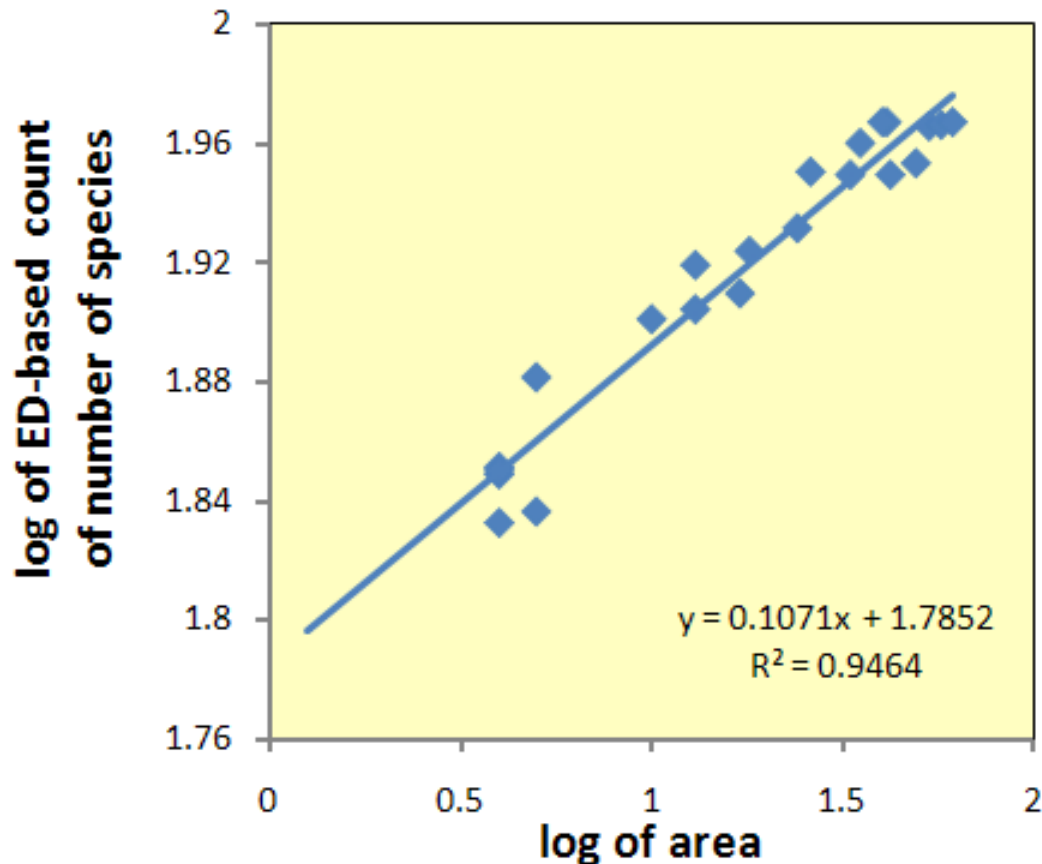


Species area relationship generated by the ED model for Panama (blue line)



Legend

The “ED” surrogates methods (1-4) provide information about regional biodiversity by integrating available environmental information with museum collections and other biotic data. ED combines models of α diversity (richness) and β diversity (compositional dissimilarity among communities) to generate hypothetical species in environmental space, and their distributions among sites in the region. Because the ED surrogates approach generates species and their distributions, we can perform many useful assessments as if we had information for all species in the region (4, see also “Biodiversity viability analysis (BVA) and the ED surrogates strategy: combining alpha and beta diversity models to fill our biodiversity knowledge gaps”

<http://australianmuseum.net.au/Biodiversity-viability-analysis-combining-alpha-and-beta-diversity-models-to-fill-our-biodiversity-knowledge-gaps>).

Under certain conditions (5), counting up species using ED generates a species area curve (or species area relationship, SAR). This provides a new model explaining how samples covering greater area capture greater environmental heterogeneity, and so also capture a greater

number of sampled species. Critically, this model depends on the general species “unimodal” response to environmental variation and its links to alpha and beta diversity through ED (1,2).

An example extends the previous ED analysis of Panama data (2,3). We start with the same environmental space summarising alpha diversity and beta diversity information (generated from a GDM model using biotic and environmental data, followed by a robust ordination of all sites 2,3). However, instead of selecting sets of areas to maximise number of species represented (the conservation planning scenario of 2), we randomly select sets of areas that achieve any nominated total area extent. Each combination of a total area sampled and the corresponding count of relative number of species sampled produces a point in a plot having area as one axis and species richness as the other axis. As expected for the general form of SAR ($S = cA^z$), log transforms of the area values and the species counts produces a roughly linear relationship (figure).

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