

A simulation study comparing methods to analyze species-habitat associations of forest trees

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Introduction

Studying small-scale habitat associations of tree populations can give insights into the importance of abiotic processes shaping the spatial patterning them [1]. There is no consensus about the importance of abiotic processes for these patterns. Apart from ecological reasons, the perceived strength of species-habitat associations may also depend on the methods used.

Therefore, we analyzed species-habitat associations of simulated patterns using methods proposed in the literature [2,3] and one novel method, namely pattern reconstruction [4].

Methods

Firstly, we created observed data, i.e. neutral habitat maps using the R-package NLMR [5] and spatial distributions (point patterns) of species in these maps with predefined positive and negative habitat associations. Secondly, we compared different methods to test for habitat associations in the observed data. All methods randomize either the habitat or the species data and compare the observed data to the randomized data.

(I) **Gamma test:** Randomized patterns are created by simulating point processes [2].

(II) **Torus-translation test:** Randomized habitat maps are created by shifting the habitat map [3].

(III) **Patch randomization test:** Randomized habitat maps are created by a random walk algorithm [3].

(IV) **Pattern reconstruction:** Randomized patterns are created by simulated annealing [4].

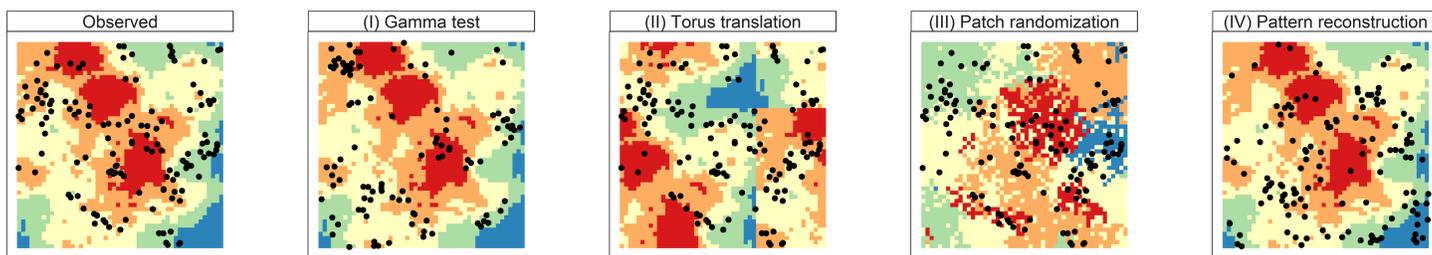


Figure 1: Example of observed data (left) and methods to randomize the observed data. We used each method as null model to randomize the observed data 199 times.

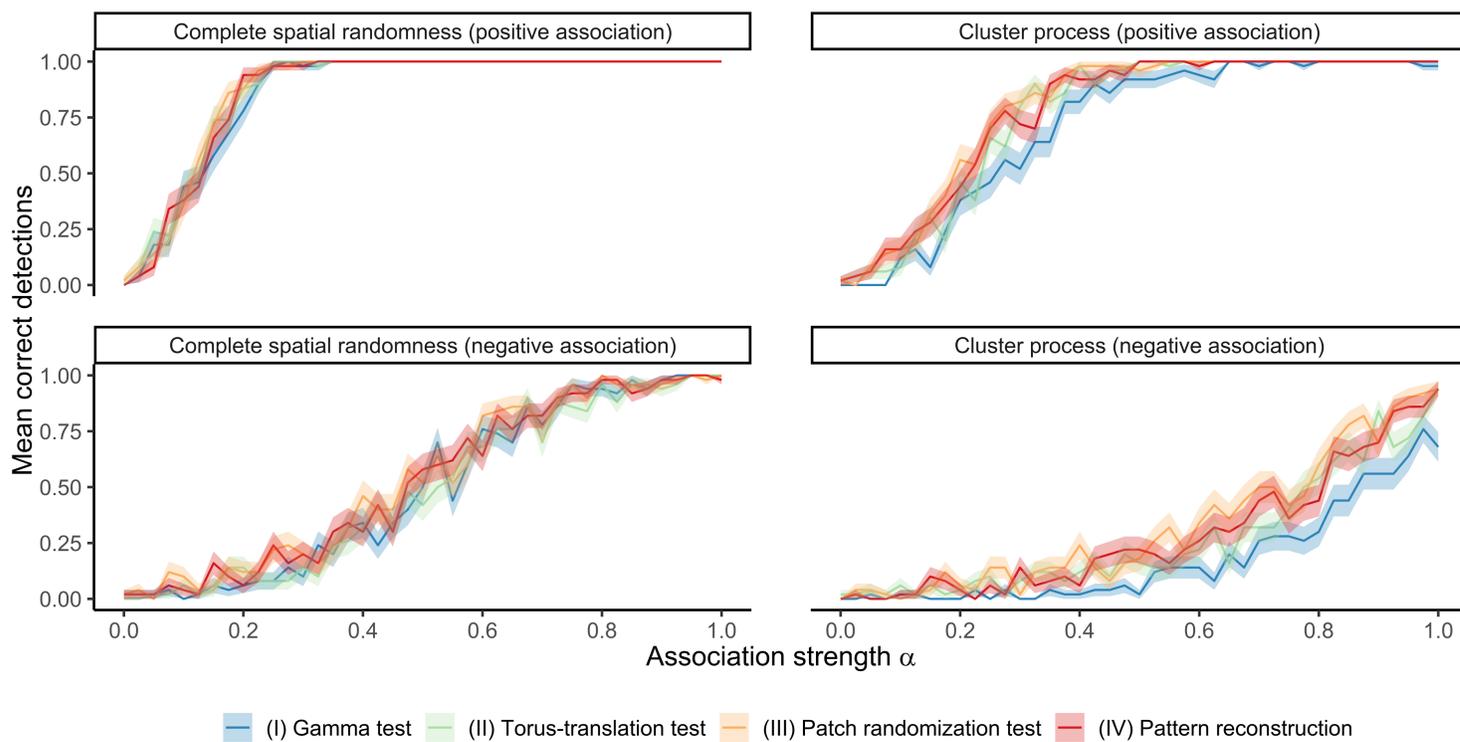


Figure 2: Correct detections of the simulation study. The results summarize 50 repetitions for each association strength. The solid line reflects the mean, the envelopes the standard error. The association strength was increased from 0 to 1 in 0.025-steps.

Conclusions

All methods work similarly well and especially positive associations are detected with a high accuracy and precision. Negative associations, especially of clustered patterns, are picked up slightly worse by all methods.

Pattern reconstruction has some advantages above all other methods, at the prize of high computational demand. The method is possible for irregular plot shapes and for complex patterns without a theoretical point process. Lastly, the spatial structure of the observed pattern is preserved best among all methods while still randomizing the pattern.

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