

Habitat network models to predict species occurrence and their sensitivity to changes in maximum dispersal distance

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Abstract

Presence or absence (occurrence-state) of a species is highly relevant for conservation. To predict occurrence-state, network models can be used, with suitable habitat patches as nodes, connected by potential species dispersal. A threshold is set at the species' maximum dispersal distance to define connections. However, for most animal species there are no trustable maximum dispersal distance estimates. This hinders the development of accurate network models to predict species occurrence-state. We present a sensitivity analysis of the performance of network models to different maximum dispersal distance settings. Our approach, applied on six amphibians in Switzerland, used habitat suitability modelling to define habitat patches, linked within a dispersal distance threshold to form habitat networks. We used network topological measures, patch suitability, and size to explain species

occurrence-state through boosted regression trees. We performed these modelling steps on each species for different maximum dispersal distances, including a literature-derived species-specific value. We evaluated predictive performance and predictor importance among network models. We found a positive relation between predictive performance and dispersal distance, and that species-specific values from literature rarely yielded the best performance. With increasing dispersal distance, the habitat-quality-related variable decreased in importance, while it increased for topology-related predictors. We conclude that model sensitivity to the dispersal distance parameter stems from the contrasting topologies formed with different movement assumptions. Most reported maximum dispersal distances are underestimated, presumably due to leptokurtism. Therefore, caution should be taken when selecting a dispersal distance threshold, considering higher values than those from field reports to account for long-distance dispersers.