on disturbance, i.e. pulse, press, pulsepress
* con.bio: mean control biomass
* treat.tot: summed community biomass in the treatment for each model run
* con.tot: summed community biomass in the control for each model run
* LRR.tot: community LRR
* deltabm.tot: community response ratio
* RR: species-specific response ratio
* treat.pi: species relative proportion in treatment
* con.pi: species relative proportion in control
* delta.pi: difference between relative proportion in treatment and control

StabAlphaAUC.csv: Absolute and relative contributions of single species to stability

* Model: information on disturbance, i.e. pulse, press, pulsepress
* runNumber: run number, 1-50
* species: species information, each run contains 5 species named species1, species2, etc.
* competition: competition term alpha of each species
* mean.con.pi: mean relative dominance in control
* AUC.totRR: AUC of community response ratio as measure for community stability
* AUC.pi: relative contribution to stability
* AUC.RR: absolute contribution to stability
* Limit: sensitivity scenario, i.e. Limit1 = all equally sensitive, Limit2 = one tolerant species, Limit3 = one sensitive species

**Description of R scripts:**

The following R scripts have been used to create and analyse our simulated communities. We saved the created data frames as csv files.

05BEFDcreateData: 5 species Lotka Volterra model to create data for 3 different disturbance types and 3 Limit scenarios.

* Functions used are stored in the functions folder and comprise of:
  + 01BEFDModel.R
  + 02BEFDgrowthRates.R
  + 03BEFDbiomassChange.R
  + 04BEFDgenerateDisturbanceSensitivities.R
  + 05BEFDgenerateCompetitionMatrix.R
  + 06BEFDrk4Solver.R
* We here create a competition-dependent model with 5 species with the same growth rate and capacity over 450 timepoints and time step 0.5.
* Disturbances are a reduction in biomass:
  + Press disturbances include a maximum biomass removal where 0.25 % of biomass is removed every time step, pulse with 50% maximum biomass removal and, pulsepress with a combination of the two (one time removal of maximum 50% of the biomass and continuous maximum biomass removal of 0.25%).
* The intensity of the disturbance is influenced by species-specific sensitivities. We considered three different sensitivity scenarios:
  + Limit 1: All species respond equally to the disturbance.
  + Limit 2: All species are equally sensitive to the disturbance, but one is resistant.
  + Limit 3: All species are equally resistant to the disturbance, but one is sensitive.
* After creating the data, here we calculate the response variables needed for the AUC calculation. See Table 1 in MS
* Write csv **LRRdata.csv**

06BEFDcalculateAUC: calculate the AUC change in biomass and proportion for each species, Model, Limit, run combination, etc.

* Biomass plot for supplement
* AUC Loop cycling trough cases using the auc() function of the MESS package
* Fig. 2: species contributions to stability
* Write csv **StabAlphaAuc.csv**

07BEFDanalyseAUC: Analysis of the AUC as function of their relative competitiveness

* Calculates relative competitiveness as inverse relative alpha
* Supplementary figure

08BEFDdominane: Analysis of the AUC as function of species dominance

Calculate relative dominance from control

* Estimates magnitude of species contributions
* Fig. 3: species contributions as function of relative dominance

**Empirical data – SITES\_Analysis**

**List of data:**

zooplankton.csv: Table contains species-specific abundance and biomass for each

zooplankton taxa. The table was downloaded from the SITES data

portal and not manipulated.

**List of R scripts:**

* 01SITES\_createTidyData\_complete.R
* 02SITES\_TidyanalyseTraits\_complete.R
* 03SITES\_lmer\_complete.R

**Description of R scripts:**

01SITES\_createTidyData\_complete.R: Data wrangling and AUC loop

* Here, we standardize the data collected in the 10 experiments (10 lakes x 2 seasons) using the complete() function, missing values of species responses were handled by replacing NAs with zeros.
* AUC Loop cycling trough cases using the auc() function of the MESS package
* Fig. 4: species contributions to stability
* **AUC\_data3.csv**

02SITES\_TidyanalyseTraits\_complete.R: Analysis of AUC as a function of dominance

* Estimates magnitude of species contributions
* Analyses species contributions as function of species relative dominance in control
* Fig. 5: species contributions as a function of relative dominance

03SITES\_lmer\_complete.R: Linear models to estimate the likelihood of a species contributing to stability in the same way among all lakes and seasons and thus being displayed in the same sector.

* Individual linear models for each perturbation type and dimension using the lmer() function within the lme4 package (Bates *et al.*, 2015).
* We used lake and season as random effects in our model and removed the intercept to test each species against zero.
* Creates a table with adjusted R2, p-values and estimates for each taxa and each disturbance.