##

"Per capita interactions and stress tolerance drive stress-induced changes in biodiversity effects on ecosystem functions"

overview of all scripts and data added as supporting material

##

Datasets

data.txt

description: raw data file containing cell densities, nutrient and atrazine concentrations

columns:	- composition:	community composition. species are represented by the original code given at isolation and correspond to column names 5-12
	- day:	day of measurement (start=0)
	- replicate:	technical replicate
	- concentration:	atrazine treatment (ug L^-1)
	- X8:	density species 1 (cells/ml), not that this is the original code given at isolation. It refers to species 1 in supplementary tables 3 and 4
	- X10:	density species 2 (cells/ml), not that this is the original code given at isolation.It refers to species 2 in supplementary tables 3 and 4
	- X17:	density species 3 (cells/ml), not that this is the original code given at isolation. It refers to species 3 in supplementary tables 3 and 4
	- X18:	density species 4 (cells/ml), not that this is the original code given at isolation. It refers to species 4 in supplementary tables 3 and 4
	- XE18:	density species 5 (cells/ml), not that this is the original code given at isolation. It refers to species 5 in supplementary tables 3 and 4
	- X23:	density species 6 (cells/ml), not that this is the original code given at isolation. It refers to species 6 in supplementary tables 3 and 4
	- X31:	density species 7 (cells/ml), not that this is the original code given at isolation. It refers to species 7 in supplementary tables 3 and 4
	- X32:	density species 8 (cells/ml), not that this is the original code given at isolation. It refers to species 8 in supplementary tables 3 and 4
	- nitrate:	nitrate concentration (mg L^-1)
	- phosphate:	nitrate concentration (mg L^-1)
	- silicate:	silicate concentration (mg L^-1)
	- atrazine:	atrazine concentration (ug L^-1)

note: some species were not detected in some samples because of low densities. However, species were still present since they could be observed after the end of the experiment. Densities for a non-detected species were therefore set to cell/ml.

data_biov.RData

description: conversion of the raw data (data.txt) into an RData object, added with some extra columns containing species biovolumes, total biovolume and diversity. Conversion can be done using "Data_analysis.R"

columns:	- composition:	community composition. species are represented by the original code given at isolation and correspond to column names 5-12
	- day:	day of measurement (start=0)
	- replicate:	technical replicate
	- concentration:	atrazine treatment (ug L^-1)
	- n8:	density species 1 (cells/ml), not that this is the original code given at isolation. It refers to species 1 in supplementary tables 3 and 4
	- n10:	density species 2 (cells/ml), not that this is the original code given at isolation. It refers to species 2 in supplementary tables 3 and 4
	- n17:	density species 3 (cells/ml), not that this is the original code given at isolation. It refers to species 3 in supplementary tables 3 and 4
	- n18:	density species 4 (cells/ml), not that this is the original code given at isolation. It refers to species 4 in supplementary tables 3 and 4
	- nE18:	density species 5 (cells/ml), not that this is the original code given at isolation. It refers to species 5 in supplementary tables 3 and 4
	- n23:	density species 6 (cells/ml), not that this is the original code given at

		isolation. It refers to species 6 in supplementary tables 3 and 4
- n31:	density species 7 (cells/ml), not that this is the original code given at isolation. It refers to species 7 in supplementary tables 3 and 4	
- n32:	density species 8 (cells/ml), not that this is the original code given at isolation. It refers to species 8 in supplementary tables 3 and 4	
- 8:	biovolume density species 1 (um^3/ml), not that this is the original code given at isolation. It refers to species 1 in supplementary tables 3 and 4	
- 10:	biovolume density species 2 (um^3/ml), not that this is the original code given at isolation. It refers to species 2 in supplementary tables 3 and 4	
- 17:	biovolume density species 3 (um^3/ml), not that this is the original code given at isolation. It refers to species 3 in supplementary tables 3 and 4	
- 18:	biovolume density species 4 (um^3/ml), not that this is the original code given at isolation. It refers to species 4 in supplementary tables 3 and 4	
- E18:	biovolume density species 5 (um^3/ml), not that this is the original code given at isolation. It refers to species 5 in supplementary tables 3 and 4	
- 23:	biovolume density species 6 (um^3/ml), not that this is the original code given at isolation. It refers to species 6 in supplementary tables 3 and 4	
- 31:	biovolume density species 7 (um^3/ml), not that this is the original code given at isolation. It refers to species 7 in supplementary tables 3 and 4	
- 32:	biovolume density species 8 (um^3/ml), not that this is the original code given at isolation. It refers to species 8 in supplementary tables 3 and 4	
- total:	total biovolume (um^3/ml)	
- diversity:	species richness (number of species)	
- nitrate:	nitrate concentration (mg L^-1)	
- phosphate:	nitrate concentration (mg L^-1)	
- silicate:	silicate concentration (mg L^-1)	
- atrazine:	atrazine concentration (ug L^-1)	

effects_analysis.RData

description: RData object containing calculations of biodiversity effects (Fox 2005, *Ecology Letters*) and its components. This object is generated by "Data_analysis.R".

columns:	- composition:	community composition. species are represented by the original code given at isolation and correspond to column names 5-12
	- diversity:	species richness (number of species)
	- day:	day of measurement (start=0)
	- replicate:	technical replicate
	- concentration:	atrazine treatment (ug L^-1)
	- cov(RY/RYT-RYe,M):	covariance between the deviation form the null hypothesis within a zero sum game (RY/RYT-RYe) and the monoculture yield (M)
	- cor(RY/RYT-RYe,M):	correlation between the deviation form the null hypothesis within a zero sum game (RY/RYT-RYe) and the monoculture yield (M)
	- sd(RY/RYT-RYe):	standard deviation of the deviation form the null hypothesis within a zero sum game (RY/RYT-RYe)
	- cov(RY-RY/RYT,M):	covariance between the deviation from a zero sum game (RY-RY/RYT) and the monoculture yield (M)
	- cor(RY-RY/RYT,M):	correlation between the deviation from a zero sum game (RY-RY/RYT) and the monoculture yield (M)
	- sd(RY-RY/RYT):	standard deviation of the deviation from a zero sum game (RY-RY/RYT
	- sd(M):	standard deviation of the monoculture yield (um^3 ml^-1)
	- mean(M):	mean monoculture yield (um^3 ml^-1)
	- mean(deltaRY):	mean deviation in relative yield from the null hypothesis
	- dY:	deviation in yield from the null hypothesis
	- dom:	dominance effect (Fox 2005, *Ecology Letters*)
	- tdc:	trait-dependent complementarity effect (Fox 2005, *Ecology Letters*)
	- tic:	trait-independent complementarity effect (Fox 2005, *Ecology Letters*)
	- total:	total biovolume (um^3 ml^-1)

note: RY=observed relative yield, RYT=relative yield total and RYe is the expected relative yield. See Methods for details

change_effects.RData

description: RData object containing the regression slopes in biodiversity effects over a concentration gradient. This object is generated by "Data_analysis.R".

columns:	- composition:	community composition. species are represented by the original code given at isolation and correspond to column names 5-12

- diversity:	species richness (number of species)
- day:	day of measurement (start=0)
- betadom:	regression coefficient between the dominance effect and the atrazine concentration (mm^3 ug ^-1)
- sddom:	standard deviation of the regression coefficient between the dominance effect and the atrazine concentration (mm^3 ug ^-1)
- pdom:	p-value of the regression coefficient
- betatdc:	regression coefficient between the trait-dependent complementarity effect and the atrazine concentration (mm^3 ug ^-1)
- sdtdc:	standard deviation of the regression coefficient between the trait-dependent complementarity effect and the atrazine concentration (mm^3 ug ^-1)
- ptedc:	p-value of the regression coefficient
- betatic:	regression coefficient between the trait-independent complementarity effect and the atrazine concentration (mm^3 ug ^-1)
- sdtic:	standard deviation of the regression coefficient between the trait-independent complementarity effect and the atrazine concentration (mm^3 ug ^-1)
- ptic:	p-value of the regression coefficient

Data_traits.RData

description: RData object containing the predictor and response variables for model 2.
This object is generated by "Data_analysis.R".

columns:

- composition:	community composition. species are represented by the original code given upon isolation and correspond to column names 5-12
- diversity:	species richness (number of species)
- day:	day of measurement (start=0)
- betadom:	regression coefficient between the dominance effect and the atrazine concentration (mm^3 ug^-1)
- betatdc:	regression coefficient between the trait-dependent complementarity effect and the atrazine concentration (mm^3 ug^-1)
- betatic:	regression coefficient between the trait-independent complementarity effect and the atrazine concentration (mm^3 ug ^-1)
- int_w:	weighted interaction strength estimated from the fitted community model under scenario 4 (-)
- sen_w:	weighted changes in monoculture yield (-)
- d_int_w:	weighted change in interaction strength estimate from the fitted community model under scenario 5 (-)

Compostitions_list.RData

description: RData object containing a list of the order in which parameters were estimated under each scenario.

M_yield.RData

description: RData object containing the monoculture yields from "data.txt".

estimates_4.RData

description: RData object containing the mean parameter estimates under scenario 4

estimates_5.RData

description: RData object containing the maenparameter estimates under scenario 5

M_out.RData

description: RData object containing 1000 Monte Carlo Simulations of monoculture yields

MC_out.RData

description: RData object containing 1000 Monte Carlo Simulations of community yields

Scripts

Data_analysis.R

      description: Main script running all statistical analysis (Table 1) and residual diagnostics (Supplementary Figures 3-13)

Calculate_biodiveristy_effects.R

      description: script transforming the raw data to the data frame used for analyis (data_biov.RData), calculating all biodiversity effects (effects_analysis.RData) and changes in biodiveristy effects (change_effects.RData).

      note: this script should either be ran from "Data_analysis.R" or the user should make sure that "data.txt" is available in the current working directory

Calculate_traits.R

      description: script calculating all predictor variables based on the estimates of the community model used for the analysis of model 2

      note: this script should either be ran from "Data_analysis.R" or the user should make sure that "data_biov.RData",

      "estimates_4.Rdata", "estimates_5.RData", "change_effects.RData" and "compositions_list.RData" are available

      in the current working directory

Figure_1.R

      description: script producing Figure 1

Figure_2.R

      description: script producing Figure 2

Figure_3.R

      description: script producing Figure 3

Figure_4.R

      description: script producing Figure 4

Relative_abundances.R

      description: script producing Supplementary Figure 1

Predicted_observed.R

      description: script producing Supplementary Figure 2