

Living on the EDGE: From the evolutionary uniqueness to the conservation status of Colombian Elapids and Viperids

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FUNCTION EDGE BY Cortés-Díaz (*in press*)

To apply this function, it is necessary to have a table with the species names (column 1), ED scores (Column 2) and GE scores (column 3)

```
edge.species <- function(data) {  
  
  #Apply the first part of the formula by Issac et a.(2007)  
  ED<-apply(data[,2, drop=F],2, function(x) {log(x+1)})  
  
  #Obtain the values of GE multiplied by the natural Logarithm  
  
  GE<-apply(data[,3, drop=F],2, function(x) {x*(log(2))})  
  
  #Create a matrix with the previously calculated data corresponding to each species.  
  
  matriz <- cbind(data[,1], as.data.frame(GE), as.data.frame(ED))  
  
  #Calculate the EDGE index  
  
  EDGE<- rowSums(matriz[,2:3])  
  
  #The results will be immersed in a matrix with the species and their EDGE values.  
  
  results<- cbind(data[,1], as.data.frame(EDGE))  
  names(results)<- c("Species", "EDGE")  
  results <- data.frame(results, row.names = "Species")  
  return(results)  
}
```