

## Solution of the spatial neutral model yields new bounds on the Amazonian species richness

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Neutral models, in which individual agents with equal fitness undergo a birth-death-mutation process, are very popular in population genetics and community ecology. A neutral community is a collection of different populations, such as different species (in ecological models) or different groups of individuals with identical genetic sequence (haplotypes, for example, in population genetics). All individuals undergo a stochastic birth-death process, where in most of the interesting cases the overall size of the community is kept fixed or almost fixed (zero-sum game). An offspring of an individual will be a member of its parent "group" (species, genotype) with probability  $1 - \nu$ , and with probability  $\nu$  it mutates or speciates, becoming the originator of a new taxon. A neutral process does not include selection: all populations are demographically equivalent, having the same rates of birth, death and mutations, and the only driver of population abundance variations is the stochastic birth-death process (also known as drift or demographic stochasticity).

Usually these models are applied to populations and communities with spatial structure, but the analytic results presented so far are limited to well-mixed or mainland-island scenarios. Here we combine analytic results and numerics to obtain an approximate solution for the species abundance distribution and the species richness for the neutral model on continuous landscape. We show how the regional diversity increases when the recruitment length decreases and the spatial segregation of species grows. Our results [1] are supported by extensive numerical simulations and allow one to probe the numerically inaccessible regime of large-scale systems with extremely small mutation/speciation rates. Model predictions are compared with the findings of recent large-scale surveys [2-3] of tropical trees across the Amazon basin, yielding new bounds for the species richness (between 13100 and 15000) and the number of singleton species (between 455 and 690).

[1] Shem-Tov et al, Sc. Rep. **7**, 42415 (2017).

[2] Ter Steege et al, Science **342**, 1243092 (2013).

[3] Slik et. al, PNAS **112**, 7472 (2015).