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SUPPLEMENTARY MATERIAL

Modelling beta diversity of aquatic macroinvertebrates in High Andean wetlands

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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)
}
```