Biodiversity model applied to the Brazilian Cerrado

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To determine the number of species (birds and mammals) that our study region could support under different land use scenarios, we applied the biological model in Polasky et al. (2008). Using three species-specific traits: (a) habitat suitability, (b) the amount of habitat required for a breeding pair, and (c) the ability of the species to move between patches of habitat, the model predicts the probability of persistence for each modeled species in a given landscape.

This section summarizes the key features of the applied biodiversity model. For more details on the model, refer to Polasky et al (2008). Details on the parameter values that underlie these equations are provided in a separate document available on The Nature Conservancy website provided above.

Model summary

This model estimates the probability that a species will persist in a given landscape as a function of its dispersal ability and habitat area requirements, in relation to habitat amount and habitat fragmentation.

Breeding pairs (BP) in a patch

Habitat patches are formed by aggregating all neighboring pixels with the same land cover/land use (LULC) type, k. The resulting patch j has an area A_j. Each species, s, has a specific area requirement per breeding pair, AR_s, and a habitat compatibility score $c_s(k)$ for each LULC. The maximum number of breeding pairs a patch j can support is given by:

$$Z_{sj} = \frac{c_s(k_j)A_j}{AR_s}$$

Potential breeding pairs in a landscape

The model estimates the total number of breeding pairs of any species s, as the weighted average of two BP estimates, $ZMax_s$ and $ZMin_s$. The first estimate, $ZMax_s$, simply adds together the Z_{sj} scores for each patch in the landscape, so that the total number of breeding pairs is:

$$ZMax_s = \sum_{j \in J} Z_{sj}$$

where *J* represents the collection of all patches comprising the landscape. The second estimate, $ZMin_s$, is the number of breeding pairs in the absence of dispersal. In this situation, smaller populations are likely to go extinct due to stochastic events or genetic drift (with high-connectivity, the "metapopulation rescue effect" would allow these populations to persist). Patch-level populations smaller than a critical value γ do not contribute to the long-term landscape population size. In $ZMin_s$, the total number of breeding pairs is as follows:

$$ZMin_s = \sum_{j \in J} Z_{sj} \psi_{sj}$$

where ψ_{sj}, is an indicator function that is 0 if $Z_{sj} < \gamma$, and 1 otherwise. For all species, we set $\gamma = 2500$ breeding pairs, based on published minimum viable population sizes for bird and mammal species (for citations, see the documentation on biodiversity parameters). These two estimates represent cases where a species experiences a fully connected landscape (for $ZMax_s$), or at the other extreme, a fully isolated landscape (for $ZMin_s$). The final BP estimate weights these values by a species-specific connectivity index.

Landscape Connectivity

The connectivity index for a landscape measures the average proximity between patches and, hence, the potential rates of population exchange. The index is determined by a species' dispersal ability and the distances between each pair of patches:

$$D_s = \frac{\sum_n^N \sum_m^M \exp(-\alpha_s d_{mn}) Z_{sm}}{N \, ZMax_s}$$

where d_{mn} is the distance between the centroids of patches *m* and *n*, and α_s is the reciprocal of the species' median dispersal distance.

Final BP estimate

Using the steps above, we approximate the final number of BPs of species *s* on the landscape as:

$$Z_s = D_s ZMax_s + (1 - D_s) ZMin_s$$

Under this relationship, a species with a very large dispersal distance relative to the inter-patch distances is estimated not to experience much extra population loss due to fragmentation (high weight on ZMax), while a species with a very small dispersal distance may be divided into many smaller nonviable subpopulations (high weight on ZMin).

Probability of persistence

To convert the estimate of BPs on the landscape to the expected likelihood that a species will persist, we calculate:

$$\pi_s = \frac{Z_s^g}{Z_s^g + \eta^g}$$

where η is the number of BPs resulting in a 50% chance of persistence, and g is a shape parameter that controls how closely π_s resembles a step function. We set η and g so there is a 50% probability of being sustained given a minimum population size of 2500 breeding pairs: $\eta = 1250$ and $g = 4.25$ (based published minimum viable population sizes for birds and mammals) (for citations, see biodiversity parameters summary).

Expected number of species

Finally, we estimate the expected number of species in a landscape by summing the species-specific probabilities to generate the final biodiversity score, B.

$$B = \sum_s \pi_s$$

References

Polasky, S., Nelson, E., Camm, J., Csuti, B., Fackler, P., Lonsdorf, E.,Montgomery, C., White, D., Arthur, J., Garber-Yonts, B., Haight, R., Kagan, J., Starfield, A., Tobalske, C. (2008). Where to put things? Spatial land management to sustain biodiversity and economic returns. *Biological Conservation*, *141*(6), 1505–1524.