Forecasting species range shifts: a Hierarchical Bayesian framework for estimating process-based models of range dynamics

J. Pagel & F. Schurr

Shifts of species ranges have been widely observed as 'fingerprints' of climate change and more drastic shifts are expected in the coming decades. Current studies projecting range shifts in response to climate change are predominantly based on phenomenological models of potential climate space (climate envelope models). These models assume that species distributions are at equilibrium with climate, both at present and in the future. A more reliable projection of range dynamics under environmental change requires process-based models that can be fitted to distribution data and permit a more comprehensive assessment of forecast uncertainties [1]. To achieve this goal, we develop a Hierarchical Bayesian framework [2] that utilizes models of local population dynamics and regional dispersal to link data on species distribution and abundance to explanatory environmental variables.

In a simulation study we investigate the performance of this approach in relation to the biological characteristics of the target species and the quantity and quality of biological information available. We use R to implement an integrated routine that combines a grid-based ecological simulation model and a 'virtual ecologist' with efficient MCMC algorithms (e.g. DRAM [3]) for sampling from the full posterior distribution of model parameters and derived predictions of spatially distributed abundances under prescribed climatic changes. This enables us to run a range of virtual scenarios differing in both ecological assumptions and sampling design in order to examine how forecast uncertainty depends on a species' ecology as well as on data quality and quantity.

References

[1] Araujo, M. B., and A. Guisan. 2006. Five (or so) challenges for species distribution modelling. Journal of Biogeography **33**:1677-1688.

[2] Clark, J. S., and A. E. Gelfand. 2006. A future for models and data in environmental science. Trends in Ecology & Evolution **21**:375-380.

[3] Haario, H., M. Laine, A. Mira, and E. Saksman. 2006. DRAM: Efficient adaptive MCMC. Statistics and Computing **16**:339-354.

Joern Pagel, Institute of Biochemistry and Biologie, University Potsdam, Germany.
joern.pagel@uni-potsdam.de