(181)

Species Distribution Modeling of Sri Lankan Endemic Genus *Stemonoporus* Thw.: Use of Stacked Species Distribution Models by Integrating Machine Learning and Regression Models

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Abstract

Genus Stemonoporus Thw. (Family Dipterocarpaceae), endemic to Sri Lanka, having 26 species showing restricted distribution mainly confined to the wet zone of the island. The National Red List 2020 recorded all the Stemonoporus species under threat categories. S. nitidus is listed as critically endangered, possibly extinct (CR(PE)). However, the potential effects of climatic variables on their distribution have not been investigated. This study aimed to model the species assemblages and compute the species diversity and richness distribution of the genus Stemonoporus using stacked species distribution modeling (SSDM). The approach integrated both machine learning and regression models including Generalized Linear Models (GLM), Generalized Additive Models (GAM), Multivariate Adaptive Regression Splines (MARS), Random Forest (RF) and Maximum Entropy (MaxEnt). Species occurrence data were obtained from reliable repositories, including international herbaria, national and international floristic databases, and field surveys. A total of 19 bioclimatic variables were acquired from Bioclim version 2.1. A multicollinearity test was conducted to prevent model overfitting. Binary maps were constructed using True Skill Statistics (TSS). The SSDM maps of local species richness and composition were generated by summing the probabilities from the habitat suitability maps. The performance of the model was evaluated using evaluation metrics including species richness error, Cohen's kappa, specificity and sensitivity. The relative contribution of environmental variables was assessed. Analysis was conducted in ntbox and SSDM R package. Results revealed that annual mean temperature and precipitation have the highest relative contribution. Mean species richness is five within a 1 km^2 grid in the wet zone of Sri Lanka. A higher sensitivity value (0.85) indicates strong model performance for detecting the presence of Stemonoporus species. A higher kappa value (0.99) indicates a strong agreement between the predicted and observed species distributions. This suggests that models accurately predict species presence and absence, reflecting strong reliability in predictions.

Keywords: *Stemonoporus, Dipterocarpaceae, SSDM, Species richness*

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47