SUPPORTING INFORMATION

for

Quantifying effects of biodiversity on ecosystem functioning across times and places

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Annotated R script for applying the additive partition to the hypothetical cases provided in Tables 1 and 2. Lines to be run in R are shown in ***bold italic small font***.

The R script on the next two pages first defines functions for quantifying the complementarity effect (***funcCE***) and the selection effect (***funcSE***), as quantified by Loreau and Hector (Loreau & Hector 2001). Second, a function named ***fune*** is defined that requires a data frame (***df***) containing five columns: (1) time, (2) place, (3) species, (4) Y, which is the species-specific levels of ecosystem functioning in mixture, and (5) M, which is the species-specific levels of ecosystem functioning in monoculture; and that returns a data frame with quantities for each of the biodiversity effects shown in Table 2. Note that this function would need to be modified for cases where there are more than two times, places, or species. For example, the expected relative yield assumes two species, planted in equal proportions and the quantification of insurance effects assumes two times and two places. Third, the ***fune*** function is applied to each of the two cases shown in Table 1 and each of the six cases shown in Table 2.

```
#Define functions

library(plyr)

funcCE <- function(df) {return(data.frame(CE = mean(df$M)*mean(df$chRY)*nrow(df)))}
funcSE <- function(df) {return(data.frame(SE = cov(df$M,df$chRY)*(nrow(df)-1)))}

fune <- function(df) {
    #add columns to df that are needed for quantifying biodiversity effects
    df$RYo <- df$Y/df$M
    df$RYe <- 1/2
    df$chRY <- df$RYo-df$RYe
    jdf <- aggregate.data.frame(df$Y,by=list(df$time,df$place),sum)
        names(jdf) <- c("time","place","Yo")
        df <- merge(df,jdf,all.x=T)
    df$p <- df$Y/df$Yo
    df$chRYo <- df$RYo-df$p
    df$dp <- df$p-df$RYe
    jdf <- aggregate.data.frame(df$M,by=list(df$species,df$time),mean)
        names(jdf) <- c("species","time","Mst")
        df <- merge(df,jdf,all.x=T)
    jdf <- aggregate.data.frame(df$M,by=list(df$species,df$place),mean)
        names(jdf) <- c("species","place","Msp")
        df <- merge(df,jdf,all.x=T)
    jdf <- aggregate.data.frame(df$dp,by=list(df$species,df$time),mean)
        names(jdf) <- c("species","time","pst")
        df <- merge(df,jdf,all.x=T)
    jdf <- aggregate.data.frame(df$dp,by=list(df$species,df$place),mean)
        names(jdf) <- c("species","place","psp")
        df <- merge(df,jdf,all.x=T)
    df <- df[order(df$time,df$place,df$species),]

return(data.frame(
    NBE = sum(df$M*df$chRY), #net biodiversity effect
    TC = mean(df$M)*mean(df$chRY)*nrow(df), #total complementarity effect
    TC2 = sum(ddply(df, .(), funcCE)$CE), #this is a different way to quantify TC
    total.se = cov(df$M,df$chRY)*(nrow(df)-1), #total selection effect
    total.se2 = sum(ddply(df, .(), funcSE)$SE), #this is a different way to quantify total.se
    NO = cov(df$M,df$chRYo)*(nrow(df)-1), #nonrandom overyielding effect
    IE = cov(df$M,df$dp)*(nrow(df)-1), #total insurance effect: IE = AS+TI+SI+ST
    AS = sum((tapply(df$M,df$species,mean)-mean(df$M))*(tapply(df$dp,df$species,mean)-
        mean(df$dp)))*2*2, #average selection effect
    TI = sum((as.vector(tapply(df$M,list(df$species,df$time),mean))-
        rep(tapply(df$M,df$species,mean),2))*(as.vector(tapply(df$dp,list(df$species,df$time),mea
        n))-rep(tapply(df$dp,df$species,mean),2)))*2, #temporal insurance effect
    SI = sum((as.vector(tapply(df$M,list(df$species,df$place),mean))-
        rep(tapply(df$M,df$species,mean),2))*(as.vector(tapply(df$dp,list(df$species,df$place),me
        an))-rep(tapply(df$dp,df$species,mean),2)))*2, #spatial insurance effect
    ST = sum((df$M-df$Mst-
        df$Msp+rep(tapply(df$M,df$species,mean),4)+rep(mean(df$M),8))*(df$dp-df$pst-
        df$psp+rep(tapply(df$dp,df$species,mean),4)+rep(mean(df$dp),8))), #spatiotemporal
        insurance effect
    local.ce = sum(ddply(df, .(time,place), funcCE)$CE), #local complementarity effect
    local.se = sum(ddply(df, .(time,place), funcSE)$SE) #local selection effect
    ))}
```

```r
#Table 1A
fune(data.frame(time=c(1,1,1,1), place=c(1,1,2,2), species=c(1,2,1,2), M=c(200,200,100,100),
Y=c(200,200,0,0)))[,c(1,2,4,12,13)]

#Table 1B
fune(data.frame(time=c(1,1,1,1), place=c(1,1,2,2), species=c(1,2,1,2), M=c(50,350,0.44,1),
Y=c(8.15,291.7,0.88,0)))[,c(1,2,4,12,13)]

#Case 1 in Table 2
fune(data.frame(time=c(1,1,1,1,2,2,2,2), place=c(1,1,2,2,1,1,2,2), species=c(1,2,1,2,1,2,1,2),
M=c(100,50,100,50,100,50,100,50), Y=c(100,0,100,0,100,0,100,0)))

#Case 2 in Table 2
fune(data.frame(time=c(1,1,1,1,2,2,2,2), place=c(1,1,2,2,1,1,2,2), species=c(1,2,1,2,1,2,1,2),
M=c(100,50,100,50,50,100,50,100), Y=c(100,0,100,0,0,100,0,100)))

#Case 3 in Table 2
fune(data.frame(time=c(1,1,1,1,2,2,2,2), place=c(1,1,2,2,1,1,2,2), species=c(1,2,1,2,1,2,1,2),
M=c(100,50,50,100,100,50,50,100), Y=c(100,0,0,100,100,0,0,100)))

#Case 4 in Table 2
fune(data.frame(time=c(1,1,1,1,2,2,2,2), place=c(1,1,2,2,1,1,2,2), species=c(1,2,1,2,1,2,1,2),
M=c(100,50,50,100,50,100,100,50), Y=c(100,0,0,100,0,100,100,0)))

#Case 5 in Table 2
fune(data.frame(time=c(1,1,1,1,2,2,2,2), place=c(1,1,2,2,1,1,2,2), species=c(1,2,1,2,1,2,1,2),
M=c(75,75,75,75,75,75,75,75), Y=c(50,50,50,50,50,50,50,50)))

#Case 6 in Table 2
fune(data.frame(time=c(1,1,1,1,2,2,2,2), place=c(1,1,2,2,1,1,2,2), species=c(1,2,1,2,1,2,1,2),
M=c(100,50,100,50,100,50,100,50), Y=c(50,50,50,50,50,50,50,50)))
```