Supplementary Text

**R code used for the data analysis.**

####------------------------------------------------------------------------------------

remove(list = ls())

require(dplyr)

require(ggplot2)

require(cowplot)

require(ggsignif)

require(car)

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#### Compute EF-Multifunctionnality (multifunctionality averaging) ####

#with all functions

kept=c("Weed.Pred.Rate","Aphid.Pred.Rate","Bee.Richness","C.orga","OSR.Pollination.SF",

"PHOS","GLU","ARS","URE","ARN")

data2016$MF=apply(data2016stand[,kept],1,sum,na.rm=T)

#with only aboveground functions

kept1=c("Weed.Pred.Rate","Aphid.Pred.Rate","Bee.Richness","OSR.Pollination.SF")

data2016$MF1=apply(data2016stand[,kept1],1,sum,na.rm=T)

#with belowground functions

kept2=c("C.orga","PHOS","GLU","ARS","URE","ARN")

data2016$MF2=apply(data2016stand[,kept2],1,sum,na.rm=T)

####Descriptive statistics for EF-Multifunctionnality per crop type

func\_summary <- data2016 %>%

group\_by(CropType) %>%

summarise(mean\_MF = mean(MF,na.rm=T),

sd\_MF = sd(MF,na.rm=T),

n\_MF = n(),

SE\_MF = sd(MF,na.rm=T)/sqrt(n()))

#### Compute Multifunctionaliy threshold approach indexes ####

cent=c(0.2,0.3,0.4,0.5,0.6,0.7,0.8,0.9)

#compute thresholds

{

Egg.Threshold=quantile(data2016$Egg.Pred.Rate.All,cent,na.rm=T)

Seed.Threshold=quantile(data2016$Weed.Pred.Rate,cent,na.rm=T)

Aphid.Threshold=quantile(data2016$Aphid.Pred.Rate,cent,na.rm=T)

Bee.Richness.Threshold=quantile(data2016$Bee.Richness,cent,na.rm=T)

Bee.Abundance.Threshold=quantile(data2016$Bee.Abundance,cent,na.rm=T)

C.orga.Threshold=quantile(data2016$C.orga,cent,na.rm=T)

Cornflowe.Threshold=quantile(data2016$Cornflower.Pollination,cent,na.rm=T)

OSR.Threshold=quantile(data2016$OSR.Pollination.SF,cent,na.rm=T)

PHOS.Threshold=quantile(data2016$PHOS,cent,na.rm=T)

GLU.Threshold=quantile(data2016$GLU,cent,na.rm=T)

ARS.Threshold=quantile(data2016$ARS,cent,na.rm=T)

URE.Threshold=quantile(data2016$URE,cent,na.rm=T)

ARN.Threshold=quantile(data2016$ARN,cent,na.rm=T)

}

fun.true=function(x){sum(x==T,na.rm=T)}

tab.MF=matrix(NA,nrow=dim(data2016)[1],ncol=length(cent))

for (i in 1:length(cent))

{

temp=data.frame(data2016$C.orga>C.orga.Threshold[i],

data2016$Bee.Richness>Bee.Richness.Threshold[i],

data2016$Aphid.Pred.Rate>Aphid.Threshold[i],

data2016$Weed.Pred.Rate>Seed.Threshold[i],

data2016$OSR.Pollination.SF>OSR.Threshold[i],

data2016$PHOS>PHOS.Threshold[i],

data2016$GLU>GLU.Threshold[i],

data2016$ARS>ARS.Threshold[i],

data2016$URE>URE.Threshold[i],

data2016$ARN>ARN.Threshold[i]

)

tab.MF[,i]=apply(temp,1,fun.true)

rm(temp)

}

colnames(tab.MF)=c("MF.T20","MF.T30","MF.T40","MF.T50","MF.T60","MF.T70","MF.T80","MF.T90")

data2016=cbind(data2016,tab.MF)

rm(tab.MF)

####--------------------------------------------------------------------------------------#### Statistics

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#Mean (sd/se) of weed richness and weed abundance per crop

func\_summary <- data2016 %>%

group\_by(CropType) %>%

summarise(mean\_WR = mean(Weed.Richness.FC,na.rm=T),

sd\_WR = sd(Weed.Richness.FC,na.rm=T),

n\_WR = n(),

SE\_WR = sd(Weed.Richness.FC,na.rm=T)/sqrt(n()),

mean\_WA = mean(Weed.Abund.FC,na.rm=T),

sd\_WA = sd(Weed.Abund.FC,na.rm=T),

n\_WA = n(),

SE\_WA = sd(Weed.Abund.FC,na.rm=T)/sqrt(n())

)

func\_summary

#Effect of Weed richness on EF-multifunctionality

mod.MF.rich=lm(MF ~ (Weed.Richness.FC+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF.rich)

anova(mod.MF.rich)

summary(mod.MF.rich)$r.squared

#Effect of Weed abundance on EF-multifunctionality

mod.MF.abund=lm(MF ~ (Weed.Abund.FC.Log+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF.abund)

anova(mod.MF.abund)

summary(mod.MF.abund)$r.squared

#Effect of Weed richness on EF-multifunctionality computed with aboveground ecological functions

mod.MF1.rich=lm(MF1 ~ (Weed.Richness.FC+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF1.rich)

anova(mod.MF1.rich)

summary(mod.MF1.rich)$r.squared

#Effect of Weed abundance on EF-multifunctionality with aboveground ecological functions

mod.MF1.abund=lm(MF1 ~ (Weed.Abund.FC.Log+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF1.abund)

anova(mod.MF1.abund)

summary(mod.MF1.abund)$r.squared

#Effect of Weed richness on EF-multifunctionality computed with belowground ecological functions

mod.MF2.rich=lm(MF2 ~ (Weed.Richness.FC+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF2.rich)

anova(mod.MF2.rich)

summary(mod.MF2.rich)$r.squared

#Effect of Weed abundance on EF-multifunctionality with belowground ecological functions

mod.MF2.abund=lm(MF2 ~ (Weed.Abund.FC.Log+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF2.abund)

anova(mod.MF2.abund)

summary(mod.MF2.abund)$r.squared

#Effect of Weed richness on Multifunctionality - threshold 20%

mod.MF.T20.rich=lm(MF.T20 ~ (Weed.Richness.FC+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF.T20.rich)

anova(mod.MF.T20.rich)

summary(mod.MF.T20.rich)$r.squared

#Effect of Weed abundance on Multifunctionality - threshold 20%

mod.MF.T20.abund=lm(MF.T20 ~ (Weed.Abund.FC.Log+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF.T20.abund)

anova(mod.MF.T20.abund)

summary(mod.MF.T20.abund)$r.squared

#Effect of Weed richness on Multifunctionality - threshold 30%

mod.MF.T30.rich=lm(MF.T30 ~ (Weed.Richness.FC+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF.T30.rich)

anova(mod.MF.T30.rich)

summary(mod.MF.T30.rich)$r.squared

#Effect of Weed abundance on Multifunctionality - threshold 30%

mod.MF.T30.abund=lm(MF.T30 ~ (Weed.Abund.FC.Log+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF.T30.abund)

anova(mod.MF.T30.abund)

summary(mod.MF.T30.abund)$r.squared

#Effect of Weed richness on Multifunctionality - threshold 40%

mod.MF.T40.rich=lm(MF.T40 ~ (Weed.Richness.FC+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF.T40.rich)

anova(mod.MF.T40.rich)

summary(mod.MF.T40.rich)$r.squared

#Effect of Weed abundance on Multifunctionality - threshold 40%

mod.MF.T40.abund=lm(MF.T40 ~ (Weed.Abund.FC.Log+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF.T40.abund)

anova(mod.MF.T40.abund)

summary(mod.MF.T40.abund)$r.squared

#Effect of Weed richness on Multifunctionality - threshold 50%

mod.MF.T50.rich=lm(MF.T50 ~ (Weed.Richness.FC+CropType)^2, data=data2016, na.action="na.exclude")

AIC(mod.MF.T50.rich)

anova(mod.MF.T50.rich)

summary(mod.MF.T50.rich)$r.squared

#Effect of Weed abundance on Multifunctionality - threshold 50%

mod.MF.T50.abund=lm(MF.T50 ~ (Weed.Abund.FC.Log+CropType)^2, data=data2016, na.action="na.exclude")

AIC(mod.MF.T50.abund)

anova(mod.MF.T50.abund)

summary(mod.MF.T50.abund)$r.squared

#Effect of Weed richness on Multifunctionality - threshold 60%

mod.MF.T60.rich=lm(MF.T60 ~ (Weed.Richness.FC+CropType)^2, data=data2016, na.action="na.exclude")

AIC(mod.MF.T60.rich)

anova(mod.MF.T60.rich)

summary(mod.MF.T60.rich)$r.squared

#Effect of Weed abundance on Multifunctionality - threshold 60%

mod.MF.T60.abund=lm(MF.T60 ~ (Weed.Abund.FC.Log+CropType)^2, data=data2016, na.action="na.exclude")

AIC(mod.MF.T60.abund)

anova(mod.MF.T60.abund)

summary(mod.MF.T60.abund)$r.squared

#Effect of Weed richness on Multifunctionality - threshold 70%

mod.MF.T70.rich=lm(MF.T70 ~ (Weed.Richness.FC+CropType)^2, data=data2016, na.action="na.exclude")

AIC(mod.MF.T70.rich)

anova(mod.MF.T70.rich)

summary(mod.MF.T70.rich)$r.squared

#Effect of Weed abundance on Multifunctionality - threshold 70%

mod.MF.T70.abund=lm(MF.T70 ~ (Weed.Abund.FC.Log+CropType)^2,data=data2016,na.action="na.exclude")

AIC(mod.MF.T70.abund)

anova(mod.MF.T70.abund)

summary(mod.MF.T70.abund)$r.squared

##Each Ecological function

## Aphid Predation Rate

#Effect of Weed richness on EF-multifunctionality

mod.aphid.rich=lm(Aphid.Pred.Rate~(Weed.Richness.FC+CropType+ Carab.Abund.Log)^2, data=data2016)

AIC(mod.aphid.rich)

anova(mod.aphid.rich)

summary(mod.aphid.rich)$r.squared

#Effect of Weed abundance on EF-multifunctionality

mod.aphid.abund=lm(Aphid.Pred.Rate~(Weed.Abund.FC.Log+CropType+ Carab.Abund.Log)^2, data=data2016)

AIC(mod.aphid.abund)

anova(mod.aphid.abund)

summary(mod.aphid.abund)$r.squared

##Weed seed Predation Rate

mod.weedseed.rich=lm(Weed.Pred.Rate~(Weed.Richness.FC+CropType+ Carab.Abund.Log)^2, data=data2016)

AIC(mod.weedseed.rich)

anova(mod.weedseed.rich)

summary(mod.weedseed.rich)$r.squared

mod.weedseed.abund=lm(Weed.Pred.Rate~(Weed.Abund.FC.Log+CropType+ Carab.Abund.Log)^2, data=data2016)

AIC(mod.weedseed.abund)

anova(mod.weedseed.abund)

summary(mod.weedseed.abund)$r.squared

##Bee richness

mod.bee.rich=lm(Bee.Richness~(Weed.Richness.FC+CropType)^2,data=data2016)

AIC(mod.bee.rich)

anova(mod.bee.rich)

summary(mod.bee.rich)$r.squared

mod.bee.abund=lm(Bee.Richness~(Weed.Abund.FC.Log+CropType)^2,data=data2016)

AIC(mod.bee.abund)

anova(mod.bee.abund)

summary(mod.bee.abund)$r.squared

##OSR pollination

mod.OSR.rich=lm(OSR.Pollination.SF~(Weed.Richness.FC+CropType)^2,data=data2016)

AIC(mod.OSR.rich)

anova(mod.OSR.rich)

summary(mod.OSR.rich)$r.squared

mod.OSR.abund=lm(OSR.Pollination.SF~(Weed.Abund.FC.Log+CropType)^2,data=data2016)

AIC(mod.OSR.abund)

anova(mod.OSR.abund)

summary(mod.OSR.abund)$r.squared

##Soil Carbon

mod.C.orga.rich=lm(C.orga~(Weed.Richness.FC+CropType)^2,data=data2016)

AIC(mod.C.orga.rich)

anova(mod.C.orga.rich)

summary(mod.C.orga.rich)$r.squared

mod.C.orga.abund=lm(C.orga~(Weed.Abund.FC+CropType)^2,data=data2016)

AIC(mod.C.orga.abund)

anova(mod.C.orga.abund)

summary(mod.C.orga.abund)$r.squared

##Phosphatase

mod.PHOS.rich=lm(PHOS~(Weed.Richness.FC+CropType)^2,data=data2016)

AIC(mod.PHOS.rich)

anova(mod.PHOS.rich)

summary(mod.PHOS.rich)$r.squared

mod.PHOS.abund=lm(PHOS~(Weed.Abund.FC+CropType)^2,data=data2016)

AIC(mod.PHOS.abund)

anova(mod.PHOS.abund)

summary(mod.PHOS.abund)$r.squared

##Arylsulfatase

mod.ARS.rich=lm(ARS~(Weed.Richness.FC+CropType)^2,data=data2016)

AIC(mod.ARS.rich)

anova(mod.ARS.rich)

summary(mod.ARS.rich)$r.squared

mod.ARS.abund=lm(ARS~(Weed.Abund.FC+CropType)^2,data=data2016)

AIC(mod.ARS.abund)

anova(mod.ARS.abund)

summary(mod.ARS.abund)$r.squared

##Urease

mod.URE.rich=lm(URE~(Weed.Richness.FC+CropType)^2,data=data2016)

AIC(mod.URE.rich)

anova(mod.URE.rich)

summary(mod.URE.rich)$r.squared

mod.URE.abund=lm(URE~(Weed.Abund.FC+CropType)^2,data=data2016)

AIC(mod.URE.abund)

anova(mod.URE.abund)

summary(mod.URE.abund)$r.squared

##Glucosidase

mod.GLU.rich=lm(GLU~(Weed.Richness.FC+CropType)^2,data=data2016)

AIC(mod.GLU.rich)

anova(mod.GLU.rich)

summary(mod.GLU.rich)$r.squared

mod.GLU.abund=lm(GLU~(Weed.Abund.FC+CropType)^2,data=data2016)

AIC(mod.GLU.abund)

anova(mod.GLU.abund)

summary(mod.GLU.abund)$r.squared

##Arylamidase

mod.ARN.rich=lm(ARN~(Weed.Richness.FC+CropType)^2,data=data2016)

AIC(mod.ARN.rich)

anova(mod.ARN.rich)

summary(mod.ARN.rich)$r.squared

mod.ARN.abund=lm(ARN~(Weed.Abund.FC+CropType)^2,data=data2016)

AIC(mod.ARN.abund)

anova(mod.ARN.abund)

summary(mod.ARN.abund)$r.squared

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#### Contribution of rare and abundant weed species to multifunctionality

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#Abundance per field

weed.abund=aggregate(tab.weed$abund,by=list(tab.weed$field,tab.weed$croptype),sum)

colnames(weed.abund)=c("id\_field","croptype","abund")

#Abundance per species and per field

tab.weed.sp=aggregate(cbind(tab.weed$abund),

by=list(tab.weed$field,tab.weed$croptype, tab.weed$species),

sum)

colnames(tab.weed.field)=c("id\_field","croptype",”species”,"abund")

#Number of rare and abundant species per field

tab.abund.perc=NULL

n=length(unique(tab.weed.sp$id\_field))

field=unique(tab.weed.sp$id\_field)

tab.nb.species=as.data.frame(matrix(NA,nrow=n,ncol=12))

colnames(tab.nb.species)=c("id\_field","croptype",

"Q10\_rare","Q10\_abund","Q20\_rare","Q20\_abund",

"Q30\_rare","Q30\_abund","Q40\_rare","Q40\_abund",

"Q50\_rare","Q50\_abund")

for (i in 1:n)

{

print(i)

temp=subset(tab.weed.sp,tab.weed.sp$id\_field==field[i])

tab.nb.species[i,2]=unique(tab.weed.field$croptype[tab.weed.field$id\_field==field[i]])

tab.nb.species[i,3]=sum(temp$abund<quantile(temp$abund,0.10))

tab.nb.species[i,4]=sum(temp$abund >quantile(temp$abund,0.90))

tab.nb.species[i,5]=sum(temp$abund <quantile(temp$abund,0.20))

tab.nb.species[i,6]=sum(temp$abund >quantile(temp$abund,0.80))

tab.nb.species[i,7]=sum(temp$abund <quantile(temp$abund,0.30))

tab.nb.species[i,8]=sum(temp$abund >quantile(temp$abund,0.70))

tab.nb.species[i,9]=sum(temp$abund <quantile(temp$abund,0.40))

tab.nb.species[i,10]=sum(temp$abund >quantile(temp$abund,0.60))

tab.nb.species[i,11]=sum(temp$abund <quantile(temp$abund,0.50))

tab.nb.species[i,12]=sum(temp$abund >quantile(temp$abund,0.50))

rm(temp)

}

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#### Relationship between Yield and ecosystem multifunctionality

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#With field area

mod=lm(Yield.std ~ (MF+Weed.std+CropType)^2 + fieldarea + fieldarea:MF + doseN + doseN:CropType, data = data2016)

Anova(mod,Type=2)