Probabilistic graphical models for species richness prediction: are current protected areas effective to face climate emergency?

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Abstract

Climate change has been related to the current loss of global biodiversity. In this paper, the effects of different scenarios of climate change on the distribution of the four classes of terrestrial vertebrate species in Andalusia (Spain) are explored. The goal is to obtain potential climatically suitable areas for each group (amphibians, reptiles, mammals and birds) under each proposed scenario and examine the usefulness of the current static design of protected areas. We propose a methodology to construct habitat suitability models, which are used to predict the expected species richness given each projected scenario of climate change. The relative change of the species richness within National and Natural Parks, remainder of Natura 2000 network and unprotected areas is compared. The results of the study show a broad effect of climate change on the species richness distribution. In general, there is a loss of specific richness and a restricted availability of suitable areas. The protected areas located in higher altitudes maintain the best conditions for the survival of the taxa considered in the proposed climate change scenarios.

Keywords: Bayesian networks, terrestrial vertebrates, effectiveness of protected areas, conservation policy

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1. Introduction

The report by IPBES (Díaz et al., 2019) considers five direct drivers related to the current loss of biodiversity: changes in land uses, direct over-exploitation of organisms, pollution, invasion of alien species and climate change. In relation to climate change, humans are estimated to have caused a likely range of 0.8-1.2 °C of global warming above to pre-industrial levels (Masson-Delmotte et al., 2018). The progressive increase in temperatures has affected many aspects of biodiversity, such as phenology (Stefanescu et al., 2003; Brown et al., 2016), population dynamics (Wittwer et al., 2015), community structure (Yang et al., 2011), or species distribution (Dyderski et al., 2018).

Protected Areas (PAs) play an essential role in the conservation of biodiversity. However, in the current context of climate change, the conservation planning and management of PAs should progress towards a suitable adaptation (Schmitz et al., 2015), improving conservation strategies (Hannah et al., 2007). With regard to planning, it is well recognized that ecosystems are dynamic, i.e., they change in space and time, for instance due to perturbations or ecological successions, while PAs have always been fixed in space (Wiens et al., 2011; D'Aloia et al., 2019). Different approaches have been proposed to deal with this static approach: increasing the size of PAs, protecting specific habitats or improving landscape connectivity, for example through stepping stones (Stein et al., 2013; Tingley et al., 2014). European Natura 2000 network highlights this static design of PAs. In Spain, the terrestrial surface of Natura 2000 network is 13,8 million ha, which approximately represents the 27,3% of the Spanish territory. Thereby, Spain is the main contributor to European Natura 2000 network.

In contrast to the static design of PAs, a dynamic perspective has been proposed (Alagador et al., 2014; Lewison et al., 2015). In this sense, dynamic area-based management considers areas temporarily protected and later released from legal protection when they are no longer needed (Alagador et al., 2014; Lewison et al., 2015). Also, this dynamic approach considers the importance of networks of PAs (Gerber et al., 2014). Integrating both approaches, dynamic ecological processes may be protected (D'Aloia et al., 2019). Therefore, decision-makers need new methodological approaches that consider the permanent PAs and the new dynamic conservation areas, public or private, to deal with climate change and biodiversity conservation.

Species distribution models (SDM) are widely used to obtain spatial pre-

dictions of environmental suitability for species (Guisan and Thuiller, 2005; Guisan et al., 2013). These models have been applied for studying climate change and biodiversity (Araújo et al., 2006; Brambilla et al., 2018) or the suitability of reserves to confront climate change (Araújo et al., 2004, 2011). Since the habitat of a species is composed of many observable characteristics, a powerful tool is necessary to analyze the relationships between the explanatory variables and the species.

Bayesian networks (BNs), which belong to the so-called probabilistic graphical models, have been proposed as a tool to model species distributions (Aguilera et al., 2010; Tantipisanuh et al., 2014; Hamilton et al., 2015; Maldonado et al., 2015; Meineri et al., 2015; Maldonado et al., 2016b) since they provide a well founded approach for handling complex systems, and also a flexible framework to allow the inclusion of expert knowledge, empirical data and automatic learning. Roughly speaking, BNs are compact representations of the joint probability distribution over a set of variables whose independence relations are encoded by the structure of an underlying directed acyclic graph (Pearl, 1988; Bielza and Larrañaga, 2014). BNs are a versatile tool since they can be used to solve a variety of problems, including characterization (Ropero et al., 2016), inference about sombe variables in the model (Ames et al., 2005; Fienen et al., 2013; Quinn et al., 2013), supervised classification (Aguilera et al., 2010; Flores et al., 2012; Palmsten et al., 2013; Maldonado et al., 2016b; Castro-Luna et al., 2019), clustering (Aguilera et al., 2013; Fernández et al., 2014; Ropero et al., 2015; Rodrıguez-Sánchez et al., 2017) or regression (Ropero et al., 2014; Scutari et al., 2014; Maldonado et al., 2016a). Some recognized advantages of BNs are their ability to perform analysis with small or incomplete data, the possibility of learning the BN structure from data, as well as their ability of combining different sources of knowledge (Uusitalo, 2007).

The aim of this paper is to explore the effects of climate change on the distribution of the four classes of terrestrial vertebrate species in Andalusia in order to obtain potential climatically suitable areas for each group and examine the usefulness of current protected areas. More specifically, we built a BN model for each group of species, ie, amphibians, reptiles, mammals and birds, and predicted the expected richness of each group of species given three different projected scenarios of climate change, proposed by the Intergovernmental Panel on Climate Change (A1B, A2, B1). The methodology followed to carry out our experiments is presented in Section 2. The obtained results are analyzed in Section 3 and discussed in Section 4. The paper ends

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with conclusions in Section 5.

2. Material and methods

2.1. Study area

Andalusia is a region located in southern Spain which occupies an area of 87000 km² and whose latitude and longitude is between 36°N - 38°44'N and 3°50'W - 0°34'E. As far as elevation is concerned, Andalusia ranges from 0 to 3479 meters above the sea level (Figure 1). The main mountain ranges of Andalusia are the Sierra Morena mountain range (in the North) and the Baetic systems (in the South), which are separated by the Baetic depression, the lowest territory in Andalusia. The flattest areas correspond to the littoral and the Baetic depression, through which the Guadalquivir river runs, and the steepest ones to the Baetic Systems.

Andalusia's geographic location and orographical diversity generate great complexity in regards to its climate. For instance, the mean annual temperature varies in accordance to altitudinal and latitudinal (coast-to-interior) gradients, ranging from 10 to 20°C. Moreover, there is a wide variation in volume of rainfall, with the rainiest area being located in western foothills of the Subbaetic System (exceeding 2000 mm per year), whereas the driest regions lie on southeastern coast (being less than 250 mm per year). In addition, potential evapotranspiration (PET) ranges from about 300 mm/year in the eastern Baetic systems to more than 1000 mm/year in both the Guadalquivir river area and the eastern Mediterranean littoral.
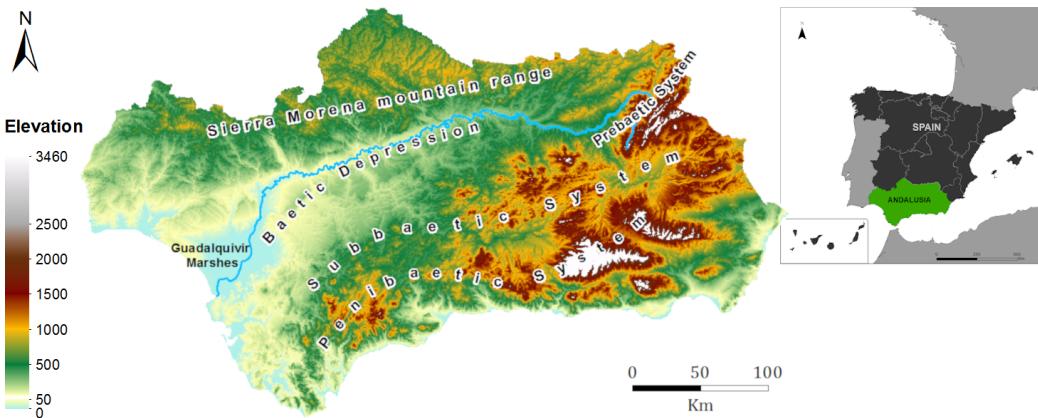

Figure 1: Location and elevation (in meters) of the study area (Andalusia, Spain).

As far as biodiversity is concerned, Andalusia has one of the highest indexes in the European continent. Regarding just the terrestrial vertebrate species, there are 259 birds, 62 mammals, 43 reptiles and 22 amphibians in the study area, which sums up to 386 different species (MAPAMA, 2013). From the conservationism point of view, there are 243 protected areas in the study area, with 24 being Natural Parks and 2 being National Parks (Figure 2). In this regard, 3 different zones will be analyzed: 1) natural and national parks; 2) Natura 2000 network (not including the aforementioned parks); and 3) unprotected areas. National Parks and Natural Parks are natural areas that have been little transformed by human exploitation and activity and have been declared of general interest by national legislation in the first case and by regional legislation (Regional Government) in the second case. However, the administrative management in both cases is carried out at regional level. The legislation on Natural Parks is considered to be somewhat more flexible in relation to permitted human activities (for example, hunting or ecotourism but always controlled and regulated). The Natura 2000 Network was created by means of a European Union (EU) Directive (92/43/EEC) for the conservation of a group of areas of high ecological value at European level, which aims to guarantee the long-term survival of the most valuable and threatened habitats and species in the EU. It includes Sites of Community Importance (SCIs), Special Areas of Conservation (SACs) and Special Protection Areas for birds (SPABs). The SCIs, SACs and SPABs in Spain are considered protected areas, under the name "Red Natura 2000 protected area".

Natural and National Parks

1. Sierra de Aracena y Picos de Aroche
2. Sierra Norte de Sevilla
3. Sierra de Hornachuelos
4. Sierra de Cardeña y Montoro
5. Sierra de Andújar
6. Despeñaperros
7. Sierras de Cazorla, Segura y Las Villas
8. Sierra de Castril
9. Sierra Mágina
10. Sierra María - Los Vélez
11. Sierras Subbéticas
12. Sierra de Huétor
13. Sierra de Baza
14. Sierra Nevada (National Park)
15. Sierra Nevada
16. Los Alcornocales
17. Sierra de Grazalema
18. Sierra de las Nieves
19. Montes de Málaga
20. Sierras de Tejeda, Almijara y Alhama
21. Doñana
22. Doñana (National Park)
23. Bahía de Cádiz
24. La Breña y Marismas del Barbate
25. Del Estrecho
26. Cabo de Gata - Nijar

FIGURE OF PROTECTION

- Natural and National Parks
- Natura 2000 network (excluding parks)

Figure 2: Location of the Natura 2000 network of Andalusia. Natural and National Parks, which are highlighted in blue color, also belong to the Natura 2000 network.

2.2. Data collection and description

The variables used to perform the experiments were obtained from different thematic maps, available in open source repositories. In particular, the land-use and climatic variables where obtained from the environmental information network of Andalusia (REDIAM); the topographic variables were computed from the Andalusian Digital Elevation Model, provided by the Spanish National Geographic Institute; and data of the presence of terrestrial vertebrates were obtained from the Spanish Inventory of Terrestrial Species.

A 10×10 km grid with presence records of different species was superimposed on the thematic maps in order to build a dataset for each group of species. Each dataset is composed of a number of explanatory variables and 1 target variable. The coordinate system for all the datasets is based on the European Terrestrial Reference System 1989 (ETRS89). The value of each variable was calculated for the grid cells which are entirely (or mainly) located in the study area. Afterwards, for each group of species, a dataset composed of 46 variables taking values over 887 cells was obtained, where the target variable is the richness of either amphibians, reptiles, mammals or birds, and the remaining 45 variables are the explanatory variables (Table A.1). This initial set of explanatory variables was selected in accordance with the scientific literature and the available information in the official repositories.

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2.3. Description of the habitat suitability model

A structured Bayesian network (BN) with variable selection was built for each group of species. In the next subsections, the details for the construction of the model for the baseline period (1960-2000) are explained. Broadly speaking, the steps to obtain the structured model are: 1) obtain a partition of the study area to find homogeneous sub-regions (Section 2.3.3); and 2) fit a sub-model to each partition, following the variable selection procedure explained in Section 2.3.2. A brief background to BNs is introduced in Section 2.3.1.

2.3.1. Bayesian networks

Bayesian networks (BNs) are compact representations of the joint probability distribution over a set of variables $\mathbf{X} = \{X_1, \ldots, X_n\}$ whose independence relations are encoded by the structure of an underlying directed acyclic graph (DAG) (Pearl, 1988). Formally, a BN is defined as a pair $(\mathcal{G}, \mathcal{P})$, where $\mathcal{G}$ is a DAG and $\mathcal{P}$ is a set of conditional probability distributions (CPDs). $\mathcal{G}$ is composed of nodes, which represent random variables ($\mathbf{X}$), and links between pairs of nodes, representing statistical dependence between them. Each node X_i has a distribution $p(x_i|pa(x_i))$ attached, where $pa(x_i)$ represents the parents of X_i in $\mathcal{G}$. Attending to the factorization encoded in the DAG, the joint probability distribution over all the variables in the network is defined as the product of the CPDs attached to each node, so that

$$p(x_1, \ldots, x_n) = \prod_{i=1}^{n} p(x_i|pa(x_i)) \qquad \forall x_1, \ldots, x_n \in \Omega_{x_1,\ldots,x_n} \tag{1}$$

where Ω_{x_i} represents the set of all possible values of variable x_i and $pa(x_i)$ denotes an instantiation of the parents of X_i.

BNs can be used as regression models (Larrañaga and Moral, 2011), whose aim is to predict the value of a continuous variable of interest, Y -in this case, the species richness-, given some values of the explanatory variables, $X_1, \ldots, X_n$. A number of restricted DAGs have been proposed to solve regression tasks, aiming at reducing the number of parameters to be estimated from data while maintaining the accuracy of the model. The simplest case is the naive Bayes (NB) structure, where the variable of interest Y is the parent of all remaining variables $X_1, \ldots, X_n$, and these are considered independent to each other given Y (Figure 3).
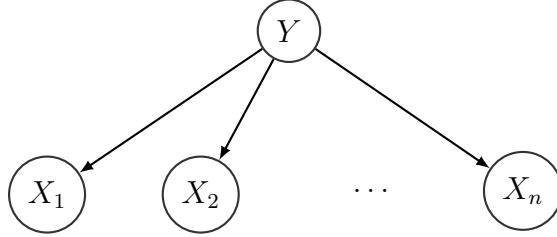
Figure 3: Structure of Naive Bayes model.

There are different ways to represent CPDs, which depend on the nature of the data, i.e. on whether the dataset contains discrete, continuous or both kinds of variables. For continuous variables, Gaussian Bayesian networks are widely used in the literature (Zhang et al., 2012; Meineri et al., 2015; Zhu et al., 2016). A linear Gaussian Bayesian network is a BN in which all the variables are continuous and all the CPDs are linear Gaussian, i.e., the mean of each random variable is a linear combination of their parents.

In this work, we built a Gaussian NB model for each group of species, where the target variable Y is the species richness of either amphibians, reptiles, mammals or birds, and the explanatory variables are selected from Table A.1 as explained in Section 2.3.2. Each model is composed of 3 sub-models (or components), as explained in Section 2.3.3. The R package bnlearn (Scutari, 2010) was used to estimate the parameters from data, following the maximum likelihood estimation (MLE) method, whose aim is to find the parameter that maximizes the likelihood function. The models were learned using variables from Table A.1, where the climate-related variables are measured for the baseline period 1960-2000. The predicted expected values of the variables of interest (species richness of amphibians, reptiles, mammals and birds) were plotted on *species richness distribution maps*.

2.3.2. Variable selection

A variable selection process was carried out among the non-climatic variables, i.e. the models were built with the 12 climate-related variables described in Table A.1 and a subset of the remaining variables. We used an incremental wrapper sequential subset with replacement method (Wang et al., 2015). Let Y be the response variable, i.e., the variable we are interested in predicting, $\mathbf{W} = \{W_1, \ldots, W_c\}$ the set of climate-related predictors and $\mathbf{X} = \{X_1, \ldots, X_n\}$ the set of non-climatic predictive variables of Y. Let $\mathbf{D}$ be the set of variables included in the model $\mathcal{M}$. Firstly, the predictive vari-

ables $\mathbf{X}$ were ordered according to their mutual information (MI) with Y, obtaining the ordered set $\mathbf{Z} = \{Z_1, \ldots, Z_n\}$. To initialize the algorithm, the first variable in $\mathbf{Z}$ (Z_1), the variables in $\mathbf{W}$ and the response Y are included in $\mathbf{D}$. Then, the variables in $\mathbf{D}$ are used to learn a regression model, $\mathcal{M}$, and a measure of predictive performance, E, is computed using the k-fold cross validation technique. Afterward, the next variable in $\mathbf{Z}$ (Z_2) takes 2 independent paths:

- it replaces the non-climatic predictive variables in $\mathbf{D}$, one by one, and the predictive performance of $\mathcal{M}'$, E', is computed. If the error of the new model $\mathcal{M}'$ is lower, i. e., $E > E'$, the new variable Z_2 replaces Z_1 and the new error (E') is set as the current error (E);

- it is inserted in $\mathbf{D}$ and the predictive performance of $\mathcal{M}'$, E', is computed. If $E > E'$, Z_2 is kept in $\mathbf{D}$ and $E = E'$.

These steps are repeated for all the variables in $\mathbf{Z}$ and the loop starts over while there is an improvement in the model's performance.

In order to measure the predictive performance of model $\mathcal{M}$, we computed the root mean square error (RMSE) between the observed and predicted values of the variable of interest. The RMSE is defined as:

$$\text{RMSE} = \sqrt{\frac{1}{n} \sum_{i=1}^{n} (y_i - \hat{y}_i)^2} , \tag{2}$$

where y_i is the observed value of instance i and $\hat{y}$ the predicted value.

As aforementioned, the models were validated by means of the k-fold cross validation technique (Stone, 1974). This technique randomly splits the complete dataset into k subsets, using k-1 for learning (train set) and the other for validation (test set). The method is repeated k times so that each time a new train set is used to learn the model and a new test set is used to compute the RMSE. The average of the k error measures gives an estimate of the out-of-sample error. In our experiments, a k-value of 10 was applied.

2.3.3. Constructing structured models

The study area shows a high spatial heterogeneity, as described in Section 2.1, and as a consequence, the ecological processes governing the distribution of species richness may be different at different locations. Therefore, the relationship between the species richness and the explanatory variables

may not be stationary but vary across the study area. A strategy to deal with non-stationarity is to use partitioning methods to find homogeneous sub-regions (Fortin and Dale, 2005; Legendre and Legendre, 2012) and fit a sub-model to each partition.

Different methods can be used to obtain a partition. In this work, the standard k-means clustering method was carried out and each observation (i.e., each cell of the grid) was identified as belonging to a specific cluster C_i, with $i = 1, \ldots, k$. The observations were clustered based on the 12 climate-related variables described in Table A.1 in order to obtain climatically homogeneous regions. Afterward, a NB model (M_i) was fit using the data (D_i) belonging to cluster C_i, as explained in Section 2.3.1 and following the variable selection procedure described in Section 2.3.2. The elbow method was followed in order to determine the number of clusters (k), obtaining an optimal of 4. However, since one of them had a size too small to train the models, the data were finally clustered in 3 groups. Therefore, a k value of 3 was used, so that each NB model is composed of 3 sub-models (or components). For prediction purposes, given a new configuration of the climate-related explanatory variables ($w_1, \ldots, w_c$) of a cell belonging to the i-th cluster, the model learned from the data corresponding to the i-th cluster was used to compute the value $\hat{y}$. Note that, in practice, there are three separate NB models and the predictions are made from a single model.

2.4. Scenarios of climate change

The Intergovernmental Panel on Climate Change (IPCC) proposed a number of scenarios of climate change (CC) based on future greenhouse gas emissions. Three of these scenarios were used to make predictions about the expected species richness distribution in Andalusia. In particular, the A1B, A2 and B1 scenarios were used since they are the ones with higher probability to occur in this region, according to the regional government. Comparing the three scenarios based on their carbon dioxide emission growth, the A2 scenario provides the highest growth, followed by the A1B and, finally, the B1 scenario, which is translated into an increase between 2°C and 4°C of global surface warming by the end of 2100 (Nakicenovic et al., 2000).

As a result of applying these scenarios to different General Circulation Models, the evolution of the climatic variables in Table A.1 were projected for the periods 2011-2040, 2041-2070 and 2071-2100. The regional Government of Andalusia adapted these variables to the regional scale by applying downscaling techniques. These data are freely available at http://www.

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. In this paper, these climatic projected variables were used to make predictions about the expected species richness distribution for each taxon, period and scenario of CC.

2.5. Scenario analysis

The three scenarios of CC were analyzed by performing probabilistic propagation over the target variable (either amphibian, reptile, mammal or bird species richness). Probabilistic propagation consists in computing the posterior probability distribution of the variable of interest Y given some evidence $\mathbf{e}$ of the observed variables $\mathbf{E} \subset \mathbf{X}$ (Lacave et al., 2007). In this regard, we can observe the changes in the posterior distribution of our target variable (richness of amphibians, reptiles, mammals or birds) when new information (IPCC projected variables) is introduced in the climate-related explanatory variables. Given that the IPCC variables are projected for three periods and three different scenarios of CC, nine evidence sets are used for the probabilistic propagation process, obtaining as many posterior probability distributions of the target variable. Then, for each group of species, period and CC scenario, a *habitat suitability map* can be obtained by depicting the posterior distribution on the grid, so that each cell is colored with an intensity, varying from red (for low species richness prediction, i.e., low suitability) to dark green (for high suitability). These maps provide spatial information about possible distributions of the four groups of species for the projected CC scenarios.

For visual purposes, the relative change of the target variable between the baseline and the projected periods were computed and plotted on *difference maps*. This maps represent changes (loss or gain) in species richness, which can be interpreted as changes in habitat suitability. The relative change (D) was computed as

$$D = \frac{y_t - y_0}{y_0} \times 100,$$

where Y_0 is the target variable in the baseline period and Y_t is the target variable in projected period t (with $t = \{2011 - 2040; 2041 - 2070; 2071 - 2100\}$).

Finally, the relative change (D) of three different zones ("Natural and National parks", "Natura 2000 network, excluding parks" and "unprotected areas") was compared for each scenario of CC (A1B, A2 and B1) and projected

period (2011-2040, 2041-2070 and 2071-2100) using the Kruskal-Wallis test. In those cases where statistical significant differences were found, Wilcoxon rank-sum test was used to analyze each pair.

3. Results

In this section, we present the results obtained from the habitat suitability model of each group of species, regarding:

- their estimated spatial distribution based on the baseline period;

- their expected distribution under three scenarios of CC for the projected periods 2011-2040, 2041-2070 and 2071-2100;

- their relative change with respect to the baseline period under each projected period and scenario of CC.

3.1. Amphibians

Figure 4 presents the estimated amphibian richness for the baseline period (right panel), based on the selected variables, as well as its observed distribution (left panel). The model identifies the general distribution pattern of the amphibian richness, with higher richness being located along the Sierra Morena mountain range and western Andalusia, whereas lower amphibian richness is spotted in the Baetic Depression, most part of the Baetic Systems and the SE. The weighted average RMSE of the 3 components of the NB model for amphibians is 2.67.
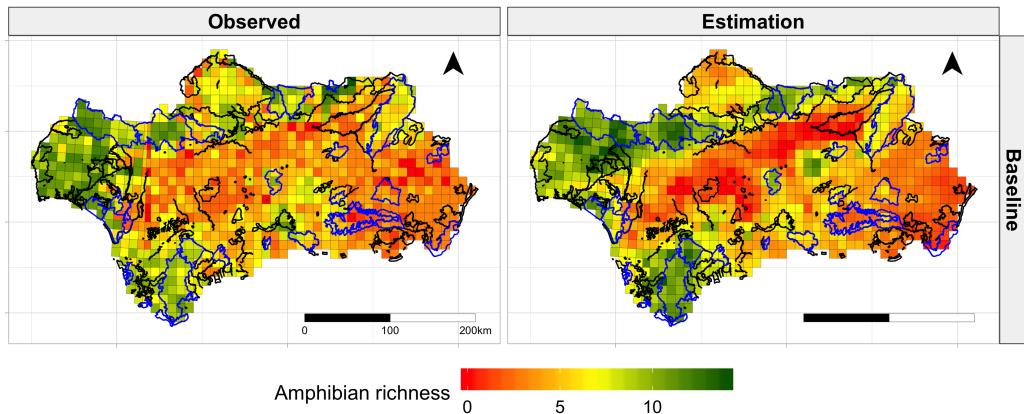

Figure 4: Observed and estimated values of species richness of amphibians.

Figure 5 shows the expected value of amphibian richness under the 3 scenarios of CC (rows) for each projected period (columns). In general, the regions with higher species richness underwent a notable drop, with special emphasis in the last projected period. Some Natural parks (Los Alcornocales, Sierra de Grazalema and Sierra de Aracena y Picos de Aroche, i.e., numbers 1, 16 an 17 in Figure 2) are able to preserve the highest amphibian richness through time.
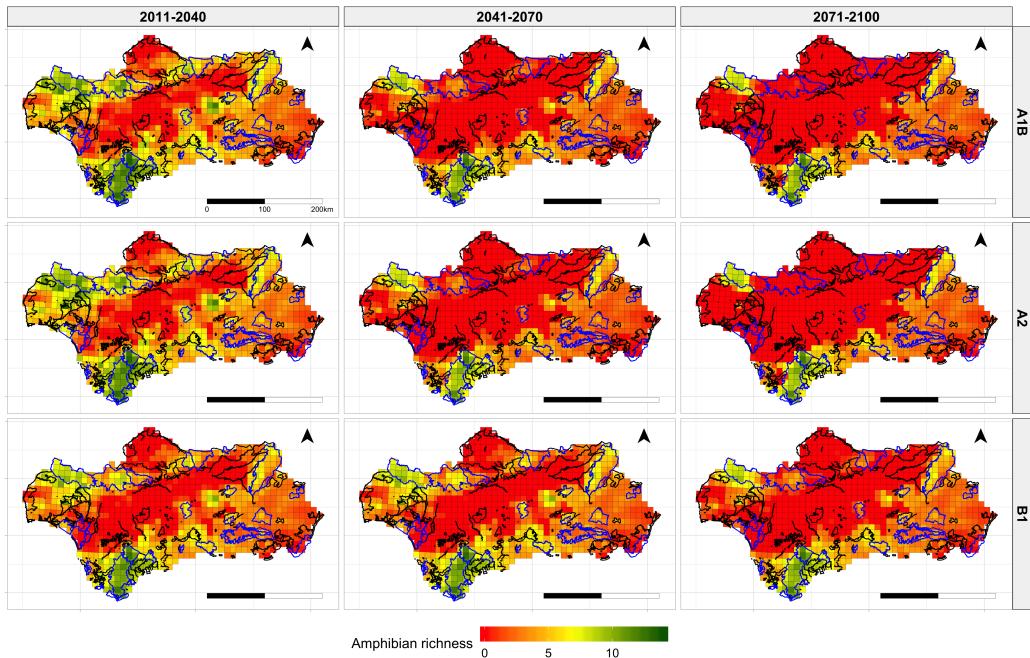

Figure 5: Habitat suitability maps of amphibian richness under the A1B, A2 and B1 scenarios of global change.

Figure 6 shows the relative change between the baseline period and each projected future, where intense red-color (-100%) indicates a loss of all the species that were present in the baseline period; white color represents no change with respect to the baseline period; and intense green color ($\geq$+100%) indicates that the number of species that were present in the baseline period has at least doubled (the relative change has been truncated to 100% for visual purposes). These maps can help visualize those areas where the predicted values increase or decrease with respect to the baseline period due to changes in the climate-related variables. The model predicts a 100% of

amphibian loss in most part of the Baetic Depression and Sierra Morena by the last projected period under the three scenarios of CC.
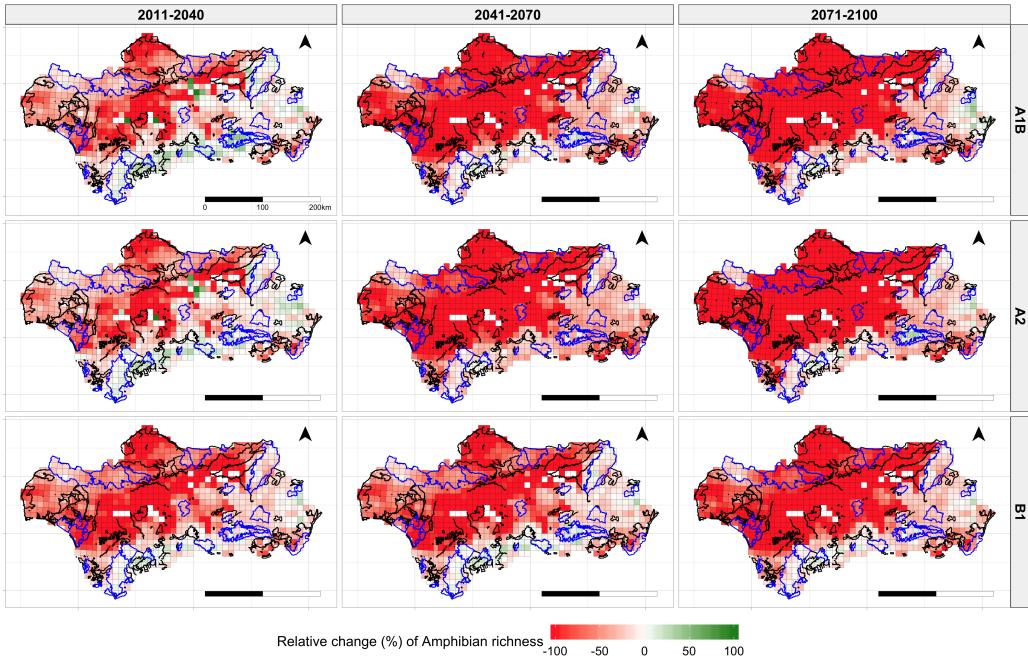

Figure 6: Difference maps showing the relative change (%) of amphibian richness under the A1B, A2 and B1 scenarios of global change with respect to the baseline period.

Figure 7 shows the results of the Kruskal-Wallis hypothesis test, where the relative change of amphibian richness is compared among zones ("unprotected", "natural and national parks" and "reminder of Natura 2000 net"), for each scenario of CC (A1B, A2 and B1) and projected period (2011-2040, 2041-2070, 2071-2100). Significant differences ($p - value < 0.05$) are found in all comparisons. In all cases, the species loss is smaller in PARKS (i.e. natural and national parks).
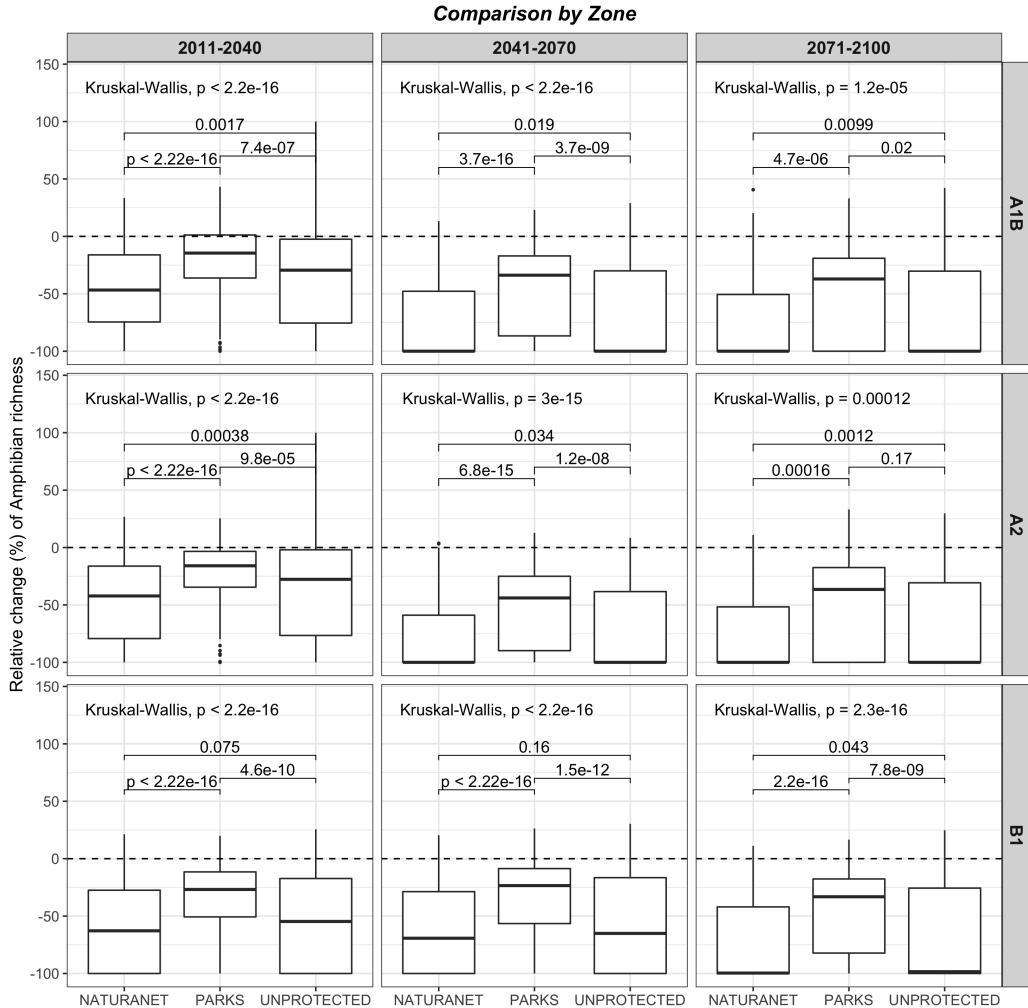
Figure 7: Comparison of relative change (%) of amphibian richness by zone (for each projected period and scenario). PARKS represents National and Natural parks; NATU-RANET represents the Natura 2000 network, excluding PARKS; and UNPROTECTED corresponds to the remainder of the territory. Some outliers are not shown for visual purposes.

3.2. Reptiles

Figure 8 presents the estimated reptile richness for the baseline period, as well as its observed distribution. The general distribution of reptile richness is captured by the model, which identifies important areas of high number of species, such as Sierra de Aracena y Picos de Aroche, Los Alcornocales,

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Doñana or Cabo de Gata-Nijar (numbers 1, 16, 22 and 26 in Figure 2, respectively). The weighted average RMSE of the 3 components of the NB model for reptiles is 4.67.
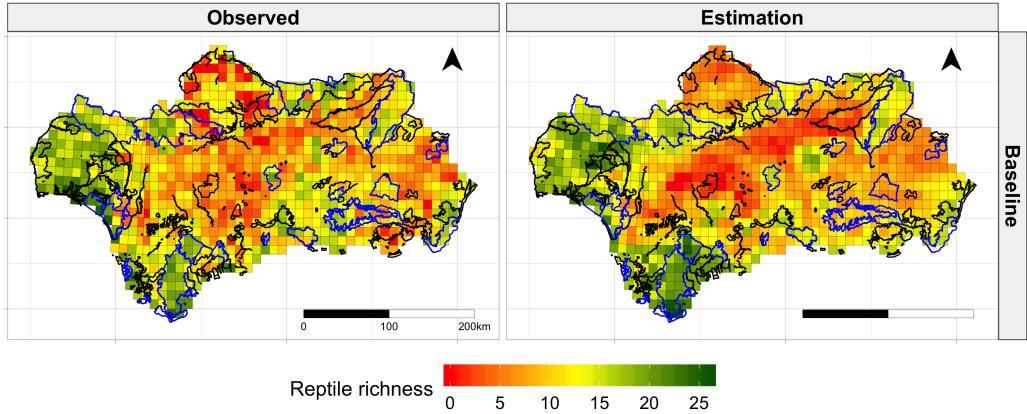
Figure 8: Observed and estimated values of species richness of reptiles.

Figure 9 shows the expected value of reptile richness under the 3 scenarios of CC (rows) for each projected period (columns). In general, regions located in the Sierra Morena mountain range will undergo a drastic drop, according to the proposed model. Some regions that will preserve the current reptile richness are located in the South-easternmost part of the study area.
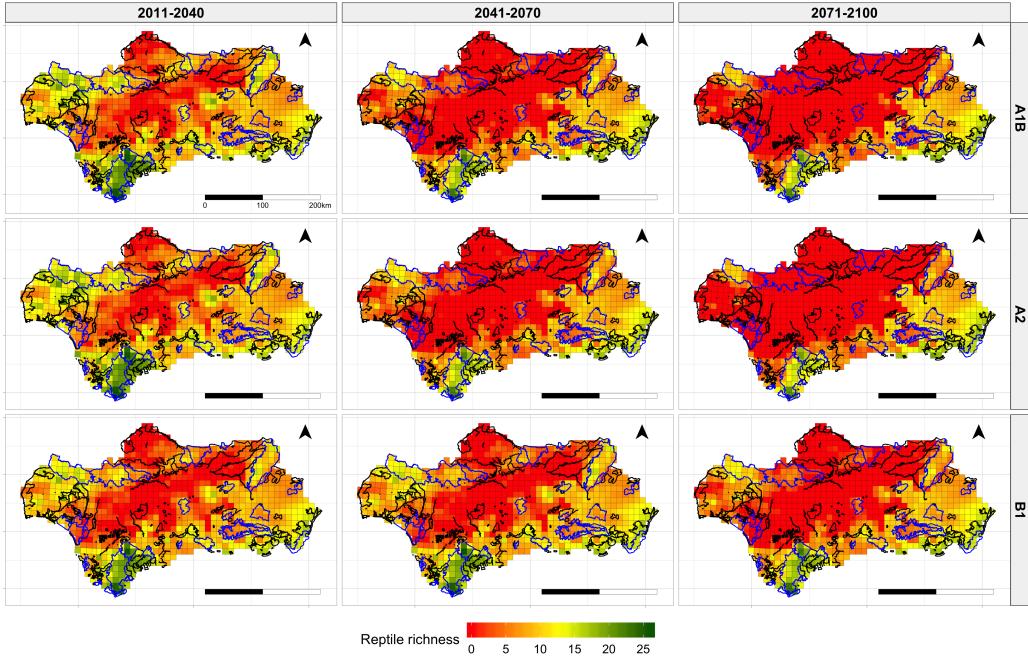
Figure 9: Habitat suitability maps of reptile richness under the 3 scenarios of global change.

Figure 10 shows the relative change (%) of reptile richness between the baseline period and each projected future, where intense red-color (-100%) indicates a loss of all species present in the baseline period. The model predicts a reduction in the number of reptiles in the area corresponding to Sierra Morena and the Baetic Depression, especially in the second and third periods. On the other hand, the reptile richness increases in the SE. Finally, the region corresponding to the Baetic Systems shows a gradual species loss through time, though the reduction is smaller than in the Baetic Depression and Sierra Morena mountain range.

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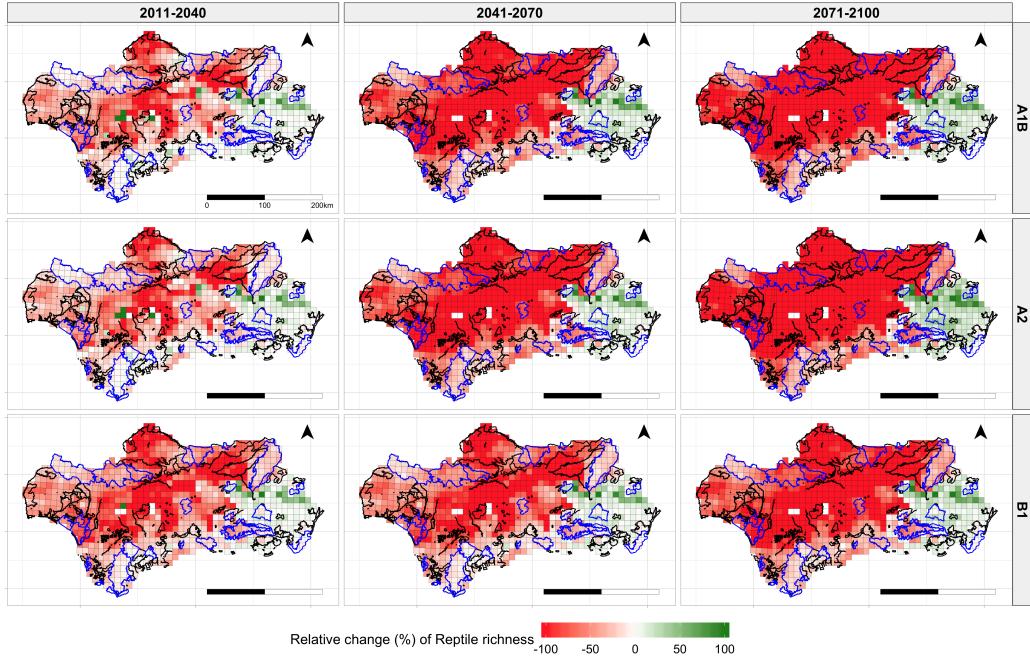
Figure 10: Difference maps showing the relative change (%) of reptile richness under the A1B, A2 and B1 scenarios of global change with respect to the baseline period.

Figure 11 shows the results of the Kruskal-Wallis hypothesis test, where the relative change of reptile richness is compared among zones, for each scenario of CC and projected period. In all comparisons, significant differences ($p - value < 0.05$) among the 3 zones are found. In all cases, PARKS presents a smaller species loss than the two other zones.

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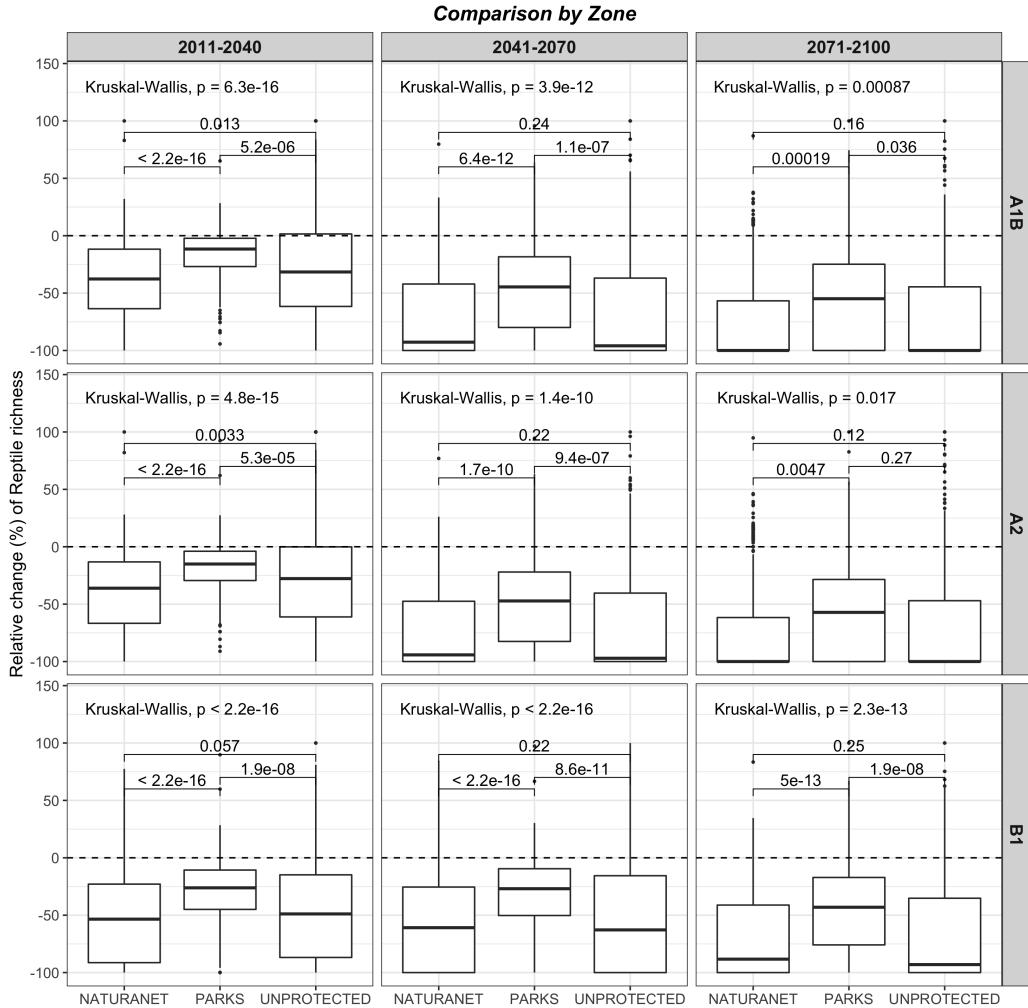
Figure 11: Comparison of relative change (%) of reptile richness by zone (for each projected period and scenario). PARKS represents National and Natural parks; NATURANET represents the Natura 2000 network, excluding PARKS; and UNPROTECTED corresponds to the remainder of the territory. Some outliers are not shown for visual purposes.

3.3. Mammals

[Figure 12](#) presents the estimated mammal richness for the baseline period, as well as its observed distribution. The general distribution of mammal richness is captured by the model, which identifies important areas of rich biodiversity, such as Sierras de Cazorla, Segura y las Villas, Sierra Nevada or Doñana (numbers 7, 14 and 22 in [Figure 2](#), respectively). However, the

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model underestimated other rich areas, such as Sierra de Andújar (number 5). The weighted average RMSE of the 3 components of the NB model for mammals is 6.85.
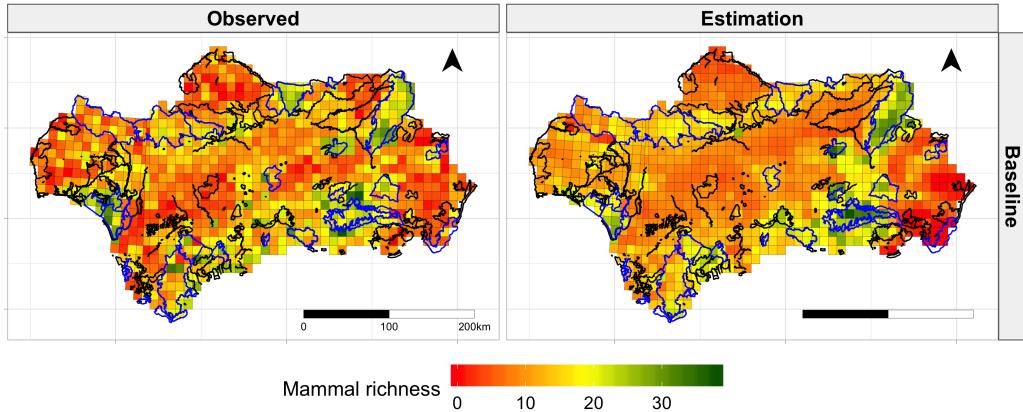

Figure 12: Observed and estimated values of species richness of mammals.

Figure 13 shows the expected value of mammal richness under the 3 scenarios of CC (rows) for each projected period (columns). In general, the mammal richness decreases through time, with only few regions maintaining higher richness than average in the most optimistic scenario (B1).
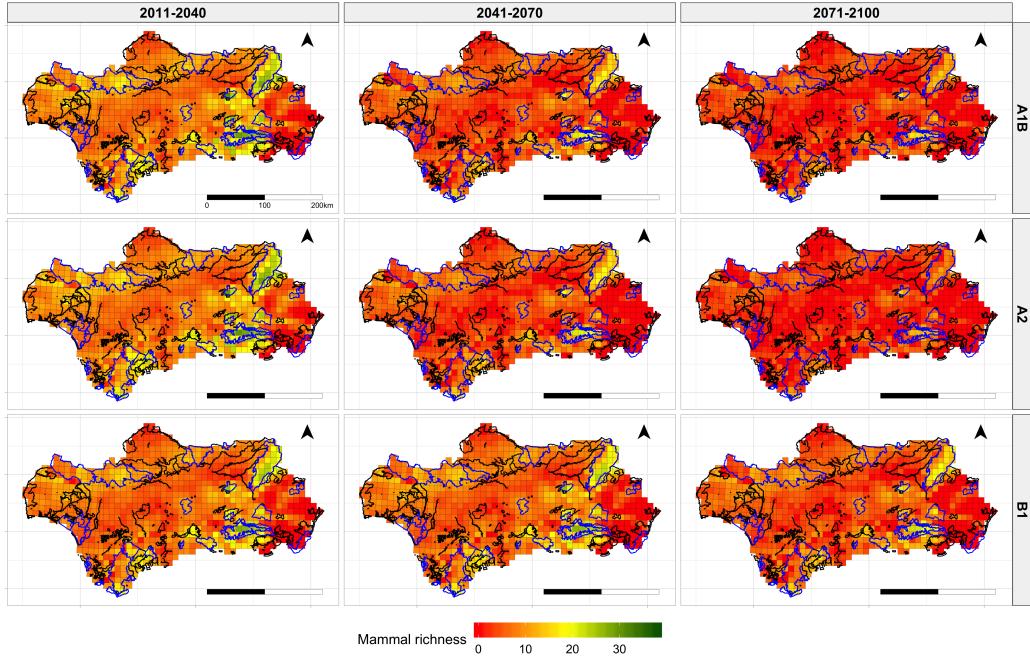
Figure 13: Habitat suitability maps of mammal richness under the 3 scenarios of global change.

Figure 14 shows the relative change between the baseline period and each projected future, where intense red-color indicates a loss of the 100% of the mammals present in the baseline period. In general, the model predicts a reduction in the number of mammal species, with respect to the baseline period, in all the study area. The northernmost part of Sierra Morena shows an area of growth in the first projected period (2011-2041), which disappears in the following periods. Only the B1 scenario maintains this area with positive change until the last period, where no change is expected, according to the model.
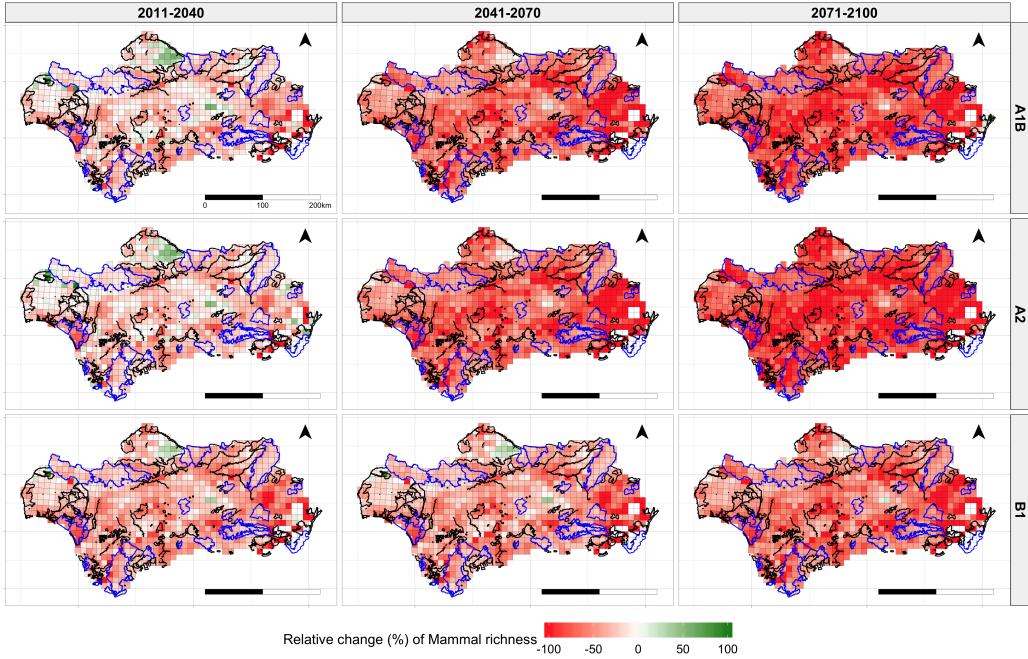
Figure 14: Difference maps showing the relative change (%) of mammal richness under the A1B, A2 and B1 scenarios of global change with respect to the baseline period.

Figure 15 shows the results of the Kruskal-Wallis hypothesis test, where the relative change of mammal richness is compared among zones, for each scenario of CC and projected period. Regarding the A1B scenario, significant differences ($p - value < 0.05$) were found among the 3 areas in the first and last periods, with PARKS undergoing a higher loss than UNPROTECTED in the former and smaller than the other two in the latter period. Concerning the A2 scenario, significant differences were found in all comparisons, with PARKS having a higher species loss than UNPROTECTED in the first period and smaller than the other two in the next periods. Finally, no statistically significant differences among the 3 zones were found under the B1 scenario.

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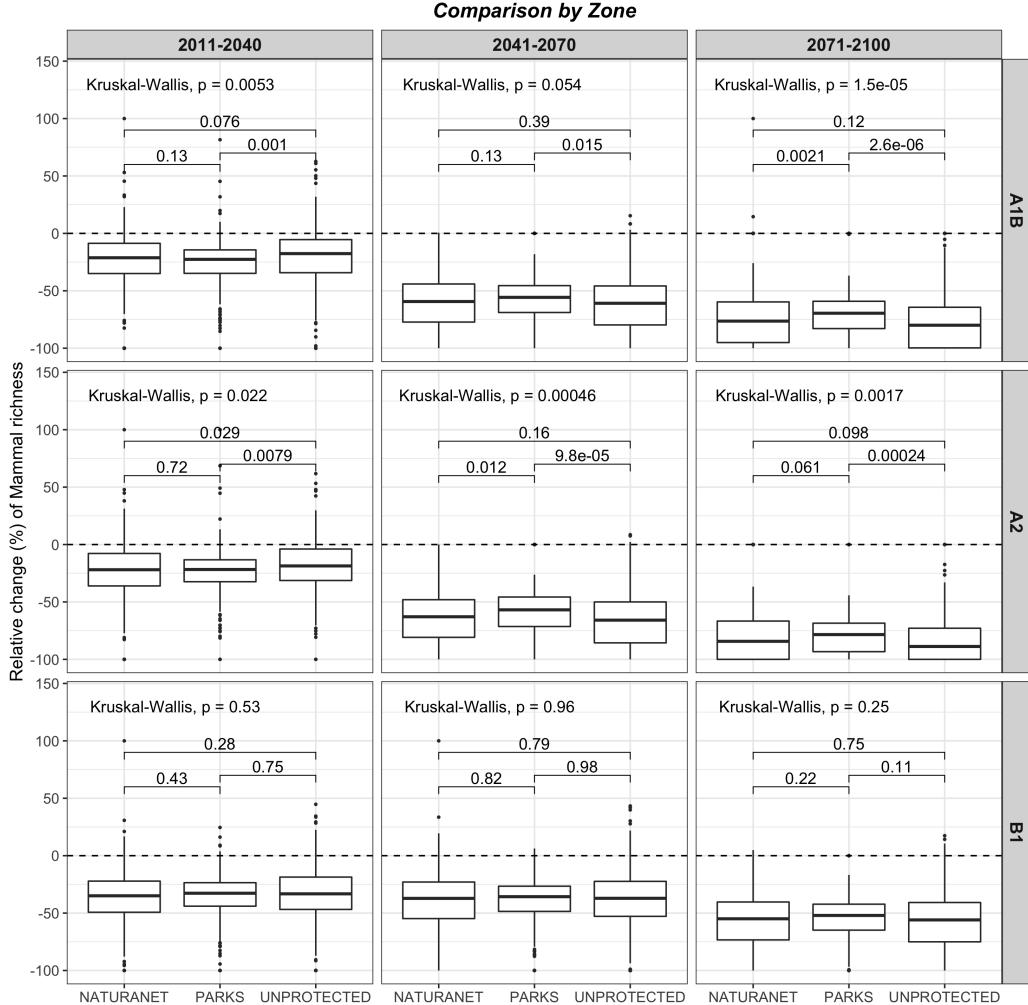
Comparison by Zone

Figure 15: Comparison of relative change (%) of mammal richness by zone (for each projected period and scenario). PARKS represents National and Natural parks; NATURANET represents the Natura 2000 network, excluding PARKS; and UNPROTECTED corresponds to the remainder of the territory. Some outliers are not shown for visual purposes.

3.4. Birds

Figure 16 presents the estimated bird richness for the baseline period, as well as its observed distribution. The general distribution of bird richness is captured by the model, which identifies important areas of rich biodiversity, such as Sierras Subbéticas, Sierra de Grazalema ot Sierra de las Nieves (num-

bers 11, 17 and 18 in Figure 2, respectively). The weighted average RMSE of the 3 components of the NB model for birds is 17.23.
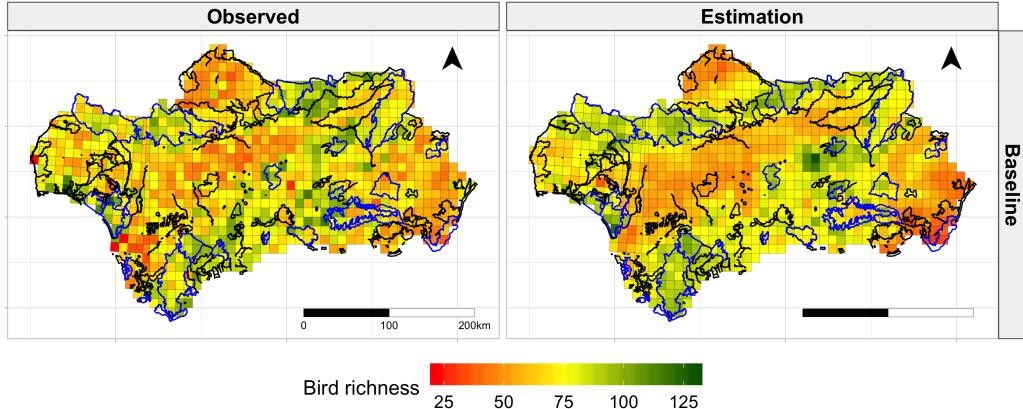
Figure 16: Observed and estimated values of species richness of birds.

Figure 17 shows the expected value of bird richness under the 3 scenarios of CC (rows) for each projected period (columns). Generally speaking, the bird richness loss will be specially severe in the Sierra Morena mountain range and the Baetic Depression.
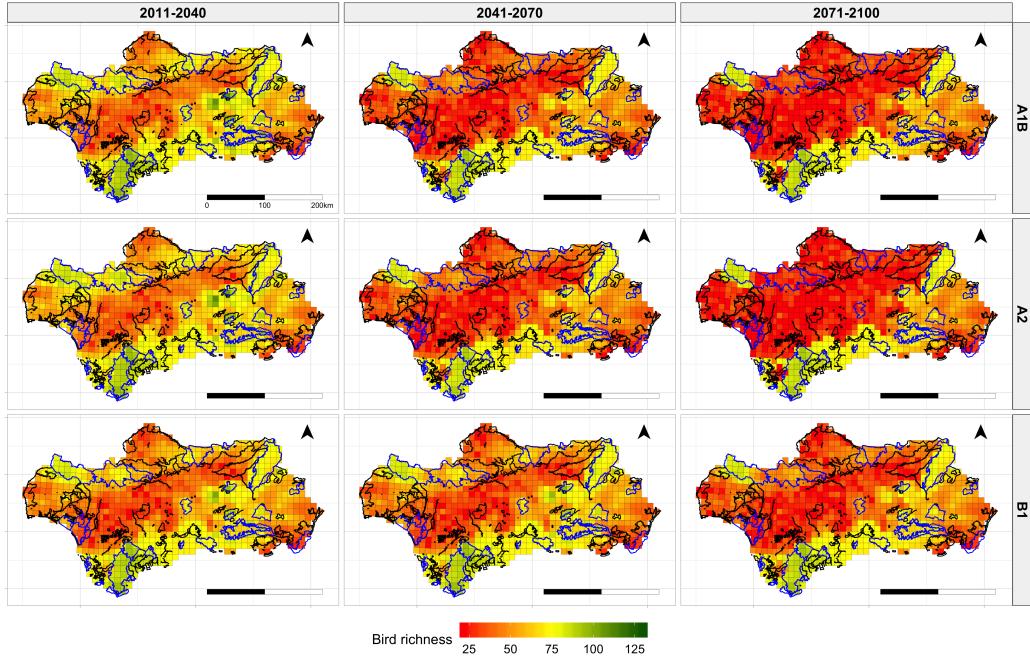
Figure 17: Habitat suitability maps of bird richness under the 3 scenarios of global change.

Figure 18 shows the relative change between the baseline period and each projected future, where intense red-color indicates a loss of the 100% of the species present in the baseline period. The model predicts a reduction in the number of birds in the Sierra Morena mountain range and in the Baetic Sistems, with respect to the baseline period, whereas protected areas located in the Baetic Systems will experience a relative loss close to 0.
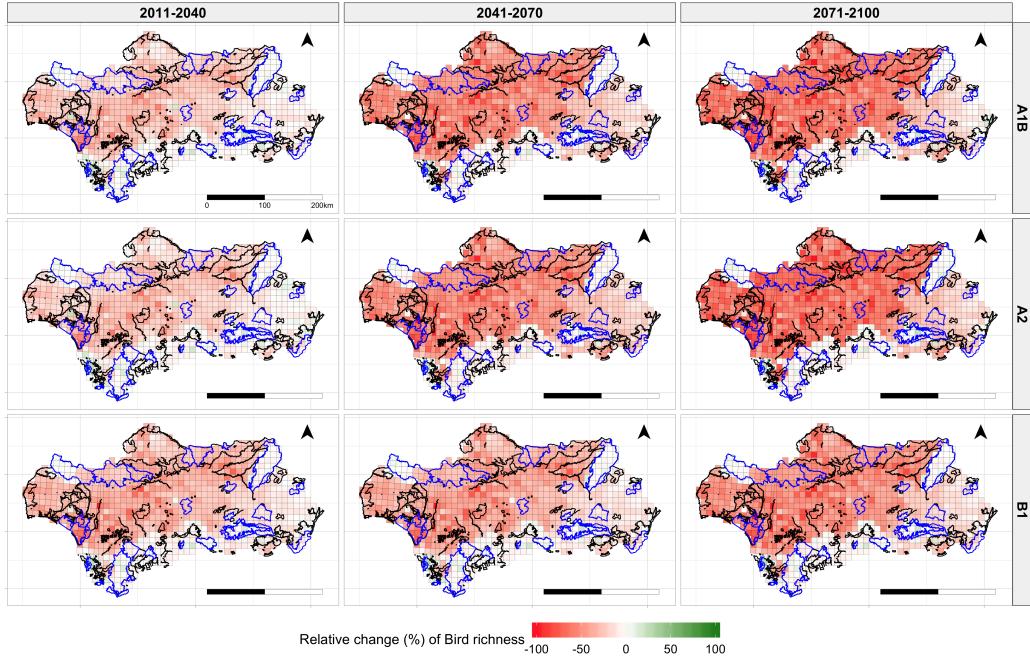
Figure 18: Difference maps showing the relative change (%) of bird richness under the A1B, A2 and B1 scenarios of global change with respect to the baseline period.

Figure 19 shows the results of the Kruskal-Wallis hypothesis test, where the relative change of bird richness is compared among zones, for each scenario of CC and projected period. In all comparisons, significant differences ($p-value < 0.05$) between pairs were found, where PARKS (i.e. natural and national parks) presented smaller species loss than the two other zones.
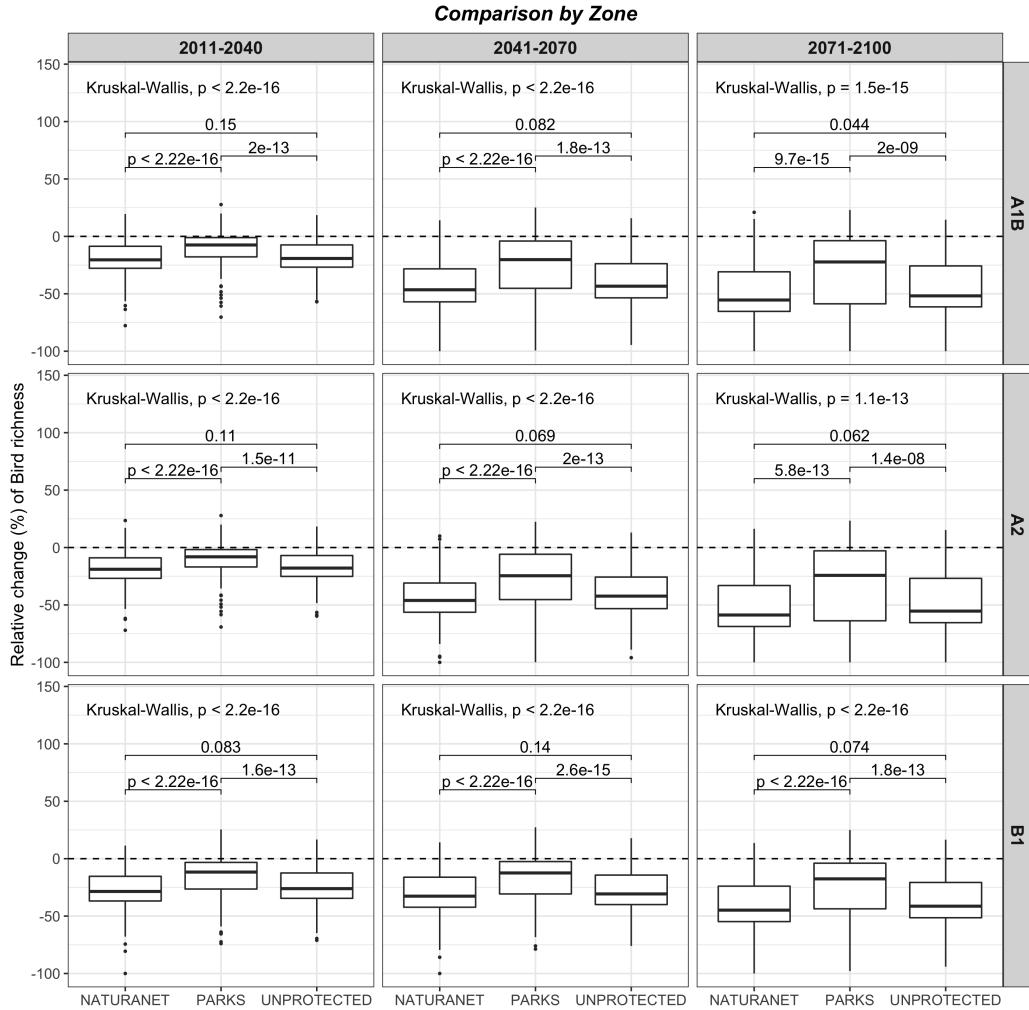
Figure 19: Comparison of relative change (%) of bird richness by zone (for each projected period and scenario). PARKS represents National and Natural parks; NATURANET represents the Natura 2000 network, excluding PARKS; and UNPROTECTED corresponds to the remainder of the territory. Some outliers are not shown for visual purposes.

4. Discussion

4.1. The habitat suitability model

We have presented a methodology to estimate the habitat suitability of four groups of species under different scenarios of climate change. The choice of using BNs was motivated by the fact that they provide a sound approach to

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deal with complex systems under uncertainty. For regression tasks, restricted structures are often used due to the reduction in the number of parameters to be estimated from data. The NB model is the simplest yet powerful BN model. It has been widely used due to the fact that, among other advantages, it is easy to build, fast and provide reliable results (Friedman et al., 1997; Fytilis and Rizzo, 2013; Maldonado et al., 2019).

Many authors have described the value of BNs (Uusitalo, 2007; Aguilera et al., 2011; Chen and Pollino, 2012; Bielza and Larrañaga, 2014), including their capability of obtaining predictions even if only partial information is available (as in this work, where only climate variables were used to make predictions) or their potential to compute the probability of a particular hypothesis (due to their probabilistic nature). Moreover, BNs are able to accommodate different conditional probability distributions, depending on the nature of data.

The presented model uses linear Gaussian distributions, which assumes linearity between the explanatory and response variables. However, this limitation has been partly overcome by carrying out a partition of the sample space. Nevertheless, we had to extrapolate beyond the observed data for some climate projections, specially the farthermost scenarios (period 2070-2100). The climate projections for the first period (2011-2040) never extrapolate further than 13% of the observed range. However, the extrapolation for the second and third periods entails higher uncertainty. One of the main problems of extrapolation is that the predictions may stop making sense. For instance, the predicted number of species could be negative. In these cases, the results were truncated to 0. Moreover, the relationship between the response and the explanatory variables might be different outside the calibration range. For these reasons, the extrapolated predictions are burdened with uncertainty since they assume that this relationship is maintained beyond the observed data.

The habitat suitability models were trained using the entire set of climate-related variables and another subset of selected variables. The decision of not dropping any climate variable allowed to use all the available information of the climate change scenarios when running predictions. As a result, the combined effect of all climate variables in each scenario is observed in the habitat suitability maps.

A drawback of NB models is their assumption of independence, i.e., the explanatory variables are considered to be independent given the response variable. As a consequence, the effects of climate on other parts of the system,

such as land uses, is only seen through the species richness node, which means that possible side effects derived from climate change (for instance, land use changes) are not taken into account to predict the species richness. In order to take these side effects into account, more complex models are needed. An example of such models is the Tree Augmented Naive Bayes (TAN), which extends the NB model by allowing the explanatory variables to have one more parent besides the response. In general, the increase in complexity results in richer and more accurate models (Friedman et al., 1997). However, TAN models are more difficult to implement and their computational cost is higher.

Another concern about the proposed models is that, even though they are able to predict the species richness of a particular group, no information about which particular species are affected by the introduced changes is obtained. As future work, the methodology presented in this work could be used to build a classifier for each single species. In this context, both the naive Bayes and TAN structures could be used to build the classifiers, so that their predictive accuracy could be compared.

4.2. Climate emergency and biodiversity alteration

Climate change (CC) and the alteration of biodiversity are some of the most important global biophysical changes derived from human activity. Variations in climate are exerting added pressure on biodiversity, habitat suitability and species distribution (Parmesan and Yohe, 2003; Root et al., 2003; Pecl et al., 2017). The severity of changes in the climate system (generalizing, temperature increase, and variation in abundance and distribution of rainfall) is such that the scientific community has declared that the planet is facing a climate emergency (Ripple et al., 2019) and the European Union has taken immediate action (European Parliament, 2019). The prevailing global warming is affecting human health and well-being as well as groups of plant and animal species (Pecl et al., 2017).

The main indicators used to detect the effects of CC on plant and animal diversity have been species richness and species distribution (Lemoine et al., 2007; Stiels and Schidelko, 2018). Using these indicators, for the case of amphibians in Andalusia, it was observed that high values of biodiversity would be maintained only in those mountainous areas with the highest rainfall. In the rest of the region, amphibians suffered a considerable decline of their species richness. By 2100, in any of the proposed CC scenarios, their richness would be less than 5 species, or they would become extinct in more

than 50% of the territory. It was also noted a persistence of amphibians in humid mountainous areas. Similar results were perceived in China where the effects of CC would cause a loss of species richness (20%) and a displacement to higher altitudes (95% of amphibians) (Duan et al., 2016). However, recent studies have admitted the uncertainty and geographic dependence on the actual effect of global warming on the amphibian species (Miller et al., 2018; Ashrafzadeh et al., 2019; von May et al., 2019). For the Mediterranean countries, the reduction of permanent wetlands and rivers due to the combined effects of land use and CC should be assessed in order to better understand the impacts on amphibian species (Hof et al., 2011). Particularly, in Andalusia there is an alarming lack of studies on amphibians and their current conservation status (Díaz et al., 2020).

Our study also revealed that species richness and habitat suitability for reptiles in Andalusia would be affected in the different CC scenarios. In general, for the three scenarios proposed there would be a loss of richness and suitable habitats, although it can be highlighted that there would be a positive change in richness in a mountainous area in the centre-east of the region. Scenario B1 would cause the least drastic changes in reptile richness whereas the three scenarios would maintain the best survival conditions in the highlands of the SW and in the arid and sub-desert area of the SE. Le Galliard et al. (2012) predicted, using niche models, that projected climatic variations over the next few years should result in substantial changes in the range and abundance of most reptiles in Europe. In some cases, these changes can be considered positive (higher growth and fecundity, earlier maturation, higher reproductive success, higher survival), but in others negative (lower survival, higher water and thermal stress, lower dispersion). The endemic species of the Mediterranean Basin, adapted to the cold and limited by the availability of water, are also expected to decrease (Foufopoulos et al., 2010). At the same time, several studies in different geographical areas established for certain reptile species increases in their range and their capacity to adapt to new environmental conditions caused by CC (Bickford et al., 2010; Bezeng et al., 2017; Berriozabal-Islas et al., 2018; Nori et al., 2018).

The effects of CC on amphibians and reptiles, according to a systematic review, were reported in 65% of the studies. In half of the cases, CC was identified as causing population declines or range restrictions (Winter et al., 2016). However, in the case of European amphibians and reptiles, Araújo et al. (2006) argued that the impact of rising temperatures may be less damaging than was postulated in previous decades and emphasize, however, that,

for amphibians, their vulnerability to changes in climate may be accentuated by the projected decline in water availability and their limited dispersal capacity. Based on the existing contrasting results, Winter et al. (2016) claim that it is impossible to draw global conclusions for amphibians and reptiles since the probability of identifying an effect of CC varies between regions, taxa and research methods.

As far as mammals are concerned, it has been noted that their demographic decrease would be drastic towards the year 2100, with special emphasis on the scenarios A1B and A2 since the first time projection. These results agree with different studies that suggest that mammal communities in a given geographic region will respond to CC by altering both taxonomic composition (through local extirpation, global extinction or species immigration) and species richness (through changes in extinction, extirpation and immigration rates). Other possible effects, also mentioned, are the alteration of the relative abundance of individuals within species, possible phenotypic modifications not necessarily accompanied by genetic change and the evolution of new species (Barnosky et al., 2003). Maiorano et al. (2013) highlighted the relevance of mountainous areas as hotspots of mammal diversity and their risk of exposure to extreme climatic situations, specifically in the Alpine, Mediterranean and Black sea biogeographic regions. For the Mediterranean Basin, the results observed on the effects of CC on the distribution of mammal species, and the communities they form, suggest that they may not suffer a drastic loss of species from their current distribution, but a change in community structure (Maiorano et al., 2011). In two studies in Spain, Santoro et al. (2017) observed a negative incidence on the abundance of certain species of small mammals due to the increase of extremely hot days whereas Aragón et al. (2010) showed that mammals, compared to birds, reptiles and amphibians, would be the taxonomic group least affected by climate variability. Our results highlight that, by 2100, mammal richness would be less than 10 species in most part of Andalusia for scenarios A1B and A2, which means a massive decline of this group.

Finally, the birds showed their highest values of specific richness in mountainous areas. In the first temporal range (2011-2040) the high biodiversity of birds is maintained in these areas for all three scenarios and, although there is a small decline, it is maintained for the rest of the temporal ranges in all three scenarios. Similarly, in a study covering the Spanish part of the Iberian Peninsula, it was observed that half of the bird species studied showed a generalized pattern towards increasing populations, while only one

tenth showed a significant decline (Seoane and Carrascal, 2008). In England, resident and short-distance migrant populations were seen to have increased in response to CC, but potentially at the expense of long-distance migratory birds, habitat specialists and species associated with the cold (Pearce-Higgins et al., 2015). Although it was suggested earlier this decade that the study of climate-induced distributive change in birds was at a predictive modelling stage (Crick, 2004), it is now assumed that CC is an increasingly important driver of changes in the distribution, abundance and life cycle of bird species, causing changes in biodiversity and community composition (Trautmann, 2018).

4.3. Effectiveness of Protected Areas: static vs dynamic approach

Our study showed that the current Andalusian PAs (Parks and Natura 2000 Network), especially those located in mountainous areas, seem to maintain the best habitat conditions and higher values of species richness for the terrestrial vertebrates studied, except for mammals where this positive condition is less clear. However, in most of them, especially in low elevation areas, the impact of global warming would be significantly negative. Specifically, in the case of amphibians, it was observed that high values of biodiversity would be maintained in humid mountainous areas corresponding to the natural parks of Sierra de Aracena y Picos de Aroche, Los Alcornocales and Sierra de Grazalema. A similar study also showed that in the face of CC, PAs were effective in maintaining the representation of amphibians, but conservation targets based on geographic range extent are achieved for only 40% of species (D'Amen et al., 2011). For reptiles, in general, for the three CC scenarios proposed there would be a loss of species richness and suitable habitats. However, reptiles would maintain the highest biodiversity values in national and natural parks and, it can be highlighted that there would be an increase in species richness in the area corresponding to the Natural Park of Sierra María-Los Vélez. Scenario B1 would cause the least drastic changes in species richness and in the three scenarios the best survival conditions would be maintained in the area corresponding to different humid and elevated PAs (Los Alcornocales and Grazalema, coinciding with amphibians) and in the Cabo de Gata-Níjar Natural Park. According to a work carried out in the Iberian Peninsula, it was found that, on the one hand, the representation of amphibians and reptiles in PAs was not higher than randomly expected (Araújo et al., 2007) and that, on the other hand, the CC would negatively affect both groups, both inside and outside PAs (Alagador et al., 2014).

The Natural Park of Sierras de Cazorla, Segura y Las Villas and the Sierra Nevada National Park showed a relatively higher mammal biodiversity for the three CC-scenarios but, contrary to the rest of the taxonomic groups studied, Andalusian PAs have not shown significant differences with unprotected areas in terms of concentrating a greater number of mammal species over time for the more optimistic scenario (B1). Other studies found a mammal species loss of up to 20% and a drastic influx of new species within national park boundaries (Burns et al., 2003) and the observed and potential mammal species richness for the Spanish peninsular National Park Network in two temporal moments (2002 and 2015) were higher within than outside the Park Network in both cases, although the favorability of national parks reduced from 2002 to 2015 (Estrada et al., 2018). In any case, it should be noted that a change in mammal species richness and an increase in extinction risk is expected for the Mediterranean Basin and, in this context, the current network of PAs is not expected to effectively conserve existing species, as most PAs will lose species according to the analyses of a recent study (Maiorano et al., 2011). In the case of birds, the results showed a clear difference between species richness inside and outside PAs, with higher values in the PAs, such as the natural parks of Grazalema, Sierras Subbéticas and Sierra de las Nieves. Similar results were found by Hole et al. (2009) and Gillingham et al. (2015) but, nevertheless, other authors showed the lack of effectiveness of PAs for the protection of birds (Beale et al., 2013; Regos et al., 2016). Specifically, Regos et al. (2016) found that in the NE of Spain in the face of two CC scenarios for the time range 2040-2069, the number of suitable habitats for the bird species studied decreased considerably both inside and outside PAs even though the number of suitable habitats is expected to decrease less inside than outside PAs.

PAs are key conservation tools used to protect species and their habitats within fixed administrative boundaries. In the face of global environmental problems, such as CC, this inflexibility of administrative boundaries calls into question the future ability of PAs to fulfil their conservation mandates. The conservation paradigm in which the declaration of PAs was historically framed was based on the ecological reference of natural biological communities of maximum successional maturity or climax. Based on this static concept of nature (metaphorically, to conserve a photograph of a given moment and space), the limits of the territory (the photograph) to be conserved were established. As the knowledge of nature progressed, it became clear that the changes are not disturbances, but part of the life cycle of the biological

communities. From this dynamic perspective, conservation implies maintaining ecological processes that develop over time and in a space that is difficult to limit (metaphorically, preserving a film without a specific end) (Van Dyke, 2008; Walker and Salt, 2012; Prober et al., 2019). At the same time, the transformation of the territory, the evidence of the finiteness of natural resources, the change in society's awareness since the Millennium Ecosystem Assessment, the economic valuation of ecosystem goods and services, the perception of the existence of critical transitions (i.e., thresholds or tipping points) in the behaviour of ecosystems, the recent global financial crisis and the emerging climate crisis, were delineating, and maintain in constant adaptation, a new conservation paradigm based on socio-ecological sustainability (Rescia et al., 2010; Balvanera et al., 2017). This paradigm, framed in the resilience thinking, assumes a society-nature relationship that must be adaptable, complex, capable of transformation and with several states of equilibrium. Under this framework, sustainability as a conservation objective would imply conserving the natural and cultural heritage, optimizing the use of natural resources and ensuring human well-being. Operationally, it means applying an ecosystem vision while preserving its integrity (processes, functioning and function -goods and services for society-) and reasonable land uses at landscape scale considering the legitimacy of adaptive multifunctional management. Administratively, it means applying alternative protection policies (administrative formats and tools) such as, dynamic or floating PAs, private areas for conservation, payment mechanisms to society (payments for ecosystem services, land stewardship) and environmental DNA -eDNA- (Rayfield et al., 2008; Alagador et al., 2014; Cristescu and Hebert, 2018; Capano et al., 2019; Hoffmann et al., 2019). Indeed, D'Aloia et al. (2019) propose a novel approach to climate adaptation that combines permanent protected areas with temporary conservation areas to create flexible networks, combined with new policies, creative financing solutions and wider acceptance of a dynamic approach to biodiversity conservation.

5. Conclusions

The results of the study show a broad effect of CC on the species richness and distribution of terrestrial vertebrates in Andalusia. Mostly, there is a loss of specific richness and a restricted availability of suitable habitats in the higher altitude areas. In general, the PAs located in mountainous areas maintain the best conditions for the survival of the taxa considered

in the proposed CC scenarios. However, and especially for mammals, the results suggest that alternative forms and formats of conservation should be considered.

Global warming and society's growing ecological footprint are making a dynamic approach to conservation increasingly useful and necessary. In recent decades, the interaction between science and policy has been strengthening and should remain iterative: policy defines the need for scientific information and the resulting science determines future policy. To maintain this interaction, scientists must provide knowledge and tools oriented to the conservation of ecological processes and genetic resources that must be supported by alternative protection policies that actively involve society (private conservation areas, stewardship mechanisms) and consider the sustainability, resilience and potential for change of the biophysical environment (dynamic conservation in situ).

Acknowledgments

Appendix A. Variable description

Table A.1: Description of variables considered in the experiments. All the variables are measured at the 100 Km^2 grid scale.

	Name	Description
Species richness *	Amphibian	Number of species of amphibians present in each cell
	Reptile	Number of species of reptiles present in each cell
	Mammal	Number of species of mammals present in each cell
	Bird	Number of species of birds present in each cell
	Mean temperature (T)	Average of the annual mean temperature (°C) over the period 1961–2000

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Climate ⋆

Table A.1: Description of variables considered in the experiments. All the variables are measured at the 100 Km² grid scale.

	Name	Description
	Maximum temperature of hottest month (Tmaxh)	Maximum temperature of the averages of the maximum monthly temperatures (°C) over the period 1961–2000
	Minimum temperature of coldest month (Tminc)	Minimum temperature of the averages of the minimum monthly temperatures (°C) over the period 1961–2000
	Precipitation (PPT)	Average of the annual total rainfall (mm) over the period 1961–2000
	Evapotranspiration (ET0)	Average of the annual evapotranspiration of reference (mm) over the period 1961–2000
	Water deficit amount	Annual sum of the negative differences between PPT and ET0
	Water surplus amount	Annual sum of the positive differences between PPT and ET0
	Water Balance	Average of water balance (mm) over the period 1961–2000
	Snow	Average of annual precipitation as snow (mm) over the period 1961–2000
	Radiation	Average of annual solar radiation (Joule/m²) over the period 1961–2000
	Availability of Time for Primary Production (ATPP)	Average (over the period 1961–2000) of time (hours/year) in which the following conditions are met: solar lighting, temperature above $7.5°$ and positive water balance
	Aridity index (AI)	Ratio of ET0 to PPT, computed as $\frac{ET0}{PPT} \times 100$
Topo †	Elevation (Z)	Average elevation (m a.s.l.) of each cell in the grid
	Slope (S)	Average slope (°) of each cell in the grid
	Urban areas	Percentage of cell covered by urban areas, parks, recreational and sport facilities and areas under construction
	Industrial areas	Percentage of cell covered by industrial areas

Table A.1: Description of variables considered in the experiments. All the variables are measured at the 100 Km^2 grid scale.

Name	Description
Mining	Percentage of occupation of mining deposits in a cell
Infrastructures	Percentage of cell covered by technical and communication infrastructure
Herbaceous crops	Percentage of cell covered by herbaceous crops, including greenhouses
Olive groves	Percentage of cell covered by olive monocultures
Vineyards	Percentage of cell covered by monocultures devoted to grape production
Fruit trees	Percentage of cell covered by monocultures devoted to fruit production
Woody crops	Percentage of cell covered by combinations of different woody crops
Crops and natural vegetation	Percentage of cell covered by combinations of different herbaceous crops and oak trees
Grassland	Percentage of cell covered by grassland
Bush	Percentage of cell covered by bush
Oaks	Percentage of cell covered by trees within the genus *Quercus*
Conifers	Percentage of cell covered by trees within the class *Pinopsida*
Eucalypts	Percentage of cell covered by trees within the genus *Eucalyptus*
Other hardwood forest	Percentage of cell covered by hardwood forest not listed above
Mixed forest	Percentage of cell covered by combinations of hardwood forest plants
Bush and forest	Percentage of cell covered by combinations of bush and forest
Grassland and forest	Percentage of cell covered by combinations of grassland and forest

Table A.1: Description of variables considered in the experiments. All the variables are measured at the 100 Km^2 grid scale.

	Name	Description
	Areas without vegetation	Percentage of cell covered by burnt areas, naked soil, deforested areas, plowed land and firebreaks
	Sand	Percentage of cell covered by beaches, dunes, cliffs and sandy areas
	Industrial wetlands	Percentage of cell covered by salt evaporation ponds and fish farms
	Artificial freshwaters	Percentage of cell covered by reservoirs, irrigation ponds and other artificial freshwaters
	Natural freshwater wetlands	Percentage of cell covered by lakes, boglands, glaciers and snowfields
	Natural brackish wetlands	Percentage of cell covered by coastal marshes, estuaries and coastal lagoons
	Rivers	Percentage of cell covered by rivers
Other	Pielou's evenness index (J)	Evenness of the 26 land-uses described above. This index reflects how many different land-uses are present in each cell and how even their relative abundances are. The J index in defined as $J = \frac{H}{H_{max}}$, where H is the Shannon index, defined as $H = -\sum_{i=1}^{n} p_i \ln p_i$, where p_i is the proportion of the i-th land-use and n is the total number of land uses; and H_{max} is the value H obtained when all the land-uses are equally frequent in a cell, i.e., $H_{max} = \ln n$. The J index ranges from 0 (the entire cell is covered by 1 land-use only) to 1 (the cell is covered by all the land-uses and their relative abundances are equal)
	Protected area (PA)	Percentage of cell protected by the Natura 2000 network.
	Roads	Number of roads per cell
	Distance to freshwater (DFW)	Distance (m) from the center of the cell to the nearest body of freshwater

Table A.1: Description of variables considered in the experiments. All the variables are measured at the 100 Km^2 grid scale.

Name	Description
Distance to urban area (DUA)	Distance (m) from the center of the cell to the nearest urban area (i.e., a municipality with more than 50000 inhabitants)

∗ Computed from presence-only data, obtained from the Spanish Inventory of Terrestrial Species, which is constantly revised and updated. In this work, the used dataset is updated to 2013, with roughly only 1% of the presences recorded being observed before year 2000.

⋆ Information obtained from the Environmental Information Network of Andalusia (REDIAM).

† Topography. Computed from the Andalusian Digital Terrain Model with a spatial resolution of 200 meters, provided by the Spanish National Geographic Institute.

‡ Computed from the Andalusian Land Use and Vegetation Cover Map of 2013 (at scale 1:10000), provided by the Andalusian Environmental Information Network.

Table A.2: Variables included (X) in each partition of the model (M1: Baetic Depression and Sierra Morena, M2: Mountain ranges and M3: East). Red cells indicate that the linear correlation between a variable a the species richness is negative, while green ones indicate a positive linear correlation. Each sub-model's RMSE is shown in parenthesis.

Variable	Amphibians			Reptiles			Mammals			Birds		
	M1	**M2**	**M3**	**M1**	**M2**	**M3**	**M1**	**M2**	**M3**	**M1**	**M2**	**M3**
	(3.5)	(1.5)	(1.4)	(4.2)	(5.9)	(4.9)	(5.6)	(8.3)	(9.2)	(16.8)	(11.7)	(24.7)
T	X	X	X	X	X	X	X	X	X	X	X	X
Tmaxh	X	X	X	X	X	X	X	X	X	X	X	X
Tminc	X	X	X	X	X	X	X	X	X	X	X	X
PPT	X	X	X	X	X	X	X	X	X	X	X	X
ET0	X	X	X	X	X	X	X	X	X	X	X	X
Water deficit amount	X	X	X	X	X	X	X	X	X	X	X	X
Water surplus amount	X	X	X	X	X	X	X	X	X	X	X	X
Water balance	X	X	X	X	X	X	X	X	X	X	X	X

Table A.2: Variables included (X) in each partition of the model (M1: Baetic Depression and Sierra Morena, M2: Mountain ranges and M3: East). Red cells indicate that the linear correlation between a variable a the species richness is negative, while green ones indicate a positive linear correlation. Each sub-model's RMSE is shown in parenthesis.

Variable	Amphibians			Reptiles			Mammals			Birds		
	M1	M2	M3	M1	M2	M3	M1	M2	M3	M1	M2	M3
	(3.5)	(1.5)	(1.4)	(4.2)	(5.9)	(4.9)	(5.6)	(8.3)	(9.2)	(16.8)	(11.7)	(24.7)
Snow	X	X	X	X	X	X	X	X	X	X	X	X
Radiation	X	X	X	X	X	X	X	X	X	X	X	X
ATPP	X	X	X	X	X	X	X	X	X	X	X	X
AI	X	X	X	X	X	X	X	X	X	X	X	X
Z	X			X			X					
S		X									X	
Urban areas		X	X	X	X	X	X		X			X
Industrial areas		X	X									
Mining	X			X	X			X				
Infrastructures			X	X	X							
Herbaceous crops			X									
Olive groves	X									X		X
Vineyards			X	X						X	X	
Fruit trees		X	X		X	X		X				X
Woody crops							X			X		X
Crops and natural vegetation				X		X				X		
Grassland												X
Bush												
Oaks						X						
Conifers							X			X		

Table A.2: Variables included (X) in each partition of the model (M1: Baetic Depression and Sierra Morena, M2: Mountain ranges and M3: East). Red cells indicate that the linear correlation between a variable a the species richness is negative, while green ones indicate a positive linear correlation. Each sub-model's RMSE is shown in parenthesis.

Variable	Amphibians			Reptiles			Mammals			Birds		
	M1	**M2**	**M3**	**M1**	**M2**	**M3**	**M1**	**M2**	**M3**	**M1**	**M2**	**M3**
	(3.5)	(1.5)	(1.4)	(4.2)	(5.9)	(4.9)	(5.6)	(8.3)	(9.2)	(16.8)	(11.7)	(24.7)
Eucalypts		X			X			X				
Other hardwood forest						X	X		X			X
Mixed forest											X	
Bush and forest												
Grassland and forest	X	X	X			X	X	X				
Areas without vegetation	X		X	X	X				X			X
Sand	X		X	X	X		X	X		X		
Industrial wetlands	X				X		X		X	X		X
Artificial freshwaters							X		X	X	X	
Natural freshwater wetlands							X	X		X		
Natural brackish wetlands	X			X	X		X			X	X	
Rivers	X			X			X			X		
J	X			X				X	X		X	X
PA	X					X	X					
Roads		X	X	X	X		X	X	X	X		
DFW	X			X								
DUA	X	X									X	

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