CZECH UNIVERSITY OF LIFE SCIENCES

Faculty of Tropical AgriSciences

Department of Animal Science and Food Processing

Determinants of the abundance of an endangered lizard:
Algyroides marchi

Master Thesis

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CZECH UNIVERSITY OF LIFE SCIENCES PRAGUE

Department of Animal Science and Food Processing

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DIPLOMA THESIS ASSIGNMENT

Jakub Strnad

Wildlife Management in the Tropics and Subtropics

Thesis title

Determinants of the abudance of an endangered lizard: Algyroides marchi

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Objectives of thesis

The aims of this thesis is to find the factors associated to the estimated abundance in different localities along the distribution range of the species.

Methodology

Algyroides marchi is an Iberian endemism restricted to some Prebetic Mountains (Alcaraz, Segura and Cazorla). It belongs to a genus evolved in humid forest environments whose members occupy relict areas across the Mediterranean Basin. Field work was carried out during 2009 by the supervisor. The student will compile all the data, and will increase the database with information from different sources (mainly distributional, geographical, topographic and climatic). For this purpose, GIS software (mainly ArcGis) and open access map sources will be used.

The proposed extent of the thesis

ca. 40 pages

Keywords

Algyroides marchi; abundance; distribution; border effect; GIS; protected areas

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Recommended information sources

Carretero MA, Ceacero F, García-Munoz E, Sillero N, Olmedo MI, Hernández-Sastre PL, Rubio JL (2010) Seguimiento de Algyroides marchi. Informe final. Monografías SARE. Asociación Herpetológica Espanola – Ministerio de Medio Ambiente y Medio Rural y Marino. Madrid.

Fernández-Cardenete JR, García-Cardenete L (2009) Lagartija de Valverde Algyroides marchi. In: Salvador A, Marco A. Enciclopedia Virtual de los Vertebrados Espanoles <http://www.vertebradosibericos.org/> Museo Nacional de Ciencias Naturales, Madrid.

Harris DJ, Arnold EN, Thomas RH (1999) A phylogeny of the European lizard genus Algyroides (Reptilia: Lacertidae) based on DNA sequences, with comments on the evolution of the group. J. Zool. Lond., 249: 49-60.

Rubio JL, Carrascal LM (1994) Habitat selection and conservation of an endemic Spanish lizard Algyroides marchi (Reptilia: Lacertidae). Biological Conservation, 70: 245-250.

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Assignment

The Assignment is printed from application Badis. It consists of two pages. Signature by supervisor is not obligatory, but recommended.

Declaration

I hereby declare that this thesis entitled "Determinants of the abundance of an endangered lizard: *Algyroides marchi*" is my own work and all the sources have been quoted and acknowledged by means of complete references.

In Prague 2015

Bc. Jakub Strnad

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Abstract

Algyroides. marchi (Spanish algyroides), from the *Lacertidae* family, was studied to determine the possible abiotic factors affecting the abundance in a dataset of 169 populations across the whole distribution area. The study was mainly focused in determining the relative effect of the 'Abundant Centre Syndrome', which has been repeatedly found in certain taxa like birds or large mammals, but has scarcely been studied in reptiles. Distribution boundaries were created in Arc GIS using the convex hull method. Two boundaries were created based on buffers of 16 and 18 km (following two criterion: avoid isolated populations and avoid gaps in the distribution). Non parametric statistics was used to analyse the data, and Generalized Linear Mixed Models were used to compare the the effects of the distance to the border (using boundaries based on the 16 and 18 km, but also excluding them from the models). In the best model, the most significant factors were the distance to the border (16 km), precipitation and macrohabitat. The degree of protection also had a marginal influence in the model. The influence of the abundant centre syndrome in the species was clearly demonstrated since the models were significantly worse when the distance to the border was included. But also highlighted the relevance of choosing the adequate boundaries: while distance to the border (16 km) was the most important factor in the best model created, distance to the border (18 km) was even not correlated with the abundance of the populations. Results also show that the species is more abundant in the transitional woodland-shrub, and is negatively affected by human activity. These factors, especially the distance to the border should be considered for further protection of the species.

1. Introduction and Literature review

1.1. *Algyroides marchi*: our animal model

1.1.1. Taxonomy

The genus *Algyroides* is mostly considered as being closely related to the genus *Lacerta*, even also as sister group of *Archaeolacerta bedriagae* (Arnold, 1973). Externally it differs just very slightly in possessing extremely enlarged dorsal scales (Arnold, 1973). *Algyroides marchi* (Valverde 1958), also known as Spanish algyroides (Fernández Cardenete and García Cardenete, 2010; Fig. 1), is one of four European species of the genus *Algyroides* (Arnold, 1973). According to internal taxonomic situation, the molecular data analysis done by Harris *et al*. (1999) indicates that relationships within the clade are: (*A. nigropunctatus* (*A. moreoticus* (*A. fitzingeri, A. marchi*))). Originally there were also three African species included, but they were moved to their own genus *Adolfus* (Arnold, 1973).

Figure 1. *Algyroides marchi*. Photo: F. Ceacero.

1.1.2. Morphological characteristics

There is a combination of features needed to determine the genus *Algyroides*. Harris *et al*. (1999) and Arnold *et al*. (2007) agreed these six key-features as essential: Small lips on the *lobe sulci* of the hemipenis, distinctive dorsal scale micro-ornamentation, dorsal scales strongly enlarged and markedly keeled, 6-8 enlarged dorsal scales in a transverse row between the hind limbs, lower number of presacral vertebrae in males than is usual in *Lacerta* and its allies (25 – 26) and sombre dorsal colouring (usually brownish, often with a darker markings). Lobes of hemipenis are equipped with plicae, with the apical section of each shorter than the basal one, and their sulcal lips are very small. In retracted hemipenis there is no armature and folding of lobes visible. Its micro-ornamentation consists of spinous tubercles in contrast with other species. Other more widely distributed features include: 7–9 premaxillary teeth in adults, no inscriptional ribs (present only in *A. fitzingeri*), tails of hatchlings not brightly coloured, hemipenial microornamentation of crown-shaped tubercles or hook-shaped spines (Arnold *et al*. 2007).

It is very difficult to distinguish particular species within the genus (*A. marchi* is very similar to *A. nigropunctatus*). For example, total body length is not very reliable feature, because Arnold (1973) described body length range from 30 to 70 cm, Harris *et al*. (1999) stated that the body length does not overcome 55 mm and later Arnold *et al*. (2007) even restated the previously published range to 45 to 70 cm. But there are many other useful features and with their combination it is possible to determine the species correctly. Skull is built delicately with absence of pterygoid teeth, which is good to determine *A. marchi* from *A. nigropunctatus* and *A. moreoticus* (Harris *et al*., 1999). Another important determination features are scaling and scales overlap. Ventral scales of *A. marchi* (opposite to *A. fitzingeri*) are significantly smaller than dorsal scales and they are just slightly overlapped (Arnold, 1973; Arnold *et al*. 2007; Harris *et al*., 1999). Arnold (1973) also mentioned well developed supratemporals (the first larger and deeper than the rest), contact of nostril with first upper labial, emarginated parietal border running medial to the outer margin of the postorbital bone (least developed from the whole genus), well defined masseteric shield, scaly eyelid and number of presacral vertebrae as features determining the species. Harris *et al*. (1999) specified the number of vertebrae of *A. marchi* to 25. Arnold *et al*. (2007) published that supraocular osteoderms are fenestrated in Spanish algyroides.

1.1.3. Ecology and behaviour

Ectothermy in lizards affects their free distribution among and within habitats, as body temperature has to be maintained by behavioural thermoregulation within a tight range where performance levels are maximized (Rubio and Carrascal, 1994). It is well documented that behavioural adjustments are the primary means by which lizards buffer fluctuations in ambient heat loads to maintain their temperature within the range that is conducive to optimal performance. García-Muñoz and Carretero (2013) stated that the most preferred body temperature of *A. marchi* is in the range 31.5 ± 0.5 °C. Behavioural thermoregulation is reached by means of cautious choice of habitat attributes within the thermal mosaic (Avery, 1982). Therefore, habitat use cannot be presented as a phenomenon independent of thermoregulation. Small lizards are characterized by fast rate of heat exchange with the surrounding environment and high relative evaporative water loss due to a high surface-to-volume ratio (Rubio and Carrascal, 1994).

The activity period of the species starts probably during first days of March, and ends at the end of September or beginning of October. In the overall study of egg-laying, the first egg-laying was observed in the second half of June and the last at the end of July (Rubio and Palacios, 1986; but during their study the minimum size of the ovary appeared coinciding with egg-laying). Within this period, annual egg-laying took place and lasted about one month (Rubio and Palacios, 1986). The reason is probably the abundance of arthropod food (mainly small spiders and flies), that is considered as its main food resource (Rubio and Carrascal, 1994). An experiment was set to find out the number and size of the eggs in the clutch. From the 31 egg-layings obtained in the laboratory, the eggs measured from 8.6 x 5.5 mm to 11.8 x 6.2 mm. Three egg-layings had 1 egg. 15 had 2 eggs, 12 had 3 eggs and 1 had 4 eggs. The appearance of young of the year from August to the beginning of September indicates an incubation period of 4 to 6 weeks (Rubio and Palacios, 1986). Regarding the water ecophysiology, much less is known in lizards in general, and only two very recent studies analysed lacertid species (Osojnik *et al.*, 2013). Nevertheless, physiological studies have provided abundant information on osmoregulation and on mechanisms of water conservation in other lizards. Thus, the resistance to water loss reflects the combined effect of two integumentary components on the rate of water loss. The first one is a structural component, including differences in skin micro-structures and lipid content. The second component is more dynamic, representing physiological, vasomotor responses to short-term variations in

the environment. This physiological response enables better and more immediate control of water loss. According to water loss, laboratory studies were conducted by García-Muñoz and Carretero (2013) in *A. marchi*. Their results displayed that *A. marchi* showed the highest water loss rates compared to other sympatric species as *Podarcis hispanica*, reaching at the end of the experiment a water loss of approximately 10% of the initial weight. If the scenarios for climate change are confirmed, the vulnerability of *A. marchi* to dehydration and competitive displacement by sympatric *P. hispanica ss* put the former species at a serious extinction risk, in fact higher than suggested by correlation models (Carvalho *et al*., 2010; García-Muñoz and Carretero, 2013).

The species is listed as endangered in the IUCN red list (Pérez Mellado *et al*., 2009) due to its reduced area of distribution (less than 500 km^2) and to the continuous decline in the range and quality of its habitat (Brakels *et al*. 2010). Conservation management should avoid forestry practices in known localities of this very local species. Gullies with streams and boulders should not be logged and used for wood extraction in order to provide an adequate habitat for the colonization or dispersion of the species between existing localities. When designing roads or tracks, special care should be taken when crossing gullies, especially avoiding the destruction of the particular habitat composed by large rocks, streams and mesophytic vegetation. The economic cost of these recommendations would be very low considering the small extent of suitable habitat for *A. marchi* in these mountainous areas (Rubio and Carrascal, 1994).

1.1.4. Species distribution

The distribution and abundance of all species are obviously affected by resources (Gaston *et al*., 2000). The geographic distribution of a species is established by factors such as its environmental niche, interspecific competition and its ability of dispersion (Ashcroft *et al*. 2012). Péron and Altwegg (2015) considered abiotic forcing and interactions with other species as the major mechanisms to shape species geographical distributions. In this regard, distribution at larger scales may be the combined reaction to local conditions, with respect to the prominent role of factors that have impact on physiological tolerances (Rubio and Carrascal, 1994). The clear preference for higher altitudes, places with water, northern aspects, and localities (and patches within localities) with low exposure to solar radiation,

casts light on the role of temperature and humidity in the distribution of this species (Rubio and Carrascal, 1994; Brakels *et al*. 2010). The pattern of habitat which is occupied by *Algyroides marchi* evidently contrasts with other larger Mediterranean lizards, which are distributed in drier and warmer habitats, and have wider distribution ranges (Rubio and Carrascal, 1994). *A. marchi* is an Iberian endemic lizard restricted to the Prebetic Mountains (Carretero *et al*., 2010). The species has been found in Sierra de Cazorla, Segura and Las Villas (Jaén, Andalucía), Sierra de Castril and Sierra de Jorquera (Granada; Andalucía), Sierra de Alcaraz, Sierra del Agua and Sierra de Segura (Albacete, Castilla - La Mancha). The new record of this strict endemism in the Murcia Region was surprising, because the particular area is relatively dry, broad and warm compared to the typical home range of the species in Andalucía and Albacete (Brakels *et al*., 2010). It belongs to a genus evolved in humid forest environments whose members occupy relict areas across the Mediterranean Basin (Carretero *et al*., 2010). Range altitude of this species is 543 to 1,790 m asl, but most populations are found between 700 to 1600 m asl (Ceacero *et al*., 2010).

Populations are not uniformly distributed in the area, but they are concentrated in certain limited locations (Rubio and Carrascal, 1994), some populations are even known to have disappeared (Rubio and Carrascal, 1994; Brakels *et al*. 2010; Carretero *et al*., 2010) and no new areas for this species were found in Jaen province during the surveys for the herpetological atlas (Ceacero *et al*. 2007). Tôrres *et al*. (2012) suggested that the more frequently occupied habitats should also present the highest suitability values, reflecting the best environmental conditions. Use of space of *A. marchi* (at local and individual levels) is directly positively connected to sources of water (streams, small pools etc.), the occurrence of large rocks, and negatively with hours of direct solar radiation and cover of small stones and vegetation. This statement was supported in a comparative study by García-Muñoz and Carretero (2013). Rubio and Palacios (1986) published that during their fieldwork throughout the activity period, a unimodal activity was observed for both sexes. The selection of large rocks may have many reasons. It can be explained by obtaining escape from predators, and better opportunities for thermoregulation and water regulation than open surfaces on rocks (Rubio and Carrascal, 1994). The study by García-Muñoz and Carretero (2013) showed that their ecophysiological results suggest that water should be more important than temperature to explain the distribution patterns of *A. marchi*. The cool, humid conditions under these rocks also tender a better source of food than open rock surfaces (Rubio and Carrascal, 1994). Northern orientations are also preferred (Brakels *et al*. 2010). Closely related species, such as

congeners, tend to have range sizes more similar than those of more distantly related species (Brown *et al*. 1996). That is why this species may be found in sympatry with *Podarcis hispanica ss*, a member of the *P. hispanica* species complex, which also inhabits rocky habitats (García-Muñoz and Carretero, 2013).

Distribution modelling displays that the lizard appears to be strongly dependent on mountains, forest cover, low temperatures and high precipitation. *A. marchi* inhabits rough and steep, rocky terrain with stone walls, so they can minimize the radiation and water loss by evaporation (García-Muñoz *et al*. 2010). Humid environments (allow to minimise lizard evaporative loss) are scarce in Mediterranean areas, which are characterised by midday and aestival draught, particularly in Southeast Iberia. Hence, it is not surprising that *A. marchi* displays such a restricted distribution (García-Muñoz and Carretero, 2013).

Figure 2. Preferred habitat of *Algyroides marchi*. Photo: F. Ceacero.

1.2. Distribution and abundance of animal populations

1.2.1. Types of animal species distribution

There are different types of animal species distribution (Davies *et al.*, 2012). First, the ideal 'free' distribution, commonly named as 'uniform', predicts the stable distribution of individuals across good and poor habitats, but this type of distribution is more theoretical than practical, at least in animal populations. The second type is the random distribution, which is quite infrequent since for this to happen the home range of each individual should be independent of the home range of others (of the same species but also independent of others) and even independent of other abiotic factors (requires adequate and consistent environmental conditions and resources). Thus, the third type is the most frequent one in animal populations. In the clumped distribution, individuals are aggregated in certain areas in high concentration groups. This is the common distribution for colonial species, but also in many other vertebrate species which frequently congregate around certain resources. Our studies species, *Algyroides marchi*, also follows this distribution with populations associated to patches of adequate habitats surrounded by unsuitable habitats where the species is absent (Carretero *et al*., 2010; although it is also possible to sporadically find some individuals in these areas, mainly young animals probably dispersing from the main population; F. Ceacero, *per. obs.*). With this distribution, *A. marchi* is a good model species to calculate the abundance of different populations and analyze the abiotic factors affecting them. Moreover, since the distribution of the species is constant across a small distribution range (along a mountainous area 125 km long and 50 km wide), the species is also suitable for analyzing the effect of the distance to the distribution boundaries as abiotic factor affecting the abundance of each population.

1.2.2. Species distribution models

The contemplation of the statistical modelling is the prognosis of species distribution in the majority of instances (Austin, 2002). Elith and Leathwick (2009) defined species distribution model (SDM) as a model that joins distribution data of species (occurrence or abundance) with information on the environmental and/or spatial features of particular areas.

It is possible to use the model for predicting the species distribution across the environment. The variation of alternative names for these models is huge. The SDMs can also be called: climate envelopes, habitat models, ecological niche models (ENMs), resource selection functions (RSFs), bioclimatic models, range maps. Other less frequently used names are correlative models or spatial models.

The use of species distribution models (SDM) to map and monitor animal and plant distributions has become increasingly important in the context of awareness of environmental change and its ecological consequences (Miller, 2010). The earliest species distribution modelling attempt found so far in the literature seems to be the niche-based spatial predictions of crop species by Henry Nix and collaborators in Australia (Guisan and Thuiller, 2005). From their original inception as resource inventory and conservation mapping tools, SDM have evolved along with the increasing variety and availability of statistical methods, digital biological and environmental data with which they are built in a geographic information system (Arc GIS). Beyond predicting species distributions, these models have become an important and widely used decision-making tool for a variety of biogeographical applications, such as studying the effects of climate change, identifying potential protected areas, determining locations potentially susceptible to invasion, and mapping vector-borne disease spread and risk (Miller, 2010). More recently, species distribution modelling (SDM), based on Geographical Information System methods, has been widely used as an alternative to subjective boundary mapping (Tôrres *et al*., 2012). The ultimate usefulness of SDMs is their ability to predict species distributions, with spatially autocorrelated residuals or biased predictors of lesser importance unless they have a detrimental effect on predictive performance (Ashcroft *et al*., 2012).

A central and recurrent problem in SDM building is identifying the appropriate scale for modelling. Scale is usually best expressed independently as resolution (grain size) and extent of the study area, because modelling a large area does not necessarily imply considering a coarse resolution. The selection of resolution and extent is a critical step in SDM building, and an inappropriate selection can yield misleading results. This issue is directly related to the transmutation problem. A first possible mismatch can occur between the resolution at which species data were sampled (*e.g.*, plot size in field surveys, grid size in atlas surveys) and the one at which environmental predictors are available. Optimally, both should be the same, but such coherence is not always possible. Furthermore, many environmental data are indeed provided in a grid lattice format – *i.e.*, regular point data –

rather than a true raster format, which complicates the story, somewhat. This is for instance the case of many digital elevation models (DEM) and derived data (*e.g.*, topographic and interpolated climatic maps; Guisan and Thuiller, 2005).

1.2.3. Calculating animal distribution area

Animal distribution area calculation allows the construction of space use maps from points representing distributions of animals or plants in space or time which are critical in addressing a range of questions in ecology from the behavioural to the landscape level. Several ways how to calculate animal distribution area exists. The modern techniques more commonly used are the minimum convex polygon and kernel methods, which are described in this chapter.

Minimum Convex Polygon

The first and simplest method for calculating the area of distribution of a species with an adequate knowledge of localities where it occurs, is through the minimum convex polygon (MCP; Burgman and Fox, 2003; Getz and Wilmers, 2004). Despite its strength due to its simplicity, Burgman and Fox (2003) have criticized MCP because of the bias increasing with sample size, and being affected by the underlying shape of the species habitat, the magnitude of errors in locations, and the spatial and temporal distribution of sampling effort. According to Getz and Wilmers (2004) the MPC is also not suitable for strongly non-convex data. There are two possibilities of using area estimates published by Burgman and Fox (2003). The first is the evaluation of thresholds for extent of occurrence used for example by IUCN to classify species vulnerability. The second, indicating the trends in range.

Kernel Methods

There is basic division of kernel methods described by Worton (1989) into fixed kernel methods and adaptive kernel methods. The simplest (fixed) method uses the smoothing

parameter value *h* (which defines the relative peakedness of the local distributions) at each point (Getz and Wilmers, 2004). Worton (1989) stated that the smaller *h* value is, the more detailed observations can be obtained. The more sophisticated (adaptive) method should perform even better than fixed methods in characterization of the tails of the utilization distributions (Getz and Wilmers, 2004). Contrary to the previous method, this one varies the smoothing parameter according to the concentration of points. Areas with lower concentration have higher *h* value and opposite (Worton, 1989).

Parametric kernel methods are frequently used in scientific studies especially for constructing animal home ranges (HRs) and utilization distributions (UDs; Getz *et al.*, 2007). Recently a local convex hull (LoCoH) nonparametric kernel method was implemented by Getz *et al.* (2007). It was also mentioned as LCH by Lichti and Swihart (2011), which generalized the minimum convex polygon (MCP) method which enables the construction of a non-uniform UD. Contrary to Kernel methods, for LoCoH a neighbourhood parameter determines *n* for each point and plays a similar role as value *h* (smoothing parameter). Getz *et al.* (2007) presented 'fixed *k*' LoCoH method and two modifications. In the 'fixed *k*' LoCoH, each local kernel is a *k*-point convex hull constructed from a root point and its *k*-1 nearest neighbours. There is a first modification of the method based on 'fixed radius' *r*, or *r*- LoCoH method, where all the points in a fixed 'sphere of influence' of radius *r* around each root point are used to construct the local hulls. In a second modification called 'adaptive', or *a*-LoCoH method, all the points within a variable sphere around a root point are used to construct the local hulls. The calculation has to fulfil the criterion that the sum of the distances between nearby points and the root point is less than or equal to *a*. LoCoH displayed to be more appropriate than parametric kernel methods for constructing HRs and UDs, because of its ability to identify hard boundaries (*e.g.*, rivers, cliff edges) and convergence to the true distribution as sample size increases (Getz *et al.*, 2007).

1.2.4. Abundance in animal populations

All species are relatively numerous in some habitats and regions and scarce or absent in others, what forms their geographic range, which is of course somehow limited (the limit of the geographic range occurs where population density over large areas declines to zero; Brown, 1984). General feature of many range boundaries is that they are extremely dynamic.

While some boundaries such as those corresponding to coastlines and other major are relatively permanent, other boundaries are constantly shifting (Brown *et al*., 1996).

For every species there should be some most favourable location where the density of the population should be greatest because the combination of environmental factors most closely matches the conditions that species requires. If autocorrelation of spatial variation in the environment occurs, then with increasing distance from this site the environment will become progressively more divergent, niche requirements of the species will correspond less frequently, and abundance will decline. There will be a decreasing amount of local spots where individuals can exist, and even within these patches population densities will tend to be lower because resources are rare and/or conditions are nearing the limits that can be tolerated (Brown, 1984). This phenomenon was also described by Péron and Altwegg (2015) as the 'Abundant Centre Syndrome'. Their statement even claim that species progressively decline in abundance from the centre to the boundaries of their range, due to abiotic conditions, competition or interaction between species, eventually leading to replacement by a functional equivalent. According to the study of Feldhammer *et al*. (2012), it does not even matter whether the species is considered abundant or rare; *i.e.*, the abundant centre syndrome is important independently of the abundance of the species.

Following the geographical patterns of target species distribution and abundance is an important and challenging subject according to conservation and time persistence of a species (Tôrres *et al*., 2012). Regarding small animals with small home ranges and lowered possibilities for dispersion (*e.g.*, lacertid lizards) is also very substantive to have as much knowledge of the factors impacting preferences of habitat choice at different spatial scales as possible, to manage their habitats within the whole geographical range and thereby to conserve their endangered populations (Rubio and Carrascal, 1994). The relationship between abundance and distribution is also crucial, because it is possible to manage conservation programs only for species for which distributional information are known. Moreover, although distribution data are relevant, indices of abundance provide information that facilitate planning of spatial conservation prioritization strategies that should help to improve species persistence ability (rather than only its presence; Tôrres *et al*. 2012).

General relationship between abundance and distribution can be divided into two parts (Brown, 1984). First, also mentioned by Péron and Altwegg (2015) is dealing with intraspecific situation. States that population density tends to be greatest in the core of the range and to decline gradually as it gets closer to the area edge. There are some exceptions

including abrupt changes in abundance that usually correspond to sharp, discontinuous changes in single environmental variables or multimodal patterns of abundance that are caused by environmental patchiness. The second principle describes interspecific relationships, which states that among closely related and ecologically similar species the spatial distribution is positively correlated with mean abundance (Brown, 1984). Both these patterns hold over a variety of spatial scales from local regions to entire geographic ranges (Brown, 1984).

There are three requirements when realizing density sampling. First is to choose arbitrary boundaries, second is to count the target subjects within them and third is to estimate the sampling area (Tôrres *et al*., 2012). Although density is a basic variable required for evaluating of any population status, accurate estimations are time-consuming and costly, especially in case of realization of large-scale conservation strategies (Tôrres *et al*., 2012). Geographical range is also an elusive variable. Considered as a simplified abstraction of a complex phenomenon driven by multiple ecological and evolutionary processes acting at distinct temporal scales (Brown *et al.*, 1996), creating the geographical range map of a species is a process usually following two basic steps: the production of a 'dot map', in which the points displays all locations where any individual of the species is sampled. Obtained map is then used to create a 'boundary map', consisting of interpolating the incidence records to establish an overall range or extent of occurrence. This 'boundary map'- based assessment unduly simplifies biotic and abiotic processes driving range patterns, such as those controlled by historic effects, limitations to dispersal, geographically structured environmental variables and habitat types (Lim *et al*., 2002).

Still, this method is not able to really acquire the comprehensive information of the geographical range of a species, a complex and dynamic reflection of the distribution of all the individuals within a population (Brown, 1995).

2. Aims of the Thesis

The main objective of this thesis is to find the factors associated to the estimated abundance in different localities along the distribution range of the target species, *Algyroides marchi*. Since this species have a small but continuous distribution range, it is an interesting model to study in detail the effects of the 'Abundant Centre Syndrome', and thus, the specific goals are:

- To compare the factors associated with the abundance of the studied populations including (or not) the distance to the distribution boundaries as explanatory factor.

- To compare the factors associated with the abundance of the studied populations in different distribution areas calculated according to the methodological constraints and the biology of the species.

- Finally, to compare the factors associated with the abundance of the studied populations with the factors affecting the distribution (presence-absence) of the species from published studies. *(Only discussion)*

3. Material and Methods

3.1. Data collection

Fieldwork: Distribution of the species and calculation of abundance

The data analyzed in this thesis is derived from the database collected by the Spanish Herpetological Association as part of an agreement with the Ministry of the Environment for the deep study of *Algyroides marchi*, as a threatened taxon which has received poor attention by scientists in the last decades. This database was built using several sources of information.

The collection of information started with the review of the database of the Spanish Herpetological Association (http://www.herpetologica.org/base_datos.asp) in which 87 records were obtained, but no exact location. More exact locations were compiled from data previously collected by the people involved in the fieldwork, and from personal communications by other herpetologists and naturalists of the study area (Jorge Escudero, Peter Brakels, Juan Manuel Pleguezuelos, Jesus Bastida, Juan Zamora, Javier Fuentes, Juan Ramón Fernández-Cardenete, Antonio Manzanares and Manuel Guerrero).

The fieldwork was conducted during summer 2009. Due to the elusiveness of this species, the restricted use made of microhabitat and the small number of known localities, the fieldwork was oriented to obtain data with maximum accuracy taken with GPS. About the design of the field surveys, it should be noted that the main goals were to extend the known distribution of the species, to collect the maximum of locations to perform detailed predictive models and collect genetic material distribution throughout the distribution range of the species. Given the possibility that the knowledge of the geographical distribution of the species could be incomplete due to its low detectability, it was developed a strategy based on extensive surveys targeted at areas of high probability (known or estimated by provisional predictive models) with active sampling in those points whose habitat characteristics prove particularly favourable. To increase the possibilities of detection of the species in each location, they were prospected in their most favourable time according to the microhabitats, weather and orientation of the area. Since many of these areas have a high degree of squeezing, commonly it was necessary to repeat the sampling at favourable times. Finally, for

each locality where the species was detected, it was recorded the locality in UTM projection (using the datum ED50, which is the reference datum for the Iberian Peninsula) and the relative abundance of the species studied, and one or more tissue samples were collected for genetic analysis (tail end preserved in pure alcohol of 70°). The literature review and field work enabled to build a database with 559 records in 45 UTM 10x10 km squares, including 224 exact localities, 169 of them with an index of relative abundance and genetic material from 84 locations.

As mentioned above, the species has a localized distribution and patterns of activity highly dependent of the microhabitat and orientation. These circumstances require making a huge fieldwork effort for collecting adequate abundance data not biased by a large number of variables (date, time, orientation, vegetation cover, type and size of rocks, relative humidity, temperature, cloudiness, wind, etc.). This effort was beyond the scope of the project. Thus, a qualitative index was used. Only four experienced observers (expert in the species) assessed each population as rare (value 1), common (value 2) or abundant (value 3), with half unit increments. Most of the populations were scored at least by two researchers, and in these situations the mean value was taken. Inter-researcher scores were tested but no differences were found.

Labwork: Calculation of geographical and climatic variables

The database previously explained was the basis for producing distribution models of the species at different scales (Carretero *et al.*, 2010). In a previous work, several geographical and climatic variables were calculated in order to produce the predictive distribution models of the species. Nevertheless, these same variables were also used as predictor variables of the abundance of the studied populations in this Thesis. Four data sources were used:

(1) Digital Atlas of the Iberian Peninsula (ADPI; Ninyerola *et al*., 2005);

(2) Shutlle Radar Topography Mission (SRTM; Farr *et al*, 2007);

(3) Advanced Spaceborne Thermal Emission and Reflection Radiometer Global Digital Elevation Model (ASTER GDEM; http://www.gdem.aster.ersdac.or.jp/).

(4) Coordination of Information on the Environment (CORINE).

The ADPI is a set of weather digital maps including average air temperature (minimum, mean and maximum), precipitation and solar radiation with a spatial resolution of 200 m. The SRTM is a digital terrain model (DTM) of almost global coverage free of charge, with a spatial resolution of 81 m. The ASTER GDEM is a project formed by the Ministry of Economy, Trade and Industry (METI) and the National Aeronautics and Space Administration (NASA) of USA to produce the first MDT Free covering all continents (between latitudes 83° N and 83° S) with a spatial resolution of 30 m. CORINE is a European database focused on collecting information relating to the environment for the European Union, including land cover.

Based on these data sources, the following variables were obtained and used in our analyses: orientation, macrohabitat, slope, altitude, precipitation, radiance, maximum annual temperature, minimal annual temperature, mean annual temperature, maximum temperature in July and minimal temperature in January.

Finally, the degree of protection of the study area was obtained from the GIS layers of the different protected areas in the distribution range of the species: Sierra de Cazorla, Segura y las Villas Natural Park, and Sierra de Castril Natural Park in Andalucía, and Los Calares del Mundo y de la Sima Natural Park, Sierra de las Cabras Natural Reserve, and la Molata y los Batanes Natural Reserve in Castilla-La Mancha. Since each figure of protection has a different degree of protection, and even each one has different subcategories also with different degrees, 4 categories were created to get some homogenous categorization of the actual degree of protection of a given area: 1) Reserve areas (full protection); 2) Protected areas with priority to conservation; 3) Protected areas with priority to human use; 4) not protected areas (Fig. 3). This variable (degree of protection) was used in the analyses alternatively as continuous and categorical.
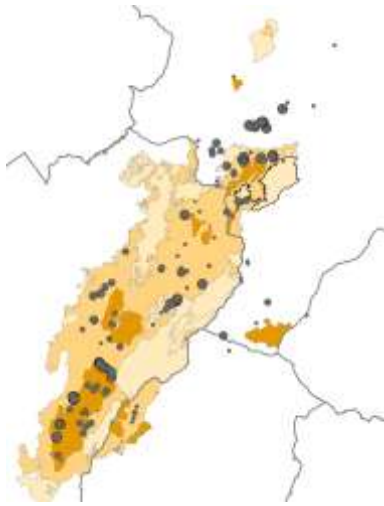
Figure 3. Degree of protection in the study area. Higher intensity of color means higher protection degree: Reserve, Protected areas with priority to conservation, Protected areas with priority to human use, and Not protected areas. The abundance of the studied populations is also indicated by the size of the dot.

3.2. Data processing: Calculation of distribution boundaries

The data set was processed in ArcGis 10.2, the licensed computer programme which is used to create and modify maps. For each known locality, a buffer zone was created around every point by using the function **buffer** in the section geoprocessing (all the ArcGIS functions used in this section are highlighted in bold). As *input features* (all the specifications of the procedures in this section are highlighted in italics) there was 'output features' (data points) chosen, *distance* was initially set to '10 km' (see further explanations about this decision) and *dissolve type* was set to 'none' (Fig. 4).
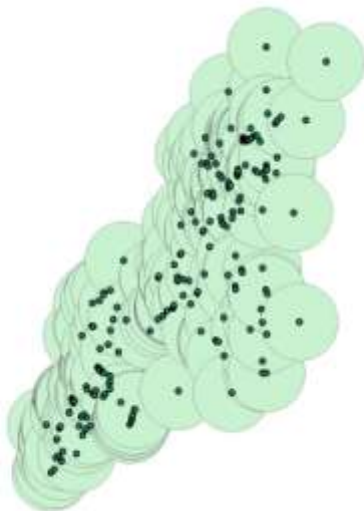

Figure 4. 10 km buffers for the studied localities of *Algyroides marchi*.

The next step was to join the data table with the buffer layer. To do so, it was used the function **intersect**. 'Output features' and 'buffer layers' were chosen as *input features*. As *join attributes* was chosen 'all'. After that, the **minimum bounding geometry** was calculated (Fig. 5). As *input* was set the previously created 'intersect', for *geometry type* was selected 'convex hull', and for *group option* it was selected 'list'. For a correct grouping of the data, the label of each observation was chosen as grouping variable.
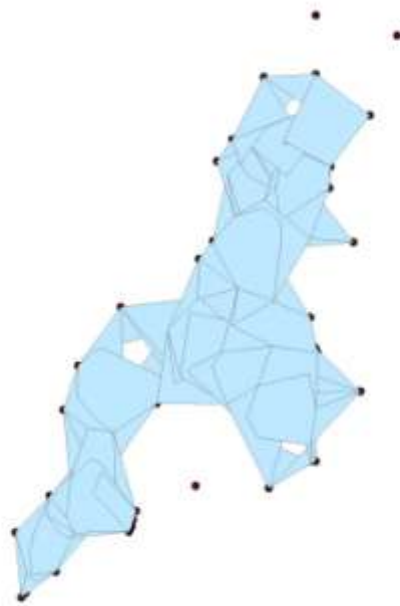

Figure 5. Convex hulls created for the 10 km buffer through the minimum bounding geometry process. It is visible how certain populations stayed isolated from the main distribution area using this 10 km buffer.

For this methodology there are no clear rules about how to choose the adequate buffer size (Getz *et al*., 2007). The main recommendation is to choose the buffer size which creates the final distribution area that most adequately reflects the actual range of the species. During the processing of our data, it was clear after this step that the initial 10 km convex hull was not suitable because it kept some isolated populations which are not supported by the genetic structure of the species (Carretero *et al*., 2010; Fig. 5). Another problem of this polygon based on a small buffer is that too many points are involved in the final creation of the distribution boundaries, which decreases the quality of the data for further analyses (the distance to the border will be 0 for a great number of populations). For these reasons, the whole process was repeated changing the buffer size to 50 km, in order to eliminate these problems. As expected, these boundaries based on a large buffer included areas behind the natural borders of occurrence of the species, which are clearly not suitable for its presence. Finally, this procedure was repeated with different buffer sizes within this range (10 − 50 km) with the

objective of finding the smallest buffer suitable for creating an uniform distribution area, *i.e.*, without isolated populations (according to the genetic structure found in the species; Carretero *et al.*, 2010).

The distribution area created by the 16 km buffer (Fig. 6) was chosen as it suited the above described criteria the best. Nevertheless, using the 16 km buffer a gap appeared within the distribution area. For that reason it was decided to obtain a second distribution area based on two criteria: not to have isolated populations and not to have gaps within the area. Following these criteria, the distribution area based on 18 km buffer (Fig. 7) was also selected for further analyses.
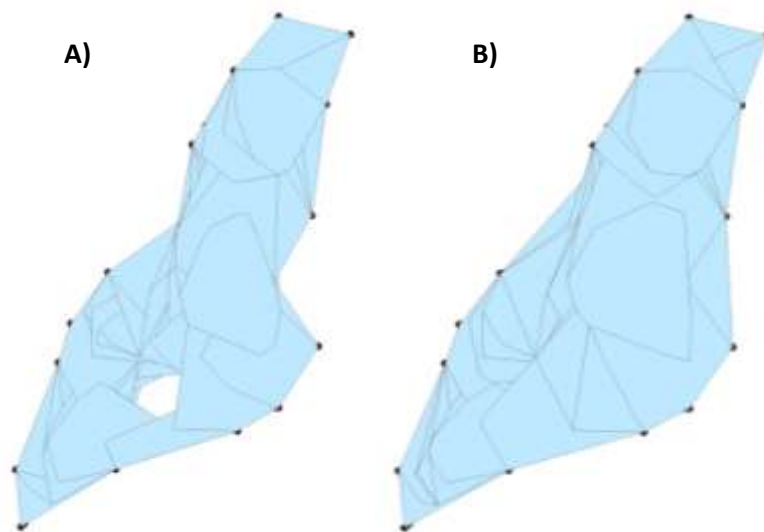

Figure 6. Convex hulls created through the minimum bounding geometry process. A) Was created with a 16 km buffer. B) Was created with an 18 km buffer.

Once selected the adequate buffer sizes, the function **dissolve** was used to obtain a single polygon (Fig. 7). The 'convex hull' was filled as the *input features*. The last step was to calculate the distance from each point to the nearest polygon border. For this purpose the function **near** fits the best. Unfortunately it is not able to calculate the distance for points lying inside the polygon. That is why it was necessary to transform **polygon to line** (Fig. 8). This procedure produced a hollow polygon which enabled the use of the function **near** to calculate the distances. For the *input features* was the 'export output' selected, for the *near* was selected 'Line'. With this calculation finished, it was included in the database the

distance of each locality to the calculated distribution boundaries, and thus it was possible to start analyzing the data.
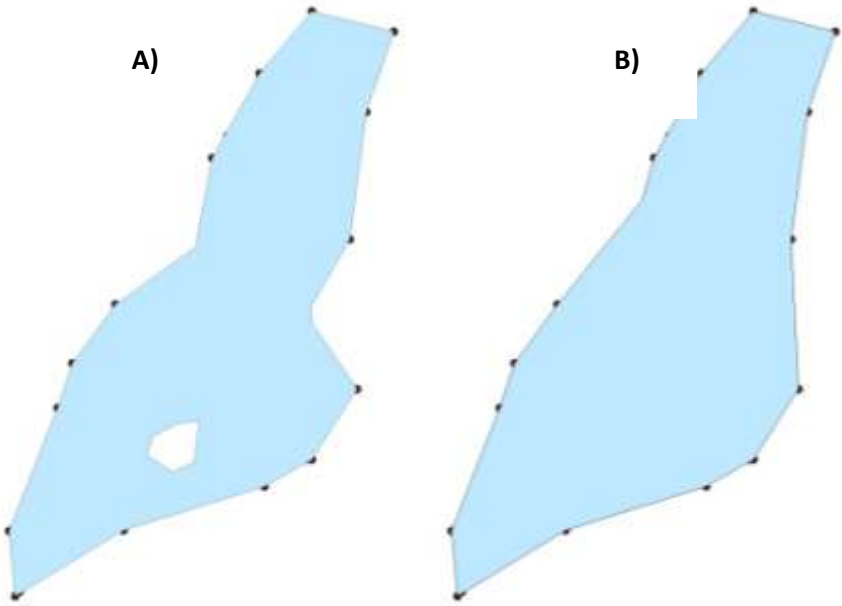

Figure 7. Dissolved convex hulls created through the minimum bounding geometry process. A) was created with a 16 km buffer. B) was created with an 18 km buffer.
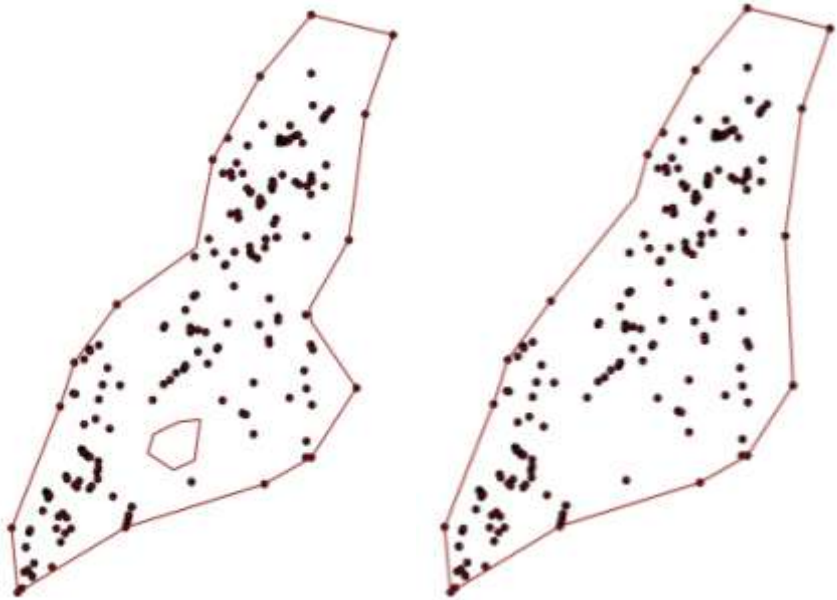

Figure 8. Distribution borders (line) created from the polygons shown in Fig. 7. A) was created with a 16 km buffer. B) was created with an 18 km buffer. Localities known for the species are also shown.

3.3. Data analysis

The dataset was analyzed using the software IBM SPSS Statistic 20. The first step was to test the normality of the continuous data [abundance, slope, altitude, precipitation, radiance, maximum temperature in July, minimum temperature in January, mean temperature, annual maximum temperature, annual minimum temperature, degree of protection, distance to the border (16 km) and distance to the border (18 km)]. The one sample Kolmogorov-Smirnov test was used for this purpose. Since few parameters did not follow a normal distribution (including the dependent variable 'abundance'), and due to the mathematical constraints to transform the variables, non-parametric statistics were used in the subsequent analyses.

Thereafter, the correlations (Spearman ranked correlations) between abundance and the continuous variables were tested. The relationships between the abundance and the categorical variables (genetic lineage, orientation, macrohabitat, and degree of protection) were tested through nonparametric tests for independent samples (Kruskal-Wallis).

The described explorative analyses showed that most of the climatic and geographical variables were not correlated with abundance, but highly correlated among themselves. In order to not to lose this information in further analyses, Factor Analysis was used to create new uncorrelated variables. All the variables which were not correlated with abundance were included in this analysis: maximum annual temperature, minimal annual temperature, mean annual temperature, maximal temperature in July, minimal temperature in January, altitude, slope and radiance. This way, the factors F_1 and F_2 were created and used in the next analyses.

Finally, Generalized Linear Mixed Models (GLMM) were conducted to analyze at once all the significant variables found in the preliminary analyses: degree of protection and macrohabitat were used as factor. Degree of protection, precipitation, distance to the border (16km), and distance to the border (18km) were included as covariates. The factors F_1 and F_2 were also included as covariates. Different models were created in order to compare the differences among them and choose the best one. As previously explained, degree of protection was used as factor or as covariate in the different models tested. Nevertheless, the main objective was to test the actual influence of the distance to the border for the different buffers created in the abundance of the populations (see Table 1 for a summary of the models tested). The first set of models excluded the distance to the border and considered the degree of protection as continuous variable; while the second set considered the degree of protection

as categorical. In the third set, distance to the border (18 km) was included, and degree of protection was considered as continuous; while the fourth set included degree of protection as categorical. Finally, the fifth set included the distance to the border (16 km) and the degree of protection as continuous; while the sixth and last set used degree of protection as categorical. Among those models which were significant for each trait, the best model was selected based on the Akaike's Information Criterion corrected for small sample size (AICc). AICc weights (AICcw) were calculated following Wagenmakers and Farrell (2004), in order to assess which of the selected models has the highest probability of being the best one.

Table 1. Factors and covariates used in the different sets of Generalized Linear Mixed Models created. The main differences among the models refers to the use of DP (as factor or covariate) and DB (for 16 km buffer, 18 km buffer or excluded from the analyses). To clarify the differences among models, these variables are highlighted in bold.

Set of Models	Factors	Covariates
1	MH	Prec, F_1, F_2, **DP**
2	MH, **DP**	Prec, F_1, F_2
3	MH	Prec, F_1, F_2, **BD18**, **DP**
4	MH, **DP**	Prec, F_1, F_2, **BD18**
5	MH	Prec, F_1, F_2, **BD16, DP**
6	MH, **DP**	Prec, F_1, F_2, **BD16**

DP = Degree of protection; MH = Macrohabitat; Prec = Precipitation; F_1 = Factor 1; F_2 = Factor 2; BD16 = Distance to the border (16 km buffer); BD18 = Distance to the border (18 km buffer).

4. Results

The results obtained in this Thesis are divided in two blocks. In the first one it is shown the individual interactions of the studied variables with the abundance. In the second part of the analyses certain selected variables were included in a set of Generalized Linear Mixed Models to clarify which are the main factors affecting the abundance of the populations of *Algyroides marchi*. Non-parametric statistic was used since some of the variables (including the dependent variable 'abundance') were not normally distributed.

4.1. Interactions of the studied variables with abundance

Table 2. Spearman ranked correlation between the abundance estimated for the 169 studied populations of *Algyroides marchi vs.* the climatic and geographical variables of each locality.

VARIABLE	r	P	n
Slope	-0.003	0.965	169
Altitude	-0.067	0.390	169
Precipitation	0.231[**]	0.002	169
Radiance	-0.058	0.456	169
Maximum annual temperature	0.011	0.889	169
Maximum temperature in July	-0.004	0.958	169
Mean annual temperature	0.043	0.577	169
Minimum annual temperature	0.062	0.420	169
Minimum temperature in January	-0.018	0.814	169
Distance to the border 16 km	0.056	0.471	169
Distance to the border 18 km	0.190[*]	0.013	169
Degree of Protection	0.211[**]	0.006	169

Significance is indicated as follows: ** = p<0.01; * = p<0.05.

Spearman ranked correlation tests showed that precipitation, distance to the border (16 km) and degree of protection were highly correlated with abundance. However, most of the geographical and climatic variables where not correlated with abundance (Table 2).

In order not to lose this information in further analyses, and because most of the climatic variables were highly correlated with each other, those variables not correlated with abundance were reduced through Factor Analysis. Table 3 shows the percentage of variance explained by the new factors (F_1=68.894 %; F_2=17.328 %), and explains the loads of the variables correlated with each extracted factor. These factors will be used in the final Generalized Linear Mixed Models.

Table 3 Relationship between the factors and continuous variables. Significant relationships are highlighted in bold [loading higher than 0.7, following Budaev (2010)]. Table also displays the variance explained by each factor.

	F1	F2
Eigenvalue	5.511	1.386
Explained variance (%)	68.894	17.328
Slope	-0.025	**-0.796**
Altitude	**-0.975**	-0.018
Radiance	-0.014	**0.846**
Maximum annual temperature	**0.967**	-0.007
Maximum temperature in July	**0.948**	-0.051
Mean annual temperature	**0.994**	-0.030
Minimum annual temperature	**0.964**	-0.046
Minimum temperature in January	**0.900**	0.182

Non-parametric tests for median comparison (Kruskal-Wallis) showed that the observed abundance values are the same across categories for the genetic linage (p=0.971) and orientation (p=0.165). Nevertheless, abundance is different for the different studied categories of degree of protection (p=0.014) and macrohabitat (p=0.008). 'Transitional

woodland-shrub' (following the nomenclature of CORINE_Land Cover) was the macrohabitat showing significantly high abundance values (mean=2.32±0.19), while 'natural grasslands' showed significantly low values (mean=1.32±0.17). For the degree of protection, reserve areas showed the greater abundance values (mean=2.28±0.10), followed by protected areas with priority to protection (mean=1.87±0.09) and not protected areas (mean=1.87±0.14). However, protected areas with priority to human use showed the lower values (mean=1.70±0.23).

4.2. Multivariate models (GLMM)

Results of the General Linear Mixed Model set performed are shown in the Table 4. In the set 1, precipitation ($p = 0.005$) and macrohabitat ($p = 0.008$) were the factors explaining abundance. In the set 2, macrohabitat ($p = 0.003$), degree of protection ($p = 0.045$) and precipitation ($p = 0.049$) were the factors explaining abundance. In the set 3 the result was the same as in the set 1. In the set 4 the result was the same as in the set 2, which means that distance to the border (18km) do not play any role explaining the abundance found in the studied populations. In the set 5, precipitation ($p = 0.001$), distance to the border (16 km) ($p = 0.002$) and macrohabitat ($p = 0.013$) were the variables explaining abundance. Finally, in the set 6 distance to the border (16 km) ($p = 0.003$), macrohabitat ($p = 0.006$), precipitation ($p = 0.013$) and degree of protection ($p = 0.064$) were the variables explaining abundance. Thereafter, the models were compared through the Akaike's Information Criterion. The Table 4 shows the probability of the different models created to be the best according to the weighed Akaike's Information Criterion (AICcw).

From all the sets tried, the set 6 generated the model with the lowest AICc value and thus was considered as the best among the four models found to be significant. The probability of this model to be the best one is 49.5 %. This model is described in Table 5. Nevertheless, a second model (that generated by the set 5) also showed a high probability to be the best one (43.8 %). Both models included the distance to the border (16 km), but in set 6 the degree of protection was included as factor and was significant in the final model, while in the set 5 it was included as covariate and it was not significant in the final model.

Table 4. Comparison of the tested Generalized Linear Mixed Models according to AICcw, which indicated the probability of each model to be the best one (that was highlighted in bold).

	Set ID[1]	AICc	ΔAICc	AICcw
M+Prec	1	393.647	7.376	0.012
M+DP+Prec	2	392.571	6.300	0.021
Prec+M	3	393.647	7.376	0.012
M+DP+Prec	4	392.571	6.300	0.021
Prec+Dist16+M	5	386.513	0.242	0.438
Dist16+M+Prec.+DP	**6**	**386.271**	**0.000**	**0.495**

[1] ID of the models and information about variables included is shown in Table 1
DP=Degree of protection; M=Macrohabitat; Prec=Precipitation; Dist16=Distance to the border (16 km).

Table 5. Significant variables in the selected Generalized Linear Mixed Model (see Table 4), which included the 16 km border and degree of protection as factor.

Variable	Wald Chi^2	df	P
(Intercept)	6.467	1	0.011
Distance to the border (16km)	8.842	1	0.003
Macrohabitat	16.156	5	0.006
Precipitation	6.255	1	0.013
Degree of protection	7.262	1	0.064

5. Discussion

This Thesis identified the abiotic factors affecting the estimated abundance in 169 populations of *Algyroides marchi*, an endemic lizard from the Iberian Peninsula, across the whole distribution range. The selected model shows that distance to the border (for a distribution area calculated with a buffer of 16 km) was the variable with greater effect in the abundance: the abundance is decreasing towards the distribution boundaries, which agrees with the 'Abundant Centre Syndrome', as was expected during the design of the experiment.

Nevertheless, there were also other significant variables influencing the abundance, like macrohabitat and precipitation. According to the macrohabitat, the transitional woodland-shrub seemed to fit the species the best meanwhile the natural grassland habitat seems to hold the populations with lower density. It has been described strong limitation of the species due to water evaporation (García-Muñoz and Carretero, 2013), which may explain the effect of precipitation in abundance detected in the model. Finally, the degree of protection also affected the abundance of the populations. This variable had a greater effect when used as categorical variable. This is due to the fact that the protected areas with priority to human use were hold less abundant populations than areas protected with priority to the conservation but also than not protected areas. This points out that the human activity affects the species abundance negatively. Thus, it seems that the most protected areas (reserve areas) actually hold the populations with greater abundance. On the other hand, the degree of protection entered in the model just marginally and it should not be considered as major determinant of the abundance. In fact, the results obtained suggest that abundance of the populations is more linked to disturbance by humans than by the protection degree: high abundance in reserve areas (no disturbance), mid abundance in areas with low disturbance (conservation areas and not protected areas, which in this situation are mountainous areas with very low human activities), and low abundance in protected areas but dedicated to human use.

Even if further analyses are necessary to fully understand the factors affecting the abundance of the populations of *Algyroides marchi*, the knowledge generated in this Thesis relative to the effect of distance to the border of the distribution area, in combination with other significant variables, may help to improve the conservation programme of the species.

The main aim of this thesis was to test the existence of the 'Abundant Centre Syndrome' in *Algyroides marchi*. Even if there are not much literature about this syndrome,

some studies have proved it in certain groups, as birds (VanDerWal *et al.*, 2009; Huntley *et al.*, 2011; Péron and Altwegg, 2015), and large mammals (Yackulic *et al.*, 2011). However, other studies failed to find this pattern in bats (Stevens *et al.*, 2004), primates (Fuller *et al.*, 2009), or rodents (Feldhamer *et al.*, 2012). Similar studies to this Thesis were published by Péron and Altwegg (2015) and Huntley *et al.* (2011) for birds. They used the same non-parametric statistic (convex hull), but the rules for selecting the distribution area were different (99 % of the cells where the species had an estimated occupancy probability above 33 %). Despite these differences, all tested species exhibited the abundant centre syndrome (but with various magnitudes), as *A. marchi* did. VanDerWal *et al.* (2009) provided also similar positive results about the effect of the 'Abundant Centre Syndrome' for 69 vertebrates in the Australian wet tropics, mainly birds but also 6 reptiles. Even that most of the species exibited positive relationship, the explained variation was generally low. Yackulic *et al.* (2011) published that 43 large mammalian species exibited lower extinction vulberavility in core of distribution due to higher abundance. On the contrary, Fuller *et al.* (2009) found that none of the 115 studies of 30 primate species examined supported the abundant centre syndrome. They also found a form of anthropogenic disturbance negatively affecting the primates abundance. This also agrees with our results, since also *A. marchi* exibited some negative effect of anthropogenic disturbance on abundance. Also Stevens *et al.* (2004), focused on bat species in Paraguay, failed to find the effect of the distance to the border in the abundance of the colonies. In summary, the there seems to be proofs against and in favour of the abundant centre syndrome which seem to work in certain taxa but not in others. It is important that this thesis is one of the first studies supporting it in lizards.

The effect of the abundant centre syndrome is clearly demonstrated for *Algyroides marchi* in this study. It was possible to create significant models without including the distance to the border, but those where much worst than the models including it (see Table 4). Moreover, the results also highlight the importance of choosing the adequate methodology: when the distance to the border was calculated using the convex hull calculated with the 18 km buffer, this variable was not significant and the final models stayed as the initial ones (those not including the distance to the border). Nevertheless, when the adequate convex hull (that created with the 16 km buffer) which was constructed paying maximum attemption to the biology of the species (as recomended by Getz *et al.*, 2007), respecting the lack of isolated populations and the existence of gaps in the distribution, the models improved significantly. Moreover, in one of the two more feasable models the distance to the border was the variable

with the greater significance. This results highlight the possibility that some of those studies which found no effect of the abundant centre syndrome in several species (like Stevens *et al.*, 2004 or Fuller *et al.*, 2009) may be due to problems in the construction of the adequate distribution borders.

Finally, another objective of this thesis was to compare the factors affecting abundance with the factors affecting the distribution (probability of presence), which was studied in earlier works (Carretero *et al.*, 2010). This study created 3 models according to different scales (1 km^2, 200 m^2, 30 m^2). Due to the incompatibility of variables tested in model 30 m^2, it is not possible to compare this one. For the 1 km^2 and 200 m^2 models, variables altitude, slope, maximum temperature in July and precipitation, sorted by significance (descending), were the most important affecting the distribution of the species. In contrary, the model found in this study showed precipitation, distance to the border and macrohabitat as the most significant factors affecting the abundance (sorted descending). It seems that the precipitation affects both the distribution and the abundance and thus it should be given high value when suggesting new possible areas of protection for the species. However, altitude, slope or temperature were important to predict presence, but not abundance. This results different are not greatly influenced by the distance to the border, since the models created not including this variable showed similar results (macrohabitat and precipitation as predictors of abundance). Thus it should be better to set eventual new protection zone in the abundant core.

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6. Conclusion

In conclusion, the main factors affecting the abundance of *Algyroides marchi* are distance to the border (if the distribution boundaries has been adequately created), macrohabitat, precipitation and marginaly by degree of protection. The results also highlight the differences between factors affecting presence and factors affecting abundance, since only precipitation seems to be a determinant factor for both as could be expected because of the ecophysiological constraints of the species (mainly water loss). The results from this work should help to understand the abundance patterns observed in this species, but also to have a first approach for other reptiles, since this topic (factors affecting abundance) has been very scarcely studied in reptiles species. Finally, several recommendations for the conservation of the species may arise from these results, specially related to higher risks of extinction in low densities populations due to anthropic disturbances.

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8. Index of Figures and Tables