

# Constructing a hybrid species distribution model from standard large-scale distribution data

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## ARTICLE INFO

### Keywords:

Biotic interaction  
Colonization  
Extinction  
Range projection  
Process-based  
Dispersal

## ABSTRACT

Species range shifts under climate change have predominantly been projected by models correlating species observations with climatic conditions. However, geographic range shifting may depend on biotic factors such as demography, dispersal and species interactions. Recently suggested hybrid models include these factors. However, parameterization of hybrid models suffers from lack of detailed ecological data across many taxa. Further, it is methodologically unclear how to upscale ecological information from scales relevant to ecological processes to the coarser resolution of species distribution data (often 100 km<sup>2</sup> or even 2500 km<sup>2</sup>). We tackle these problems by developing a novel modelling and calibration framework, which allows hybrid model calibration from (static) presence-absence data that is available for many species. The framework improves understanding of the influence of biotic processes on range projections and reveals critical sources of uncertainty that limit projection reliability. We demonstrate its performance for the case of the butterfly *Titania's* Fritillary (*Boloria titania*).

## 1. Introduction

Projections of species distributions under changing environmental conditions are needed to support the conservation of biodiversity (Dawson et al., 2011; Pereira et al., 2010). Most models (such as bioclimatic envelope models, synonyms: ecological niche models, habitat models or species distribution models) statistically correlate species observations and environmental conditions (Elith and Leathwick, 2009; Guisan and Zimmermann, 2000; Yalcin and Leroux, 2017). Because of their correlative calibration approach, we refer to them as correlative species distribution models (C-SDMs). The correlative approach takes advantage of the type of widely available data, such as raster maps of species occurrence and environmental factors, usually derived from atlas data. The models, however, often for technical reasons (Singer et al., 2016), ignore key biotic mechanisms that affect species distributions (Urban et al., 2016).

Recent methodological advances suggest ways to enhance structural realism of species distribution models by incorporating biotic factors (Bocedi et al., 2014; Cabral et al., 2017; Evans et al., 2016; Kissling et al., 2012; Schurr et al., 2012; Talluto et al., 2016; Zurell, 2017) and

have been shown to improve range projections (Zurell et al., 2016). One approach are hybrid species distribution models (H-SDMs; Dormann et al., 2012; also called niche population models Fordham et al., 2013). H-SDMs are based on C-SDMs that constitute filtering by the abiotic environment but add further relevant biotic processes or factors, such as interspecific interactions (Kissling et al., 2010; Meier et al., 2012; Schweiger et al., 2012), individual variability and local adaptation (Swab et al., 2015), dispersal or transport (Buse and Griebeler, 2011; Chapman et al., 2016; De Cáceres and Brotons et al., 2012; Kramer-Schadt et al., 2004), or demography (Keith et al., 2008). These studies used additional ecological knowledge to parameterize the biotic processes, and showed differences in range projections compared to such based on abiotic environmental information only.

However, for many species, ecological process knowledge is lacking. Therefore, it would be desirable to parameterize H-SDMs from widely available data similarly to C-SDMs. Clearly such an endeavor has its limitations, because model projections cannot be more reliable than the information from which they are constructed. Missing knowledge on model and process structure or model parameters can compromise projection reliability (Singer et al., 2016). Nevertheless, we will show

Abbreviations: C-SDM, correlative species distribution model; G-ECM, grid cell extinction-colonization model; H-SDM, hybrid species distribution model

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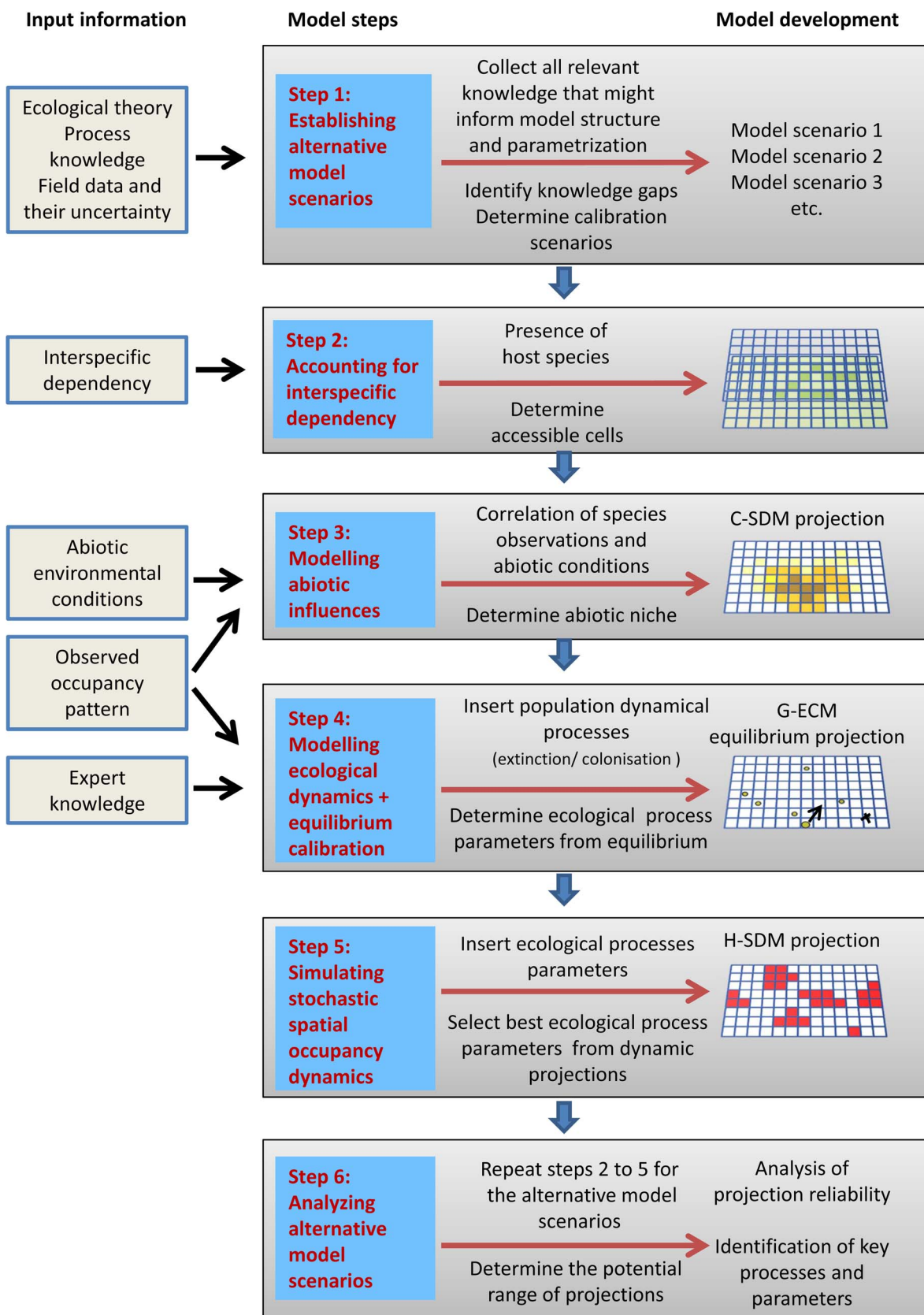


Fig. 1. H-SDM modelling framework. Embedded in a framework of model critique, the H-SDM hierarchically combines two submodels, a correlative species distribution model (C-SDM) and a grid-cell extinction colonization model (G-ECM). In a knowledge survey, available and lacking information is identified and condensed in model scenarios (step 1). Interspecific dependency on host species limits spatial extent (step2). From environmental filtering, the C-SDM projects abiotic grid cell suitability for each geographic grid cell (step 3). This grid cell suitability affects population dynamical processes in the G-ECM. Parametrization via the G-ECM equilibrium solution (step 4) is further improved by stochastic H-SDM projections (step 5). Steps 2–5 are repeated in uncertainty and sensitivity analyses (step 6). Models (right column) and data (left column) are linked by modelling steps (central column). For further information refer to Sec. 2.2.

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