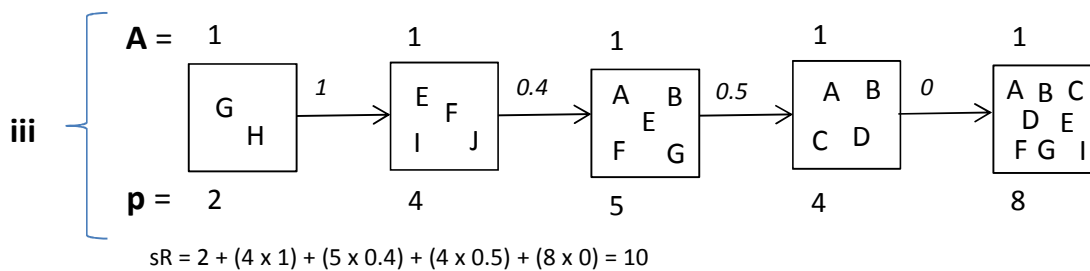
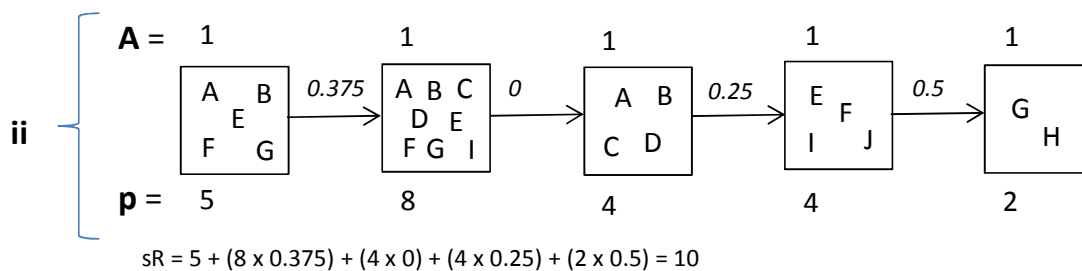
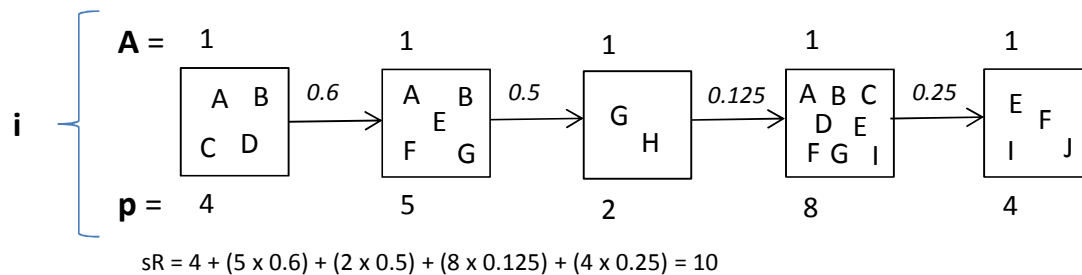


**Appendix S4:** Schematic showing the calculation of species richness using species density combined with turnover among accumulated samples. The example is for five quadrats, sampled in three contrasting sequences (i-iii), and including ten species (A-J), showing the area of each quadrat (A), the species density per unit area ( $\rho$ ), and in italics, associated with each arrow, the proportion of species occurring in each consecutive quadrat which have not been recorded for the previously accumulated samples.

Part A. An example with species density calculated for quadrats which have the same area (A). In each case species richness ( $sR^{Ob} = 10$ ) is calculated exactly, regardless of the order of the samples.



Part B. An example with species density calculated based on the mean area ( $A_m$ ), for spatially variable quadrats (A). This corresponds to a situation in which the area of individual quadrats is slightly different, such as when correcting for local bole curvature and bark roughness in estimating epiphyte species density. Species density ( $\rho$ ) is adjusted to the mean area of the quadrats on a tree bole. In this case, species richness depends on the sequence of the samples (sR is different for examples i-iii), and can be estimated ( $sR^{Est}$ ) by repeatedly randomising the sequence of quadrats (resampling) to find the mean species richness for a given sampling effort.

