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 warrented, 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)

require(ggplot2)
```

```
## Loading required package: ggplot2
```

```
## Warning: package 'ggplot2' was built under R version 3.2.4
```

```
require(gridExtra)
```

```
## Loading required package: gridExtra
```

```
## Warning: package 'gridExtra' was built under R version 3.2.4
```

```
require(plyr)
```

```
## Loading required package: plyr
```

```
require(reshape2)
```

```
## Loading required package: reshape2
```

```
require(metafor)
```

```
## Loading required package: metafor
```

```
## Loading required package: Matrix
```

```
## Warning: package 'Matrix' was built under R version 3.2.4
```

```
## Loading 'metafor' package (version 1.9-8). For an overview
## and introduction to the package please type: help(metafor).
```

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

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

```r
source('CODE/metaAnalysis/fxn_PrepForestPlot.R')
source('CODE/metaAnalysis/fxn_SaveQstats.R')
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/metaDataset.txt", header=TRUE, sep="\t")
metaSummary<-read.table("DATA/metaSummary.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=","))

```r
#subset unique effect size data
dat1<-dat[!is.na(dat$yi),]
dat.meas<-ddply(dat1, ~obsID+measCat, summarize,
                yi = unique(yi),
                vi = unique(vi),
                n1i<-unique(n1i),
                n2i<-unique(n2i),
                paperID = unique(paperID))

colnames(dat.meas)<-c('obsID','measCat','yi','vi','n1i','n2i','paperID')

#run random effects models to determine grand effect sizes and produce funnel plots
res.list<-list()
res.pubBias.list<-list()
i<-0
newfilename<-"funnelPlots.png"
png(paste(figuresPath,'globalForest',newfilename, sep='/'), units='in', width = fig.width*3, height = f
par(mfrow=c(3,3))
for(i in 1:length(MEASCAT)){

  #subset by MEASCAT
  df<-subset(dat.meas, measCat==MEASCAT[i])
```

```r
  #random effects model
  res <- rma.mv(yi, vi,
                random= ~1 | paperID/obsID,
                data=df,
                slab=as.character(obsID),
                method='REML')
  res.list[[i]]<-res

  #evaluate publication bias
  ## funnel plot
  funnel(res, main=labels[i])

  ## correlation between effect size and sample size
  modtab<-summary(lm(yi~n1i, data=df))$coefficients
  est<-round(modtab['n1i','Estimate'], digits=3)
  pval<-round(modtab['n1i','Pr(>|t|)'], digits=3)
  spearman.r<-round(cor(x=df$n1i, y=df$yi, method='spearman'), digits=3)
  #file-drawer problem (aka fail-safe number)
  res.fsn<-fsn(yi, vi, data=df)
  fsnum.n<-res.fsn$fsnum
  fsnum.pval<-round(res.fsn$pval, digits=3)
  #save everything
  res.pubBias.list[[i]]<-data.frame(MEASCAT[i], est, pval, spearman.r, fsnum.n, fsnum.pval)

  #print progress
  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"
```

```r
dev.off()
```

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

```r
names(res.list)<-MEASCAT
names(res.pubBias.list)<-MEASCAT

#random effects model results
resultdf<-PrepForestPlot(res.list) #save estimates, pvalues, and prep dataframe for plotting
resultdf
```

```
##   measCAT              labels    est   var    cil   ciu   k  pval
## 1      nh            Ammonium  0.258 0.005  0.119 0.396 141 0.000
## 2      no             Nitrate  0.169 0.008 -0.004 0.343 150 0.055
## 3    toti   Total inorganic N  0.147 0.011 -0.057 0.350 195 0.157
## 4 ammonif      Ammonification -0.046 0.018 -0.311 0.218  50 0.731
## 5  nitrif       Nitrification  0.457 0.016  0.209 0.704  79 0.000
## 6   nminz      Mineralization  0.361 0.013  0.134 0.588 101 0.002
## 7   soiln              Soil N  0.532 0.013  0.307 0.758 187 0.000
## 8  soilcn            Soil C:N -0.054 0.010 -0.249 0.142 100 0.590
## 9     som Soil organic matter  0.591 0.045  0.175 1.006  90 0.005
##   intraPaperCorr heterogen NoOverlap0 alpha05
## 1          0.536     0.205       TRUE    TRUE
## 2          0.829     0.346      FALSE   FALSE
## 3          0.876     0.470      FALSE   FALSE
## 4          1.000     0.239      FALSE   FALSE
## 5          1.000     0.382       TRUE    TRUE
## 6          0.847     0.406       TRUE    TRUE
## 7          0.712     0.945       TRUE    TRUE
## 8          1.000     0.258      FALSE   FALSE
## 9          0.596     1.621       TRUE    TRUE
```

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

#extract QE and QM information from res.list
Qstats<-SaveQstats(res.list) #save Q stats
Qstats
```

```
##   measCAT              labels      QE QEdf   QEp     QM   QMp
## 1      nh            Ammonium 307.859  140 0.000 13.225 0.000
## 2      no             Nitrate 405.181  149 0.000  3.674 0.055
## 3    toti   Total inorganic N 492.204  194 0.000  2.000 0.157
## 4 ammonif      Ammonification  74.517   49 0.011  0.119 0.731
## 5  nitrif       Nitrification 166.976   78 0.000 13.021 0.000
## 6   nminz      Mineralization 207.895  100 0.000  9.739 0.002
## 7   soiln              Soil N 608.337  186 0.000 21.385 0.000
## 8  soilcn            Soil C:N 190.683   99 0.000  0.291 0.590
## 9     som Soil organic matter 368.530   89 0.000  7.758 0.005
```

```r
newfilename<-'globalMeans_Qstats.txt'
write.table(Qstats, file=paste(figuresPath,'globalForest',newfilename, sep='/'), sep='\t')

#evaluate publication bias -- correlation table
pubBias1.tab<-ldply(res.pubBias.list)
pubBias1.tab
```

```
##        .id MEASCAT.i.    est  pval spearman.r fsnum.n fsnum.pval
## 1      nh         nh -0.006 0.708      0.009    1827      0.000
## 2      no         no -0.005 0.845     -0.166     314      0.002
## 3    toti       toti -0.006 0.666     -0.062     404      0.002
## 4 ammonif    ammonif  0.005 0.634      0.074       0      0.117
## 5  nitrif     nitrif -0.027 0.094     -0.326    1321      0.000
## 6   nminz      nminz -0.073 0.046     -0.191    1143      0.000
## 7   soiln      soiln -0.006 0.612     -0.014    8416      0.000
## 8  soilcn     soilcn  0.009 0.558      0.063       0      0.143
## 9     som        som -0.018 0.682      0.046    1508      0.000
```

```
newfilename<-'globalMeans_pubBias1.txt'
write.table(pubBias1.tab, file=paste(figuresPath,'globalForest',newfilename, sep='/'), sep='\t')

#show that yi's are normally distributed
# Q-Q plots
dat.measP<-dat.meas
dat.measP$measCat<-factor(dat.measP$measCat, levels=MEASCAT)
levels(dat.measP$measCat)<-labels
qq<-ggplot(dat.measP, aes(sample=yi)) +
  facet_wrap(~measCat, scales='free', ncol=3) +
  stat_qq() + mytheme + ggtitle('QQ Plots of effect sizes')
qq
```


QQ Plots of effect sizes
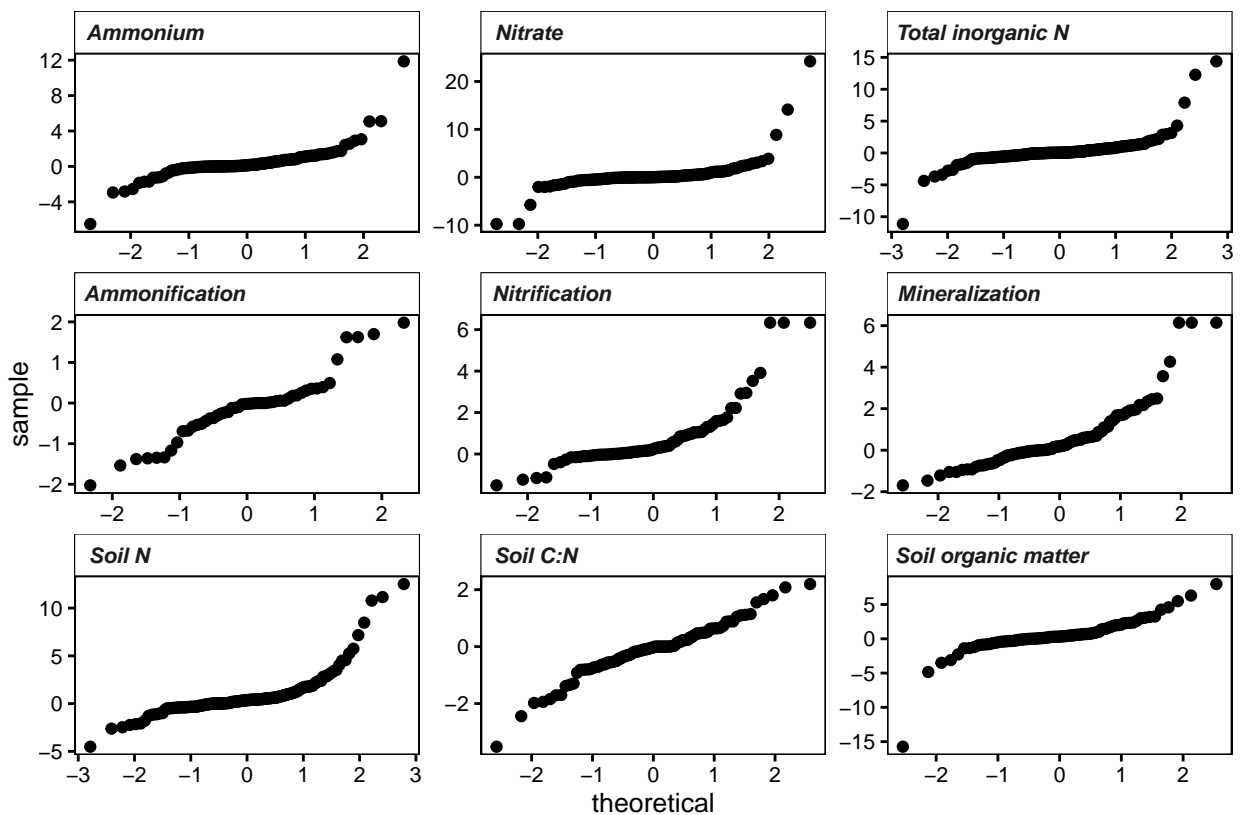
```
newfilename<-"globalMeans_qqPlots.png"
png(paste(figuresPath,'globalForest',newfilename, sep='/'),
    units='in', width = fig.width*3, height = fig.height*3, res=fig.res)
qq
dev.off()
```

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

1B. Plot the results of this study relative to previous meta-analyses

---

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
```

```r
which(temp$n==1)
```

```
## integer(0)
```

```r
#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= ~1 | paperID/obsID,
                    data=subdat, slab=as.character(obsID),
                    method='REML')

  #full models
  res.quality[[i]]<- rma.mv(yi, vi,
                            mods= ~factor(measQuality),
                            random= ~1 | paperID/obsID,
                            data=subdat, slab=as.character(obsID),
                            method='REML')
```

```
  res.ecosyst[[i]]<- rma.mv(yi, vi,
                            mods= ~factor(ecosystCat),
                            random= ~1 | paperID/obsID,
                            data=subdat, slab=as.character(obsID),
                            method='REML')
  res.studytype[[i]]<- rma.mv(yi, vi,
                              mods= ~factor(studyType),
                              random= ~1 | paperID/obsID,
                              data=subdat, slab=as.character(obsID),
                              method='REML')
  res.Nfix[[i]]<- rma.mv(yi, vi,
                         mods= ~factor(Nfix),
                         random= ~1 | paperID/obsID,
                         data=subdat, slab=as.character(obsID),
                       method='REML')
  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 warrented
ANOVAParams<-function(fullMod, reducedMod){

  #do anova comparison
  #anova.comp<-anova(fullMod,reducedMod)
  QM<-fullMod$QM
  QMp<-fullMod$QMp

  #manually calculate the pseudo R2 values
  #compute the proportional reduction in the variance components as a sort of pseudo R-squared value
  pseudoR2.1<-(reducedMod$sigma2[1] - fullMod$sigma2[1]) / reducedMod$sigma2[1]
  pseudoR2.2<-(reducedMod$sigma2[2] - fullMod$sigma2[2]) / reducedMod$sigma2[2]
  pseudoR2.perc<-(sum(reducedMod$sigma2) - sum(fullMod$sigma2)) / sum(reducedMod$sigma2)
  anova.comp.df<-data.frame(QM=round(QM, digits=3),
                            QMp=round(QMp, digits=3),
                            pseudoR2.1=round(pseudoR2.1, digits=3), #pseudo R2 for the 1st sigma2
                            pseudoR2.2=round(pseudoR2.2, digits=3), #pseudo R2 for the 2nd sigma2
```

```
                            pseudoR2.perc=round(pseudoR2.perc, digits=3)
                            )
#    #put everything in a table
#    anova.comp.df<-data.frame(p.f=anova.comp$p.f, #number of parameters in the full model
#                             LRT=round(anova.comp$LRT, digits=3), #likelihood ratio statistic
#                             pval=round(anova.comp$pval, digits=3), #p-value for the likelihood ratio
#                             pseudoR2.1=round(pseudoR2.1, digits=3), #pseudo R2 for the 1st sigma2
#                             pseudoR2.2=round(pseudoR2.2, digits=3), #pseudo R2 for the 2nd sigma2
#                             pseudoR2.perc=round(pseudoR2.perc, digits=3) #the proportional reduction
#                             #)
  return(anova.comp.df)
}
i<-0
tmp.list<-list()
for(i in 1:length(MEASCAT)){

#    #reduced model parameters
#    p.r<-anova(res.quality[[i]], res[[i]])$p.r

  #full vs reduced model anova and extract params
  qualityA<-ANOVAParams(fullMod=res.quality[[i]], reducedMod=res[[i]])
  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

#    #add a column to hold the reduced model information
#    p.rCol<-rep(p.r, dim(tmpdf)[1])

  #save df
  tmp.list[[i]]<-data.frame(anovaLabels, tmpdf)


}
names(tmp.list)<-MEASCAT
anovaMods<-ldply(tmp.list)
anovaMods
```

```
##        .id anovaLabels     QM   QMp pseudoR2.1 pseudoR2.2 pseudoR2.perc
## 1       nh     qualityA  4.616 0.202      0.024      0.053         0.037
## 2       nh     ecosystA  6.644 0.084      0.213     -0.029         0.102
## 3       nh   studytypeA  5.654 0.130     -0.195      0.154        -0.034
## 4       nh        NfixA  1.308 0.727     -0.116     -0.040        -0.081
## 5       no     qualityA  3.193 0.363     -0.092      0.079        -0.064
## 6       no     ecosystA  5.536 0.137     -0.065      0.105        -0.037
## 7       no   studytypeA  9.909 0.019      0.250     -0.127         0.188
## 8       no        NfixA  7.007 0.072      0.245     -0.468         0.129
## 9     toti     qualityA  2.499 0.476     -0.035     -0.092        -0.043
## 10    toti     ecosystA  1.743 0.627      0.003     -0.133        -0.015
## 11    toti   studytypeA  4.361 0.225      0.015      0.117         0.028
## 12    toti        NfixA 11.043 0.011      0.060      0.042         0.058
## 13 ammonif     qualityA  2.193 0.533     -0.074     -0.078        -0.074
## 14 ammonif     ecosystA 10.199 0.017      0.454     -0.028         0.454
```

```
## 15 ammonif   studytypeA  2.480 0.479    -0.007    -0.081    -0.007
## 16 ammonif       NfixA  2.073 0.557    -0.166    -0.053    -0.166
## 17  nitrif     qualityA 10.244 0.017     0.052     0.411     0.052
## 18  nitrif     ecosystA  2.954 0.399    -0.150    -0.015    -0.150
## 19  nitrif    studytypeA  2.280 0.516   -0.317     0.409    -0.317
## 20  nitrif       NfixA  5.773 0.123     0.270    -0.129     0.270
## 21   nminz     qualityA  8.124 0.044     0.228    -0.031     0.188
## 22   nminz     ecosystA  0.806 0.848    -0.267    -0.052    -0.234
## 23   nminz    studytypeA  6.001 0.112   -0.051     0.324     0.006
## 24   nminz       NfixA  6.680 0.083     0.030     0.489     0.100
## 25   soiln     qualityA  2.973 0.396    -0.047    -0.012    -0.037
## 26   soiln     ecosystA 12.892 0.005    -0.208     0.281    -0.066
## 27   soiln    studytypeA  0.048 0.976   -0.061    -0.012    -0.047
## 28   soiln       NfixA 14.379 0.002    -0.039     0.282     0.054
## 29  soilcn     qualityA  3.999 0.262     0.002    -0.040     0.002
## 30  soilcn     ecosystA  4.061 0.255     0.053    -0.138     0.053
## 31  soilcn    studytypeA  3.024 0.221    0.055    -0.700     0.055
## 32  soilcn       NfixA 10.701 0.013     0.142     0.008     0.142
## 33     som     qualityA  7.884 0.019     0.292    -0.070     0.140
## 34     som     ecosystA  3.159 0.368    -0.093     0.007    -0.051
## 35     som    studytypeA  8.739 0.033    0.300     0.017     0.181
## 36     som       NfixA  2.548 0.467    -0.071    -0.011    -0.046
```

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

2Bi. Study type

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

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

```r
#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 0.0055
## 2   no     fs_er 0.0133
## 3   no     fs_gh 0.0038
## 4   no     ea_er 0.2746
## 5   no     ea_gh 0.4892
## 6   no     er_gh 0.5776
## 7  som     fs_ea 0.7719
## 8  som     fs_er 0.3242
## 9  som     fs_gh 0.0584
## 10 som     ea_er 0.4480
## 11 som     ea_gh 0.1627
## 12 som     er_gh 0.3131
```

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

```
##   .id          studyType1        pred        cilb      ciub        se   k
## 1  no          field study  0.29974513  0.10778312 0.4917071 0.0979416 103
## 2  no  field expt addition -0.51883831 -1.21491747 0.1772408 0.3551490   7
## 3  no   field expt removal -0.06825904 -0.48068864 0.3441706 0.2104271  16
## 4  no      greenhouse expt -0.24431313 -0.71211402 0.2234878 0.2386783  20
## 5 som          field study  0.36008507 -0.02406679 0.7442369 0.1959994  78
## 6 som  field expt addition  0.34726970 -2.05458477 2.7491242 1.2254585   1
## 7 som   field expt removal  1.38261898  0.20670798 2.5585300 0.5999656   6
## 8 som      greenhouse expt  2.37794642  0.84262514 3.9132677 0.7833416   4
```

```
#update effect size table for plotting
colnames(predR)[1]<-'MeasFac'
selectMeas<-unique(predR$MeasFac)
MeasFacl<-rev(levels(factor(MEASCAT[MEASCAT %in% selectMeas], levels=MEASCAT[MEASCAT %in% selectMeas])))
MeasNamesl<-rev(measTab[measTab$MEASCAT %in% selectMeas,'labels'])
colnames(predR)[2]<-'CAT'
CAT<-levels(dat$studyType)
predR$y<-NA
i<-0
for(i in 1:length(MeasFacl)){
```

```
  predR[predR$CAT==CAT[1] & predR$MeasFac==MeasFacl[i],'y']<-i+0.3
  predR[predR$CAT==CAT[2] & predR$MeasFac==MeasFacl[i],'y']<-i+0.1
  predR[predR$CAT==CAT[3] & predR$MeasFac==MeasFacl[i],'y']<-i-0.1
  predR[predR$CAT==CAT[4] & predR$MeasFac==MeasFacl[i],'y']<-i-0.3
}
predR
```

```
##   MeasFac                CAT        pred        cilb       ciub        se
## 1      no        field study  0.29974513  0.10778312 0.4917071 0.0979416
## 2      no field expt addition -0.51883831 -1.21491747 0.1772408 0.3551490
## 3      no  field expt removal -0.06825904 -0.48068864 0.3441706 0.2104271
## 4      no      greenhouse expt -0.24431313 -0.71211402 0.2234878 0.2386783
## 5     som        field study  0.36008507 -0.02406679 0.7442369 0.1959994
## 6     som field expt addition  0.34726970 -2.05458477 2.7491242 1.2254585
## 7     som  field expt removal  1.38261898  0.20670798 2.5585300 0.5999656
## 8     som      greenhouse expt  2.37794642  0.84262514 3.9132677 0.7833416
##     k   y
## 1 103 2.3
## 2   7 2.1
## 3  16 1.9
## 4  20 1.7
## 5  78 1.3
## 6   1 1.1
## 7   6 0.9
## 8   4 0.7
```

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

#assign pretty names and symbols
faclimits<-rev(c('Greenhouse study',
           'Field removal',
           'Field addition',
           'Field observation'))
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=2) +
  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=MeasNamesl) +
  scale_shape_manual(name="Study design",
                  labels=faclimits,
                  values=facShapes)+
  geom_text(aes(x=ciub, y=y, hjust=-0.3, vjust=0.5),size=2.2,show_guide = FALSE) +
```
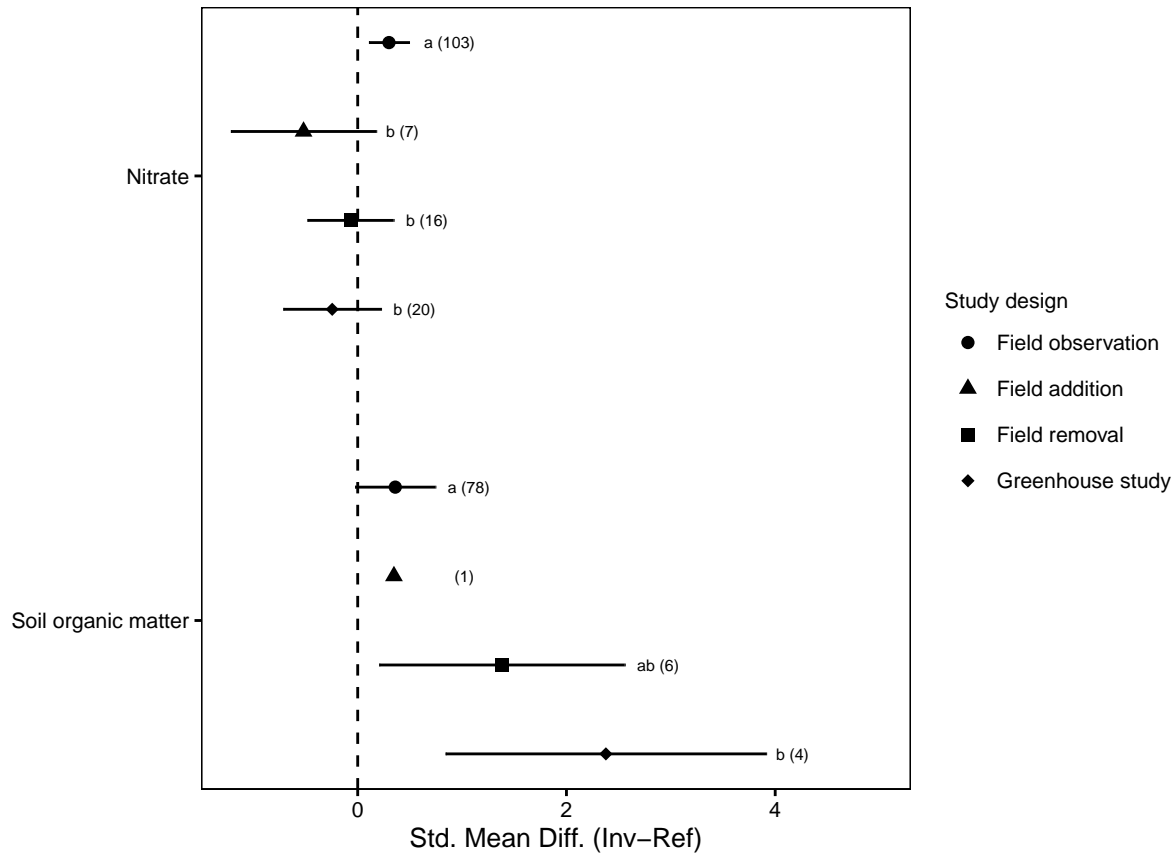
```
    annotate("text", x=1, y=1.1, label=' (1)', size=2.2)+ #manually add the posthoc letters and k here
    scale_x_continuous(expand=c(0,0), limits=c(-1.5,5.3)) +
    theme(legend.title=element_text(size=8))
stud.sp
```



```
#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*1.8, height = f
stud.sp
dev.off()
```

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

2Bii. Nfix status

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

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

```r
#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 0.0021
## 2     toti    none_i 0.6240
## 3     toti none_both 0.7769
## 4     toti       r_i 0.0017
## 5     toti    r_both 0.1378
## 6     toti    i_both 0.5473
## 7    soiln    none_r 0.3991
## 8    soiln    none_i 0.0354
## 9    soiln none_both 0.2588
## 10   soiln       r_i 0.2839
## 11   soiln    r_both 0.7766
## 12   soiln    i_both 0.4181
## 13  soilcn    none_r 0.0011
## 14  soilcn    none_i 0.2575
## 15  soilcn none_both 0.5161
## 16  soilcn       r_i 0.0174
## 17  soilcn    r_both 0.0135
## 18  soilcn    i_both 0.7055
```

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

```
##       .id                          Level         pred          cilb
## 1    toti                      No N-fixers  0.146246046 -0.067756563
## 2    toti          Resident N-fixers only -0.643704892 -1.161870005
## 3    toti          Invasive N-fixers only  0.436950103 -0.008218357
## 4    toti Invasive and resident N-fixers  0.148215167 -0.762828477
## 5   soiln                      No N-fixers  0.206021415 -0.085702267
## 6   soiln          Resident N-fixers only  0.771963352  0.172335981
## 7   soiln          Invasive N-fixers only  1.187337310  0.720806052
## 8   soiln Invasive and resident N-fixers  0.895860774  0.285475550
## 9  soilcn                      No N-fixers -0.180519873 -0.408598758
## 10 soilcn          Resident N-fixers only  0.929631290  0.300006755
## 11 soilcn          Invasive N-fixers only  0.002477821 -0.430919328
## 12 soilcn Invasive and resident N-fixers -0.124210622 -0.674450871
##          ciub        se    k
## 1   0.36024865 0.1091870 162
## 2  -0.12553978 0.2643748  14
## 3   0.88211856 0.2271309  14
## 4   1.05925881 0.4648267   3
## 5   0.49774510 0.1488413 120
## 6   1.37159072 0.3059380  19
## 7   1.65386857 0.2380305  29
## 8   1.50624600 0.3114268  18
## 9   0.04755901 0.1163689  69
## 10  1.55925582 0.3212429   8
## 11  0.43587497 0.2211251  14
## 12  0.42602963 0.2807400   7
```

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

```
##     MeasFac                          CAT         pred          cilb
## 1      toti                  No N-fixers  0.146246046 -0.067756563
## 2      toti          Resident N-fixers only -0.643704892 -1.161870005
## 3      toti          Invasive N-fixers only  0.436950103 -0.008218357
```

```
## 4     toti Invasive and resident N-fixers  0.148215167 -0.762828477
## 5    soiln                    No N-fixers  0.206021415 -0.085702267
## 6    soiln          Resident N-fixers only  0.771963352  0.172335981
## 7    soiln           Invasive N-fixers only  1.187337310  0.720806052
## 8    soiln Invasive and resident N-fixers  0.895860774  0.285475550
## 9   soilcn                    No N-fixers -0.180519873 -0.408598758
## 10  soilcn          Resident N-fixers only  0.929631290  0.300006755
## 11  soilcn           Invasive N-fixers only  0.002477821 -0.430919328
## 12  soilcn Invasive and resident N-fixers -0.124210622 -0.674450871
##          ciub        se   k   y
## 1   0.36024865 0.1091870 162 3.3
## 2  -0.12553978 0.2643748  14 3.1
## 3   0.88211856 0.2271309  14 2.9
## 4   1.05925881 0.4648267   3 2.7
## 5   0.49774510 0.1488413 120 2.3
## 6   1.37159072 0.3059380  19 2.1
## 7   1.65386857 0.2380305  29 1.9
## 8   1.50624600 0.3114268  18 1.7
## 9   0.04755901 0.1163689  69 1.3
## 10  1.55925582 0.3212429   8 1.1
## 11  0.43587497 0.2211251  14 0.9
## 12  0.42602963 0.2807400   7 0.7
```

```r
#assign post-hoc letters (order:field study, expt addition, expt removl, gh)
#subset(posthocR, .id=='litterbiom')
phTtoti<-c('b','a','b','ab')
phTsoiln<-c('a','ab','b','ab')
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
faclimits_new<-c('No N-fixers','Ref. community N-fixers only','Invasive sp. N-fixers only','Ref. and inv

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=MeasNamesl) +
  scale_shape_manual(name="N-fixing status",
                     labels=faclimits_new,
                     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))+
  theme(legend.title=element_text(size=8))
nfix.sp
```
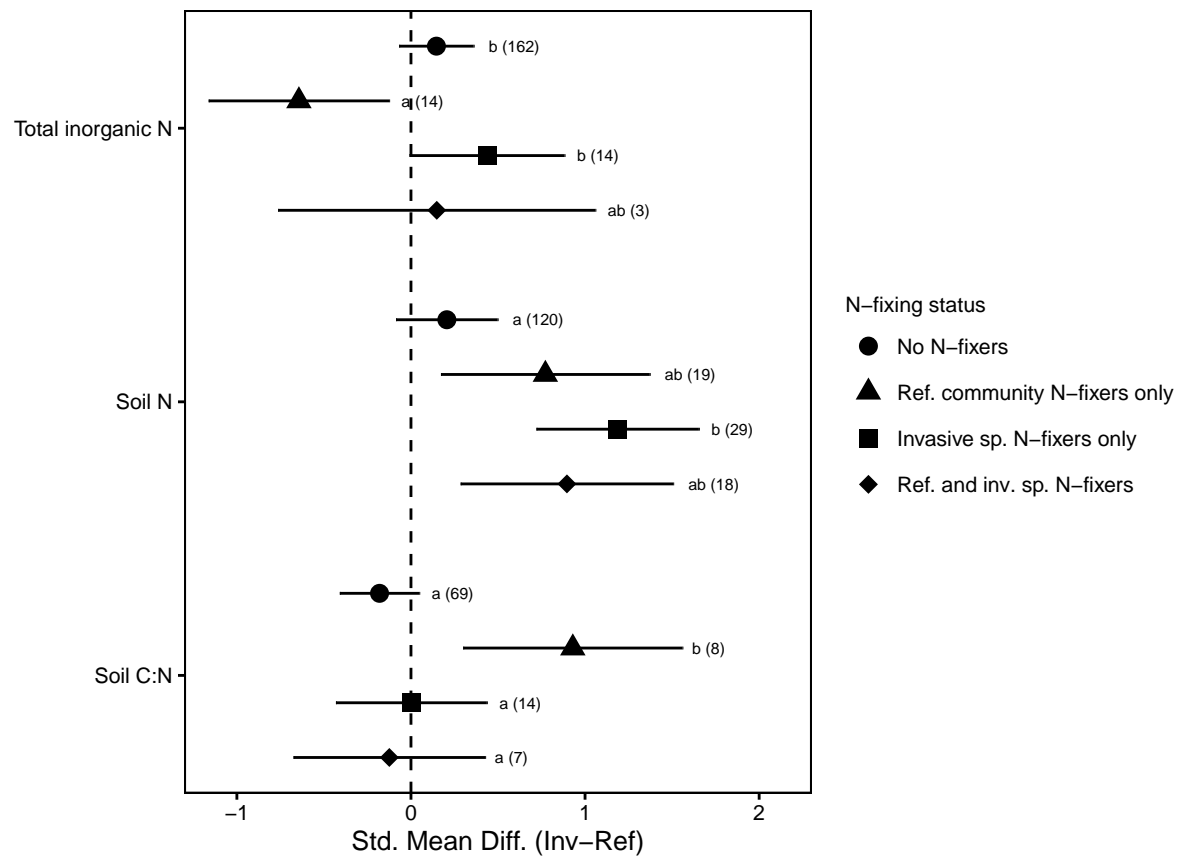
```
#theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))

newfilename<-"nfixForest.png"
png(paste(figuresPath,'modForests',newfilename, sep='/'), units='in', width = fig.width*2, height = fig
nfix.sp
dev.off()
```

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

2Biii. Quality

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

```
## character(0)
```

```
#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 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
```

```
#    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
#
# names(pred.list)<-currMeasFac
# predR<-ldply(pred.list)
# predR
#
# #update effect size table for plotting
# colnames(predR)[1]<-'MeasFac'
# selectMeas<-unique(predR$MeasFac)
# MeasFacl<-rev(levels(factor(MEASCAT[MEASCAT %in% selectMeas], levels=MEASCAT[MEASCAT %in% selectMeas]
# MeasNamesl<-rev(measTab[measTab$MEASCAT %in% selectMeas,'labels'])
```

```
# colnames(predR)[2]<-'CAT'
# CAT<-levels(dat$measQuality)
# predR$y<-NA
# i<-0
# for(i in 1:length(MeasFacl)){
#    predR[predR$CAT==CAT[1] & predR$MeasFac==MeasFacl[i],'y']<-i+0.3
#    predR[predR$CAT==CAT[2] & predR$MeasFac==MeasFacl[i],'y']<-i+0.1
#    predR[predR$CAT==CAT[3] & predR$MeasFac==MeasFacl[i],'y']<-i-0.1
#    predR[predR$CAT==CAT[4] & predR$MeasFac==MeasFacl[i],'y']<-i-0.3
# }
# predR
#
# #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=0.03
# 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(MeasFacl)),
#                       labels=MeasNamesl) +
#    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 = f
# qual.sp + theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))
# dev.off()
```

2Biv. Ecosystem type

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

```
## character(0)
```

```
# #levels(dat.tmp$ecosystCat) #check to make sure that this lines up with the way I organized the contr
# #Run post-hoc comparisions among Nfix levels, pull out means and CI
# i<-0
# posthoc.list<-list()
# pred.list<-list()
# for(i in 1:length(currMeasFac)){
#    #1. calc posthoc pvals
#    # forest, shrubland, grassland, wetland
#    posthocR<-anova(res.ecosyst[[currMeasFac[i]]],
#        L=rbind(c(1,-1,0,0), #forest vs shrub
#                c(1,0,-1,0), #forest vs grass
#                c(1,0,0,-1), #forest vs wet
#                c(0,1,-1,0), #shrub vs grass
#                c(0,1,0,-1), #shrub vs wet
#                c(0,0,1,-1) #grass vs wet
#                ))
#    levelcomp<-c('f_s','f_g','f_w',
#                      's_g','s_w',
#                          'g_w')
#    posthoc.list[[i]]<-data.frame(levelcomp, pval=round(posthocR$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$se)
#    ind.Fac<-ddply(dat.tmp, ~obsID, summarize, Level=unique(ecosystCat))
#    tmp1<-merge(tmp, ind.Fac)
#    tmp2<-ddply(tmp1, ~Level, summarize,
#          pred = unique(pred),
#          cilb = unique(cilb),
#          ciub = unique(ciub),
#          se = unique(se),
#          k = length(obsID))
#    pred.list[[i]]<-tmp2
#    }
# names(posthoc.list)<-currMeasFac
# posthocR<-ldply(posthoc.list)
# posthocR
#
# names(pred.list)<-currMeasFac
# predR<-ldply(pred.list)
# predR
#
# #update effect size table for plotting
# colnames(predR)[1]<-'MeasFac'
# selectMeas<-unique(predR$MeasFac)
# MeasFacl<-rev(levels(factor(MEASCAT[MEASCAT %in% selectMeas], levels=MEASCAT[MEASCAT %in% selectMeas]
# MeasNamesl<-rev(measTab[measTab$MEASCAT %in% selectMeas,'labels'])
# colnames(predR)[2]<-'CAT'
# CAT<-levels(dat.tmp$ecosystCat)
# predR$y<-NA
# i<-0
# for(i in 1:length(MeasFacl)){
#    predR[predR$CAT==CAT[1] & predR$MeasFac==MeasFacl[i],'y']<-i+0.3
#    predR[predR$CAT==CAT[2] & predR$MeasFac==MeasFacl[i],'y']<-i+0.1
```

```
#   predR[predR$CAT==CAT[3] & predR$MeasFac==MeasFacl[i],'y']<-i-0.1
#   predR[predR$CAT==CAT[4] & predR$MeasFac==MeasFacl[i],'y']<-i-0.3
# }
# predR
#
# #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(MeasFacl)),
#                      labels=MeasNamesl) +
#   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 =
# eco.sp + theme(axis.text.y=element_text(angle=90, hjust=0.5, size=10))
# dev.off()
```

---

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;

```
### update to include new calculation of pseudo R2
INVlist<-FitPlot(dat, k=1, qualColumn<-'InvSpInvArea_qualRank', colorN=5)
```

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

```
NATlist<-FitPlot(dat, k=2, qualColumn<-'NatArea_qualRank', colorN=5)
```

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

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

```r
DIFFlist<-FitPlot(dat, k=3, qualColumn<-'CWMDiff_qualRank', colorN=10)
```

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

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

```r
DIFF2list<-FitPlot(dat, k=4, qualColumn<-'CWMDiff2_qualRank', colorN=10)
```

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

```r
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]
DIFF2tab<-rbind(ldply(DIFF2list[['results']][['percN']]),
            ldply(DIFF2list[['results']][['litterpercN']]),
            ldply(DIFF2list[['results']][['cn']]),
            ldply(DIFF2list[['results']][['littercn']]))[,-1]


newfilename<-'INVtab.txt'
write.table(INVtab, file=paste(figuresPath,'allRegressionTable',newfilename, sep='/'), sep='\t', row.nam
newfilename<-'NATtab.txt'
write.table(NATtab, file=paste(figuresPath,'allRegressionTable',newfilename, sep='/'), sep='\t', row.nam
newfilename<-'DIFFtab.txt'
write.table(DIFFtab, file=paste(figuresPath,'allRegressionTable',newfilename, sep='/'), sep='\t', row.na
newfilename<-'DIFF2tab.txt'
write.table(DIFF2tab, file=paste(figuresPath,'allRegressionTable',newfilename, sep='/'), sep='\t', row.r


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

```
##           plantType   traitType measType studies   est pVal pseudoR2.1
## 7  InvSpInvArea_cwm      percN    soiln     170  0.34 0.00       0.00
## 8  InvSpInvArea_cwm      percN   soilcn      89 -0.20 0.04       0.14
## 17 InvSpInvArea_cwm litterpercN  soilcn      10 -0.46 0.05       1.00
## NA            <NA>        <NA>     <NA>      NA    NA   NA         NA
##    pseudoR2.2 pseudoR2.perc
## 7        0.25          0.06
## 8        0.82          0.14
## 17       1.00          1.00
## NA         NA           NA
```

```
INVlist[['qual']][['percN']][['soiln']] #trait quality has a marginal influence - studies with low qual
```

```
##
## Multivariate Meta-Analysis Model (k = 170; method: REML)
##
## Variance Components:
##
##            estim    sqrt  nlvls  fixed   factor
## sigma^2.1 0.7228  0.8502     72     no  paperID
## sigma^2.2 0.2639  0.5137    170     no    obsID
##
## Test for Residual Heterogeneity:
## QE(df = 168) = 562.4749, p-val < .0001
```

```
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 1.9167, p-val = 0.1662
##
## Model Results:
##
##          estimate      se     zval     pval     ci.lb    ci.ub
## intrcpt    1.0639   0.3762   2.8283   0.0047    0.3267   1.8012   **
## qual      -0.1585   0.1145  -1.3844   0.1662   -0.3830   0.0659
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

INVlist[['qual']][['percN']][['soilcn']]

```
##
## Multivariate Meta-Analysis Model (k = 89; method: REML)
##
## Variance Components:
##
##              estim    sqrt   nlvls   fixed    factor
## sigma^2.1   0.3112  0.5579      39      no   paperID
## sigma^2.2   0.0007  0.0266      89      no     obsID
##
## Test for Residual Heterogeneity:
## QE(df = 87) = 186.4902, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.0743, p-val = 0.7852
##
## Model Results:
##
##          estimate      se     zval     pval     ci.lb    ci.ub
## intrcpt   -0.1357   0.3175  -0.4273   0.6692   -0.7580   0.4867
## qual       0.0266   0.0977   0.2725   0.7852   -0.1648   0.2180
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

INVlist[['qual']][['litterpercN']][['soilcn']]

```
##
## Multivariate Meta-Analysis Model (k = 10; method: REML)
##
## Variance Components:
##
##              estim    sqrt   nlvls   fixed    factor
## sigma^2.1   0.2424  0.4923       6      no   paperID
## sigma^2.2   0.0000  0.0000      10      no     obsID
##
## Test for Residual Heterogeneity:
## QE(df = 8) = 12.6065, p-val = 0.1261
##
```

```
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 1.7322, p-val = 0.1881
##
## Model Results:
##
##           estimate      se     zval     pval    ci.lb   ci.ub
## intrcpt     0.6919  0.9334   0.7413   0.4585  -1.1375  2.5212
## qual       -0.4041  0.3070  -1.3161   0.1881  -1.0059  0.1977
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
##       plantType traitType measType studies   est  pVal pseudoR2.1 pseudoR2.2
## 24 NatArea_cwm        cn    nminz      46  0.02  0.01          0          1
## 26 NatArea_cwm        cn   soilcn      66 -0.02  0.00          0          1
##    pseudoR2.perc
## 24             0
## 26             0
```

```
NATlist[['qual']][['cn']][['nminz']]
```

```
##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.2296  0.4792     17     no   paperID
## sigma^2.2  0.0000  0.0001     46     no     obsID
##
## Test for Residual Heterogeneity:
## QE(df = 44) = 77.2734, p-val = 0.0014
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 2.5523, p-val = 0.1101
##
## Model Results:
##
##           estimate      se     zval     pval    ci.lb   ci.ub
## intrcpt    -0.2823  0.3783  -0.7462   0.4556  -1.0237  0.4592
## qual        0.1918  0.1201   1.5976   0.1101  -0.0435  0.4272
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
NATlist[['qual']][['cn']][['soilcn']]
```

```
##
## Multivariate Meta-Analysis Model (k = 66; method: REML)
##
```

```
## Variance Components:
##
##             estim   sqrt  nlvls  fixed   factor
## sigma^2.1  0.2195  0.4686    26     no   paperID
## sigma^2.2  0.0252  0.1589    66     no    obsID
##
## Test for Residual Heterogeneity:
## QE(df = 64) = 113.9193, p-val = 0.0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.5171, p-val = 0.4721
##
## Model Results:
##
##          estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt    0.2649  0.3377   0.7843  0.4329  -0.3971  0.9269
## qual      -0.0740  0.1029  -0.7191  0.4721  -0.2757  0.1277
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
##        plantType    traitType  measType  studies    est  pVal  pseudoR2.1
## 10  CWMDiff_cwm  litterpercN        nh       26   0.61  0.02        0.00
## 12  CWMDiff_cwm  litterpercN      toti       24   1.55  0.00        1.00
## 21  CWMDiff_cwm           cn      toti       70  -0.02  0.03        0.22
## 24  CWMDiff_cwm           cn     nminz       46  -0.03  0.00        0.00
## 26  CWMDiff_cwm           cn    soilcn       66   0.03  0.00        0.00
## 28  CWMDiff_cwm     littercn        nh       17  -0.02  0.09        0.23
## 30  CWMDiff_cwm     littercn      toti       23  -0.02  0.00        0.59
## 33  CWMDiff_cwm     littercn     nminz       22  -0.01  0.06        0.42
##     pseudoR2.2  pseudoR2.perc
## 10        0.94           0.45
## 12        0.63           1.00
## 21        0.00           0.22
## 24        1.00           0.00
## 26        1.00           0.04
## 28        0.15           0.15
## 30        0.52           0.59
## 33        0.00           0.42
```

```
DIFFlist[['qual']][['litterpercN']][['nh']]
```

```
##
## Multivariate Meta-Analysis Model (k = 26; method: REML)
##
## Variance Components:
##
##             estim   sqrt  nlvls  fixed   factor
## sigma^2.1  0.0779  0.2791    16     no   paperID
## sigma^2.2  0.0455  0.2134    26     no    obsID
##
```

```
## Test for Residual Heterogeneity:
## QE(df = 24) = 35.3580, p-val = 0.0633
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.6290, p-val = 0.4277
##
## Model Results:
##
##          estimate      se    zval    pval    ci.lb   ci.ub
## intrcpt    0.1325  0.4202  0.3153  0.7525  -0.6911  0.9561
## qual       0.0548  0.0691  0.7931  0.4277  -0.0806  0.1901
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFFlist[['qual']][['litterpercN']][['toti']]

```
##
## Multivariate Meta-Analysis Model (k = 24; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed   factor
## sigma^2.1  0.8126  0.9014     13     no  paperID
## sigma^2.2  0.0000  0.0000     24     no    obsID
##
## Test for Residual Heterogeneity:
## QE(df = 22) = 61.9410, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.0107, p-val = 0.9174
##
## Model Results:
##
##          estimate      se    zval    pval    ci.lb   ci.ub
## intrcpt    0.5642  0.8175  0.6902  0.4901  -1.0381  2.1666
## qual       0.0144  0.1389  0.1037  0.9174  -0.2579  0.2867
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFFlist[['qual']][['cn']][['toti']] *#trait quality has a marginal influence - studies with low quality*

```
##
## Multivariate Meta-Analysis Model (k = 70; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed   factor
## sigma^2.1  0.2102  0.4585     28     no  paperID
## sigma^2.2  0.0000  0.0000     70     no    obsID
##
## Test for Residual Heterogeneity:
```

```
## QE(df = 68) = 116.6071, p-val = 0.0002
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.1285, p-val = 0.7200
##
## Model Results:
##
##          estimate      se     zval     pval    ci.lb   ci.ub
## intrcpt    0.1137  0.2722   0.4176   0.6762  -0.4198  0.6471
## qual      -0.0203  0.0567  -0.3585   0.7200  -0.1314  0.0908
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFFlist[['qual']][['cn']][['nminz']]

```
##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.2203  0.4694     17     no   paperID
## sigma^2.2  0.0143  0.1194     46     no     obsID
##
## Test for Residual Heterogeneity:
## QE(df = 44) = 79.4231, p-val = 0.0008
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 1.1291, p-val = 0.2880
##
## Model Results:
##
##          estimate      se     zval     pval    ci.lb   ci.ub
## intrcpt   -0.1132  0.3905  -0.2899   0.7719  -0.8786  0.6522
## qual       0.0801  0.0754   1.0626   0.2880  -0.0676  0.2278
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFFlist[['qual']][['cn']][['soilcn']]

```
##
## Multivariate Meta-Analysis Model (k = 66; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.2162  0.4650     26     no   paperID
## sigma^2.2  0.0256  0.1601     66     no     obsID
##
## Test for Residual Heterogeneity:
## QE(df = 64) = 114.1358, p-val = 0.0001
```

```
## 
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.0529, p-val = 0.8181
## 
## Model Results:
## 
##           estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt     0.1121  0.3413   0.3284  0.7426  -0.5568  0.7809
## qual       -0.0144  0.0625  -0.2300  0.8181  -0.1370  0.1082
## 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFFlist[['qual']][['littercn']][['nh']]

```
## 
## Multivariate Meta-Analysis Model (k = 17; method: REML)
## 
## Variance Components:
## 
##             estim    sqrt  nlvls  fixed   factor
## sigma^2.1  0.0000  0.0001     12     no  paperID
## sigma^2.2  0.4926  0.7019     17     no    obsID
## 
## Test for Residual Heterogeneity:
## QE(df = 15) = 31.0951, p-val = 0.0085
## 
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.0004, p-val = 0.9831
## 
## Model Results:
## 
##           estimate      se    zval    pval    ci.lb   ci.ub
## intrcpt     0.3122  0.7223  0.4322  0.6656  -1.1035  1.7280
## qual        0.0024  0.1115  0.0211  0.9831  -0.2162  0.2209
## 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFFlist[['qual']][['littercn']][['toti']]

```
## 
## Multivariate Meta-Analysis Model (k = 23; method: REML)
## 
## Variance Components:
## 
##             estim    sqrt  nlvls  fixed   factor
## sigma^2.1  0.7731  0.8792     14     no  paperID
## sigma^2.2  0.0000  0.0000     23     no    obsID
## 
## Test for Residual Heterogeneity:
## QE(df = 21) = 62.6574, p-val < .0001
## 
```

```
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 1.0136, p-val = 0.3140
##
## Model Results:
##
##          estimate      se     zval     pval     ci.lb    ci.ub
## intrcpt   -0.4403   0.8972  -0.4908   0.6236   -2.1988   1.3181
## qual       0.1437   0.1428   1.0068   0.3140   -0.1361   0.4235
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFFlist[['qual']][['littercn']][['nminz']]

```
##
## Multivariate Meta-Analysis Model (k = 22; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed   factor
## sigma^2.1  0.4964  0.7046     12     no  paperID
## sigma^2.2  0.0000  0.0000     22     no    obsID
##
## Test for Residual Heterogeneity:
## QE(df = 20) = 31.3104, p-val = 0.0512
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.0660, p-val = 0.7972
##
## Model Results:
##
##          estimate      se     zval     pval     ci.lb    ci.ub
## intrcpt    0.4878   0.8300   0.5877   0.5568   -1.1391   2.1146
## qual      -0.0345   0.1343  -0.2569   0.7972   -0.2977   0.2287
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFF2tab[DIFF2tab$pVal <0.1 & DIFF2tab$measType %in% MEASCAT,]

```
##       plantType    traitType  measType  studies    est   pVal  pseudoR2.1
## 1  CWMDiff2_cwm        percN        nh      111   0.22   0.04        0.00
## 17 CWMDiff2_cwm  litterpercN    soilcn        8  -0.52   0.03        1.00
## 19 CWMDiff2_cwm           cn        nh       47  -0.01   0.08        1.00
## 24 CWMDiff2_cwm           cn     nminz       43  -0.04   0.00        0.00
## 26 CWMDiff2_cwm           cn    soilcn       62   0.02   0.00        0.23
## 28 CWMDiff2_cwm     littercn        nh       11  -0.02   0.08        0.55
## 30 CWMDiff2_cwm     littercn      toti       14  -0.01   0.04        0.00
## NA         <NA>         <NA>      <NA>       NA     NA     NA          NA
##    pseudoR2.2 pseudoR2.perc
## 1        0.04          0.00
## 17       1.00          1.00
## 19       0.00          0.11
```

```
## 24          1.00              0.00
## 26          1.00              0.25
## 28          0.19              0.19
## 30          0.61              0.00
## NA            NA                NA
```

DIFF2list[['qual']][['percN']][['nh']] *#trait quality has a marginal influence - studies with low quali*

```
##
## Multivariate Meta-Analysis Model (k = 111; method: REML)
##
## Variance Components:
##
##            estim    sqrt  nlvls  fixed   factor
## sigma^2.1  0.1276  0.3573     54     no  paperID
## sigma^2.2  0.1366  0.3696    111     no    obsID
##
## Test for Residual Heterogeneity:
## QE(df = 109) = 271.9014, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.0251, p-val = 0.8740
##
## Model Results:
##
##          estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt    0.3367  0.2639   1.2757  0.2021  -0.1806  0.8539
## qual      -0.0082  0.0515  -0.1585  0.8740  -0.1091  0.0928
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFF2list[['qual']][['litterpercN']][['soilcn']]

```
##
## Multivariate Meta-Analysis Model (k = 8; method: REML)
##
## Variance Components:
##
##            estim    sqrt  nlvls  fixed   factor
## sigma^2.1  0.6818  0.8257      5     no  paperID
## sigma^2.2  0.0000  0.0000      8     no    obsID
##
## Test for Residual Heterogeneity:
## QE(df = 6) = 12.4730, p-val = 0.0522
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.8291, p-val = 0.3625
##
## Model Results:
##
##          estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt    0.5695  1.4772   0.3856  0.6998  -2.3257  3.4648
```

```
## qual       -0.2428   0.2666  -0.9106   0.3625  -0.7653   0.2798
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFF2list[['qual']][['cn']][['nh']] *# trait quality has a influence - studies with low quality trait da*

```
##
## Multivariate Meta-Analysis Model (k = 47; method: REML)
##
## Variance Components:
##
##            estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0000  0.0000     26     no   paperID
## sigma^2.2  0.1400  0.3742     47     no     obsID
##
## Test for Residual Heterogeneity:
## QE(df = 45) = 74.7853, p-val = 0.0035
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 4.5431, p-val = 0.0331
##
## Model Results:
##
##          estimate      se    zval    pval   ci.lb   ci.ub
## intrcpt    0.5987  0.2237  2.6764  0.0074  0.1603  1.0371  **
## qual      -0.0972  0.0456 -2.1315  0.0331 -0.1866 -0.0078   *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

DIFF2list[['qual']][['cn']][['nminz']]

```
##
## Multivariate Meta-Analysis Model (k = 43; method: REML)
##
## Variance Components:
##
##            estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.1841  0.4290     15     no   paperID
## sigma^2.2  0.0295  0.1717     43     no     obsID
##
## Test for Residual Heterogeneity:
## QE(df = 41) = 73.2892, p-val = 0.0014
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.1208, p-val = 0.7281
##
## Model Results:
##
##          estimate      se    zval    pval   ci.lb   ci.ub
## intrcpt    0.0600  0.4112  0.1460  0.8839 -0.7458  0.8659
## qual       0.0303  0.0873  0.3476  0.7281 -0.1407  0.2014
```

```
## 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
DIFF2list[['qual']][['cn']][['soilcn']]
```

```
## 
## Multivariate Meta-Analysis Model (k = 62; method: REML)
## 
## Variance Components:
## 
##             estim    sqrt   nlvls  fixed   factor
## sigma^2.1  0.2316  0.4813      23     no   paperID
## sigma^2.2  0.0048  0.0690      62     no     obsID
## 
## Test for Residual Heterogeneity:
## QE(df = 60) = 100.0343, p-val = 0.0009
## 
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.0512, p-val = 0.8211
## 
## Model Results:
## 
##           estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt     0.1050  0.3817   0.2752  0.7832  -0.6431  0.8532
## qual       -0.0169  0.0748  -0.2262  0.8211  -0.1636  0.1297
## 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
DIFF2list[['qual']][['littercn']][['nh']]
```

```
## 
## Multivariate Meta-Analysis Model (k = 11; method: REML)
## 
## Variance Components:
## 
##             estim    sqrt   nlvls  fixed   factor
## sigma^2.1  0.0000  0.0001       9     no   paperID
## sigma^2.2  0.7775  0.8817      11     no     obsID
## 
## Test for Residual Heterogeneity:
## QE(df = 9) = 24.0768, p-val = 0.0042
## 
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.8298, p-val = 0.3623
## 
## Model Results:
## 
##           estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt    -0.5529  1.2127  -0.4559  0.6484  -2.9297  1.8239
## qual        0.1917  0.2105   0.9110  0.3623  -0.2208  0.6043
## 
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
DIFF2list[['qual']][['littercn']][['toti']]
```

```
##
## Multivariate Meta-Analysis Model (k = 14; method: REML)
##
## Variance Components:
##
##            estim    sqrt  nlvls  fixed   factor
## sigma^2.1  0.1586  0.3983     10     no  paperID
## sigma^2.2  0.0000  0.0000     14     no    obsID
##
## Test for Residual Heterogeneity:
## QE(df = 12) = 17.6772, p-val = 0.1258
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.5176, p-val = 0.4718
##
## Model Results:
##
##          estimate      se     zval     pval    ci.lb   ci.ub
## intrcpt   -0.2580  0.7662  -0.3368   0.7363  -1.7597  1.2436
## qual       0.1044  0.1451   0.7195   0.4718  -0.1799  0.3887
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

3B. Plot some/all of the regressions 3Bi. Loop through all plots: 1 page per trait type x community with 9 ES panels

```
#plot notes:
#predicted values calculated based on only the fixed effects
#ci = 95% confidence interval on the fixed effect coefficients

#add panel labels
INVlist1<-AddPanelTitles(INVlist)
NATlist1<-AddPanelTitles(NATlist)
DIFFlist1<-AddPanelTitles(DIFFlist)
DIFF2list1<-AddPanelTitles(DIFF2list)

#plot and save
PLANTlist<-list(INVlist1, NATlist1, DIFFlist1, DIFF2list1)
PLANTlabel<-c('INV','NAT','DIFF','DIFF2')
xlabel.PlantText<-c('Invasive species','Reference area','Invaded - Reference area','Inv Sp. - Reference
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()

  }
}
```

a. Invasive sp. traits

```
newfilename<-"INVreg.png"
png(paste(figuresPath,newfilename, sep='/'), units='in', width = fig.width*1.8, height = fig.height*1.75
grid.arrange(
  INVlist[['figures']][['percN']][['soiln']] +
    xlab('Invasive sp. leaf %N') + ylab('Soil N effect size') + ggtitle('a'),
  INVlist[['figures']][['percN']][['soilcn']] +
    xlab('Invasive sp. Leaf %N') + ylab('Soil C:N effect size') + ggtitle('b'),
  INVlist[['figures']][['litterpercN']][['soilcn']] +
    xlab('Invasive sp. Litter %N') + ylab('Soil C:N effect size') + ggtitle('c'),
  ncol=2
)
dev.off()


## pdf
##   2

#small points have large variance
#large points have small variance
```

b. Reference traits

```
newfilename<-"NATreg.png"
png(paste(figuresPath,newfilename, sep='/'), units='in', width = fig.width*1.8, height = fig.height*.88
grid.arrange(
  NATlist[['figures']][['cn']][['nminz']] +
    xlab('Ref. CWM leaf C:N') + ylab('Mineralization effect size') + ggtitle('a'),
  NATlist[['figures']][['cn']][['soilcn']] +
    xlab('Ref. CWM leaf C:N') + ylab('Soil C:N effect size') + ggtitle('b'),
```

```
  ncol=2
)
dev.off()
```

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

```
#small points have large variance
#large points have small variance
```

c. Trait dissimilarity - invaded and reference areas

```
newfilename<-"DIFFreg.png"
png(paste(figuresPath,newfilename, sep='/'), units='in', width = fig.width*1.8, height = fig.height*3.5
grid.arrange(
  DIFFlist[['figures']][['litterpercN']][['nh']] +
    xlab('Inv.-Ref. CWM litter %N') + ylab('Ammonium effect size') + ggtitle('a'),
  DIFFlist[['figures']][['litterpercN']][['toti']] +
    xlab('Inv.-Ref. CWM litter %N') + ylab('Total inorg. N effect size') + ggtitle('b'),
  DIFFlist[['figures']][['littercn']][['nh']] +
    xlab('Inv.-Ref. CWM litter C:N') + ylab('Ammonium effect size') + ggtitle('c'),
  DIFFlist[['figures']][['littercn']][['toti']] +
    xlab('Inv.-Ref. CWM litter C:N') + ylab('Total inorg. N effect size') + ggtitle('d'),
  DIFFlist[['figures']][['littercn']][['nminz']] +
    xlab('Inv.-Ref. CWM litter C:N') + ylab('Mineralization effect size') + ggtitle('e'),
  DIFFlist[['figures']][['cn']][['toti']] +
    xlab('Inv.-Ref. CWM leaf C:N') + ylab('Total inorg. N effect size') + ggtitle('f'),
  DIFFlist[['figures']][['cn']][['nminz']] +
    xlab('Inv.-Ref. CWM leaf C:N') + ylab('Mineralization effect size') + ggtitle('g'),
  DIFFlist[['figures']][['cn']][['soilcn']] +
    xlab('Inv.-Ref. CWM leaf C:N') + ylab('Soil C:N effect size') + ggtitle('h'),
  ncol=2
)
dev.off()
```

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

```
#small points have large variance
#large points have small variance
```

d. Trait dissimilarity - comparison of plots

```
newfilename<-"DIFF2reg_compare.png"
png(paste(figuresPath,newfilename, sep='/'), units='in', width = fig.width*1.8, height = fig.height*3.5

grid.arrange(

  arrangeGrob(
    DIFFlist[['figures']][['littercn']][['nh']] + ggtitle('a'),
    DIFF2list[['figures']][['littercn']][['nh']] + ggtitle('b'),
```

```
    DIFFlist[['figures']][['littercn']][['toti']] + ggtitle('c'),
    DIFF2list[['figures']][['littercn']][['toti']] + ggtitle('d'),

    DIFFlist[['figures']][['cn']][['nminz']] + ggtitle('e'),
    DIFF2list[['figures']][['cn']][['nminz']] + ggtitle('f'),

    DIFFlist[['figures']][['cn']][['soilcn']] + ggtitle('g'),
    DIFF2list[['figures']][['cn']][['soilcn']] + ggtitle('h'),
    ncol=2
  ),
  left=textGrob('     Soil C:N ES          Mineralization ES          Total inorg. N ES          Amm
  bottom=textGrob('Inv.-Ref. CWM leaf C:N                    Inv Sp.- Ref leaf C:N', rot=0, vjust=0)

)

dev.off()
```

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

```
#small points have large variance
#large points have small variance
```