















ate snail host at regional scales. This means that we face an enormous challenge, as reliable future projections for changes in, for example, land use and land cover are not available. Currently, we have little choice but to treat these variables as static, and adopt a *no change-assumption*, that is not very realistic, although it is better than excluding them altogether (Stanton *et al.*, 2012). However, we are not alone facing this challenge. Conservation scientists, to give one example, are also exploring new avenues (de Chazal and Rounsevell, 2009; Riordan and Rundel, 2014), and a combined effort here could perhaps lead to new ways to address this challenge.

## Conclusions

In conclusion, we suggest that ways to combine, hybridise or couple statistical-empirical distribution modelling with process-based models of snail lifecycles and parasite development, underpinned by a solid knowledge of snail ecology, be further explored. One approach is not intrinsically superior to the other (Dormann *et al.*, 2012), and by combining them, the knowledge and insight that can be gained from available data, experimental and/or empirical, is maximised.

This approach, however, can only be fully exploited, if the current paucity of biological data needed to parameterise the different models to single species' responses to changes in abiotic conditions is addressed (McCreesh *et al.*, 2013). Combining a full set of such species-specific details with knowledge of the complex ecological, evolutionary and societal aspects that determine the variation in the distribution and intensity of disease may be the most promising way forward in the challenging field of predicting the impacts of climate change on schistosomiasis, and vector-borne diseases in general.

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