

# On the inference of positive and negative interactions and their relation to abundance

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A recent paper inferred species-species interactions from spatially replicated abundance data and further tied those inferred interactions to abundances<sup>1</sup>. Specifically, the authors found that inferred positive interactions were disproportionately associated with rare species, a result they interpreted as rare species being stabilized by facilitative interactions.

```
library(knitr)
opts_chunk$set(echo = TRUE, cache = TRUE,
               fig.width = 4, fig.height = 4, fig.align = 'center')

library(pika)
library(RarePlusComMinus)

## Loading required package: vegan
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.5-3

library(parallel)
library(MASS)
library(socorro)

# plotting defaults
parArgs <- list(mar = c(3, 3, 0, 0) + 0.5, mgp = c(1.75, 0.5, 0), tcl = -0.25)
cexDefault <- 1.4
lwdDefault <- 2
```

First we explore the shape of the spatial abundance patters in the real data provided by ref. 1.

```
data('abundance_matrices')

summStats <- mclapply(1:length(abun.mat), mc.cores = 3, FUN = function(i) {
  x <- round(abun.mat[[i]])

  o <- sapply(1:ncol(x), function(j) {
    params <- try(fitdistr(x[, j], 'negative binomial'))
    if(class(params) == 'try-error') {
      params <- c(size = NA, mu = NA, loglik = NA)
    } else {
      params <- c(params$estimate, loglik = params$loglik)
    }
    nocc <- sum(x[, j] > 0)
    abund <- sum(x[, j])

    return(c(nsite = nrow(x), nspp = ncol(x), nocc = nocc, abund = abund, J = sum(x),
             params))
  })
})
```

```

summStats <- data.frame(study = rep(names(abun.mat), sapply(summStats, ncol)),
                        t(do.call(cbind, summStats)))

# remove failed optims
summStats <- summStats[!is.na(summStats$size), ]

# looks like an optim bug around size = 100, remove it
summStats <- summStats[round(summStats$size) != 100, ]

par(parArgs)
plot(summStats$nocc / summStats$nsite, summStats$mu, log = 'xy')
plot(summStats$nocc / summStats$nsite, summStats$size, log = 'xy')
plot(summStats$nocc, summStats$mu, log = 'xy')
plot(summStats$nocc, summStats$size, log = 'xy')
plot(summStats$mu, summStats$size, log = 'xy')

plot(summStats$abund / summStats$J, summStats$mu, log = 'xy')
plot(summStats$abund / summStats$J, summStats$size, log = 'xy')
plot(summStats$abund / summStats$nsite, summStats$mu, log = 'xy')
plot(summStats$abund / summStats$nsite, summStats$size, log = 'xy')
plot(summStats$abund, summStats$mu, log = 'xy')
plot(summStats$abund, summStats$size, log = 'xy')

plot(summStats$abund / summStats$J, summStats$nocc / summStats$nsite, log = 'xy')
plot(summStats$abund, summStats$nocc, log = 'xy')

plot(summStats$nsite, summStats$J, log = 'xy')
plot(summStats$J, summStats$nspp, log = 'xy')

plot(summStats$nspp, summStats$mu, log = 'xy')
plot(summStats$nspp, summStats$size, log = 'xy')
plot(summStats$nspp, summStats$nocc / summStats$nsite, log = 'xy')

commStats <- mclapply(abun.mat, mc.cores = 3,
                     FUN = function(x) unlist(plusMinus(x)))

## Warning in mclapply(abun.mat, mc.cores = 3, FUN = function(x)
## unlist(plusMinus(x))): all scheduled cores encountered errors in user code

commStats <- do.call(rbind, commStats)

```

## References

1. Calatayud, J. *et al.* Positive associations among rare species and their persistence in ecological assemblages. *Nat Ecol Evol* (2019).