



Exhaustive search for conservation networks of populations representing genetic diversity

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ABSTRACT. Conservation strategies routinely use optimization methods to identify the smallest number of units required to represent a set of features that need to be conserved, including biomes, species, and populations. In this study, we provide R scripts to facilitate exhaustive search for solutions that represent all of the alleles in networks with the smallest possible number of populations. The script also allows other variables to be added to describe the populations, thereby providing the basis for multi-objective optimization and the construction of Pareto curves by averaging the values in the solutions. We applied this algorithm to an empirical dataset that comprised 23 populations of *Eugenia dysenterica*, which is a tree species with a widespread distribution in the Cerrado biome. We observed that 15 populations would be necessary to represent all 249 alleles based on 11 microsatellite loci, and that the likelihood of representing all of the alleles with random networks is less than 0.0001. We selected the solution (from two with the smallest number

of populations) obtained for the populations with a higher level of climatic stability as the best strategy for *in situ* conservation of genetic diversity of *E. dysenterica*. The scripts provided in this study are a simple and efficient alternative to more complex optimization methods, especially when the number of populations is relatively small (i.e., <25 populations).

Key words: Cerrado; Computational search; Conservation planning; Genetic diversity; Optimization; R platform