# Testing the relevance of using spatial modeling to predict foraging habitat suitability around bat maternity: A case study in Mediterranean landscape

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## ARTICLE INFO

## ABSTRACT

Habitat suitability models (HSMs) have so far been used mainly to study broad-scale patterns of species distribution based on environmental variables; however, they can also be applied to address conservation needs at finer scales. In this study, we evaluated the feasibility of using HSMs based on presence-only data to predict bat foraging habitat suitability around maternity roosts using radio-tracking location data. We radio-marked 34 *Rhinolophus ferrumequinum* and 29 *Myotis emarginatus* from two mixed-species maternity roosts (21.5 km apart) in a Mediterranean landscape. We generated foraging habitat suitability maps for the two species and the two colonies incorporating 17 land cover variables as well as distance from the maternity roosts. We then compared the performance of four presence-only models: Mahalanobis distance, ENFA, MADIFA and MaxEnt. Our study found that all four models generated foraging habitat suitability maps that performed well at predicting the species-specific quality of foraging habitat based on the configuration of the landscape. Riparian vegetation, woodland and distance from roosts play a key role in foraging habitat selection around colonies both for *R. ferrumequinum* and *M. emarginatus*. MaxEnt was the model that best predicted suitable foraging habitats. These are also the best models at predicting foraging habitat suitability with relatively good performance around another colony maternity roost using independent radio-tracking locations. Because many bat species are threatened by foraging habitat loss, habitat suitability modeling offers a useful tool in defining appropriate conservation guidelines that protect foraging habitats around bat maternity roosts.

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## 1. Introduction

During the last decade, habitat suitability models (HSMs), or species distribution models (SDMs), have received considerable attention in conservation studies and have generated a wide range of applications (Elith and Leathwick, 2009; Guisan and Thuiller, 2005). These models have been used both to identify the most influential environmental variables that may explain species occurrence or abundance at known locations and to predict species distribution in relation to biotic and abiotic variables. They have thus enabled a better understanding of species–environment relationships at large spatial scales (Bellamy et al., 2013; Sattler et al., 2007), with the assumption that the probability of the occurrence or abundance of a species is proportional to the degree of habitat suitability (Calenge et al., 2008).

HSMs have also been the subject of significant and rapid methodological development (Elith and Leathwick, 2009). Among the numerous available methods, the widely used generalized linear models (GLMs) are known to provide pertinent results for abundant species (Brotons et al., 2004), but are less reliable for rare species, which produce a high proportion of zero values in the datasets because they are present at only a few locations (Wisz et al., 2008). Moreover, GLMs are based on presence–absence or abundance datasets, whereas many of the datasets available for HSM are presence-only, which raises the issue of choosing "pseudo-absences" to determine whether the species is truly absent or whether it has simply not been observed because of insufficient exploration effort (Hirzel and Le Lay, 2008; Mcardle, 1990).

More recently, several novel HSMs that use presence-only data have been proposed in response to the limitations of models based on presence–absence data: ecological niche factor analysis (ENFA; Hirzel et al., 2002), Mahalanobis distance factor analysis (MADIFA; Calenge et al., 2008) and maximum entropy method (MaxEnt; Phillips et al., 2006). HSMs using presence-only data (e.g. ENFA, MADIFA, MaxEnt) are more suitable for elusive species such as bats, for which local

absence data are often not available or reliable because of their low detectability due to their nocturnal behavior, the difficulties of acoustic identification (Ahlén and Baagøe, 1999; Barclay, 1999) and their high mobility (Jaberg and Guisan, 2001; Walsh and Harris, 1996). HSMs in bat studies have mostly been developed with the primary goal of predicting species distribution in relation to environmental variables, especially climatic variables, at a large spatial scale (see e.g. Greaves et al., 2006; Rebelo and Jones, 2010; Sattler et al., 2007). However, HSMs may also offer opportunities for predicting habitat suitability at finer scales, for instance, in relation to landscape configuration (see e.g. Razgour et al., 2011). However, characterizing or predicting habitat suitability at a fine spatial scale in relation to landscape configuration can be more problematic for mobile species than for sessile species, as the former tend to use intermittent resources that are patchily distributed across a landscape (Elith and Leathwick, 2009). To date only one study (Razgour et al., 2011) has explored the feasibility of predicting bat foraging habitat suitability at a fine spatial scale using HSM based on presence-only data. The satisfactory results obtained for the gray long-eared bat *Plecotus austriacus* in the UK (Razgour et al., 2011) need to be tested for other bat species in different contexts.

Many bat species around the world are increasingly threatened by anthropogenic land-use intensification (Mickleburgh et al., 2002) which affects both their access to foraging habitat and their ability to establish colonies: two key elements for the conservation (Fenton, 1997). Because the majority of bat species form colonies, they are vulnerable to local disturbance. Bat conservation efforts mainly focus on hibernacula or maternity roosts and rarely on the foraging habitat surrounding maternity roosts. Despite the significant development of telemetry studies on bats in recent years, the characterization of favorable foraging habitat surrounding maternity roosts and its explicit spatialization using predictive models – both of which are needed to plan effective conservation management actions for habitats – remain very limited (see however Rainho and Palmeirim, 2013). In this context, HSM could be used to generate foraging habitat suitability maps surrounding maternity roosts that allow the species-specific quality of the foraging habitat to be predicted based on the landscape configuration of the study area (Rainho and Palmeirim, 2013; Razgour et al., 2011). These models could be useful tools to help identify where and how species use foraging habitats.

Indeed, by helping conservation management staff to better identify key foraging habitats, HSMs could be used to define appropriate conservation guidelines for protecting foraging habitats around maternity roosts of threatened species.

The aim of this study was to evaluate the relevance of HSM based on presence-only data to predict bat foraging habitat suitability around maternity roosts using as a biological model two different bat species of conservation concern, the greater horseshoe bat *Rhinolophus ferrumequinum* and Geoffroy's bat *Myotis emarginatus*. More specifically, we compared the performance of four different presence-only models (Mahalanobis distance or MD, ENFA, MADIFA and MaxEnt) using radio-tracking location datasets of these two species within the foraging areas of two mixed-species maternity colonies in the French Mediterranean area. Our objectives were: (1) to characterize the selection of foraging habitat of the two bat species at a fine spatial scale; (2) to assess the relative performance of the four presence-only models in creating suitability maps for foraging habitat around the two colonies; and (3) to assess the performance of these models at predicting foraging habitat suitability around another independent bat colony.

## 2. Materials and methods

### 2.1. Study area

Our study site was located in the Camargue (the delta of the Rhône River) on the French Mediterranean coast (43° 34′ N, 4° 34′ E; Fig. 1). The climate is typically Mediterranean, with warm average daily temperatures (3–11 °C in January, 19–30 °C in August) and low rainfall (590 mm year$^{-1}$ on average) (Chauvelon, 1998). Northerly and northwesterly winds are very common throughout the year, and there is significant evapotranspiration (1300 mm year$^{-1}$) (Chauvelon, 1998). The Camargue is characterized by flat landscapes with soil containing an increasing gradient of salt as it approaches the Mediterranean Sea. The area consists mainly of lagoons and a marshy network with some salt grasslands. Forest areas are small and dominated by *Populus alba* (L.) and *Pinus pinea* (L.). The drainage system of the Camargue is entirely controlled by man-made dykes located where marine and river water
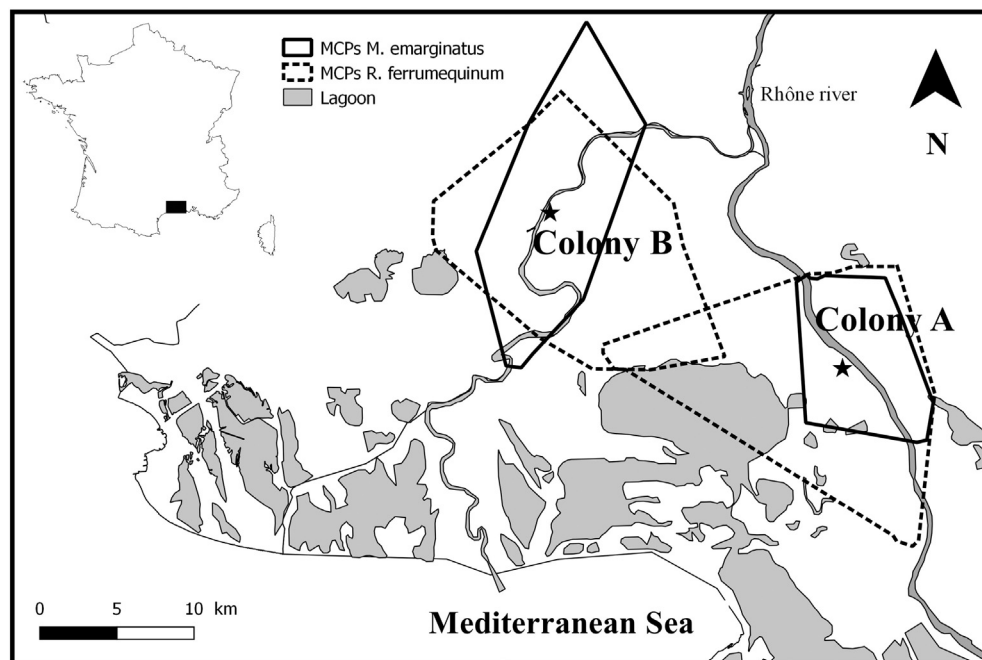


**Fig. 1.** Location of the study area with the four minimum convex polygons (MCPs) for *Rhinolophus ferrumequinum* and *Myotis emarginatus* around the two mixed-species maternity roosts (colonies A and B indicated by a star).