Are niche-based species distribution models transferable in space?

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)

ID 996709
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Year 2006
Title Are niche-based species distribution models transferable in space?
Journal Journal of Biogeography
Volume 33
Number 10
Pages / **Article-Number** 1689-1703
Aim To assess the geographical transferability of niche-based species distribution models fitted with two modelling techniques. Location Two distinct geographical study areas in Switzerland and Austria, in the subalpine and alpine belts. Methods Generalized linear and generalized additive models (GLM and GAM) with a binomial probability distribution and a logit link were fitted for 54 plant species, based on topoclimatic predictor variables. These models were then evaluated quantitatively and used for spatially explicit predictions within (internal evaluation and prediction) and between (external evaluation and prediction) the two regions. Comparisons of evaluations and spatial predictions between regions and models were conducted in order to test if species and methods meet the criteria of full transferability. By full transferability, we mean that: (1) the internal evaluation of models fitted in region A and B must be similar; (2) a model fitted in region A must at least retain a comparable external evaluation when projected into region B, and vice-versa; and (3) internal and external spatial predictions have to match within both regions. Results The measures of model fit are, on average, 24% higher for GAMs than for GLMs in both regions. However, the differences between internal and external evaluations (AUC coefficient) are also higher for GAMs than for GLMs (a difference of 30% for models fitted in Switzerland and 54% for models fitted in Austria). Transferability, as measured with the AUC evaluation, fails for 68% of the species in Switzerland and 55% in Austria for GLMs (respectively for 67% and 53% of the species for GAMs). For both GAMs and GLMs, the agreement between internal and external predictions is rather weak on average (Kulczynski's coefficient in the range 0.3-0.4), but varies widely among individual species. The dominant pattern is an asymmetrical transferability between the two study regions (a mean decrease of 20% for the AUC coefficient when the models are transferred from Switzerland and 13% when they are transferred from Austria). Main conclusions The large inter-specific variability observed among the 54 study species underlines the need to consider more than a few species to test properly the transferability of species distribution models. The pronounced asymmetry in transferability between the two study regions may be due to peculiarities of these regions, such as differences in the ranges of environmental predictors or the varied impact of land-use history, or to species-specific reasons like differential phenotypic plasticity, existence of ecotypes or varied dependence on biotic interactions that are not properly incorporated into niche-based models. The lower variation between internal and external evaluation of GLMs compared to GAMs further suggests that overfitting may reduce transferability. Overall, a limited geographical transferability calls for caution when projecting niche-based models for assessing the fate of species in future environments.
Publisher Wiley
ISSN/ISBN 0305-0270 ; 1365-2699
edoc-URL http://edoc.unibas.ch/46762/

Full Text on edoc No;
Digital Object Identifier DOI 10.1111/j.1365-2699.2006.01466.x
ISI-Number 000240367800002
Document type (ISI) ArticleProceedings Paper