

Calculation of endemism indices

To estimate endemism at the ecoregion level, we calculated five endemism indices (E_1 - E_5). Weighted endemism indices were calculated based on these five indices using z-transformation of residuals in regression analyses against sequencing and sampling depth.

Five endemism indices

E_1 Number of endemic species

$$E_1$$

E_2 Proportion of endemic species

$$E_2 = \frac{E_1}{S}$$

S , total species richness in ecoregion

E_3 Mean maximum range of species (average weighted endemism; Crisp et al. 2001)

$$E_3 = \frac{\sum_i d_i}{S}$$

d_i , range of species i

E_4 Jaccard index of similarity (Jaccard 1912)

$$E_4(C_1, C_2) = \frac{C_1 \cap C_2}{C_1 \cup C_2}$$

C , ecoregion communities

E_5 β_{SIM} index of similarity (multiple-site Simpson-based community similarity index, Baselga et al. 2010)

$$E_5 = \frac{\sum_{i < j} \min(b_{ij}, b_{ji})}{\sum_i (S_i - S_T) + \sum_{i < j} \min(b_{ij}, b_{ji})}$$

S_i , number of species in site i

S_T , total number of species

b_{ij} and b_{ji} , number of species exclusive to sites i and j , respectively

Accounting for sampling and sequencing depth for endemism indices

E_{nR} residuals of n endemism index

$$E_{nR} = E_n - \hat{E}_n; \\ \hat{E}_n = \beta_1 \log(L_1 + L_2) + \beta_2 \log(R_1 + R_2) + \beta_3 \log(L_1) + \beta_4 \log(L_2) + \beta_5 \log(R_1) + \beta_6 \log(R_2) + \beta_7(L_1 + L_2) + \beta_8(R_1 + R_2) + \beta_9 L_1 + \beta_{10} L_2 + \beta_{11} R_1 + \beta_{12} R_2 + \epsilon$$

L_1 , number of soil sampling localities

L_2 , number of UNITE localities

R_1 , number of reads of soil samples

R_2 , number of UNITE Sanger reads

Residuals are calculated based on the best-fitting model.

Standardizing residuals of endemism indices

E_{nRz} Z-transformed E_{nR}

$$E_{nRz} = \frac{E_{nR} - \mu}{\sigma}$$

μ , mean E_{nR}

σ , standard deviation of E_{nR} .

Weighting standardised endemism indices

E_{ave} weighted E_{nRz}

$$E_{ave} = \frac{E_{1Rz} + E_{2Rz} + 2E_{3Rz} + E_{4Rz} + E_{5Rz}}{6}$$

E_3 receives double weight, because E_1 and E_2 as well as E_3 and E_4 are calculated on a similar basis.

Correlation matrix of endemism indices

	E_{ave}	E_{1Rz}	E_{2Rz}	E_{3Rz}	E_{4Rz}	E_{5Rz}
E_{ave}	1.000	0.767	0.805	0.554	0.754	0.816
E_{1Rz}	0.767	1.000	0.806	0.188	0.452	0.540
E_{2Rz}	0.805	0.806	1.000	0.072	0.788	0.745
E_{3Rz}	0.554	0.188	0.072	1.000	0.169	0.270
E_{4Rz}	0.754	0.452	0.788	0.169	1.000	0.782
E_{5Rz}	0.816	0.540	0.745	0.270	0.782	1.000

Correlation matrix of average endemism of fungal groups

	1	2	3	4	5	6	7	8	9
all fungi (1)	1.000	0.797	0.591	0.517	0.568	0.628	0.675	0.619	0.523
non-EcM Agaricomycetes (2)	0.797	1.000	0.790	0.398	0.461	0.470	0.460	0.595	0.532
AM fungi (3)	0.591	0.790	1.000	0.280	0.375	0.232	0.233	0.578	0.461
EcM fungi (4)	0.517	0.398	0.280	1.000	0.234	0.268	0.250	0.270	0.176
molds (5)	0.568	0.461	0.375	0.234	1.000	0.600	0.413	0.364	0.513
OHP (6)	0.628	0.470	0.232	0.268	0.600	1.000	0.809	0.159	0.354
pathogens (7)	0.675	0.460	0.233	0.250	0.413	0.809	1.000	0.264	0.331
unicellular fungi (8)	0.619	0.595	0.578	0.270	0.364	0.159	0.264	1.000	0.463
yeasts (9)	0.523	0.532	0.461	0.176	0.513	0.354	0.331	0.463	1.000

References

- Baselga, A. (2010). Partitioning the turnover and nestedness components of beta diversity. *Global Ecology and Biogeography*, 19, 134-143.
- Jaccard, P. (1912). The distribution of the flora in the alpine zone. *New Phytologist*, 11, 37-50.

BOX S1. Calculation of endemism indices and correlation among standardised indices for all fungi and among functional groups.