

# Experimental evidence for the importance of multi-trophic structure 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(1111) #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') #function to plot triangles
load(file = "data/matrices/plants.RData") #plant matrices as calculayted in plant_parameters.R
load(file = "data/matrices/pollinators.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 (feasibility domain) for PLANTS ONLY:
C <- diag(c(1,1,1), 3) # constraints -> assume 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] 0.2886096
```

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

```
## [1] 0.7512334
```

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

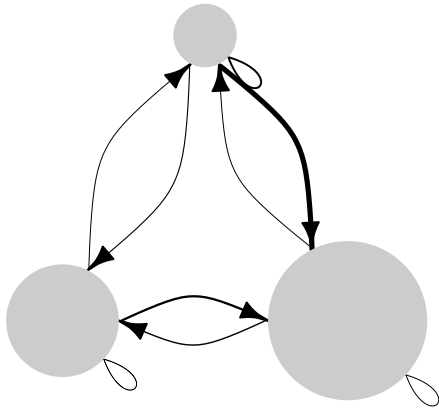
```
## [1] 0.6007499
```

```
#PLOT Fig 2
```

```
#A) Ntw
```

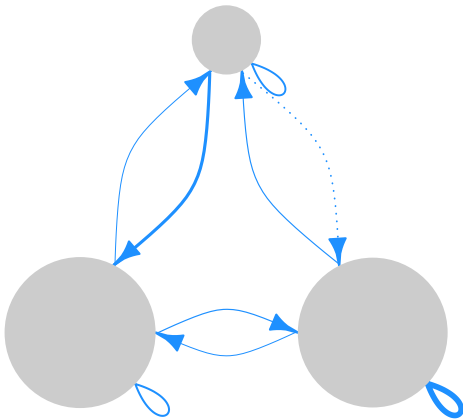
```
mk_graph_3sp(alphamat = alpha, rs = r/2, title = "\n No pollinators", superunname = TRUE
, line_col = "black")
```

## No pollinators



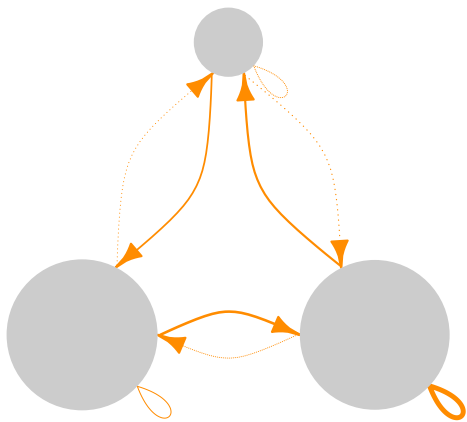
```
mk_graph_3sp(alphamat = alpha_link, rs = r_link/2, title = "\n Link", superunname = TRUE  
             , line_col = "DodgerBlue")
```

## Link

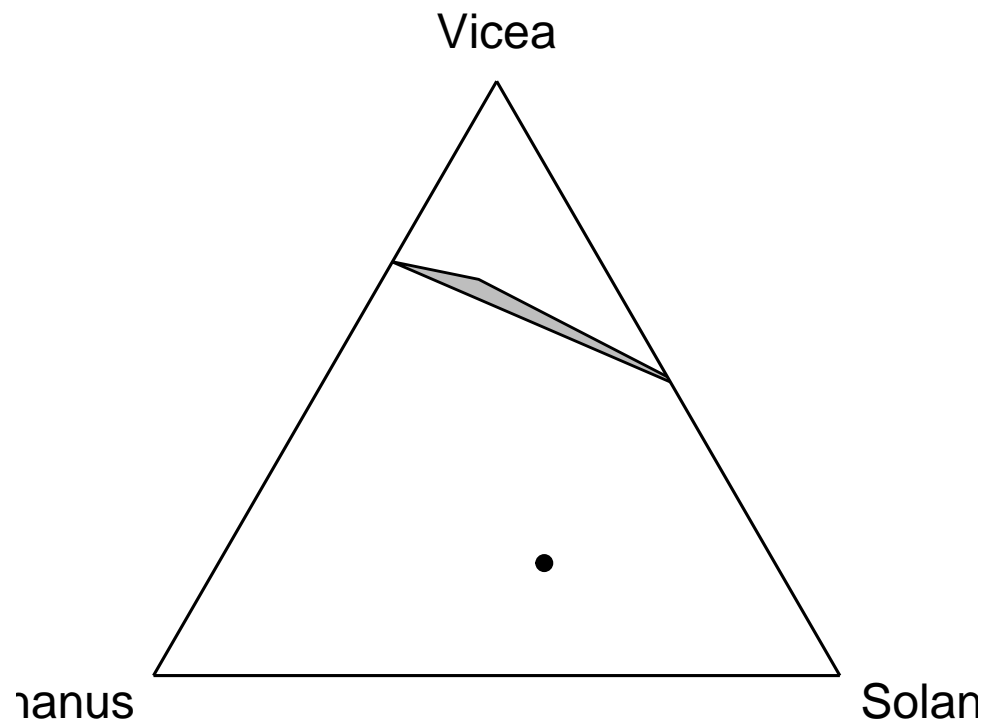


```
mk_graph_3sp(alphamat = alpha_no_link, rs = r_link/2, title = "\n No link",  
             superunname = TRUE, line_col = "darkorange")
```

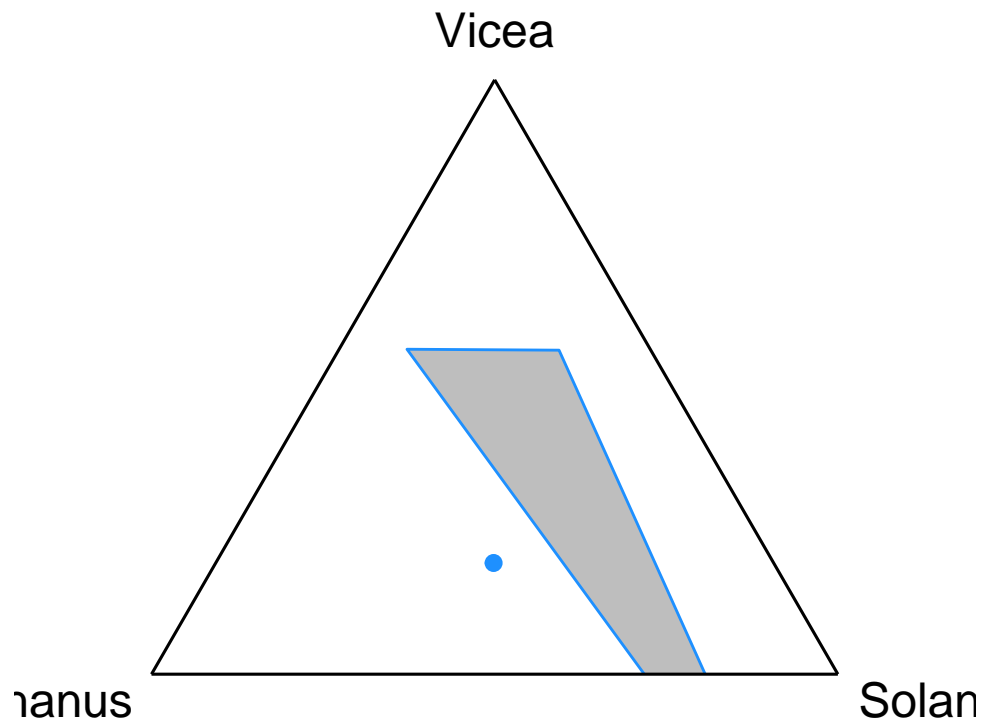
No link



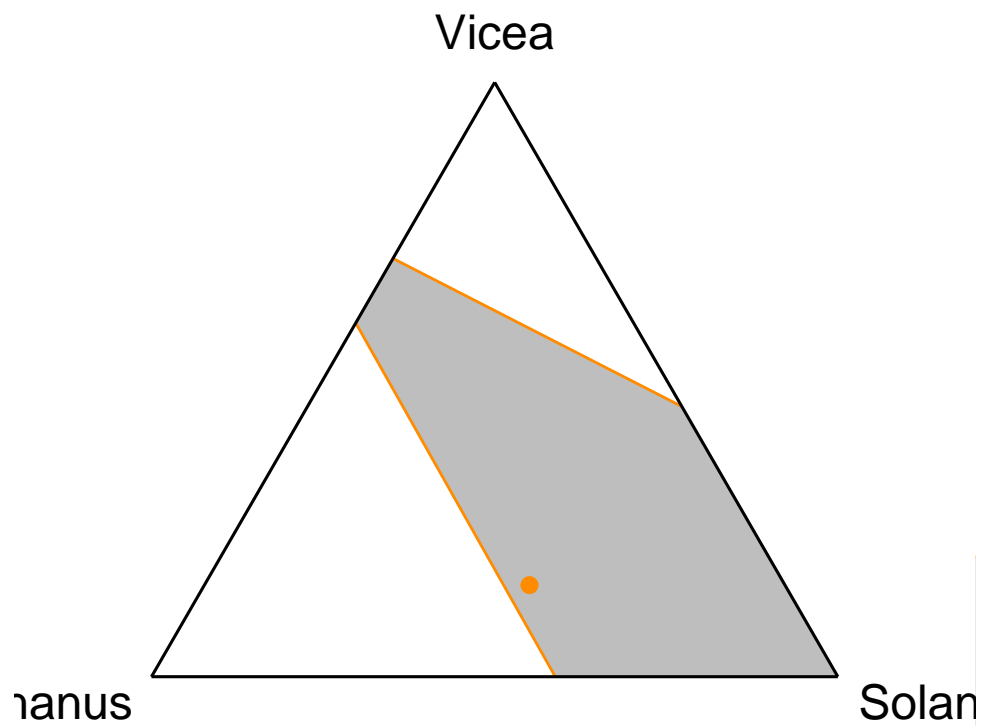
```
#B) triangles
nopol <- print(simplex_plot(alpha, r, col = "black", line_col = "black"))
```



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



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



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

```

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] 0.2480612 1.0000000 0.1200000 0.5080000 0.5220000 0.0600000 0.2620000
print(c(Omega_fit_link,probs_link))

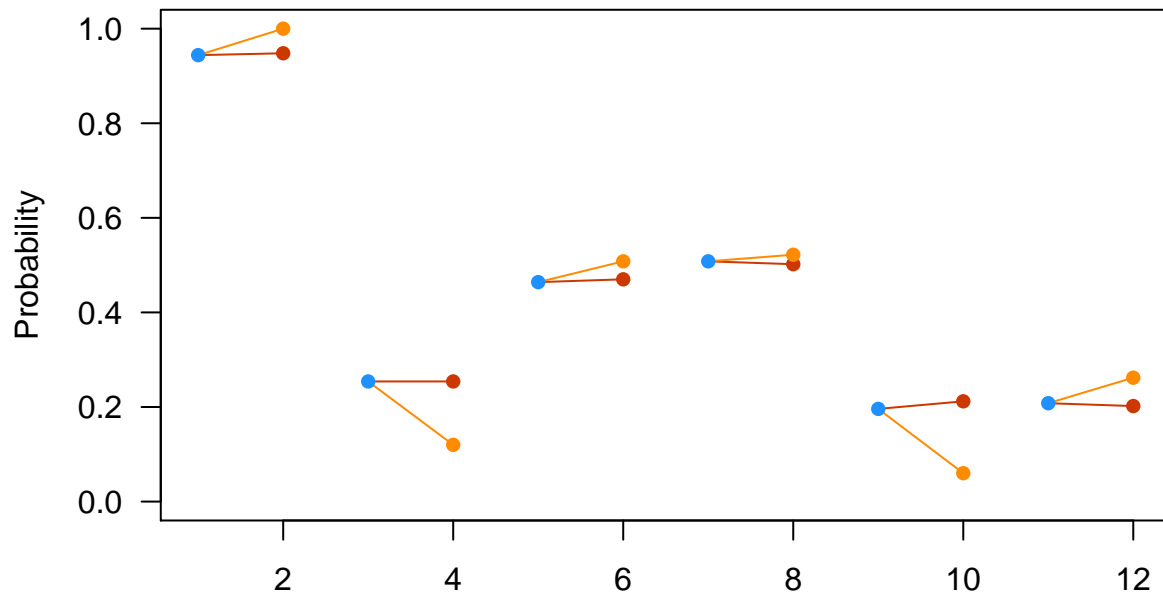
## [1] 0.239591 0.944000 0.254000 0.464000 0.508000 0.196000 0.208000
print(c(Omega_fit_analitical,probs_analitical))

## [1] 0.2492628 0.9480000 0.2540000 0.4700000 0.5020000 0.2120000 0.2020000
#Those are probabilities of species coexisting.
#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("DodgerBlue",
#          "orangered3",
#          "darkorange")
#          #legend.text = c("no link", "link", "anal. removed")
#          )

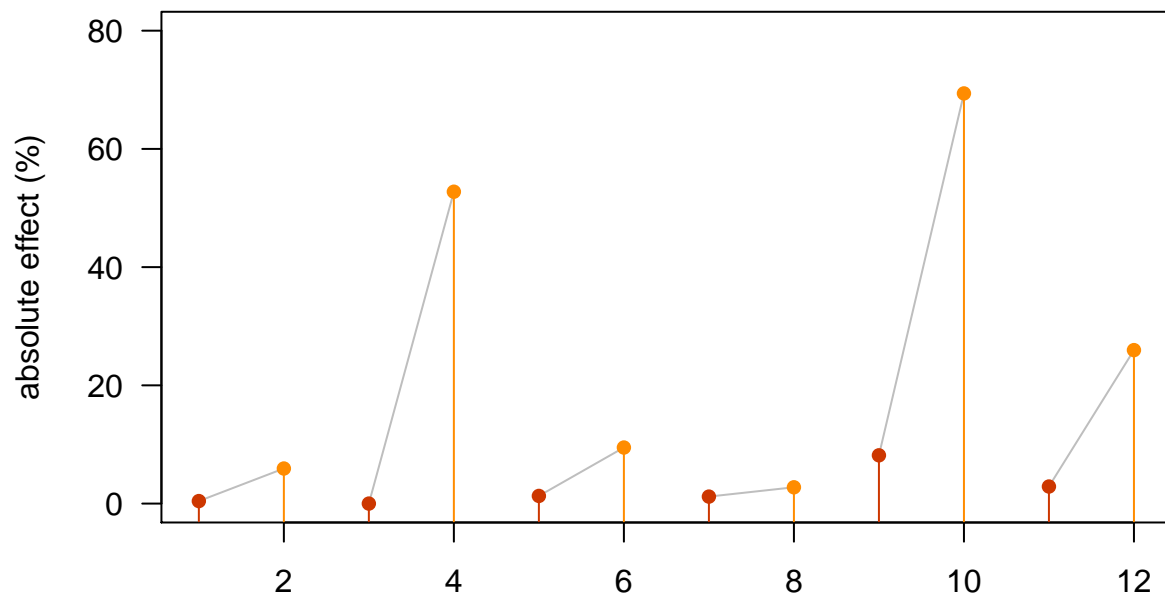
plot(x = 1,
     xlab = " ", ylab = "Probability",
     xlim = c(1, 12), ylim = c(0, 1),
     type = "n", las = 1)
segments(x0 = c(1,3,5,7,9,11),
         y0 = probs_link,
         x1 = c(2,4,6,8,10,12),
         y1 = probs_analitical,
         col = "orangered3")
segments(x0 = c(1,3,5,7,9,11),
         y0 = probs_link,
         x1 = c(2,4,6,8,10,12),
         y1 = probs_no_link,
         col = "darkorange")
points(x = c(1,3,5,7,9,11), y = probs_link, pch = 16, col = "DodgerBlue")
points(x = c(2,4,6,8,10,12), y = probs_analitical, pch = 16, col = "orangered3")
points(x = c(2,4,6,8,10,12), y = probs_no_link, pch = 16, col = "darkorange")

```



```
#in %
change_analitical <- abs(100-(probs_analitical*100)/probs_link)
change_nolink <- abs(100-(probs_no_link*100)/probs_link)
plot(x = 1,
     xlab = " ", ylab = "absolute effect (%)",
     xlim = c(1, 12), ylim = c(0, 80),
     type = "n", las = 1)
segments(x0 = c(1,3,5,7,9,11),
         y0 = change_analitical,
         x1 = c(2,4,6,8,10,12),
         y1 = change_nolink,
         col = "grey")
points(x = c(1,3,5,7,9,11), y = change_analitical, pch = 16, col = "orangered3")
points(x = c(2,4,6,8,10,12), y = change_nolink, pch = 16, col = "darkorange")

segments(x0 = c(1,3,5,7,9,11),
         y0 = c(-3,-3,-3,-3,-3,-3),
         x1 = c(1,3,5,7,9,11),
         y1 = change_analitical,
         col = "orangered3")
segments(x0 = c(2,4,6,8,10,12),
         y0 = c(-3,-3,-3,-3,-3,-3),
         x1 = c(2,4,6,8,10,12),
         y1 = change_nolink,
         col = "darkorange")
```



```
wilcox.test(change_analitical, change_nolink, paired = TRUE, alternative = "two.sided")
```

```
##
## Wilcoxon signed rank test
##
## data: change_analitical and change_nolink
## V = 0, p-value = 0.03125
## alternative hypothesis: true location shift is not equal to 0
```

```
mean(change_analitical)
```

```
## [1] 2.324303
```

```
mean(change_nolink)
```

```
## [1] 27.71268
```

```
mean(change_analitical)-mean(change_nolink)
```

```
## [1] -25.38838
```