Predicting elusiveness: potential distribution model of the Southern smooth snake, *Coronella girondica*, in Italy

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Abstract. Predictive models of species distribution may be very useful for understanding actual distribution of elusive species, including several snakes. The southern smooth snake (*Coronella girondica*) is likely the most elusive snake species of peninsular Italy, and is therefore well-suited for predicting potential distribution studies. In this paper we predict the potential distribution map of this species in Italy by using MAXENT algorithm, that finds the probability distribution of maximum entropy that is constrained by considered ecological parameters. Presence data for *Coronella girondica* were gotten from CKmap. The potential distribution model of *Coronella girondica* showed a very good overall performance (AUC = 0.959), and indicated that high suitability areas correspond mainly to Tyrrhenian north and central regions, including Liguria, western Emilia-Romagna, Tuscany, Umbria, and northern Latium. Southern Italian regions were clearly unsuitable for this snake species. Overall, our study revealed that previous distribution maps indicating the occurrence of *Coronella girondica* in southern Italy and Sicily were poorly reliable. The conservation and management implications of our study are also addressed.

Keywords. Distribution modelling, elusive species, Serpentes, Colubridae, Italy.

INTRODUCTION

Analysis of many aspects of ecology and conservation may be helped by the use of predictive models of species distribution (Graham et al., 2004), including for instance modelling studies of invasive species spread (e.g., Thuiller et al., 2005), impacts of climate change (Thomas et al., 2004), and spatial patterns of species diversity (Guisan and Zimmermann, 2000; Graham et al., 2006). Modelling potential distribution of a given species based on presence-only data is also a useful tool for predicting new localities of presence for rare and

threatened species that are hardly found in the wild (Godown and Peterson, 2000; Engler et al., 2004), or for species that are simply very elusive and whose distribution is therefore little known (Guisan et al., 2006). The utility of these presence-only modelling methods is that they only require a set of known occurrences together with predictor variables such as topographic, climatic, edaphic, biogeographic and remotely sensed variables (Phillips and Dudik, 2008). The main advantage of presence-only data methods is that it is not necessary to confirm absence records, a big problem especially in elusive species.

Several snake species are genuinely elusive, and therefore their distribution may be somewhat underestimated and least known compared to other reptiles. For instance, in recent years it has been demonstrated that the true distribution of the snake *Hemorrhois hippocrepis* is considerably wider in Sardinia than previously suspected (e.g., compare maps in Razzetti and Bonini, 2006 with that in Bruno and Maugeri, 1977). Among the snake species found in the Italian peninsula, the Southern smooth snake (*Coronella girondica*) is likely the most elusive, and certainly one of the least known in terms of both ecology and distribution. Indeed, this snake spends much of the time below-ground or behind flat stones, and is active in the open only at night (Agrimi and Luiselli, 1994; Capula et al., 1995). As a consequence, its local distribution is often very little known (Razzetti and Bonini, 2006; Bologna et al., 2007). *Coronella girondica* is therefore a well-suited species for modelling its niche in order to find new suitable areas, also because there is circumstantial evidence that this species is declining over wide sectors of its current range (Bologna et al., 2007).

Our aim in this paper is to present a model of distribution for *Coronella girondica* in Italy, and to discuss the potential importance of distribution maps in terms of ecological and conservation purposes.

MATERIALS AND METHODS

Presence data for *Coronella girondica* were gotten from CKmap (Stoch, 2000-2005). The CKmap databank represents the largest, most authoritative, and most updated resource of faunistic knowledge in Italy, being composed by more than 500000 records regarding approximately 10000 terrestrial and freshwater species (Ruffo and Stoch, 2005). CKmap data indicates the occurrence of each species within the cells of the Universal Transverse Mercator (UTM, 10 × 10 km) grid that intersect the Italian territory. The presence data was downscaled to the resolution of environmental predictors (e.g., Araújo et al., 2005) and implemented in the modelling procedure. In order to build a reliable model of habitat suitability, one distribution record from north-eastern Italy was excluded from the computations, as in recent studies it has been considered to be likely the result of an introduction event (e.g., Lapini et al., 1999).

Potential distribution of *Coronella girondica* in Italy was assessed by MAXENT algorithm (Phillips et al., 2004, 2006). In order to estimate the target probability distribution, MAXENT finds the probability distribution of maximum entropy that is constrained by considered ecological parameters. In the case of modelling ecological niches of species, these constraints consist of the values of those pixels at which the species has been detected (Phillips et al., 2004, 2006; Peterson et al., 2007). MAXENT models produce predictions in the form of real numbers between 0 and 100, representing cumulative probabilities of occurrence (Phillips et al., 2004, 2006; Peterson et al., 2007). MAXENT can combine predictors to manage over-fitting by regularizing factors (Phillips et al., 2006; Phillips and Dudík, 2008). We performed this algorithm by using the 19 climatic variables (Table 1), with a resolution of 30" of geographic degree, provided by WorldClim (Hijmans et al., 2004).

Table 1. Climatic variables used to elaborate the models

Var no.	Description
var 1	Annual Mean Temperature
Var 2	Mean Diurnal Range [Mean of monthly (max temp - min temp)]
Var 3	Isothermality [(var2 / var7) * 100]
Var 4	Temperature Seasonality (standard deviation * 100)
Var 5	Maximum Temperature of Warmest Month
Var 6	Minimum Temperature of Coldest Month
Var 7	Temperature Annual Range (var5 - var6)
Var 8	Mean Temperature of Wettest Quarter
Var 9	Mean Temperature of Driest Quarter
Var 10	Mean Temperature of Warmest Quarter
Var 11	Mean Temperature of Coldest Quarter
Var 12	Annual Precipitation
Var 13	Precipitation of Wettest Month
Var 14	Precipitation of Driest Month
Var 15	Precipitation Seasonality (standard deviation / mean)
Var 16	Precipitation of Wettest Quarter
Var 17	Precipitation of Driest Quarter
Var 18	Precipitation of Warmest Quarter
Var 19	Precipitation of Coldest Quarter

The reliability of the potential distribution model was assessed by Area Under Curve (AUC) criterion through a jack-knife procedure. This validation procedure compares the predicted values of habitat suitability assigned to presence and pseudo-absence data in the test subset by producing the Receiver Operating Characteristic (ROC) plots (Fielding and Bell, 1997) and deriving the relative AUC value (Faraggi and Reiser, 2002). The main positive feature of AUC consists of being a single threshold-independent measure for model performance (Fielding and Bell, 1997; Manel et al., 2001; Allouche et al., 2006; Peterson et al., 2007). An AUC value can be interpreted as the probability that a presence site, randomly chosen from the dataset, has a higher predicted value than an absence site (Elith et al., 2006, Phillips et al., 2006).

Models were run by using MAXENT 3.1 (Phillips et al., 2006), which was also utilized for the jack-knife procedure for the model validation.

RESULTS

The potential distribution model of *Coronella girondica* showed a very good overall performance (AUC = 0.959; see Fig. 1). The potential distribution map (Fig. 2) showed that high suitability areas correspond mainly to Tyrrhenian north and central regions,
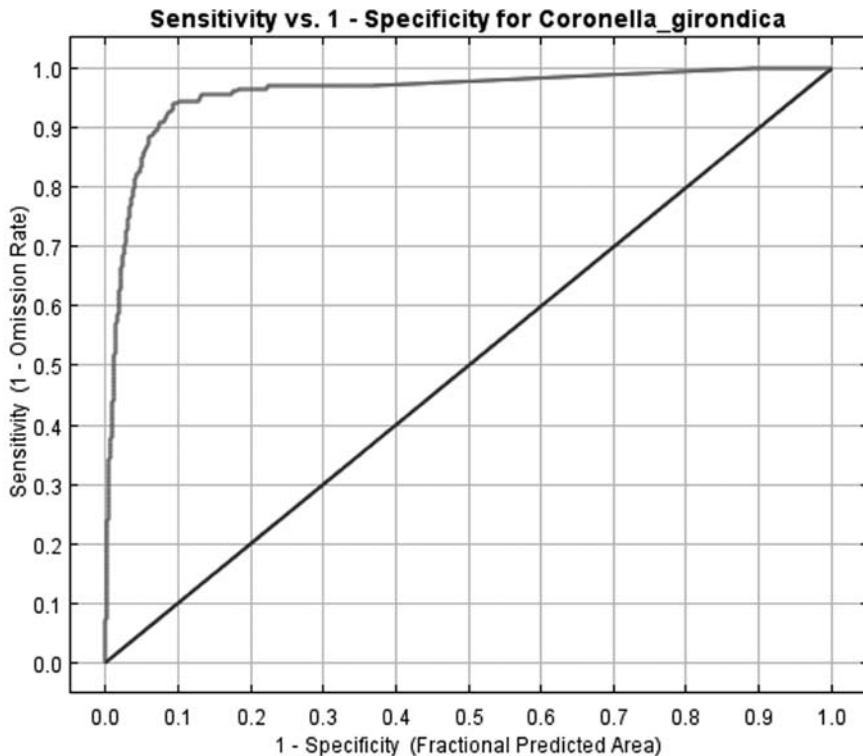
Fig. 1. Receiver Operating Characteristic (ROC) plots for the potential distribution model of *Coronella girondica* in Italy. The "Area Under ROC Curve" is the AUC value.

including Liguria, western Emilia-Romagna, Tuscany, Umbria, and northern Latium. These regions indeed correspond to the areas with the higher number of known presences (Razzetti and Bonini, 2006). Wide regions in both northern and southern Italy appeared completely unsuitable for *Coronella girondica* (Fig. 2).

DISCUSSION

The most updated and reliable distribution map for *Coronella girondica* in Italy is given in Razzetti and Bonini (2006). These authors pointed out that several historical records are unreliable, and that the species is likely more common on the Tyrrhenian side of Italy than on the Adriatic side. Razzetti and Bonini (2006) map was considerably different from previous distribution maps for this species (Bruno and Maugeri, 1977), where *Coronella girondica* was claimed to be widespread also in the southern regions of Italy, i.e. Campania, Calabria, Basilicata, Puglia, and Sicily. Our modelling analysis clearly confirmed the reliability of Razzetti and Bonini (2006) map compared to Bruno and Maugeri (1977) map, indicating that the southern Italian regions are unsuitable for the presence of this
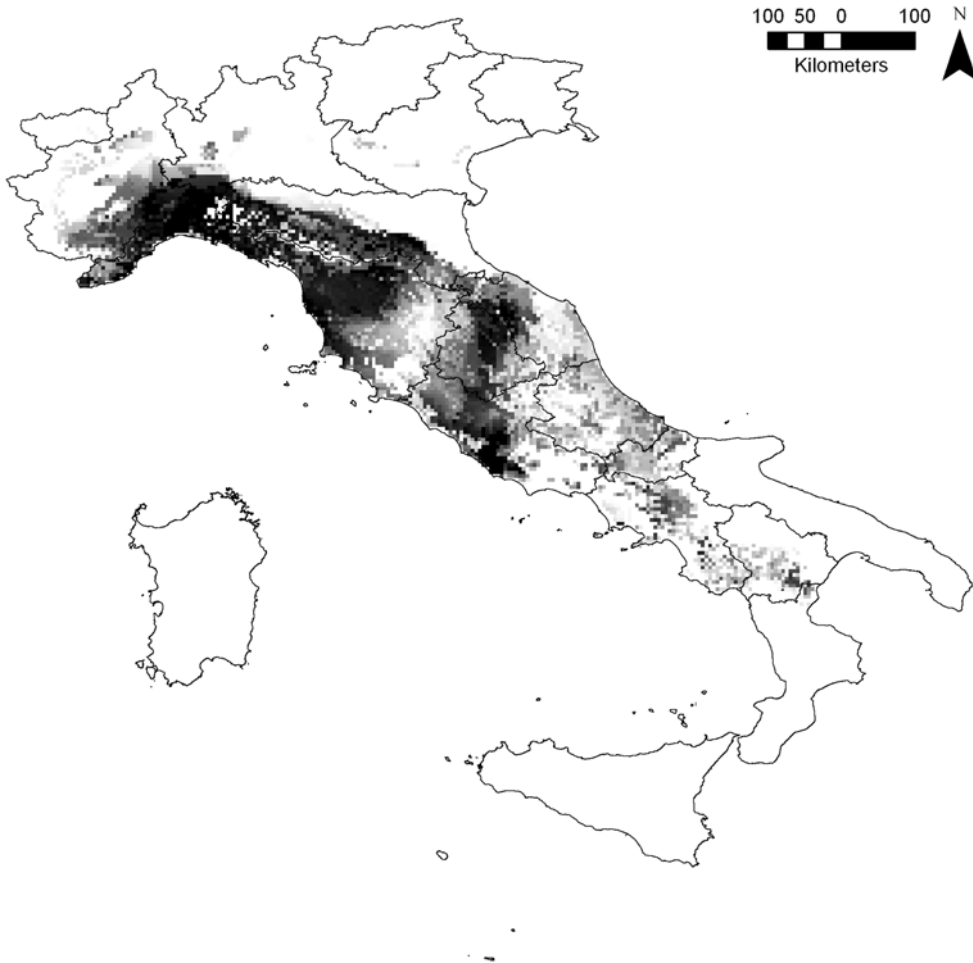
Fig. 2. Potential distribution model for *Coronella girondica*. Probability of presence increases from white to black.

colubrid species. Thus, our study reveals that at least 14 presence records in Bruno and Maugeri (1977) map are unreliable. On the other hand, the potential distribution map given in this study mirrors widely the map drawn by Capula et al. (1995), which was built in consideration of the reproductive ecology characteristics of *Coronella girondica* that were considered inappropriate for the life in the southern Italian climates.

However, if we compare the map of true distribution given in Razzetti and Bonini (2006) with the potential distribution map given here, some differences also do exist. Indeed, we can stress that the potential range of this snake is much wider in Tuscany, Umbria and Latium than currently demonstrated. For instance, there are very few recent records for presence sites in Tuscany, Umbria, and Latium whereas the distribution suitability map indicated that wide sectors of these regions are very well suited for *Coronella girondica*. We would

therefore urge further accurate research in these regions to improve the knowledge of the local distribution of this species. In conservation terms, it is however necessary to stress that some areas that are depicted as potentially very good for this snake (for instance the areas surrounding Rome) are currently strongly altered due to human intervention on the natural habitat. *Coronella girondica* may have been therefore extirpated from these areas, and the remnant populations that are still eventually found should be carefully managed and protected in order to avoid further decline in these potentially important areas for the species. The well-suited areas in Tuscany and Umbria are likely less exploited than those in Latium, suggesting that the relatively few presence records should depend more on unsatisfying field research than on extirpation of the species from potentially good areas. It is, therefore, likely that *Coronella girondica* is not really threatened or in decline in these latter regions, but that its presence may have simply gone undetected in many sites due to its elusiveness accomplished with suboptimal field research by herpetologists. Nevertheless these hypotheses need to be confirmed by including human impact variables in the analysis.

In conclusion, we suggest that careful field research should be done especially in Tuscany and Umbria to improve the number of presence data for this species, and that special conservation and management actions should be done in the suitable areas of Latium, where the suitability of the areas for *Coronella girondica* is high but where the human intervention on the habitat has been very intense.

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