#Kurt Reinhart June 11, 2020

setwd("C:/Users/Kurt.Reinhart/Documents/Research/manuscripts/Soil feedback study 2010/meta-analysis/abund-PSF project/data")

#import datafile

PSF1 <- [read.csv](http://stat.ethz.ch/R-manual/R-devel/library/utils/html/read.csv.html) ('PSF\_data\_2020.csv', [row.names](http://stat.ethz.ch/R-manual/R-devel/library/base/html/row.names.html) = 1)

colnames(PSF1)

summary(PSF1)

str(PSF1)

#meta-data information

#source info: (names correspond with citations from Fig. 2 in the main paper

#G1-G3 Reinhart 2012

#F1 McCarthy-Neumann & Kobe 2010, i= low light portion, ii= high light portion

#F2 McCarthy-Neumann & Ibáñez 2012, i= low light portion, ii= high light portion

#F3 Mangan et al. 2010

#G4 Giesen 2006

#G5 Klironomos 2002

#G6 MacDougall, Rillig, & Klironomos 2011

#G7-G12 Bauer, Mack & Bever 2015

#G13 Chiuffo, MacDougall, & Hierro 2015

#G14 Diez et al. 2010

#G15 Heinze, Bergmann, & Joshi unpublished

#F4 Rutten et al. 2016

#G16 Heinze, Wacker, & Kulmatiski 2020

#for a given data source, data are plant-soil feedback (ln[conspecific/heterospecific]) then metrics of abundance #which can be cross-referenced with Table A1.

#G1-G3: feedback1= biomass, feedback2= mortality and biomass combined, abund1= frequency, abund2= biomass

#F1: i= grown in shade, ii= grown in light, feedback1= lifespan, feedback2= biomass,

#F1 continued: feedback3= lifespan and biomass combined, abund1= density, abund2= basal area

#F2: i= grown in shade, ii= grown in light, feedback1= lifespan, feedback2= growth rate,

#F2 continued: feedback3= lifespan and growth rate combined, abund1= density, abund2= basal area

#F3: abund1= density, abund2= basal area

#G6: abund1= frequency, abund2= % cover

#G14: abund1=number of plots each species was present, abund2= dominance metric

#default is Pearson correlations

#Determine correlation coefficients for every dataset

outer(PSF1[, c(1,2)], PSF1[, c(3,4)], function(g1x, g1y){

mapply(function(...) cor.test(..., na.action = "na.exclude")$estimate,

g1x, g1y)

})

outer(PSF1[, c(5,6)], PSF1[, c(7,8)], function(g2x, g2y){

mapply(function(...) cor.test(..., na.action = "na.exclude")$estimate,

g2x, g2y)

})

outer(PSF1[, c(9,10)], PSF1[, c(11,12)], function(g3x, g3y){

mapply(function(...) cor.test(..., na.action = "na.exclude")$estimate,

g3x, g3y)})

outer(PSF1[, c(13,14,15,16,17,18)], PSF1[, c(19,20)], function(f1x, f1y){

mapply(function(...) cor.test(..., na.action = "na.exclude")$estimate,

f1x, f1y)

})

outer(PSF1[, c(21,22,23,24,25,26)], PSF1[, c(27,28)], function(f2x, f2y){

mapply(function(...) cor.test(..., na.action = "na.exclude")$estimate,

f2x, f2y)

})

outer(PSF1[, c(29,30)], PSF1[, c(30,31)], function(f3x, f3y){

mapply(function(...) cor.test(..., na.action = "na.exclude")$estimate,

f3x, f3y)

})

g4\_cor <- cor(PSF1[,c(32:33)], use="pairwise")

g5\_cor <- cor(PSF1[,c(34:35)], use="pairwise")

g6\_cor <- cor(PSF1[,c(36:38)], use="pairwise")

g7\_cor <- cor(PSF1[,c(39:40)], use="pairwise")

g8\_cor <- cor(PSF1[,c(41:42)], use="pairwise")

g9\_cor <- cor(PSF1[,c(43:44)], use="pairwise")

g10\_cor <- cor(PSF1[,c(45:46)], use="pairwise")

g11\_cor <- cor(PSF1[,c(47:48)], use="pairwise")

g12\_cor <- cor(PSF1[,c(49:50)], use="pairwise")

g13\_cor <- cor(PSF1[,c(51:52)], use="pairwise")

g14\_cor <- cor(PSF1[,c(53:55)], use="pairwise")

f4\_cor <- cor(PSF1[,c(56:57)], use="pairwise")

g15\_cor <- cor(PSF1[,c(58:59)], use="pairwise")

g16\_cor <- cor(PSF1[,c(60:61)], use="pairwise")

#metacor is also in library meta

library(meta)

PSF2 <- read.csv ('meta-analysis parameters2\_2020.csv', row.names = 1)

#meta-data information

#study1 refers to column coding (e.g. “G1”, “G2”) listed and described on page 1 of this document

#name refers to site location names

#life\_form (herbs= data for herbaceous species, woody= data for woody species)

#n (number of species)

#r (selected correlation coefficient, refer to main manuscript for selection criteria)

#mr (mean correlation coefficient)

colnames(PSF2)

PSF2

PSF2 <- PSF2[order(PSF2$r),]

PSF2.herb <- PSF2[-c(12,13,15,18,21,22),] #del empty row #create herbaceous dataset

PSF2.woody <- PSF2[-c(1:11,14,16,17,19,20),] #del empty row #create woody dataset

library(meta) #load using Rstudio

library(metafor)

PSF2 <- PSF2[order(PSF2$r),]

# DerSimonian-Laird estimator (method.tau="DL") (default)

PSF2.meta.dl <- metacor(PSF2$r, PSF2$n, studlab=PSF2$study1, method.tau="DL")

write.table(PSF2.meta.dl, "results\_all\_PSF3.2020.meta.dl", sep="\t")

#table did not seem to write correctly?

forest(PSF2.meta.dl)

#Let repeat on mr

PSF2mr <- PSF2[order(PSF2$mr),]

# DerSimonian-Laird estimator (method.tau="DL") (default)

PSF2mr.meta.dl <- metacor(PSF2mr$mr, PSF2mr$n, studlab=PSF2mr$study1, method.tau="DL")

PSF2mr.meta.dl

forest(PSF2mr.meta.dl)

#lets test how sensitive the ‘r’ result is to the largest dataset

PSF2b <- PSF2[-c(19),] #del JK dataset

PSF2b <- PSF2b[order(PSF2b$r),]

PSF2b.meta.dl <- metacor(PSF2b$r, PSF2b$n, studlab=PSF2b$study1, method.tau="DL")

PSF2b.meta.dl

forest(PSF2b.meta.dl)

#Let repeat on ‘mr’ without JK study

PSF2bmr <- PSF2b[order(PSF2b$mr),]

# DerSimonian-Laird estimator (method.tau="DL") (default)

PSF2bmr.meta.dl <- metacor(PSF2bmr$mr, PSF2bmr$n, studlab=PSF2bmr$study1, method.tau="DL")

PSF2bmr.meta.dl

#below herb portion done on 6-11-2020

PSF2.herb <- PSF2.herb[order(PSF2.herb$r),]

PSF2.herb.meta.dl <- metacor(PSF2.herb$r, PSF2.herb$n, studlab=PSF2.herb$study1, method.tau="DL")

PSF2.herb.meta.dl

#Let repeat on mr portion of herb

PSF2mr.herb <- PSF2.herb[order(PSF2.herb$mr),]

PSF2mr.herb.meta.dl <- metacor(PSF2mr.herb$mr, PSF2.herb$n, studlab=PSF2.herb$study1, method.tau="DL")

PSF2mr.herb.meta.dl

#lets test the sensitivity of the herbaceous dataset to removing the most #influential dataset

PSF2.herb.jk <- PSF2.herb[-c(15),] #del JK dataset

PSF2.herb.jk <- PSF2.herb.jk[order(PSF2.herb.jk$r),]

PSF2r.herb.jk.meta.dl <- metacor(PSF2.herb.jk$r, PSF2.herb.jk$n, studlab=PSF2.herb.jk$study1, method.tau="DL")

PSF2r.herb.jk.meta.dl

#lets test the sensitivity of the herbaceous dataset ‘mr’ to removing the #most influential dataset

PSF2mr.herb.jk <- PSF2.herb.jk[order(PSF2.herb.jk$mr),]

PSF2mr.herb.jk.meta.dl <- metacor(PSF2mr.herb.jk$mr, PSF2mr.herb.jk$n, studlab=PSF2mr.herb.jk$study1, method.tau="DL")

PSF2mr.herb.jk.meta.dl