DOES THE NATURA 2000 NETWORK REALLY PROTECT THE SPECIES? A CASE STUDY OF THE CRETAN HERPETOFAUNA.

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ABSTRACT

The Natura 2000 is a network of protected areas designed and implemented by European Union. The main purpose of the Natura 2000 network is to protect the biodiversity. However, systematic assessment studies on the effectiveness of the Natura 2000 network are still scarce.

The aim of this study is to assess the Natura 2000 Special Areas of Conservation network, and to answer does it protect the amphibians and reptiles of Crete. Species distribution modelling platform biomod2 was used to create distribution maps. We have explored using multiple modelling techniques for this purpose (GLM, GBM/BRT, CTA, RF, MARS and MAXENT), and multiple pseudo-absence approaches in order to find the optimal model with the highest performance, measured by kappa, TSS and AUC. We have used one optimal combination to create distribution models. Spatial conservation prioritization software Zonation was used to identify areas of high conservation priority from the distribution maps of 15 species of amphibians and reptiles of Crete. We assessed how well does the Natura 2000 Special Areas of Conservation network represents species for three different scenarios: (i) we assessed all 15 species of amphibians and reptiles, (ii) we assessed species from the Annex II of the Habitats Directive, and (iii) we assessed the species from the IUCN Red List. Percentage of overlap and kappa value of agreement was calculated between the extent of the Natura 2000 Special Area of Conservation sites and priority conservation areas for these three scenarios. Furthermore, we calculated importance of every Natura 2000 Special Area of Conservation site for the conservation of amphibians and reptiles in all three scenarios.

The results showed that MAXENT and GBM/BRT had high value of performance evaluation metrics, and the best strategy for generating pseudo-absences is disk strategy in biomod2. MAXENT was used as a best method to create the distribution maps. Our assessment showed that the Natura 2000 network Special Area of Conservation sites was performing poorly when it comes to representing the priority conservation areas: (i) all species – 34.7% overlap and kappa = 0.101, (ii) Annex II species – 19.8% overlap and kappa = -0.104, and (iii) Red List species – 38.6% overlap and kappa = 0.154. Natura 2000 Special Area of Conservation sites that are representing these three scenarios the best are: Drapano, Lefka Ori and Limni Agias, and that represent them the worst are: Moni Kapsa, Ormos Sougias and Dytika Asterousia.

This method showed to be useful for gap analysis of protected areas, however modelling approach should be carefully considered, as well as the input data quality, as they can negatively influence the performance of the models.

Keywords: Natura 2000, Crete, amphibians, reptiles, species distribution modelling, biomod2, Zonation, gap analysis

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LIST OF ABBREVIATIONS

ABF	Additive benefit function
AIC	Akaike information criteron
ASTER	Advanced Spaceborne Thermal Emission and Reflection Radiometer
AUC	Area under the curve
BIC	Bayesian information criterion
BRT	Boosted regression trees
CAZ	Core area Zonation
CR	Critically endangered
CTA	Classification tree analysis
DEM	Digital elevation model
EEA	European Environment Agency
EN	Endangered
EU	European Union
GBM	Generalised boosting models
GLM	Generalised linear models
IUCN	International Union for Conservation of Nature
LC	Least concern
MARS	Multivariate adaptive regression splines
MAXENT	Maximum entropy
NDVI	Normalized difference vegetation index data
NHMC	Natural History Museum of Crete University
PA	Pseudo-absence
RF	Random forest
ROC	Receiver operating characteristic
SAC	Special Areas of Conservation
SDM	Species distribution modelling
SPA	Special Protection Areas
TSS	True skill statistics
VIF	Variance inflation factor
VU	Vulnerable

1. INTRODUCTION

Nature areas of particular value have been set aside as protected areas since 19th century for benefit and enjoyment of people (Eagles, McCool, Haynes, & Phillips, 2002; Margules & Pressey, 2000), or in order to protect habitats, species and populations (Gaston, Jackson, Nagy, Cantú-Salazar, & Johnson, 2008; Margules & Pressey, 2000). Various legal mechanism exist to protect areas with particular value, and amongst them some are designed to protect areas recognized for their biodiversity (Margules & Pressey, 2000). For example, the system of protected areas designed by the International Union for Conservation of Nature (IUCN) designates areas that are recognized for their biodiversity values to categories I – IV (IUCN, 2008). Currently, between 10.1 and 15.5% of land area is under some form of protection globally (Abellán & Sánchez-Fernández, 2015), yet a unique action plan on a global level for nominating protected areas does not exist (Gruber et al., 2012).

Network of protected areas known as Natura 2000 has been designed by the European Union to protect biodiversity (Jongman, 1995; Rondinini & Pressey, 2007). The Natura 2000 network has been established by designating areas which protect habitats and species contained under the Birds Directive (Directive 79/409/EEC for the conservation of wild birds), and the Habitats Directive (Directive 92/43/EEC for the conservation of natural habitats, wild fauna and flora) (Gaston et al., 2008; Gruber et al., 2012; Louette et al., 2011; Trochet & Schmeller, 2013; Vokou et al., 2014). Special Protection Areas (SPAs) are designated under the Birds Directive, while Special Areas of Conservation (SACs) are designated under the Habitats Directive (Gaston et al., 2008). Habitats Directive has six Annexes that cover protection of species and habitats (EC, 2007). Annex II specifically covers species that require designation under Special Areas of Conservation, while Annex IV covers species in need of strict protection (EC, 2007). More precisely, a species is listed in Annex II when the conservation of its habitat is the principal factor determining their survival and well-being, therefore the species listed in Annex II is defined as "*animal or plant species of Community interest whose conservation requires the designation of Special Areas of Conservation*" (EC, 2007).

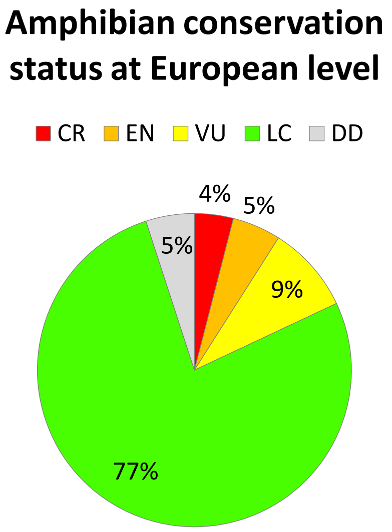
Methodology of choosing sites for Natura 2000 network has not been uniform between the European Union Member States (Davis, Naumann, Mcfarland, Graf, & Evans, 2014; Rauschmayer, van den Hove, & Koetz, 2009). Historically, protected areas were often designated using an *ad hoc* way of decision-making (de Novaes e Silva et al., 2014; Dimitrakopoulos, Memtsas, & Troumbis, 2004; Jantke & Schneider, 2010; Margules & Pressey, 2000; Kostas Papageorgiou & Vogiatzakis, 2006). In many cases the Natura 2000 sites were not planned so that they complement existing national and regional protected areas, as it has been shown in studies in Greece, Romania, the Czech Republic and Italy (Davis et al., 2014; Gruber et al., 2012; Pa, Popescu, & Verghelet, 2010; Kostas Papageorgiou & Vogiatzakis, 2006). Instead, they were either superimposed on existing protected areas, or planned without taking existing protected areas into consideration and complementarily with those protected areas. And as it is common practice to designate protected areas based only on their scenic beauty (Eagles et al., 2002), without taking biodiversity into consideration, superimposing Natura 2000 sites would often mean that they do not represent the local biodiversity (Margules & Pressey, 2000).

Around 27% of Greek territory is covered by Natura 2000 network sites (EEA, 2012), making it one of the European Union countries with the highest proportion of area covered by the Natura 2000 network. However, out of 359 Natura 2000 sites in Greece, 214 have been nominated based on previous designations (Kostas Papageorgiou & Vogiatzakis, 2006). Since the 1990's there has been a significant increase in the number of protected areas in Greece. However, despite the increased effort, selection of locations for new protected areas is still mainly politically motivated (Apostolopoulou & Pantis, 2009). This is contrary to using a scientific approach for finding the optimal locations of protected areas (Margules & Pressey, 2000), and also implies that newly created protected areas do not represent (cover) important segments of biodiversity of an area (Jennings, 2000).

Assessment of protected areas and identification of elements of biodiversity which are not sufficiently covered by protected areas is done using gap analysis (Jennings, 2000). Convention on Biological Diversity defines gap analysis within the conservation context as "an assessment of the extent to which a protected area system meets protection goals set by a nation or region to represent its biological diversity (Davis et al., 2014; Dudley & Parish, 2006). In other words, gap analysis is used to assess the representation of protected area network, and also to identify area of conservation priority that are not included within the existing network of protected areas (Davis et al., 2014; Jennings, 2000; Kujala, Araújo, Thuiller, & Cabeza, 2011; Margules & Pressey, 2000).

Amphibians and reptiles are one of the most endangered vertebrate taxa in Europe, making their conservation a priority in policies of European Union (Abellán & Sánchez-Fernández, 2015). Amphibians and reptiles are taxonomic groups with highest proportion of declining species numbers from all assessed groups at European level. Indeed, 42% of reptile species have declining populations (Cox & Temple, 2009), while amphibian species are under even greater stress, with 59% of species that are declining in numbers (Temple, H. J., Cox, 2009). IUCN has listed 18% of amphibian species and 13% of reptile species (Figure 1) under one of the threatened categories - critically endangered (CR), endangered (EN) and vulnerable (VU) (Cox & Temple, 2009; Temple, H. J., Cox, 2009).

Amphibians and reptiles are usually studied together, mainly because of their ecological, physiological and behavioural similarities (Vitt & Caldwell, 2013). Therefore the branch of zoology that studies amphibians and reptiles is called herpetology and amphibian and reptilian fauna is referred to as herpetofauna (from greek "herpien" = "to creep") (Vitt & Caldwell, 2013).



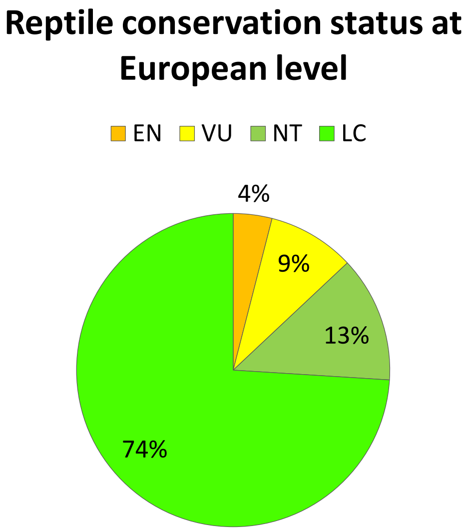


Figure 1: IUCN conservation status of European amphibian and reptile species (CR: Critically Endangered; EN: Endangered; VU: Vulnerable; NT: Near Threatened; LC: Least Concern; DD: Data Deficient. Adapted from Cox & Temple, (2009) and Temple, H. J., Cox, (2009).

Gap analysis requires accurate information on the distribution of analyzed species or habitats (Boitani et al., 2011; Rondinini, Wilson, Boitani, Grantham, & Possingham, 2006). Data on the distribution of species can come in three forms: (i) point data - locations where presence of species has been observed, (ii) geographic range - broad boundary of the area where the occurrence of the species is known, and (iii) predicted distribution - the area where presence can be expected based on environmental suitability (Rondinini et al., 2006; Sillero et al., 2014). Most of the species occurrence data comes in point data form, either from museum collections, surveys with predetermined sampling design or random sightings without any sampling design (Boitani et al., 2011). However, this data is often sparse, incomplete and spatially biased, which can lead to errors that eventually underestimate or overestimate the distribution (Fajardo, Lessmann, Bonaccorso, Devenish, & Muñoz, 2014). Therefore, due to the lack of detail and quality, point data on species occurrence can rarely be used effectively for conservation planning (Carvalho, Brito, Pressey, Crespo, & Possingham, 2010). However, point data on species occurrence combined with proper environmental variables and expert knowledge on how to use this data can be used to create predicted species distribution models(Guisan & Zimmermann, 2000).

Predictions from species distribution models are often used an input data for gap analysis (Abellán & Sánchez-Fernández, 2015; Boitani et al., 2011; de Novaes e Silva et al., 2014; Díaz-Gómez et al., 2013; Guisan et al., 2013; Jennings, 2000; Wu, Walther, Chen, Lin, & Lee, 2013) and systematic conservation planning (Boitani et al., 2011; de Novaes e Silva et al., 2014; Fajardo et al., 2014; Franklin, 2010; Rondinini et al., 2006). Species distribution modelling is based on the assumption that environmental niche of a species can be inferred by associating locations of known occurrences (such as those in point data), with environmental predictor variables for these locations (Figure 2) that are relevant in the terms of ecology of the organism (Jane Elith & Leathwick, 2009; Franklin, 2010; Hijmans & Elith, 2013; T. Peterson & Soberón, 2012). Information on the environmental niche of the species can be used to project the models from environmental space to the geographical space (Jane Elith & Leathwick, 2009; Guisan & Zimmermann, 2000; Soberón & Peterson, 2005). This quantification of the interactions and relationship between the species and its environment represents the essential part of predictive modelling of the distribution of species, or the habitat suitability of the species (Guisan & Zimmermann, 2000).

Usage of different terminology in literature is common when it comes to this association of the species' environment with its distribution. Terms that are most commonly used are "species distribution modelling", "ecological niche modelling", "habitat suitability modelling" and "bioclimatic envelope modelling" (A. T. Peterson & Soberón, 2012). The issue is often more than just a semantic issue, and the usage of the term can depend on the application (Jane Elith & Leathwick, 2009; A. T. Peterson & Soberón, 2012). For this analysis we will use the term species distribution modelling.

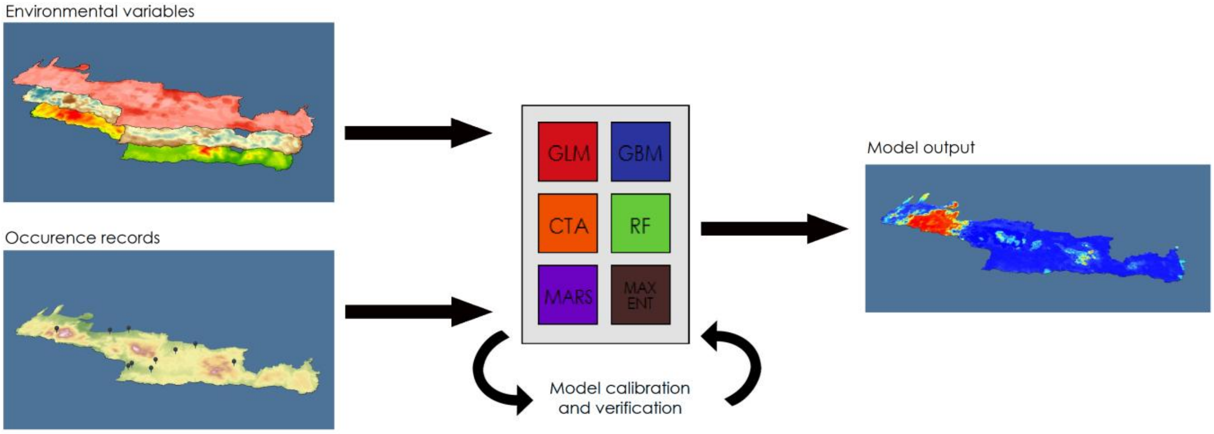


Figure 2: Simplified workflow of species distribution modelling. Modelling techniques depicted correspond to the modelling techniques used in this analysis.

Multiple methods and techniques exist for modelling the distribution of species, asll with varying degree of performance and robustness (Araújo & New, 2007; Pearson et al., 2006). Selection of the appropriate modelling technique is an issue when performing these analyses. Most common approach when choosing modelling technique is to pick a specific technique and justify the choice by citing a particular study (Araújo & New, 2007). However, one single technique has not been shown as consistently dominant over other techniques. Results often depend on the study area extent, data quality, modelled organisms and model parameters. For this reason, selection of the appropriate modelling technique is important for the quality and robustness of the output models.

Data on species' distribution can be used to determine the areas of high biodiversity and conservation value by using specific software. Various software packages have been developed for this purpose such as C-Plan, Marxan and Zonation (Sharafi, Moilanen, White, & Burgman, 2012). Zonation is software for spatial conservation prioritization that identifies areas important for retaining habitat quality for multiple species (Moilanen, 2007). Zonation has been used for gap analysis and reserve planning in different areas and ecosystems, and for different groups of organisms (Early & Thomas, 2007; Fiorella, Cameron, Sechrest, Winfree, & Kremen, 2010; Guisan et al., 2013; Kremen et al., 2008; Langford et al., 2011; Leathwick et al., 2008; Lehtomäki & Moilanen, 2013; Sharafi et al., 2012). It can be used for individual species, ecosystems, or any biodiversity feature (Lehtomäki & Moilanen, 2013). Furthermore, it is computationally effective and it can be applied to large scale analyses with high resolution data having up to tens of millions of grid cells (Sharafi et al., 2012).

1.1. Research problem

Conservation planning practice in Greece has not been systematic, and protected areas may not be located in areas that do contribute to the representation of biodiversity (Apostolopoulou & Pantis, 2009; Margules & Pressey, 2000; Kostas Papageorgiou & Vogiatzakis, 2006). There has been few studies that assessed protected areas in Greece. Three studies focused on vegetation (Boteva, Griffiths, & Dimopoulos, 2004; Dimitrakopoulos et al., 2004; K. Papageorgiou, Malounis, & Vogiatzakis, 2005), and one study assessed the effectiveness of Natura 2000 network for wolf conservation (Votsi, Zomeni, & Pantis, 2015). However, there were no studies that focused on other groups of organisms. Therefore, it is necessary to assess the Natura 2000 Special Areas of Conservation in regards of representing one of the most threatened vertebrate groups, amphibians and reptiles. This is especially important since as Crete is located within the Mediterranean basin that has particularly important species of herpetofauna. Furthermore, herpetofauna of Crete has several species which have been recognized as important on European and global level. Crete has three species listed in Annex II of the Habitats Directive, and by definition, Natura SAC sites have to be designated to conserve these species. European Red List includes three species of Cretan herpetofauna that are recognized as threatened.

1.2. Research objectives

1.2.1. General objective

- General objective of this research is to assess the effectiveness of Natura 2000 Special Areas of Conservation in representing the amphibians and reptiles of Crete (Cretan herpetofauna).

1.2.2. Specific objectives

- To determine which areas are a conservation priority.
- To assess the representativeness of Natura 2000 Special Areas of Conservation for specific groups of Cretan herpetofauna
- To assess which Natura 2000 SAC sites contribute to the protection of Cretan herpetofauna the most and the least.

1.3. Research questions

1.3.1. General research question

- Are the priority areas for conservation of Cretan herpetofauna represented by the current extent of Natura 2000 Special Areas of Conservation?

1.3.2. Specific research questions

- Which modeling technique is optimal for this study?
- Are Natura 2000 Special Areas of Conservation sites representing the Annex II species in Crete more than random?
- Are Natura 2000 Special Areas of Conservation sites representing the IUCN Red List species in Crete more than random?

1.4. Research hypotheses

- H_0: Annex II species are not represented significantly more by Natura 2000 SAC sites than all species
- H_1: Annex II species are represented significantly more by Natura 2000 SAC sites than all species
- H_0: Red List species are not represented significantly more by Natura 2000 SAC sites than all species
- H_1: Red List species are represented significantly more by Natura 2000 SAC sites than all species

2. RESEARCH METHODS

Workflow of this study can be separated into several parts: (i) data processing and preparation, (ii) preparation of input data for Zonation analysis, and (iii) Zonation analysis and analysis of the output data (gap analysis). We have used two types of input data for Zonation analysis – species distribution model outputs and species presence points. Major part of this study was species distribution modelling, and we have performed them in several steps in order to find the most suitable approach of using SDM techniques for our study area (section 2.5). Final part of the study was comparing the Zonation output (priority conservation areas), and extent of the Natura 2000 SAC sites (section 2.6). The workflow carried out during this study is summarized in Figure 3.

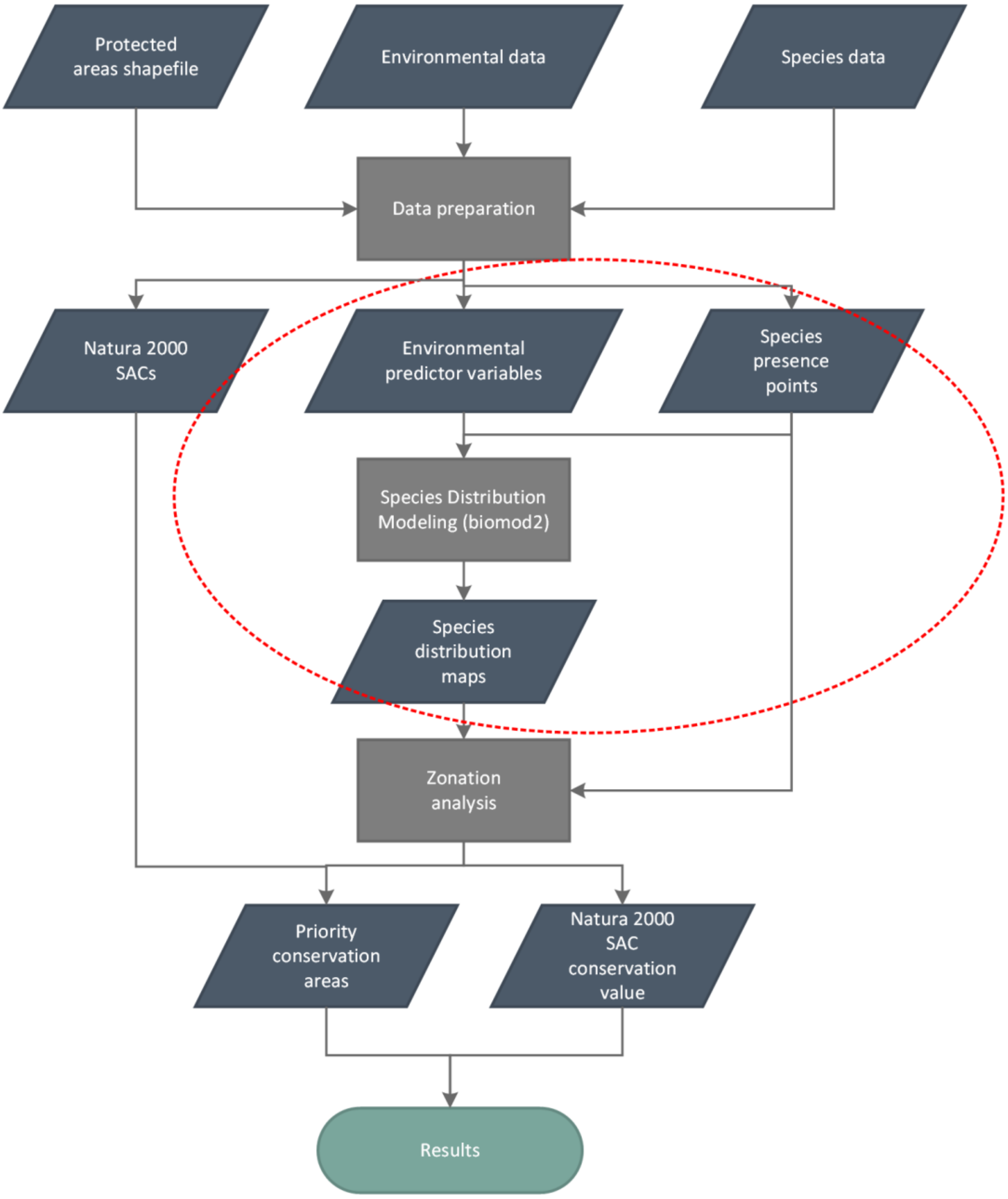


Figure 3: Methodology flow chart. Circled in red is the species distribution modelling method which is given in more detail in Figure 2.

2.1. Study area

Mediterranean Basin is one of the richest biodiversity areas in the world, and it has been recognized as one of the first 25 global biodiversity hotspots (Cuttelod, García, Malak, & Temple, 2008; Gaston et al., 2008; Myers, Mittermeier, Mittermeier, da Fonseca, & Kent, 2000). Indeed, Greece as a part of Mediterranean region is a biodiversity hotspot (Kostas Papageorgiou & Vogiatzakis, 2006), with its 6 600 taxa of vascular plants and 23 130 animal taxa, out of which 19% and 17% of the taxa are endemic, respectively (Vokou et al., 2014).

With an area of 8 336 km², Crete is the largest Greek island (Figure 4). It is located in southern part of the Aegean Sea. It has an elongated shape, and is 260 km long in east-west direction, and its maximum width is 60 km. Crete has rugged topography, with more than 50 peaks above 2000 m above sea level (Lymberakis & Poulakakis, 2010). It has three distinct mountain ranges crossing from east to west. Two climatic zones characterize Crete, the Mediterranean and the North African climate zone. However, most of the island area is characterized by Mediterranean climate, while southern coast falls in the North African climatic zone. In biogeographical terms, Crete has floral and faunal elements from three continents, which resulted in high species richness and endemism (Lymberakis & Poulakakis, 2010).

In Greece there are currently 359 Natura 2000 network sites; 151 SPAs and 239 SACs, while 31 sites fell in both categories (Kostas Papageorgiou & Vogiatzakis, 2006). Highest number of Natura 2000 sites in Greece can be found in South Aegean and Crete (Kostas Papageorgiou & Vogiatzakis, 2006). These high numbers in this case reflect the biogeographical and ecological importance of those areas (Kostas Papageorgiou & Vogiatzakis, 2006). Crete has one National park, one aesthetic forest site, five protected natural monuments and 55 Natura 2000 sites (Figure 4) (Kostas Papageorgiou & Vogiatzakis, 2006) .

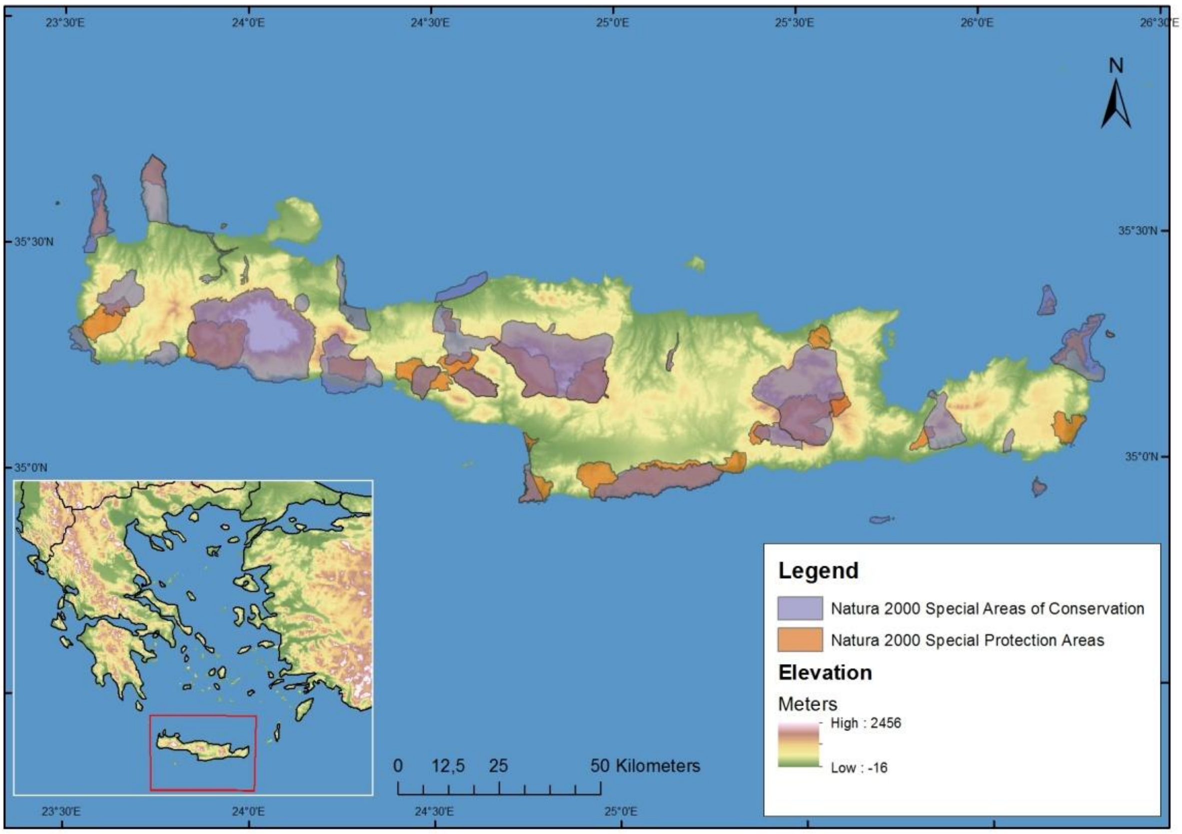


Figure 4: Map of Crete with Natura 2000 network sites.

2.2. Field work

Field work was carried out between September 22nd and October 19th. Field work involved collecting species presence points. Specific regions of Crete were under-sampled in the database provided by the Natural History Museum of Crete University, namely east part of Crete, and the western stretch of the coast of Crete, and mountain massifs in central and west Crete. Lack of proper road network and inaccessibility made sampling in the massif region not possible in this time-frame. Very few records exist for the east part of the island, and particular weight was given to sampling in that area. However, out of seven days of field work spent there, for four days not a single species was recorded. This was most likely due to inadequate weather conditions and sampling during the late part of the season. Livestock fences are very common element of Cretan landscape. They are usually set up along the roads and in the pastures. For this reason, many locations are inaccessible, which made moving freely difficult and restricted our sampling methodology. Therefore, sampling strategy used was purposive sampling. Only species that could be identified with certainty were recorded, and GPS coordinates were recorded for the location, as well as the time of the day, temperature, number of individuals and habitat characteristics. We recorded in total 97 points for 9 species (Table 1) of Cretan herpetofauna.

Table 1: Number of recorded presence points during the field work for every species.

Species name	Number of recorded points
Bufotes viridis	6
Pelophylax cretensis	1
Mauremys rivulata	1
Hemidactylus turcicus	5
Tarentola mauritanica	1
Lacerta trilineata	21
Podarcis cretensis	29
Chalcides ocellatus	28
Hierophis gemonensis	5

2.3. Target species

Cretan herpetofauna consists of 18 species (Spaneli & Lymberakis, 2014; Valakos et al., 2008); four amphibian species, and 14 species of reptiles. Out of 17 species, American Bullfrog *Rana catesbeiana* Shaw, 1802, is non-native and has been introduced locally (Valakos et al., 2008) in lake Agia in north-west part of Crete. It is considered as threat since it will outcompete native species of frogs (Valakos et al., 2008). *Ablepharus kitaibelii* Bibron & Bory, 1833 lives only on small islet Mikronisi off the coast of Crete (Valakos et al., 2008). Stable population of the rough-tailed agama, *Stellagama stellio* (Linnaeus, 1758) was recently observed in a small locality near the town of Sitia (Spaneli & Lymberakis, 2014). Most plausible hypothesis is that this population is in fact alien species introduced to Crete (Spaneli & Lymberakis, 2014). Although it is not mentioned in Valakos et al. (2008), the red-eared terrapin *Trachemys scripta-elegans* (Wied-Neuwied, 1839) was introduced to Crete (Lymberakis & Poulakakis, 2010), and it was observed by the author during field work in several lakes and ponds. It is popular in the pet trade, and it is common that when it grows too large, people that had it as a pet release it into the wild where it will often act as an invasive species (Invasive Species Specalist Group ISSG 2015, 2015). Since these 4 species either occur in very restricted localities where they have been introduced (*Rana catesbeiana*, *Trachemys scripta-elegans* and likely *Stellagama stellio*), or they have extremely narrow range which is also off the mainland Crete area (*Ablepharus kitaibelli*), they were not included into further analyses. It is worth noting that the Mediterranean chameleon *Chamaeleo chamaeleon* (Linnaeus, 1758) used to live in Crete, however there are no recent records, and is considered extinct locally (Valakos et al., 2008).

Ultimately, we have analyzed 15 species of Cretan herpetofauna. In Table 2 we have given taxonomic rank for each species, as well as its common name according to Valakos et al. (2008). More detailed description of the species is given in Appendix I, namely their taxonomy, habitat characteristics and conservation status.

Table 2: Taxonomic rank of analyzed species, along with their common names.

Class	Order	Family	Species name	Common name
Amphibia	Anura	Bufonidae	*Bufotes viridis* (Laurenti, 1768)	Green toad
		Hylidae	*Hyla arborea* (Linnaeus, 1758)	Common tree frog
		Ranidae	*Pelophylax cretensis* (Beerli, Hotz, Tunner, Heppich & Uzzell, 1994)	Cretan water frog
Reptilia	Testudines	Cheloniidae	*Caretta caretta* (Linnaeus, 1758)	Loggerhead turtle
		Geoemydidae	*Mauremys rivulata* (Valenciennes, 1833)	Balkan terrapin
	Squamata	Gekkoniadae	*Cyrtopodion kotschyi* (Steindachner, 1870)	Kotschy's gecko
			Hemidactylus turcicus (Linnaeus, 1758)	Turkish gecko
			Tarentola mauritanica (Linnaeus, 1758)	Moorish wall gecko
		Lacertidae	*Lacerta trilineata* Bedriaga, 1886	Balkan green lizard
			Podarcis cretensis (Wettstein, 1952)	Cretan wall lizard
		Scincidae	*Chalcides ocellatus* (Forskkål, 1775)	Ocellated skink
		Colubridae	*Hierophis gemonensis* (Laurenti, 1768)	Balkan whip snake
			Natrix tessellata (Laurenti, 1768)	Dice snake
			Telescopus fallax (Fleischmann, 1831)	European cat snake
			Zamenis situla (Linnaeus, 1758)	Leopard snake

For 14 species of Cretan herpetofauna we have used species distribution models in order to get the input data for Zonation analysis. Fifteenth species, *Caretta caretta,* is a species of marine turtle that nests in the beaches on Crete (Valakos et al., 2008). For *Caretta caretta* we have used data of nests and nesting beaches in order to get the species extent to use for Zonation analysis (Carvalho et al., 2010). Data was available for 357 nesting sites of *Caretta caretta*. Binary raster layer was created with the cell value of 1 where the species is present, and 0 for where it is absent. Extent of occurrence was made by creating 1km buffer around the 357 recorded nesting sites.

Several species of the herpetofauna of Crete that were included in the analysis are recognized as threatened on European (Table 3). Three species are included on the Annex II of the Habitats Directive: the loggerhead turtle *Caretta caretta*, the Balkan terrapin *Mauremys rivulata* and the leopard snake *Zamenis situla* (EC, 2007). Species listed on Annex II are the species whose conservation requires the designation of Natura 2000 Special Areas of Conservation (EC, 2007). Three species are also on the IUCN European Red List: the loggerhead sea turtle *Caretta caretta,* which is also included in the Annex II of Habitats Directive, Cretan water frog *Pelophylax cretensis,* and the Cretan wall lizard *Podarcis cretensis* (Cox & Temple, 2009; Temple, H. J., Cox, 2009). IUCN refers to the species that are listed under the categories of critically endangered (CR), endangered (EN) and vulnerable (VU) as threatened species (Cox & Temple, 2009; Temple, H. J., Cox, 2009). Furthermore, Greek national law recognizes most of the species that were analyzed as protected (Valakos et al., 2008).

Table 3: Conservation status of the target species.

Species	Greek National Law	Habitats Directive Annexes	European IUCN Red List status
Bufotes viridis	✓	IV[1]	LC
Hyla arborea	✓	IV	LC
Pelophylax cretensis	✗	-	EN
Caretta caretta	✓	II/IV	VU
Mauremys rivulata	✓	II/IV[2]	LC
Cyrtopodion kotschyi	✓	IV	LC
Hemidactylus turcicus	✓	-	LC
Tarentola mauritanica	✓	-	LC
Lacerta trilineata	✓	IV	LC
Podarcis cretensis	✓[3]	IV[3]	EN
Chalcides ocellatus	✓	IV	LC
Hierophis gemonensis	✓	-	LC
Natrix tessellata	✓	IV	LC
Telescopus fallax	✓	IV	LC
Zamenis situla	✓	II/IV[4]	LC

[1] As *Bufo viridis*
[2] As a part of *Mauremys caspica*
[3] As a part of *Podarcis erhardii*
[4] As *Elaphe situla*

2.4. Data preprocessing

2.4.1. Species presence data

Species presence data was provided by Natural History Museum of Crete University (NHMC), and additional presence data was collected during the fieldwork. Database provided by NHMC contained 4050 presence points. Species presence points had varying degree of spatial accuracy: 20 m to 100 m, 100 m to 300 m, 300 m to 1 km, and 1 km to 5 km. For our analysis we only used presence points that had spatial accuracy lower than 1 km. Presence points for several species were removed, such as for species that were introduced to Crete in particular locations (such as *Rana catesbeiana* Shaw, 1802 and *Trachemys scripta-elegans* (Wied-Neuwied, 1839), or for *Chamaeleo chameleon* (Linnaeus, 1758), that is most likely extinct in Crete (Valakos et al., 2008). In total, 815 presence points that were removed. All data was reprojected to WGS84 UTM zone 35N reference system and merged.

One of the general assumptions of distribution modelling is that the entire study area has been properly sampled, however in majority of cases presence data is spatially biased towards areas that are accessible (such us areas near major roads and towns) or better surveyed (Kramer-Schadt et al., 2013). This sampling bias can increase spatial auto-correlation and over-fitting of models (Boria, Olson, Goodman, & Anderson, 2014), and environmental bias manifested in over-representation of particular environmental features (Kramer-Schadt et al., 2013). The effect of sampling bias can be reduced by removing presence records in regions that have been oversampled by using spatial filtering (Kramer-Schadt et al., 2013).

In order to remove the spatial bias, presence data was filtered by proximity using a custom function (Pascal, 2014) in R (R Core Team, 2015). If within the set distance threshold multiple presence points exist, presence points would be removed randomly until there is a single presence point remaining within the set range. For the range we chose a threshold of 1 km, which is equal to spatial resolution of the coarsest environmental variable is 1 km. When the proximity filtering was performed, 2 284 points were removed, leaving 951 presence points of 14 species for the modelling process.

2.4.2. Environmental predictor variables

Species distribution models are based on environmental factors that control the distribution of species and their relations to the presence data of the species (Guisan & Zimmermann, 2000). Environmental predictor variables for species distribution modelling should therefore be chosen based on the knowledge of ecological processes that influence distribution of modelled species. We have used available literature to identify commonly used variables for modelling the distribution of amphibians and reptiles. Summary of environmental variables used for the process of species distribution modelling is given in Table 4. As biomod2 requires that all environmental variables have same extent and cell size, we have resample all variables down to the cell size of the variable with the finest spatial resolution (ASTER DEM – 30 meter) All environmental variables were reprojected to WGS84 UTM zone 35N reference system.

Climate variables

We used a subset of the freely available BIOCLIM variables to describe climatic characteristics of the habitats. BIOCLIM variables are derived from the monthly values of temperature and rainfall in order to derive ecologically meaningful variables (Hijmans, Cameron, Parra, Jones, & Jarvis, 2005). They represent extreme or limiting factors, seasonality, or annual trends. BIOCLIM variables are created by interpolating ground weather station data (Hijmans et al., 2005). The spatial resolution is 30 arc-seconds (~1 km). Unfortunately, BIOCLIM grids have a data gap in southern part of Crete. In order to fill the data gaps we used inverse distance weighted (IDW) interpolation technique which is incorporated in ArcGIS 10.3. Inverse distance weighting has adjustable parameter of the distance exponent, which determines the importance of surrounding points on the interpolated value, and the number of sample points used for the interpolation can be selected. For the distance exponent we used the value of 2, and 5 nearest points were used to perform the interpolation.

Topographical variables

Advanced Space-borne Thermal Emission and Reflection Radiometer (ASTER) Digital Elevation Model (DEM) was used as elevation serves as a proxy for important variables such as temperature and precipitation that influence the distribution of amphibians and reptiles, and it was also used to derive other topographical variables. ASTER has spatial resolution of 30 m and as a layer with finest spatial resolution out of all environmental variables; it was used to resample all other environmental variables to this resolution. Aspect was derived from ASTER DEM. Aspect is an important factor in the life cycle of amphibians and reptiles, as it influences the amount of energy the area is receiving. Aspect is a circular variable (0-360°), and as such, high values can be very close to low values (359° and 1° for example). For this reason, measures of northness and eastness were derived from aspect by calculating cosine and sine respectively. Northness and eastness have a range of values from -1 to 1. For northness, northward aspects will have value of 1, and southward aspects will have value of -1, while for eastness, eastward aspect will have value of 1, and westward aspect will have value of -1.

As ectothermic animals, amphibians and reptiles are reliant on external sources of heat to regulate their body temperature (Vitt & Caldwell, 2013). Reptiles especially regulate their body temperature by basking in the sun. Solar radiation can be calculated in GIS software, where the algorithm accounts for latitude, elevation, slope, shadows and seasonal shifts of the sun angle. Data on direct incoming solar radiation was generated from ASTER DEM using ESRI ArcGIS 10.3 Area Solar Radiation tool. Time period for calculating incoming solar radiation was from April 1st – September 31st, which we considered as season in which the animals are the most active on Crete. The output raster for direct incoming solar radiation has units of watt hours per square meter.

NDVI variables

NDVI (normalized difference vegetation index data) is commonly used to describe vegetation characteristics, quantify productivity and above-ground biomass of the ecosystem, and it has been used successfully to predict the distribution of amphibians and reptiles (Leyequien et al., 2007; Taheri, 2010). We used SPOT-Vegetation S10 NDVI data to create NDVI environmental variables (VITO NV, 2016). VGT S10 data are maximum value composite 10-day syntheses products, meaning that single image represents maximum NDVI value with temporal resolution of 10 days and spatial resolution of 1x1 km^2 (Bie et al., 2016). By taking the average pixel values for imagery captured in specific months, two NDVI predictor variables were created; mean NVDI value for April 2013, and mean NDVI value for September 2013. We considered these months as start and end of most active season for amphibians and reptiles on Crete.

Other variables

Distribution of amphibian and reptile species is often influenced by factors such as presence of water, and also by factors such as anthropogenic pressure and impact (Vitt & Caldwell, 2013). Distance layers are often used in species distribution modelling as they can capture the dependency of the species on these factors (Gibson, Wilson, Cahill, & Hill, 2004; Niamir, Skidmore, Toxopeus, Muñoz, & Real, 2011; Use et al., 2014).

Two distance variables were generated by using ESRI ArcGIS 10.3 Euclidian distance tool. Pixel value in generated layers corresponds to a distance in meters from a feature. Distance variables calculated were distance from rivers and distance from built-up areas. Shapefile obtained from the ITC database was used to generate distance from rivers raster variable. Distance from built-up areas layer was generated from two merged data sources; (i) shapefile with road network obtained from the ITC database from which we have selected only highway roads and primary roads, and (ii) urban morphological zone dataset obtained from EEA (European Environment Agency) which includes major urban areas on Crete. We also included human footprint index data which contains the information on the anthropogenic impacts on the environment (WCS & University, 2005). The human footprint index is created from 9 global data layers that include population density, land use and infrastructure, and human access (WCS & University, 2005).

Table 4: Environmental variables used for the SDM process.

Environmental variable	**Spatial resolution – original**	**Data source**
Climate data		
Annual mean temperature	1000 m	WorldClim
Annual precipitation	1000 m	WorldClim
Isothermality (Mean diurnal range/annual range * 100)	1000 m	WorldClim
Maximum temperature of the warmest month	1000 m	WorldClim
Minimum temperature of the coldest month	1000 m	WorldClim
Mean temperature of the coldest quarter	1000 m	WorldClim
Mean temperature of the warmest quarter	1000 m	WorldClim
Precipitation of the driest month	1000 m	WorldClim
Precipitation of the wettest month	1000 m	WorldClim
Precipitation of the driest quarter	1000 m	WorldClim
Precipitation of the wettest quarter	1000 m	WorldClim
Temperature seasonality (standard deviation * 100)	1000 m	WorldClim
Topographic		
Elevation (DEM)	30 m	ASTER GDEM
Eastness	30 m	ASTER GDEM
Northness	30 m	ASTER GDEM
Direct incoming solar radiation	30 m	ASTER GDEM
Vegetation		
NDVI April	1000 m	SPOT VGT
NDVI September	1000 m	SPOT VGT
Other variables		
Distance to rivers	30 m	ITC database
Distance to built-up areas	30 m	ITC database and EEA
Human footprint index	1000 m	SEDAC

2.5. Species distribution modelling methods

2.5.1. Modelling methods

In order to get the information on the distribution of species from the presence data, we have used species distribution modelling package "biomod2" (Thuiller, Georges, Engler, & Breiner, 2015) implemented within the environment for statistical computing R (R Core Team, 2015). To deal with the issue of selecting the appropriate modelling technique, we have ran models using 6 different techniques, and used the technique that yielded the best results for producing the final distribution models. In general, the process consisted of running all modelling techniques on all species, choosing appropriate pseudo-absence generation strategy, choosing the best performing modelling technique, and removing the low-performing variables.

Modelling methods we used were two regression-based techniques: GLM (Generalised Linear Models) and MARS (Multivariate Adaptive Regression Splines), and 4 machine-learning techniques: GBM (Generalized Boosting Models, also known as Boosted Regression Trees (BRT)), CTA (Classification Tree Analysis), RF (Random Forests) and MAXENT (MAXimum ENTropy modelling) (Thuiller, Lafourcade, & Araujo, 2010). Default settings of biomod2 (version 3.3-6) were used for every modelling technique.

- GLM (Generalized Linear Models): GLMs establishes the relationship between species occurrences and the environmental variables by fitting a linear, quadratic or cubic term (Guisan, Edwards, & Hastie, 2002). GLM runs a stepwise procedure which removes the redundant variables by using the AIC or BIC criteria (Thuiller et al., 2010).
- GBM (Generalized Boosted Models): GBMs combine two methods: regression trees and boosting (J. Elith, Leathwick, & Hastie, 2008). Regression trees establish a relationship between species occurrence variable and environmental predictor by recursive binary splits. Boosting is an adaptive method for combining multiple simple models in order to give improved predictive performance.
- CTA (Classification Tree Analysis): This method is based on building a recursive partitions within the environmental variables (Thuiller et al., 2010). The recursive partitions are groups that are as homogeneous as possible in the term of species response. The "tree" is built by splitting the data into groups, and the actual algorithm seeks to decrease variance within the subset as much as possible.
- RF (Random Forest): Random forest algorithm grows multiple classification trees, and each tree is grown with a randomized subset of predictors (Prasad, Iverson, & Liaw, 2006). Number of predictor variables that are used to find the optimal split of new trees is randomly chosen subset of the total number of predictor variables. The classification given by considering each tree as a 'vote', and the predicted class of an observation is determined by the majority vote among all trees (Naimi, Skidmore, Groen, & Hamm, 2011).
- MARS (Multivariate Adaptive Regression Splines): This method builds regression models by fitting separate splines to distinct intervals in the predictor variables (Prasad et al., 2006). Breakpoints between the intervals that define a change in model coefficient is called a spline knot (Thuiller et al., 2010). MARS will then in stepwise manner remove knots that have the smallest contribution to the overall fit (Prasad et al., 2006).
- MAXENT (Maximum Entropy): MAXENT is a machine-learning technique that uses the method of finding the probability distribution of maximum entropy (most spread out or closest to uniform distribution). It will estimate probability distribution of the target species by setting constraints that represent our incomplete information about the species' distribution (S. J. Phillips, Anderson, & Schapire, 2006).

2.5.2. Pseudo-absence selection

Absence records were not available for the study extent, and pseudo-absences (PA's) have to be generated when no absence records are available (Barbet-Massin, Jiguet, Albert, & Thuiller, 2012). Biomod2 package has three methods of generating PA's (Thuiller et al., 2015): (i) randomly generating PA's in all the cells of initial background given the number of PA's ("random"), (ii) generating PA's randomly within defined minimum and maximum distance from the presence points ("disk"), (iii) generating PA's randomly outside of the broadly area of defined environmental conditions of the modelled species, defined by the surface range presence only model ("sre"). Besides the PA generation method, the number of PA points and the number of runs in which PA's are generated is important when it comes to model performance (Barbet-Massin et al., 2012). We have used recommended parameters according to Barbet-Massin et al. (2012), where they have shown that models created with of 10 runs randomly generated 1000 PA's perform well, as well as models created with the disk strategy. We have also explored the effect of prevalence (proportion of presences in regards to absences), which was shown as influential on modelling results (Barbet-Massin et al., 2012). We used equal prevalence of 50%, and created pseudo-absences where we have created twice as many PA's as presences for each species. In order to select the optimal method of generating and determining the number of PA's across multiple techniques, we ran the models with four different strategies: (i) random PA generation, 1000 PA's (1k), (ii) random PA generation, twice as many PA's as presences (2x – equal prevalence), (iii) disk PA generation, 1000 PA's (1k), (iv) disk PA generation, twice as many PA's as presences (2x – equal prevalence). For the distance threshold of disk method we used 5 km, meaning the PA's would be generated in area that is outside of 5 km buffer Performance of the models in regards to different PA generation methods was assessed with kappa value, TSS and AUC measures, that are explained in more detail in the section 2.5.4. 10. We ran 100 model repetitions for all species with all 6 modelling techniques, and the pseudo-absence generation strategy that performed the best was used afterwards.

2.5.3. Multicollinearity analysis

When two or more predictor variables are correlated in regression models, then the data are said to be affected by multi(collinearity) (Quinn & Keough, 2002). Multicollinearity is common in ecological datasets and it can be an issue for parameter estimation since it inflates the regression parameter variance (Dormann et al., 2013), and it can inflate the variable importance of highly correlated variables (Baldwin, 2009). Often in ecological data, variables are collinear since they are different manifestations of the same underlying process, which is immeasurable in some cases (Dormann et al., 2013). Multicollinearity of predictor variables used for species distribution models can lead to over-fitting of models and issues with identifying relevant predictor variables. Common method of detecting multicollinearity is using the variance inflation factor (VIF) (Quinn & Keough, 2002). VIF gives us the extent to which every variable is collinear to other variables in the dataset. However, thresholds of VIF values where multicollinearity starts affecting environmental variables are often arbitrarily determined.

Thresholds of VIF > 5, or VIF > 10, or even VIF > 20 have been suggested by different authors to identify highly collinear variables (Legendre & Legendre, 2012), or even thresholds as low as VIF > 2 or VIF > 3 (Zuur, Ieno, & Elphick, 2010). Most commonly used rule of thumb is that VIF values greater than 10 can be considered as signs of strong collinearity (Dormann et al., 2013).

Multicollinearity analyses were done using vif() and vifstep() functions from the R package "usdm" (Naimi, 2015). Function vif() gives us VIF values for stack of raster objects (in our case environmental variables), while vifstep() performs stepwise analysis and removes correlated variable with the highest VIF value higher than set threshold. Function vifstep() was run for thresholds of VIF > 20 and VIF > 10.

2.5.4. Model evaluation

Species distribution models are usually validated using new or independent data, or by partitioning the data in two parts (two-fold cross-validation), where one part is used to calibrate the model, and the second part is used for validating the predictions (Franklin, 2010). Independent datasets are rarely used to validate the models, due to the lack of independent data and high cost of collecting new data. It is therefore common to use aforementioned two-fold cross-validation. In two-fold cross-validation the data used for calibrating the model is often called training data, while data set aside for validation is called testing data (Franklin, 2010). We used 80% of the data for model calibration, and remaining 20% were used to validate the models. The calibration and validation process was repeated 10 times for every model run.

Evaluating the performance of models is an important step of model-building and evaluating process (Barry & Elith, 2006; Liu, White, & Newell, 2009). Performance metrics of SDM can give us information on what is the model's discrimination ability and what is the reliability of the model (Liu et al., 2009). We have used three commonly used performance metrics: (i) Cohen's kappa index of agreement, (ii) true skill statistics (TSS), often referred to as the Youden index (Liu et al., 2009), and (iii) area under the curve of the receiver operating characteristic curve (AUC of the ROC) (Liu et al., 2009).

Continuous output from the models needs to be transformed into binary presence-absence output by using a specific threshold in order to create confusion matrix to calculate values of kappa and TSS (Anderson, Lew, & Townsend-Peterson, 2003). For this reason performance metrics can be divided into threshold-dependent and threshold-independent metrics (Franklin, 2010). For threshold-dependent accuracy measures, biomod2 uses threshold maximization, where it will set the threshold for binary transformation which returns the highest value of kappa or TSS. All performance assessment measures were done by using the get_evaluations() function implemented within biomod2 package.

From threshold-dependent performance measures we used Cohen's kappa coefficient (kappa) and true skill statistics (TSS) (Allouche, Tsoar, & Kadmon, 2006; Franklin, 2010; Liu et al., 2009). Kappa gives us the agreement between modelled predictions and observations, corrected for the agreement expected to occur by chance (McPherson, Jetz, & Rogers, 2004). Values of kappa range from -1 to +1, where +1 indicates perfect agreement, while zero value indicates performance no better than chance (Cohen, 1960).

TSS is defined as Sensitivity + Specificity – 1, where sensitivity is proportion of true presences that are being predicted as presences, and specificity is proportion of true absences that are being predicted as absences (Allouche et al., 2006). TSS is not affected by prevalence, nor is it affected by the validation set size (Allouche et al., 2006). Values of TSS range from -1 to +1, where +1 indicates perfect agreement, while zero values or lower indicate performance no better than random (Allouche et al., 2006).

Receiver operating curves are generated by plotting sensitivity against the corresponding proportion of false positives (1 – specificity) (Allouche et al., 2006). Since all possible thresholds are used to plot the curve, ROC is considered as independent from threshold. In SDM literature, AUC (area under the receiver operating curve) is used more often as a performance metric. AUC values can be interpreted as the discrimination ability of the model (Lobo, Jiménez-Valverde, & Real, 2008; A. T. Peterson, Papeş, & Soberón, 2008). In other words, in models with high AUC value areas with high predicted suitability values are areas with known presences (Hijmans & Elith, 2013). However, this means that AUC value cannot be used to measure accuracy of the model, since it is possible that poorly fitted model has a good discrimination power (Lobo et al., 2008). AUC values range from 0 to 1, and values lower than 0.5 indicate that the model discriminates against presences and absences worse than chance.

Performance evaluation metrics were used to select the most optimum modelling technique for our study area and study organisms. We have selected the modelling technique according to the mean values of performance metrics and standard deviation. Furthermore, after the best modelling technique was selected, we have analyzed model's performance for every species. All measures were generated by using the get_evaluations() function implemented within the biomod2 package.

2.5.5. Variable importance

In order to select a specific set of environmental variables for every single species used for modelling, we used measure of variable importance to eliminate variables that were not important. R package biomod2 has implemented function variables_importance() with which the importance of variables can be calculated. Principle that this function uses is that one of the environmental variables is being randomized and a new prediction is made, then correlation is being calculated between the standard models and the new prediction with the randomized variable (Thuiller et al., 2010). Value that is returned for variable importance is 1-correlation. The higher the variable importance value is, the more influence the variable will have on the model (Thuiller et al., 2015). Value of 0 assumes no influence of variable to the model.

In our case, we ran distribution models for 14 species. Species that we have analyzed have more or less similar ecological requirements (Vitt & Caldwell, 2013). However, assessment of protected areas is often performed on a large number of species that may have very different ecology, and choosing environmental variables according to the ecological needs of every species is often not practical when several hundreds of species are analyzed (Abellán & Sánchez-Fernández, 2015; Fajardo et al., 2014; Maiorano, Falcucci, & Boitani, 2006; Tantipisanuh, Savini, Cutter, & Gale, 2016). Therefore, we have examined the impact of removing low performing variables from a larger set of more general variables. We ran the best performing model for all species with environmental variable dataset that remained after the multicollinearity analysis. Variables that had consistent low importance for analyzed species were eliminated, and separate set of environmental variables was created for each species. In order to identify which variables have low importance for modelled species, we have looked which variables appear as outliers with 90% confidence interval. Variables that were identified as outliers in the low range (variables with low contribution to the model) were eliminated, and the models were re-run. We compared the results of two runs by using TSS and AUC performance metrics.

2.6. Zonation analysis

To identify areas important for the conservation of amphibians and reptiles, we have used Zonation version 4.0.0 (Moilanen, 2007; Moilanen, Pouzols, Meller, Veach, Arponen, Leppanenm, et al., 2014). Zonation develops conservation priority ranking for the whole landscape (Lehtomäki & Moilanen, 2013). It assumes that protecting the full landscape is the optimal solution. Then, it will iteratively rank cells, and remove at each step the cell that will lead to the smallest marginal loss of biodiversity (Lehtomäki & Moilanen, 2013; Moilanen, 2007; Moilanen, Pouzols, Meller, Veach, Arponen, Leppänen, et al., 2014). This iterative process is called the Zonation meta-algorithm, and it will result in ranked output of removed cells, with cells that were ranked as the least valuable receiving value of 0, and most valuable of 1 (Lehtomäki & Moilanen, 2013). The values can be interpreted as the value of conservational potential, or conservation value, where the higher pixel value means that the cell has higher conservation value (Moilanen, Pouzols, Meller, Veach, Arponen, Leppanenm, et al., 2014).

Raster grids of species distribution or other biodiversity features are used as input data for Zonation. Biodiversity features can include distribution of individual features, such as observed or predicted occurrences, abundance values or other suitability measures, or it can include features such as distribution of community types (Moilanen, Pouzols, Meller, Veach, Arponen, Leppanenm, et al., 2014). Zonation workflow in general can be separated into two parts; the Zonation meta-algorithm and the way that marginal loss is defined (i.e. cell-removal rule). The Zonation meta-algorithm (Moilanen, 2007):

1. Start from the full landscape, where the rank is $r = 1$.
2. Marginal loss is calculated after the removal of each remaining site i, δ_i.
3. The cell with the smallest δ_i is removed. Removal rank of i is defined as r. Set $r = r + 1$, and return to step 2 until there are no cells remaining in the landscape.

There are several ways in which the marginal loss can be defined (cell-removal rule). Different definitions of the cell-removal rule enable emphasizing various conservation value concepts. Some prioritize species richness (such as in the case of the additive benefit function, ABF), while others give priority to the rare species (core-area Zonation, CAZ), and also random cell-removal rule removes the cells in a random order (Lehtomäki & Moilanen, 2013; Moilanen, 2007). We have used the additive benefit function that takes into account all features in the cell instead of one feature with the highest value such as CAZ (Moilanen, Pouzols, Meller, Veach, Arponen, Leppanenm, et al., 2014). We have also used the random cell-removal rule in order to have null-control state.

In the case of ABF, the marginal loss (δ_i) value of the particular cell is the sum over feature-specific declines after the cell i is removed (Moilanen, Pouzols, Meller, Veach, Arponen, Leppanenm, et al., 2014):

$$\delta_i = \frac{1}{c_i}\omega_j \sum_j \Delta V_j = \sum_j \left[V_j\left(q_j\right) - V_j\left(q_j - i\right)\right], \qquad \text{Equation 1}$$

where q_j is the probability of occurrence of species j contained within the remaining set of sites, and (q_j-i) indicates set of remaining cells minus the cell i (Moilanen, 2007). Term ω_j is the weight of the species j, and it can be set manually in order to give higher or lower priority to a specific species.Term c_i is the cost of planning unit i. Cost layers are optional, and can be added to force inclusion or exclusion of specific areas, such as important agricultural areas, or current protected areas. After the cell i gets removed, representation of all species (ΔR_j) that were in removed cell will decrease. According to the additive benefit function (Figure 5), representation value will decrease by ΔV_j (Moilanen, Pouzols, Meller, Veach, Arponen, Leppanenm, et al., 2014).

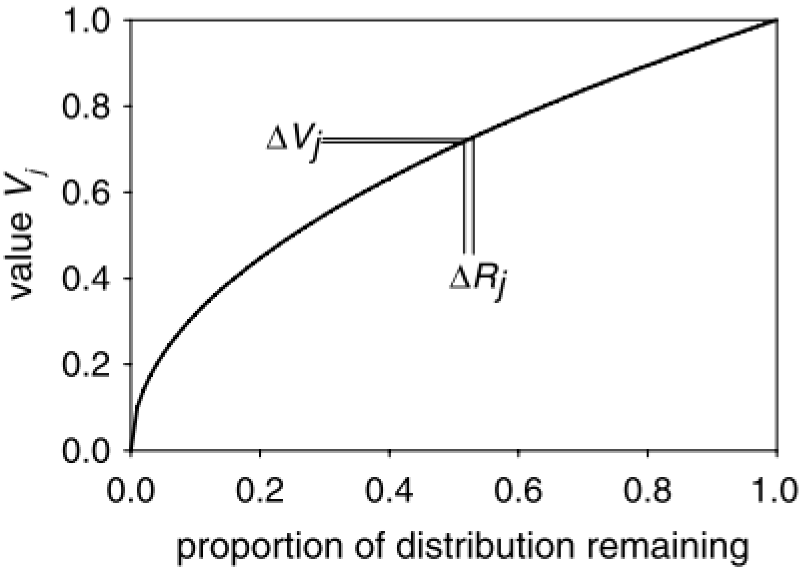


Figure 5: Additive benefit function in Zonation (Reprinted from Moilanen (2007)).

2.7. Gap analysis

In order to evaluate how well the current network of Natura 2000 Special Areas of Conservation does accomplish its proposed goals, we have performed species-focused gap analysis for their priority conservation areas and site-focused gap analysis (Fajardo et al., 2014; Groves et al., 2002).

2.7.1. Gap analysis for priority areas for conservation

Output of Zonation's process is hierarchically ranked order of removed cells. In other words, cells with low conservation value get removed sooner than cell with high conservation value. Cell with the lowest conservation value will get the value in the output of 0, while the cell with highest conservation value will get the value of 1. Natura 2000 SAC shapefile clipped to the study extent covers of its 27.5% area. Therefore we used the same area coverage and identified top 27.5% of most valuable cells in the Zonation output. In this way we were able to compare most important areas the herpetofauna of Crete with Natura 2000 Special Areas of Conservation. The highest ranked 27.5% cells of the Zonation output we are referring to as priority conservation areas.

Priority conservation areas were identified for three scenarios: (i) all species, (ii) only species included on Annex II of the Habitats Directive (EC, 2007), (iii) only species from European IUCN Red List threatened categories (Cox & Temple, 2009; Temple, H. J., Cox, 2009). Natura 2000 SAC sites should be designated to cover the extent of species included in Annex II of the Habitats Directive (EC, 2007). Different scenarios were created by using the Zonation feature weights option. Weights were set according to the Fiorella, Cameron, Sechrest, Winfree, & Kremen (2010) equal weighing scheme. For example, in the case of the Annex II scenario, species included to the Annex II of Habitats Directive were weighted by the factor of 1, while species not included on the list get the weight of 0. We have also used Zonation's random cell removal rule, and identified top 27.5% of those cells in order to have null control run.

We analyzed the representativeness of the priority areas for conservation by Natura 2000 SAC sites in two ways: (i) by overlaying them with priority conservation areas and calculating the percentage of overlap, (ii) by calculating the level of agreement using Cohen's kappa coefficient (kappa) (Cohen, 1960). Kappa gives us the agreement between predictions and observations, corrected for the agreement expected to occur by chance (McPherson et al., 2004). Values of kappa range from -1 to +1, where +1 indicates perfect agreement, while zero value indicates performance no better than chance (Cohen, 1960). To calculate the kappa statistics, we reclassified priority area and Natura 2000 SAC raster layers into two categories: priority area or not priority area, and SAC site or not SAC site. Afterwards we have used GRASS 7.1 r.kappa tool to calculate to kappa statistics.

2.7.2. Gap analysis per Natura 2000 SAC site

We calculated zonal statistics for individual Natura 2000 SAC sites for the whole Zonation output of conservation value. All three scenarios were used to calculate zonal statistics. In this way we were able to compare individual Natura 2000 SAC sites in regards to their mean conservation value for different groups of Cretan herpetofauna. We have identified Natura 2000 SAC sites with the highest and the lowest mean conservation value for every scenario. Zonal statistics weas calculated using QGIS 2.12.

2.8. Web map

In order to have better overview of the Natura 2000 SAC sites and its conservation value, we have created online map using QGIS 2.12 and gis2web plugin. Attribute table of every site contains the link for the data forms of that particular site with detailed description of each site.

3. RESULTS

3.1. Multicollinearity analysis

VIF values were calculated for the whole set of environmental variables, and stepwise procedure was performed to remove the highly collinear variables based on set VIF thresholds. Results of the multicollinearity analyses are given in Table 5. Stepwise analysis of variables with VIF threshold set at VIF = 10, showed that 9 variables out of 21 input variables had collinearity issues. Stepwise removal procedure was repeated with higher threshold (VIF = 20), and 8 variables out of 21 input variables had collinearity problem. Common procedure with collinearity analysis is to automatically remove variables that have VIF values greater than arbitrarily set threshold (O'Brien, 2007). However, environmental variables should not be rejected *a priori* using only rule-of-thumb VIF thresholds, but underlying ecological processes should always be considered (Dormann et al., 2013; Zuur et al., 2010). Variables used for ecological analyses will be often correlated due to the interactions between the variables, and the true ecological effect on the distribution of the species is often difficult to isolate (Zuur et al., 2010).

Dormann et al. (2013) argued that if statistical analysis suggests removal of variables that has ecological relevance or importance, priority should be given to the ecological importance. Environmental variable for the precipitation of the driest month had value of VIF = 11.62 (Table 5). Nevertheless, this variable was kept for further analyses since it may be ecologically important for amphibian and reptilian species as a limiting factor, especially for the amphibian species (Cunningham, Rissler, Buckley, & Urban, 2015).

Table 5: Results of the multicollinearity analyses for VIF threshold set at VIF = 10 and VIF = 20. Highlighted with grey are the environmental variables that have been selected as predictors.

Variables	**VIF value**	**VIF of the remained variables (th = 10)**	**VIF of the remained variables (th = 20)**
Annual mean temperature	6180,50	-	-
Annual precipitation	1132,84	-	-
Built-up distance	1,99	2,03	1,90
ASTER DEM	34,37	-	-
Eastness	1,04	1,01	1,01
Human footprint index	1,57	1,54	1,54
Isothermality	17,90	5,76	7,63
Maximum temperature warmest month	779,71	4,78	8,31
Mean temperature coldest quarter	5603,54	-	-
Mean temperature warmest quarter	4275,08	-	-
Min temperature coldest month	3652,07	-	-
NDVI April	5,42	4,10	4,17
NDVI September	3,35	3,03	2,91
Northness	1,52	1,39	1,41
Precipitation driest month	36,92	-	11,62
Precipitation driest quarter	129,48	-	-
Precipitation wettest month	1097,68	-	-
Precipitation wettest quarter	548,48	4,33	4,36
Rivers distance	1,15	1,11	1,13
Solar radiation	1,61	1,57	1,59
Temperature seasonality	158,01	6,41	6,40

3.2. Pseudo-absence method selection

We have compared model performance evaluation metrics in regards to different pseudo-absence creation strategies. Results have showed that random method had systematically lower performance than disk pseudo-absence strategies. When different numbers of pseudo-absences are concerned, models with 1000 pseudo-absences had slightly higher TSS and AUC metrics compared to the equal prevalence models (twice as many pseudo-absences as presences). On the other hand, equal prevalence models had higher kappa values than models with 1000 PA's.

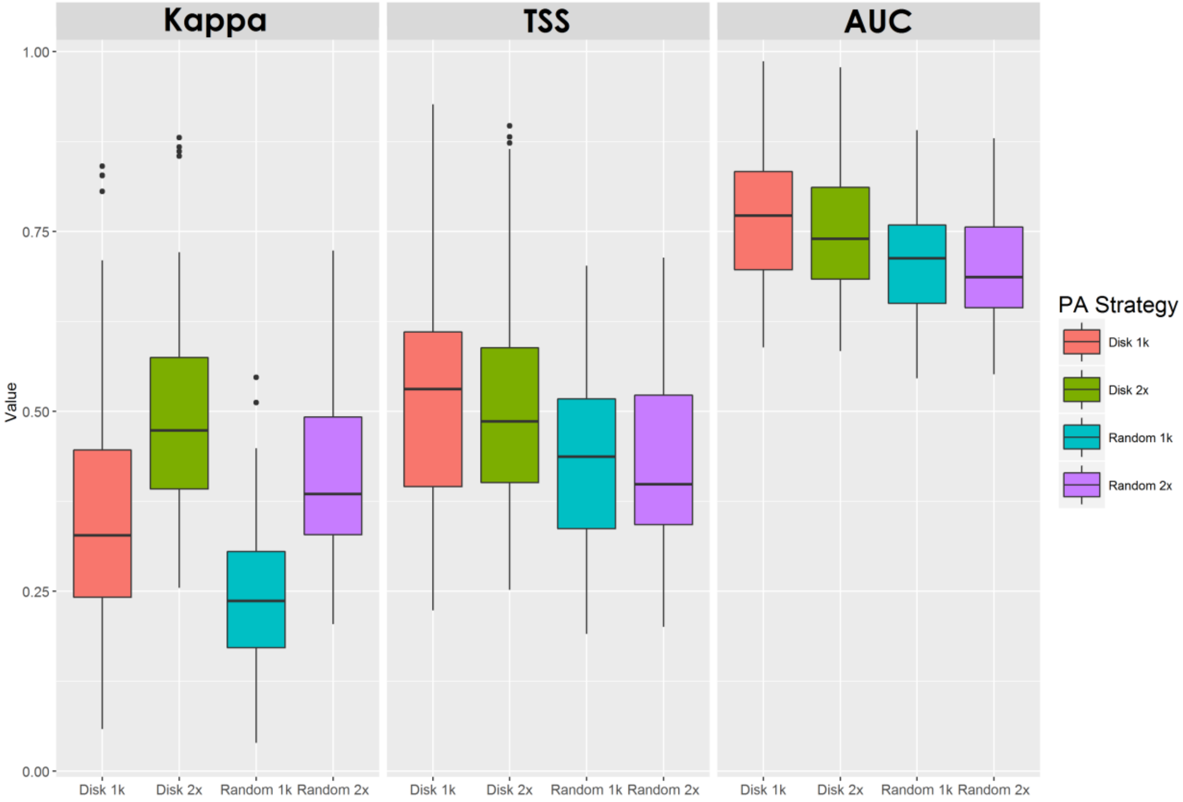


Figure 6: Evaluation metrics for 100 repetitions of all 6 modelling techniques for all species in regards to different pseudo-absence creation strategies and number of pseudo-absences. 1k = 1000 pseudo-absences, 2x = twice as many absences as presences.

As the analysis of evaluation metrics for number of generated PA's did not produce conclusive results, except higher kappa value for the equal prevalence strategy, we have analyzed effect of the dataset size (number of presences) to the value of TSS. The number of presences in our dataset ranged from 14 points for *Cyrtopodion kotschyi*, up to 202 points for *Lacerta trilineata*. Figure 7 shows the behaviour of TSS values in regards to the number of presence points for disk strategy with 1000 PA's and with twice as many PA's as presences. We have fitted a linear model to the data, and the values for the slope of linear fit that describe the behaviour of TSS are given in Table 6.

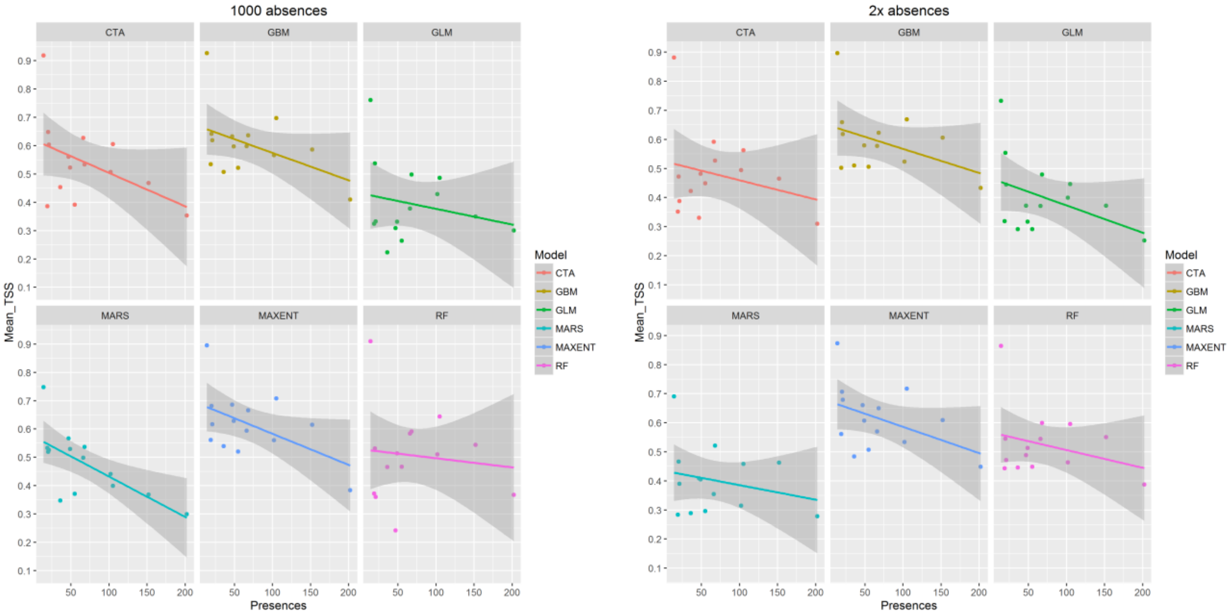


Figure 7: Scatterplots of TSS value plotted against the number of species presences. Left is given TSS value for models created with 1000 PA's, and right is given TSS value for models where we created twice as many pseudo-absences as presences. Each point represents mean TSS value for 100 repetitions of a model for a single species. Linear models were fitted, and the gray area around the line represents 95% confidence interval.

If the slope value of linear fit is 0, then the line will be plotted completely flat. Slope value of 0 can be interpreted that TSS value will remain constant if the number of presences increase, and larger negative slope values mean that TSS value will drop with increase in presence number. Value of slope determines amount of drop in TSS value when one presence point is added.

Random forest with 1000 PA's was the most stable technique in regards to prevalence with the slope value of -0.00032. On the other hand, MARS with 1000 PA's had the largest change in regards to prevalence with slope value of -0.00143. However, models that used twice as many pseudo-absences as presences (equal prevalence) had overall smaller change of TSS value, indicated by lower mean value of slope (Table 6). When it comes to 2x PA strategy, in this case MARS had the most stable results (slope = -0.0005), and GLM was the most sensitive technique (slope = -0.00094) in regards to the number of presences.

Table 6: Slope values for linear fit line from Figure 7 scatterplots. 1000 PA's = 1000 pseudo-absences; 2x PA's = twice as many pseudo-absences as presences.

Modelling technique	**1000 PA's**	**2x PA's**
GLM	-0,00055	-0,00094
GBM	-0,00097	-0,00083
CTA	-0,00118	-0,00066
RF	-0,00032	-0,00061
MARS	-0,00143	-0,00050
MAXENT	-0,00110	-0,00090
Mean	**-0,00093**	**-0,00074**

3.3. Modelling technique selection

Analysis of model performance metrics showed that with using the same datasets and settings, MAXENT and GBM were the modelling techniques with the highest TSS and AUC scores. Out of these two, MAXENT had slightly higher mean AUC and TSS values compared to GBM (Table 7). Furthermore, it has yielded the most robust models, measured by the low standard deviation of AUC and TSS values for 100 model replicates (Table 7), and by the height of the boxes plotted in the boxplot (Figure 8).

Table 7: Mean and standard deviation (St. Dev.) values of AUC and TSS for multiple modelling techniques, across all species. Best values are accentuated in bold (higher mean value and lower standard deviation value are better).

		GLM	**GBM**	**CTA**	**RF**	**MARS**	**MAXENT**
AUC	**Mean**	0.69	0.819	0.772	0.759	0.74	**0.83**
	St. Dev.	0.077	0.071	0.092	0.1	0.071	**0.069**
TSS	**Mean**	0.395	0.605	0.541	0.507	0.477	**0.618**
	St. Dev.	0.139	0.117	0.143	0.159	**0.116**	**0.116**
Kappa	**Mean**	0.228	0.428	0.344	0.352	0.356	**0.443**
	St. Dev.	0.161	0.186	0.17	0.181	**0.132**	0.171

MARS showed to have robust results as well when it comes to the standard deviation of TSS, and GBM had low standard deviation for AUC and TSS as well. On the other hand, GLM had the lowest mean (Table 7) and median (Figure 8) performance metrics out of all six modelling techniques. Although random forest and classification tree analysis had moderate values of mean AUC and TSS compared to the other techniques, their results were not as robust as other modelling techniques.

MAXENT was the only technique that had consistent high scores of evaluation metrics. Therefore, we chose MAXENT as the modelling technique to use for projecting the models in geographic space.

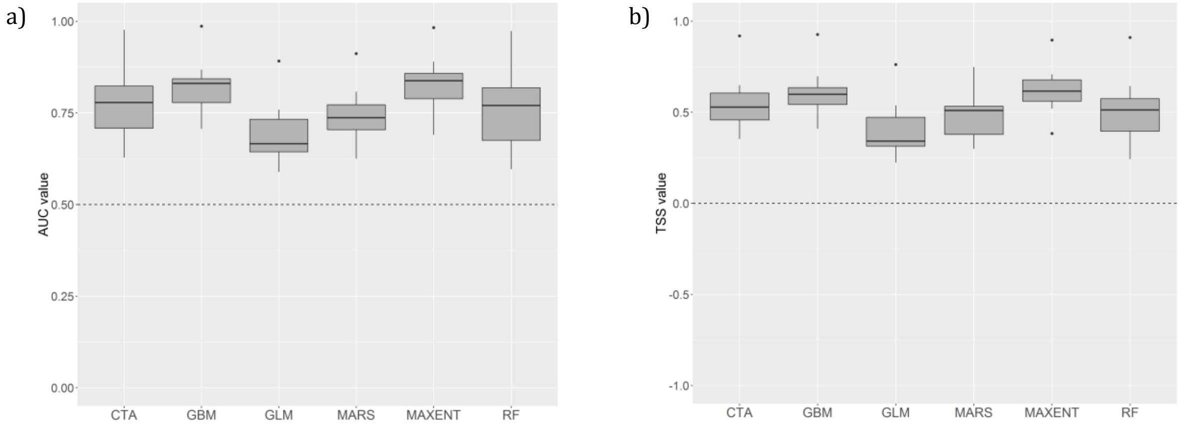


Figure 8: Boxplots of the AUC values (a) and TSS values (b) for each of 6 models across all species; the dashed line represents the threshold at which the model has performance not better than random.

3.4. Variable importance and variable selection

We used biomod2 variable importance function in order to identify level of contribution of environmental predictor variable. Detailed plots of variables importance for each species are given in Appendix II. Certain variables proved to have dominant predictive power, while the others contribution to the model was lower. Solar radiation level showed to have low predictive power, where we have found that for 8 out of 14 modelled species, it had the lowest ranking out of all variables. Only other variable that had the lowest value for multiple species (two species) was the precipitation of driest month.

On the other hand, precipitation of the wettest quarter was the most important variable for 4 species. Precipitation of the wettest quarter was most influential on the distribution of *Bufotes vidiris*, *Cyrtopodion kotschyi*, *Zamenis situla* and *Hierophis gemonensis*. High predictive power was also demonstrated with climatic temperature variables such as temperature seasonality (standard deviation of temperature * 100) and maximum temperature of warmest month. Both variables were the most important variables for 3 species each.

To create environmental variable dataset for each species, we have removed variables that were identified as lower limit outliers with 90% confidence interval in order to assess the effect of removing the low-performing variables. Variables that were removed were solar radiation, precipitation of the driest month and mean NDVI value for September. Solar radiation was an outlier for 4 species, and the precipitation of the driest month was an outlier for two species, while NDVI value for September was and outlier for one species.

We compared the differences in performance evaluation metrics for two runs of 100 MAXENT model repetitions (standard run and run with removed outliers). The results are given in Table 8 and the numbers represent the difference between two runs. For most of the species, evaluation metrics difference was not considerably different. The largest discrepancy between the two runs was for species *Bufotes viridis* and *Telescopus fallax*.

Table 8: Difference in evaluation metrics between the standard MAXENT run, and no outliers run. Light grey – 1 removed variable, dark grey – 2 removed variables, no highlight – no variables were removed. Positive number shows improvement in the performance metrics, while negative values mean that the metrics were lower in the second run.

Species name	**TSS difference**	**AUC difference**
Bufotes viridis	-0,07	-0,04
Chalcides ocellatus	0,00	0,00
Cyrtopodion kotschyi	0,00	-0,01
Hemidactylus turcicus	-0,03	-0,01
Hierophis gemonensis	0,02	0,01
Hyla arborea	0,01	0,00
Lacerta trilineata	0,01	0,01
Mauremys rivulata	0,00	0,00
Natrix tessellata	0,03	0,02
Pelophylax cretensis	0,00	0,00
Podarcis cretensis	0,02	0,01
Tarentola mauritanica	0,02	0,01
Telescopus fallax	0,06	0,04
Zamenis situla	0,01	-0,01

3.5. Model evaluation

In order to assess the performance of the models, we have used kappa, TSS and AUC of the ROC performance metrics. Mean values of kappa, TSS and AUC with the standard deviation are given in Table 9 for each species. The values were calculated from evaluation metrics of 100 repetitions of MAXENT model run with disk 2x PA strategy. Highest performance metrics were recorded for *Podarcis cretensis*: Performance metrics values were highest for all three measures for *Podarcis cretensis*, and also it had robust results of performance evaluation metrics, measured by low standard deviation. The lowest values overall were recorded for *Hierophis gemonensis*.

Table 9: Mean values of performance evaluation metrics with their standard deviations for 100 repetitions of MAXENT.

Species	**Kappa**	**TSS**	**AUC**
Bufotes viridis	0,32 ± 0,16	0,37 ± 0,21	0,71 ± 0,13
Hyla arborea	0,39 ± 0,11	0,53 ± 0,1	0,79 ± 0,07
Pelophylax cretensis	0,37 ± 0,11	0,5 ± 0,15	0,78 ± 0,09
Mauremys rivulata	0,34 ± 0,14	0,4 ± 0,2	0,7 ± 0,11
Cyrtopodion kotschyi	0,26 ± 0,14	0,57 ± 0,18	0,74 ± 0,13
Hemidactylus turcicus	0,31 ± 0,14	0,37 ± 0,18	0,68 ± 0,11
Tarentola mauritanica	0,42 ± 0,19	0,52 ± 0,24	0,76 ± 0,12
Lacerta trilineata	0,53 ± 0,07	0,54 ± 0,08	0,81 ± 0,05
Podarcis cretensis	0,71 ± 0,08	0,75 ± 0,09	0,91 ± 0,04
Chalcides ocellatus	0,34 ± 0,11	0,44 ± 0,14	0,73 ± 0,08
Hierophis gemonensis	0,25 ± 0,12	0,3 ± 0,14	0,62 ± 0,08
Natrix tessellata	0,31 ± 0,19	0,53 ± 0,24	0,74 ± 0,15
Telescopus fallax	0,24 ± 0,13	0,53 ± 0,19	0,73 ± 0,14
Zamenis situla	0,2 ± 0,13	0,35 ± 0,21	0,65 ± 0,12

3.6. Zonation output

Figure 9 shows the Zonation ranking of individual cells which is interpreted as the conservation value of the cell. Maps of the Zonation output are given for three scenarios, all species, Annex II species and Red List species (Figure 9). All three scenarios identified area around Iraklio as a priority conservation area. Some areas that are not within the Natura 2000 SAC network also appeared in all three scenarios, such as the Messara plain in the south part of Crete. Several areas had very low conservation value for the herpetofauna of Crete. Region north of Keratokampos had low conservation value for all three scenarios, and the same case was for the eastern region of Crete.

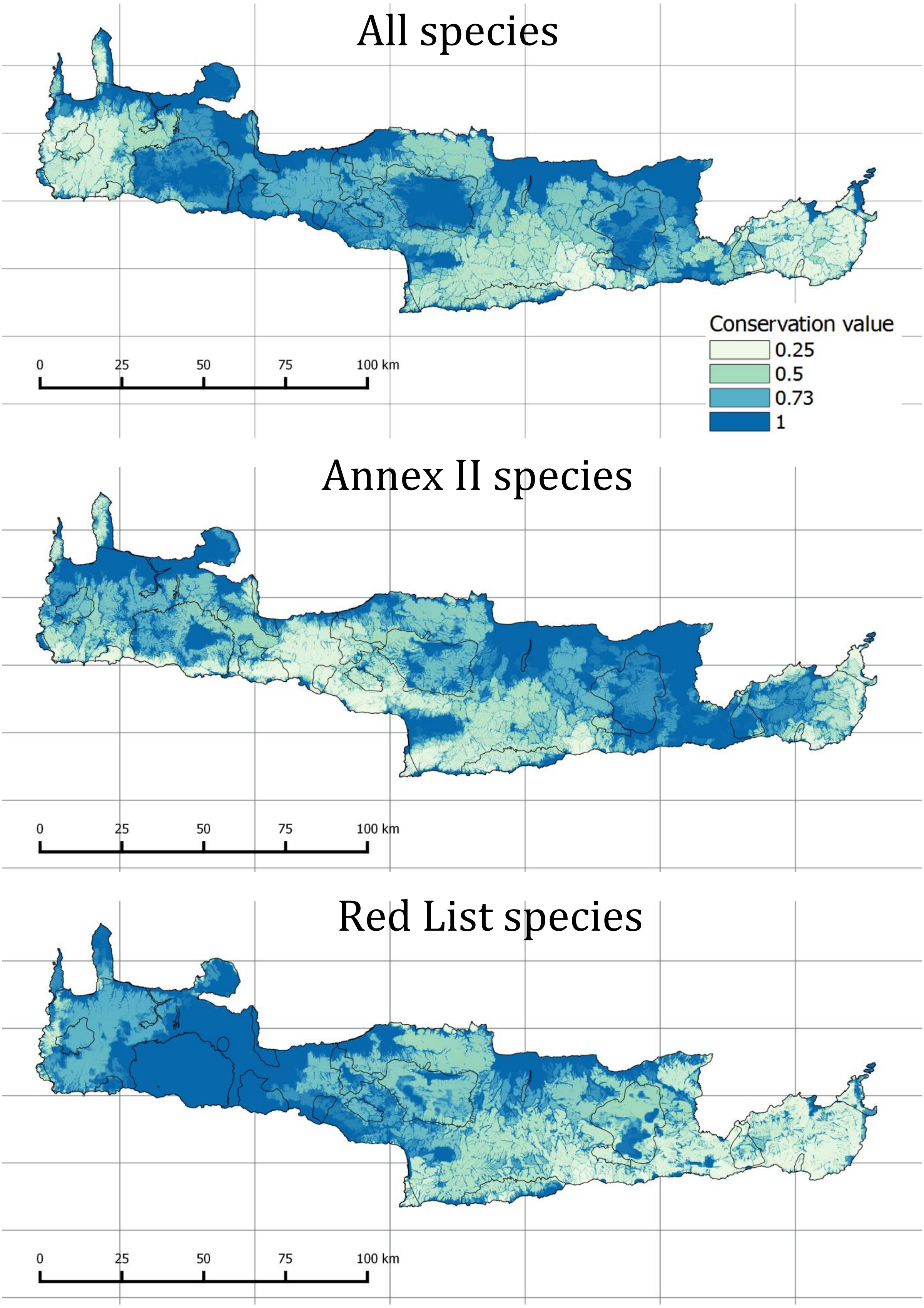


Figure 9: Output maps of the Zonation process for all species, Annex II species, Red List species. Darker hue represents higher conservation value. The darkest hue represents priority conservation areas. Boundaries of the Natura 2000 SAC sites are also given.

3.7. Gap analysis

Gap analysis of Natura 2000 SAC sites in Crete was performed in two ways: (i) gap analysis in regards to priority conservation areas for different groups of species, and (ii) Natura 2000 SAC site specific gap analysis.

3.7.1. Gap analysis for priority conservation areas

As expected, value of kappa for random priority areas was very close to zero (indicating agreement not better or worse than chance), with kappa = 0.0004. Species from the Annex II scenario were covered by Natura 2000 SAC sites worse than if the areas were randomly delineated, with negative value of kappa = -0.104. On the other hand, agreement was better than chance when all species were included (kappa = 0.101), and when only the Red List species were looked upon (kappa = 0.154). These values are reflected as well in the percent of overlap, where priority areas for the conservation of Annex II species overlapped 19.8% of Natura 2000 SAC sites. Highest overlap was recorded for the Red List species priority areas, with 38.6% of those areas covered by Natura 2000 SAC sites.

Table 10: Mean values of kappa statistics of agreement (2nd row) and overlap percentage (3rd row) between Natura 2000 SAC and priority conservation areas for different scenarios.

Scenario	**All species**	**Annex II species**	**Red list species**	**Random**
Kappa value	0.102	-0.104	0.154	0.0004
Overlap (%)	34.72	19.81	38.57	27.39

3.7.2. Gap analysis per Natura 2000 SAC site

In Table 11 we have presented the mean conservation value for the top and bottom three Natura 2000 SAC sites. Drapano and Lefka Ori, which coincides with Samaria gorge National Park, had high conservation value for all species and Red List scenarios. Drapano also had the highest conservation value overall (Figure 10). On the other hand, Ormos Sougias and Moni Kapsa showed to be not important sites when it comes to representing the biodiversity of herpetofauna (Table 11).

Table 11 Top and bottom three Natura 2000 SAC sites according to their mean conservation values for three scenarios.

Natura 2000 sites with highest conservation value					
All species		Annex II species		Red List species	
Site	**Value**	**Site**	**Value**	**Site**	**Value**
Drapano	0,8	Giouchtas	0,77	Drapano	0,93
Oros Idi	0,71	Limni Agias	0,74	Fre - Tzitzifes	0,89
Lefka Ori	0,69	Oropedio lasithiou	0,66	Lefka Ori	0,89
Natura 2000 sites with lowest conservation value					
All species		Annex II species		Red List species	
Site	**Value**	**Site**	**Value**	**Site**	**Value**
Ormos Sougias	0,2	Ormos Sougias	0,08	Moni Kapsa	0,09
Moni Kapsa	0,11	Kourtaliotiko Farangi	0,11	Omalos Viannou	0,17
Elos - Topolia	0,14	Oros Kedros	0,19	Oros Thryptis	0,2

Some sites had different relative impact on the conservation of specific groups of herpetofanual biodiversity (Figure 10). For example, even though Ormos Sougias site had very low relevance when it comes to all species and Annex II species, its relevance in representing only the Red List species was much higher (mean conservation value = 0.68). On the other hand, Natura site that encompass the Kourtaliotis gorge, Kourtaliotiko Farangi, represents all species and Red List species well, however its conservation value when it comes to the Annex II species is low (0.08).

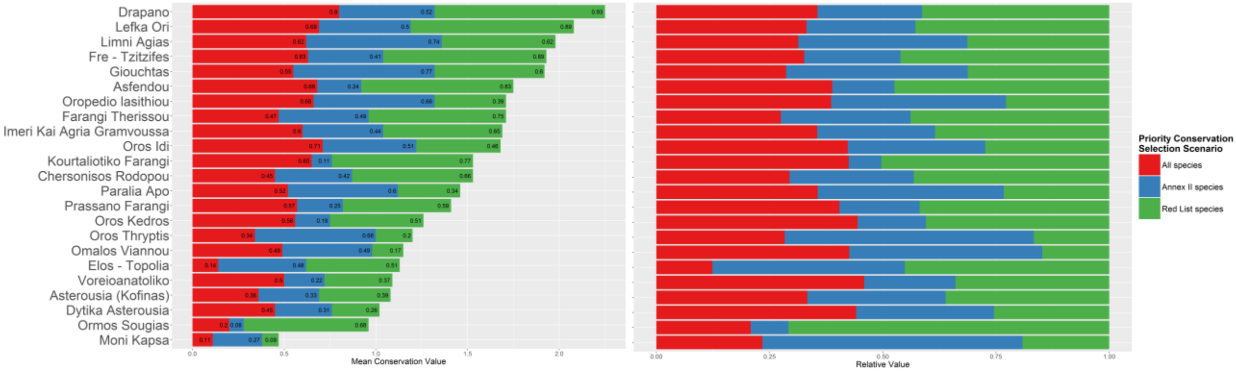


Figure 10: Mean conservation value per every Natura 2000 SAC site for all scenarios (left), and relative conservation value of each scenario per Natura 2000 SAC site (right).

3.8. Webmap

We have produced an interactive web map with Natura 2000 SAC sites in Crete. The map is accessible online on http://tiny.cc/Natura_Crete. It is possible to visualize the map in regards to different scenarios, and also every site has in its attribute table link for the official data forms which gives the detailed description for each site (Figure 11).

OBJECTID: 184
CODE: GR4320002
Site: Oropedio lasithiou
Allspecies: 0.66
Annex II: 0.66
Red List: 0.39
URL: natura2000.eea.europa.eu/Natura2000/SDF.aspx?site=GR4320002

Figure 11: Screenshot of web map interface (left), and working QR code which can be scanned with mobile phone to access the website.

4. DISCUSSION

4.1. Assessment of Natura 2000 Special Areas of Conservation

Our results showed that Natura 2000 Special Areas of Conservation represented poorly the most important areas for the conservation of amphibian and reptilian species. This was especially the case for species included in the Annex II of the Habitats Directive, which are the species that basically would had to be represented well by the Natura 2000 SAC sites. In fact, our results showed that priority conservation areas for species included in Annex II of the Habitats Directive were extremely poor, with kappa value of kappa = -0.1104 (Table 10). Although in most of analyses kappa values will range from 0 to 1, negative kappa values are also possible (Cohen, 1960; Juurlink & Detsky, 2005). Although not very common, negative kappa value results when agreement occurs less often than predicted by chance alone (Juurlink & Detsky, 2005). In other words, priority areas for the conservation of Annex II species are mostly contained outside of the Natura 2000 SAC sites. Multiple studies have also reached the conclusion that Natura 2000 network does not represent well the biodiversity that it should cover, and it was demonstrated for multiple taxa on various scales (Abellán & Sánchez-Fernández, 2015; Bagella, Caria, & Filigheddu, 2013; Dimitrakopoulos et al., 2004; Jantke, Schleupner, & Andreas, 2011; Maiorano et al., 2006; Trochet & Schmeller, 2013).

Natura 2000 SAC sites covered the priority areas for Red List species more than Annex II species. The Natura 2000 SAC sites represented priority areas for Red List species 15.4% more than chance, compared to 10.4% less than chance representation for Annex II species priority areas. These results however are not in agreement with Trochet & Schmeller (2013), where they have found that the coverage of species included in annexes of the Habitats Directive and coverage of threatened species as recognized by IUCN Red List did not differ significantly. On the other hand, these results may support the claim by Papageorgiou & Vogiatzakis (2006) that many Natura 2000 sites have been nominated based on previous designations of protected areas. Crete has one National Park, the Samaria gorge, and one aesthetic forest site. Samaria gorge is a large National Park on the west part of Crete, and Natura 2000 SAC site Lefka Ori (White Mountains) is superimposed over its region. Lefka Ori is the largest Natura 2000 SAC site, and it represents 23% of the total area of Natura 2000 SAC sites. All of the above may imply that protected areas other than Natura 2000 SAC sites represent better the important aspects of biodiversity than the actual Natura 2000 sites.

It should be noted that lists such as Annex II of the Habitats Directive and IUCN Red List are made on European level. In that regard, species that are included in these lists may have very stable and numerous populations in specific areas, or on the other hand their populations might be very threatened on a local scale, but on European level they are not recognized as threatened, or their local populations might be stable, but on European level they are recognized as threatened (Battisti & Fanelli, 2015; Louette et al., 2011). Biodiversity of the herpetofauna on Crete does not follow the general patterns in the region. Several species have dense populations on smaller islands of the Aegean archipelago (Lymberakis & Poulakakis, 2010). For example, the populations status of *Cyrtopodion kotschyi* on Crete is much different than on surrounding islands and *Cyrtopodion kotschyi* is usually very rare on Crete (Lymberakis & Poulakakis, 2010). Therefore, in areas with specific biogeography such as Crete, local conservation status should also be considered, as the status of local populations may greatly differ from the status of populations of same species on a European level.

Current diversity of Cretan herpetofauna is considered poor when compared to the whole Greece or nearby islands that are much smaller in size (Lymberakis & Poulakakis, 2010). There could be several reasons why Crete has small number of species which can have small populations. Human impact on

Crete is apparent, from the current agricultural and touristic practice, to the early evidences of civilization throughout history. Absence of venomous snakes on Crete may suggest early human influence on the distribution of Cretan herpetofauna, as they could have been extinct from the area by humans. However it is more likely that the reason behind the absence of venomous snakes on Crete can be explained by palaeogeography. The mid-Aegean trench opened ~8 million years ago, and made an island of current-day Crete before the viperid snakes had the opportunity to migrate to those areas (Lymberakis & Poulakakis, 2010). Small number of species in Crete may also imply that there are a number of ecological niches available for the other species to occupy. This claim is supported by several alien species that have established populations in Crete (Lymberakis & Poulakakis, 2010). Availability of niches could imply that the local populations of species are still in the process of speciation and they have not yet developed the traits that would enable them to utilize all available niches.

Economic aspects of the Natura 2000 network

Surveys have showed that in member states of EU15, the cost of establishing and managing the Natura 2000 network in the year 2020 will be around 28.6 billion Euros (Bladt, Strange, Abildtrup, Svenning, & Skov, 2009). Out of those, 5.6 billion Euros goes to management planning and administration, 15.2 billion to the ongoing management activities and incentives, and 7.8 billion to the occasional capital investment. Management planning and administration costs are mainly costs linked to establishment of the conservation programme, ongoing activities include compensation of landowners or habitat management, and occasional capital investment costs include projects of research and data collection, developing infrastructure and habitat regeneration projects (Bladt et al., 2009).

European Union Member State is mostly responsible to provide the financing of its Natura 2000 network, however Article 8 of the Habitats Directive (EC, 2000) describes the co-financing scheme with which the EU supports the Member State to achieve the necessary conservation measures (European Commission, 2011). Report by WEDA Urban Task Force (2010) showed that most of the funding for EU Member States Natura 2000 network comes in fact from the EU financial instruments rather than from the national funding mechanisms. It has been shown that some countries could potentially benefit in the terms of resource allocation from the coordinated financing approach (Bladt et al., 2009). Greece is mentioned as one of these countries, because of its high biodiversity and large proportion of endemic species, and also because of its labour-intensive agriculture which would imply high costs of compensating the farmers if the land is set aside for protection of biodiversity (Bladt et al., 2009). In this regard, more designated sites could ultimately mean greater access to EU funding mechanisms. Therefore, question arises how much is the designation of Natura 2000 sites motivated by financial incentives? The analysis and justification of the scientific reasons behind designation of each individual Natura 2000 should be conducted, but it is out of the scope of this analysis.

4.2. Species distribution modeling for gap analysis

As suggested in Margules & Pressey (2000), species distribution modelling proved to be a useful tool for gap analysis. Our results have showed also that the results of these models can be very different according to which modelling tools we use. Therefore, focus should be directed to finding the appropriate tools, i.e. finding the optimal modelling technique and optimal modelling parameters such as pseudo-absence generation strategy and the number of pseudo-absences.

Pseudo-absence selection

In studies where multiple modelling methods are used, the optimal way of creating pseudo-absences would be to use different strategies for different modelling techniques, or for different groups of modelling techniques (Barbet-Massin et al., 2012). However, approach in most of studies is to use pseudo-absence strategy that was shown to perform well, even though the optimal strategy and number of pseudo-absences depends on the spatial extent of the study, spatial resolution and modelled organisms (Barbet-Massin et al., 2012).

Disk strategy creates pseudo-absences outside of the defined disk threshold, while randomly generated pseudo-absences can be created in the vicinity of presence. This means that similar environmental space can be potentially sampled for absence of species when random strategy is used. Pseudo-absences created with disk strategy probably have better chance of being true-absences than with random strategy, as there is a geographical exclusion of areas near the presence points (Barbet-Massin et al., 2012). This may be the reason why disk strategy had higher performance metrics, as the models were able to distinguish more clearly where the species is absent.

In the case where we have used constant number of 1000 pseudo-absences for each species, prevalence (proportion of presences in regards to absences) ranged from 1.4% to 20.2%. On the other hand, models with twice as many pseudo-absences as presences had equal prevalence of 50% for all species. Allouche et al. (2006) showed that while TSS and kappa values will have different responses in regards to prevalence. TSS in general is not affected by prevalence, but kappa values will have unimodal response to prevalence. This is accordance to our results shown in Figure 6, where models that used species data with unequal prevalence (ranging between 1.4% and 20.2%) had lower values of kappa compared to the species data with equal prevalence (50%). On the other hand, TSS values for our models were not affected by prevalence, which is in agreement with Allouche et al. (2006).

When the effect of prevalence on AUC values is considered, Allouche et al. (2006) showed that AUC showed a negative response to prevalence, although the effect was not statistically significant. On the other hand, Santika (2011) found that the AUC value had inverted U-shaped response in regards to prevalence, where the AUC value would decrease when the prevalence approached 50%. In our case the AUC values were slightly lower for models with equal prevalence (Figure 6). In reality, prevalence means that the species will occur more frequently, and usually prevalent species occupy wider niches and are considered habitat generalist (Allouche et al., 2006), The ability of models to discriminate species' presence (interpreted by AUC values) is lesser when it comes to generalist species with wide niches (Evangelista et al., 2008; Lobo et al., 2008). However, whether our results have ecological or statistical explanation in our case should be researched further.

Environmental variables

In species distribution modelling, usage of proper environmental variables is crucial for producing good-quality models (Guisan & Zimmermann, 2000). Choice of proper environmental variables is complex and preferably iterative process where ecological characteristics of organisms have to be considered, but also characteristics of available data such as data quality or spatial resolution.

Distribution of species is determined by environmental factors which occur at different spatial scales (Franklin, 2010; Mackey & Lindenmayer, 2001). At the global scale, latitudinal variations in climate drive the distribution of biomes (Mackey & Lindenmayer, 2001). Local climatic environmental factors such as local precipitation and temperature can be described as meso-scale variables, while local topographical factors control the distribution of resources via slope, aspect, hillslope position on a topo-scale (Franklin, 2010; Mackey & Lindenmayer, 2001). In regards to the ecological hierarchy (Wandrei, 2016), distribution of populations of species can be described on a topo-scale, while distribution of species itself is usually linked with the meso-scale (Mackey & Lindenmayer, 2001).

In general, our results revealed that bioclimatic environmental variables had greater contribution to the prediction of models than all other groups of predictors (Appendix II). This can imply that the distribution of modelled species is mainly influenced by climate at the meso-scale. Furthermore, Guisan & Hofer (2003) showed that climatic variables at the meso-scale have greater predictive power than topo-scale variables when it comes to the distribution of reptiles. They have also found that topographical variables had low predictive power where strong response was expected for lizard and snake species.

The fact that distribution of amphibians and reptiles can be explained well with climatic variables is not surprising, since the physiological processes of ectotherms and their reproductive behaviour are influenced by temperature (Vitt & Caldwell, 2013). It could be also expected that the solar radiation would have high predictive power, considering the relationship of ectotherms with temperature, especially when it comes to their basking behaviour (Vitt & Caldwell, 2013). Solar radiation and local variations of terrain at topo-scale did not explain well the distribution of the species. However, this is in accordance with van Gils, Conti, Ciaschetti, & Westinga (2012), where they have found that incoming solar radiation has low predictive power for the distribution of plants, since it may not represent ecologically meaningful solar radiation. In this study, we have used direct incoming solar radiation that gives the amount of solar radiation in watt hours per square meter for the set time-span. This type of solar radiation may not be particularly relevant when it comes to the influence on the basking behaviour of amphibians and reptiles.

Usage of fine-resolution environmental variables for our analysis (30m variables derived from ASTER DEM) may not have improved the accuracy of our models. Positional uncertainty in the species presence data can be an issue at this scale level, since incorrect positioning of species data can lead to incorrect sampling of environmental space (Naimi, Hamm, Groen, Skidmore, & Toxopeus, 2014). Furthermore, even though SRTM DEM with its 90m resolution is coarser, it has been shown that SRTM DEM has better quality than ASTER DEM, especially when it comes to the vertical accuracy (Forkuor & Maathuis, 2012; Wong, Tsuyuki, Ioki, & Phua, 2014). Crete is topographically heterogeneous (Lymberakis & Poulakakis, 2010), and it has many gorges and steep cliffs. In case of lower quality DEM, complex terrain features such as these can cause inaccurate values of the DEM (Forkuor & Maathuis, 2012). In this case the performance of models may improve by using coarser data of higher quality. This was shown to be the case in van Gils et al. (2012), where they have found that AUC values were higher for 90m DEM compared to the 30m DEM.

Variable selection

Removal of low-performing variables for specific species had no noticeable impact on the performance evaluation metrics. In fact, the greatest difference between two runs was recorded for species that were modelled using the same environmental variable data sets, namely *Bufotes viridis* and *Telescopus fallax*. This could be interpreted that the results for these species have greater uncertainty, therefore the results of the model will deviate more between runs. This is supported by the fact that there was no consistency in the results, but for *Bufotes viridis* the performance metrics were worse for the second run, while *Telescopus fallax* had better metrics in the second run. Species that had low performing variables removed (highlighted species in the Table 8) also had inconsistent results between the two runs. This can be attributed to the random variation in the modelling results, and no to the actual statistical effect of lowering the number of variables to reduce the overfitting.

However, it is also the case that MAXENT uses the regularization term in its equation (Anderson & Gonzalez, 2011; S. J. Phillips et al., 2006), which penalizes complex models with many environmental variables in order to reduce the tendency of overfitting the models. This term will in effect force MAXENT to work only with the most important features (Anderson & Gonzalez, 2011). This is also in accordance to our results where lowering the number of variables did not produce different results.

Using an approach where ecological requirements and responses to different environmental variables are considered for every individual species can be implemented in studies where the analyses are conducted on a small number of species such as here. However, gap analyses are often performed on a large number of species of multiple taxa with different ecological requirements (Abellán & Sánchez-Fernández, 2015; Fajardo et al., 2014; Maiorano et al., 2006; Tantipisanuh et al., 2016). In these cases, analyzing each species response may not be appropriate, but a more general set of environmental variables may be used. Our results have showed that removing small number of low-performing variables from a set of general variables when MAXENT is used did not make significant difference when it comes to ecologically similar taxa such as amphibians and reptiles. Therefore, this implies that cases where the variables are carefully chosen *a priori* for taxa with similar ecology, more general set of environmental variables may be used for all species.

Species' ecological characteristics and model evaluation

Models with poor performance metrics usually lack in important environmental variables that are required to identify the species' niche (Evangelista et al., 2008). On the other hand, in case where important environmental variables are identified *a priori*, the models will have better performance (Gibson et al., 2004). Accuracy of the models is often determined by the width of the species' ecological niche (Evangelista et al., 2008). Species whose habitats are more general and wide have models with lower performing metrics than the species who are specialists and whose niche is narrower (Evangelista et al., 2008). This was also demonstrated for reptilian species by Guisan & Hofer (2003), where they showed that widespread species had lower performance scores. Species that had the lowest performance metrics scores overall was *Hierophis gemonensis* (Table 9), which can actually be considered as habitat generalist (Scali, Mangiacotti, & Bonardi, 2008). On the other hand, highest performance metrics were recorded for the endemic Cretan wall lizard *Podarcis cretensis*. Endemic species indeed have the need for specialized ecological niche, and they usually occupy only one or a few specialized habitats (Işik, 2011).

Sources of error and uncertainty

Species distribution models are in general based on modelling the fundamental niche of the species, which is constrained by physiological responses of species on it environment (Anderson et al., 2003; Jane Elith & Leathwick, 2009; Guisan & Zimmermann, 2000; A. T. Peterson & Soberón, 2012). However, the realized niche includes other factors such as ecological interactions (Guisan & Zimmermann, 2000). This difference can be also interpreted to a degree as difference between potential and actual distribution (T. Peterson & Soberón, 2012). In this analysis we did not consider ecological interactions such as competitive exclusion or mutualism, or dispersal barriers; therefore we have only modelled the fundamental niche of the species. This can have effect on our results, as some areas that model identifies as suitable may be already occupied by species with similar ecological niche, or the species may be absent from those areas due to the physical barriers or it was extinct due to different environmental pressures. This can in turn cause uncertainty in the Zonation output, as the Zonation's additive benefit function is based on suitability values of all species in the cell, and the remaining distribution of those species in the remaining cells.

It is important to distinguish the effects of ecological causation on one hand, and improper sampling on the other when it comes to explaining the distribution of species. Although particular variables showed to have high predictive power in our case, the correlation does not necessarily mean that there is real ecological causation in the model. For example, some species such as *Hemidactylus turcicus* are closely linked to human settlements (Lymberakis & Poulakakis, 2010; Valakos et al., 2008). In our case the model did indeed recognize distance from built-up areas as a factor that is important for the distribution of *Hemidactylus turcicus*. However, question that arises is when the factors such as built-up distance are important because it is related to species' ecology, and when they are important because the model captured sampling bias, since it is common to take presence points in the vicinity of accessible roads and urban centres (Kramer-Schadt et al., 2013). It can be expected that in datasets where sampling efforts have been biased towards particular areas, that models will identify those areas as suitable (Boitani et al., 2011; Gaston et al., 2008; Kramer-Schadt et al., 2013). Multitude of species presence points in our case were captured in the vicinity of major cities, especially Iraklio. The database used for modelling comes from the Natural History Museum of Crete University, which is based in Iraklio, so it is not surprising that the sampling effort is based around that area. In all scenarios this area was recognized as an area of high conservation value. Specific areas that are heavily used for agriculture, such as the Messara plain, were also identified as areas with high conservation value in all three scenarios. Some of these areas might be might be actually suitable habitats for multiple species from which they were expelled as a result of anthropogenic activities.

5. CONCLUSIONS AND RECOMMENDATIONS

Overall aim of this research was to assess the effectiveness of Natura 2000 SAC network in representing the herpetofauna of Crete. The study showed that the priority areas for conservation of specific groups of the Cretan herpetofauna are not sufficiently represented by the Natura 2000 SAC network. Out of those groups, species from the IUCN Red List were represented the most, followed by all species. Species included on the Annex II of the Habitats Directive, which Natura 2000 SAC sites should cover, showed to have the least amount of protection by the Natura 2000 SAC network.

Out of all individual Natura 2000 SAC sites, Drapano and Lefka Ori were identified as the most important sites for the conservation of the Cretan herpetofauna. They had high conservation value for all species, and also for species from the IUCN Red List. On the other hand, Sougias and Moni Kapsa showed to have low importance when it comes to the conservation of amphibians and reptiles.

No matter to what extent do protected areas represent the local biodiversity, key part of reaching the conservation goals of protected areas is proper implementation of proper management practices. This requires existence of an iterative process of scientific reasoning for the designation of protected areas, assessment of those areas (as in studies such as this one), and the implementation of conservation actions.

Usage of Zonation proved to be useful for gap analysis, although the results of Zonation analysis are heavily dependent on the quality of input data. For creating the input data with species distribution modelling, we have found that MAXENT was the most optimal modelling technique for our study area and our target species. GBM/BRT also has showed to perform well in this case. Choice of pseudo-absence generation strategy did have an influence on the performance of the models, with disk strategy performing better than random strategy. However, it was difficult to reach strong argument for any of two ways of determining the number of created pseudo-absences.

When it comes to species distribution modelling, having the access to high quality data is crucial. In our study the results showed that sampling bias had an impact on our results, as major urban areas appeared to be important for conservation. Improving the quality of the species' data and usage of adequate sampling techniques is of high importance for the quality of the gap analysis. In future cost layers, such as for urban areas and important agricultural areas where they could be weighted or forced out in order to account for the spatial bias or unsuitable areas. These issues could be also accounted for in the modelling stage, for example with using land use categories or different set of variables that explain anthropogenic factors. In addition, inclusion of better environmental variables and environmental variables that explain different species-environment relationship could improve the performance of the models. For example, in this study we have not used any data on soil or land cover, nor we have used any type of categorical environmental variables.

However, assessment of protected areas should not be delayed due to the lack of high-quality data, especially when the studies are done on threatened groups of organisms such as amphibians and reptiles. Instead, sense of general patterns and trends could be inferred from the results, and immediate and adequate actions should be undertaken to improve namely the methods of designating protected areas, and more importantly, implementation of conservation actions.

"All models are wrong, but some are useful..."
George E.P. Box

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7. APPENDICES

7.1. Appendix I - Taxonomy, habitat characteristics and conservation status of the target species

Class: Amphibia Gray, 1825
  - Order: Anura Duméril, 1806
    - Family: Bufonidae Gray, 1825

Bufotes viridis (Laurenti, 1768) - Green toad
Its range spans from eastern France all the way up to Central Asia and south Sweden in the northern limits of its range (Arnold & Ovenden, 2002). In Greece it is found all over the mainland and on most of the islands. The green toad lives in wide variety of habitats, ranging from sea level, and up to 2500 m elevation. It tolerates dry conditions well. Threats present for the green toad are destruction of meadows, reclaiming of wetlands, urbanization and recreation. The green toad is listed in Appendix II of the Bern Convention, Annex IV of the EU Habitats Directive, and is protected by Greek Law (Presidential Decree 67/1981) (Valakos et al., 2008).

- Class: Amphibia Gray, 1825
  - Order: Anura Duméril, 1806
    - Family: Hylidae Rafinesque, 1815

Hyla arborea (Linnaeus, 1758) – Common tree frog
It can be found in most parts of Europe except for the north, and southernmost regions of the Iberian Peninsula and France (Arnold & Ovenden, 2002). In Greece it is found all across the mainland, and on some larger, more humid islands. Common habitats for the common tree frog are mixed and broad-leaved forests, cultivated areas, shores of lakes and streams and floodplains. It uses stagnant waters (lakes, ponds, swamps and reservoirs) for breeding. Threats include loss of breeding habitats, habitat isolation and fragmentation, pollution and climate change. The common tree frog is listed in Appendix II of the Bern Convention, Annex IV of the EU Habitats Directive, and is protected by Greek Law (Presidential Decree 67/1981) (Valakos et al., 2008).

- Class: Amphibia Gray, 1825
  - Order: Anura Duméril, 1806
    - Family: Ranidae Rafinesque, 1814

Pelophylax cretensis (Beerli, Hotz, Tunner, Heppich & Uzzell, 1994) – Cretan water frog
Cretan water frog is a species endemic for the island of Crete. It can be found in wetlands, lakes and marshes, slow-moving rivers and streams. It is listed in Appendix III of the Bern Convention. Main threat is loss of aquatic habitats due to the agricultural irrigation. In general, further research on population abundance and distribution of the Cretan water frog is needed.

- Class: Reptilia Laurenti, 1768
  - Order: Testudines Batsch, 1788
    - Family: Cheloniidae Oppel, 1811

Caretta caretta (Linnaeus, 1758) – Loggerhead turtle
Loggerhead turtle is a marine turtle species that has one of the most important nesting sites in Crete. Loggerhead turtle is an endangered species protected by Greek Law (Presidential Decree 67/1981), and it is considered a priority species of community interest, listed on Annex II and IV of the Habitats Directive,

and on Appendix II of the Bern Convention. All of its main nesting sites and most of the sites with moderate nesting activity have been included in the NATURA 2000 network. Populations of the loggerhead turtle are threatened by habitat destruction and the alteration of nesting beaches due to the development of tourism and infrastructure.

- Class: Reptilia Laurenti, 1768
  - Order: Testudines Batsch, 1788
    - Family: Geoemydidae Theobald, 1868

Mauremys rivulata (Valenciennes, 1833) – Balkan terrapin
The Balkan terrapin's can be found in Balkan peninsula, north up to southern Croatia, and can be found in parts of Asiatic Turkey and Israel (Arnold & Ovenden, 2002). In Greece it can be found throughout its mainland and also in larger islands that have appropriate wetlands. Its habitats are usually stagnant or slow-flowing freshwaters. It is threatened by the habitat degradation and destruction due to irrigation. It is protected by Greek Law (Presidential Decree 67/1981). It is also a species of community interest, listed in Annexes II and IV of the Habitats Directive under *Mauremys caspica*, and it is included in Annex II of the Bern Convention (Valakos et al., 2008).

- Class: Reptilia Laurenti, 1768
  - Order: Squamata Oppel, 1811
    - Family: Gekkoniadae Gray, 1825

Cyrtopodion kotschyi (Steindachner, 1870) – Kotschy's gecko
Its range extends from south Italy, Greece, and east up to the Trans-Caucasus region. It can be found in dry, stony habitats with a scrub, maquis vegetation. There are no major threats to this species over most of its range (Böhme et al., 2009). It is listed in Appendix II of the Bern Convention, Annex IV of the EU Habitats Directive, and is also protected by Greek Law (Presidential Decree 67/1981) (Valakos et al., 2008).

- Class: Reptilia Laurenti, 1768
  - Order: Squamata Oppel, 1811
    - Family: Gekkoniadae Gray, 1825

Hemidactylus turcicus (Linnaeus, 1758) – Turkish gecko
Distribution of the Turkish gecko ranges from the Mediterranean region all the way to Pakistan, Arabian Peninsula and Somalia. It lives in a great variety of stony habitats. It is common in abandoned agricultural areas, and also is commonly found in houses. This species is very adaptable and it has no major threats. Animals can be occasionally mistreated in tourist resorts, although this does not have a significant impact on its population (Agasyan et al., 2009). It is listed in the Annex III of the Bern Convention, and it is also protected by Greek Law (Presidential Decree 67/1981) (Valakos et al., 2008).

- Class: Reptilia Laurenti, 1768
  - Order: Squamata Oppel, 1811
    - Family: Gekkoniadae Gray, 1825

Tarentola mauritanica (Linnaeus, 1758) – Moorish wall gecko
It is found throughout the Mediterranean countries. It prefers dry places, close to human habitation. It is listed in Annex III of the Bern Convention, and also it is protected by Greek Law (Presidential Decree 67/1981).

- Class: Reptilia Laurenti, 1768

  - Order: Squamata Oppel, 1811
    - Family: Lacertidae Oppel, 1811

Lacerta trilineata Bedriaga, 1886 – Balkan green lizard
Range of the Balkan green lizard is the larger part of the southern Balkans, including the European part of Turkey. It prefers habitats with dense vegetation, although can be sometimes found foraging in open areas. Depending on the site, it can be found on bushes, meadows and abandoned cultivated land, sand dunes, stone walls, buildings and roadsides. It is protected by Greek Law (Presidential Decree 67/1981), and it is also considered a species of community interest, listed in Annex IV of the Habitats Directive, and in Annex II of the Bern Convention.

- Class: Reptilia Laurenti, 1768
  - Order: Squamata Oppel, 1811
    - Family: Lacertidae Oppel, 1811

Podarcis cretensis (Wettstein, 1952) – Cretan wall lizard
Cretan wall lizard is a species endemic to Crete and its satellite islands. On the island of Crete it is present only in the western part. It prefers dry, rocky habitats with low vegetation, but can be also found in open areas and sand dunes. It is protected under Appendix II of Bern Convention and Annex IV of the EU Habitats Directive (as part of *Podarcis erhardii*, from which it was recently separated as a distinct species) (Lymberakis, 2009).

- Class: Reptilia Laurenti, 1768
  - Order: Squamata Oppel, 1811
    - Family: Scincidae Gray, 1825

Chalcides ocellatus (Forskkål, 1775) – Ocellated skink
In Europe it is distributed on the Mediterranean islands, and some parts of mainland Greece and Italy. It is frequently encountered on sandy beaches, in cultivated areas, in gardens, in vineyards. It can be found both in dry and damp places. It is protected by Greek Law (Presidential Decree 67/1981), and it is listed in Annex II of the Bern Convention, and in Annex IV of the EU Habitats Directive.

- Class: Reptilia Laurenti, 1768
  - Order: Squamata Oppel, 1811
    - Family: Colubridae Oppel, 1811

Hierophis gemonensis (Laurenti, 1768) – Balkan whip snake
It can be found along the Adriatic coast all the way up to northeast Italy, and in Greece throughout the mainland Greece west of Pindos. It prefers dry habitats with low vegetation. It is most common in phrygana, degraded maquis and cultivations. It is listed in Annex II of the Bern Convention. It is also protected by Greek Law (Presidential Decree 67/1981).

- Class: Reptilia Laurenti, 1768
  - Order: Squamata Oppel, 1811
    - Family: Colubridae Oppel, 1811

Natrix tessellata (Laurenti, 1768) – Dice snake
It has a wide range of distribution, ranging from Europe to China in the east, and southwards to the Nile delta. In Greece it can be found throughout the mainland and in some islands. It prefers wetland habitats, and it is dependent on the presence of water. It is listed in Annex II of the Bern Convention and in the

Annex IV of the EU Habitats Directive as a priority species. It is also protected by Greek Law (Presidential Decree 67/1981).

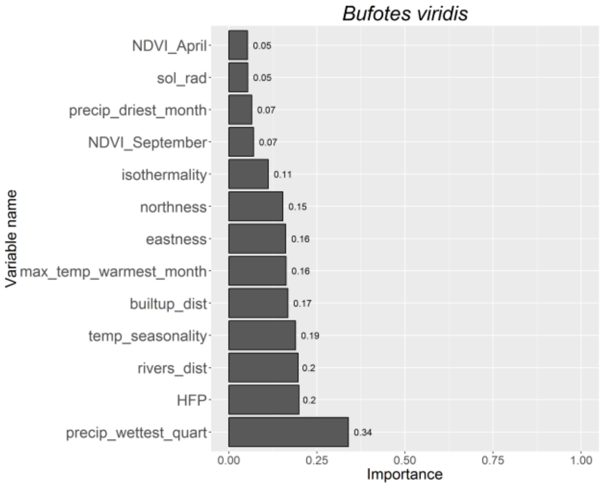
- Class: Reptilia Laurenti, 1768
    - Order: Squamata Oppel, 1811
        - Family: Colubridae Oppel, 1811

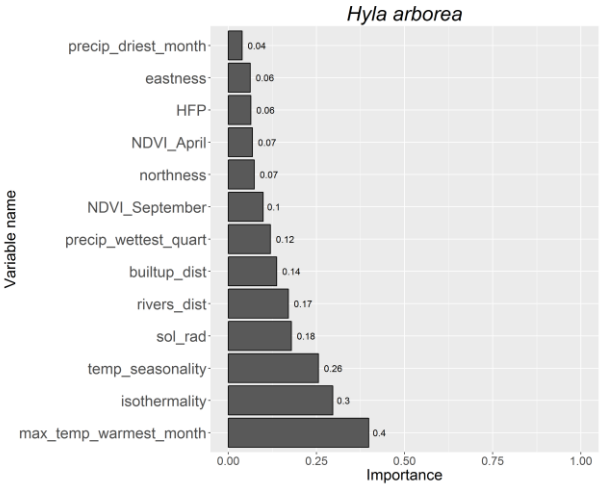
*Telescopus fallax (*Fleischmann, 1831) – European cat snake
It is present along the Adriatic coast, and it can be found all the way east to the Caucasus region. In Greece it is found throughout the mainland, and on most of the Ionian and Aegean islands. The cat snake is usually found in rocky and stony areas with degraded vegetation, abandoned cultivated areas, in Mediterranean maquis or phrygana. It is listed in Annex II of the Bern Convention, and also in Annex IV of the EU Habitats Directive as a priority species. It is protected by Greek Law (Presidential Decree 67/1981).

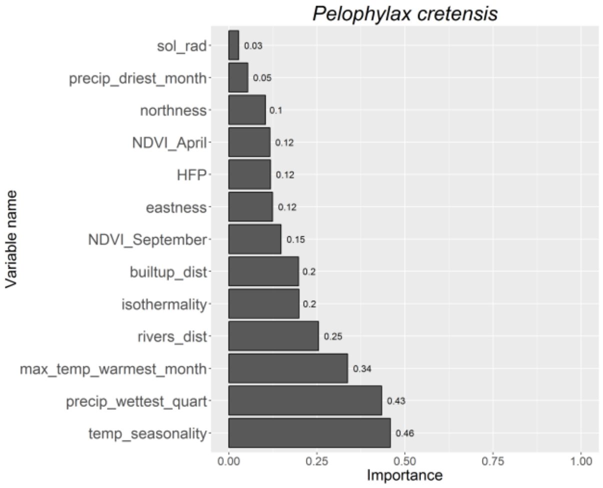
- Class: Reptilia Laurenti, 1768
    - Order: Squamata Oppel, 1811
        - Family: Colubridae Oppel, 1811

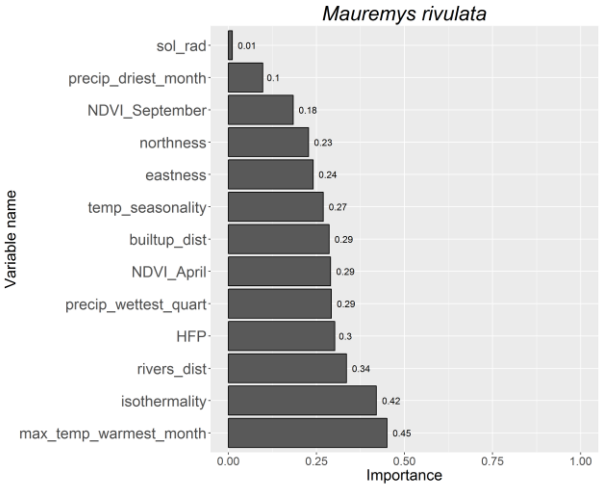
Zamenis situla (Linnaeus, 1758) – Leopard snake
It can be found in Mediterranean region along the Adriatic Sea, eastward to Turkey and Crimea. In Greece it is distributed throughout mainland Greece, and in most of Ionian and Aegean islands. It is found in maquis and in cultivated areas such as vineyards and olive groves. It is listed in Annex II of the Bern Convention, and in Annex II of the EU Habitats Directive as a priority species. It is protected by Greek Law (Presidential Decree 67/1981) and it is included in the IUCN Red List of threatened species.

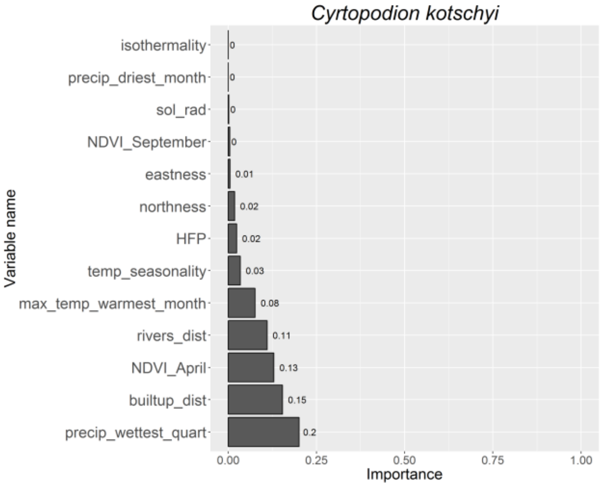
7.2. Appendix II - Variable importance

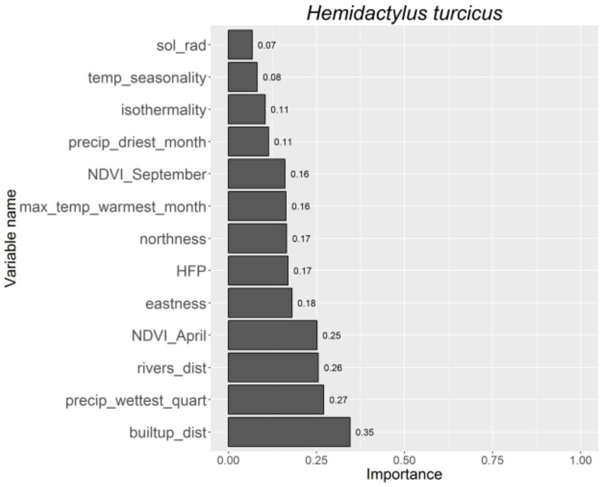


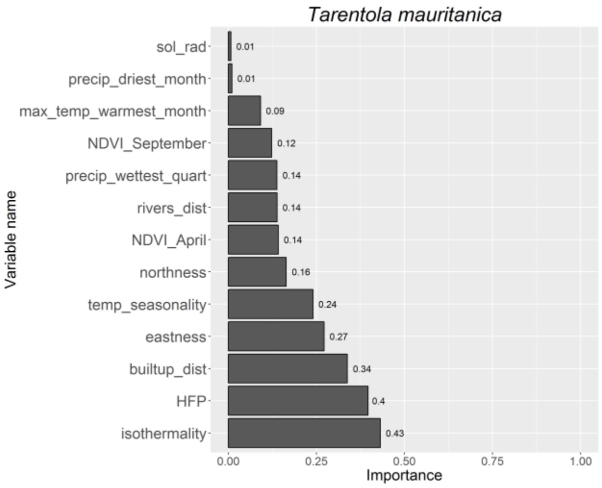


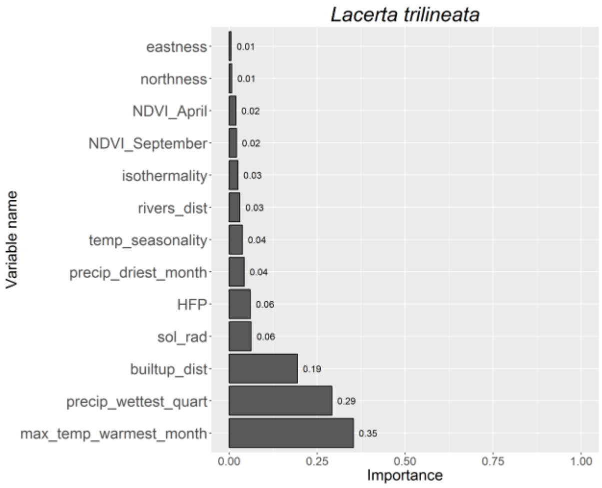


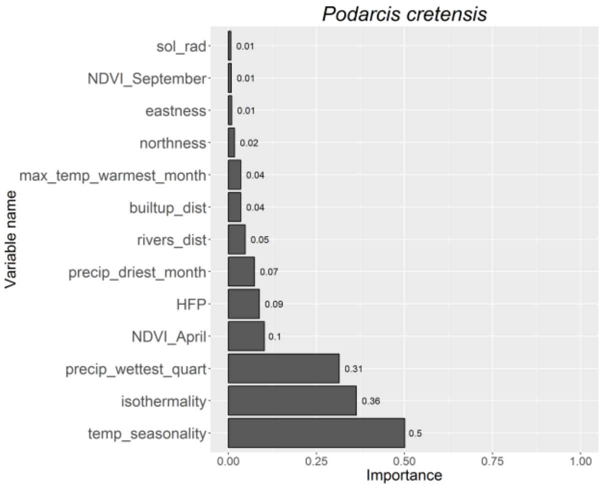


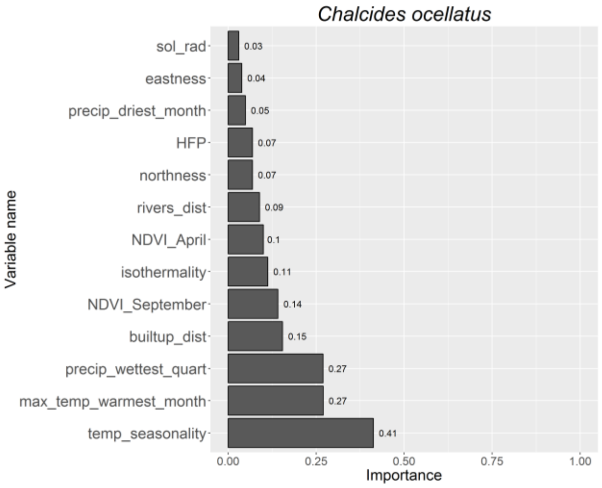


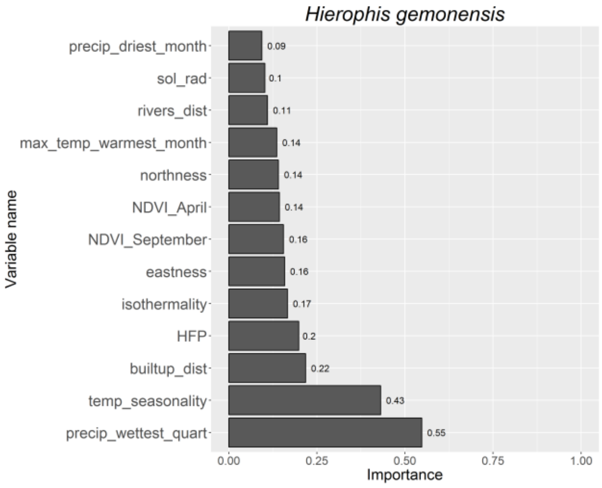


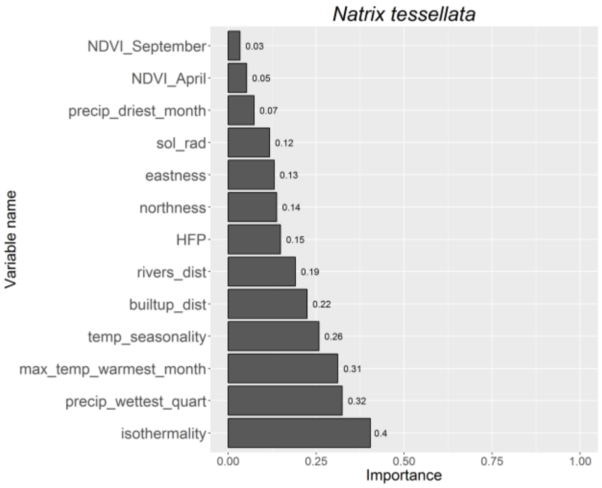

Tarentola mauritanica

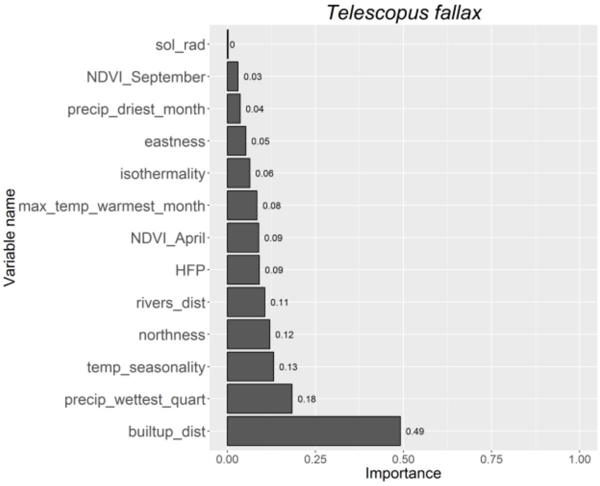

Lacerta trilineata

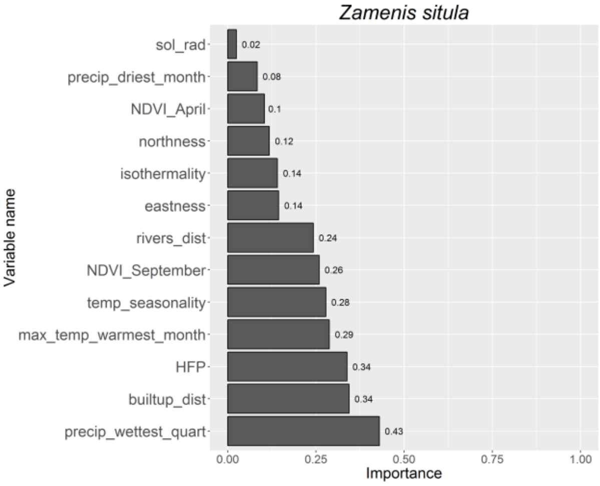

Podarcis cretensis


Chalcides ocellatus


Hierophis gemonensis


Natrix tessellata


Telescopus fallax
Variable name
sol_rad
NDVI_September
precip_driest_month
eastness
isothermality
max_temp_warmest_month
NDVI_April
HFP
rivers_dist
northness
temp_seasonality
precip_wettest_quart
builtup_dist
0
0.03
0.04
0.05
0.06
0.08
0.09
0.09
0.11
0.12
0.13
0.18
0.49
0.00
0.25
0.50
0.75
1.00
Importance


Zamenis situla
Variable name
sol_rad
precip_driest_month
NDVI_April
northness
isothermality
eastness
rivers_dist
NDVI_September
temp_seasonality
max_temp_warmest_month
HFP
builtup_dist
precip_wettest_quart
0.02
0.08
0.1
0.12
0.14
0.14
0.24
0.26
0.28
0.29
0.34
0.34
0.43
0.00
0.25
0.50
0.75
1.00
Importance