

Supplementary material of: Combining food-web theory and population dynamics to assess the impact of invasive species

R-code part 1: Inferences of trophic interactions

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Function definition

Function 1: `get_niche_attributes`

Infer the niche attributes of species in the species inventory based on their body size and their category. Niche parameters of primary producers are automatically set at 0. The function requires the package “stringr”.

Input: Data are ordered by decreasing body sizes.

1. `species_name` = the name of the species to use
2. `body_size` = \log_{10} (vector of species body sizes in μm)
3. `species_category` = “vertebrate”, “invertebrate”, “zooplankton”, or other. If “other” is mentioned, the species will automatically be considered as producer and not as consumer. Capital and lowercase letters are allowed for the species category. Species category can also be provided in French.

Outputs : A data frame with the Niche attributes of each species containing:

1. `name` = the species name
2. `n` = the \log_{10} (species body sizes in μm)
3. `low` = the lower bound of the species diet range (QR at 5%)
4. `high` = the higher bound of the species diet range (QR at 95%)
5. `c` = the center of the species diet range

```
get_niche_attributes <- function(name,body_size, species_category) {  
  
  Niche <- data.frame(name=NA,n=NA,c=NA,low=NA,high=NA)  
  
  for(i in 1:length(body_size)){  
    Niche2<-data.frame(name=NA,n=NA,c=NA,low=NA,high=NA)  
  
    # For primary producers  
    if(!str_detect(species_category[i], regex("vertebrate", ignore_case = TRUE)) |  
        !str_detect(species_category[i], regex("invertebrate", ignore_case = TRUE)) |  
        !str_detect(species_category[i], regex("vertebre", ignore_case = TRUE)) |  
        !str_detect(species_category[i], regex("invertebre", ignore_case = TRUE)) |  
        !str_detect(species_category[i], regex("zoop", ignore_case = TRUE))){  
      Niche2$name <- name[i]
```

```

Niche2$n <- body_size[i]
Niche2$low <- 0
Niche2$high <- 0
Niche2$c <- 0
}

# For vertebrates
if(str_detect(species_category[i], regex("vertebrate", ignore_case = TRUE)) |
   str_detect(species_category[i], regex("vertebre", ignore_case = TRUE))){
  qrsup <- Param_regvert[[2]]
  qrintf <- Param_regvert[[3]]
  Niche2$name <- name[i]
  Niche2$n <- body_size[i]
  Niche2$low <- qrintf[1] + qrintf[2]*body_size[i]
  Niche2$high <- qrsup[1] + qrsup[2]*body_size[i]
  Niche2$c <- Niche2$low+(Niche2$high-Niche2$low)/2
}

# For invertebrates
if(str_detect(species_category[i], regex("invertebrate", ignore_case = TRUE)) |
   str_detect(species_category[i], regex("invertebre", ignore_case = TRUE)) |
   str_detect(species_category[i], regex("zoop", ignore_case = TRUE))){
  qrsup <- Param_reginvert[[2]]
  qrintf <- Param_reginvert[[3]]
  Niche2$name <- name[i]
  Niche2$n <- body_size[i]
  Niche2$low <- qrintf[1] + qrintf[2]*body_size[i]
  Niche2$high <- qrsup[1] + qrsup[2]*body_size[i]
  Niche2$c <- Niche2$low+(Niche2$high-Niche2$low)/2
}
Niche <- rbind(Niche,Niche2)
}
return(na.omit(Niche))
}

```

Function 2: L_fn2

Transform the parameters from get_niche_attributes into an binary interaction matrix from Gravel et al. 2013

Inputs:

1. name = the species name
2. n = the log10(species body sizes in μm)
3. low = the lower bound of the species diet range (QR at 5%)
4. high= the higher bound of the species diet range (QR at 95%)
5. c = the center of the species diet range
6. table= "NO" to only obtain the binary matrix, "YES" to only obtain the binary matrix + a data.frame with one observation = one interaction

Outputs :

A binary interaction matrix with 0 indicating absence of a link and 1 indicating the presence of a link with consumers in columns (j) and resources in rows (i) OR A list with the binary interaction matrix + a table referencing each link with :

1. Res = the resource name
2. Cons = the consumer name
3. Log10Size_Res = log10(resource body size)
4. Log10Size_Cons = log10(consumer body size)

```
L_fn2 <- function(name,n,c,low,high,table) {

  S <- length(n)
  L <- matrix(0,nr=S,nc=S)

  for(j in 1:S)
    for(i in 1:S)
      if(n[i]>low[j] && n[i]<high[j]) L[i,j] = 1
  colnames(L) <-name
  rownames(L) <-name

  Table<-data.frame(Res=NA,Cons=NA,Log10Size_Res=NA,Log10Size_Cons=NA)
  for(i in 1:S){
    if(length(which(L[,j]==1))!=0){
      Table2 <- data.frame(Res=names(which(L[,j]==1)),
                           Cons=rep(colnames(L)[j],length(which(L[,j]==1))),
                           Log10Size_Res=n[which(L[,j]==1)],
                           Log10Size_Cons=n[j])
    }
    else{Table2<-data.frame(Res=NA,Cons=NA,Log10Size_Res=NA,Log10Size_Cons=NA)}
    Table <- rbind(Table,Table2)}

  if(table=="NO"){
    return(L)
  }
  if(table=="YES"){
    return(list(Bmat=L,Table=na.omit(Table)))
  }
}
```

Function3: Ref_L_Diet

Refine links for impossible results according to species diet trait. Fish do not eat primary producers. Carnivorous macroinvertebrates do not eat primary producers Other diet refinement can be implemented after applying the function as they are considered as site-specific.

Inputs:

1. Bmat = binary matrix of trophic links inferred from L_fn2 function with : colnames and rownames = names of species in the inventory
2. diet = "invP" or "inv" for invertebrates | "p"=piscivorous or "o"=omnivorous for fish | "prod" for primary producers
3. table = "YES" or "NO" to obtain or note the matrix with links refined
4. LinksTab = if Table is "YES" provide the table of links obtained with the function L_fn2

Outputs :

1. if table="NO", returns th Binary matrix after link refinement
2. if table="YES", returns th Binary matrix after link refinement + the table of links after links refinement

```

Ref_L_Diet <- function(Bmat, diet, table, LinksTab) {
  if(table=="NO"){

    for(j in 1:ncol(Bmat)){
      for (i in 1:nrow(Bmat)){

        if(diet[j]=="omnivorous" & diet[i]=="prod" |

          diet[j]=="piscivorous" & diet[i]=="prod"){
          Bmat[i,j]<-0
        }else{Bmat[i,j]<-Bmat[i,j]}

        if(diet[j]=="invP" &
          diet[i]=="prod"){
          Bmat[i,j]<-0
        }else{Bmat[i,j]<-Bmat[i,j]}
      }
    }
    return(Bmat_ref=Bmat)
  }

  if (table == "YES") {
    for(j in 1:ncol(Bmat)){
      for (i in 1:nrow(Bmat)){
        if(length(which(Bmat[,j]==1))!=0){

          if(diet[j]=="omnivorous" & diet[i]=="prod" |
            diet[j]=="piscivorous" & diet[i]=="prod"){
            Bmat[i,j]<-0
          }else{Bmat[i,j]<-Bmat[i,j]}

          if(diet[j]=="invP" & diet[i]=="prod"){
            Bmat[i,j]<-0
          }else{Bmat[i,j]<-Bmat[i,j]}

        }else{Bmat[,j]<-0}
      }
    }

    for (j in 1:ncol(Bmat)) {
      for (i in 1:nrow(Bmat)) {
        if(Bmat[i,j]==0){
          LinksTab$Prey[LinksTab$Prey==rownames(Bmat)[i]&
            LinksTab$Pred==colnames(Bmat)[j]]<-NA
        }else{

        }
      }
    }
    return(list(Bmat_ref = Bmat, Table_ref=na.omit(LinksTab)))
  }
}

```

Function 4: Ref_L_Hab

Refine links for impossible results according to the habitat trait

Inputs:

1. Bmat = binary matrix of trophic links inferred from L_fn2 function with : colnames and rownames = names of species in the inventory
2. habitat = "pel" or "ben" or "pel/ben"
3. Table = "YES" or "NO" to obtain or note the matrix with links refined

Outputs :

1. if Table="NO", returns th Binary matrix after link refinement
2. if Table="YES", returns th Binary matrix after link refinement and the table of links after links refinement

```
Ref_L_Hab <- function(Bmat, habitat, table, LinksTab) {  
  if(table=="NO"){  
    for(j in 1:ncol(Bmat)){  
      for (i in 1:nrow(Bmat)){  
        if(length(which(Bmat[,j]==1))!=0){  
  
          if(habitat[j]=="pel" &  
             habitat[i]=="ben" |  
             habitat[j]=="ben" &  
             habitat[i]=="pel"){  
            Bmat[i,j]<-0  
          }else{Bmat[i,j]<-Bmat[i,j]}  
  
        }else{Bmat[,j]<-0}  
      }  
    }  
  
    return(Bmat_ref=Bmat)  
  }  
  
  if (table == "YES") {  
    for (j in 1:ncol(Bmat)) {  
      for (i in 1:nrow(Bmat)) {  
        if (length(which(Bmat[, j] == 1)) != 0) {  
          if (habitat[j] == "pel" &  
              habitat[i] == "ben" |  
              habitat[j] == "ben" &  
              habitat[i] == "pel") {  
            Bmat[i, j] <- 0  
          } else{  
            Bmat[i, j] <- Bmat[i, j]  
          }  
  
        } else{  
          Bmat[, j] <- 0  
        }  
      }  
    }  
  }  
  
  for (j in 1:ncol(Bmat)) {
```

```

for (i in 1:nrow(Bmat)) {
  if(Bmat[i,j]==0){
    LinksTab$Prey[LinksTab$Prey==rownames(Bmat)[i]&
                  LinksTab$Pred==colnames(Bmat)[j]]<-NA
  }else{
  }
}
}
}
return(list(Bmat_ref = Bmat,Table_ref = na.omit(LinksTab)))
}
}

```

Function 5: Weighting

Used to obtain the likelihood of an occurring trophic link between a consumer and a resource. This “weighting” is scaled to the resource body size range obtained from diet range for each consumer.

Inputs :

1. Niche_attributes = data frame resulting from the function “get_niche_attribute” with :
 - names = species name also used as colnames/rownames for the binary matrix
 - n = log10(species body size (μm))
 - c = optimal center of the niche (log10(μm))
 - low = lower bound of the niche range (log10(μm))
 - high =higher bound of the niche range (log10(μm))
2. Bmat = initial binary interaction matrix

Outputs :

1. the “weighted” interaction matrix

```

Weighting <- function(Niche_attributes,Bmat){
  for(j in 1:ncol(Bmat)){
    if(length(which(Bmat[,j]==1))!=0){
      Bmat[which(Bmat[,j]==1),j] <- dnorm(Niche_attributes$n[which(Bmat[,j]==1)],
      mean=Niche_attributes$c[j],
      sd=sd(seq(from=Niche_attributes$low[j],to=Niche_attributes$high[j],
      by=((Niche_attributes$high[j]-Niche_attributes$low[j])/100))))/
      max(dnorm(Niche_attributes$n[which(Bmat[,j]==1)],
      mean=Niche_attributes$c[j],
      sd=sd(seq(from=Niche_attributes$low[j],to=Niche_attributes$high[j],
      by=((Niche_attributes$high[j]-Niche_attributes$low[j])/100))))))
    }else{Bmat[which(Bmat[,j]!=1),j]<-0}
  }
  return(Bmat)
}

```

Example: Inference and refinement of the trophic links among species in an inventory

Loading library and data

```
library(stringr)

#Parameters to calculate the consumers diet range (regressions quantiles)
load("Param_reginvert.Rdata") # For invertebrates
load("Param_regvert.Rdata")  # For vertebrates

#Loading of the species inventory created for the example
load("Example_SpInventory.Rdata")
DATA2<-DATA[order(DATA$bs,decreasing=TRUE),] # species are ordered by decreasing body size
DATA2$Log10bs<-log10(DATA2$bs) #Body size is transformed to log10
```

A) The resource body sizes range are reconstructed for consumers based on :

1. species category (i.e., primary producers, zooplankton,invertebrate, vertebrate)
2. body size

Note that rows corresponding to primary producers are automatically filled with 0.

```
bs_r<-get_niche_attributes(name=DATA2$Species,
                          body_size = DATA2$Log10bs,
                          species_category = DATA2$Category)
```

B) Inferences of all trophic links (binary matrix)

```
Bmat<-L_fn2(name=bs_r$name,n=bs_r$n,c=bs_r$c,low=bs_r$low,high=bs_r$high,table="NO")
```

C) Links refinement based on consumers' diet

```
Bmat_Diet<-Ref_L_Diet(Bmat=Bmat, diet=DATA2$Diet,table="NO")
```

D) Links refinement based on consumers' habitat

```
Bmat_Hab<-Ref_L_Hab(Bmat=Bmat_Diet,habitat =DATA2$Habitat,table="NO")
# Note that supplementary refinement can be implemented depending on the ecosystems or the
# species studied.In this example fish and predatory invertebrates are not allowed to consume
# primary producers.
# Final binary matrix Mb is given by:
Mb<-Bmat_Hab
```

E) Weighting of refined trophic links

```
Mb_W<-Weighting(Niche_attributes = bs_r,Bmat=Mb)
```

F) Use weightings as resources i proportions in diet of consumer j

$$\omega_{ji} = \frac{WeightedLink_{ji}}{\sum_{i \in resources\ of\ j} WeightedLink_{ji}} \quad (eq.1)$$

```
Wji<-Mb_W
Wji[,which(colSums(Wji)!=0)]<-t((1/colSums(Wji[,which(colSums(Wji)!=0)])) *
                                t(Wji[,which(colSums(Wji)!=0)]))
```

G) Save matrices used in the simulations of population dynamics

```
save(DATA2,file="DATA2.Rdata")# Species inventory with supplementary data  
save(Mb,file="Mb.Rdata") # Binary interaction matrix  
save(Wji,file="Wji.Rdata") # Matrix of resources  $i$  proportions in diet of consumer  $j$ 
```