

Diversity Measures (beta and abundance)

PT ANJ Jan - Jun 2020

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8/4/2020

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Load packages

```
library(tabula)
library(magrittr)
library(khroma)
library(ggplot2)
library(openxlsx)
library(RFLPtools)
library(knitr)
```

Reading and preparing data

```
dat <- "data_jml_spesies_ANJ.xlsx"
df <- read.xlsx(paste0("C:/Users/rbbutar/Documents/R/Konservasi_ANJ/indeks_kehati/"), dat),
             sheet = "grafik_beta", cols = 1:8)
rownames(df) <- df[,1]
df <- df[, -1]
df <- t(df)

#Dropping columns sum 0
df <- as.data.frame(df)
df <- df[, !sapply(df, function(x) sum(x)==0)]
#kable(df, caption = )
```

A. Beta -diversity

Beta diversity is a comparison of diversity between ecosystems, usually measured as the amount of species change between the ecosystem.

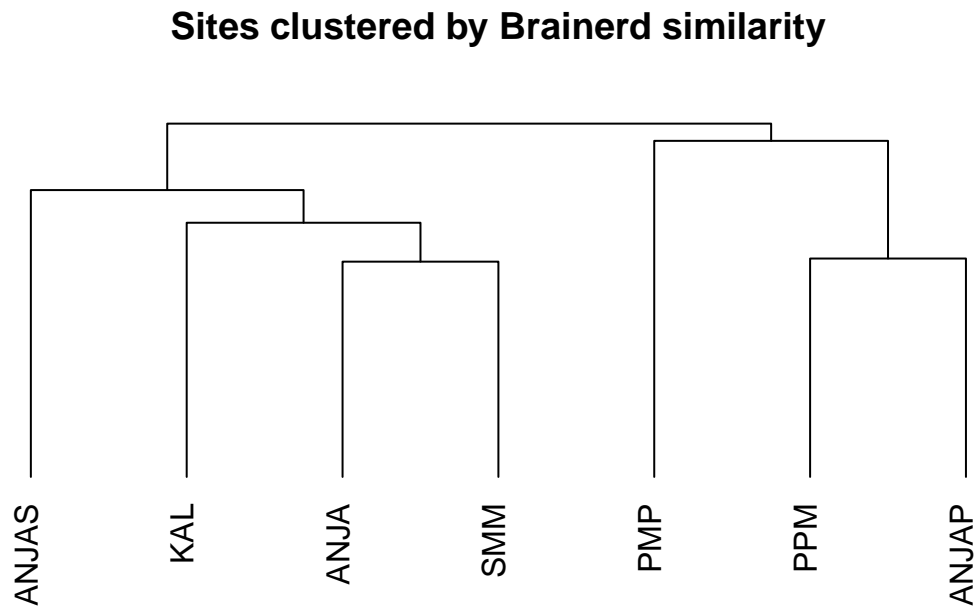
1. Similarity

Jaccard, Morisita-Horn and Sorenson indices provide a scale of similarity from 0-1 where 1 is perfect similarity and 0 is no similarity. The Brainerd-Robinson index is scaled between 0 and 200.

a. Brainerd-Robinson (similarity between assemblages)

- **Quantitative** similarity measures (between samples)
- Brainerd-Robinson quantitative index. This is a city-block metric of similarity between pairs of samples/cases.

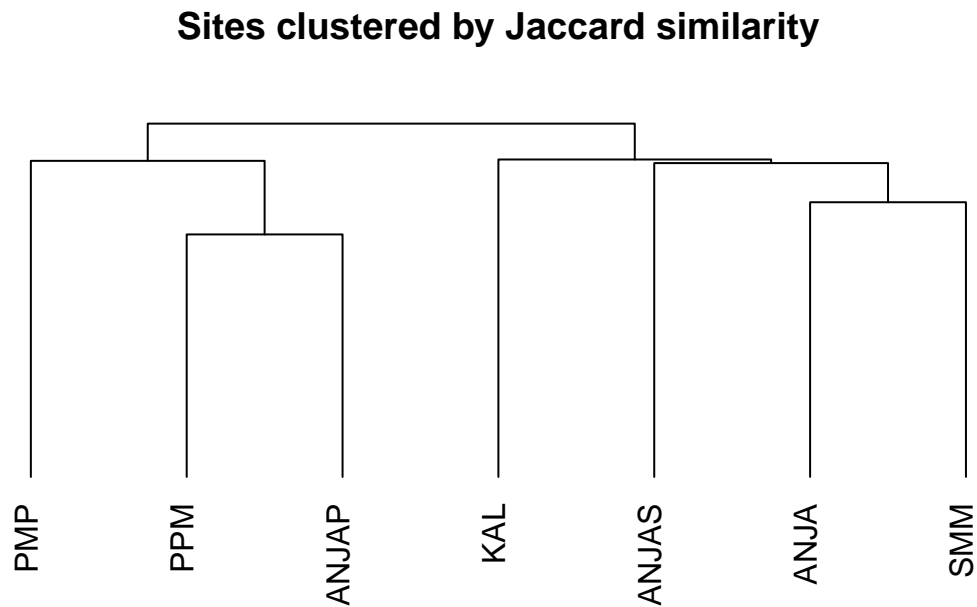
```
brainerd <- df %>% as_count %>% similarity(method = "brainerd")
brainerddata <- sim2dist(brainerd@.Data, maxSim = 200)
plot(
  hclust(brainerddata),
  hang = -1,
  main = "Sites clustered by Brainerd similarity",
  xlab = "Quantitative Index",
  axes = FALSE, ylab = ""
)
```



b. Jaccard index (similarity between assemblages)

- **Qualitative** similarity measures (between samples)
- This analysis includes presence/absence standardization using `decostand`

```
jaccard <- df %>% as_count %>% similarity(method = "jaccard")
jaccarddata <- sim2dist(jaccard@.Data, maxSim = 1)
plot(
  hclust(jaccarddata),
  hang = -1,
  main = "Sites clustered by Jaccard similarity",
  xlab = "includes presence/absence standardization using `decostand`",
  sub = "Qualitative index",
  axes = FALSE, ylab = ""
)
```



B. Abundance Model

Ranks vs abundance plot can be used for abundance models

```
abund.model <- df %>% as_count() %>%  
  plot_rank(log = "xy", facet = FALSE) +  
  ggplot2::theme_bw() + khroma::scale_color_discreterainbow()  
print(abund.model)
```

