

# MIIN Part 5: Meta-analysis

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Filename: MIIN\_5\_metaAnalysis.Rmd

This markdown file does the following tasks:

1. Calculate global effect sizes and plot
2. Test for inclusion of categorical moderators. Where a categorical moderator is warranted, make a forest plot and conduct post-hoc Tukeys: A) Study type, B) N fixer status, C) Ecosystem type, D) Quality
3. Test for correlation between CWM traits and effect size values. Record the outcomes in a table. In cases where the slope coefficient significantly differs from 0, plot it.

```
knitr::opts_chunk$set(cache=TRUE)
```

```
library(ggplot2)
library(gridExtra)
library(plyr)
library(reshape2)
library(metafor)
```

```
## Loading required package: Matrix
## Loading 'metafor' package (version 1.9-7). For an overview
## and introduction to the package please type: help(metafor).
```

```
source('CODE/mytheme.R')
```

```
## Loading required package: grid
```

```
source('CODE/metaAnalysis/fxn_PrepForestPlot.R')
#source('CODE/metaAnalysis/fxn_FactorForests.R') #this is fxn calculated whether each level differed fr
source('CODE/metaAnalysis/fxn_FitPlot.R')
```

```
figuresPath<-file.path(getwd()[1], "FIGURES_TABLES", "metaAnalysis") #where to put the saved plots
fig.height<-2.5 #inches
fig.width<- 2.5 #inches
fig.res<-300
```

```
dat<-read.table("DATA/DATA_SYNTHESIZED/calcES/metaDataset.txt", header=TRUE, sep="\t")
source('CODE/metaAnalysis/script_orderLevels.R')
```

```
#dat structure
summ<-ddply(dat, ~measCat+traitCat, summarize,
            uniqueObs = length(unique(obsID)))
#summ
```

# 1. Calculate global effect sizes and plot

1A. Fit a nested random effects model. Model syntax is `res <- rma.mv(yi, vi, random=list(~1 | paperID, ~1 | obsID), data=dat1, subset=measCat==MEASCAT[i], slab=paste(paperID,obsID, sep=","))`

```
dat1<-dat[!is.na(dat$yi),]
dat.meas<-ddply(dat1, ~obsID+measCat, summarize,
  yi = unique(yi),
  vi = unique(vi),
  paperID = unique(paperID))
res.list<-list()
i<-0
for(i in 1:length(MEASCAT)){
  res <- rma.mv(yi, vi,
    random=list(~1 | paperID, ~1 | obsID),
    data=dat.meas, subset=measCat==MEASCAT[i],
    slab=as.character(obsID),
    method='ML')
  res.list[[i]]<-res
  print(paste(i, 'of', length(MEASCAT)))
}
```

```
## [1] "1 of 9"
## [1] "2 of 9"
## [1] "3 of 9"
## [1] "4 of 9"
## [1] "5 of 9"
## [1] "6 of 9"
## [1] "7 of 9"
## [1] "8 of 9"
## [1] "9 of 9"
```

```
names(res.list)<-MEASCAT
resultdf<-PrepForestPlot(res.list) #save estimates, pvalues, and prep dataframe for plotting
resultdf
```

##	measCAT	labels	est	var	cil	ciu	k	pval
## 1	nh	Ammonium	0.257	0.005	0.120	0.395	141	0.000
## 2	no	Nitrate	0.168	0.008	-0.003	0.339	150	0.054
## 3	toti	Total inorganic N	0.146	0.010	-0.054	0.347	195	0.153
## 4	ammonif	Ammonification	-0.050	0.017	-0.305	0.204	50	0.699
## 5	nitrif	Nitrification	0.452	0.015	0.210	0.694	79	0.000
## 6	nminz	Mineralization	0.359	0.013	0.136	0.581	101	0.002
## 7	soiln	Soil N	0.531	0.013	0.308	0.754	187	0.000
## 8	soilcn	Soil C:N	-0.054	0.010	-0.246	0.139	100	0.586
## 9	som	Soil organic matter	0.586	0.043	0.180	0.992	90	0.005
##	intraPaperCorr	heterogen	NoOverlap0	alpha05				
## 1		0.531	0.200	TRUE	TRUE			
## 2		0.821	0.334	FALSE	FALSE			
## 3		0.873	0.456	FALSE	FALSE			
## 4		1.000	0.211	FALSE	FALSE			
## 5		1.000	0.356	TRUE	TRUE			
## 6		0.841	0.384	TRUE	TRUE			

## 7	0.706	0.923	TRUE	TRUE
## 8	1.000	0.246	FALSE	FALSE
## 9	0.580	1.552	TRUE	TRUE

```
newfilename<-'globalMeans.txt'
write.table(resultdf, file=paste(figuresPath,'globalForest',newfilename, sep='/'), sep='\t')
#intraPaperCorr #if this # is high, it means that the underlying true effects within paperIDs are estim
#Heterogen #the sum of the two variance components can be interpreted as the total amount of heterogene

# #View profile likelihood plots
# par(mfrow=c(2,1))
# i<-0
# for(i in 1:length(res.list)){
#   res<-res.list[[i]]
#   profile(res, sigma2=1)
#   mtext(labels[i])
#   profile(res, sigma2=2)
#   mtext(labels[i])
# }
#if both have 1 peak, we can be sure that both variance components are identifiable
```

1B. Fit just the Liao 2008 subset.

```
dat.Liao<-subset(dat1, source2 == 'Liao 2008')
dat.Liao.meas<-ddply(dat.Liao, ~obsID+measCat, summarize,
  yi = unique(yi),
  vi = unique(vi),
  paperID = unique(paperID))
res.Liao.list<-list()
i<-0
for(i in 1:length(MEASCAT)){
  res <- rma.mv(yi, vi,
    random=list(~1 | paperID, ~1 | obsID),
    data=dat.Liao.meas, subset=measCat==MEASCAT[i],
    slab=as.character(obsID),
    method='ML')
  res.Liao.list[[i]]<-res
  print(paste(i, 'of', length(MEASCAT)))
}
```

```
## [1] "1 of 9"
## [1] "2 of 9"
## [1] "3 of 9"
## [1] "4 of 9"
## [1] "5 of 9"
## [1] "6 of 9"
## [1] "7 of 9"
## [1] "8 of 9"
## [1] "9 of 9"
```

```
names(res.Liao.list)<-MEASCAT
resultdf.Liao<-PrepForestPlot(res.Liao.list) #save estimates and prep dataframe for plotting
resultdf.Liao
```

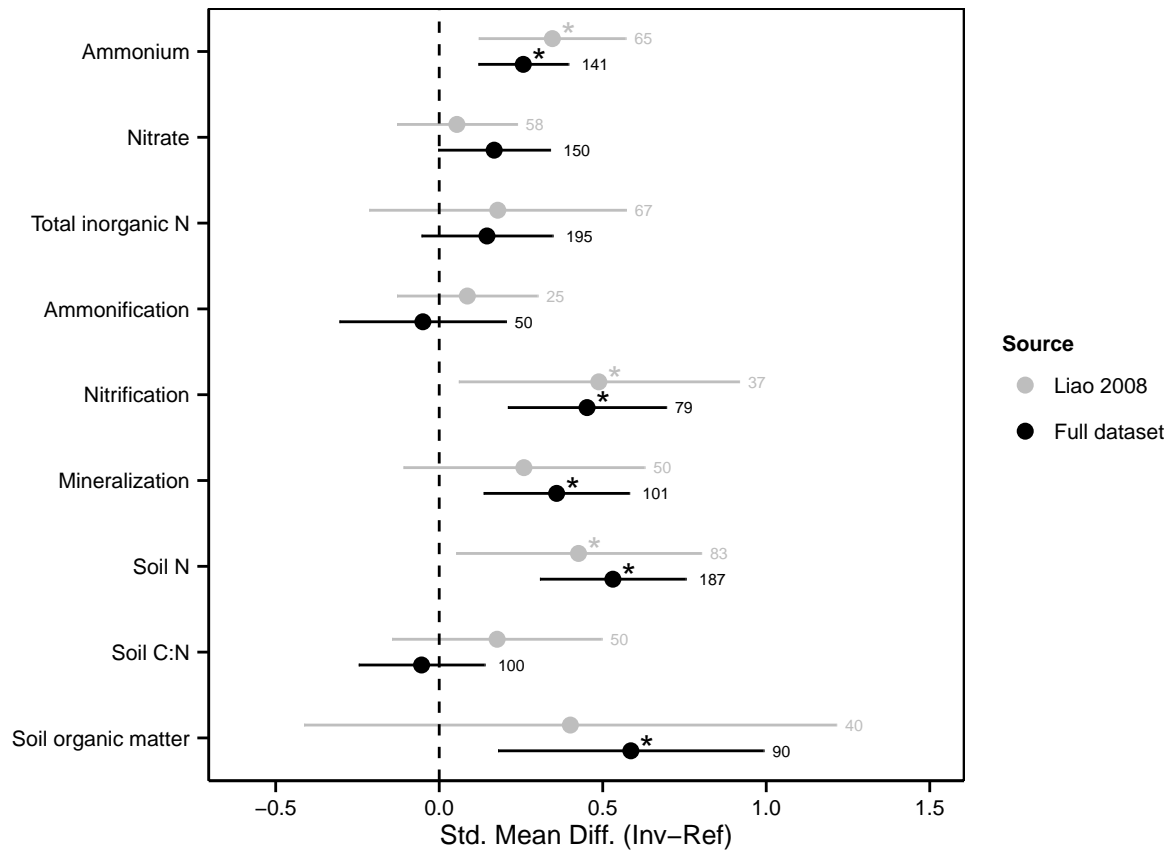
```
## measCAT      labels  est  var  cil  ciu  k  pval
## 1      nh      Ammonium 0.346 0.013 0.121 0.570 65 0.003
## 2      no      Nitrate 0.054 0.009 -0.129 0.238 58 0.562
## 3      toti    Total inorganic N 0.179 0.040 -0.214 0.571 67 0.372
## 4 ammonif     Ammonification 0.086 0.012 -0.129 0.301 25 0.432
## 5 nitrif      Nitritification 0.488 0.048 0.060 0.917 37 0.025
## 6 nminz       Mineralization 0.259 0.035 -0.109 0.628 50 0.168
## 7 soiln       Soil N 0.426 0.036 0.052 0.801 83 0.026
## 8 soilcn      Soil C:N 0.177 0.027 -0.144 0.497 50 0.281
## 9      som Soil organic matter 0.401 0.172 -0.413 1.214 40 0.334
## intraPaperCorr heterogen NoOverlap0 alpha05
## 1      0.577      0.219      TRUE      TRUE
## 2      0.000      0.176      FALSE     FALSE
## 3      1.000      0.831      FALSE     FALSE
## 4      1.000      0.026      FALSE     FALSE
## 5      0.929      0.540      TRUE      TRUE
## 6      0.536      0.628      FALSE     FALSE
## 7      1.000      0.891      TRUE      TRUE
## 8      1.000      0.257      FALSE     FALSE
## 9      0.761      2.321      FALSE     FALSE
```

```
newfilename<-'globalMeans_Liao.txt'
write.table(resultdf.Liao, file=paste(figuresPath,'globalForest',newfilename, sep='/'), sep='\t')
```

1C. Make global forest plot comparing Liao 2008 and the full dataset

```
#update effect size table for plotting with ggplot
resultdf$y<-NA
resultdf.Liao$y<-NA
CATl<-rev(levels(resultdf$measCAT))
i<-0
for(i in 1:length(CATl)){
  resultdf[resultdf$measCAT==CATl[i], 'y']<-i-0.15
  resultdf.Liao[resultdf.Liao$measCAT==CATl[i], 'y']<-i+0.15
}
resultdf$source2<-'Full dataset'
resultdf.Liao$source2<-'Liao 2008'
resultdf.full<-rbind(resultdf, resultdf.Liao)
cols <- c("Liao 2008" = "gray", "Full dataset" = "black")

#make ggplot plot
glob.sp<-ggplot(data=resultdf.full, aes(x=est, y=y, label=k, color=source2)) +
  geom_point(size=3) +
  geom_errorbarh(aes(xmin=cil, xmax=ciu), height=0, show_guide=FALSE) +
  geom_vline(xintercept=0, linetype="dashed") +
  mytheme + xlab('Std. Mean Diff. (Inv-Ref)') + ylab('') +
  scale_y_continuous(breaks=seq(1, length(MEASCAT)), labels=rev(labels),
    limits=c(0.5, 9.5), expand=c(0, 0)) +
  geom_text(aes(x=ciu, y=y, hjust=-0.5, vjust=0.5), size=2.2, show_guide = FALSE) +
  xlim(-0.6, 1.5) +
  geom_text(aes(label=ifelse(alpha05==TRUE, "*", ""), hjust=-0.6, vjust=0.4),
    size=5, show_guide=FALSE) +
  scale_color_manual(name='Source', values=cols, breaks=c('Liao 2008', 'Full dataset'))
glob.sp
```



```
#save global forest plot
newfilename<-"globalForest.png"
png(paste(figuresPath,'globalForest',newfilename, sep='/'), units='in', width = fig.width*2, height = f
glob.sp
dev.off()
```

```
## pdf
## 2
```

## 2. Test for inclusion of categorical moderators.

2A. Fit a random-effects model with 1 of the categorical variables as a fixed effect. Model syntax is `res <- rma.mv(yi, vi, mods= ~factor(Xmod), random=list(~1 | paperID, ~1 | obsID), data=dat1, subset=measCat==MEASCAT[i], slab=paste(paperID,obsID, sep=","))` where Xmod is one of the following: (1) Quality, (2) Ecosystem type, (3) Study type, (4) Invasive legumes present/absent, (5) Reference legumes present/absent

```
dat.meas<-ddply(dat, ~obsID+measCat, summarize,
  yi = unique(yi),
  vi = unique(vi),
  paperID = unique(paperID),
  measQuality= unique(measQuality),
```

```

ecosystCat= unique(ecosystCat),
studyType= unique(studyType),
Nfix= unique(Nfix))
dat.tmp<-dat.meas[dat.meas$measCat %in% MEASCAT,]
dat.tmp<-dat.tmp[!is.na(dat.tmp$yi),]

#look for singularities
temp<-ddply(dat.tmp, ~measCat+Nfix, summarize, n=length(paperID))
temp

```

```

##      measCat                                Nfix      n
## 1  ammonif                                No N-fixers 42
## 2  ammonif          Resident N-fixers only      2
## 3  ammonif          Invasive N-fixers only      4
## 4  ammonif Invasive and resident N-fixers      2
## 5      nh                                No N-fixers 93
## 6      nh          Resident N-fixers only      18
## 7      nh          Invasive N-fixers only      20
## 8      nh Invasive and resident N-fixers      10
## 9  nitrif                                No N-fixers 61
## 10 nitrif          Resident N-fixers only       3
## 11 nitrif          Invasive N-fixers only       8
## 12 nitrif Invasive and resident N-fixers       7
## 13 nminz                                No N-fixers 80
## 14 nminz          Resident N-fixers only       5
## 15 nminz          Invasive N-fixers only      10
## 16 nminz Invasive and resident N-fixers       6
## 17    no                                No N-fixers 102
## 18    no          Resident N-fixers only      18
## 19    no          Invasive N-fixers only      19
## 20    no Invasive and resident N-fixers      11
## 21 soilcn                                No N-fixers 69
## 22 soilcn          Resident N-fixers only       8
## 23 soilcn          Invasive N-fixers only      16
## 24 soilcn Invasive and resident N-fixers       7
## 25 soiln                                No N-fixers 120
## 26 soiln          Resident N-fixers only      19
## 27 soiln          Invasive N-fixers only      30
## 28 soiln Invasive and resident N-fixers      18
## 29    som                                No N-fixers 57
## 30    som          Resident N-fixers only      15
## 31    som          Invasive N-fixers only       8
## 32    som Invasive and resident N-fixers      10
## 33  toti                                No N-fixers 162
## 34  toti          Resident N-fixers only      14
## 35  toti          Invasive N-fixers only      15
## 36  toti Invasive and resident N-fixers       4

```

```

which(temp$n==1)

```

```

## integer(0)

```

```

#for the ecosystCat, remove the 'other' level from the model
dat.tmp<-dat.tmp[dat.tmp$ecosystCat != 'other',]
dat.tmp$ecosystCat<-droplevels(dat.tmp$ecosystCat)

### fit 3-level random-effects models with a categorical mod
res<-list()
res.quality<-list()
res.ecosyst<-list()
res.studytype<-list()
res.Nfix<-list()
i<-0
for(i in 1:length(MEASCAT)){
  subdat<-subset(dat.tmp, measCat==MEASCAT[i])

  #reduced model
  res[[i]]<- rma.mv(yi, vi,
                    random=list(~1 | paperID, ~1 | obsID),
                    data=subdat, slab=as.character(obsID),
                    method='ML')

  #full models
  res.quality[[i]]<- rma.mv(yi, vi,
                            mods= ~factor(measQuality),
                            random=list(~1 | paperID, ~1 | obsID),
                            data=subdat, slab=as.character(obsID),
                            method='ML')
  res.ecosyst[[i]]<- rma.mv(yi, vi,
                            mods= ~factor(ecosystCat),
                            random=list(~1 | paperID, ~1 | obsID),
                            data=subdat, slab=as.character(obsID),
                            method='ML')
  res.studytype[[i]]<- rma.mv(yi, vi,
                              mods= ~factor(studyType),
                              random=list(~1 | paperID, ~1 | obsID),
                              data=subdat, slab=as.character(obsID),
                              method='ML')
  res.Nfix[[i]]<- rma.mv(yi, vi,
                        mods= ~factor(Nfix),
                        random=list(~1 | paperID, ~1 | obsID),
                        data=subdat, slab=as.character(obsID),
                        method='ML')
  print(paste(i, 'of', length(MEASCAT)))
}

```

```

## [1] "1 of 9"
## [1] "2 of 9"
## [1] "3 of 9"
## [1] "4 of 9"
## [1] "5 of 9"
## [1] "6 of 9"
## [1] "7 of 9"
## [1] "8 of 9"
## [1] "9 of 9"

```

```

names(res)<-MEASCAT
names(res.quality)<-MEASCAT
names(res.ecosyst)<-MEASCAT
names(res.studytype)<-MEASCAT
names(res.Nfix)<-MEASCAT

#Test whether inclusion of any of these moderators are warranted
ANOVAParams<-function(fullMod, reducedMod){
  anova.comp<-anova(fullMod,reducedMod)
  anova.comp.df<-data.frame(p.f=anova.comp$p.f,
                             LRT=round(anova.comp$LRT, digits=3),
                             pval=round(anova.comp$pval, digits=3))

  return(anova.comp.df)
}
i<-0
tmp.list<-list()
for(i in 1:length(MEASCAT)){
  p.r<-anova(res.quality[[i]], res[[i]])$p.r #reduced model parameters
  qualityA<-ANOVAParams(fullMod=res.quality[[i]], reducedMod=res[[i]]) #full vs reduced model anova and
  ecosystA<-ANOVAParams(fullMod=res.ecosyst[[i]], reducedMod=res[[i]])
  studytypeA<-ANOVAParams(fullMod=res.studytype[[i]], reducedMod=res[[i]])
  NfixA<-ANOVAParams(fullMod=res.Nfix[[i]], reducedMod=res[[i]])
  tmpdf<-rbind(qualityA, ecosystA, studytypeA, NfixA) #same anova params in a dataframe
  anovaLabels<-c('qualityA','ecosystA','studytypeA','NfixA') #name all the rows
  p.rCol<-rep(p.r, dim(tmpdf)[1]) #add a column to hold the reduced model information
  tmp.list[[i]]<-data.frame(anovaLabels, p.rCol, tmpdf)
}
names(tmp.list)<-MEASCAT
anovaMods<-ldply(tmp.list)
anovaMods

```

```

##      .id anovaLabels p.rCol p.f    LRT  pval
## 1    nh    qualityA      3    6  4.743 0.192
## 2    nh    ecosystA      3    6  6.620 0.085
## 3    nh  studytypeA      3    6  5.507 0.138
## 4    nh      NfixA      3    6  1.297 0.730
## 5    no    qualityA      3    6  3.257 0.354
## 6    no    ecosystA      3    6  5.649 0.130
## 7    no  studytypeA      3    6  9.752 0.021
## 8    no      NfixA      3    6  6.820 0.078
## 9   toti    qualityA      3    6  2.593 0.459
## 10   toti    ecosystA      3    6  1.869 0.600
## 11   toti  studytypeA      3    6  4.428 0.219
## 12   toti      NfixA      3    6 11.114 0.011
## 13 ammonif    qualityA      3    6  2.499 0.475
## 14 ammonif    ecosystA      3    6 10.427 0.015
## 15 ammonif  studytypeA      3    6  2.865 0.413
## 16 ammonif      NfixA      3    6  2.138 0.544
## 17 nitrif    qualityA      3    6 10.586 0.014
## 18 nitrif    ecosystA      3    6  3.145 0.370
## 19 nitrif  studytypeA      3    6  1.895 0.594
## 20 nitrif      NfixA      3    6  5.738 0.125
## 21 nminz    qualityA      3    6  8.287 0.040

```



```
## 22  nminz  ecosystA      3  6  0.648 0.885
## 23  nminz  studytypeA    3  6  6.156 0.104
## 24  nminz   NfixA       3  6  6.759 0.080
## 25  soiln  qualityA     3  6  3.082 0.379
## 26  soiln  ecosystA     3  6 11.536 0.009
## 27  soiln  studytypeA    3  5  0.048 0.976
## 28  soiln   NfixA       3  6 13.430 0.004
## 29  soilcn  qualityA     3  6  4.169 0.244
## 30  soilcn  ecosystA     3  6  4.340 0.227
## 31  soilcn  studytypeA    3  5  3.140 0.208
## 32  soilcn   NfixA       3  6 10.788 0.013
## 33    som  qualityA     3  5  7.717 0.021
## 34    som  ecosystA     3  6  3.435 0.329
## 35    som  studytypeA    3  6  8.662 0.034
## 36    som   NfixA       3  6  2.693 0.441
```

```
newfilename<-'anovaMods.txt'
write.table(anovaMods, file=paste(figuresPath,'modForests',newfilename, sep='/'), sep='\t')
```

2Bi. Study type

```
currMeasFac<-anovaMods[anovaMods$anovaLabels=='studytypeA' & anovaMods$pval < 0.05, '.id']
currMeasFac
```

```
## [1] "no"  "som"
```

```
#Run post-hoc comparisions among Study type levels, pull out means and CI
i<-0
posthoc.list<-list()
pred.list<-list()
for(i in 1:length(currMeasFac)){
  #1. calc posthoc pvals
  posthocR<-anova(res.studytype[[currMeasFac[i]]],
    L=rbind(c(1,-1,0,0), #fs vs ea
            c(1,0,-1,0), #fs vs er
            c(1,0,0,-1), #fs vs gh
            c(0,1,-1,0), #ea vs er
            c(0,1,0,-1), #ea vs gh
            c(0,0,1,-1)  #er vs gh
          ))
  levelcomp<-c('fs_ea','fs_er','fs_gh','ea_er','ea_gh','er_gh')
  posthoc.list[[i]]<-data.frame(levelcomp, pval=round(posthocR$pval, digits=4))
  #2. calc predicted values by level
  predR<-predict(res.studytype[[currMeasFac[i]]])
  tmp<-data.frame(obsID=predR$slab, pred=predR$pred,
                  cilb=predR$ci.lb, ciub=predR$ci.ub, se=predR$se)
  ind.studyType<-ddply(dat.tmp, ~obsID, summarize, studyType1=unique(studyType))
  tmp1<-merge(tmp, ind.studyType)
  tmp2<-ddply(tmp1, ~studyType1, summarize,
    pred = unique(pred),
    cilb = unique(cilb),
    ciub = unique(ciub),
    se = unique(se),
```

```

      k = length(obsID))
    pred.list[[i]]<-tmp2
  }
names(posthoc.list)<-currMeasFac
posthocR<-ldply(posthoc.list)
posthocR

```

```

##      .id levelcomp   pval
## 1    no      fs_ea 0.0039
## 2    no      fs_er 0.0096
## 3    no      fs_gh 0.0030
## 4    no      ea_er 0.2700
## 5    no      ea_gh 0.4742
## 6    no      er_gh 0.5969
## 7    som     fs_ea 0.7703
## 8    som     fs_er 0.2789
## 9    som     fs_gh 0.0395
## 10   som     ea_er 0.4162
## 11   som     ea_gh 0.1368
## 12   som     er_gh 0.2868

```

```

names(pred.list)<-currMeasFac
predR<-ldply(pred.list)
predR

```

```

##      .id      studyType1      pred      cilb      ciub      se
## 1    no      field study  0.29783013  0.114407596  0.4812527  0.09358465
## 2    no field expt addition -0.51480152 -1.178114568  0.1485115  0.33843124
## 3    no field expt removal -0.07993938 -0.477091849  0.3172131  0.20263253
## 4    no      greenhouse expt -0.24097216 -0.690481877  0.2085376  0.22934591
## 5    som      field study  0.34911578 -0.003748808  0.7019804  0.18003626
## 6    som field expt addition 0.34726970 -1.900631589  2.5951710  1.14690949
## 7    som field expt removal 1.38687827  0.279021097  2.4947354  0.56524364
## 8    som      greenhouse expt 2.36687822  0.944130304  3.7896261  0.72590513
##      k
## 1 103
## 2   7
## 3  16
## 4  20
## 5  78
## 6   1
## 7   6
## 8   4

```

```

#update effect size table for plotting
colnames(predR)[1]<-'MeasFac'
selectMeas<-unique(predR$MeasFac)
MeasFac1<-rev(levels(factor(MEASCAT[MEASCAT %in% selectMeas], levels=MEASCAT[MEASCAT %in% selectMeas])))
MeasNames1<-rev(measTab[measTab$MEASCAT %in% selectMeas,'labels'])
colnames(predR)[2]<-'CAT'
CAT<-levels(dat$studyType)
predR$y<-NA

```

```

i<-0
for(i in 1:length(MeasFac1)){
  predR[predR$CAT==CAT[1] & predR$MeasFac==MeasFac1[i], 'y']<-i+0.3
  predR[predR$CAT==CAT[2] & predR$MeasFac==MeasFac1[i], 'y']<-i+0.1
  predR[predR$CAT==CAT[3] & predR$MeasFac==MeasFac1[i], 'y']<-i-0.1
  predR[predR$CAT==CAT[4] & predR$MeasFac==MeasFac1[i], 'y']<-i-0.3
}
predR

```

```

##      MeasFac          CAT      pred      cilb      ciub
## 1      no      field study  0.29783013  0.114407596 0.4812527
## 2      no field expt addition -0.51480152 -1.178114568 0.1485115
## 3      no field expt removal -0.07993938 -0.477091849 0.3172131
## 4      no      greenhouse expt -0.24097216 -0.690481877 0.2085376
## 5      som      field study  0.34911578 -0.003748808 0.7019804
## 6      som field expt addition 0.34726970 -1.900631589 2.5951710
## 7      som field expt removal 1.38687827  0.279021097 2.4947354
## 8      som      greenhouse expt 2.36687822  0.944130304 3.7896261
##          se    k    y
## 1 0.09358465 103 2.3
## 2 0.33843124   7 2.1
## 3 0.20263253  16 1.9
## 4 0.22934591  20 1.7
## 5 0.18003626  78 1.3
## 6 1.14690949   1 1.1
## 7 0.56524364   6 0.9
## 8 0.72590513   4 0.7

```

```

#assign post-hoc letters (order:field study, expt addition, expt removal, gh)
#subset(posthocR, .id=='biom')
phTno<-c('a','b','b','b')
phTsom<-c('',' ',' ',' ')
predR$posthocL<-c(phTno,phTsom)

#assign pretty names and symbols
faclimits<-rev(c('Greenhouse study',
                 'Removal expt',
                 'Addition expt',
                 'Observational study'))
facShapes<-c(16,17,15,18)
predR$annLabel<-paste(predR$posthocL, '(',predR$k,')', sep='')

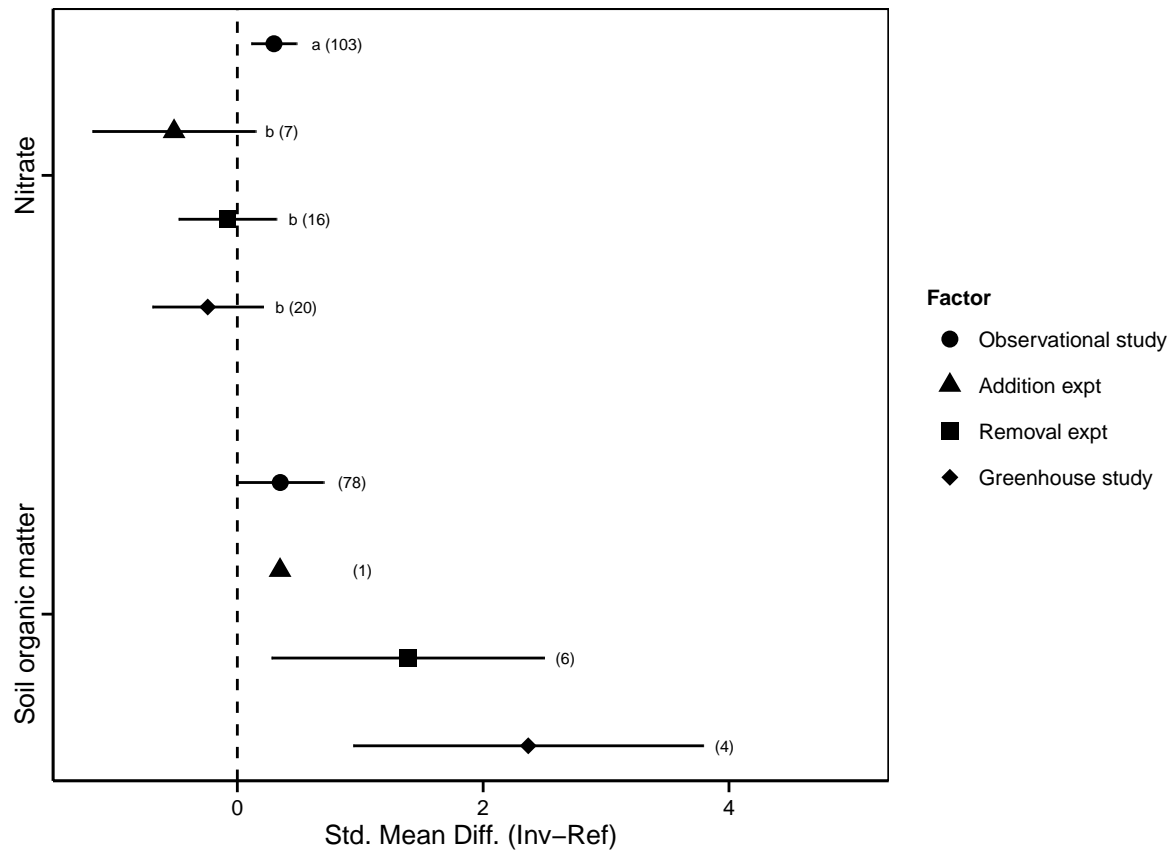
#ggplot
predR1<-predR #get rid of the CIs for a level with only 1 data point
predR1[predR1$MeasFac == 'som' & predR1$CAT == 'field expt addition',c('cilb','ciub')]<-NA
stud.sp<-ggplot(data=predR1,aes(x=pred,y=y, shape=CAT, label=annLabel)) +
  geom_point(aes(shape=CAT),size=3) +
  geom_errorbarh(aes(xmin=cilb,xmax=ciub), height=0)+
  geom_vline(xintercept=0,linetype="dashed") + mytheme +
  xlab('Std. Mean Diff. (Inv-Ref)') + ylab('') +
  scale_y_continuous(breaks=c(1,2),labels=MeasNames1) +
  scale_shape_manual(name="Factor",
                     labels=faclimits,

```

```

      values=facShapes)+
    geom_text(aes(x=ciub, y=y, hjust=-0.3, vjust=0.5),size=2.2,show_guide = FALSE) +
    annotate("text", x=1, y=1.1, label=' (1)', size=2.2)+ #manually add the posthoc letters and k here
    scale_x_continuous(expand=c(0,0), limits=c(-1.5,5.3))
stud.sp + theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))

```



```

newfilename<-"studytypeForest.png"
png(paste(figuresPath,'modForests',newfilename, sep='/'), units='in', width = fig.width*2, height = fig
stud.sp + theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))
dev.off()

```

```

## pdf
## 2

```

2Bii. Nfix status

```

currMeasFac<-anovaMods[anovaMods$anovaLabels=='NfixA' & anovaMods$pval < 0.05, '.id']
currMeasFac

```

```

## [1] "toti" "soiln" "soilcn"

```

```

#levels(dat.tmp$Nfix) #check to make sure that this lines up with the way I organized the contrasts
#Run post-hoc comparisions among Nfix levels, pull out means and CI
i<-0

```

```

posthoc.list<-list()
pred.list<-list()
for(i in 1:length(currMeasFac)){
  #1. calc posthoc pvals
  posthocR<-anova(res.Nfix[[currMeasFac[i]]],
    L=rbind(c(1,-1,0,0), #I-R- vs I-R+
            c(1,0,-1,0), #I-R- vs I+R-
            c(1,0,0,-1), #I-R- vs I+R+
            c(0,1,-1,0), #I-R+ vs I+R-
            c(0,1,0,-1), #I-R+ vs I+R+
            c(0,0,1,-1) #I+R- vs I+R+
          ))
  levelcomp<-c('none_r','none_i','none_both','r_i','r_both','i_both')
  posthoc.list[[i]]<-data.frame(levelcomp, pval=round(posthocR$pval, digits=4))
  #2. calc predicted values by level
  predR<-predict(res.Nfix[[currMeasFac[i]]])
  tmp<-data.frame(obsID=predR$slab, pred=predR$pred, cilb=predR$ci.lb, ciub=predR$ci.ub, se=predR$se)
  ind.Fac<-ddply(dat.tmp, ~obsID, summarize, Level=unique(Nfix))
  tmp1<-merge(tmp, ind.Fac)
  tmp2<-ddply(tmp1, ~Level, summarize,
    pred = unique(pred),
    cilb = unique(cilb),
    ciub = unique(ciub),
    se = unique(se),
    k = length(obsID))
  pred.list[[i]]<-tmp2
}
names(posthoc.list)<-currMeasFac
posthocR<-ldply(posthoc.list)
posthocR

```

```

##      .id levelcomp  pval
## 1  toti   none_r 0.0019
## 2  toti   none_i 0.6139
## 3  toti none_both 0.7692
## 4  toti      r_i 0.0015
## 5  toti   r_both 0.1337
## 6  toti   i_both 0.5357
## 7  soiln   none_r 0.4035
## 8  soiln   none_i 0.0349
## 9  soiln none_both 0.2652
## 10 soiln      r_i 0.2750
## 11 soiln   r_both 0.7800
## 12 soiln   i_both 0.4073
## 13 soilcn   none_r 0.0008
## 14 soilcn   none_i 0.2619
## 15 soilcn none_both 0.5133
## 16 soilcn      r_i 0.0134
## 17 soilcn   r_both 0.0110
## 18 soilcn   i_both 0.7210

```

```
names(pred.list)<-currMeasFac
predR<-ldply(pred.list)
predR
```

```
##      .id      Level      pred      cilb
## 1  toti      No N-fixers  0.145819164 -0.06264507
## 2  toti      Resident N-fixers only -0.639073459 -1.14949297
## 3  toti      Invasive N-fixers only  0.436906288  0.00152190
## 4  toti      Invasive and resident N-fixers 0.145524712 -0.74608223
## 5  soiln      No N-fixers  0.209141810 -0.07021320
## 6  soiln      Resident N-fixers only  0.760156852  0.18454234
## 7  soiln      Invasive N-fixers only  1.167400723  0.71647139
## 8  soiln      Invasive and resident N-fixers 0.877499527  0.28887503
## 9  soilcn      No N-fixers -0.175307201 -0.39229343
## 10 soilcn      Resident N-fixers only  0.920641747  0.31550562
## 11 soilcn      Invasive N-fixers only -0.006455591 -0.42258342
## 12 soilcn      Invasive and resident N-fixers -0.122424077 -0.65141389
##      ciub      se      k
## 1  0.35428339 0.1063613 162
## 2 -0.12865395 0.2604229  14
## 3  0.87229068 0.2221390  14
## 4  1.03713166 0.4549099   3
## 5  0.48849682 0.1425307 120
## 6  1.33577136 0.2936863  19
## 7  1.61833006 0.2300702  29
## 8  1.46612403 0.3003241  18
## 9  0.04167902 0.1107093  69
## 10 1.52577788 0.3087486   8
## 11 0.40967224 0.2123140  14
## 12 0.40656573 0.2698977   7
```

*#update effect size table for plotting*

```
colnames(predR)[1]<-'MeasFac'
selectMeas<-unique(predR$MeasFac)
MeasFac1<-rev(levels(factor(MEASCAT[MEASCAT %in% selectMeas], levels=MEASCAT[MEASCAT %in% selectMeas])))
MeasNames1<-rev(measTab[measTab$MEASCAT %in% selectMeas,'labels'])
colnames(predR)[2]<-'CAT'
CAT<-levels(dat$Nfix)
predR$y<-NA
i<-0
for(i in 1:length(MeasFac1)){
  predR[predR$CAT==CAT[1] & predR$MeasFac==MeasFac1[i], 'y']<-i+0.3
  predR[predR$CAT==CAT[2] & predR$MeasFac==MeasFac1[i], 'y']<-i+0.1
  predR[predR$CAT==CAT[3] & predR$MeasFac==MeasFac1[i], 'y']<-i-0.1
  predR[predR$CAT==CAT[4] & predR$MeasFac==MeasFac1[i], 'y']<-i-0.3
}
predR
```

```
##      MeasFac      CAT      pred      cilb
## 1  toti      No N-fixers  0.145819164 -0.06264507
## 2  toti      Resident N-fixers only -0.639073459 -1.14949297
## 3  toti      Invasive N-fixers only  0.436906288  0.00152190
```

```
## 4      toti Invasive and resident N-fixers  0.145524712 -0.74608223
## 5      soiln                No N-fixers  0.209141810 -0.07021320
## 6      soiln                Resident N-fixers only  0.760156852  0.18454234
## 7      soiln                Invasive N-fixers only  1.167400723  0.71647139
## 8      soiln Invasive and resident N-fixers  0.877499527  0.28887503
## 9      soilcn                No N-fixers -0.175307201 -0.39229343
## 10     soilcn                Resident N-fixers only  0.920641747  0.31550562
## 11     soilcn                Invasive N-fixers only -0.006455591 -0.42258342
## 12     soilcn Invasive and resident N-fixers -0.122424077 -0.65141389
##          ciub          se    k    y
## 1  0.35428339 0.1063613 162 3.3
## 2 -0.12865395 0.2604229  14 3.1
## 3  0.87229068 0.2221390  14 2.9
## 4  1.03713166 0.4549099   3 2.7
## 5  0.48849682 0.1425307 120 2.3
## 6  1.33577136 0.2936863  19 2.1
## 7  1.61833006 0.2300702  29 1.9
## 8  1.46612403 0.3003241  18 1.7
## 9  0.04167902 0.1107093  69 1.3
## 10 1.52577788 0.3087486   8 1.1
## 11 0.40967224 0.2123140  14 0.9
## 12 0.40656573 0.2698977   7 0.7
```

```
#assign post-hoc letters (order:field study, expt addition, expt removal, gh)
```

```
#subset(posthocR, .id=='litterbiom')
```

```
phTtoti<-c('b','a','b','b')
```

```
phTsoiln<-c('a','a','b','a') #check this one
```

```
phTsoilcn<-c('a','b','a','a')
```

```
predR$posthocL<-c(phTtoti,phTsoiln, phTsoilcn)
```

```
#assign pretty names and symbols
```

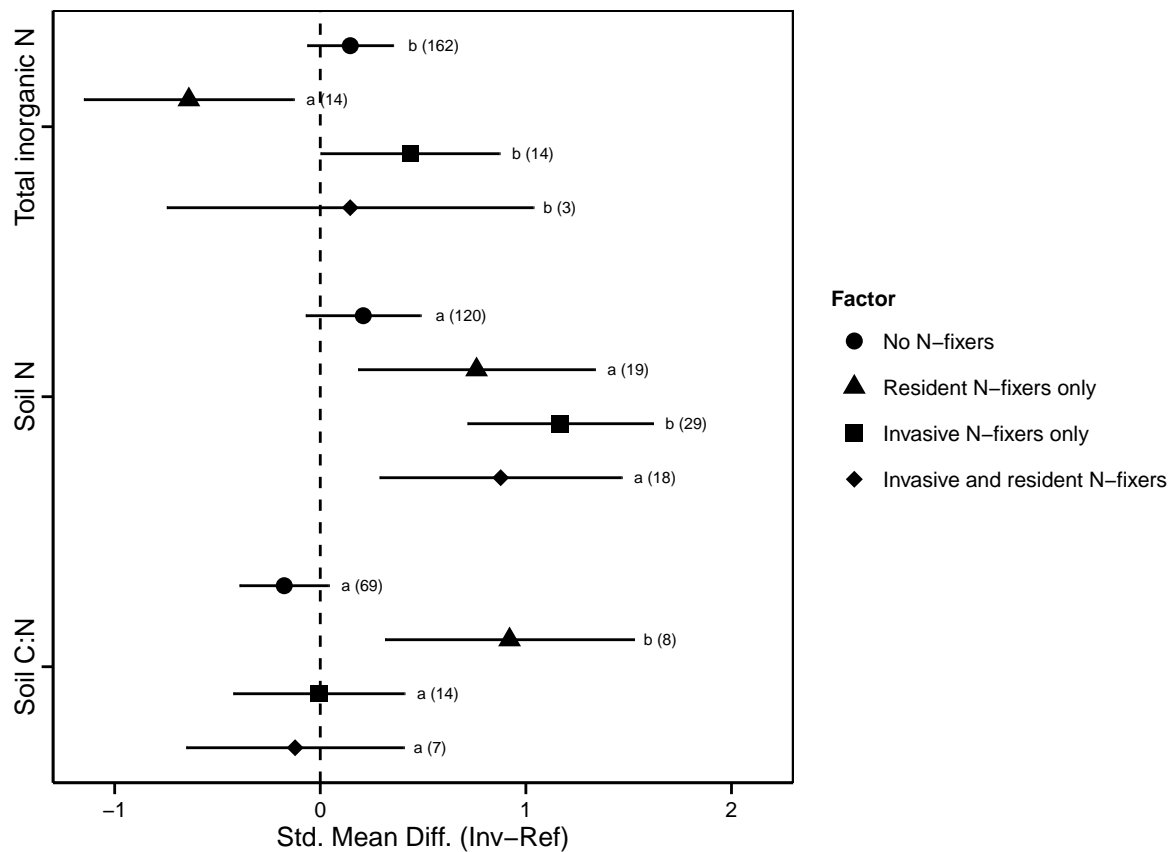
```
faclimits<-unique(predR$CAT)
```

```
facShapes<-c(16,17,15,18)
```

```
predR$annLabel<-paste(predR$posthocL, '(',predR$k,')', sep='')
```

```
#ggplot
```

```
nfix.sp<-ggplot(data=predR,aes(x=pred,y=y, shape=CAT,label=annLabel)) +
  geom_point(aes(shape=CAT),size=3) +
  geom_errorbarh(aes(xmin=cilb,xmax=ciub), height=0)+
  geom_vline(xintercept=0,linetype="dashed") + mytheme +
  xlab('Std. Mean Diff. (Inv-Ref)') + ylab('') +
  scale_y_continuous(breaks=seq(1,length(MeasFacl)),
    labels=MeasNames1) +
  scale_shape_manual(name="Factor",
    labels=faclimits,
    values=facShapes)+
  geom_text(aes(x=ciub, y=y, hjust=-0.3, vjust=0.5),size=2.2,show_guide = FALSE) +
  scale_x_continuous(expand=c(0,0), limits=c(-1.3,2.3))
nfix.sp + theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))
```



```
newfilename<-"nfixForest.png"
png(paste(figuresPath,'modForests',newfilename, sep='/'), units='in', width = fig.width*2, height = fig
nfix.sp + theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))
dev.off()
```

```
## pdf
## 2
```

2Biii. Quality

```
currMeasFac<-anovaMods[anovaMods$anovaLabels=='qualityA' & anovaMods$pval < 0.05, '.id']
currMeasFac
```

```
## [1] "nitrif" "nminz" "som"
```

```
#note - som doesn't have all levels of measQuality, so you need to have a different set of contrasts
#levels(dat.tmp$measQuality) #check to make sure that this lines up with the way I organized the contra
#Run post-hoc comparisons among Nfix levels, pull out means and CI
i<-0
posthoc.list<-list()
pred.list<-list()
for(i in 1:length(currMeasFac)){
  #1. calc posthoc pvals
  if(i %in% c(1,2)){
    posthocR<-anova(res.quality[[currMeasFac[i]]],
```



```

      # A+C+, A+C-, A-C+, A-C-
      L=rbind(c(1,-1,0,0), #A+C+ vs A+C-
              c(1,0,-1,0), #A+C+ vs A-C+
              c(1,0,0,-1), #A+C+ vs A-C-
              c(0,1,-1,0), #A+C- vs A-C+
              c(0,1,0,-1), #A+C- vs A-C-
              c(0,0,1,-1)  #A-C+ vs A-C-
      ))
    levelcomp<-c('both_a','both_c','both_none','a_c','a_none','c_none')
    posthoc.list[[i]]<-data.frame(levelcomp, pval=round(posthocR$pval, digits=4))
  }else{
    temp1<-subset(dat.tmp, measCat=='som')
    unique(temp1$measQuality)
    #levels: A+C-, A-C+, A-C-
    posthocR<-anova(res.quality[[currMeasFac[i]]],
                    L=rbind(c(1,-1,0), #A+C- vs A-C+
                            c(1,0,-1), #A+C- vs A-C-
                            c(0,1,-1)  #A-C+ vs A-C-
                    ))
    levelcomp<-c('a_c','a_none','c_none')
    posthoc.list[[i]]<-data.frame(levelcomp, pval=round(posthocR$pval, digits=4))
  }

  #2. calc predicted values by level
  predR<-predict(res.quality[[currMeasFac[i]]])
  tmp<-data.frame(obsID=predR$slab, pred=predR$pred, cilb=predR$ci.lb, ciub=predR$ci.ub, se=predR$se)
  ind.Fac<-ddply(dat.tmp, ~obsID+measCat, summarize, Level=measQuality)
  ind.Fac.sub<-subset(ind.Fac, measCat==currMeasFac[i])
  tmp1<-merge(tmp, ind.Fac.sub)
  tmp2<-ddply(tmp1, ~Level, summarize,
              pred = unique(pred),
              cilb = unique(cilb),
              ciub = unique(ciub),
              se = unique(se),
              k = length(obsID))
  pred.list[[i]]<-tmp2
}
names(posthoc.list)<-currMeasFac
posthocR<-ldply(posthoc.list)
posthocR

```

```

##      .id levelcomp  pval
## 1  nitrif   both_a 0.5775
## 2  nitrif   both_c 0.0464
## 3  nitrif both_none 0.2574
## 4  nitrif     a_c 0.2806
## 5  nitrif   a_none 0.6763
## 6  nitrif   c_none 0.3621
## 7   nminz   both_a 0.8532
## 8   nminz   both_c 0.0783
## 9   nminz both_none 0.6363
## 10  nminz     a_c 0.1244

```

```
## 11 nminz a_none 0.8140
## 12 nminz c_none 0.0273
## 13 som a_c 0.6740
## 14 som a_none 0.3003
## 15 som c_none 0.0094
```

```
names(pred.list)<-currMeasFac
predR<-ldply(pred.list)
predR
```

```
##      .id      Level      pred      cilb      ciub      se k
## 1  nitrif    Agg.Conv  0.02492035 -0.35065764  0.4004983  0.1916249 26
## 2  nitrif    Agg.NoConv 0.36678677 -0.45760090  1.1911744  0.4206137  5
## 3  nitrif    NoAgg.Conv 0.86774573  0.48239011  1.2531013  0.1966136 29
## 4  nitrif NoAgg.NoConv 0.57265116  0.06840542  1.0768969  0.2572730 17
## 5  nminz     Agg.Conv  0.03211934 -0.34683847  0.4110771  0.1933494 21
## 6  nminz     Agg.NoConv 0.16505566 -0.58676186  0.9168732  0.3835874  6
## 7  nminz     NoAgg.Conv 0.82265567  0.45071697  1.1945944  0.1897681 28
## 8  nminz NoAgg.NoConv 0.26356829 -0.06548470  0.5926213  0.1678873 45
## 9      som    Agg.NoConv -0.28242249 -1.49038684  0.9255419  0.6163197  6
## 10     som    NoAgg.Conv -1.16140073 -2.53594654  0.2131451  0.7013118  5
## 11     som NoAgg.NoConv  0.72704021  0.35288533  1.1011951  0.1908989 78
```

```
#update effect size table for plotting
colnames(predR)[1]<-'MeasFac'
selectMeas<-unique(predR$MeasFac)
MeasFac1<-rev(levels(factor(MEASCAT[MEASCAT %in% selectMeas], levels=MEASCAT[MEASCAT %in% selectMeas])))
MeasNames1<-rev(measTab[measTab$MEASCAT %in% selectMeas,'labels'])
colnames(predR)[2]<-'CAT'
CAT<-levels(dat$measQuality)
predR$y<-NA
i<-0
for(i in 1:length(MeasFac1)){
  predR[predR$CAT==CAT[1] & predR$MeasFac==MeasFac1[i], 'y']<-i+0.3
  predR[predR$CAT==CAT[2] & predR$MeasFac==MeasFac1[i], 'y']<-i+0.1
  predR[predR$CAT==CAT[3] & predR$MeasFac==MeasFac1[i], 'y']<-i-0.1
  predR[predR$CAT==CAT[4] & predR$MeasFac==MeasFac1[i], 'y']<-i-0.3
}
predR
```

```
##      MeasFac      CAT      pred      cilb      ciub      se k  y
## 1  nitrif    Agg.Conv  0.02492035 -0.35065764  0.4004983  0.1916249 26 3.3
## 2  nitrif    Agg.NoConv 0.36678677 -0.45760090  1.1911744  0.4206137  5 3.1
## 3  nitrif    NoAgg.Conv 0.86774573  0.48239011  1.2531013  0.1966136 29 2.9
## 4  nitrif NoAgg.NoConv 0.57265116  0.06840542  1.0768969  0.2572730 17 2.7
## 5  nminz     Agg.Conv  0.03211934 -0.34683847  0.4110771  0.1933494 21 2.3
## 6  nminz     Agg.NoConv 0.16505566 -0.58676186  0.9168732  0.3835874  6 2.1
## 7  nminz     NoAgg.Conv 0.82265567  0.45071697  1.1945944  0.1897681 28 1.9
## 8  nminz NoAgg.NoConv 0.26356829 -0.06548470  0.5926213  0.1678873 45 1.7
## 9      som    Agg.NoConv -0.28242249 -1.49038684  0.9255419  0.6163197  6 1.1
## 10     som    NoAgg.Conv -1.16140073 -2.53594654  0.2131451  0.7013118  5 0.9
## 11     som NoAgg.NoConv  0.72704021  0.35288533  1.1011951  0.1908989 78 0.7
```

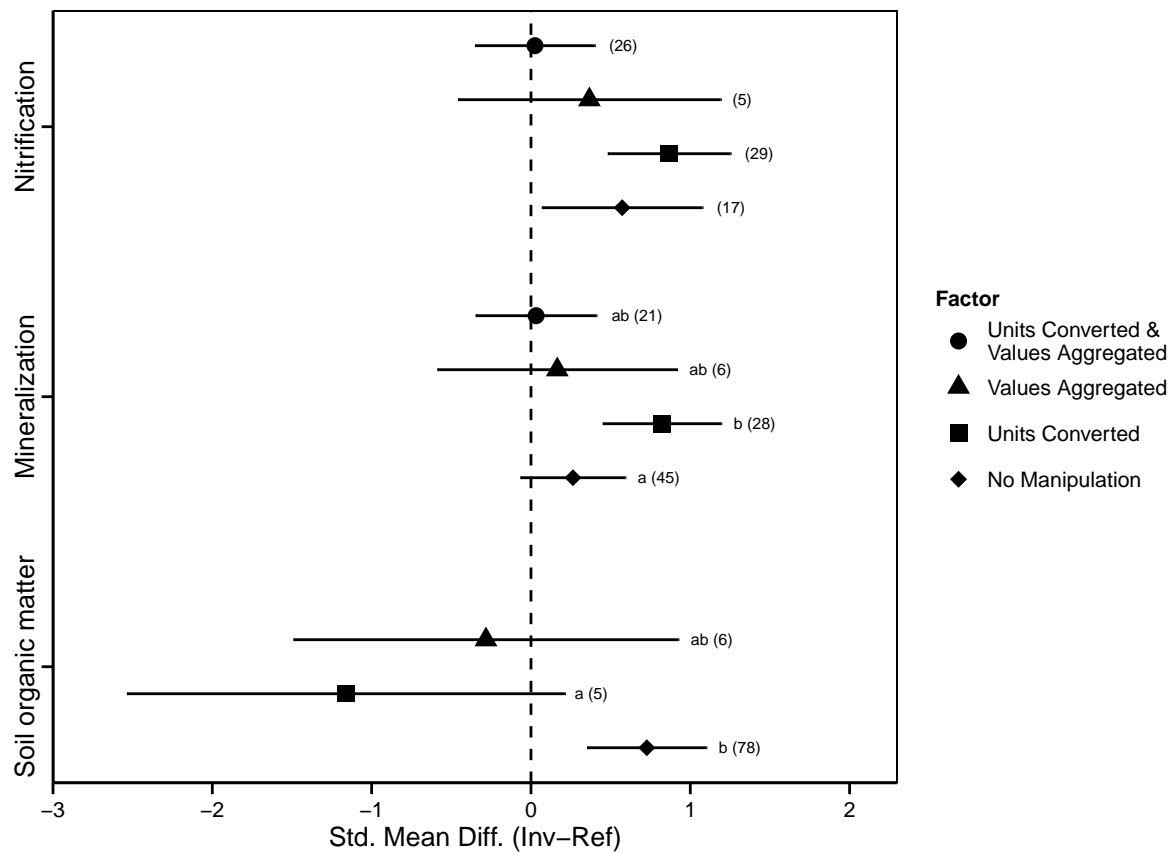
```

#assign post-hoc letters (order ex:both, a, c, none)
#subset(posthocR, .id=='som')
phTnitrif<-c('',' ',' ') #both vs c is marginally signif (p=0.059)
phTnminz<-c('ab','ab','b','a') #both vs c is marginally signif (p=0.080), c vs none is signif (p=0.038)
phTsom<-c('ab','a','b') #c vs none pval=0.0128
predR$posthocL<-c(phTnitrif,phTnminz, phTsom)

#assign pretty names and symbols
faclimits<-rev(c('No Manipulation','Units Converted',
                'Values Aggregated','Units Converted &\nValues Aggregated'))
facShapes<-c(16,17,15,18)
predR$annLabel<-paste(predR$posthocL, '(',predR$k,')', sep='')

#ggplot
qual.sp<-ggplot(data=predR,aes(x=pred,y=y, shape=CAT,label=annLabel)) +
  geom_point(aes(shape=CAT),size=3) +
  geom_errorbarh(aes(xmin=cilb,xmax=ciub), height=0)+
  geom_vline(xintercept=0,linetype="dashed") + mytheme +
  xlab('Std. Mean Diff. (Inv-Ref)') + ylab('') +
  scale_shape_manual(name="Factor",
                    labels=faclimits,
                    values=facShapes) +
  scale_y_continuous(breaks=seq(1,length(MeasFac1)),
                    labels=MeasNames1) +
  geom_text(aes(x=ciub, y=y, hjust=-0.3, vjust=0.5),size=2.2,show_guide = FALSE) +
  scale_x_continuous(expand=c(0,0),limits=c(-3,2.3))
qual.sp + theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))

```



```
newfilename<-"qualityForest.png"
png(paste(figuresPath,'modForests',newfilename, sep='/'), units='in', width = fig.width*2, height = fig
qual.sp + theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))
dev.off()
```

```
## pdf
## 2
```

2Biv. Ecosystem type

```
currMeasFac<-anovaMods[anovaMods$anovaLabels=='ecosystA' & anovaMods$pval < 0.05, '.id']
currMeasFac
```

```
## [1] "ammonif" "soiln"
```

```
#levels(dat.tmp$ecosystCat) #check to make sure that this lines up with the way I organized the contras
#Run post-hoc comparisions among Nfix levels, pull out means and CI
i<-0
posthoc.list<-list()
pred.list<-list()
for(i in 1:length(currMeasFac)){
  #1. calc posthoc pvals
  # forest, shrubland, grassland, wetland
  posthocR<-anova(res.ecosyst[[currMeasFac[i]]],
    L=rbind(c(1,-1,0,0), #forest vs shrub
```

```

      c(1,0,-1,0), #forest vs grass
      c(1,0,0,-1), #forest vs wet
      c(0,1,-1,0), #shrub vs grass
      c(0,1,0,-1), #shrub vs wet
      c(0,0,1,-1) #grass vs wet
    ))
levelcomp<-c('f_s','f_g','f_w',
             's_g','s_w',
             'g_w')
posthoc.list[[i]]<-data.frame(levelcomp, pval=round(posthocR$pval, digits=4))
#2. calc predicted values by level
predR<-predict(res.ecosyst[[currMeasFac[i]]])
tmp<-data.frame(obsID=predR$slab, pred=predR$pred, cilb=predR$ci.lb, ciub=predR$ci.ub, se=predR$se)
ind.Fac<-ddply(dat.tmp, ~obsID, summarize, Level=unique(ecosystCat))
tmp1<-merge(tmp, ind.Fac)
tmp2<-ddply(tmp1, ~Level, summarize,
            pred = unique(pred),
            cilb = unique(cilb),
            ciub = unique(ciub),
            se = unique(se),
            k = length(obsID))
pred.list[[i]]<-tmp2
}
names(posthoc.list)<-currMeasFac
posthocR<-ldply(posthoc.list)
posthocR

```

```

##      .id levelcomp  pval
## 1  ammonif      f_s 0.0003
## 2  ammonif      f_g 0.0008
## 3  ammonif      f_w 0.0066
## 4  ammonif      s_g 0.5443
## 5  ammonif      s_w 0.8235
## 6  ammonif      g_w 0.8520
## 7   soiln      f_s 0.1035
## 8   soiln      f_g 0.0003
## 9   soiln      f_w 0.0078
## 10  soiln      s_g 0.0034
## 11  soiln      s_w 0.0937
## 12  soiln      g_w 0.6649

```

```

names(pred.list)<-currMeasFac
predR<-ldply(pred.list)
predR

```

```

##      .id   Level    pred    cilb    ciub    se  k
## 1 ammonif forest -0.5341463 -0.84447712 -0.2238154 0.1583350 25
## 2 ammonif shrubland 0.3136574 -0.08882315 0.7161379 0.2053510 7
## 3 ammonif grassland 0.1481908 -0.20399709 0.5003786 0.1796910 12
## 4 ammonif wetland 0.2223072 -0.47209769 0.9167120 0.3542947 5
## 5  soiln forest 0.8785069 0.47144766 1.2855661 0.2076871 67
## 6  soiln shrubland 0.9757642 0.50476195 1.4467664 0.2403117 25

```

```
## 7   soiln grassland  0.1361788 -0.20894752  0.4813051 0.1760881 79
## 8   soiln  wetland  0.3061949 -0.38500646  0.9973962 0.3526602 15
```

```
#update effect size table for plotting
colnames(predR)[1]<-'MeasFac'
selectMeas<-unique(predR$MeasFac)
MeasFac1<-rev(levels(factor(MEASCAT[MEASCAT %in% selectMeas], levels=MEASCAT[MEASCAT %in% selectMeas])))
MeasNames1<-rev(measTab[measTab$MEASCAT %in% selectMeas,'labels'])
colnames(predR)[2]<-'CAT'
CAT<-levels(dat.tmp$ecosystCat)
predR$y<-NA
i<-0
for(i in 1:length(MeasFac1)){
  predR[predR$CAT==CAT[1] & predR$MeasFac==MeasFac1[i], 'y']<-i+0.3
  predR[predR$CAT==CAT[2] & predR$MeasFac==MeasFac1[i], 'y']<-i+0.1
  predR[predR$CAT==CAT[3] & predR$MeasFac==MeasFac1[i], 'y']<-i-0.1
  predR[predR$CAT==CAT[4] & predR$MeasFac==MeasFac1[i], 'y']<-i-0.3
}
predR
```

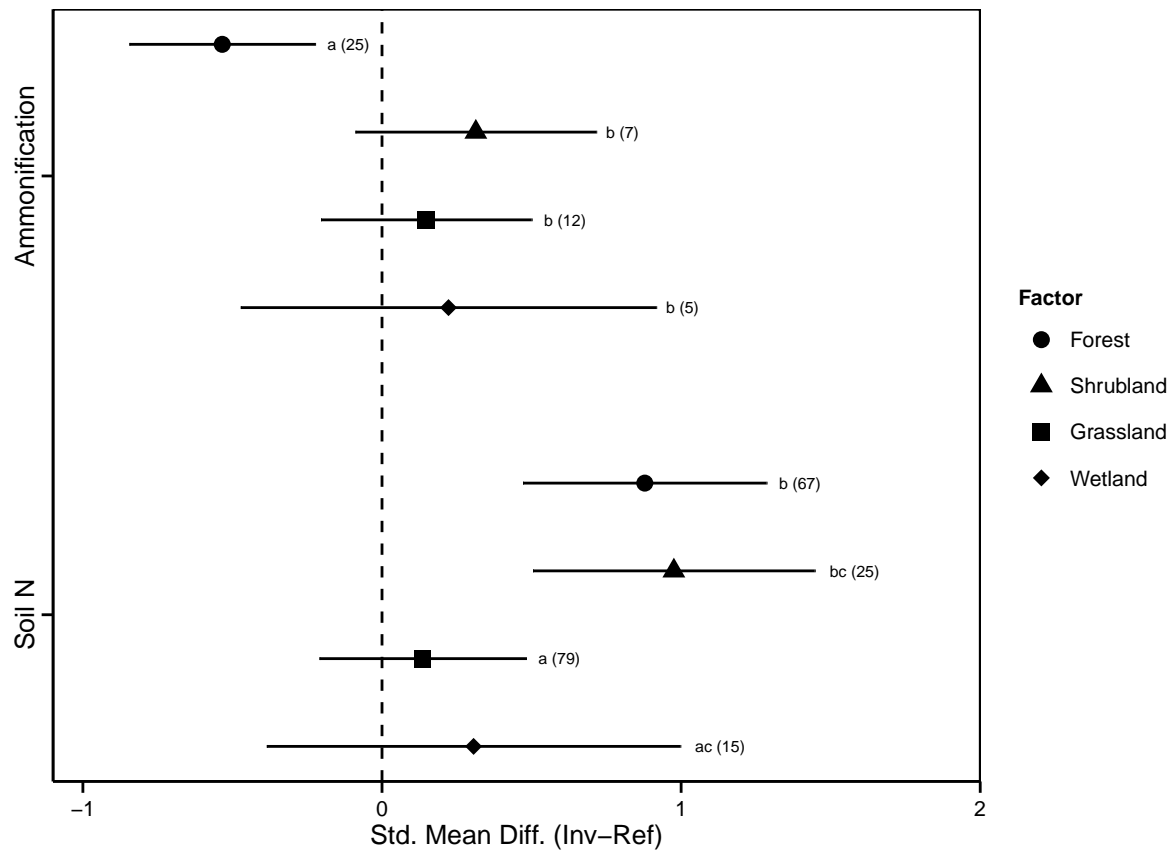
```
##   MeasFac      CAT      pred      cilb      ciub      se k  y
## 1 ammonif forest -0.5341463 -0.84447712 -0.2238154 0.1583350 25 2.3
## 2 ammonif shrubland 0.3136574 -0.08882315 0.7161379 0.2053510 7 2.1
## 3 ammonif grassland 0.1481908 -0.20399709 0.5003786 0.1796910 12 1.9
## 4 ammonif wetland 0.2223072 -0.47209769 0.9167120 0.3542947 5 1.7
## 5 soiln forest 0.8785069 0.47144766 1.2855661 0.2076871 67 1.3
## 6 soiln shrubland 0.9757642 0.50476195 1.4467664 0.2403117 25 1.1
## 7 soiln grassland 0.1361788 -0.20894752 0.4813051 0.1760881 79 0.9
## 8 soiln wetland 0.3061949 -0.38500646 0.9973962 0.3526602 15 0.7
```

```
#assign post-hoc letters (order:f, s, g, w)
#subset(posthocR, .id=='soiln')
phTammonif<-c('a','b','b','b')
phTsoiln<-c('b','bc','a','ac') #check this one
predR$posthocL<-c(phTammonif,phTsoiln)

#assign pretty names and symbols
facLimits<-rev(c('Wetland','Grassland','Shrubland','Forest'))
facShapes<-c(16,17,15,18)
predR$annLabel<-paste(predR$posthocL, '(',predR$k,')', sep='')

#ggplot
eco.sp<-ggplot(data=predR,aes(x=pred,y=y, shape=CAT,label=annLabel)) +
  geom_point(aes(shape=CAT),size=3) +
  geom_errorbarh(aes(xmin=cilb,xmax=ciub), height=0)+
  geom_vline(xintercept=0,linetype="dashed") + mytheme +
  xlab('Std. Mean Diff. (Inv-Ref)') + ylab('') +
  scale_y_continuous(breaks=seq(1,length(MeasFac1)),
    labels=MeasNames1) +
  scale_shape_manual(name="Factor",
    labels=facLimits,
    values=facShapes)+
  geom_text(aes(x=ciub, y=y, hjust=-0.3, vjust=0.5),size=2.2,show_guide = FALSE) +
```

```
scale_x_continuous(expand=c(0,0), limits=c(-1.1,2))
eco.sp + theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))
```



```
newfilename<-"ecosystForest.png"
png(paste(figuresPath,'modForests',newfilename, sep='/'), units='in', width = fig.width*1.5, height = f
eco.sp + theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))
dev.off()
```

```
## pdf
## 2
```

### 3. Test for correlation between CWM traits and effect size values

3A. Fit a random-effects model with 1 of the continuous trait variables as a fixed effect. Model syntax is `res <- rma.mv(yi, vi, mods= ~Xmod, random=list(~1 | paperID, ~1 | obsID), data=dat1, subset=measCat==MEASCAT[i], slab=paste(paperID,obsID, sep=","))` where Xmod is one of the following 12 combinations:

-> 1 of 3 plant communities: (1) InvSpInvArea\_cwm, (2) NatArea\_cwm, (3) CWMDiff\_cwm

-> 1 of 4 trait types: (1) percN, (2) litterpercN, (3) cn, (4) littercn

where... 'InvSpInvArea\_cwm' is the invasive species community weighted mean trait value; 'NatArea\_cwm' is the reference area plant community weighted mean trait value; 'CWMDiff\_cwm' is the dissimilarity between

the Invaded - Reference area plant community weighted mean trait value; 'percN' is leaf %N; 'litterpercN' is litter %N; 'cn' is leaf C:N; 'littercn' is litter C:N;

```
INVlist<-FitPlot(dat, k=1)
NATlist<-FitPlot(dat, k=2)
DIFFlist<-FitPlot(dat, k=3)

INVtab<-rbind(ldply(INVlist[['results']][['percN']],
  ldply(INVlist[['results']][['litterpercN']],
  ldply(INVlist[['results']][['cn']],
  ldply(INVlist[['results']][['littercn']])))[, -1]
NATtab<-rbind(ldply(NATlist[['results']][['percN']],
  ldply(NATlist[['results']][['litterpercN']],
  ldply(NATlist[['results']][['cn']],
  ldply(NATlist[['results']][['littercn']])))[, -1]
DIFFtab<-rbind(ldply(DIFFlist[['results']][['percN']],
  ldply(DIFFlist[['results']][['litterpercN']],
  ldply(DIFFlist[['results']][['cn']],
  ldply(DIFFlist[['results']][['littercn']])))[, -1]

newfilename<-'INVtab.txt'
write.table(INVtab, file=paste(figuresPath, 'allRegressionTable', newfilename, sep='/'), sep='\t', row.names=FALSE)
newfilename<-'NATtab.txt'
write.table(NATtab, file=paste(figuresPath, 'allRegressionTable', newfilename, sep='/'), sep='\t', row.names=FALSE)
newfilename<-'DIFFtab.txt'
write.table(DIFFtab, file=paste(figuresPath, 'allRegressionTable', newfilename, sep='/'), sep='\t', row.names=FALSE)
```

```
INVtab[INVtab$pVal < 0.1 & INVtab$measType %in% MEASCAT,]
```

##	plantType	traitType	measType	studies	pr2	est	pVal
## 7	InvSpInvArea_cwm	percN	soiln	170	0.02	0.34	0.00
## 8	InvSpInvArea_cwm	percN	soilcn	89	0.02	-0.20	0.03
## 9	InvSpInvArea_cwm	percN	som	88	0.01	0.27	0.09
## 17	InvSpInvArea_cwm	litterpercN	soilcn	10	0.22	-0.46	0.05

```
NATtab[NATtab$pVal < 0.1 & NATtab$measType %in% MEASCAT,]
```

##	plantType	traitType	measType	studies	pr2	est	pVal
## 24	NatArea_cwm	cn	nminz	46	0.05	0.02	0.02
## 26	NatArea_cwm	cn	soilcn	66	0.05	-0.02	0.01
## 27	NatArea_cwm	cn	som	22	0.04	0.02	0.08

```
DIFFtab[DIFFtab$pVal < 0.1 & DIFFtab$measType %in% MEASCAT,]
```

##	plantType	traitType	measType	studies	pr2	est	pVal
## 10	CWMDiff_cwm	litterpercN	nh	26	0.09	0.55	0.01
## 12	CWMDiff_cwm	litterpercN	toti	24	0.28	1.55	0.00
## 21	CWMDiff_cwm	cn	toti	70	0.03	-0.02	0.03
## 24	CWMDiff_cwm	cn	nminz	46	0.06	-0.03	0.00
## 26	CWMDiff_cwm	cn	soilcn	66	0.09	0.03	0.00
## 28	CWMDiff_cwm	littercn	nh	17	0.06	-0.02	0.08
## 30	CWMDiff_cwm	littercn	toti	23	0.13	-0.02	0.00
## 33	CWMDiff_cwm	littercn	nminz	22	0.07	-0.01	0.04



3B. Plot some/all of the regressions 3Bi. CWM Diff Litter %N and Litter C:N VS nh, toti, nminz

```
#CWM Diff Litter %N and Litter C:N VS nh, toti, nminz

#set up panel margins
top<-0
right<-0.05
bottom<-0
left<-0.05

#set up labels
ylabel <- textGrob(c('Ammonium','Total inorg. N','Mineralization',
  'Std. Mean Diff. (Inv-Ref)'),
  y=c(0.83,0.5,0.15,
    0.5),
  x=unit(c(2,2,2,
    1),'lines'), rot=90)
xlabel<- textGrob(c('Invaded - Reference area\nLitter %N', 'Invaded - Reference area\nLitter C:N'),
  x=c(0.25,0.75),
  y=unit(c(1,1), 'lines'))

#open image file connection
newfilename<-"exampleRegression.png"
png(paste(figuresPath,newfilename, sep='/'), units='in', width = fig.width*3, height = fig.height*4, res=)

#plot
grid.arrange(

  ylabel, # topleft

  arrangeGrob(

    DIFFlist[['figures']][['litterpercN']][['nh']] + ggtitle('a') +
      theme(plot.margin = unit(c(top,right,bottom,left),"in")),
    DIFFlist[['figures']][['littercn']][['nh']] + ggtitle('d') +
      theme(plot.margin = unit(c(top,right,bottom,left),"in")),

    DIFFlist[['figures']][['litterpercN']][['toti']] + ggtitle('b') +
      theme(plot.margin = unit(c(top,right,bottom,left),"in")),
    DIFFlist[['figures']][['littercn']][['toti']] + ggtitle('e') +
      theme(plot.margin = unit(c(top,right,bottom,left),"in")),

    DIFFlist[['figures']][['litterpercN']][['nminz']] + ggtitle('c')+
      theme(plot.margin = unit(c(top,right,bottom,left),"in")),
    DIFFlist[['figures']][['littercn']][['nminz']] + ggtitle('f') +
      theme(plot.margin = unit(c(top,right,bottom,left),"in")),

    nrow=3, ncol=2),

  textGrob(" "), #bottom left

  xlabel, #bottom right

  widths = unit.c(unit(2.5, "lines"), unit(1, "npc") - unit(2.5, "lines")),
```

```

heights = unit.c(unit(1, "npc") - unit(2.5, "lines"), unit(2.5, "lines")),
nrow=2, ncol=2)

dev.off()

```

```

## pdf
## 2

```

3Bii. Loop through all plots: 1 page per trait type x community with 9 ES panels

```

#add panel labels
INVlist1<-AddPanelTitles(INVlist)
NATlist1<-AddPanelTitles(NATlist)
DIFFlist1<-AddPanelTitles(DIFFlist)

#plot and save
PLANTlist<-list(INVlist1, NATlist1, DIFFlist1)
PLANTlabel<-c('INV','NAT','DIFF')
xlabel.PlantText<-c('Invasive species','Reference area','Invaded - Reference area')
xlabel.TraitText<-c('Leaf %N','Litter %N','Leaf C:N','Litter C:N')
l<-0
for(l in 1:length(PLANTlist)){
  i<-0
  for (i in 1:length(TRAIT)){
    CURRTRAIT<-PLANTlist[[l]][[i]]
    xlabel<- textGrob(paste(xlabel.PlantText[l],xlabel.TraitText[i], sep=", "), x=0.5, y=unit(1,'lines'))

    #open image file connection
    newfilename<-paste(paste(PLANTlabel[l],TRAIT[i], sep="_"),'.png',sep="")
    png(paste(figuresPath,'allRegressionPlots',newfilename, sep='/'), units='in',
        width = fig.width*3.5, height = fig.height*3.5, res=fig.res)

    grid.arrange(
      textGrob('Std. Mean Diff. (Inv-Ref)', y=0.5,x=unit(1,'lines'), rot=90), # ylabel topleft
      do.call(arrangeGrob, CURRTRAIT),
      textGrob(" "), #bottom left
      xlabel, #bottom right
      widths = unit.c(unit(2.5, "lines"), unit(1, "npc") - unit(2.5, "lines")),
      heights = unit.c(unit(1, "npc") - unit(2.5, "lines"), unit(2.5, "lines")),
      nrow=2, ncol=2
    )

    dev.off()
  }
}

```