Experimental evidence for the importance of multi-trophicstructure in regulating species persistence

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This code allows reproducing all results and raw figures from the paper. We start by loading the data and functions needed.

```
set.seed(1234) #to ensure reproducibility
source('functions/toolbox.R') #set of tools and functions
source('functions/alphantw.R') #function to plot aphas ntw
source('functions/feasibility_domain_simplex.R') #funcion to plot triangles
load(file = "data/matrices/plants.RData") #plant matrices as calculayted in plant_parameters.R
load(file = "data/matrices/polinators.RData") #pollinator matrices directly from raw data.
load(file = "data/matrices/betas.Rdata") #Beta matrices ordered as required for the functions
if(!require(ggtern)) {install.packages("ggtern"); library(ggtern)}
if(!require(deSolve)) {install.packages("deSolve"); library(deSolve)}
if(!require(matrixcalc)) {install.packages("matrixcalc"); library(matrixcalc)}
```

First we ask if plant coexistence within trophic level changes when considering pollintors.

```
#Calculate Omegas (feasability domain) for PLANTS ONLY:
C <- diag(c(1,1,1), 3) # constraints -> assuming that r can be positive only
### loops are useful to eliminate numerical instabilities and allow the value to converge
print(Omega_overlap(alpha,C)*2)
```

```
## [1] 0.2890077
```

```
print(Omega_overlap(alpha_no_link,C)*2)
```

```
## [1] 0.7503123
```
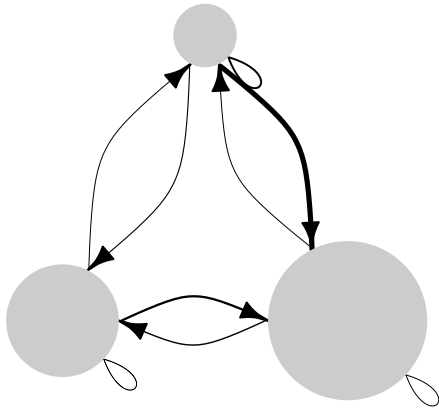
```
print(Omega_overlap(alpha_link,C)*2)
```

```
## [1] 0.6007772
```
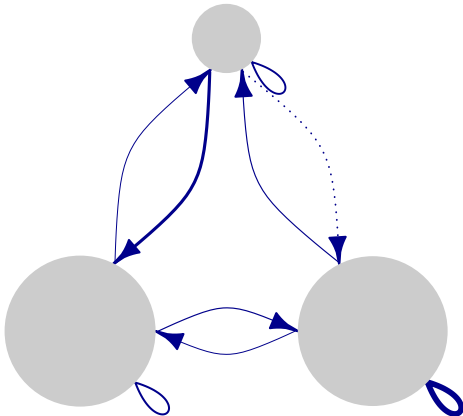
```
#PLOT Fig 2
#A) Ntw
mk_graph_3sp(alphamat = alpha, rs = r/2, title = "\n No pollinators", superunname = TRUE
            , line_col = "black")
```
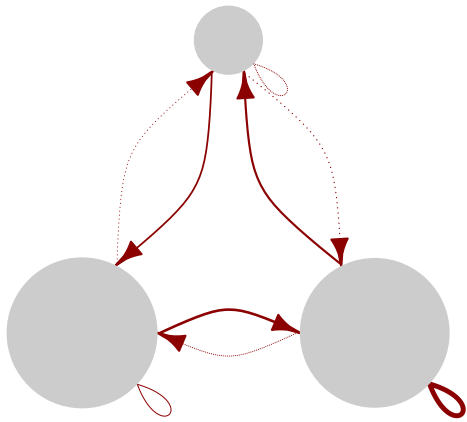
No pollinators


```
mk_graph_3sp(alphamat = alpha_link, rs = r_link/2, title = "\n Link", superunname = TRUE
             , line_col = "darkblue")
```
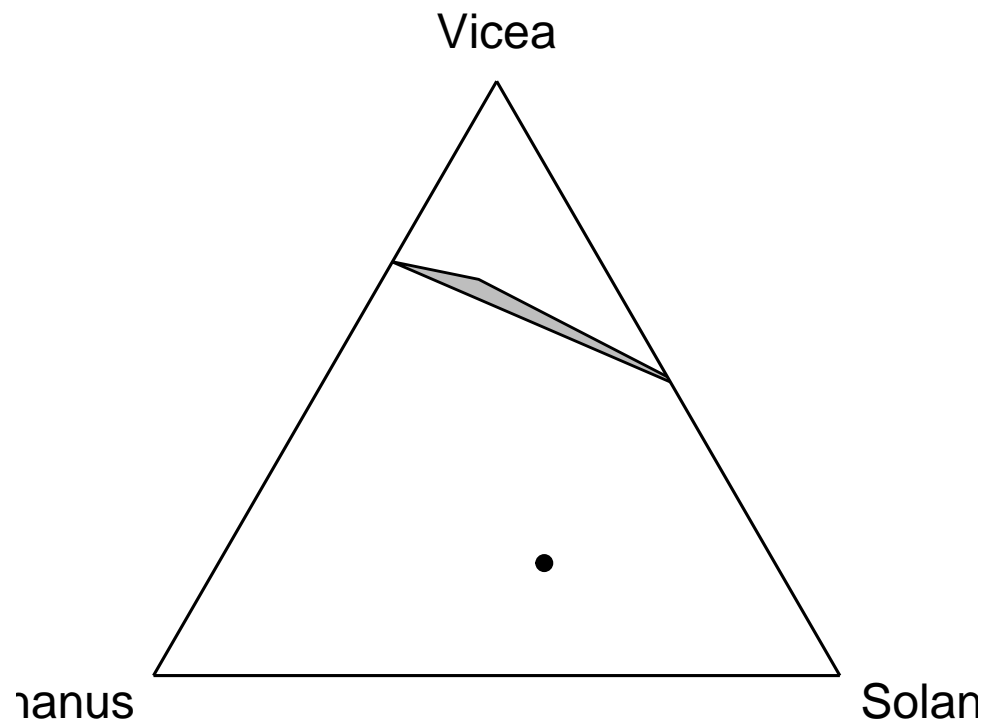
Link


```
mk_graph_3sp(alphamat = alpha_no_link, rs = r_link/2, title = "\n No link",
             superunname = TRUE, line_col = "darkred")
```
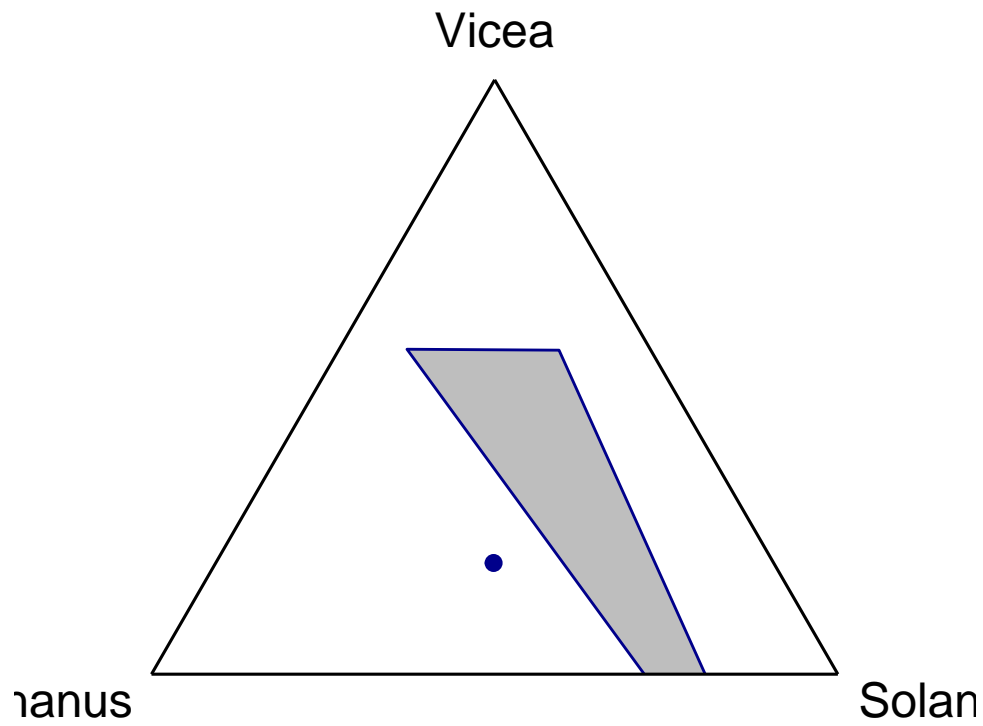
No link

```
#B) triangles
nopol <- print(simplex_plot(alpha, r, col = "black", line_col = "black"))
```
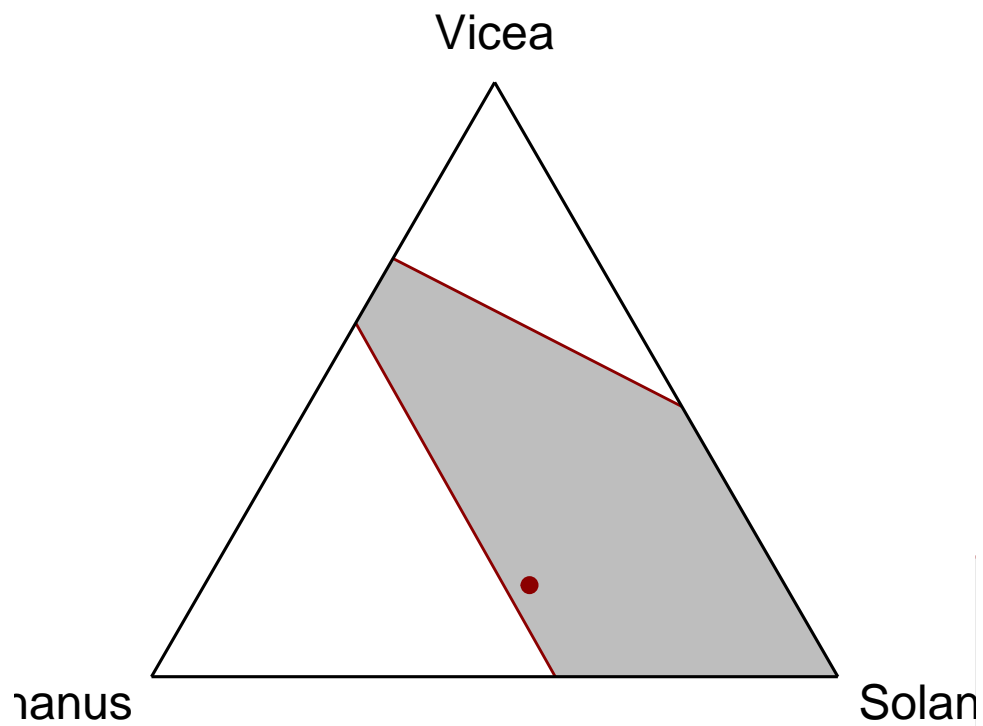
Vicea

hanus   Solan

```
link <- print(simplex_plot(alpha_link, r_link, col = "darkblue", line_col = "darkblue"))
```

```
no_link <- print(simplex_plot(alpha_no_link, r_no_link, col = "darkred", line_col = "darkred"))
```


Next, we ask if the full community coexistence changes for the full community

```r
C <- diag(c(1,1,1,1,1,1), 6) # constraints

Omega_fit_no_link <- Omega_overlap(beta_no_link,C)*2
probs_no_link <- Probabilities_plant_pos(beta_no_link,6)

Omega_fit_link <- Omega_overlap(beta_link,C)*2
probs_link <- Probabilities_plant_pos(beta_link,6)

Omega_fit_analitical <- Omega_overlap(beta_no_link_analitical2,C)*2
probs_analitical <- Probabilities_plant_pos(beta_no_link_analitical2,6)

print(c(Omega_fit_no_link,probs_no_link))
```

```
## [1] 0.2359025 1.0000000 0.1060000 0.4980000 0.5360000 0.0600000 0.2440000
```

```r
print(c(Omega_fit_link,probs_link))
```

```
## [1] 0.2118445 0.9460000 0.2740000 0.4580000 0.5200000 0.1740000 0.2040000
```

```r
print(c(Omega_fit_analitical,probs_analitical))
```

```
## [1] 0.2335425 0.9320000 0.2780000 0.4540000 0.4720000 0.2320000 0.2420000
```

```r
#Those are probabilities of species coexsisting.
#Notice Omega's a very close...

#plot
barplot(as.matrix(rbind(probs_link, probs_analitical, probs_no_link)), beside = TRUE,
        las = 2, names.arg = c("Solanum", "Raphanus", "Vicea", "Osmia",
                               "Bombus", "Lucilia"), ylim = c(0,1), col = c("darkblue",
                                                                            "orangered3",
                                                                            "darkred")

        #legend.text = c("no link", "link", "anal. removed")
        )
```