

```

spedisparam <-
function(comm, method = c("D", "Delta", "L", "M"), abundance =
c("relative", "absolute"), alpha = 2, tol = 1e-8, ...)
{
  q <- alpha[1]
  if(!is.numeric(q)) stop("q must be a numeric")
  if(!inherits(comm, "matrix") && !inherits(comm, "data.frame"))
stop("Incorrect definition of comm")
  method <- method[1]
  if(!method%in%c("D", "Delta", "L", "M")) stop("Incorrect definition
for method")
  abundance <- abundance[1]
  if(!abundance%in%c("relative", "absolute"))
stop("Incorrect definition for abundance")
  dataset <- t(comm)
  total <- colSums(dataset)
  if(abundance == "relative")
    abu <- sweep(dataset, 2, total, "/")
  else abu <- dataset
  num.plot <- dim(dataset)[2]
  num.sp <- dim(dataset)[1]
  names<-list(colnames(dataset), colnames(dataset))
  dis.matrix<-matrix(0, nrow=num.plot, ncol=num.plot, dimnames=names)
  for (i in 2:num.plot) {
  for (j in 1:(i-1)) {
    Zik <- abu[, j]
    Zih <- abu[, i]
    tabZ <- rbind.data.frame(Zik, Zih)
    garde <- apply(tabZ, 2, sum)>tol
    Zik <- Zik[garde]
    Zih <- Zih[garde]
    tabZ <- tabZ[, garde]

    NUM <- (sum(((abs(Zik-Zih))^q))^(1/q)

    if(method == "D")
      DEN <- (sum(((Zik+Zih)^q))^(1/q)
    else if(method == "Delta")
      DEN <- ( sum((Zik^q))+ sum((Zih^q) )^(1/q)
    else if(method == "M")
      DEN <- 1
    else
      DEN <- (sum((Zik^q))^(1/q) + (sum((Zih^q))^(1/q)
    index <- NUM/DEN
    dis.matrix[i, j] <- index
  }
}
  dis.matrix <- dis.matrix + t(dis.matrix)
return(as.dist(dis.matrix, ...))
}

```

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fundisparam <-
function(comm, dis, method = c("D", "Delta", "L", "M"), abundance =
c("relative", "absolute"), alpha = 2, tol = 1e-8, ...)
{
  q <- alpha[1]
  if(!is.numeric(q)) stop("q must be a numeric")
  if(inherits(dis, "dist")) dis <- as.matrix(dis)

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if(!inherits(dis, "matrix")) stop("Incorrect definition of dis")
if(any(dis< (-tol))) stop("Incorrect definition of dis")
dis[dis<0] <- 0
if(!inherits(comm, "matrix") && !inherits(comm, "data.frame"))
stop("Incorrect definition of comm")
if(any(dis>1)){
  warning("dissimilarities in dis are not in the range 0-1. They
have been normalized by the maximum")
  dis <- dis/max(dis)
}
if(any(!colnames(comm) %in%rownames(dis))) stop("At least one species
in the matrix of abundances is missing in the matrix of dissimilarities")
if(any(!colnames(comm) %in%colnames(dis))) stop("At least one species
in the matrix of abundances is missing in the matrix of dissimilarities")
method <- method[1]
if(!method%in%c("D", "Delta", "L", "M")) stop("Incorrect definition
for method")
abundance <- abundance[1]
if(!abundance%in%c("relative", "absolute"))
stop("Incorrect definition for abundance")
dis <- dis[colnames(comm), colnames(comm)]
dataset <- t(comm)
similarities <- 1-as.matrix(dis)
total <- colSums(dataset)
if(abundance == "relative")
  abu <- sweep(dataset, 2, total, "/")
else abu <- dataset
num.plot <- dim(dataset)[2]
num.sp <- dim(dataset)[1]
names<-list(colnames(dataset), colnames(dataset))
dis.matrix<-matrix(0, nrow=num.plot, ncol=num.plot, dimnames=names)
for (i in 2:num.plot) {
for (j in 1:(i-1)) {
  mat_folk <- similarities*abu[, j]
  mat_folk2 <- similarities*abu[, i]
  Zik <- colSums(mat_folk)
  Zih <- colSums(mat_folk2)
  tabZ <- rbind.data.frame(Zik, Zih)
  garde <- apply(tabZ, 2, sum)>tol & apply(abu[,c(i,j)], 1,
sum)>tol
  Zik <- Zik[garde]
  Zih <- Zih[garde]
  tabZ <- tabZ[, garde]
  wk <- (abu[, j]+abu[, i])/sum(abu[, c(i,j)])
  wk <- wk[garde]

  NUM <- (sum((wk*(abs(Zik-Zih))^q))^(1/q)

  if(method == "D")
    DEN <- (sum(wk*(Zik+Zih)^q))^(1/q)
  else if(method == "Delta")
    DEN <- ( sum(wk*(Zik^q))+ sum(wk*(Zih^q)) )^(1/q)
  else if(method == "M")
    DEN <- 1
  else
    DEN <- (sum(wk*(Zik^q))^(1/q) + (sum(wk*(Zih^q))^(1/q)
index <- NUM/DEN
dis.matrix[i, j] <- index

```

```
    }  
  }  
  dis.matrix <- dis.matrix + t(dis.matrix)  
  return(as.dist(dis.matrix, ...))  
}
```