## 1. Calculate dissimilarities

Dissimilarity Index (DI) measures the relative separation (high dissimilarity) or closeness (low dissimilarity) between two richness of islands It is a symmetrical measure so that this interpretation can apply to either richness

- A DI of 0 indicates conditions of total closeness under which richness and their species are distributed in the same proportions across all islands.

- A DI of 1 indicates conditions of total segregation such that the species are located in completely different islands than other species.

### 1.1. Simpson

It is an asymetrical index, it means that ignores double-zero attributes (co-absences) in the similarity calculation (Todeschini et al., 2012)

nº of species both samples share / nº of all species occurring in the SMALLER sample. Recommended in a situation when there are large differences in species richness between the islands. It also quantifies the nestedness. (https://davidzeleny.net/blog/2017/03/18/simpsons-similarity-index-vs-simpsons-diversity-index/)

### 1.2. Jaccard

It is an asymetrical index, it means that ignores double-zero attributes (co-absences) in the similarity calculation (Todeschini et al., 2012)

nº of species both samples share / nº of all species occurring in both samples together. Recommended in a situation when there are few differences in species richness between the islands. (https://davidzeleny.net/blog/2017/03/18/simpsons-similarity-index-vs-simpsons-diversity-index/). It is also very sensitive to small sample sizes. Co-absences are eliminated!

### 1.3. Bray-Curtis

It is a simetrical index, it means that takes into account double-zero attributes (co-absences). Bray-Curtis treats in exactly the same way co-absences as any other pair of values

and should be used when the zero state is a valid basis for comparing two objects in the similarity calculation (Greenacre, 2008; Todeschini et al., 2012).

The Formula is 1 - 2\* (sum of the lesser values for species both samples share) / total number of species counted at both sites. It is an inverse index due to '1-'. . This measure is very reasonable if we want to take into account ABSENCES of species in our data. However, it does not satisfy the triangle inequality axiom, and hence is not a true distance. It means that the sum of the dissimilarities between islands A and B and islands A and C is not necessarily greater than between islands B and C (Oksanen et al., 2020) (Greenacre, 2008; Post-ResearchGate.

This dissimilarity index ranges from zero, when species are similar among sites, to unity, when no single species is shared among them (Castro-Urgal, R. & Traveset, A., 2014).

In our data, absences are true absences because these species haven't been found in the islands that are marked as absences. Moreover, our matrix have 71% of absences and 29% of presences. So there are probably quite co-absences between islands that we think have to be taken into account to compare islands.

Studies that have used Bray-Curtis index for oceanic islands:

- Castro-Urgal, R. & Traveset, A. (2014)

- Florencio et al, (2013)

- Thuesen et al, (2011)

### 1.4. Bibliography

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Todeschini, R. et al. (2012). Similarity Coefficients for Binary Chemoinformatics Data: Overview and Extended Comparison Using Simulated and Real Data Sets. Journal of Chemical Information and