Micro food web

knitr::opts\_knit$set(root.dir = "D:/Knowledge-based/BISE/meta-bio-net/Bionet\_V2/")  
knitr::opts\_knit$set(warning = FALSE, include=FALSE)

#### Setting global parameters

#### Load KB

taxo=read.csv2(file\_taxo)  
tg=read.csv2(file\_tg)  
tg\_fw=read.csv2(file\_tg\_fw)  
  
taxo\_tg=merge(tg,taxo,by.x="scientificName",by.y="verbatimScientificName")[taxa\_attributes]  
rm(taxo)  
rm(tg)  
  
taxo\_tg$surf=rep(1,dim(taxo\_tg)[1])  
taxo\_tg$subsurf=rep(1,dim(taxo\_tg)[1])  
taxo\_tg$soil=rep(1,dim(taxo\_tg)[1])

#### Generate taxa-level KB

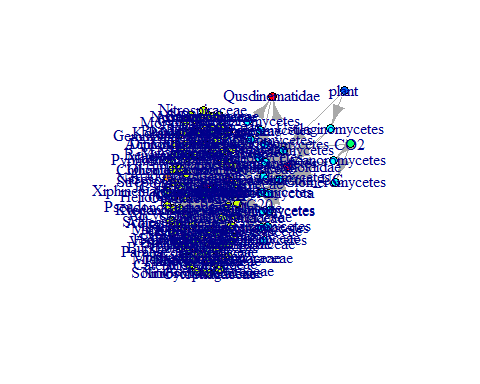
consumers=merge(tg\_fw,taxo\_tg[c("scientificName","key","trophicGroup")],by.x="consumer\_TG",by.y="trophicGroup")  
taxa\_fw=merge(consumers,taxo\_tg[c("scientificName","key","trophicGroup")],by.x="resource\_TG",by.y="trophicGroup",suffixes = c("\_consumer","\_resource"))  
  
taxa\_fw$cooccur<-rep(1,dim(taxa\_fw)[1])  
write.csv2(taxa\_fw,"metafoodweb.csv")  
rm(consumers)  
  
taxa\_metadata<-unique(taxo\_tg[,-2])

#### Creating metanetwork

taxa\_nodes=apply(taxa\_metadata,1, function(x){  
 microhab=list(surf=x["surf"],subsurf=x["subsurf"],soil=x["soil"])  
 node=Taxon$new(gbif\_id=as.character(x['key']),  
 label = as.character(x['scientificName']),  
 broad=as.character(x['kingdom']),  
 rank=as.character(x['rank']),  
 microhab=microhab)  
 })  
  
metaweb=MetaWeb$new(  
 mwebname="microfoodweb", taxa=taxa\_nodes, edge\_list=taxa\_fw[,edge\_ends\_taxa],   
 edge\_metadata=taxa\_fw[,edge\_attributes],res\_name="key\_resource",cons\_name="key\_consumer",type="interaction\_type",cooccur="cooccur")  
  
metaweb$print()

## Metaweb:   
## Name: microfoodweb  
## Network statistics:   
## Number of taxa: 117  
## Number of interactions: 797  
## Connectivity: 0.05872384

g=metaweb$graph  
plot(g,  
 vertex.label=V(g)$scName,  
 vertex.color=rainbow(10)[as.factor(V(g)$broad)],  
 vertex.size=10,  
 plot.layout=layout\_as\_tree)



#### Load data

occur=merge(subset(read.csv2(file\_occur),(ScientificName %in% taxa\_metadata$scientificName)),taxa\_metadata[c("key","scientificName")],by.x="ScientificName",by.y="scientificName")  
design=read.csv2(file\_design)  
pt\_names=as.character(design[,lev])

### Creating local networks

subnets=lapply(as.vector(pt\_names), function(x){  
 community\_compos=as.character(occur[which(occur[,x]>=min\_occur),"key"])  
 subnetwork=metaweb$project\_metanetwork(sublist\_taxa\_keys = community\_compos,net\_name = x,verbose=verb)   
 return(subnetwork)  
 })

## Projected trophic web:   
## Name: P1  
## Network statistics:   
## Number of taxa: 100  
## Number of interactions: 669  
## Connectivity: 0.06757576   
## Projected trophic web:   
## Name: P2  
## Network statistics:   
## Number of taxa: 99  
## Number of interactions: 675  
## Connectivity: 0.06957328   
## Projected trophic web:   
## Name: P3  
## Network statistics:   
## Number of taxa: 94  
## Number of interactions: 625  
## Connectivity: 0.07149394   
## Projected trophic web:   
## Name: P4  
## Network statistics:   
## Number of taxa: 90  
## Number of interactions: 472  
## Connectivity: 0.05892634   
## Projected trophic web:   
## Name: P5  
## Network statistics:   
## Number of taxa: 92  
## Number of interactions: 550  
## Connectivity: 0.06569517   
## Projected trophic web:   
## Name: P6  
## Network statistics:   
## Number of taxa: 89  
## Number of interactions: 470  
## Connectivity: 0.06001021   
## Projected trophic web:   
## Name: P7  
## Network statistics:   
## Number of taxa: 97  
## Number of interactions: 653  
## Connectivity: 0.07012457   
## Projected trophic web:   
## Name: P8  
## Network statistics:   
## Number of taxa: 100  
## Number of interactions: 674  
## Connectivity: 0.06808081   
## Projected trophic web:   
## Name: P9  
## Network statistics:   
## Number of taxa: 95  
## Number of interactions: 616  
## Connectivity: 0.06898096   
## Projected trophic web:   
## Name: P10  
## Network statistics:   
## Number of taxa: 106  
## Number of interactions: 635  
## Connectivity: 0.05705301   
## Projected trophic web:   
## Name: P11  
## Network statistics:   
## Number of taxa: 104  
## Number of interactions: 707  
## Connectivity: 0.06600075   
## Projected trophic web:   
## Name: P12  
## Network statistics:   
## Number of taxa: 105  
## Number of interactions: 714  
## Connectivity: 0.06538462   
## Projected trophic web:   
## Name: P13  
## Network statistics:   
## Number of taxa: 89  
## Number of interactions: 585  
## Connectivity: 0.07469356   
## Projected trophic web:   
## Name: P14  
## Network statistics:   
## Number of taxa: 94  
## Number of interactions: 625  
## Connectivity: 0.07149394   
## Projected trophic web:   
## Name: P15  
## Network statistics:   
## Number of taxa: 98  
## Number of interactions: 657  
## Connectivity: 0.06911424   
## Projected trophic web:   
## Name: P16  
## Network statistics:   
## Number of taxa: 103  
## Number of interactions: 693  
## Connectivity: 0.06596231   
## Projected trophic web:   
## Name: P17  
## Network statistics:   
## Number of taxa: 100  
## Number of interactions: 665  
## Connectivity: 0.06717172   
## Projected trophic web:   
## Name: P18  
## Network statistics:   
## Number of taxa: 101  
## Number of interactions: 690  
## Connectivity: 0.06831683   
## Projected trophic web:   
## Name: P19  
## Network statistics:   
## Number of taxa: 102  
## Number of interactions: 699  
## Connectivity: 0.0678509   
## Projected trophic web:   
## Name: P20  
## Network statistics:   
## Number of taxa: 103  
## Number of interactions: 685  
## Connectivity: 0.06520084   
## Projected trophic web:   
## Name: P21  
## Network statistics:   
## Number of taxa: 101  
## Number of interactions: 667  
## Connectivity: 0.0660396   
## Projected trophic web:   
## Name: P22  
## Network statistics:   
## Number of taxa: 104  
## Number of interactions: 706  
## Connectivity: 0.06590739   
## Projected trophic web:   
## Name: P23  
## Network statistics:   
## Number of taxa: 107  
## Number of interactions: 733  
## Connectivity: 0.06462705   
## Projected trophic web:   
## Name: P24  
## Network statistics:   
## Number of taxa: 105  
## Number of interactions: 705  
## Connectivity: 0.06456044   
## Projected trophic web:   
## Name: P25  
## Network statistics:   
## Number of taxa: 103  
## Number of interactions: 698  
## Connectivity: 0.06643823   
## Projected trophic web:   
## Name: P26  
## Network statistics:   
## Number of taxa: 97  
## Number of interactions: 649  
## Connectivity: 0.06969502   
## Projected trophic web:   
## Name: P27  
## Network statistics:   
## Number of taxa: 105  
## Number of interactions: 714  
## Connectivity: 0.06538462   
## Projected trophic web:   
## Name: P28  
## Network statistics:   
## Number of taxa: 99  
## Number of interactions: 669  
## Connectivity: 0.06895485   
## Projected trophic web:   
## Name: P29  
## Network statistics:   
## Number of taxa: 104  
## Number of interactions: 687  
## Connectivity: 0.06413368   
## Projected trophic web:   
## Name: P30  
## Network statistics:   
## Number of taxa: 105  
## Number of interactions: 699  
## Connectivity: 0.06401099

#### Compute alpha metrics on the metaweb and local networks

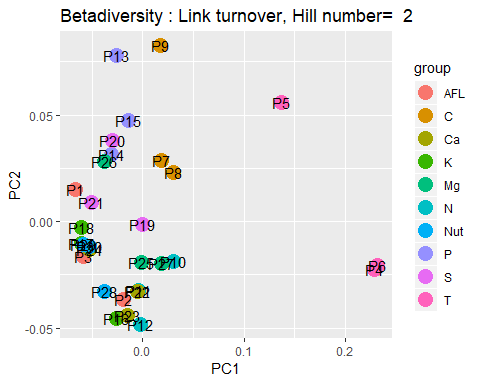
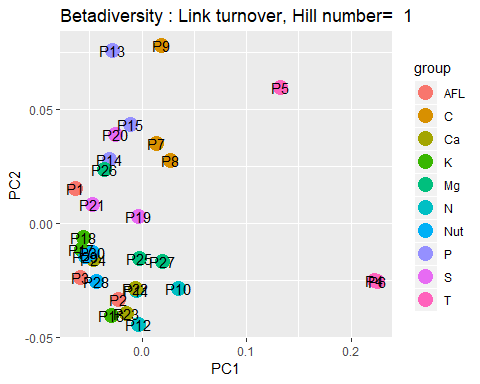
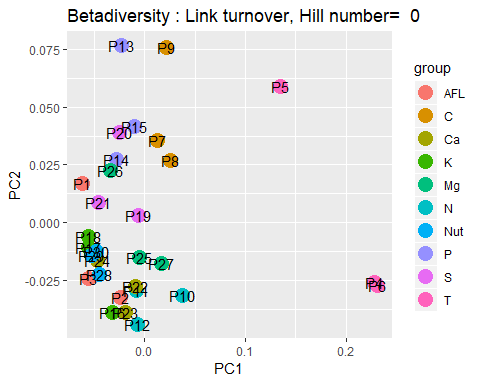
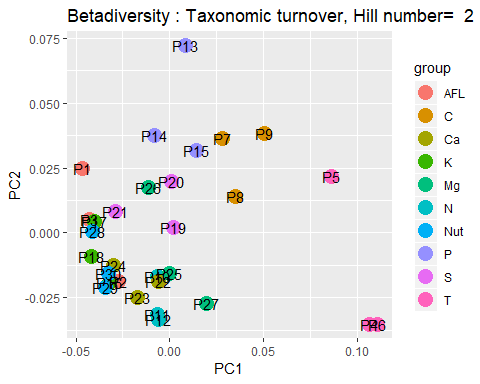
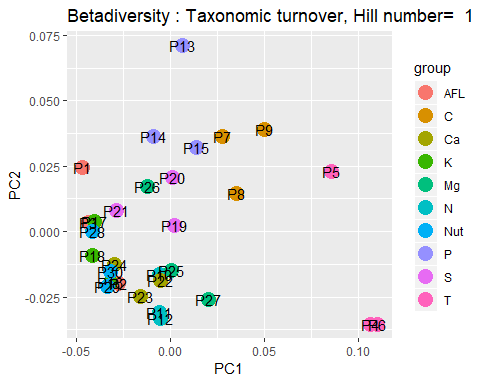
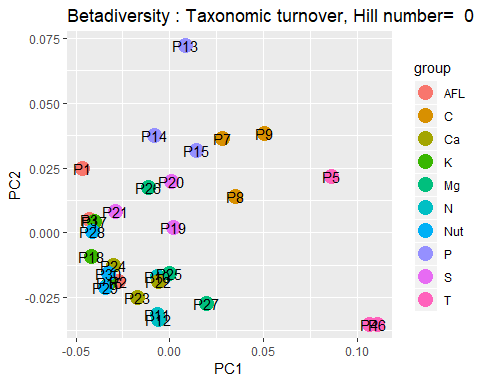
broad\_light=c("plant")  
broad\_som=c("SOM")  
  
broad\_fungi=c("Fungi")  
broad\_bacteria=c("Bacteria","Archaea")  
  
att="broad"  
scNames\_opp=c()  
scNames\_min=c()  
  
topoenerg\_metrics=lapply(subnets,topoenergetic\_metrics)  
topoenerg\_metrics[[length(topoenerg\_metrics)+1]]=topoenergetic\_metrics(metaweb$graph)  
  
topometrics\_df=do.call(rbind,lapply(topoenerg\_metrics, as.data.frame))  
topometrics\_df$observation\_id=c(as.character(design$Pot),"metaweb")  
write.csv2(topometrics\_df,outfile\_metrics)

#### Compute betadiversity between plots

eta=c(0,1,2)  
div=c('P','L')  
labdiv=c('Taxonomic','Link')  
names(labdiv)=div  
groups=as.character(design$Trt)  
  
params=vector(mode="list",length=length(eta)\*length(div))  
cpt=1  
for(d in div) for (e in eta){  
 params[[cpt]]=list(e=e,d=d)  
 cpt=cpt+1  
}   
  
beta\_list=lapply(1:length(params),function(x){  
 betadivdf=betanet(gList=subnets,groups=NULL,  
 file\_beta =   
 paste(outfile\_beta,params[[x]]$e,"\_",params[[x]]$d,".csv",sep=""),  
 pt\_names = pt\_names,div=params[[x]]$d,eta=params[[x]]$e)  
   
 return(betadivdf)  
})

## PCOA of betadiversity between plots

pcoa\_list=lapply(1:length(params), function(x) {  
 pcoa=pcoa\_plot(D=as.dist(beta\_list[[x]]),Y=NULL,  
 corr="none",groups=groups,  
 title=paste(  
 "Betadiversity :",labdiv[params[[x]]$d],  
 "turnover, Hill number= ",params[[x]]$e))  
   
 print(pcoa$plot)  
   
})



#### Functional redundancy within plots

###Occurrence of groups  
occur\_tg=merge(taxo\_tg,occur,by="key")  
func\_redund=aggregate(x=occur\_tg[,as.character(design$Pot)],  
 FUN = sum,by = list(TG=occur\_tg$trophicGroup))  
  
write.csv2(func\_redund,outfile\_fredund)  
  
fct\_div=redund\_fct(func\_redund,as.character(design$Pot))  
write.csv2(fct\_div,outfile\_fdiv)