

Appendix S3: Equations for calculating species accumulation curves based on species density and species turnover.

It is possible to describe the exact accumulation of species richness across multiple samples (i.e. quadrats) as the relationship between species density, and species turnover:

$$sR_{1,2} = [\rho_1 + (\rho_2 * sT_{2 \vee 1})] \quad [\text{Eq. 1}]$$

In Eq. 1, the species density (number of species per unit area) from the first sampling unit (ρ_1) is added to the species density in the second sampling unit (ρ_2) multiplied by the proportion of species which are unique to this unit ($sT_{2 \vee 1}$), and which do not occur in the first sample. This provides the number of species across the first two samples ($sR_{1,2}$). Considering a third sampling unit:

$$sR' = [sR_{1,2} + [\rho_3 * sT_{3 \vee 1,2})] \dots \quad [\text{Eq. 2}]$$

In Eq. 2, the number of species accumulated by the first two samples ($sR_{1,2}$, derived from Eq. 1), is added to the species density in the third sampling unit (ρ_3) multiplied by the proportion of species which are unique to this unit ($sT_{3 \vee 1\&2}$), and which do not occur in the first two samples combined. This provides the number of species across the first three samples, and this accumulative procedure continues across all sample units to provide the sampled species richness (sR^{Ob} , see Appendix S4, Part A). An estimate of total species richness (sR^T) might be derived if the accumulation curve is extrapolated using an appropriate function, to the habitat area which circumscribes the sampling regime.