

Published in final edited form as:

*Glob Chang Biol.* 2014 December ; 20(12): 3591–3592. doi:10.1111/gcb.12728.

## Editorial commentary on “BIOMOD – optimizing predictions of species distributions and projecting potential future shifts under global change”

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Climate is changing at an unprecedented rate, resulting in early signs of biodiversity loss and community reshuffling throughout the globe (Bertrand *et al.*, 2011, Parmesan, 2006). Considering the irreversibility of species extinction and the social and political needs for risk assessments, scientists have tried to extrapolate the likely effects of forecasted climate change over this next century on various entities (e.g. species, communities). Among the various strategies to address this issue, empirical models relating field observations or atlas surveys to climatic variables, based on statistically or theoretically derived response surfaces, have become a tool of choice. In the early 2000s, the use of these species distribution models (SDMs) in ecology was still in its infancy (see key review by, Guisan & Zimmermann, 2000). SDMs, which allow for investigating, explaining and predicting the relationships between a given species distribution and its environment, have emerged as a key player in the Big Data revolution in ecology. Ten to fifteen years ago, few standalone packages were available for non-aficionados. The pioneering ones mostly relied on minimal rectilinear envelopes in a multi-dimensional climatic space (Busby, 1991). The most well-known and applied algorithm at that period was GARP, a standalone and user-friendly package based on a genetic algorithm (Stockwell & Peters, 1999). What struck me in the early 2000's was the paucity of comparative analyses and more generally frameworks to run a set of models on the same data and contrast the results. In other words, while ecology was entering an era of prediction, triggered by the climate and land use change context, most researchers were left without appropriate tools necessary to address burning questions related to the future of biodiversity.

I do not intend here to state that this paper “BIOMOD....” changed the way ecologists or biogeographers carried out predictive science, but that it set the first stone for the use of multiple models in ecology. In others words, ecologists discovered that the description of the relationships between a species occurrence or abundance and environmental variables was conditioned by the type of algorithm used and its underlying hypotheses. Since then, there are now an important number of tools, standalone packages and frameworks to work with species distribution models. In 2009, we released an important upgrade of *BIOMOD*, called *biomod2* (Thuiller *et al.*, 2009), fully object-oriented and developed as a library in the ever-developing R community and that integrates around ten different algorithms. The main advantage of *biomod2* lies in its capability to compare or combine a suite of algorithms using the same set of initial data and parameterization. It also built on the power of R that

now fully integrates geographic information systems and data queries on web-servers (*rgdal* and *raster* packages). In parallel, the community was enriched with other frameworks such as MAXENT (Phillips *et al.*, 2006), point-pattern models (*ppmlasso*, (Renner & Warton, 2013)) and lately hierarchical Bayesian species distribution models (<http://hsdm.sourceforge.net>). Although all these approaches are powerful and allow potential users to build models in a relatively simple way, there are important issues to consider beforehand: choosing a limited but relevant number of variables, understanding the assumptions behind the models, choosing between simplicity versus complexity in the parameterization of the algorithms, assessing the quality of the data used to build but also to evaluate the models and finally evaluating the uncertainty and errors. These are the essential steps to take into account before making any statement about the drivers of species ranges and the future state of biodiversity (Elith & Leathwick, 2009, Guisan & Thuiller, 2005, Merow *et al.*, 2015). *BIOMOD* and other tools developed since have greatly enhanced the ability of ecologists and biogeographers to take these steps into account.

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