

Modelling beta diversity of aquatic macroinvertebrates in High Andean wetlands

Carolina NIETO,^{1,2} Daniel A. DOS SANTOS,^{1,2*} Andrea E. IZQUIERDO,^{2,3}

José S. RODRÍGUEZ,¹ Héctor R. GRAU^{2,3}

¹Instituto de Biodiversidad Neotropical (IBN), CONICET-UNT, Crisóstomo Álvarez 722, San Miguel de Tucumán, Tucumán 4000

²Facultad de Ciencias Naturales e I.M.L., Miguel Lillo 205, San Miguel de Tucumán, Tucumán 4000

³Instituto de Ecología Regional (IER), CONICET-UNT, Horco Molle s/n, Yerba Buena, Tucumán 4107, Argentina.

***Corresponding Author:** dadosantos@csnat.unt.edu.ar

Supplementary Material. Function coded in R language to calculate the compositional dissimilarity between pairs of sampled communities.

```
compdiss <- function(Amatrix, taxaincols = TRUE) {  
  if(taxaincols) Amatrix <- as.matrix(Amatrix)  
  else Amatrix <- as.matrix(t(Amatrix))  
  n <- ncol(Amatrix)  
  s <- nrow(Amatrix)  
  Rmatrix <- prop.table(Amatrix, 1)  
  CSmatrix <- matrix(0, s, s)  
  rownames(CSmatrix) <- colnames(CSmatrix) <- rownames(Amatrix)  
  for(y in 1:(s - 1))  
    for(z in (y+1):s) {  
      aux1 <- sweep(Rmatrix, 2, Rmatrix[y, ], "-")*sweep(Rmatrix, 2, Rmatrix[z, ], "-")  
      aux2 <- sweep(Amatrix, 2, Amatrix[y, ], "-")*sweep(Amatrix, 2, Amatrix[z, ], "-")  
      total <- sum(aux1 > 0) + sum(aux2 > 0)  
      CSmatrix[y, z] <- CSmatrix[z, y] <- total/(2*n*(s - 2))  
    }  
  DS <- as.dist(1 - CSmatrix)  
  return(DS)  
}
```