

## S1 - Partitioning beta diversity

We used the procedure of Baselga [1], where Sørensen beta diversity for multiple-sites can be expressed as:

$$\beta_{SOR} = \frac{\left[ \sum_{i < j} \min(b_{ij}, b_{ji}) \right] + \left[ \sum_{i < j} \max(b_{ij}, b_{ji}) \right]}{2 \left[ \sum_j S_i - S_T \right] + \left[ \sum_{i < j} \min(b_{ij}, b_{ji}) \right] + \left[ \sum_{i < j} \max(b_{ij}, b_{ji}) \right]} \quad (1)$$

Where  $S_i$  is the richness in each site,  $b_{ij}$  is the number of species in site  $i$  not in site  $j$  and  $b_{ji}$  is the number of species in site  $j$  not in site  $i$  and  $S_T$  is total richness across all sites.

Sørensen dissimilarity ( $\beta_{SOR}$ ) accounts for both species turnover and nestedness. Beta diversity accounting only for pure spatial turnover is ( $\beta_{SIM}$ ):

$$\beta_{SIM} = \frac{\left[ \sum_{i < j} \min(b_{ij}, b_{ji}) \right]}{2 \left[ \sum_j S_i - S_T \right] + \left[ \sum_{i < j} \min(b_{ij}, b_{ji}) \right]} \quad (2)$$

Therefore we can use Sørensen dissimilarity ( $\beta_{SOR}$ ) and spatial turnover ( $\beta_{SIM}$ ) to calculate the total nestedness of species assemblages ( $\beta_{NES}$ ):

$$\beta_{NES} = \beta_{SOR} - \beta_{SIM} \quad (3)$$

Therefore,

$$\beta_{NES} = \frac{\left[ \sum_{i < j} \min(b_{ij}, b_{ji}) \right] + \left[ \sum_{i < j} \max(b_{ij}, b_{ji}) \right]}{2 \left[ \sum_j S_i - S_T \right] + \left[ \sum_{i < j} \min(b_{ij}, b_{ji}) \right] + \left[ \sum_{i < j} \max(b_{ij}, b_{ji}) \right]} - \frac{\left[ \sum_{i < j} \min(b_{ij}, b_{ji}) \right]}{2 \left[ \sum_j S_i - S_T \right] + \left[ \sum_{i < j} \min(b_{ij}, b_{ji}) \right]} \quad (4)$$

## References

1. Baselga A. Partitioning the turnover and nestedness components of beta diversity. *Glob Ecol Biogeogr.* 2009;19: 134–143.