

# Supporting Information

A.T. Tredennick, P.B. Adler, & F.R. Adler, “The relationship between species richness and...”  
*Ecology Letters*

## Section SI.1 R Code for Consumer-Resource Model

Below is the R code for our model function, which is represented mathematically in the main text in Equations 1-4. The same code, along with all the code to reproduce our results, has been archived on Figshare (link) and is available on GitHub (<http://github.com/atredennick/Coexistence-Stability/releases>).

```
simulate_model <- function(seasons, days_to_track, Rmu,
                           Rsd_annual, sigE, rho,
                           alpha1, alpha2, alpha3, alpha4,
                           eta1, eta2, eta3, eta4,
                           r1, r2, r3, r4,
                           a1, a2, a3, a4,
                           b1, b2, b3, b4,
                           eps1, eps2, eps3, eps4,
                           D1, D2, D3, D4,
                           N1, N2, N3, N4, R) {

  require('deSolve') # for solving continuous differential equations
  require('mvtnorm') # for multivariate normal distribution functions

  ## Assign parameter values to appropriate lists
  DNR <- c(D=c(D1,D2,D3,D4), # initial dormant state abundance
           N=c(N1,N2,N3,N4), # initial live state abundance
           R=R)              # initial resource level

  parms <- list (
    r = c(r1,r2,r3,r4),      # max growth rate for each species
    a = c(a1,a2,a3,a4),      # rate parameter for Hill function
    b = c(b1,b2,b3,b4),      # shape parameter for Hill function
    eps = c(eps1,eps2,eps3,eps4) # resource-to-biomass efficiency
  )

  #####
```

```

#### Sub-Model functions -----
####
## Continuous model
updateNR <- function(t, NR, parms){
  with(as.list(c(NR, parms)), {
    dN1dt = N1*eps[1]*(uptake_R(r[1], R, a[1], b[1]))
    dN2dt = N2*eps[2]*(uptake_R(r[2], R, a[2], b[2]))
    dN3dt = N3*eps[3]*(uptake_R(r[3], R, a[3], b[3]))
    dN4dt = N4*eps[4]*(uptake_R(r[4], R, a[4], b[4]))
    dRdt = -1 * (dN1dt/eps[1] + dN2dt/eps[2] + dN3dt/eps[3] + dN4dt/eps[4])
    list(c(dN1dt, dN2dt, dN3dt, dN4dt, dRdt)) # output as list
  })
} # end continuous function

## Discrete model
update_DNR <- function(t, DNR, gammas,
                        alpha1, alpha2, alpha3, alpha4,
                        eta1, eta2, eta3, eta4) {
  with (as.list(DNR),{
    g1 <- gammas[1]
    g2 <- gammas[2]
    g3 <- gammas[3]
    g4 <- gammas[4]
    D1new <- (1-g1)*(alpha1*N1 + D1)*(1-eta1)
    D2new <- (1-g2)*(alpha2*N2 + D2)*(1-eta2)
    D3new <- (1-g3)*(alpha3*N3 + D3)*(1-eta3)
    D4new <- (1-g4)*(alpha4*N4 + D4)*(1-eta4)
    N1new <- g1*(alpha1*N1 + D1)*(1-eta1)
    N2new <- g2*(alpha2*N2 + D2)*(1-eta2)
    N3new <- g3*(alpha3*N3 + D3)*(1-eta3)
    N4new <- g4*(alpha4*N4 + D4)*(1-eta4)
    Rnew <- Rvector[t]
    return(c(D1new, D2new, D3new, D4new, N1new, N2new, N3new, N4new, Rnew))
  })
}

## Resource uptake function (Hill function)
uptake_R <- function(r, R, a, b) {
  return((r*R^a) / (b^a + R^a))
}

```

```

}

## Generate germination fractions
getG <- function(sigE, rho, nTime, num_spp) {
  varcov      <- matrix(rep(rho*sigE,num_spp*2), num_spp, num_spp)
  diag(varcov) <- sigE
  if(sigE > 0) { varcov <- Matrix::nearPD(varcov)$mat } # crank through nearPD to fix rounding
  varcov <- as.matrix(varcov)
  e      <- rmvnorm(n = nTime, mean = rep(0,num_spp), sigma = varcov)
  g      <- exp(e) / (1+exp(e))
  return(g)
}

####
#### Simulate model -----
####
days      <- c(1:days_to_track)
num_spp    <- length(parms$r)
nmsDNR     <- names(DNR)
dormants   <- grep("D", names(DNR))
NR         <- DNR[-dormants]
nmsNR      <- names(NR)
gVec       <- getG(sigE = sigE, rho = rho, nTime = seasons, num_spp = num_spp)
Rvector    <- rlnorm(seasons, Rmu, Rsd_annual)
saved_outs <- matrix(ncol=length(DNR), nrow=seasons+1)
saved_outs[1,] <- DNR

## Loop over seasons
for(season_now in 1:seasons) {
  # Simulate continuous growing season
  output <- ode(y = NR, times=days, func = updateNR, parms = parms)
  NR     <- output[nrow(output),nmsNR]
  dormants <- grep("D", names(DNR))
  DNR     <- c(DNR[dormants], NR)

  # Save end of season biomasses, before discrete transitions
  saved_outs[season_now+1,] <- DNR

```

```

names(DNR) <- nmsDNR
DNR      <- update_DNR(season_now, DNR, gVec[season_now,],
                      alpha1 = alpha1, alpha2 = alpha2,
                      alpha3 = alpha3, alpha4 = alpha4,
                      eta1 = eta1, eta2 = eta2, eta3 = eta3, eta4 = eta4)

names(DNR) <- nmsDNR
NR        <- DNR[-dormants]
names(NR)  <- nmsNR
} # next season

return(saved_outs)

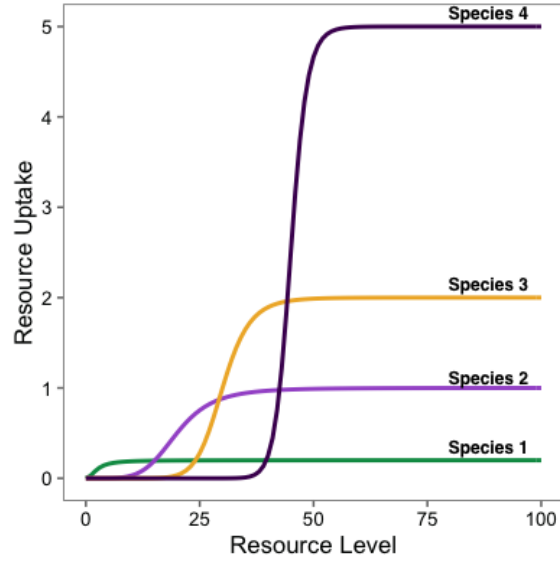
} #end simulation function

```

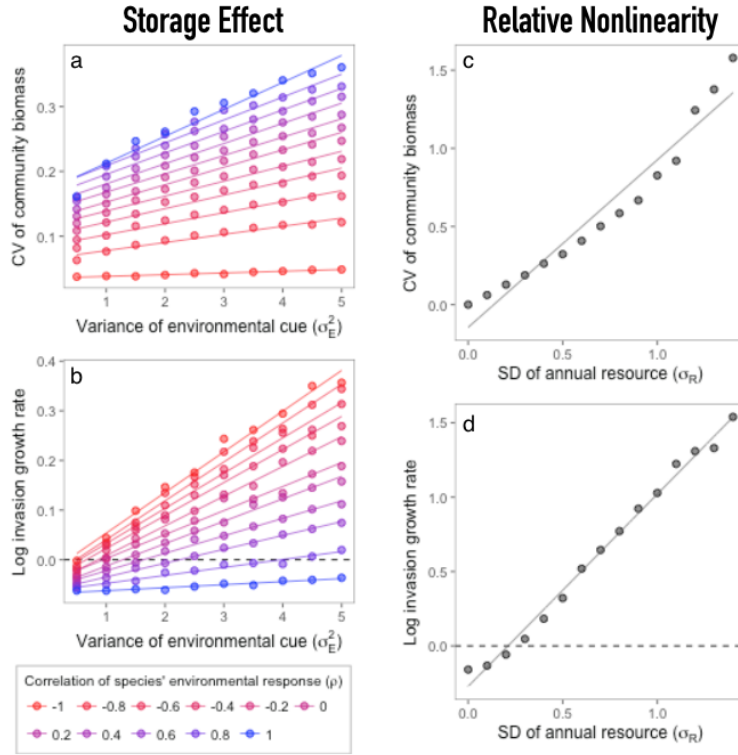
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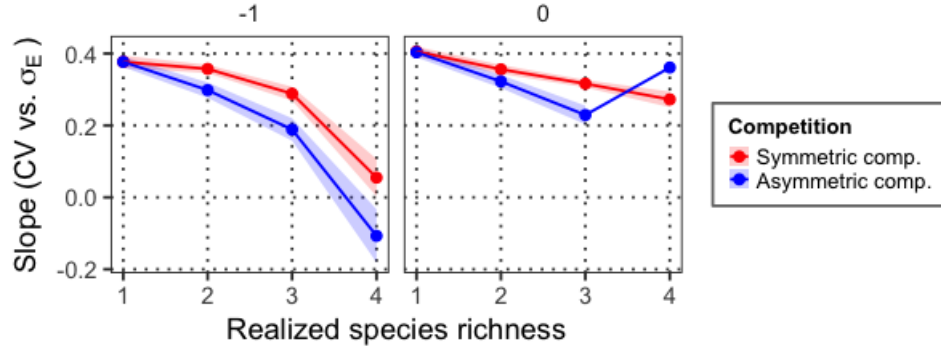


**Figure S1-1** Resource uptake curves for each species (represented by different colors) as used in relative nonlinearity simulations. The equation for resource uptake is:  $f_i(R) = r_i R^{a_i} / (b_i^{a_i} + R^{a_i})$ . Parameter values are as follows. Species 1:  $r = 0.2$ ,  $a = 2$ ,  $b = 2.5$ ; Species 2:  $r = 1$ ,  $a = 5$ ,  $b = 20$ ; Species 3:  $r = 2$ ,  $a = 10$ ,  $b = 30$ ; Species 4:  $r = 5$ ,  $a = 25$ ,  $b = 45$ .

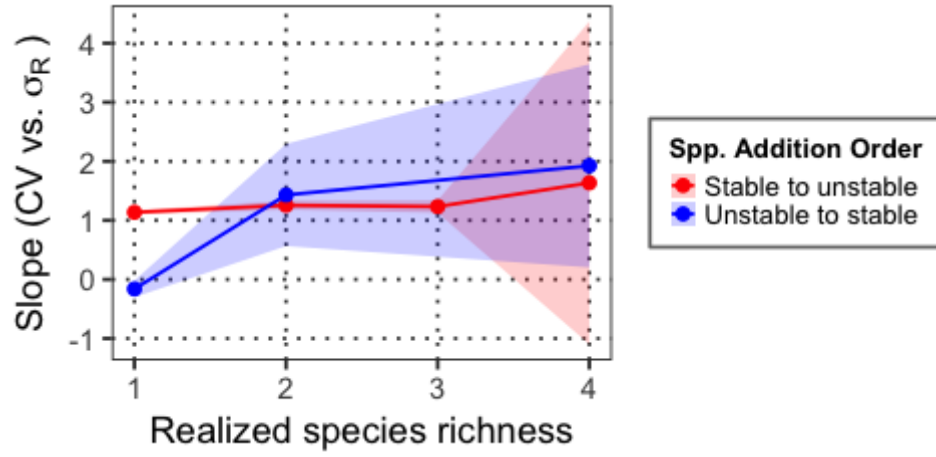


**Figure S1-2** Variability of community biomass and invasion growth rates of the inferior competitor in a two-species community under different parameter combinations. Points are mean values from 5,000 growing seasons and lines are linear fits to show trends. In **Storage Effect** plots (a,b), resource supply is held constant between growing seasons. Resource supply varies each year in **Relative Nonlinearity** simulations (c,d), while the environmental cue variance is set to 0.





**Figure S1-3** Slopes of linear fits for the relationship between  $\log(CV)$  and  $\log(\sigma_E)$  at different levels of realized species richness from storage effect simulations. The slopes come from linear models fit to log-transformed versions of Figure 3 in the main text. For these simulations, “symmetric competition” (•) refers to similar live-to-dormant biomass allocation fractions ( $\alpha = [0.5, 0.495, 0.49, 0.485]$  for the four species), and “asymmetric competition” (•) refers to more dissimilar live-to-dormant biomass allocation fractions ( $\alpha = [0.5, 0.49, 0.48, 0.47]$  for the four species).



**Figure S1-4** Slopes of linear fits for the relationship between  $\log(CV)$  and  $\log(\sigma_R)$  at different levels of realized species richness from relative nonlinearity simulations. The slopes come from linear models fit to log-transformed versions of Figure 4 in the main text.