**caf.R**

don<-as.matrix(filename)

nbrrel= ncol(don)

nbrsp= nrow(don)

nomsp<-rownames(don)

nomrel<-colnames(don)

nrang= 1+nbrsp+nbrrel

nbrcol=nax\*3

nomrang<-list(1:nrang)

nomcol<-list(1:nax\*3)

for(j in 1:nax)

{

  nomcol[1+(j-1)\*3]<-paste("coord",j)

  nomcol[2+(j-1)\*3] <-paste("Cr%",j)

  nomcol[3+(j-1)\*3] <-paste("P",j)

}

resulca<-matrix(1:nrang\*nbrcol, nrow=nrang,ncol=nbrcol,byrow=TRUE)

colnames(resulca)<- nomcol

#calculation of the transformed and the covariance matrices

donc<- matrix(1 :nbrsp\*nbrrel, nrow=nbrsp,ncol=nbrrel)

don1<-matrix(1 :nbrsp\*nbrrel, nrow=nbrsp,ncol=nbrrel)

donc<-don

covar1<-matrix(rep(0,nbrrel\*nbrrel),nbrrel,nbrrel)

covar1<-covarca(donc,nbrsp,nbrrel)

#distribution histogram of the covariance coefficients with the function hist()

nbrcel= nbrrel\*(nbrrel-1)/2 +nbrrel

matcov<-as.matrix(1 :nbrcel, nrow=1,ncol=nbrcel)

i=0

for (j1 in 1:nbrrel)

{

  for (j2 in 1:j1)

  {

    i=i+1

    matcov[i]=covar1[j1,j2]

  }

}

hist(matcov, breaks=40, include.lowest = TRUE, right = TRUE,

     labels=FALSE, border = NULL,

     main = paste("Matrice de covariance CA"), plot=TRUE,

     axes = TRUE,

     warn.unused = TRUE)

#calculation of the trace, of the eigenvectors and eigenvalues

Lam<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Lam2<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

R<-eigen(covar1, symmetric=TRUE, only.values=FALSE)

V <- R$vectors; Lam <- R$values

trace = sum(Lam)

trace

Lam2<-Lam\*100/trace

#calculation of the coordinates and relative contributions of the individuals on axes

hr<-rowSums(don)

hc<-colSums(don)

somme=sum(don)

coordrel<-matrix(1:nbrrel\*nax,nrow=nbrrel,ncol=nax)

contrerel<-matrix(1:nbrrel\*nax,nrow=nbrrel,ncol=nax)

for(j in 1:nbrrel)

{

  for(b in 1:nax)

  {

    coordrel[j,b]=V[j,b]\*sqrt(Lam[b])\*sqrt(somme/hc[j])

    contrerel[j,b] = 100 \* V[j,b] \* V[j,b]

  }

}

#calculation of the coordinates and relative contributions of the species on axes

coordsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

contrelsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

for (b in 1:nax)

{

  for(i in 1:nbrsp)

  {

    cosp=0

    for( j in 1:nbrrel)

    {

      cosp= cosp + don[i,j]\*V[j, b]\*sqrt(somme/hc[j])/hr[i]

    }

    coordsp[i,b]=cosp

    contrelsp[i, b]= cosp^2\*100\*hr[i] /(Lam[b]\*somme)

  }

}

#permutations of the matrix and new calculations

prob1<-matrix(1:nax\*1,nrow=1,ncol=nax,byrow=TRUE)

prob2<-matrix(1:nax\*nbrrel,nrow=nbrrel,ncol=nax,byrow=TRUE)

prob3<-matrix(1:nax\*nbrsp,nrow=nbrsp,ncol=nax,byrow=TRUE)

prob1[]<-0

prob2[]<-0

prob3[]<-0

nombreper=0

for(np in 1:nper)

{

  Lamp<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  Lamp2<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  donc<-matrix(rep(0,nbrsp\*nbrrel),nbrsp,nbrrel)

  don1<-matrix(rep(0,nbrsp\*nbrrel),nbrsp,nbrrel)

  hc<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  covar1<-matrix(rep(0,nbrrel\*nbrrel),nbrrel,nbrrel)

  for(i in 1 :nbrsp)

  {

    donc[i,]<-sample(don[i,],nbrrel,replace=FALSE)

  }

  hc<-colSums(donc)

  if (min(hc)==0){

    next

  }

  nombreper=nombreper+1

  covar1<-covarca(donc,nbrsp,nbrrel)

  #calculation of the eigenvectors, of the eigenvalues and of the trace after permutations

  Rp<-eigen(covar1, symmetric=TRUE, only.values=FALSE)

  Vp <- Rp$vectors; Lamp <- Rp$values

  trace2=sum(Lamp)

  Lamp2<-Lamp\*100/trace2

  for(b in 1:nax)

  {

    if (Lamp[b]>=Lam[b])

    {

      prob1[b]=prob1[b]+1

    }

  }

  #calculation of the relative contributions of the individuals on axes after permutations

  contrerelp<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

  for(j in 1:nbrrel)

  {

    for(b in 1:nax)

    {

      contrerelp[j,b] = 100 \* Vp[j,b] \* Vp[j,b]

      if(contrerelp[j,b] >=contrerel[j,b]){

        prob2[j,b]=prob2[j,b]+1

      }

    }

  }

  #calculation of the relative contributions of the species on axes after permutations

  contrelspp<-matrix(1 :nbrsp\*nax,nrow=nbrsp,ncol=nax)

  for(b in 1:nax)

  {

    for (i in 1:nbrsp)

    {

      cosp=0

      for( j in 1:nbrrel)

      {

        cosp= cosp + donc[i,j]\*Vp[j, b]\*sqrt(somme/hc[j])/(hr[i])

      }

      contrelspp[i, b]= cosp^2\*100\*hr[i]/(Lamp[b]\*somme)

      if (contrelspp[i,b]>=contrelsp[i,b])

      {

        prob3[i,b]=prob3[i,b]+1

      }

    }

  }

}

nombreper

prob1=prob1/nombreper\*100

prob2=prob2/nombreper\*100

prob3=prob3/nombreper\*100

for(j in 1:nax)

{

  resulca[1,3\*(j-1)+1]=Lam[j]

  resulca[1,3\*(j-1)+2]=Lam2[j]

  resulca[1,3\*(j-1)+3]=prob1[j]

}

nomrang[1]<- paste("Vp,Vp% et P")

for(i in 1 :nbrsp)

{

  for(j in 1:nax)

  {

    resulca[i+1,3\*(j-1)+1]=coordsp[i,j]

    resulca[i+1,3\*(j-1)+2]=contrelsp[i,j]

    resulca[i+1,3\*(j-1)+3]=prob3[i,j]

  }

  nomrang[i+1]=nomsp[i]

}

for(i in 1 :nbrrel)

{

  for(j in 1:nax)

  {

    resulca[i+1+nbrsp,3\*(j-1)+1]=coordrel[i,j]

    resulca[i+1+nbrsp,3\*(j-1)+2]=contrerel[i,j]

    resulca[i+1+nbrsp,3\*(j-1)+3]=prob2[i,j]

  }

  nomrang[i+1+nbrsp]=nomrel[i]

}

rownames(resulca)<-nomrang

**covarca.R**

covarca<-function(donc,nbrsp,nbrrel)

{

  somme<-0

  hr<-rowSums(donc)

  hc<-colSums(donc)

  somme=sum(donc)

  for(i in 1:nbrsp)

  {

    for(j in 1 :nbrrel)

    {

      don1[i,j]=donc[i,j]\*(somme/(hc[j]\*hr[i]))-1

    }

  }

  for(j1 in 1:nbrrel)

  {

    for(j2 in 1:nbrrel)

    {

      for (i in 1:nbrsp)

      {

        covar1[j1,j2]= covar1[j1,j2]+don1[i,j1]\*don1[i,j2]\*hr[i]\*sqrt(hc[j1]\*hc[j2])

      }

      covar1[j1,j2]= covar1[j1,j2]/somme^2

    }

  }

  covar1

}

covarnsca.R

covarnsca<-function(donc,nbrsp,nbrrel)

{

  somme = 0

  hr<-rowSums(donc)

  hc<-colSums(donc)

  somme=sum(donc)

  for(i in 1:nbrsp)

  {

    for(j in 1:nbrrel)

    {

      don1[i,j]= (donc[i,j]/hc[j]-hr[i]/somme)\*nbrsp

    }

  }

  for(j1 in 1:nbrrel)

  {

    for(j2 in 1:nbrrel)

    {

      for (i in 1:nbrsp)

      {

        covar1[j1,j2] = covar1[j1,j2] +don1[i,j1]\*don1[i,j2]\*sqrt(hc[j1]\*hc[j2])

      }

      covar1[j1,j2]= covar1[j1,j2]/(nbrsp\*somme)

    }

  }

  covar1

}

**Cs.R**

don<-as.matrix(filename)

ng=length(co)

nbrsp= nrow(don)

nomsp<-rownames(don)

nomrel<-colnames(don)

nbrrel2=0

nbrrel=0

for(i in 1:ng)

{

  nbrrel2=nbrrel2+co[i]+3

  nbrrel=nbrrel+co[i]

}

nbrrel2=nbrrel2+2

sligne<-rowSums(don)

nomcol1<-list(1:nbrrel2)

#Writing the frequencies of the complete table

res<-matrix(1 :nbrrel2\*nbrsp,nrow=nbrsp,ncol=nbrrel2,byrow=TRUE)

for(i in 1:nbrsp)

{

  res[i,1]=sligne[i]

  res[i,2]=sligne[i]/nbrrel

}

nomcol1[1]<-paste("sum")

nomcol1[2]<-paste("fr")

#Frequency calculation in each cluster

k=0 ;l=0

sumg<-matrix(rep(0,nbrsp\*ng), nbrsp,ng)

frg<-matrix(rep(0,nbrsp\*ng), nbrsp,ng)

for(p in 1:ng)

{

  nrg=co[p]

  k=l+1

  l=l+nrg

  for(i in 1:nbrsp)

  {

    for(j in k: l)

    {

      sumg[i,p]=sumg[i,p]+don[i,j]

    }

    frg[i,p]=sumg[i,p]/nrg

  }

}

#Line permutation

prg<-matrix(rep(0,nbrsp\*ng), nbrsp,ng)

nbrrel

for(np in 1:nper)

{

  donp<-matrix(rep(0,nbrsp\*nbrrel),nbrsp,nbrrel)

  for(i in 1:nbrsp)

  {

    donp[i,]<-sample(don[i,],nbrrel,replace=FALSE)

  }

  #For each line

  for(i in 1 :nbrsp)

  {

    #For each cluster

    #nrg : releve number in each cluster

    k=0 ; l=0

    for(g in 1 : ng)

    {

      nrg=co[g]

      k=l+1 ;l=l+nrg

      sumgp=0

      for(j in k :l)

      {

        sumgp=sumgp+donp[i,j]

      }

      if (sumgp>=sumg[i,g])

      {

        prg[i,g]=prg[i,g]+1

      }

    }

  }

}

for(i in 1 :nbrsp)

{

  for(g in 1 :ng)

  {

    prg[i,g]=prg[i,g]/nper

  }

}

#Writing the results

for(g in 1:ng)

{

  if(g==1)

  {

    nbrrel1=1

    nbrrel2=co[1]

  }

  else

  {

    nbrrel1=nbrrel1+co[g-1]

    nbrrel2=nbrrel2+co[g]

  }

  for(i in 1:nbrsp)

  {

    for(j in nbrrel1: nbrrel2)

    {

      nomcol1[j+2+(g-1)\*3]=nomrel[j]

      res[i,j+2+(g-1)\*3]=don[i,j]

    }

    res[i,nbrrel2+3+(g-1)\*3]=sumg[i,g]

    res[i,nbrrel2+4+(g-1)\*3]=frg[i,g]

    res[i,nbrrel2+5+(g-1)\*3]=prg[i,g]

  }

  nomcol1[nbrrel2+3+(g-1)\*3]<-paste("sum")

  nomcol1[nbrrel2+4+(g-1)\*3]<-paste("fr")

  nomcol1[nbrrel2+5+(g-1)\*3]<-paste("pr")

}

rownames(res)<-nomsp

colnames(res)<-nomcol1

resul<-data.frame(res)

**disj113.R**

don<-as.matrix(filename)

nbrrel= ncol(don)

nbrsp= nrow(don)

nomsp<-rownames(don)

nomrel<-colnames(don)

#calcul nombre de lignes du nouveau tableau

nbrl=0

don1<-don

res3<-apply(don,1,max)

for(i in 1:nbrsp)

{

  if(res3[i]>3)

  {

    nbrl=nbrl+1

    for(j in 1:nbrrel)

    {

      if(don[i,j]>3)

      {

        don[i,j]=0

      }

    }

  }

}

res2<-apply(don,1,max)

for(i in 1:nbrsp)

{

  if(res2[i]>1)

  {

    nbrl=nbrl+1

    for(j in 1:nbrrel)

    {

      if(don[i,j]>1)

      {

        don[i,j]=0

      }

    }

  }

}

res1<- apply(don,1,max)

for(i in 1:nbrsp)

{

  if(res1[i]==1)

  {

    nbrl=nbrl+1

  }

}

nbrl

#definition of a new table

nomsp2<-list(1 :nbrl)

don2<-matrix(rep(0,nbrl\*nbrrel),nbrl,nbrrel)

nbrl=0

for(i in 1:nbrsp)

{

  if(res3[i]>3)

  {

    nbrl=nbrl+1

    nomsp2[nbrl]<-paste(nomsp[i],">3")

    for(j in 1:nbrrel)

    {

      if(don1[i,j]>3)

      {

        don2[nbrl,j]=1

      }

    }

  }

  if(res2[i]>1)

  {

    nbrl=nbrl+1

    nomsp2[nbrl]<-paste(nomsp[i],">1")

    for(j in 1:nbrrel)

    {

      if(don1[i,j]>1)

      {

        don2[nbrl,j]=1

      }

    }

  }

  if(res1[i]==1)

  {

    nbrl=nbrl+1

    nomsp2[nbrl]<-paste(nomsp[i])

    for(j in 1:nbrrel)

    {

      if(don1[i,j]>0)

      {

        don2[nbrl,j]=1

      }

    }

  }

}

nbrl

rownames(don2)<-c(nomsp2)

colnames(don2)<-c(nomrel)

resul<-data.frame(don2)

**disj12345.R**

don<-as.matrix(filename)

nbrrel= ncol(don)

nbrsp= nrow(don)

nomsp<-rownames(don)

nomrel<-colnames(don)

#calcul nombre de lignes du nouveau tableau

nbrl=0

for(i in 1:nbrsp)

{

  for(j in 1:nbrrel)

  {

    if (don[i,j] == 1)

    {

      nbrl=nbrl+1

      break

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j] ==2)

    {

      nbrl=nbrl+1

      break

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j] ==3)

    {

      nbrl=nbrl+1

      break

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j] == 4)

    {

      nbrl=nbrl+1

      break

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j] == 5)

    {

      nbrl=nbrl+1

      break

    }

  }

}

nbrl

#definition of a new table

nomsp2<-list(1 :nbrl)

don1<-matrix(rep(0,nbrl\*nbrrel),nbrl,nbrrel)

nbrl=0

for(i in 1:nbrsp)

{

  for(j in 1:nbrrel)

  {

    if (don[i,j] == 1)

    {

      nbrl=nbrl+1

      nomsp2[nbrl]<-paste(nomsp[i])

      break

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j] == 1)

    {

      don1[nbrl,j] = 1

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j] ==2)

    {

      nbrl=nbrl+1

      nomsp2[nbrl]<-paste(nomsp[i],"2")

      break

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j] ==2)

    {

      don1[nbrl,j] =1

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j]==3)

    {

      nbrl=nbrl+1

      nomsp2[nbrl]<-paste(nomsp[i] ,"3")

      break

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j]==3)

    {

      don1[nbrl,j]=1

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j]==4)

    {

      nbrl=nbrl+1

      nomsp2[nbrl]<-paste(nomsp[i] ,"4")

      break

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j]==4)

    {

      don1[nbrl,j]=1

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j]==5)

    {

      nbrl=nbrl+1

      nomsp2[nbrl]<-paste(nomsp[i] ,"5")

      break

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j]==5)

    {

      don1[nbrl,j]=1

    }

  }

}

nbrl

rownames(don1)<-c(nomsp2)

colnames(don1)<-c(nomrel)

resul<-data.frame(don1)

**mfaca.R**

don<-as.matrix(filename)

nomsp<-rownames(don)

nomrel<-colnames(don)

nbrsp= nrow(don)

nbrsp1=nbrsp

nbrrel= ncol(don)

nb=length(co)

nrang=nb+2+nbrsp+nbrrel

nbrcol=nax\*2

nomrang<-list(1:nrang)

nomcol<-list(1:nbrcol)

for(j in 1:nax)

{

  nomcol[1+(j-1)\*2]<-paste("coord",j)

  nomcol[2+(j-1)\*2] <-paste("Cr%",j)

}

resulmfaca<-matrix(1:1\*nbrcol\*nrang,nrow=nrang,ncol=nbrcol,byrow=TRUE)

colnames(resulmfaca)<-nomcol

#Eigenvalues of the originel table

donc<-matrix(1:nbrsp\*nbrrel,nrow=nbrsp,ncol=nbrrel)

donc<-don

hr<-matrix(1:nbrsp)

hc<-matrix(1:nbrrel)

hr<-rowSums(don)

hc<-colSums(don)

somme<-sum(don)

covar1<-matrix(rep(0,nbrrel\*nbrrel),nbrrel,nbrrel)

covar1<-covarca(donc,nbrsp,nbrrel)

Lam<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Lam2<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

R<-eigen(covar1,symmetric=TRUE)

V<- R$vectors

Lam<-R$values

trace=sum(Lam)

Lam2<-Lam\*100/trace

for(j in 1 :nax)

{

  resulmfaca[1,2\*(j-1)+1]=Lam[j]

  resulmfaca[1,2\*(j-1)+2]=Lam2[j]

}

nomrang[1]<-paste("Vp & Vp% of the original table")

#Sub-tables and 1st eigenvalues of the sub-tables

v1st<-matrix(1 :nb)

i1=0

for(k in 1:nb)

{

  nbrsp= co[k]

  donc<-matrix(1 :nbrsp\*nbrrel, nrow = nbrsp,ncol = nbrrel)

  for(i in 1 :nbrsp)

  {

    i1=i1+1

    for(j in 1 :nbrrel)

    {

      donc[i,j]=don[i1,j]

    }

  }

  covarst<-matrix(rep(0,nbrrel\*nbrrel), nbrrel,nbrrel)

  covarst<-covarca(donc,nbrsp,nbrrel)

  Lamst<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

  Lamst2<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

  Rst<-eigen(covarst, symmetric=TRUE, only.values=FALSE)

  Lamst<- Rst$values

  tracest = sum(Lamst)

  Lamst2=Lamst\*100/tracest

  v1st[k]=Lamst[1]

  for(j in 1 :nax)

  {

    resulmfaca[1+k,2\*(j-1)+1]=Lamst[j]

    resulmfaca[1+k,2\*(j-1)+2]=Lamst2[j]

  }

  nomrang[1+k]<-paste("Vp & Vp% du sous-tableau",k)

}

#Weighting of the sub-tables by the 1st eigenvalues of the sub-tables

nbrsp=nbrsp1

donc<-matrix(1:nbrsp\*nbrrel,nrow=nbrsp,ncol=nbrrel)

v1<-matrix(1 :nbrsp)

i1=0

for(k in 1:nb)

{

  nbrspp= co[k]

  for(i in 1:nbrspp)

  {

    i1=i1+1

    v1[i1]=v1st[k]

  }

}

for(i in 1:nbrsp)

{

  for(j in 1:nbrrel)

  {

    donc[i,j]=don[i,j]/sqrt(v1[i])

  }

}

covar1p<-matrix(1 :nbrrel\*nbrrel,nrow = nbrrel,ncol = nbrrel)

covar1p<-covarca(donc,nbrsp,nbrrel)

#Distribution histogram of the covariance coefficients with the function hist()

nbrcel=nbrrel\*(nbrrel-1)/2+nbrrel

matcov<-as.matrix(1 :nbrcel, nrow=1,ncol=nbrcel)

i=0

for (j1 in 1:nbrrel)

{

  for (j2 in 1:j1)

  {

    i=i+1

    matcov[i]=covar1p[j1,j2]

  }

}

hist(matcov, breaks=40, include.lowest = TRUE, right = TRUE,

     border = NULL,

     main = paste("Covariance distribution-mfaca"), plot=TRUE,

     axes = TRUE,

     warn.unused = TRUE)

Lamp<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Lamp2<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Rp<-eigen(covar1p, symmetric=TRUE, only.values=FALSE)

Vp<- Rp$vectors; Lamp <- Rp$values

tracep= sum(Lamp)

Lamp2<-Lamp\*100/tracep

for(j in 1 :nax)

{

  resulmfaca[2+nb,2\*(j-1)+1]=Lamp[j]

  resulmfaca[2+nb,2\*(j-1)+2]=Lamp2[j]

}

nomrang[2+nb]<-paste("Vp & Vp% of the weighted table")

coordsp<-matrix(rep(0,nbrsp\*nax),nrow=nbrsp,ncol=nax)

contrelsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

#Calculation of the coordinates and relative contributions of the individuals, on axes

coordrel<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

contrelrel<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

hr<-rowSums(donc)

hc<-colSums(donc)

somme=sum(donc)

for(j in 1:nbrrel)

{

  for(b in 1 :nax)

  {

    coordrel[j,b]=Vp[j,b]\*sqrt(Lamp[b])/sqrt(somme/ hc[j])

    contrelrel[j,b]=100\* Vp[j,b]\* Vp[j,b]

  }

}

#Calculation of the coordinates and relative contributions of the species, on axes

coordsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

contrelsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

for(b in 1 :nax)

{

  for(i in 1 : nbrsp)

  {

    cosp=0

    for(j in 1 :nbrrel)

    {

      cosp= cosp + donc[i,j]\*Vp[j,b]\*sqrt(somme/hc[j])/hr[i]

    }

    coordsp[i,b]=cosp

    contrelsp[i,b]= cosp^2\*100\*hr[i]/(Lamp[b]\*somme)

  }

}

for(i in 1 :nbrsp)

{

  nomrang[i+2+nb]<-nomsp[i]

  for(j in 1:nax)

  {

    resulmfaca[i+2+nb,2\*(j-1)+1]=coordsp[i,j]

    resulmfaca[i+2+nb,2\*(j-1)+2]=contrelsp[i,j]

  }

}

for(i in 1 :nbrrel)

{

  for(j in 1:nax)

  {

    resulmfaca[i+2+nb+nbrsp,2\*(j-1)+1]=coordrel[i,j]

    resulmfaca[i+2+nb+nbrsp,2\*(j-1)+2]=contrelrel[i,j]

  }

  nomrang[i+2+nb+nbrsp]<-nomrel[i]

}

rownames(resulmfaca)<-nomrang

**mfansca.R**

don<-as.matrix(filename)

nomsp<-rownames(don)

nomrel<-colnames(don)

nbrsp= nrow(don)

nbrrel= ncol(don)

somme=sum(don)

hr<-matrix(1:nbrsp)

hc<-matrix(1:nbrrel)

hr<-rowSums(don)

hc<-colSums(don)

nb=length(co)

nrang1=nb+1

nrang2=1+nbrsp+nbrrel

ncol1=2

ncol2=nax\*3

nomrang1<-list(1:nrang1)

nomrang2<-list(1:nrang2)

nomcol1<-list(1:ncol1)

nomcol2<-list(1:ncol2)

nomcol1[1]<-paste("line numbers")

nomcol1[2]<-paste("table densities")

resul1mfansca<-matrix(1:nrang1\*ncol1,nrow=nrang1,ncol=ncol1,byrow=TRUE)

resul2mfansca<-matrix(1:nrang2\*ncol2,nrow=nrang2,ncol=ncol2,byrow=TRUE)

#Eigenvalues of the originel table

donc<- matrix(1 :nbrsp\*nbrrel, nrow=nbrsp,ncol=nbrrel)

don1<-matrix(1 :nbrsp\*nbrsp, nrow=nbrsp,ncol=nbrsp)

donc<-don

covar1<-matrix(rep(0,nbrrel\*nbrrel),nbrrel,nbrrel)

covar1<-covarnsca(donc,nbrsp,nbrrel)

Lam<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Lam2<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

density<-matrix(1 :nb+1)

R<-eigen(covar1,symmetric=TRUE)

Lam<-R$values

trace<-sum(Lam)

density[1]<-somme/(nbrsp\*nbrrel)

Lam2<-Lam\*100/trace

resul1mfansca[1,1]<-nbrsp

resul1mfansca[1,2]<-density[1]

nomrang1[1]<-paste("Complete table")

#densities of sub-tables

v1st<-matrix(1 :nb)

i1=0

for(k in 1:nb)

{

  nbrspp= co[k]

  donst<-matrix(1 :nbrspp\*nbrrel, nrow = nbrspp,ncol = nbrrel)

  for(i in 1 :nbrspp)

  {

    i1=i1+1

    for(j in 1 :nbrrel)

    {

      donst[i,j]=don[i1,j]

    }

  }

  sommest=sum(donst)

  density[k+1]<-sommest/(nbrrel\*nbrspp)

  v1st[k]=density[k+1]

  resul1mfansca[1+k,1]<-nbrspp

  resul1mfansca[1+k,2]<-density[k+1]

  nomrang1[k+1]<-paste("subtable" ,k)

}

#Weighting of the original tables by the densities of the sub-tables

donc<-matrix(1:nbrsp\*nbrrel,nrow=nbrsp,ncol=nbrrel)

v1<-matrix(1 :nbrsp)

i1=0

for(k in 1:nb)

{

  nbrspp= co[k]

  for(i in 1:nbrspp)

  {

    i1=i1+1

    v1[i1]=v1st[k]

  }

}

for(i in 1:nbrsp)

{

  for(j in 1:nbrrel)

  {

    donc[i,j]=don[i,j]/sqrt(v1[i])

  }

}

covar1p<-matrix(1 :nbrrel\*nbrrel,nrow = nbrrel,ncol = nbrrel)

covar1p<-covarnsca(donc,nbrsp,nbrrel)

somme = sum(donc)

hr<-rowSums(donc)

hc<-colSums(donc)

#Distribution histogram of the covariance - coefficients with the function hist()

nbrcel=nbrrel\*(nbrrel-1)/2 + nbrrel

matcov<-as.matrix(1 :nbrrel, nrow=1,ncol=nbrcel)

i=0

for (j1 in 2:nbrrel)

{

  for (j2 in 2:j1)

  {

    i=i+1

    matcov[i]=covar1p[j1,j2]

  }

}

hist(matcov, breaks=40, include.lowest = TRUE, right = TRUE,

     labels=FALSE, border = NULL,

     main = paste("Covariance distribution-mfansca"), plot=TRUE,

     axes = TRUE,

     warn.unused = TRUE)

Lamp<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Lamp2<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Rp<-eigen(covar1p, symmetric=TRUE, only.values=FALSE)

Vp<- Rp$vectors; Lamp <- Rp$values

tracep= sum(Lamp)

Lamp2<-Lamp\*100/tracep

nomrang2[2+nb]<-paste("Vp & Vp% of weighted tables")

coordsp<-matrix(rep(0,nbrsp\*nax),nrow=nbrsp,ncol=nax)

contrelsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

#Calculation of the coordinates and relative contributions of the individuals, on axes

coordrel<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

contrelrel<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

for(j in 1:nbrrel)

{

  for(b in 1 :nax)

  {

    coordrel[j,b]=Vp[j,b]/sqrt(hc[j])\*sqrt(somme)

    contrelrel[j,b]=100\* Vp[j,b]\* Vp[j,b]

  }

}

#Calculation of the coordinates and relative contributions of the species, on axes

coordsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

contrelsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

for(b in 1 :nax)

{

  for(i in 1 : nbrsp)

  {

    cosp=0

    const= sqrt(nbrsp/(Lamp[b]\*somme))

    const

    for(j in 1 :nbrrel)

    {

      cosp= cosp + donc[i,j]\*Vp[j, b]/sqrt(hc[j])\*const

    }

    coordsp[i,b]=cosp

    contrelsp[i,b]= cosp^2\*100

  }

}

#permutations of the weighted matrix and new calculations

prob1<-matrix(1:nax\*1,nrow=1,ncol=nax,byrow=TRUE)

prob2<-matrix(1:nax\*nbrrel,nrow=nbrrel,ncol=nax,byrow=TRUE)

prob3<-matrix(1:nax\*nbrsp,nrow=nbrsp,ncol=nax,byrow=TRUE)

prob1[]<-0

prob2[]<-0

prob3[]<-0

nombreper<-0

for(np in 1:nper)

{

  Lampp<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  Lampp2<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  donpp<-matrix(rep(0,nbrsp\*nbrrel),nbrsp,nbrrel)

  don1pp<-matrix(rep(0,nbrsp\*nbrrel),nbrsp,nbrrel)

  hcpp<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  covar1pp<-matrix(1 :nbrrel\*nbrrel,nrow=nbrrel,ncol = nbrrel)

  for(i in 1 :nbrsp)

  {

    donpp[i,]<-sample(donc[i,],nbrrel,replace=FALSE)

  }

  hcpp<-colSums(donpp)

  if(min(hcpp)==0){

    next

  }

  nombreper=nombreper+1

  donc<-donpp

  covar1pp<-covarnsca(donc,nbrsp,nbrrel)

  #calculation  of the eigenvectors, of the eigenvalues and of the trace after permutations

  Rpp<-eigen(covar1pp, symmetric=TRUE, only.values=FALSE)

  Vpp <- Rpp$vectors; Lampp <- Rpp$values

  tracepp<-sum(Lampp)

  Lampp2<-Lampp\*100/tracepp

  for(b in 1 :nax)

  {

    if (Lampp[b]>=Lamp[b])

    {

      prob1[b]=prob1[b]+1

    }

  }

  #calculation of the relative contributions of the individuals on axes after permutations

  contrerelpp<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

  for(j in 1:nbrrel)

  {

    for(b in 1 :nax)

    {

      contrerelpp[j,b]=100\* Vpp[j,b]\* Vpp[j,b]

      if(contrerelpp[j,b] >=contrelrel[j,b]){

        prob2[j,b]=prob2[j,b]+1

      }

    }

  }

  #calculation of the relative contributions of the species on axes after permutations

  contrelspp<-matrix(1 :nbrsp\*nax,nrow=nbrsp,ncol=nax)

  for(b in 1 :nax)

  {

    for(i in 1 : nbrsp)

    {

      cosp=0

      const= sqrt(nbrsp/(Lampp[b]\*somme))

      for(j in 1 :nbrrel)

      {

        cosp= cosp + donpp[i,j]\*Vpp[j, b]/sqrt(hcpp[j])\*const

      }

      contrelspp[i,b]=cosp^2\*100

      if (contrelspp[i,b] >=contrelsp[i,b]){

        prob3[i,b]=prob3[i,b]+1

      }

    }

  }

}

nombreper

prob1=prob1\*100/nombreper

prob2=prob2\*100/ nombreper

prob3=prob3\*100/ nombreper

for(j in 1:nax)

{

  nomcol2[1+(j-1)\*3]<-paste("coord",j)

  nomcol2[2+(j-1)\*3] <-paste("CR",j)

  nomcol2[3+(j-1)\*3] <-paste("P",j)

}

nomrang2[1]<-paste("Vp, Vp%, P")

for(j in 1:nax)

{

  resul2mfansca[1,3\*(j-1)+1]=Lamp[j]

  resul2mfansca[1,3\*(j-1)+2]=Lamp2[j]

  resul2mfansca[1,3\*(j-1)+3]=prob1[j]

}

for(i in 1 :nbrsp)

{

  nomrang2[i+1]=nomsp[i]

  for(j in 1:nax)

  {

    resul2mfansca[i+1,3\*(j-1)+1]=coordsp[i,j]

    resul2mfansca[i+1,3\*(j-1)+2]=contrelsp[i,j]

    resul2mfansca[i+1,3\*(j-1)+3]=prob3[i,j]

  }

}

for(i in 1 :nbrrel)

{

  nomrang2[i+1+nbrsp]=nomrel[i]

  for(j in 1:nax)

  {

    resul2mfansca[i+1+nbrsp,3\*(j-1)+1]=coordrel[i,j]

    resul2mfansca[i+1+nbrsp,3\*(j-1)+2]=contrelrel[i,j]

    resul2mfansca[i+1+nbrsp,3\*(j-1)+3]=prob2[i,j]

  }

}

rownames(resul1mfansca)<-nomrang1

colnames(resul1mfansca)<-nomcol1

rownames(resul2mfansca)<-nomrang2

colnames(resul2mfansca)<-nomcol2

**mfanscaEV.R**

don<-as.matrix(filename)

nomsp<-rownames(don)

nomrel<-colnames(don)

nbrsp= nrow(don)

nbrsp1=nbrsp

nbrrel= ncol(don)

somme=sum(don)

don<-log1p(don)

hr<-matrix(1:nbrsp)

hc<-matrix(1:nbrrel)

hr<-rowSums(don)

hc<-colSums(don)

nb=length(co)

nrang1=nb+1

nrang2=1+nbrsp+nbrrel

ncol1=2

ncol2=nax\*3

nomrang1<-list(1:nrang1)

nomrang2<-list(1:nrang2)

nomcol1<-list(1:ncol1)

nomcol2<-list(1:ncol2)

nomcol1[1]<-paste("line numbers")

nomcol1[2]<-paste("eigenvalues")

resul1mfansca<-matrix(1:nrang1\*ncol1,nrow=nrang1,ncol=ncol1,byrow=TRUE)

resul2mfansca<-matrix(1:nrang2\*ncol2,nrow=nrang2,ncol=ncol2,byrow=TRUE)

#Eigenvalues of the originel table

donc<- matrix(1 :nbrsp\*nbrrel, nrow=nbrsp,ncol=nbrrel)

don1<- matrix(1 :nbrsp\*nbrrel, nrow=nbrsp,ncol=nbrrel)

donc<-don

somme=0

hr<-rowSums(donc)

hc<-colSums(donc)

somme=sum(donc)

covar1<-covarnsca(donc,nbrsp,nbrrel)

Lam<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Lam2<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

R<-eigen(covar1,symmetric=TRUE)

Lam<-R$values

trace<-sum(Lam)

Lam2<-Lam\*100/trace

resul1mfansca[1,1]<-nbrsp

resul1mfansca[1,2]<-Lam[1]

nomrang1[1]<-paste("Complete table")

#Sub-tables and 1st eigenvalues of the sub-tables

v1st<-matrix(1 :nb)

i1=0[]

for(k in 1:nb)

{

  nbrsp= co[k]

  donc<-matrix(1 :nbrsp\*nbrrel, nrow = nbrsp,ncol = nbrrel)

  for(i in 1 :nbrsp)

  {

    i1=i1+1

    for(j in 1 :nbrrel)

    {

      donc[i,j]=don[i1,j]

    }

  }

  covarst<-matrix(rep(0,nbrrel\*nbrrel), nbrrel,nbrrel)

  covarst<-covarnsca(donc,nbrsp,nbrrel)

  Lamst<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

  Lamst2<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

  Rst<-eigen(covarst, symmetric=TRUE, only.values=FALSE)

  Lamst<- Rst$values

  tracest = sum(Lamst)

  Lamst2=Lamst\*100/tracest

  v1st[k]=Lamst[1]

  for(j in 1 :nax)

  {

    resul1mfansca[1+k,1]=nbrsp

    resul1mfansca[1+k,2]=Lamst[1]

  }

  nomrang[1+k]<-paste("Vp & Vp% du sous-tableau",k)

}

v1st

#Weighting of the original tables by the eigenvalues of the sub-tables

nbrsp=nbrsp1

donc<-matrix(1:nbrsp\*nbrrel,nrow=nbrsp,ncol=nbrrel)

v1<-matrix(1 :nbrsp)

i1=0

for(k in 1:nb)

{

  nbrspp= co[k]

  for(i in 1:nbrspp)

  {

    i1=i1+1

    v1[i1]=v1st[k]

  }

}

for(i in 1:nbrsp)

{

  for(j in 1:nbrrel)

  {

    donc[i,j]=don[i,j]/sqrt(v1[i])

  }

}

covar1p<-matrix(1 :nbrrel\*nbrrel,nrow = nbrrel,ncol = nbrrel)

covar1p<-covarnsca(donc,nbrsp,nbrrel)

#Distribution histogram of the covariance - coefficients with the function hist()

nbrcel=nbrrel\*(nbrrel-1)/2 + nbrrel

matcov<-as.matrix(1 :nbrrel, nrow=1,ncol=nbrcel)

i=0

for (j1 in 2:nbrrel)

{

  for (j2 in 2:j1)

  {

    i=i+1

    matcov[i]=covar1p[j1,j2]

  }

}

hist(matcov, breaks=40, include.lowest = TRUE, right = TRUE,

     labels=FALSE, border = NULL,

     main = paste("Covariance distribution-mfansca"), plot=TRUE,

     axes = TRUE,

     warn.unused = TRUE)

Lamp<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Lamp2<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Rp<-eigen(covar1p, symmetric=TRUE, only.values=FALSE)

Vp<- Rp$vectors; Lamp <- Rp$values

tracep= sum(Lamp)

Lamp2<-Lamp\*100/tracep

nomrang2[2+nb]<-paste("Vp & Vp% of weighted tables")

coordsp<-matrix(rep(0,nbrsp\*nax),nrow=nbrsp,ncol=nax)

contrelsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

#Calculation of the coordinates and relative contributions of the individuals, on axes

coordrel<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

contrelrel<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

for(j in 1:nbrrel)

{

  for(b in 1 :nax)

  {

    coordrel[j,b]=Vp[j,b]/sqrt(hc[j])\*sqrt(somme)

    contrelrel[j,b]=100\* Vp[j,b]\* Vp[j,b]

  }

}

#Calculation of the coordinates and relative contributions of the species, on axes

coordsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

contrelsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

for(b in 1 :nax)

{

  for(i in 1 : nbrsp)

  {

    cosp=0

    const= sqrt(nbrsp/(Lamp[b]\*somme))

    const

    for(j in 1 :nbrrel)

    {

      cosp= cosp + donc[i,j]\*Vp[j, b]/sqrt(hc[j])\*const

    }

    coordsp[i,b]=cosp

    contrelsp[i,b]= cosp^2\*100

  }

}

#permutations of the weighted matrix and new calculations

prob1<-matrix(1:nax\*1,nrow=1,ncol=nax,byrow=TRUE)

prob2<-matrix(1:nax\*nbrrel,nrow=nbrrel,ncol=nax,byrow=TRUE)

prob3<-matrix(1:nax\*nbrsp,nrow=nbrsp,ncol=nax,byrow=TRUE)

prob1[]<-0

prob2[]<-0

prob3[]<-0

nombreper<-0

for(np in 1:nper)

{

  Lampp<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  Lampp2<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  donpp<-matrix(rep(0,nbrsp\*nbrrel),nbrsp,nbrrel)

  don1pp<-matrix(rep(0,nbrsp\*nbrrel),nbrsp,nbrrel)

  hcpp<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  covar1pp<-matrix(1 :nbrrel\*nbrrel,nrow=nbrrel,ncol = nbrrel)

  for(i in 1 :nbrsp)

  {

    donpp[i,]<-sample(don[i,],nbrrel,replace=FALSE)

  }

  hcpp<-colSums(donpp)

  if(min(hcpp)==0){

    next

  }

  nombreper=nombreper+1

  donc<-donpp

  covar1pp<-covarnsca(donc,nbrsp,nbrrel)

  #calculation  of the eigenvectors, of the eigenvalues and of the trace after permutations

  Rpp<-eigen(covar1pp, symmetric=TRUE, only.values=FALSE)

  Vpp <- Rpp$vectors; Lampp <- Rpp$values

  tracepp<-sum(Lampp)

  Lampp2<-Lampp\*100/tracepp

  for(b in 1 :nax)

  {

    if (Lampp[b]>=Lamp[b])

    {

      prob1[b]=prob1[b]+1

    }

  }

  #calculation of the relative contributions of the individuals on axes after permutations

  contrerelpp<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

  for(j in 1:nbrrel)

  {

    for(b in 1 :nax)

    {

      contrerelpp[j,b]=100\* Vpp[j,b]\* Vpp[j,b]

      if(contrerelpp[j,b] >=contrelrel[j,b]){

        prob2[j,b]=prob2[j,b]+1

      }

    }

  }

  #calculation of the relative contributions of the species on axes after permutations

  contrelspp<-matrix(1 :nbrsp\*nax,nrow=nbrsp,ncol=nax)

  for(b in 1 :nax)

  {

    for(i in 1 : nbrsp)

    {

      cosp=0

      const= sqrt(nbrsp/(Lampp[b]\*somme))

      for(j in 1 :nbrrel)

      {

        cosp= cosp + donpp[i,j]\*Vpp[j, b]/sqrt(hcpp[j])\*const

      }

      contrelspp[i,b]=cosp^2\*100

      if (contrelspp[i,b] >=contrelsp[i,b]){

        prob3[i,b]=prob3[i,b]+1

      }

    }

  }

}

nombreper

prob1=prob1\*100/nombreper

prob2=prob2\*100/ nombreper

prob3=prob3\*100/ nombreper

for(j in 1:nax)

{

  nomcol2[1+(j-1)\*3]<-paste("coord",j)

  nomcol2[2+(j-1)\*3] <-paste("CR",j)

  nomcol2[3+(j-1)\*3] <-paste("P",j)

}

nomrang2[1]<-paste("Vp, Vp%, P")

for(j in 1:nax)

{

  resul2mfansca[1,3\*(j-1)+1]=Lamp[j]

  resul2mfansca[1,3\*(j-1)+2]=Lamp2[j]

  resul2mfansca[1,3\*(j-1)+3]=prob1[j]

}

nomsp

for(i in 1 :nbrsp)

{

  nomrang2[i+1]=nomsp[i]

  for(j in 1:nax)

  {

    resul2mfansca[i+1,3\*(j-1)+1]=coordsp[i,j]

    resul2mfansca[i+1,3\*(j-1)+2]=contrelsp[i,j]

    resul2mfansca[i+1,3\*(j-1)+3]=prob3[i,j]

  }

}

nomrel

for(i in 1 :nbrrel)

{

  nomrang2[i+1+nbrsp]=nomrel[i]

  for(j in 1:nax)

  {

    resul2mfansca[i+1+nbrsp,3\*(j-1)+1]=coordrel[i,j]

    resul2mfansca[i+1+nbrsp,3\*(j-1)+2]=contrelrel[i,j]

    resul2mfansca[i+1+nbrsp,3\*(j-1)+3]=prob2[i,j]

  }

}

rownames(resul1mfansca)<-nomrang1

colnames(resul1mfansca)<-nomcol1

rownames(resul2mfansca)<-nomrang2

colnames(resul2mfansca)<-nomcol2

**mfapca.R**

don<-as.matrix(filename)

nbrsp= nrow(don)

nbrrel= ncol(don)

nomsp<-rownames(don)

nomrel<-colnames(don)

nb=length(co)

nrang= nb+2+nbrsp+nbrrel

nbrcol=nax\*2

nomrang<-list(1:nrang)

nomcol<-list(1:nbrcol)

for(j in 1:nax)

{

  nomcol[1+(j-1)\*2]<-paste("coord",j)

  nomcol[2+(j-1)\*2] <-paste("Cr%",j)

}

resulmfapca<-matrix(1:nbrcol\*nrang, nrow=nrang,ncol=nbrcol,byrow=TRUE)

colnames(resulmfapca)<-nomcol

correl<-cor(t(don))

R<-eigen(correl,symmetric=TRUE)

V<- R$vectors; Lam <- R$values

Lam2=Lam\*100/nbrsp

for(j in 1:nax)

{

  resulmfapca[1,2\*(j-1)+1]=Lam[j]

  resulmfapca[1,2\*(j-1)+2]=Lam2[j]

}

nomrang[1]<- paste("Vp & Vp% du tableau originel")

#Subtables and 1st eigenvalues for each subtable

vp1<-matrix(1 :nb)

i1=0

for(k in 1:nb)

{

  nbrspp= co[k]

  donst<-matrix(1:nbrspp\*nbrrel,nrow=nbrspp,ncol=nbrrel)

  for(i in 1 :nbrspp)

  {

    i1=i1+1

    for(j in 1 :nbrrel)

    {

      donst[i,j]=don[i1,j]

    }

  }

  correlst<-cor(t(donst))

  Rst<-eigen(correlst,symmetric=TRUE)

  Lamst<-Rst$values

  Lamst2<-matrix(1:nax)

  vp1[k]=Lamst[1]

  Lamst2=Lamst\*100/nbrspp

  for(j in 1:nax)

  {

    resulmfapca[1+k,2\*(j-1)+1]=Lamst[j]

    resulmfapca[1+k,2\*(j-1)+2]=Lamst2[j]

  }

  nomrang[1+k]<-paste("Vp & Vp% du sous-tableau", k)

}

#Complete weighted table by the 1rst eigenvalues of sub-tables

v1<-matrix(1 :nbrsp)

correlp<-matrix(1:nbrsp\*nbrsp,nrow=nbrsp,ncol=nbrsp)

i1=0

for(k in 1:nb)

{

  nbrspp= co[k]

  for(i in 1 :nbrspp)

  {

    i1=i1+1

    v1[i1]=vp1[k]

  }

}

for(i in 1 :nbrsp)

{

  for(j in 1:nbrsp)

  {

    correlp[i,j]= correl[i,j]/sqrt(v1[i]\*v1[j])

  }

}

#Distribution histogram of correlations with function hist()

nbrcel=nbrsp\*(nbrsp-1)/2

matcor<-as.matrix(1 :nbrcel, nrow=1,ncol=nbrcel)

i=0

for (j1 in 2:nbrsp)

{

  for (j2 in 2:j1)

  {

    i=i+1

    matcor[i]=correlp[j1,j2]

  }

}

hist(matcor, breaks=40, include.lowest = TRUE, right = TRUE,

     labels=FALSE, border = NULL,

     main = paste("Correl distribution-mfapca"), plot=TRUE,

     axes = TRUE,

     warn.unused = TRUE)

Rp<-eigen(correlp,symmetric=TRUE)

Vp<- Rp$vectors; Lamp <- Rp$values

trace =sum(Lamp)

trace

Lamp2<-matrix(1 :nbrsp)

Lamp2=Lamp\*100/trace

for(j in 1:nax)

{

  resulmfapca[2+nb,2\*(j-1)+1]=Lamp[j]

  resulmfapca[2+nb,2\*(j-1)+2]=Lamp2[j]

}

nomrang[2+nb]<- paste("Vp & Vp% of the weighted table")

#Calculation of species coordinates and relative contributions on axes

coordsp<-matrix(1 :nbrsp\*nax,nrow=nbrsp,ncol=nax)

contrelsp<-matrix(1 :nbrsp\*nax,nrow=nbrsp,ncol=nax)

for(i in 1:nbrsp)

{

  for(a in 1:nax)

  {

    coordsp[i,a] =Vp[i,a]\*sqrt(Lamp[a]\*v1[i])

    contrelsp[i,a] =coordsp[i,a]^2

  }

}

# Calculation of releve coordinates and relative contributions on axes

coordrel<-matrix(1:nbrrel\*nax,nrow=nbrrel,ncol=nax)

contrelrel<-matrix(1:nbrrel\*nax,nrow=nbrrel,ncol=nax)

nrmp<-matrix(rep(0,1\*nbrrel),1,nbrrel)

#Calculation of weighted reduced centered variables

don1<-matrix(1:nbrsp\*nbrrel, nrow = nbrsp,ncol=nbrrel)

sec<-matrix(1 :nbrsp)

moy<-rowMeans(don)

for(i in 1 :nbrsp)

{

  for(j in 1:nbrrel)

  {

    sec[i]=sec[i] +(don[i,j]-moy[i])^2

  }

  sec[i]=sqrt(sec[i]/nbrrel)

}

for(i in 1 :nbrsp)

{

  for(j in 1:nbrrel)

  {

    don1[i,j]=(don[i,j]-moy[i])/(sec[i]\*sqrt(v1[i]))

  }

}

for(i in 1:nbrrel)

{

  for (j in 1:nbrsp)

  {

    nrmp[i] = nrmp[i]+(don1[j,i])^2

  }

}

for(i in 1:nbrrel)

{

  for(a in 1:nax)

  {

    coind=0

    for(j in 1:nbrsp)

    {

      coind= coind+ don1[j,i]\*Vp[j,a]

    }

    coordrel[i,a]=coind

    contrelrel[i,a]= coordrel[i,a]\* coordrel[i,a]/nrmp[i]

  }

}

for(i in 1 :nbrsp)

{

  nomrang[i+2+nb]<-nomsp[i]

  for(j in 1:nax)

  {

    resulmfapca[i+2+nb,2\*(j-1)+1]=coordsp[i,j]

    resulmfapca[i+2+nb,2\*(j-1)+2]=contrelsp[i,j]

  }

}

for(i in 1 :nbrrel)

{

  for(j in 1:nax)

  {

    resulmfapca[i+nbrsp+2+nb,2\*(j-1)+1]=coordrel[i,j]

    resulmfapca[i+nbrsp+2+nb,2\*(j-1)+2]=contrelrel[i,j]

  }

  nomrang[i+2+nb+nbrsp]<-nomrel[i]

}

rownames(resulmfapca)<-nomrang

**nscaf.R**

don<-as.matrix(filename)

nbrsp= nrow(don)

nbrrel= ncol(don)

nomsp<-rownames(don)

nomrel<-colnames(don)

somme=sum(don)

nrang= 1+nbrsp+nbrrel

nbrcol=nax\*3

nomrang<-list(1:nrang)

nomcol<-list(1:1+nax\*3)

for(j in 1:nax)

{

  nomcol[1+(j-1)\*3]<-paste("coord",j)

  nomcol[2+(j-1)\*3] <-paste("Cr%",j)

  nomcol[3+(j-1)\*3] <-paste("P",j)

}

resulnsca<-matrix(1:nrang\*nbrcol, nrow=nrang,ncol=nbrcol,byrow=TRUE)

colnames(resulnsca)<- nomcol

#calculation of the transformed and covariance matrices

donc<- matrix(1 :nbrsp\*nbrrel, nrow=nbrsp,ncol=nbrrel)

donc<-don

covar1<-matrix(rep(0,nbrrel\*nbrrel),nbrrel,nbrrel)

covar1<-covarnsca(donc,nbrsp,nbrrel)

#distribution histogram of the covariance coefficients with the function hist()

nbrcel=nbrrel\*(nbrrel-1)/2 +nbrrel

matcov<-as.matrix(1 :nbrcel, nrow=1,ncol=nbrcel)

i=0

for (j1 in 1:nbrrel)

{

  for (j2 in 1:j1)

  {

    i=i+1

    matcov[i]=covar1[j1,j2]

  }

}

hist(matcov, breaks=40, include.lowest = TRUE, right = TRUE,

     labels=FALSE, border = NULL,

     main = paste("NSCA"), plot=TRUE,

     axes = TRUE,

     warn.unused = TRUE)

#calculation of the trace, of the eigenvectors and eigenvalues

Lam<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

Lam2<-matrix(1:nbrrel,nrow=1,ncol=nbrrel)

R<-eigen(covar1, symmetric=TRUE, only.values=FALSE)

V <- R$vectors; Lam <- R$values

trace = sum(Lam)

trace

Lam2<-Lam\*100/trace

#calculation of the coordinates and relative contributions of the individuals on axes

coordrel<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

contrerel<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

hc<-colSums(don)

for(j in 1:nbrrel)

{

  for(b in 1 :nax)

  {

    coordrel[j,b]=V[j,b]/sqrt(hc[j])\*sqrt(somme)

    contrerel[j,b]=100\* V[j,b]\* V[j,b]

  }

}

coordrel

contrerel

#calculation of the coordinates and relative contributions of the species on axes

coordsp<-matrix(1 :nbrsp\*nax,nrow=nbrsp,ncol=nax)

contrelsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

for(b in 1 :nax)

{

  for(i in 1 : nbrsp)

  {

    cosp=0

    const= sqrt(nbrsp/(Lam[b]\*somme))

    for(j in 1 :nbrrel)

    {

      cosp= cosp+don[i,j]\*V[j,b]/sqrt(hc[j])\*const

    }

    coordsp[i,b]=cosp

    contrelsp[i,b]= cosp^2\*100

  }

}

#permutations of the matrix and new calculations

prob1<-matrix(1:nax\*1,nrow=1,ncol=nax,byrow=TRUE)

prob2<-matrix(1:nax\*nbrrel,nrow=nbrrel,ncol=nax,byrow=TRUE)

prob3<-matrix(1:nax\*nbrsp,nrow=nbrsp,ncol=nax,byrow=TRUE)

prob1[]<-0

prob2[]<-0

prob3[]<-0

nombreper<-0

for(np in 1:nper)

{

  Lamp<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  Lamp2<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  donc<-matrix(rep(0,nbrsp\*nbrrel),nbrsp,nbrrel)

  hc<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  covar1<-matrix(rep(0,nbrrel\*nbrrel),nbrrel,nbrrel)

  for(i in 1 :nbrsp)

  {

    donc[i,]<-sample(don[i,],nbrrel,replace=FALSE)

  }

  hc<-colSums(donc)

  if(min(hc)==0){

    next

  }

  nombreper=nombreper+1

  covar1<-covarnsca(donc,nbrsp,nbrrel)

  #calculation  of the eigenvectors, of the eigenvalues and of the trace after permutations

  Rp<-eigen(covar1, symmetric=TRUE, only.values=FALSE)

  Vp <- Rp$vectors; Lamp <- Rp$values

  trace2=sum(Lamp)

  Lamp2<-Lamp\*100/trace2

  for(b in 1 :nax)

  {

    if (Lamp[b]>=Lam[b])

    {

      prob1[b]=prob1[b]+1

    }

  }

  #calculation of the relative contributions of the individuals on axes after permutations

  contrerelp<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

  for(j in 1:nbrrel)

  {

    for(b in 1 :nax)

    {

      contrerelp[j,b]=100\* Vp[j,b]\* Vp[j,b]

      if(contrerelp[j,b] >=contrerel[j,b]){

        prob2[j,b]=prob2[j,b]+1

      }

    }

  }

  #calculation of the relative contributions of the species on axes after permutations

  contrelspp<-matrix(1 :nbrsp\*nax,nrow=nbrsp,ncol=nax)

  for(b in 1 :nax)

  {

    for(i in 1 : nbrsp)

    {

      cosp=0

      const= sqrt(nbrsp/(Lamp[b]\*somme))

      for(j in 1 :nbrrel)

      {

        cosp=cosp+donc[i,j]\*Vp[j,b]/sqrt(hc[j])\*const

      }

      contrelspp[i,b]=cosp^2\*100

      if (contrelspp[i,b] >=contrelsp[i,b]){

        prob3[i,b]=prob3[i,b]+1

      }

    }

  }

}

nombreper

prob1=prob1\*100/nombreper

prob2=prob2\*100/ nombreper

prob3=prob3\*100/ nombreper

for(j in 1:nax)

{

  resulnsca[1,3\*(j-1)+1]=Lam[j]

  resulnsca[1,3\*(j-1)+2]=Lam2[j]

  resulnsca[1,3\*(j-1)+3]=prob1[j]

}

nomrang[1]<- paste("Vp,Vp% and P")

for(i in 1 :nbrsp)

{

  for(j in 1:nax)

  {

    resulnsca[i+1,3\*(j-1)+1]=coordsp[i,j]

    resulnsca[i+1,3\*(j-1)+2]=contrelsp[i,j]

    resulnsca[i+1,3\*(j-1)+3]=prob3[i,j]

  }

  nomrang[i+1]=nomsp[i]

}

for(i in 1 :nbrrel)

{

  for(j in 1:nax)

  {

    resulnsca[i+1+nbrsp,3\*(j-1)+1]=coordrel[i,j]

    resulnsca[i+1+nbrsp,3\*(j-1)+2]=contrerel[i,j]

    resulnsca[i+1+nbrsp,3\*(j-1)+3]=prob2[i,j]

  }

  nomrang[i+1+nbrsp]=nomrel[i]

}

rownames(resulnsca)<-nomrang

pca.R

don<-as.matrix(filename)

nbrsp= nrow(don)

nbrrel= ncol(don)

nomsp<-rownames(don)

nomrel<-colnames(don)

nrang= 1+nbrsp+nbrrel

nbrcol=nax\*3

nomrang<-list(1:nrang)

nomcol<-list(1:nax\*3)

nomcol[1]<-paste("sp./releves")

for(j in 1:nax)

{

  nomcol[1+(j-1)\*3]<-paste("coord",j)

  nomcol[2+(j-1)\*3] <-paste("Cr%",j)

  nomcol[3+(j-1)\*3] <-paste("P",j)

}

resulpca<-matrix(1:nrang\*nbrcol, nrow=nrang,ncol=nbrcol,byrow=TRUE)

colnames(resulpca)<- nomcol

#calculation of the centered reduced matrix

don1<-matrix(1 :nbrsp\*nbrrel, nrow=nbrsp, ncol=nbrrel)

sce<-matrix(rep(0,1\*nbrsp),1,nbrsp)

moyenne<-rowMeans(don)

for(i in 1 :nbrsp)

{

  for(j in 1:nbrrel)

  {

    sce[i]=sce[i]+ (don[i,j]-moyenne[i])\* (don[i,j]-moyenne[i])

  }

  sce[i]=sqrt(sce[i]/nbrrel)

}

for(i in 1 :nbrsp)

{

  for(j in 1:nbrrel)

  {

    don1[i,j]=(don[i,j]-moyenne[i])/sce[i]

  }

}

#calculation of the correlation matrix, of eigenvectors and of eigenvalues

correlation<-cor(t(don1))

R<-eigen(correlation, symmetric=TRUE)

V <- R$vectors; Lam <- R$values

trace=sum(Lam)

Lam2<-matrix(1 :nbrsp)

Lam2=Lam\*100/trace

#correlation distribution histogram with function hist()

nbrcel=nbrsp\*nbrsp

matcov<-as.matrix(1 :nbrcel, nrow=1,ncol=nbrcel)

i=0

for (j1 in 1:nbrsp)

{

  for (j2 in 1:nbrsp)

  {

    i=i+1

    matcov[i]<-correlation[j1,j2]

  }

}

hist(matcov, breaks=40, include.lowest = TRUE, right = TRUE,labels=FALSE, border = NULL,main = paste("PCA"), plot=TRUE,axes = TRUE,warn.unused = TRUE)

#calculation of coordinates and relatives contributions of species on axes

coordsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

contrelsp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

contrelrel<-matrix(1 :nbrrel\*nax,nrow=nbrrel,ncol=nax)

for(i in 1:nbrsp)

{

  for(j in 1:nax)

  {

    coordsp[i,j] =V[i,j]\*sqrt(Lam[j])

    contrelsp[i,j] <- coordsp[i,j]^2

  }

}

# calculation of coordinates and relatives contributions of releves on axes

coordrel<-matrix(rep(0,nbrrel\*nax),nbrrel,nax)

nrm<-matrix(rep(0,1\*nbrrel),1,nbrrel)

for(i in 1:nbrrel)

{

  for (j in 1:nbrsp)

  {

    nrm[i] = nrm[i]+don1[j,i]^2

  }

}

for(i in 1:nbrrel)

{

  norme=nrm[i]

  for(a in 1:nax)

  {

    for(j in 1:nbrsp)

    {

      coordrel[i,a]= coordrel[i,a]+don1[j,i]\*V[j,a]

    }

    contrelrel[i,a]= coordrel[i,a]\* coordrel[i,a]/norme

  }

}

#permutations of the matrix and new calculations

prob1<-matrix(1:nax\*1,nrow=1,ncol=nax,byrow=TRUE)

prob2<-matrix(1:nax\*nbrsp,nrow=nbrsp,ncol=nax,byrow=TRUE)

prob3<-matrix(1:nax\*nbrrel,nrow=nbrrel,ncol=nax,byrow=TRUE)

prob1[]<-0

prob2[]<-0

prob3[]<-0

Lamp<-matrix(1:nbrsp,nrow=1,ncol= nbrsp)

Lamp2<-matrix(1:nbrsp,nrow=1,ncol= nbrsp)

don1p<-matrix(1 :nbrsp\*nbrrel, nbrsp,nbrrel)

coordspp<-matrix(1:nbrsp\*nax,nrow=nbrsp,ncol=nax)

for(np in 1:nper)

{

  for(i in 1 :nbrsp)

  {

    don1p[i,]<-sample(don1[i,],nbrrel,replace=FALSE)

  }

  #calculation of the correlation matrices and of eigenvalues and eigenvectors after permutations

  correlationp = cor(t(don1p))

  Rp<-eigen(correlationp, symmetric=TRUE)

  Vp <- Rp$vectors; Lamp <- Rp$values

  Lamp2<-Lamp\*100/nbrsp

  for(a in 1 :nax)

  {

    if (Lamp[a]>=Lam[a]){

      prob1[a]=prob1[a]+1

    }

  }

  #calculation of the coordinates and relative contributions of species on axes after permutations

  for(i in 1:nbrsp)

  {

    for(a in 1:nax)

    {

      coordspp[i,a] =Vp[i,a]\*sqrt(Lamp[a])

    }

  }

  # calculation of releve coordinates on axes after permutations

  for(i in 1:nbrsp)

  {

    for(a in 1:nax)

    {

      contrelspp =coordspp[i,a]\*coordspp[i,a]

      if (contrelspp>=contrelsp[i,a]){

        prob2[i,a]=prob2[i,a]+1

      }

    }

  }

  # calculation of the coordinates and relative contributions of species on axes after permutations

  nrmp<-matrix(rep(0,1\*nbrrel),1,nbrrel)

  for(i in 1:nbrrel)

  {

    for (j in 1:nbrsp)

    {

      nrmp[i] = nrmp[i]+(don1p[j,i]\* don1p[j,i])

    }

  }

  for(i in 1:nbrrel)

  {

    for(a in 1:nax)

    {

      coind=0

      for(j in 1:nbrsp)

      {

        coind= coind+don1p[j,i]\*Vp[j,a]

      }

      contrelrelp= coind\* coind/nrmp[i]

      if (contrelrelp>=contrelrel[i,a]){

        prob3[i,a]=prob3[i,a]+1

      }

    }

  }

}

prob1=prob1\*100/nper

prob2=prob2\*100/ nper

prob3=prob3\*100/ nper

for(j in 1:nax)

{

  resulpca[1,3\*(j-1)+1]=Lam[j]

  resulpca[1,3\*(j-1)+2]=Lam2[j]

  resulpca[1,3\*(j-1)+3]=prob1[j]

}

nomrang[1]<- paste("Vp,Vp% and P")

for(i in 1 :nbrsp)

{

  for(j in 1:nax)

  {

    resulpca[i+1,3\*(j-1)+1]=coordsp[i,j]

    resulpca[i+1,3\*(j-1)+2]=contrelsp[i,j]

    resulpca[i+1,3\*(j-1)+3]=prob2[i,j]

  }

  nomrang[i+1]=nomsp[i]

}

for(i in 1 :nbrrel)

{

  for(j in 1:nax)

  {

    resulpca[i+1+nbrsp,3\*(j-1)+1]=coordrel[i,j]

    resulpca[i+1+nbrsp,3\*(j-1)+2]=contrelrel[i,j]

    resulpca[i+1+nbrsp,3\*(j-1)+3]=prob3[i,j]

  }

  nomrang[i+1+nbrsp]=nomrel[i]

}

rownames(resulpca)<-nomrang

phyto1.R

don<-as.matrix(filename)

nbrrel= ncol(don)

nbrsp= nrow(don)

nomsp<-rownames(don)

nomrel<-colnames(don)

res<-matrix(1 :nbrrel\*nbrsp,nrow=nbrsp,ncol=nbrrel,byrow=TRUE)

for(i in 1:nbrsp)

{

  for(j in 1:nbrrel)

  {

    if (don[i,j]!=".")

    {

      res[i,j]=1

    }

    else

    {

      res[i,j]=0

    }

  }

}

rownames(res)<-c(nomsp)

colnames(res)<-c(nomrel)

resul<-data.frame(res)

phyto12345.R

don<-as.matrix(filename)

nbrrel= ncol(don)

nbrsp= nrow(don)

nomsp<-rownames(don)

nomrel<-colnames(don)

#calcul nombre de lignes du nouveau tableau

#definition of a new table

nomsp2<-list(1 :nbrsp)

don1<-matrix(1 :nbrrel\*nbrsp,nrow=nbrsp,ncol=nbrrel,byrow=TRUE)

for(i in 1:nbrsp)

{

  nomsp2[i]<-paste(nomsp[i])

}

for(i in 1:nbrsp)

{

  for(j in 1:nbrrel)

  {

    if (don[i,j] ==".")

    {

      don1[i,j]=0

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j] =="+"| don[i,j] =="r"| don[i,j] =="i"| don[i,j] ==1)

    {

      don1[i,j]=1

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j]==1)

    {

      don1[i,j]=1

    }

  }

  for(j in 1:nbrrel)

  {

    if (don[i,j]>1)

    {

      don1[i,j]<-paste(don[i,j])

    }

  }

}

rownames(don1)<-c(nomsp2)

colnames(don1)<-c(nomrel)

resul<-data.frame(don1)