hSDM, an R package for hierarchical species distribution models taking into account imperfect detection and spatial correlation of the observations.

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Abstract:

Imperfect detection of individuals (Iknayan et al., *in press*) and spatial correlation of the observations (Lichstein et al., 2002) must be taken into account to obtain unbiased estimates of species distribution from presence and count data.

To do so, hierarchical Bayesian models that incorporate multiple hierarchical processes (detection process, suitability process and spatial correlation process) provide a promising way forward (Latimer et al., 2006). These hierarchical models are relatively complex and beyond the experience of many potential users (Iknayan et al., *in press*). Classical softwares used for hierarchical models (such as WinBUGS) usually fail at estimating the parameters of such complex models for large data-sets (number of spatial cells superior to tens of thousands).

Here we present the hSDM R package to estimate the parameters of site-occupancy (MacKenzie et al., 2002) and N-mixture models (Royle, 2004) for large data-sets. Models take into account the spatial correlation of the observations. Functions from the hSDM R package provide user-friendly and fast implementations of these models that would facilitate their use and acceptance by the scientific community in ecology.

References

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