History_Diversity.R

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Thu Jun 15 23:59:12 2017

```
#Diferentes analisis de diversidad y rarefracción usando funciones del paquete Vegan


#Para Cargar el paquete
library(vegan) #se requiere esta libreria para bajar la base de datos BCI
```

```
## Loading required package: permute
```

```
## Loading required package: lattice
```

```
## This is vegan 2.4-3
```

```
data(BCI)
TablaH <- BCI[1:23,] #Solo escojo unos renglones (En este caso sitios)
nrow(TablaH)
```

```
## [1] 23
```

```
UU <- rep("Veg",nrow(TablaH))
UUU <- seq(1:nrow(TablaH))
FactoresH <- paste(UU,UUU, sep=".")
FactoresH
```

```
##  [1] "Veg.1"  "Veg.2"  "Veg.3"  "Veg.4"  "Veg.5"  "Veg.6"  "Veg.7"
##  [8] "Veg.8"  "Veg.9"  "Veg.10" "Veg.11" "Veg.12" "Veg.13" "Veg.14"
## [15] "Veg.15" "Veg.16" "Veg.17" "Veg.18" "Veg.19" "Veg.20" "Veg.21"
## [22] "Veg.22" "Veg.23"
```

```
#head(TablaH,3)
apply(TablaH,1,sum)
```

```
##   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18
## 448 435 463 508 505 412 416 431 409 483 401 366 409 438 462 437 381 347
##  19  20  21  22  23
## 433 429 408 418 340
```

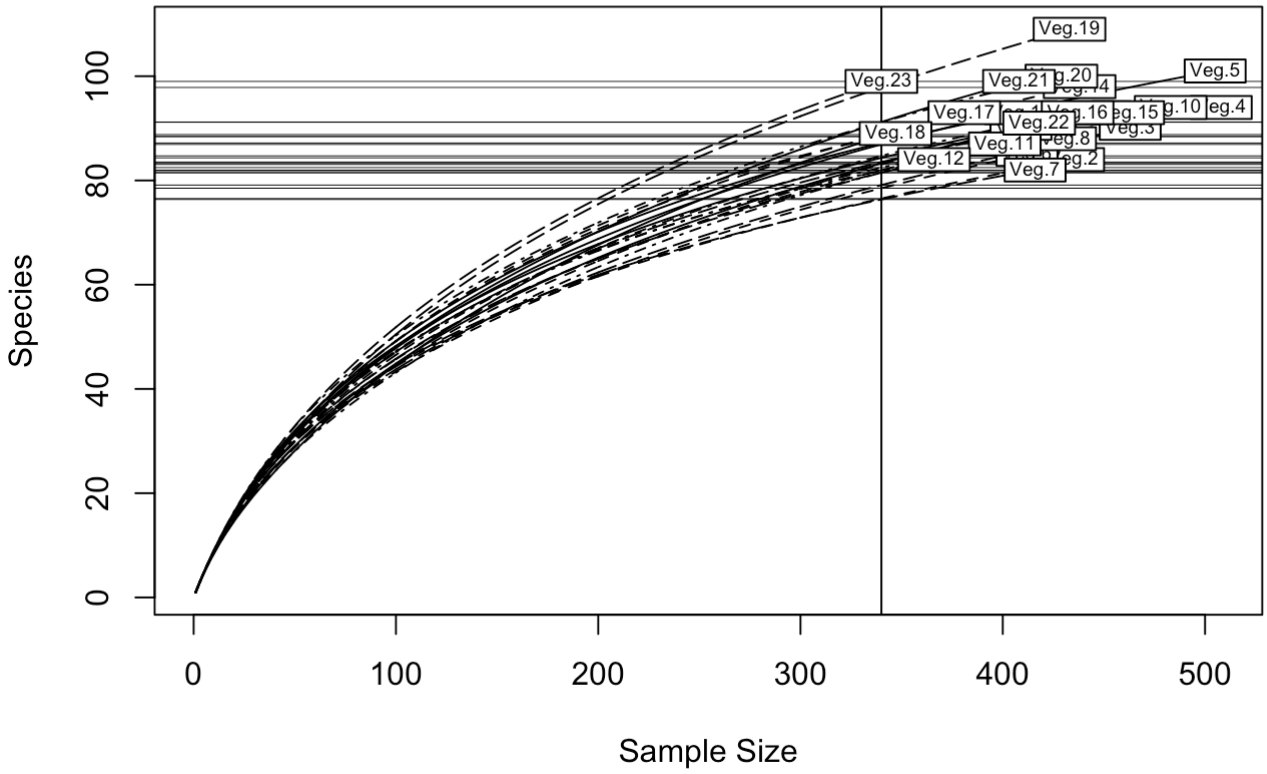
```
nrow(TablaH)
```

```
## [1] 23
```

```
#Este seria el indicador de los ocho renglones de la TablaH


########################################
######## Diversidad Varios analisis
#Aqui analizamos varios parametros de diversidad: Shannon, Inversa de Simpson, equidad d
e Pielou y el numero total de especies
#Factor seria las variables alfanumericas que escogeriamos para hacer el analisis (e.g.
 vegetacion, sitios de muestreo)

#Variable "Tabla" debe tener el mismo numero de renglones que la variable "factor"
#Variable "factor" debe tener distinto nombre

DiversidadCC <- function(Tabla,factor){
        require(vegan)
        SpecNum <- specnumber(Tabla) ## #rowSums(BCI > 0)#  Species         richness
        ShannonD <- diversity(Tabla)#Shannon entropy
    Pielou <- ShannonD/log(SpecNum)#Pielou's evenness
        Simp <- diversity(Tabla, "simpson")#        Indice de dominacia de Simpson
        TablaF <- data.frame(factor,SpecNum, ShannonD, Simp, Pielou)
        print("Indicadors de Diversidad")
        print(TablaF)
}
DiversidadCC(TablaH,FactoresH)
```

```
## [1] "Indicadors de Diversidad"
##    factor SpecNum ShannonD      Simp    Pielou
## 1   Veg.1      93 4.018412 0.9746293 0.8865579
## 2   Veg.2      84 3.848471 0.9683393 0.8685692
## 3   Veg.3      90 3.814060 0.9646078 0.8476046
## 4   Veg.4      94 3.976563 0.9716117 0.8752597
## 5   Veg.5     101 3.969940 0.9678267 0.8602030
## 6   Veg.6      85 3.776575 0.9627557 0.8500724
## 7   Veg.7      82 3.836811 0.9672014 0.8706729
## 8   Veg.8      88 3.908381 0.9671998 0.8729254
## 9   Veg.9      90 3.761331 0.9534257 0.8358867
## 10 Veg.10      94 3.889803 0.9663808 0.8561634
## 11 Veg.11      87 3.859814 0.9658398 0.8642843
## 12 Veg.12      84 3.698414 0.9550599 0.8347024
## 13 Veg.13      93 3.982373 0.9692075 0.8786069
## 14 Veg.14      98 4.017494 0.9718626 0.8762317
## 15 Veg.15      93 3.956635 0.9709057 0.8729284
## 16 Veg.16      93 3.916821 0.9686598 0.8641446
## 17 Veg.17      93 3.736897 0.9545126 0.8244489
## 18 Veg.18      89 3.944985 0.9676685 0.8788828
## 19 Veg.19     109 4.013094 0.9655820 0.8554245
## 20 Veg.20     100 4.077327 0.9748589 0.8853802
## 21 Veg.21      99 3.969925 0.9686058 0.8639438
## 22 Veg.22      91 3.755413 0.9548316 0.8325271
## 23 Veg.23      99 4.062575 0.9723529 0.8841064
```

```
##############################################
##############Para Rarefraccion
#Variable "Tabla" debe tener el mismo numero de renglones que la variable "factor"
#Variable "factor" debe tener distinto nombre


RarefraccionCC <- function(Tabla,factor){
    require(vegan)
    Tabla1 <- data.frame(Tabla, row.names = factor)
    raremax <- min(rowSums(Tabla1))
    col1 <- seq(1:nrow(Tabla1)) #Para poner color a las lineas
    lty1 <- c("solid","dashed","longdash","dotdash")
    rarecurve(Tabla1, sample = raremax, col = "black", lty = lty1, cex = 0.6)
  #Para calcular el numero de especies de acuerdo a rarefraccion
  UUU <- rarefy(Tabla1, raremax)
  print(UUU)
}


RarefraccionCC(TablaH,FactoresH)
```

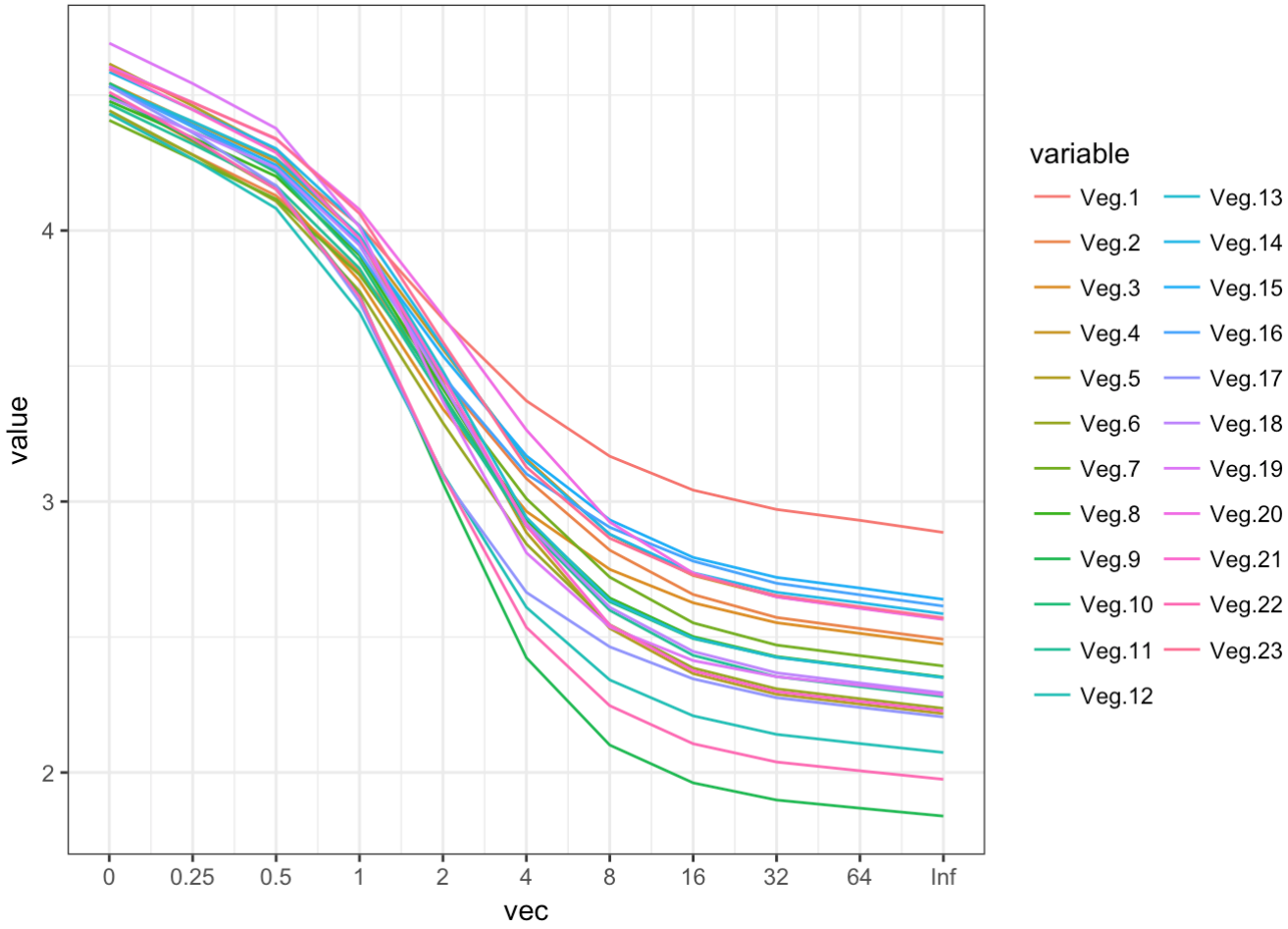



```
##    Veg.1    Veg.2    Veg.3    Veg.4    Veg.5    Veg.6    Veg.7    Veg.8
## 84.33992 76.53165 79.11504 82.46571 86.90901 78.50953 76.34768 81.88136
##    Veg.9   Veg.10   Veg.11   Veg.12   Veg.13   Veg.14   Veg.15   Veg.16
## 83.26880 81.97148 81.50075 81.48412 87.18673 88.80562 83.52890 84.72147
##   Veg.17   Veg.18   Veg.19   Veg.20   Veg.21   Veg.22   Veg.23
## 88.43415 88.42566 97.83931 91.17334 91.20346 83.07428 99.00000
## attr(,"Subsample")
## [1] 340
```

```
##############################################
####Para Calcular Renyi#######
#Variable "Tabla" debe tener el mismo numero de renglones que la variable "factor"
#Variable "factor" debe tener distinto nombre

RenyiCC <- function(Tabla, factor){
        require(vegan) #Paquete para la funcion "renyi"
        require(ggplot2)#Paquete para hacer la funcion "qplot"
        require(reshape)#Paquete para la funcion "melt"
        Tabla <- data.frame(Tabla, row.names = factor)
        mod <- renyi(Tabla)
        vec <- seq(1:11)
        mod1 <- data.frame(vec,t(mod))
        mod2 <- melt(mod1, id = c("vec"))
        mod2
        #mod2$variable <- as.numeric(mod2$variable)
    orange <- qplot(vec, value, data = mod2, colour = variable, geom =  "line") + theme_
bw()
    orange + scale_x_continuous(breaks = c(1,2,3,4,5,6,7,8,9,10,11),        labels =
c("0","0.25","0.5","1","2","4","8","16","32","64","Inf"))
}

RenyiCC(TablaH, FactoresH)
```

```
## Loading required package: ggplot2
```

```
## Loading required package: reshape
```



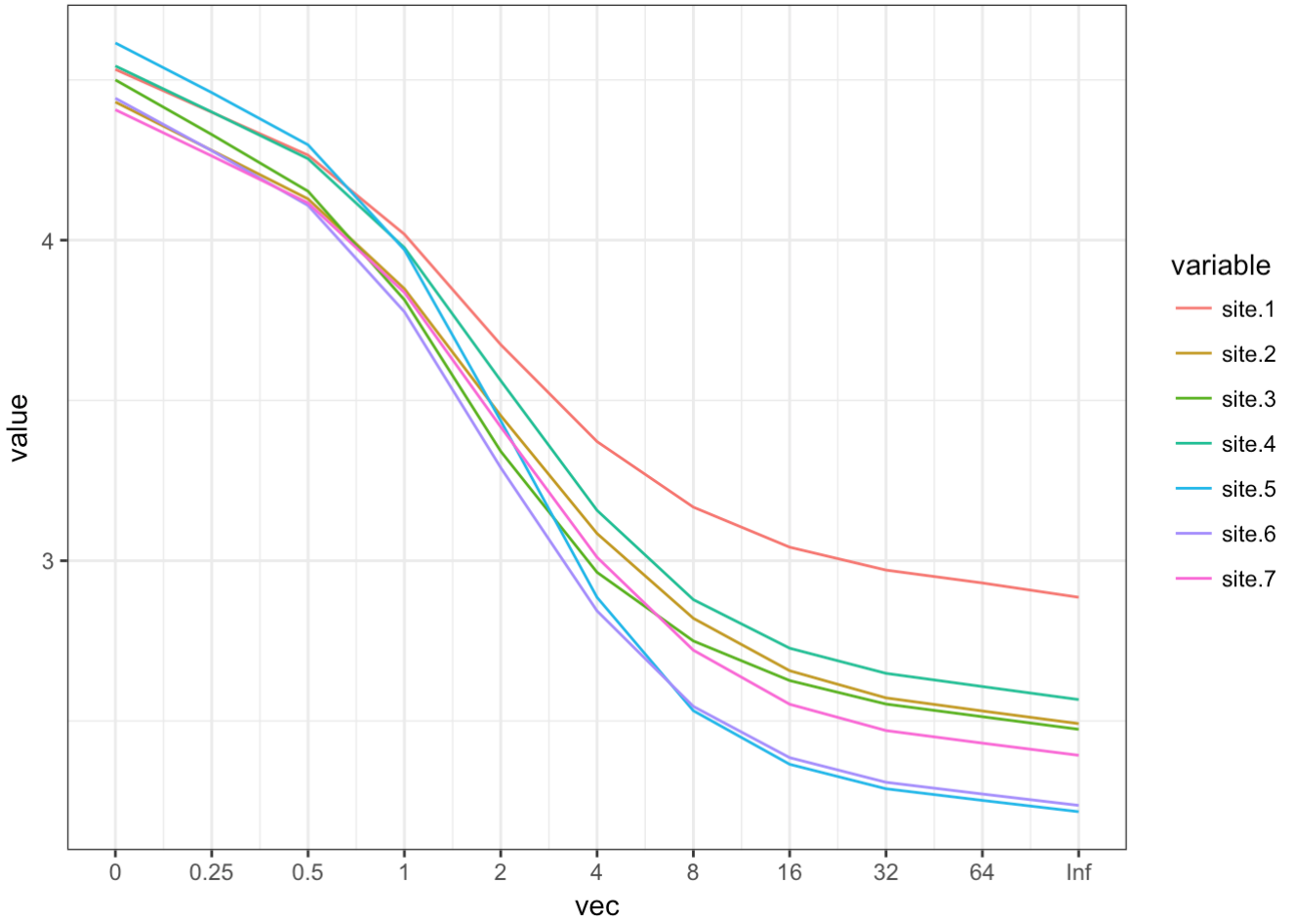

```
library(vegan)

data(BCI)
dim(BCI)
```

```
## [1]  50 225
```

```
BCI1 <- BCI[1:7,]
vec1 <- paste(rep("site",7),seq(1:7), sep = ".")

DiversidadCC(BCI1,vec1)
```

```
## [1] "Indicadors de Diversidad"
##   factor SpecNum ShannonD      Simp    Pielou
## 1 site.1      93 4.018412 0.9746293 0.8865579
## 2 site.2      84 3.848471 0.9683393 0.8685692
## 3 site.3      90 3.814060 0.9646078 0.8476046
## 4 site.4      94 3.976563 0.9716117 0.8752597
## 5 site.5     101 3.969940 0.9678267 0.8602030
## 6 site.6      85 3.776575 0.9627557 0.8500724
## 7 site.7      82 3.836811 0.9672014 0.8706729
```

```
RenyiCC(BCI1, vec1)
```



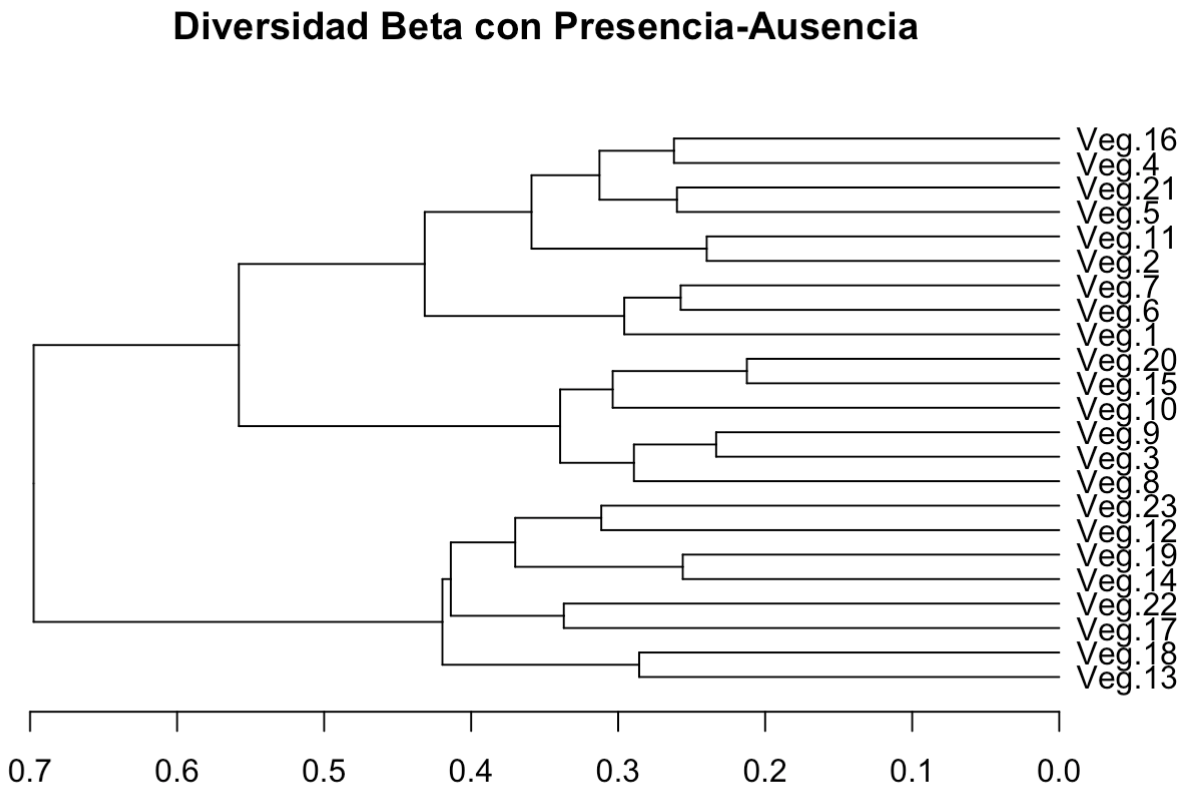

```
############################################################

# Calcular Diversidad Beta para presencia y ausencia o abundancia
# Tabla, debera de tener los valores de cada sitio
# variable factor debe tener distinto nombre
# el valor "n" es el tipo de metodo de analisis de la diversidad beta
# el valor de "n" debe de ir del 1 al 24 de acuerdo al articulo de
# Koleff et al., 2003 o buscar el numero en: betadiver(help = TRUE)

#Alex quiza hacer una opcion para que si el usuario quiere abundancia
# o los datos en presencia y ausencia?

#Para presencia y ausencia
DivBetaPA <- function(Tabla, Factor, n1){
  require(vegan) #Paquete para la funcion "betadiver"
  #Diversidad Beta de acuerdo a Koleff et al., con presencia y ausencia
  Tabla <- data.frame(Tabla, row.names = Factor)
  Tabla
  Tabla <- decostand(Tabla, "pa")
  mod <- betadiver(Tabla, method = n1, binary = F)
  mod
  hca <- hclust(mod, method = "ward.D")
  plot(as.dendrogram(hca), horiz = T, main = "Diversidad Beta con Presencia-Ausencia")
  print(mod)
}
ls()
```

```
##  [1] "BCI"            "BCI1"           "DivBetaPA"      "DiversidadCC"
##  [5] "FactoresH"      "RarefraccionCC" "RenyiCC"        "TablaH"
##  [9] "UU"             "UUU"            "vec1"
```

```
#Para abundancia
DivBetaAbun <- function(Tabla, Factor, n1){
  require(vegan) #Paquete para la funcion "vegdist"
  Tabla <- data.frame(Tabla, row.names = Factor)
  Tabla

  #Los distintos tipos de analisis
  if (n1 == 1) {
    n2 <- "manhattan"
  } else if (n1 == 2) {
    n2 <- "euclidean"
  } else if (n1 == 3) {
    n2 <- "canberra"
  } else if (n1 == 4) {
    n2 <- "bray"
  } else if (n1 == 5) {
    n2 <- "kulczynski"
  } else if (n1 == 6) {
    n2 <- "jaccard"
  } else if (n1 == 7) {
    n2 <- "gower"
  } else if (n1 == 8) {
    n2 <- "altGower"
  } else if (n1 == 9) {
    n2 <- "morosita"
  } else if (n1 == 10) {
    n2 <- "horn"
  } else if (n1 == 11) {
    n2 <- "mountford"
  }else if (n1 == 12) {
    n2 <- "raup"
  } else if (n1 == 13) {
    n2 <- "binomial"
  } else if (n1 == 14) {
    n2 <- "chao"
  } else if (n1 == 15) {
    n2 <- "cao"
  } else if (n1 == 16) {
    n2 <- "mahalanobis"
  }

  mod <- vegdist(Tabla, method = n2)
  mod
  hca <- hclust(mod, method = "ward.D")
  plot(as.dendrogram(hca), horiz = T, main = "Diversidad Beta con Abundancia")
  print(mod)
}

ls()
```

```
##  [1] "BCI"            "BCI1"           "DivBetaAbun"    "DivBetaPA"
##  [5] "DiversidadCC"   "FactoresH"      "RarefraccionCC" "RenyiCC"
##  [9] "TablaH"         "UU"             "UUU"            "vec1"
```

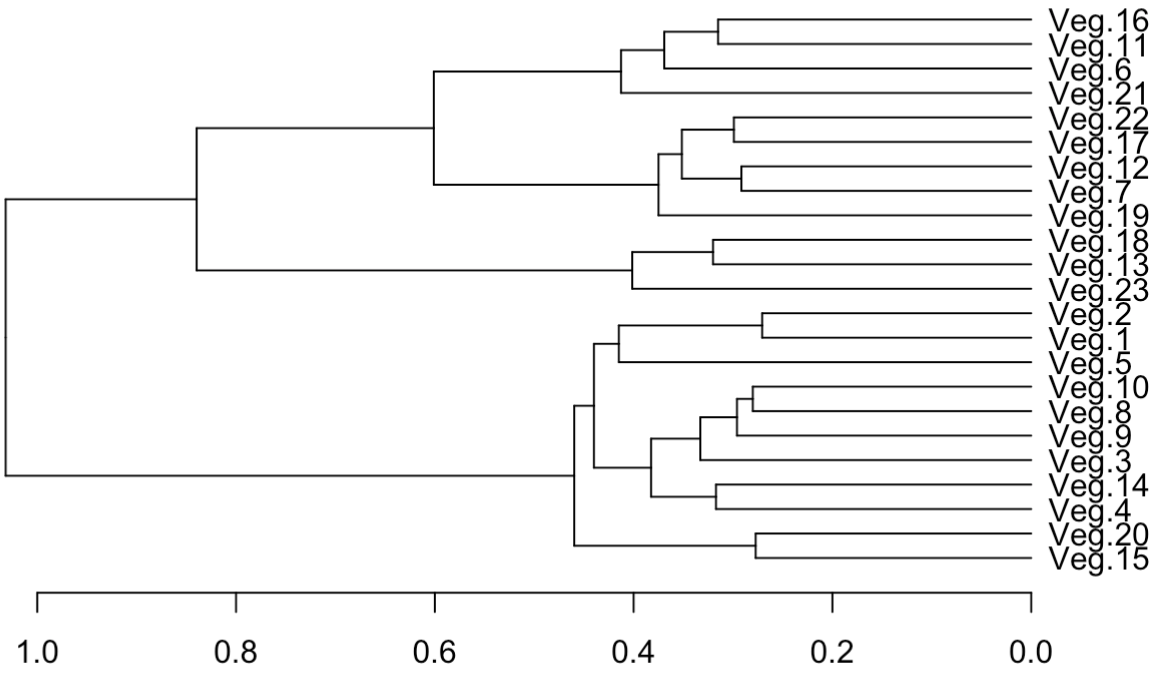
```
par(mfrow = c(1,1))
DivBetaPA(TablaH, FactoresH, 9)
```



```
##            Veg.1     Veg.2     Veg.3     Veg.4     Veg.5     Veg.6
## Veg.2  0.2768362
## Veg.3  0.3005464 0.2873563
## Veg.4  0.2834225 0.2808989 0.2717391
## Veg.5  0.2989691 0.3081081 0.2984293 0.2615385
## Veg.6  0.2696629 0.3372781 0.3600000 0.2849162 0.3225806
## Veg.7  0.3028571 0.3253012 0.3372093 0.2954545 0.3442623 0.2574850
## Veg.8  0.3370166 0.3023256 0.2921348 0.2967033 0.2910053 0.3872832
## Veg.9  0.3442623 0.2758621 0.2333333 0.2826087 0.2670157 0.3371429
## Veg.10 0.3475936 0.3258427 0.2826087 0.2659574 0.3025641 0.3407821
## Veg.11 0.3111111 0.2397661 0.2768362 0.2707182 0.2978723 0.2906977
## Veg.12 0.4237288 0.3452381 0.3908046 0.3370787 0.3189189 0.3727811
## Veg.13 0.4086022 0.4124294 0.4098361 0.4010695 0.3917526 0.4044944
## Veg.14 0.3612565 0.3406593 0.2872340 0.3020833 0.3266332 0.3224044
## Veg.15 0.3333333 0.3220339 0.2896175 0.2620321 0.3092784 0.3932584
## Veg.16 0.3440860 0.2881356 0.3333333 0.2620321 0.2989691 0.2921348
## Veg.17 0.3225806 0.3333333 0.3224044 0.3262032 0.3092784 0.3595506
## Veg.18 0.4285714 0.4450867 0.4301676 0.3989071 0.4631579 0.4367816
## Veg.19 0.3168317 0.3264249 0.3266332 0.2906404 0.3238095 0.3402062
## Veg.20 0.3367876 0.3478261 0.3368421 0.2783505 0.3233831 0.3945946
## Veg.21 0.3750000 0.3442623 0.3439153 0.3056995 0.2600000 0.3586957
## Veg.22 0.4239130 0.4057143 0.3812155 0.3621622 0.3854167 0.3522727
## Veg.23 0.3854167 0.3114754 0.4179894 0.3471503 0.3400000 0.3369565
##            Veg.7     Veg.8     Veg.9    Veg.10    Veg.11    Veg.12
## Veg.2
## Veg.3
## Veg.4
## Veg.5
## Veg.6
## Veg.7
## Veg.8  0.4000000
## Veg.9  0.3139535 0.2584270
## Veg.10 0.3863636 0.3186813 0.2717391
## Veg.11 0.3609467 0.2914286 0.2994350 0.3038674
## Veg.12 0.3132530 0.3488372 0.3103448 0.4044944 0.3450292
## Veg.13 0.3485714 0.3812155 0.3661202 0.4224599 0.4111111 0.3559322
## Veg.14 0.3444444 0.3225806 0.2659574 0.3541667 0.3189189 0.3736264
## Veg.15 0.4057143 0.2596685 0.2459016 0.2834225 0.3000000 0.4011299
## Veg.16 0.2914286 0.4143646 0.3005464 0.3368984 0.3000000 0.2881356
## Veg.17 0.3257143 0.3480663 0.3661202 0.3368984 0.3222222 0.3672316
## Veg.18 0.3450292 0.4802260 0.4078212 0.4754098 0.4431818 0.4104046
## Veg.19 0.3193717 0.3401015 0.2864322 0.3201970 0.3163265 0.3160622
## Veg.20 0.3626374 0.2872340 0.2842105 0.2783505 0.3155080 0.4021739
## Veg.21 0.3591160 0.3155080 0.3439153 0.3367876 0.3010753 0.2896175
## Veg.22 0.3641618 0.3854749 0.3480663 0.3729730 0.3595506 0.3714286
## Veg.23 0.2817680 0.3796791 0.3227513 0.3782383 0.3440860 0.3114754
##           Veg.13    Veg.14    Veg.15    Veg.16    Veg.17    Veg.18
## Veg.2
## Veg.3
## Veg.4
## Veg.5
## Veg.6
## Veg.7
```

```
## Veg.8
## Veg.9
## Veg.10
## Veg.11
## Veg.12
## Veg.13
## Veg.14 0.3403141
## Veg.15 0.4086022 0.3403141
## Veg.16 0.3763441 0.3612565 0.3118280
## Veg.17 0.3118280 0.3298429 0.3870968 0.3870968
## Veg.18 0.2857143 0.3368984 0.4835165 0.4065934 0.3736264
## Veg.19 0.3168317 0.2560386 0.3069307 0.3465347 0.3267327 0.3333333
## Veg.20 0.3782383 0.3131313 0.2124352 0.3367876 0.3575130 0.3968254
## Veg.21 0.4062500 0.3705584 0.3854167 0.2812500 0.3333333 0.4468085
## Veg.22 0.3695652 0.3544974 0.3913043 0.3152174 0.3369565 0.4111111
## Veg.23 0.3020833 0.3197970 0.3645833 0.3125000 0.3958333 0.3617021
##           Veg.19    Veg.20    Veg.21    Veg.22
## Veg.2
## Veg.3
## Veg.4
## Veg.5
## Veg.6
## Veg.7
## Veg.8
## Veg.9
## Veg.10
## Veg.11
## Veg.12
## Veg.13
## Veg.14
## Veg.15
## Veg.16
## Veg.17
## Veg.18
## Veg.19
## Veg.20 0.3205742
## Veg.21 0.3461538 0.3668342
## Veg.22 0.3600000 0.3717277 0.3368421
## Veg.23 0.2980769 0.3567839 0.3535354 0.3473684
```

```
DivBetaAbun(TablaH, FactoresH, 4)
```


Diversidad Beta con Abundancia
Veg.16
Veg.11
Veg.6
Veg.21
Veg.22
Veg.17
Veg.12
Veg.7
Veg.19
Veg.18
Veg.13
Veg.23
Veg.2
Veg.1
Veg.5
Veg.10
Veg.8
Veg.9
Veg.3
Veg.14
Veg.4
Veg.20
Veg.15
1.0
0.8
0.6
0.4
0.2
0.0

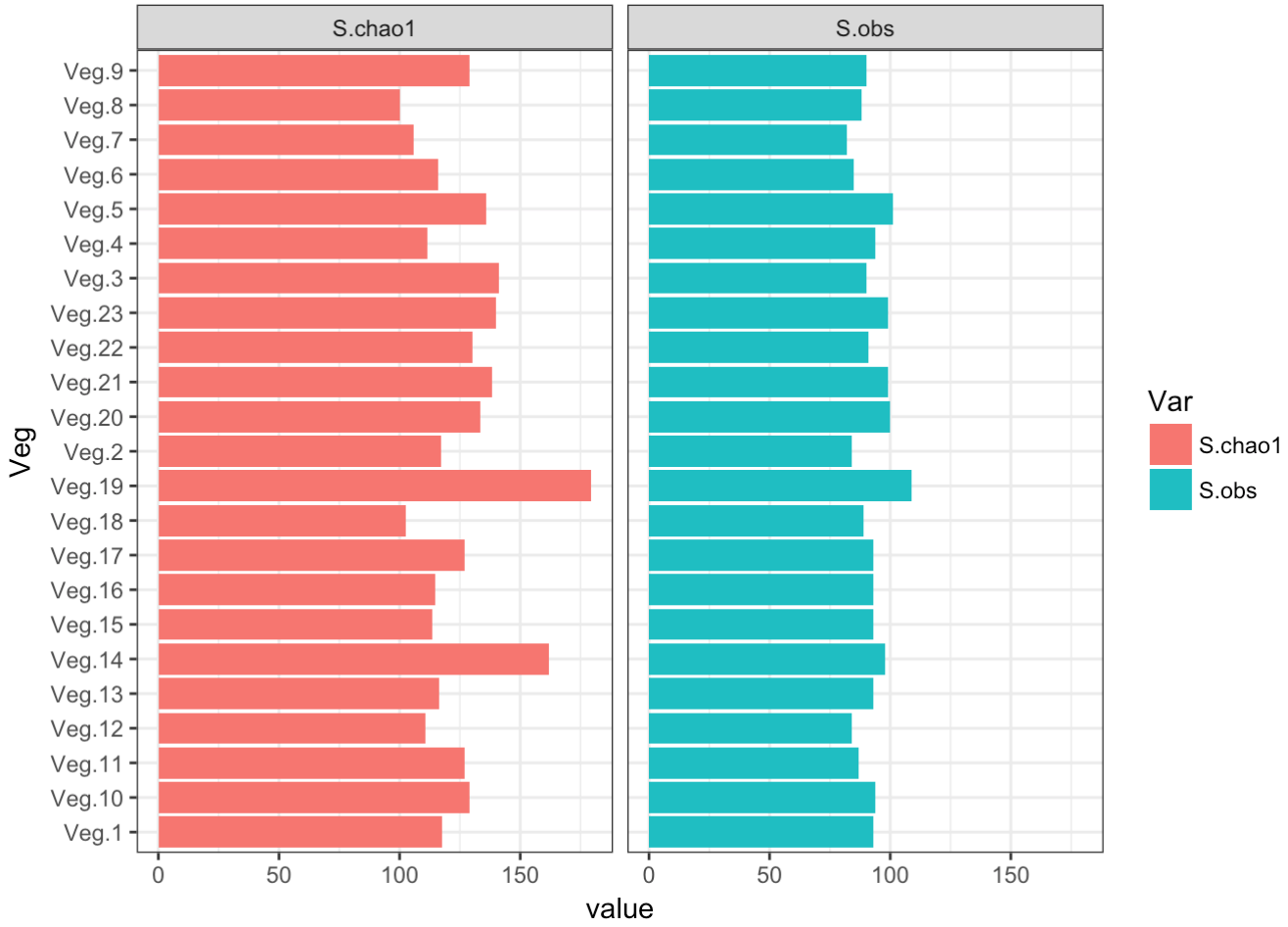
```
##            Veg.1     Veg.2     Veg.3     Veg.4     Veg.5     Veg.6
## Veg.2  0.2706682
## Veg.3  0.3501647 0.2873051
## Veg.4  0.3682008 0.3149523 0.3244078
## Veg.5  0.3725079 0.3851064 0.3595041 0.3721619
## Veg.6  0.3744186 0.3530106 0.3760000 0.4239130 0.3762268
## Veg.7  0.3518519 0.2925969 0.3242321 0.3766234 0.4375679 0.3115942
## Veg.8  0.3424346 0.2748268 0.2885906 0.3141640 0.3717949 0.3570581
## Veg.9  0.4235706 0.3744076 0.3692661 0.3784079 0.4223195 0.4129111
## Veg.10 0.3770140 0.3355120 0.2959831 0.3118063 0.3846154 0.4279330
## Veg.11 0.3804476 0.3468900 0.3634259 0.3773377 0.4437086 0.3308733
## Veg.12 0.4520885 0.3732834 0.4065139 0.3981693 0.5063146 0.3778920
## Veg.13 0.5612602 0.5094787 0.5481651 0.5005453 0.5776805 0.5493301
## Veg.14 0.3724605 0.3264605 0.3762486 0.3171247 0.3913043 0.4070588
## Veg.15 0.4241758 0.3489409 0.3556757 0.3505155 0.3919338 0.4736842
## Veg.16 0.3468927 0.3463303 0.3644444 0.3756614 0.3927813 0.3804476
## Veg.17 0.4499397 0.3921569 0.4478673 0.4353206 0.5530474 0.4224464
## Veg.18 0.5748428 0.5115090 0.5703704 0.5181287 0.6009390 0.5230567
## Veg.19 0.3916005 0.3479263 0.4084821 0.3900106 0.4818763 0.4106509
## Veg.20 0.3819840 0.3541667 0.3923767 0.3532551 0.4068522 0.4411415
## Veg.21 0.4018692 0.3831554 0.4236510 0.4694323 0.4238773 0.4512195
## Veg.22 0.4457275 0.3974209 0.4392736 0.4125270 0.5341278 0.4000000
## Veg.23 0.5279188 0.4425806 0.5491905 0.4882075 0.5242604 0.5026596
##            Veg.7     Veg.8     Veg.9    Veg.10    Veg.11    Veg.12
## Veg.2
## Veg.3
## Veg.4
## Veg.5
## Veg.6
## Veg.7
## Veg.8  0.3152302
## Veg.9  0.3672727 0.2880952
## Veg.10 0.3882091 0.2800875 0.2959641
## Veg.11 0.3537332 0.3677885 0.4222222 0.3755656
## Veg.12 0.2915601 0.3601004 0.3806452 0.4087161 0.3298566
## Veg.13 0.4472727 0.4619048 0.4963325 0.5291480 0.5061728 0.4529032
## Veg.14 0.3793911 0.3026467 0.3364817 0.3463626 0.3992849 0.4054726
## Veg.15 0.4692483 0.3281075 0.3846154 0.3164021 0.4414832 0.4855072
## Veg.16 0.3341149 0.4078341 0.4397163 0.3978261 0.3150358 0.3848070
## Veg.17 0.3751568 0.3965517 0.4607595 0.4537037 0.3708440 0.3012048
## Veg.18 0.4442988 0.4935733 0.5317460 0.5710843 0.5080214 0.4474053
## Veg.19 0.3804476 0.3217593 0.3610451 0.3624454 0.3812950 0.3416771
## Veg.20 0.4272189 0.3302326 0.3890215 0.3179825 0.3831325 0.4817610
## Veg.21 0.4538835 0.4374255 0.4957160 0.4298541 0.3671199 0.4702842
## Veg.22 0.3213429 0.3945819 0.4268440 0.4228635 0.3699634 0.2959184
## Veg.23 0.4417989 0.4811933 0.5113485 0.5236938 0.4736842 0.4419263
##           Veg.13    Veg.14    Veg.15    Veg.16    Veg.17    Veg.18
## Veg.2
## Veg.3
## Veg.4
## Veg.5
## Veg.6
## Veg.7
```

```
## Veg.8
## Veg.9
## Veg.10
## Veg.11
## Veg.12
## Veg.13
## Veg.14 0.4214876
## Veg.15 0.5476464 0.3688889
## Veg.16 0.5130024 0.3965714 0.4149055
## Veg.17 0.4329114 0.4285714 0.5160142 0.4254279
## Veg.18 0.3201058 0.4394904 0.6019778 0.5306122 0.4313187
## Veg.19 0.4156770 0.3340987 0.4324022 0.4413793 0.3538084 0.4000000
## Veg.20 0.5035800 0.3148789 0.2772166 0.4018476 0.5160494 0.5283505
## Veg.21 0.5740514 0.4326241 0.4689655 0.3491124 0.5158428 0.6000000
## Veg.22 0.4292624 0.4018692 0.5045455 0.3684211 0.2991239 0.4431373
## Veg.23 0.3938585 0.4293059 0.5586035 0.4594595 0.4729542 0.3682678
##           Veg.19    Veg.20    Veg.21    Veg.22
## Veg.2
## Veg.3
## Veg.4
## Veg.5
## Veg.6
## Veg.7
## Veg.8
## Veg.9
## Veg.10
## Veg.11
## Veg.12
## Veg.13
## Veg.14
## Veg.15
## Veg.16
## Veg.17
## Veg.18
## Veg.19
## Veg.20 0.4176334
## Veg.21 0.4744352 0.4145759
## Veg.22 0.3325499 0.4710744 0.4842615
## Veg.23 0.4282018 0.4954486 0.4973262 0.4406332
```

```
########################################
#Chao data
#Many species will always remain unseen or undetected in a
#collection of sample plots.
#The function uses some popular ways of estimating
#the number of these unseen species and adding them
#to the observed species richness (Palmer 1990, Colwell & Coddington 1994).
########################################
ChaoF <- function(Tabla, Factor){
  require(vegan)
  require(ggplot2)
  require(reshape)
  Tabla <- data.frame(Tabla, row.names = Factor)
  Tabla
  UNO <- estimateR(Tabla)[1:2,]
  UNO1 <- melt(UNO)
  names(UNO1)[1] <- c("Var")
  names(UNO1)[2] <- c("Veg")
  LL <- ggplot(UNO1, aes(x = Veg, y = value, fill = Var))
  LL <- LL + geom_bar(position = "stack", stat = "identity")
  LL <- LL + facet_wrap( ~ Var) + theme_bw() + coord_flip()
  print(LL)
  print(UNO)
}
ls()
```

```
##  [1] "BCI"            "BCI1"           "ChaoF"          "DivBetaAbun"
##  [5] "DivBetaPA"      "DiversidadCC"   "FactoresH"      "RarefraccionCC"
##  [9] "RenyiCC"        "TablaH"         "UU"             "UUU"
## [13] "vec1"
```

```
ChaoF(TablaH, FactoresH)
```




```
##            Veg.1    Veg.2    Veg.3  Veg.4 Veg.5    Veg.6   Veg.7 Veg.8
## S.obs    93.0000  84.0000  90.0000  94.00   101  85.0000  82.000    88
## S.chao1 117.4737 117.2143 141.2308 111.55   136 116.1667 105.625   100
##            Veg.9 Veg.10   Veg.11   Veg.12 Veg.13   Veg.14   Veg.15
## S.obs    90.0000     94  87.0000  84.0000  93.00  98.0000  93.0000
## S.chao1 129.1765    129 127.0714 110.7143 116.25 161.9091 113.7143
##           Veg.16  Veg.17 Veg.18 Veg.19   Veg.20   Veg.21 Veg.22   Veg.23
## S.obs    93.0000  93.000   89.0  109.0 100.0000  99.0000     91  99.0000
## S.chao1 114.5652 126.913  102.5  179.5 133.4762 138.2609    130 140.1304
```

```
##############################################
#Curvas de Whitaker

#legend("bottomright","foo")

Whitaker1 <- function(Tabla, Factor){
  require(vegan)
  Tabla <- data.frame(Tabla, row.names = Factor)
  Tabla
  mod <- radfit(Tabla)
  mod
  plot(mod, pch = 19)
  }
ls()
```

```
##  [1] "BCI"           "BCI1"          "ChaoF"         "DivBetaAbun"
##  [5] "DivBetaPA"     "DiversidadCC"  "FactoresH"     "RarefraccionCC"
##  [9] "RenyiCC"       "TablaH"        "UU"            "UUU"
## [13] "vec1"          "Whitaker1"
```

```
Whitaker1(TablaH, FactoresH)
```