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Appendix A. Jaccard's dissimilarity index in terms of the slope of the species-area relationship.

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In this appendix, our goal is to relate average pairwise turnover as computed by the Jaccard's index of dissimilarity (T_J) with the slope of the log-log species-area relationship (SAR, z).

Legendre and Legendre (1998, p. 256) defined the Jaccard's (1912) index of similarity (S_J) as

$$S_J = \frac{\mathbf{a}}{\mathbf{a} + \mathbf{b} + \mathbf{c}} = 1 - T_J \tag{A.1}$$

where (as defined in Legendre and Legendre 1998, p. 254) a is the number of species shared between the two samples, and b and c are the number of species unique to samples one and two respectively. Now it is beneficial to express T_J in terms of species richness because z is typically expressed in this way:

$$T_J = \frac{\mathbf{b} + \mathbf{c}}{\mathbf{a} + \mathbf{b} + \mathbf{c}} = \frac{2\gamma - (\alpha_1 + \alpha_2)}{\gamma}$$
(A.2)

where α_1 is the number of species in sample 1, and α_2 is the number of species in sample 2, and γ is the total number of species in both samples together.

The slope of the log-log SAR, *z*, for two samples each of area *A*:

$$z = \frac{\log_2 \frac{2(a+b+c)}{a+2b+c}}{\log_2 2A/A} = \log_2 \frac{2\gamma}{\alpha_1 + \alpha_2}$$
(A.3)

Here is it is worth noting that T_J and z both have the exact same input parameters, namely: γ , α_1 and α_2 . We wish to define T_J in terms of z therefore we must use (A.3) to express one of the variables in (A.2) in terms of z.

$$2^{z} = \frac{2\gamma}{\alpha_{1} + \alpha_{2}} \tag{A.4}$$

$$2^{z-1}(\alpha_1 + \alpha_2) = \gamma \tag{A.5}$$

Now we may substitute (A.5) into (A.2) and simplify the expression.

$$T_{J} = \frac{2 \cdot 2^{z-1} (\alpha_{1} + \alpha_{2}) - (\alpha_{1} + \alpha_{2})}{2^{z-1} (\alpha_{1} + \alpha_{2})} = \frac{2^{z} - 1}{2^{z-1}}$$
(A.6)

$$T_J = 2 - 2^{1-z} \tag{A.7}$$

Equation A.7 provides the scale-invariance expectation for Jaccard's turnover index for two equal area samples. Note that although the assumption of constant species richness (i.e., $\alpha_1 = \alpha_2$) is not necessary to derive (A.7) in the two quadrat context, this assumption is necessary to apply (A.7) in the context considered in the manuscript in which four samples are considered simultaneously and we relate \overline{T}_j calculated as the average of six pairwise comparisons to z which is calculated from $\overline{\alpha}$ and γ where in this context $\overline{\alpha} = (\alpha_1 + \alpha_2 + \alpha_3 + \alpha_4)/4$ and γ is the number of unique species in across all four quadrats. Assuming quadrat richness is constant is equivalent to assuming that the same spatially explicit Type IIA or Type IIIA species-area relationship holds across all four quadrats (Harte and Kinzig 1997, Scheiner et al. 2011). Additionally we will treat each of the six pairwise comparisons as independent of all other comparisons. In theory, it should be possible to derive the fraction of shared species between each pairwise comparison by considering the joint probability distribution of co-occurrences that strictly satisfy scale-invariance; however, this is a non-trivial problem and currently formulations of this sort only exist for Harte's bisection scaling scheme (Hui and McGeoch 2008).

Therefore, we will precede here assuming independence of the pairwise comparisons, in which case it should be clear that:

$$\overline{T}_{J} = \frac{1}{6} \sum_{i=1}^{3} \sum_{j=i+1}^{4} 2 - 2^{1-z_{ij}}$$
(A.8)

where z_{ij} represents the *z*-value for the comparison of the *i*th and *j*th quadrats. Because we have assumed that *z* is constant for the set of four quadrats we can simplify (A.8) to:

$$\overline{T}_J = 2 - 2^{1-z} \tag{A.9}$$

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