Predicting The Invasion Risk of Non-Native Reptiles as Pets in The Middle East

Azita Farashi (✉ farashi@um.ac.ir)

Ferdowsi University of Mashhad

Mohammad Alizadeh-Noughani

Ferdowsi University of Mashhad

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Abstract

Wildlife trade for non-native pets is an important and increasing driver of biodiversity loss and often compromises the standards required for protection. However, the growing interest in non-native pets has posed the issue of invasive non-native species to wildlife managers and conservationists. Instituting effective policies regarding non-native species requires a thorough understanding of the potential range of the species in new environments. In this study, we used an ensemble of ten species distribution models to predict the potential distribution for 23 commonly traded species of reptiles across the Middle East. We used ten modeling techniques implemented in the Biomod2 package and ensemble forecasts. Final models contained fourteen environmental variables, including climatic, topographic, and land cover/land use variables. Our results indicate that all Middle Eastern countries included suitable habitats for at least six species, except Qatar, Kuwait and Bahrain for which the models did not predict any suitable habitats. Our study showed that Lebanon, Palestine, Turkey, and Israel face the highest risk of biological invasion by the species on the whole. Also, the results showed that *Centrochelys sulcata*, *Chamaeleo calyptatus*, and *Trachemys scripta* posed the highest risk of spreading in this area. Information on which species pose a greater danger as invaders and the possible impacts of their introduction will be a valuable contribution to the development of conservation plans and policies.

Introduction

Over the past two decades, non-native pet trade has become the main source of non-native reptile and amphibian species worldwide (Capinha et al., 2017; Stringham & Lockwood, 2018). The aesthetic and entertainment value of some species has made them coveted non-native pets (Reed, 2005) and created a market around capturing, breeding and selling them (Bush et al., 2014) while docility in captivity, large size and rarity has contributed to the popularity of other species as pets (e.g. pythons and boas) (Luiselli et al., 2012; Reed, 2005). As a result, over half a million live reptiles are traded annually across the globe (Kareesh et al., 2005). "Non-native pets" refers to species without a history of domestication by humans which are sold as pets; these species are caught from their natural habitats or grown in human-made environments. These animals are not sold with the goal of being released into the wild. However, non-native species are frequently observed as free-living, indicating that large numbers of these species eventually find their way into natural ecosystems (Hulme, 2015). The released individuals might establish populations in the wild, which could in turn lead to negative consequences for native species and the environment (Stringham & Lockwood, 2018).

Invasive reptiles can disturb ecosystems through predation, herbivory, competition, genetic hybridization (Kraus, 2015), or introduction of non-native pathogens (Burrige et al., 2000; Nowak, 2010). The introduction of non-native species can lead to disturbance in local ecosystems and cause decline or change in local populations (Holbrook & Chesnes, 2011); extinction of native species as a consequence of the introduction of non-native species has also been reported (Savidge, 1987). The detrimental consequences of invasive reptiles are not limited to ecosystems and can extend into economic and social realms as well (Bomford et al., 2005). Wildlife managers should also take note that many of the illegally traded reptile species are venomous (García-Díaz et al., 2017) which could pose a threat to both humans and native animal populations if it becomes established in the region.

Reptiles are commonly traded as pets in the Middle East. Turtles such as *Trachemys scripta* (Thunberg in Schoepff, 1792) are widely traded as pets while other species such as snakes and chameleons are chiefly kept and traded by seasoned enthusiasts. Although there are no records of non-native reptiles establishing a population in some countries such as Iran (Rastegar-Pouyani et al., 2015), reptilian species might have already established populations in other countries (Soorae et al., 2010). Very little research has been conducted to catalog non-native reptiles in the Middle East. However, the growing interest in non-native pets has posed the issue of invasive non-native species to wildlife managers and conservationists.

Knowledge about the invasion range of these species plays a vital role in understanding the ecology of invasive species and in creating a sustainable conservation and management plan. Predictive models, such as species distribution models (SDMs), have become an essential tool for researchers to predict and assess the distribution of non-native species by quantifying species–environment relationships (Guisan and Thuiller, 2005; Elith and Leathwick, 2009). SDM first became species in Australia (Guisan and Thuiller, 2005). In the 1990s the approach experienced a renaissance caused by simultaneous developments in computer- and statistical sciences (Elith and Leathwick, 2009). Another 20 years later, within the past decade significant advancements in predictive modelling have occurred with thousands of new publications on SDM, and their applications, in the fields of ecology, conservation, biogeography and evolution (Zimmermann et al., 2010; Choudhary et al., 2019; Jha and Jha, 2021). There are now many methods used for distribution modelling, varying in how they approach model selection, how they define fitted functions and interactions, whether they can handle imperfect detection and sampling biases and so on (Franklin, 2010; Guisan et al., 2017). Predictive outcomes across SDM methods are known to be variable, and the choice of modelling method can significantly affect model predictive performance. However, no one method is consistently superior in performance across species, regions and applications (Segurado & Araujo, 2004). This makes it difficult to choose which method (individual model hereafter) to use, prompting the idea of combining predictive outputs from different models in a so-called ensemble (Araújo & New, 2007). The underlying philosophy of ensemble modelling is that each individual model carries both some true "signal" about the relationships the model is aiming to capture, and some "noise" created by errors and uncertainties in the data and the model structure. Ensembles combine models with the intention of obtaining better separation of the signal from noise (Araújo & New, 2007; Dormann et al., 2018). These types of ensembles have been shown in many cases to have superior predictive performance to individual models (Seni & Elder, 2010).

In this study, an ensemble framework of ten SDMs was used to investigate the potential distribution of the 23 most commonly traded non-native reptile species in the Middle East. Thus, the aims of this study were as follows: (1) to identify potential distributions of the 23 most commonly traded non-native reptile species in the Middle East; (2) to determine the important environmental variables that shape the variations in the potential geographic range of non-native species; and (3) identify countries in the Middle East that are at risk of biological invasion by these 23 species.

Methods

Studied species and presence points

In this study, 23 species which met two criteria were selected: 1) the species had to be widely traded globally and 2) an adequate number of presence points had to be accessible for the species (more than 50 presence points). We initially found 89 species that were traded on social media, unofficial platforms, and on the black market, but only 23 species of the initial set had enough presence points to be used for modeling. We compiled presence points for the 23 species from the Global Biodiversity Information Facility (GBIF), VertNet, iNaturalist, and Berkeley Ecoinformatics Engine. GBIF is an international platform aiming to provide publicly-available data on life on Earth. GBIF focuses on providing templates, standards, and tools for sharing information between institutions and individuals. Data available on GBIF come from a number of sources including field observations by experts and citizen scientists, museum records, and surveys. VertNet is an NSF-funded project created through the combination of four taxon-specific repositories (FishNet, MaNIS, HerpNet, ORNIS) to make biodiversity data available online. iNaturalist, jointly funded by California Academy of Sciences and National Geographic is a crowdsourced species identification system and a platform to record presence points. Berkeley Ecoinformatics Engine allows access to several biodiversity information repositories (<https://holos.berkeley.edu/LearnMore/datasources/>) through its R package. Each database was accessed through their respective packages in R ("rgbif", "rvertnet", "rinat", and "ecoengine" respectively). Queries were made using the scientific name of the species, and georeferenced presence points from January 1, 1998 to January 1, 2018 were extracted. In this study, we used data from the last 20 years to minimize the error in the data (Alhajeri and Fourcade, 2019). Here, we used the datasets for both native and non-native geographical ranges of the specie. In order to obtain more accurate results in modelling, presence points were compared with the native range of the species. In the next step, only the none-native range in countries where established populations of the species had been reported was included (Cordier et al., 2020). In cases where the same data point was recorded more than once, duplicates were omitted in R. After removing duplicates, presence points were used to model the potential distribution of the species. Moran's correlograms were created in Spatial Analysis in Macroecology (SAM; Rangel et al., 2006) to determine spatial autocorrelation for the species. The significance of Moran's I was tested using a randomization test with 9,999 Monte Carlo permutations, adjusted for multiple testing. In instances where spatial autocorrelation was detected, we restricted the testing and training data as follows: first, a distance threshold was set using distance lags which showed positive spatial autocorrelation (from 10 to 25 km); in the next step, the distance between data pairs was compared with the threshold, and pairs which had a distance smaller than the threshold were placed in the same partition (Parolo et al., 2008). Given that we only had access to species presence points, a number of pseudo-absences were randomly generated (Elith et al., 2011).

Environmental variables

Environmental variables include climatic, topographic, and land cover/land use variables. The variables were selected according to species ecology, the factors determining the distribution of reptiles, and availability of data (e.g. Block et al., 2016; Ribeiro-Júnior & Amaral, 2016; Sanchooli, 2017). An initial set of 19 climatic variables were downloaded from WorldClim 1.4 (Hijmans et al., 2005) at 1-km resolution (<https://www.worldclim.org/>). Four topographic variables (mean and standard deviation (SD) of elevation, and slope of all raster cells) were derived from the digital elevation model provided by the Shuttle Radar Topography Mission (SRTM) digital elevation model at 90-m resolution (<http://srtm.csi.cgiar.org>). 16-day composite normalized difference vegetation index (NDVI) data collected by the Moderate Resolution Imaging Spectrometer for the year 2019 at 500-m resolution (MODIS; <http://lpdaac.usgs.gov>). The land cover map (including 17 classes: 11 natural vegetation classes, three human-altered classes, and three non-vegetated classes) were derived from the combination of MODIS Terra and Aqua data at 500-m resolution (<https://modis.gsfc.nasa.gov>). To evaluate human impact on the reptile, we calculated the human footprint index using data on settlements, land transformation, accessibility and infrastructure.

To exclude highly-correlated inputs, all pairs of variables were checked for correlation using Pearson's correlation coefficient (r) in SDMTtoolbox (Brown, 2014) for ArcGIS. $r > 0.70$ and $r < -0.75$ were considered as the threshold values, and variables with stronger correlation were excluded (Kalboussi & Achour, 2018), resulting in a final set of 14 variables (including: 9 climatic, 2 topographic, and 3 land cover/land use variables) (Table 1).

Modelling techniques and ensemble forecasting

Four categories of modelling techniques, encompassing 10 algorithms, were implemented in the Biomod2 package with 80/20 calibration and evaluation, bootstrapping with 10 cycles, 0.5 prevalence, and a high 0.70 quality threshold (Thuiller et al., 2009; 2014) for R version 3.1.25 (R Core Team, 2014). Algorithms in the regression category included generalized linear models (GLMs) and generalized additive models (GAMs), which respectively calculate linear and non-linear correlation between input variables and species presence. Algorithms in the machine learning category included, maximum entropy (MaxEnt), boosted regression trees (BRT), random forest (RF), artificial neural networks (ANN), and multivariate adaptive regression splines (MARS). These algorithms directly predict the environmental space of species according to training data. The classification algorithms included classification and regression trees (CART) and flexible discriminate analyses (FDA), both of which divide data into homogeneous groups in a series of consecutive steps. Finally, the surface range envelope (SRE) algorithm attempts to first describe the ecological conditions in which a species is found, and then find areas with similar conditions (Elith and Leathwick, 2009; Franklin, 2010; Guisan and Thuiller, 2005; Merow et al., 2014).

Only algorithms that met the 0.7 quality threshold were included in the ensemble calculations; those that do not meet this standard were discarded (Thuiller et al., 2009, 2014). To compensate for variation between the number of pseudo-absences (PA), replicates, and model runs based on which algorithm is used, we grouped the 10 algorithms into three PA subsets to allow for optimal ensemble model performance Groups 1, 2, and 3 (Table 3; Barbet-Massin et al., 2012; Brown and Yoder, 2015; Bevan et al., 2019). Group results were compared for accuracy using the true skill statistic (TSS; scaled -1 to +1, where performance ≤ 0 means the model output is no better than random and > 0 means the proposed model successfully distinguishes between suitable and unsuitable habitat). Models were also evaluated for sensitivity and specificity. Sensitivity is the accuracy rate for true positive outcomes (i.e., the probability that the model correctly predicted presence). Specificity is the accuracy rate for true negative outcomes (i.e., the probability that the model correctly predicted absence) (Allouche et al., 2006). Finally, we used a quality threshold to accept models and TSS, sensitivity and specificity values to compare and select among alternative ensemble SDMs (Table 4).

Variable importance is determined in Biomod2 package using permutation as follows: after models are calibrated, a baseline prediction is generated. In the next step, the values of one variable are randomized and a new prediction is generated using the randomized values of the randomized variable and the unchanged values of other variables. The correlation between the baseline prediction and the new prediction (using one randomized variable) indicates the relative importance of the variable that has been randomized (Thuiller et al., 2009). This procedure does not depend on the modelling algorithms employed.

Results

Evaluation of modeling results based on the TSS, sensitivity and specificity values showed that the ensemble SDMs performed better than individual models (Table 4).

Results of variable importance tests showed that the importance of environmental variables varied for different species. The three most important environment variables that determine species potential geographic distributions are shown in Table 2. The most important environmental variables in predicting potential geographic distribution for most of the species were temperature seasonality, land cover, and NDVI.

The potential distribution maps of the ensemble model for each species are presented in Fig 1. The current overlap between suitable habitats and the Middle East is shown in Table 5. The results show that only small parts of the Middle East are suitable for most species. The results also demonstrated that different countries vary in terms of the percentage of their land area that can be considered suitable for different species. Among Middle Eastern countries, Iran and Oman have the potential to host more species than others, whereas Iraq and UAE provide suitable habitats for fewer species. Yellow Bellied Slider had the highest (17.25%), and Amazon Tree Boa and Burmese Python had the lowest (0%) the area of suitable habitats among all studied species in the Middle East as a whole. The models did not predict suitable habitats for any of the species in Bahrain, Kuwait, and Qatar. No Middle Eastern country showed the potential distribution for Amazon Tree Boa and Burmese Python. More than 50% of the land area of Palestine, Lebanon, and Israel is a suitable habitat for Veiled Chameleon and African Spurred Tortoise. The risk of invasion by African Spurred Tortoise is high in Lebanon and Palestine since more than 90% of the land area of these countries is suitable habitat for African Spurred Tortoise. Similarly, more than 60% percent of the land area of Turkey, Palestine and Lebanon were defined as suitable for Yellow Bellied Slider. Turkey was the only country with suitable areas for Reticulated Python and Wood Turtle. While the model predicted suitable habitats for Radiated Tortoise to be located exclusively in Yemen, all countries except Bahrain, Kuwait, and Qatar contain regions that are potentially suitable habitats for Veiled Chameleon. Furthermore, the model showed that African Spurred Tortoise's suitable habitat can be found in all countries except Bahrain, Kuwait, Qatar, and Yemen.

Considering the area of suitable habitats for the studied species, this study showed that Lebanon, Palestine, Turkey, and Israel face the highest risk of biological invasion by the species on the whole. We ranked countries in the Middle East in the order of highest to lowest risk of biological invasion (Fig 2a). We also ranked the studied species based on their risk of biological invasion; accordingly, African Spurred Tortoise, Veiled Chameleon, and Yellow Bellied Slider had the highest risk of spreading in this area (Fig 2b).

Discussion And Conclusion

The results revealed the significant role of climatic and land cover/land use variables in determining the suitable habitat for the studied species. Our results are in line with findings by similar studies in other regions such as the Zagros Mountains, western Iran (Hosseinzadeh et al., 2017), South Central USA (Salas et al., 2017), Northwest China (Xu, 2015), North Africa (Martínez-Freiría et al., 2013), Egypt (El-Gabbas et al., 2016), northern Mexico (Gadsden et al., 2012), and India (Rakholia et al., 220).

Our results indicate that all Middle Eastern countries included suitable habitats for at least six species, except Qatar, Kuwait and Bahrain for which the models did not predict any suitable habitats. Our study showed that Lebanon, Palestine, Turkey, and Israel face the highest risk of biological invasion by the species on the whole (Fig. 2a). Previous studies in these countries have not paid much attention to the invasion and trade of non-native reptiles, which makes the management and conservation of these species difficult or even impossible. Also, the results showed that African Spurred Tortoise, Veiled Chameleon, and Yellow Bellied Slider posed the highest risk of spreading in this area (Fig. 2b). Although these species have limited global range, their ability to spread in other parts of the world should be taken into consideration.

The Veiled Chameleon is natively found in Saudi Arabia and Yemen, mostly in plateaus and grasslands (Showler, 1995; Schmidt, 2001). The species has been introduced in Hawaii (Kraus and Duvall, 2004; Kraus 2009) and Florida (Gillette and Krysko, 2012; Edwards et al., 2014; Dalaba et al., 2019) in the United States, where it is now commonly found. The Yellow Bellied Slider naturally occurs in the Mississippi Valley, its range stretching from Illinois to the Gulf of Mexico. In the last five decades, the Yellow Bellied Slider has been grown commercially in the US for pet trade, and grown turtles have been accidentally released into urban and natural landscapes (Cadi, et al., 2004). The species has been reported from a number of countries including Australia (Burgin, 2006), Brazil (Ferronato et al., 2009), France (Prévot-Julliard et al., 2007), Japan (Oi et al., 2012), and South Africa (Newbery, 1984). Due to its extensive global spread, the species has been categorized as one of the 100 worst invasive species (ISSG, 2021). The African Spurred Tortoise ranks second among terrestrial turtles in terms of size, and naturally occurs in the western parts of the Sahel region. Although it is a threatened species and its population has been in decline through its range, little information is available about the causes of this decline. Researchers have pointed to competition with cattle, wildfires, and pet trade as the possible drivers of the decline in its population (Petrozzi et al., 2018). Despite the species having been reported from other countries, it is not clear whether it has been able to establish populations outside its native range.

Wildlife managers should pay attention to species potential of invasion when making decisions about the import of non-native species into their countries. Although the model did not indicate any areas with a potential distribution for Amazon Tree Boa and Burmese Python, managers should exercise caution when making decisions about these species as well, and refer to previous studies or conduct more detailed research to further assess the risks associated with non-native species.

SDMs take into account only the bioclimatic realized niche of species, meaning that the model assumes the species is only able to establish in areas with a similar climate to its native range (Kearney 2006). It is obvious that biotic and abiotic factors and their interactions can alter a species' realized niche (Broennimann et al., 2007). This leads to the generated niche predictions in the new environments being only rough approximations. Consequently, a mismatch between bioclimatic conditions in the native and introduced range can lead models to underestimate the extent of suitable areas. Further studies focusing on each species and utilizing a wider range of data with better accuracy, including biotic variables, abiotic variables, and their interactions are needed to make more nuanced judgments about each species. Such studies would also benefit from a comparison with areas that have the studied species as invasive species.

In the meantime, managers should not interpret the absence of suitable habitats for some of the studies species as a license for unrestricted import or introduction. Thus, the findings of this study are mainly helpful as a basis for imposing restrictions on species for which a suitable habitat was found; our findings should not be seen as justification for allowing the introduction of species or loosening regulations. However, SDMs can still serve as the first step in understanding the biological invasion history of species (Silva Rocha et al., 2015). The results of the current model need refinement and further investigation to clarify the role of different factors in determining species distributions. Future studies should address niche shift and resolve the most important factors underlying species distribution.

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Availability of data and materials

Some or all data, models, or code that support the findings of this study are available from the corresponding author upon reasonable request.

Competing interests

Not applicable

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Not applicable

Authors' contributions

Azita Farashi: Writing and modelling, Mohammad Alizadeh-Noughani: Writing

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Tables

Table 1
Pearson correlation coefficient matrix of environmental variables (values in bold are $r > 0.70$ and $r < -0.70$)

Variable	C19	C18	C17	C16	C15	C14	C13	C12	C11	C10	C9	C8	C7	C6	C5	C4	C3	C2
C19																		
C18	0.34																	
C17	0.67	0.55																
C16	0.50	0.77	0.39															
C15	-0.29	-0.09	-0.52	0.16														
C14	0.65	0.53	0.99	0.36	-0.51													
C13	0.47	0.74	0.35	0.99	0.21	0.32												
C12	0.68	0.82	0.71	0.91	-0.14	0.68	0.87											
C11	0.19	0.13	0.01	0.38	0.42	-0.01	0.38	0.30										
C10	-0.13	-0.20	-0.28	-0.02	0.48	-0.28	0.01	-0.15	0.71									
C9	0.15	-0.11	-0.06	0.15	0.29	-0.08	0.16	0.10	0.84	0.74								
C8	-0.12	0.17	-0.12	0.20	0.47	-0.13	0.22	0.09	0.58	0.62	0.24							
C7	-0.42	-0.41	-0.32	-0.59	-0.12	-0.29	-0.58	-0.61	-0.79	-0.17	-0.56	-0.30						
C6	0.24	0.20	0.08	0.43	0.37	0.06	0.44	0.37	0.99	0.65	0.82	0.56	-0.85					
C5	-0.21	-0.27	-0.35	-0.11	0.51	-0.35	-0.08	-0.25	0.64	0.98	0.69	0.72	-0.05	0.56				
C4	-0.33	-0.30	-0.19	-0.52	-0.25	-0.17	-0.51	-0.50	-0.89	-0.32	-0.66	-0.39	0.96	-0.92	-0.24			
C3	0.07	0.05	0.03	0.10	0.07	0.03	0.10	0.09	0.18	0.12	0.14	0.12	-0.14	0.17	0.11	-0.17		
C2	-0.36	-0.76	-0.46	-0.37	0.44	-0.45	-0.35	-0.50	0.24	0.52	0.31	0.26	0.28	0.12	0.67	0.01	0.08	
C1	0.07	0.03	-0.10	0.26	0.48	-0.11	0.27	0.16	0.96	0.87	0.85	0.65	-0.62	0.64	0.66	-0.64	0.17	0.3
TMS	0.01	0.03	0.01	0.03	0.03	0.01	0.03	0.03	0.03	0.01	0.01	0.03	0.00	0.01	0.03	-0.03	0.02	0.1
TSS	0.01	0.03	0.01	0.03	0.03	0.01	0.03	0.03	0.03	0.01	0.01	0.03	0.00	0.01	0.03	-0.03	0.02	0.1
TME	-0.10	-0.05	-0.14	-0.06	0.11	-0.14	-0.06	-0.09	-0.10	-0.20	-0.09	-0.17	0.08	-0.13	-0.11	0.01	0.04	0.2
TSE	-0.10	-0.05	-0.14	-0.06	0.11	-0.14	-0.06	-0.09	-0.10	-0.20	-0.09	-0.17	0.08	-0.13	-0.11	0.01	0.04	0.2
LV	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.0
NDVI	0.06	0.03	0.00	0.30	0.71	-0.70	0.29	0.20	0.43	0.67	0.51	0.50	-0.41	0.64	0.71	-0.70	0.12	0.3
HFI	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.0
Climatic variables: C1 (Annual Mean Temperature), C2 (Mean Diurnal Range), C3 (Isothermality), C4 (Temperature Seasonality), C5 (Max Temperature of Warmest Quarter), C6 (Mean Temperature of Wettest Quarter), C7 (Mean Temperature of Driest Quarter), C8 (Mean Temperature of Warmest Quarter), C9 (Mean Temperature of Driest Quarter), C10 (Mean Temperature of Warmest Quarter), C11 (Precipitation of Wettest Month), C12 (Precipitation of Driest Month), C13 (Precipitation of Wettest Month), C14 (Precipitation of Driest Month), C15 (Precipitation Seasonality), C16 (Precipitation of Wettest Quarter), C17 (Precipitation of Driest Quarter), C18 (Precipitation of Wettest Quarter), C19 (Precipitation of Driest Quarter)																		
Topographic variables: TME (Mean of the Elevation), TSE (Standard Deviation of the Elevation), TMS (Mean of the Slope), TSS (Standard Deviation of the Slope)																		
Land cover/land use variables: LV (Land Cover), NDVI (Normalized Difference Vegetation Index), HFI (Human Footprint Index)																		
Selected variables to model: C1, C3, C4, C5, C12, C16, C17, C18, C19, TME, TMS, LV, NDVI, HFI																		

Table 2
Studied reptile species and the three most important environmental variables that determine their potential geographic distributions.

Scientific name	Common name	Statues		The number of presence points	Important environmental variables		
		IUCN	CITES		(Relative contribution, %)		
<i>Anolis carolinensis</i> (Voigt, 1832)	Green Anole	LC	-	9938	C17 (60)	C3 (10)	TME (9)
<i>Astrochelys radiata</i> (Shaw, 1802)	Radiated Tortoise	CR	I	62	C18 (40)	C3 (30)	C4 (10)
<i>Boa constrictor</i> (Linnaeus, 1758)	Common Boa	DD	II	585	C12 (40)	C6 (39)	C16 (11)
<i>Centrochelys sulcata</i> (Miller, 1779)	African Spurred Tortoise	VU	II	89	NDVI (35)	C12 (28)	NDVI (17)
<i>Chamaeleo calypttratus</i> (Duméril & Bibron, 1851)	Veiled Chameleon	LC	II	84	C19 (54)	C3 (18)	C12 (10)
<i>Corallus hortulanus</i> (Linnaeus, 1758)	Amazon Tree Boa	LC	II	102	C4 (52)	NDVI (19)	C12 (11)
<i>Emys orbicularis</i> (Linnaeus, 1758)	European Pond Turtle	NT	-	1136	C1 (47)	C12 (20)	C4 (8)
<i>Eunectes murinus</i> (Linnaeus, 1758)	Green Anaconda	DD	-	80	C19 (49)	C4 (20)	NDVI (10)
<i>Glyptemys insculpta</i> (Le Conte, 1830)	Wood Turtle	EN	II	344	C16 (32)	C17 (19)	C19 (11)
<i>Gopherus agassizii</i> (Cooper, 1863)	Desert Tortoise	VU	II	614	C1 (51)	C6 (21)	C5 (9)
<i>Iguana iguana</i> (Linnaeus, 1758)	Green Iguana	DD	II	4114	C6 (50)	C4 (22)	TME (5)
<i>Morelia viridis</i> (Schlegel, 1872)	Green Tree Python	LC	II	134	C18 (44)	C4 (14)	C1 (8)
<i>Pantherophis guttatus</i> (Linnaeus, 1766)	Corn Snake	LC	-	667	C17 (45)	C16 (28)	TME (7)
<i>Physignathus Cocincinus</i> (Cuvier, 1829)	Asian Water Dragon	DD	-	60	C12 (45)	NDVI (30)	C18 (8)
<i>Pogona barbata</i> (Cuvier, 1829)	Common Bearded Dragon	LC	-	1921	C4 (48)	C3 (26)	C6 (11)
<i>Python bivittatus</i> (Kuhl, 1820)	Burmese Python	VU	II	855	C18 (46)	C6 (32)	C4 (8)
<i>Python regius</i> (Shaw, 1802)	Ball Python	LC	II	347	C19 (41)	C12 (30)	NDVI (12)
<i>Python reticulatus</i> (Schneider, 1801)	Reticulated Python	DD	II	51	C6 (51)	C4 (31)	C1 (7)
<i>Stigmochelys pardalis</i> (Bell, 1828)	Leopard Tortoise	LC	II	308	C3 (49)	C18 (14)	C1 (7)
<i>Terrapene carolina</i> (Linnaeus, 1758)	Common Box Turtle	VU	II	7854	C17 (61)	C12 (15)	NDVI (5)
<i>Testudo hermanni</i> (Gmelin, 1789)	Hermann's Tortoise	NT	II	498	C1 (51)	C12 (13)	C19 (5)
<i>Trachemys scripta</i> (Thunberg in Schoepff, 1792)	Yellow Bellied Slider	LC	-	9055	NDVI (50)	C12 (19)	NDVI (12)
<i>Varanus niloticus</i> (Linnaeus, 1766)	Nile Monitor	DD	II	660	C3 (34)	C4 (21)	NDVI (8)
IUCN Red List Categories: CR (Critically Endangered), EN (Endangered), VU (Vulnerable), NT (Near Threatened), LC (Least Concern), and DD (Data Deficient).							
CITES Appendices: I (it lists species that are the most endangered among CITES-listed animals and plants), and II (it lists species that are not necessarily now threatened with extinction but that may become so unless trade is closely controlled).							

Table 3
The species distribution models in Biomod2 used in this research and their required type of dependent variables

Group	Algorithms	Replicates	Runs	Number of pseudo-absences
1	Artificial neural networks (ANN) (Lek and Guegan, 1999) Surface range envelope (SRE) (Busby, 1991) Generalized additive models (GAM) (Guisan et al., 2002) Generalized linear models (GLM) (Guisan et al., 2002) Maximum entropy (MaxEnt) (Phillips et al., 2006)	5	10	1000
2	Random forest (RF) (Breiman, 2001) Boosted regression trees (BRT) (Elith et al., 2008) Classification and regression trees (CART) (Vayssieres et al., 2000)	5	10	1000
3	Flexible discriminant analysis (FDA) (Hastie et al., 1994) Multivariate adaptive regression splines (MARS) (Friedman, 1991)	7	10	100

Table 4 Accuracy metrics for all models (SEN: sensitivity, SPE: specificity, TSS: true skill score)																			
Species	ANN		SRE			GAM			GLM			MaxEnt			RF			E	
	SEN	SPE	TSS	SEN	SPE	TSS	SEN	SPE	TSS	SEN	SPE	TSS	SEN	SPE	TSS	SEN	SPE	TSS	S
Green Anole	0.76	0.73	0.81	0.70	0.70	0.71	0.81	0.77	0.70	0.88	0.73	0.81	0.82	0.83	0.71	0.74	0.75	0.73	C
Radiated Tortoise	0.84	0.72	0.88	0.66	0.70	0.73	0.81	0.90	0.90	0.85	0.90	0.73	0.80	0.73	0.92	0.73	0.70	0.80	C
Common Boa	0.81	0.90	0.83	0.72	0.59	0.73	0.92	0.72	0.76	0.72	0.84	0.85	0.69	0.80	0.78	0.91	0.72	0.72	C
African Spurred Tortoise	0.85	0.72	0.85	0.59	0.70	0.72	0.90	0.89	0.89	0.76	0.69	0.89	0.72	0.65	0.82	0.69	0.89	0.74	C
Veiled Chameleon	0.82	0.84	0.81	0.70	0.70	0.73	0.81	0.76	0.84	0.66	0.84	0.81	0.89	0.70	0.73	0.80	0.85	0.81	C
Amazon Tree Boa	0.85	0.70	0.90	0.59	0.65	0.72	0.83	0.69	0.89	0.69	0.76	0.81	0.65	0.84	0.70	0.84	0.66	0.74	C
European Pond Turtle	0.73	0.84	0.78	0.76	0.70	0.72	0.79	0.70	0.76	0.85	0.85	0.92	0.85	0.72	0.72	0.89	0.73	0.74	C
Green Anaconda	0.81	0.73	0.83	0.65	0.59	0.73	0.88	0.81	0.81	0.66	0.65	0.84	0.80	0.66	0.73	0.69	0.70	0.74	C
Wood Turtle	0.73	0.85	0.83	0.70	0.70	0.72	0.90	0.73	0.75	0.65	0.80	0.75	0.81	0.85	0.85	0.72	0.66	0.85	C
Desert Tortoise	0.72	0.76	0.81	0.59	0.69	0.70	0.80	0.65	0.84	0.81	0.76	0.73	0.81	0.66	0.76	0.65	0.81	0.74	C
Green Iguana	0.84	0.70	0.82	0.65	0.70	0.79	0.83	0.76	0.73	0.73	0.89	0.76	0.77	0.70	0.77	0.89	0.89	0.72	C
Green Tree Python	0.81	0.72	0.92	0.65	0.70	0.70	0.83	0.80	0.89	0.80	0.81	0.89	0.76	0.76	0.81	0.70	0.76	0.74	C
Corn Snake	0.82	0.81	0.91	0.77	0.59	0.72	0.84	0.72	0.80	0.82	0.73	0.76	0.80	0.70	0.70	0.66	0.77	0.76	C
Asian Water Dragon	0.70	0.73	0.93	0.72	0.70	0.75	0.65	0.65	0.72	0.66	0.77	0.72	0.65	0.89	0.72	0.85	0.84	0.92	C
Common Bearded Dragon	0.73	0.82	0.88	0.72	0.70	0.73	0.85	0.66	0.85	0.84	0.72	0.77	0.84	0.85	0.89	0.69	0.70	0.80	C
Burmese Python	0.84	0.73	0.83	0.59	0.66	0.72	0.65	0.81	0.73	0.77	0.73	0.84	0.89	0.69	0.70	0.72	0.73	0.72	C
Ball Python	0.72	0.73	0.84	0.70	0.70	0.73	0.81	0.65	0.90	0.72	0.80	0.89	0.80	0.72	0.76	0.80	0.90	0.84	C
Reticulated Python	0.81	0.72	0.81	0.69	0.59	0.72	0.65	0.80	0.84	0.65	0.65	0.72	0.69	0.66	0.92	0.82	0.89	0.74	C
Leopard Tortoise	0.72	0.81	0.80	0.72	0.76	0.73	0.84	0.73	0.90	0.73	0.72	0.92	0.82	0.65	0.73	0.90	0.72	0.92	C
Common Box Turtle	0.73	0.69	0.90	0.69	0.72	0.76	0.65	0.70	0.70	0.77	0.76	0.76	0.89	0.76	0.89	0.76	0.90	0.85	C
Hermann's Tortoise	0.84	0.70	0.85	0.70	0.69	0.73	0.73	0.69	0.90	0.73	0.77	0.73	0.73	0.73	0.76	0.90	0.73	0.80	C
Yellow Bellied Slider	0.73	0.70	0.79	0.59	0.70	0.72	0.70	0.77	0.81	0.69	0.70	0.70	0.81	0.70	0.73	0.84	0.69	0.92	C
Nile Monitor	0.89	0.77	0.75	0.70	0.77	0.73	0.77	0.89	0.77	0.89	0.80	0.77	0.89	0.90	0.80	0.90	0.77	0.89	C

Table 5
The areas of suitable habitats for studied species (the highest values are in bold).

Species	Suitable habitats for studied species											
		Emirates	Egypt	Iran	Iraq	Israel	Jordan	Lebanon	Oman	Palestine	Saudi Arabia	Syria
Green Anole	Km ²	38.59	0	24368.84	34.25	0	0	3156.97	38.53	0	0	139
	%	0.05	0	1.50	0.01	0	0	31.53	0.01	0	0	7.5
Radiated Tortoise	Km ²	0	0	0	0	0	0	0	0	0	0	0
	%	0	0	0	0	0	0	0	0	0	0	0
Common Boa	Km ²	38.59	0	19987.60	0	380.57	108.39	1225.33	1990.37	127.99	0	426
	%	0.05	0	1.23	0	1.71	0.12	12.24	0.64	2.05	0	2.30
African Spurred Tortoise	Km ²	57.91	39047.87	166030.71	53941.71	18415.04	21219.85	9391.26	2757.50	6057.29	1646.56	338
	%	0.08	3.91	10.25	12.36	82.72	23.88	93.80	0.89	97.08	0.09	18.1
Veiled Chameleon	Km ²	4171.19	4873.81	232053.38	2958.64	11803.12	8830.22	6469.14	25438.67	5511.16	104402.26	203
	%	5.85	0.49	14.32	0.68	53.02	9.94	64.62	8.17	88.33	5.43	10.9
Amazon Tree Boa	Km ²	0	0	0	0	0	0	0	0	0	0	0
	%	0	0	0	0	0	0	0	0	0	0	0
European Pond Turtle	Km ²	0	454.49	90487.52	0	0	0	3119.83	59.06	0	58.94	911
	%	0	0.05	5.59	0	0	0	31.16	0.02	0	0.00	4.9
Green Anaconda	Km ²	57.91	54.87	648.52	0	1756.87	0	2896.81	250.61	146.22	0	175
	%	0.08	0.01	0.04	0	7.89	0	28.93	0.08	2.34	0	0.91
Wood Turtle	Km ²	0	0	0	0	0	0	0	0	0	0	0
	%	0	0	0	0	0	0	0	0	0	0	0
Desert Tortoise	Km ²	0	0	216799.14	0	0	0	0	433.52	0	560.12	433
	%	0	0	13.38	0	0	0	0	0.14	0	0.03	0.21
Green Iguana	Km ²	0	0	1185.07	0	0	0	2149.38	1308.34	0	1122.11	131
	%	0	0	0.07	0	0	0	21.47	0.42	0	0.06	0.7
Green Tree Python	Km ²	1774.32	677.79	38632.42	0	3623.75	1992.91	106.81	329.73	1459.78	780.48	89.1
	%	2.49	0.07	2.38	0	16.28	2.24	1.07	0.11	23.40	0.04	0.01
Corn Snake	Km ²	0	0	25860.74	0	0	0	1821.93	253.31	0	0	126
	%	0	0	1.60	0	0	0	18.20	0.08	0	0	6.8
Asian Water Dragon	Km ²	0	33725.08	3612.00	0	0	0	0	79.07	0	0	0
	%	0	3.37	0.22	0	0	0	0	0.03	0	0	0
Common Bearded Dragon	Km ²	0	0	996.29	0	0	0	0	2504.10	18.28	1152.75	0
	%	0	0	0.06	0	0	0	0	0.80	0.29	0.06	0
Burmese python	Km ²	0	0	0	0	0	0	0	0	0	0	0
	%	0	0	0	0	0	0	0	0	0	0	0
Ball Python	Km ²	0	0	532.52	0	468.76	126.47	106.62	134.91	0	0	123
	%	0	0	0.03	0	2.11	0.14	1.06	0.04	0	0	0.01
Reticulated Python	Km ²	0	0	0	0	0	0	0	0	0	0	0
	%	0	0	0	0	0	0	0	0	0	0	0
Leopard Tortoise	Km ²	0	36.85	125.05	0	941.00	90.31	0	511.91	181.38	8691.56	0

	%	0	0.00	0.01	0	4.23	0.10	0	0.16	2.91	0.45	0
Common Box Turtle	Km ²	0	0	2416.07	102.35	0	0	88.39	117.45	0	0	140
	%	0	0	0.15	0.02	0	0	0.88	0.04	0	0	0.76
Hermann's Tortoise	Km ²	0	0	28835.95	0	287.80	0	2881.39	0	0	0	452
	%	0	0	1.78	0	1.29	0	28.78	0	0	0	2.44
Yellow Bellied Slider	Km ²	77.22	0	614677.89	8218.48	2442.59	7977.13	6393.26	5340.91	4131.13	12577.05	310
	%	0.11	0	37.94	1.88	10.97	8.98	63.86	1.72	66.21	0.65	16.7
Nile Monitor	Km ²	0	0	0	0	0	0	0	415.05	0	0	0
	%	0	0	0	0	0	0	0	0.13	0	0	0

Figures

Figure 1
Potential distribution map of the studied species in the world (red: suitable habitats, gray: unsuitable habitats)

Figure 2

The areas of suitable habitats for countries (a) and studied species (b).