DISTRIBUTION PATTERNS OF BATS IN EASTERN MEDITERRANEAN REGION THROUGH A CLIMATE CHANGE PERSPECTIVE

by

Ari Keşişoğlu

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This thesis is dedicated to my wife Selay, who fully supported me throughout the process.

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DISTRIBUTION PATTERNS OF BATS IN EASTERN MEDITERRANEAN REGION THROUGH A CLIMATE CHANGE PERSPECTIVE

The impact of climate change on different species has been analyzed multiple times in various geographies. The main aim of this study was to determine how climate change will affect 18 different bats species in the eastern Mediterranean region. Using presence only modelling techniques and relevant bioclimatic data forecasts according to two different climate change scenarios (A2A and B2A) of Intergovernmental Panel on Climate Change (IPCC), the potential geographic distribution of bat species in the eastern Mediterranean region for current period and the years 2020, 2050 and 2080 was modelled. The results suggest that climate change will affect bats negatively throughout the 21st century in the studied area on two fronts: i) species richness will deteriorate, and ii) the total area occupied by bats will decline. These impacts will be more severely observed in Turkey's coastal areas, northwest Turkey, Red Sea coasts, Israel, and west of Syria and Jordan. Using only bioclimatic variables as factors and thus not using any land cover (or habitat) data was the main limitation of the study. Hence the models and results of the study present "best case" scenarios.

İKLİM DEĞİŞİKLİĞİ PERSPEKTİFİNDE DOĞU AKDENİZ BÖLGESİ'NDE BULUNAN YARASALARIN DAĞILIM ŞEKİLLERİ

İklim değişikliğinin farklı türlere etkisi çeşitli coğrafyalarda birçok kez analiz edilmesine rağmen Türkiye ve çevresini kapsayan bölgede bu tür araştırmalar pek bulunmamaktadır. Bu çalışmanın amacı iklim değişikliğinin 18 farklı yarasa türünü Doğu Akdeniz Bölgesi'nde nasıl etkileyeceğini belirlemektir. Çalışmada türlerin farklı noktalardaki gözlem verisi ve bu noktalardaki ilgili iklim tahminleri kullanılarak yarasa türlerinin 2020, 2050 ve 2080 yıllarındaki potansiyel coğrafi dağılımı hesaplandı. Modellemelerde Intergovernmental Panel on Climate Change (IPCC)'nin iki farklı iklim değişikliği senaryoları (A2A ve B2A) ana faktör olarak kullanıldı. Sonuçlar iklim değişikliğinin yarasaların çalışılan coğrafyada 21.yüzyıl boyunca iki alanda (yarasa tür çeşitliliğinin azalması ve yarasaların yaşayabilecekleri toplam alanın azalması) olumsuz olarak etkileneceğini ortaya çıkardı. Bu etkiler daha ciddi olarak Türkiye'nin kıyı alanlarında, Türkiye'nin kuzeybatısında, Kızıldeniz'in kıyı alanlarında, İsrail, ve Suriye ve Ürdün'ün batısında gözleneceği sonucu ortaya çıkmıştır. Çalışmadaki ana sınırlama, etkileyici faktör olarak sadece iklim değişkenlerinin kullanılması ve buna bağlı olarak herhangi bir arazi örtüsü veya yaşama alanı verisinin gözardı edilmesi oldu.Bu kısıtlamalar dolayısıyla bu modelleme çalışması "olabilecek en iyi senaryo" şeklinde yorumlanmalıdır.

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LIST OF SYMBOLS/ABBREVIATIONS

Abbreviation	Explanation
AUC	Area Under Curve
HadCM3	Hadley Centre Coupled Model, version 3
IPCC	Intergovernmental Panel on Climate Change
ROC	Receiver Operating Characteristics

1. INTRODUCTION

1.1. Climate Change and Recent Climate Data

Throughout the history of the earth, the climate has shown certain volatility, over a wide range of climatic parameters including temperature levels. It is believed that temperature volatility has been slightly but consistently on the positive side in the last few decades. The evidence can be observed in the consistent pattern of increase in global temperature levels since 1850s. It has been stated that current and predicted climate change may result from natural climate oscillations of the planet (IPCC, 2007).

The sun warms our planet through radiation energy, and the thermal radiation from the Earth and the atmosphere is radiated out to space (Houghton, 2005). Under normal conditions these two forces should balance each other out, leaving the temperature constant over time. If there has been an increase in the temperature, something should have been affecting this process. Global warming due to an increase in greenhouse gases is the most accepted explanation to this increase.

Some gases such as carbon dioxide, methane, nitrous oxide and chlorofluorocarbons (called greenhouse gases as a group) can absorb thermal radiation emitted by the earth. This provides a warmer climate in the planet and is necessary for the creation of climate conditions preferable to humans.

For the greenhouse effect to actually result in global warming, an increase in the global temperature should have been preceded by an increase in the amount of greenhouse gases in the atmosphere. An analysis of the data on greenhouse concentrations over time shows that the concentration of these gases started to increase during the first half of the 20th century and has been growing at an increasing pace (Working Group I of the Intergovernmental Panel on Climate Change, 2001). These data confirm that there was an increase in greenhouse gas concentrations prior to temperature increases observed in the second half of 20th century. The data also suggests that the slight increases in temperature will continue in the coming decades as the greenhouse gases only increased in concentration during last few decades (Working Group I of the Intergovernmental Panel on Climate Change, 2001).

One way of assessing whether current temperature increase is normal or unexpected is to forecast the average temperature based on past data, and compare the observed temperatures against this forecast. With recent technological improvements, more accurate quantifications of the forecasted climate conditions can be made. Such a comparison of actual observations and forecasts of temperature for the 20th century reveals that observed temperatures have been consistently higher than the forecasted ones since 1960s (IPCC, 2007). The temperature increase is directly coupled with an expected increase in global sea levels and decrease in areas covered by snow and glaciers (IPCC, 2007).

1.2. Impact of Climate Change on Animal Species

There is evidence that this warming has already had ecological impacts. For instance, Root et al. (2003) examined 143 studies on the impact of climate change on wild animals and plants. They have observed a consistent temperature related geographical shift, or "fingerprint", of various animals and plants. Within these studies, they looked at data for 1468 species, of which 81.1% (90% confidence interval: 74.2-86.5%) had a temperature related shift in the expected direction (Root et al., 2003). The shifts are observed even in minor (<1°C) temperature changes. The basic implication of this finding is that temperature change causes animals with high dispersal ability to change their geographic distribution.

1.3. IPCC Scenarios for Climate Change

As it is impossible to predict exactly how the world dynamics will develop in the future, a sensible approach is to create a few scenarios that take into account different assumptions around the major factors. IPCC developed such long-term emission scenarios in 1990 and 1992, which were used for forecasting future climate change by various parties. In 2000, IPCC updated these scenarios with the latest understanding of global dynamics, covering a time span until the year 2100. These scenarios include three key measurable factors of climate change: economic activity, population and technology. To cover most of the possible paths the world development can follow, IPCC created four scenario “families”: A1, A2, B1 and B2. Every family has sub-scenarios, and altogether 40 scenarios have been developed by IPCC. There are two important points to note about these scenarios:

First, as with every long term forecast, it is extremely difficult to predict the likelihood of any scenario. Thus, IPCC publishes the scenarios without providing any guidance on their probabilities. Second, every scenario has a storyline and the results of the scenarios are based on assumptions that match the storyline. Therefore, the results of each scenario for different metrics are to be considered together and not to be mixed with the outputs of other scenarios. A summary of selected factors’ change to 1990 levels in each scenario can be found in Table 1.1.

Table 1.1. Levels of selected indicators in the year 2100 when compared to 1990 in IPCC scenarios (IPCC, 2000).

	A1	A2	B1	B2
World Population	x1.3	x2.8	x1.3	x2.0
World GDP	x25.2	x11.6	x15.6	x11.2
Share of zero carbon in primary energy	x3.6	x1.6	x2.9	x2.7
CO_2 level	x1.9	x4.1	x0.6	x1.9

1.4. Biodiversity and its Importance

Biodiversity is defined as "the variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species and of ecosystems." (Millennium Ecosystem Assessment, 2005).

As biodiversity forms the base of many ecosystems that critically contribute to the human well-being (Millennium Ecosystem Assessment, 2005), forecasting its aspects for the coming decades bears significant importance in highlighting the need to take precautionary action if necessary. There are many indicators and measures of biodiversity but no single indicator can capture all of its dimensions. Among many others, existence of different animal species is a key indicator of biodiversity in a region.

There is evidence that climate change is affecting geographic distributions of animal species globally (Parmesan & Yohe, 2003). While there is a relatively strong research base analyzing the impact of climate change on animal distributions in different parts of the world, such analysis is lacking for the eastern Mediterranean region.

1.5. Objective of the Study

Within the perspective outlined above, this study focuses on the relationship between two major IPCC scenarios (A2 and B2) and the change in animal distributions in the Eastern Mediterranean region during the coming century, using bats as a model family of species. The results will enable the determination of potential changes in species ranges over the course of the 21st century and suggestion of recommendations for their conservation. Such an approach is novel for studying any group of organisms in this region.

2. LITERATURE REVIEW

One of the underlying aims of this study is to forecast changes in biodiversity and species richness in the 21st century. Species richness in an area has been forecasted best by summing the individual distribution models (Newbold et al., 2009), which requires building models that calculate presence of each species in a particular area one by one and then summing the number of the species present in that particular area in order to come up with the total number of species. Consequently, the first part of the study consisted of the selection of a species distribution model, sometimes referred as the ecological model.

Ecological modelling techniques, including the one this study has used, have been thoroughly analyzed (Elith et al., 2006; Hernandez et al, 2006). The general conclusion is that although it is impossible to predict the future with full certainty, due to extremely complicated nature of ecosystems and many variables that affect the dynamics in them, the modelling has produced some success and it can be claimed that the predictive results are directionally right (Bell & Collins, 2008).

As with any forecasting technique, one way of assessing the predictive power of a model is to use data from the past and use the same model to predict a date still in the past but more recent (or current) for which we have actual data. This way, modelled results can be easily compared to actual results, and if actual results are consistently similar to modelled ones (assessed with a statistically sound approach) then it can be assumed that modelling exercise is powerful. Martínez-Meyer et al. (2004) have performed this analysis using 23 extant mammal species and 8 extinct mammal taxa in North America. They concluded that the species they analyzed have followed the patterns the models had predicted using climatic variables. Waltari et al. (2007) performed a similar analysis and compared molecular genetic and phylogeographic predictions to ecological niche modelling. The former methodologies are more established but also manual techniques requiring extremely detailed observations. The results were similar and they found that both approaches converged on similar results. Both of these results significantly strengthen the argument that the modelling technique used in this study has robust predictive abilities and models can be extrapolated to conditions different than the ones they were originally calculated in.

All modelling methodologies use variable inputs, and the selection of the type of input is highly dependent on the purpose. There is evidence that in determining species richness at large scales, climate and productivity are crucial factors, especially for non-insular and terrestrial habitats (Field et al., 2008) such as the geographical area of this study. It also has been suggested that for large geographical areas (200-10,000+ km.) climate is the dominant force in delimiting species distributions (Pearson & Dawson, 2003). Taking these two results into account, climate has been the factor of choice in this study.

We would expect living organisms to adapt to changes in environment, such as in climate, in three forms: phenological, genetic and geographical (Root et al., 2003). Phenology can be defined as "the annual timing of life history events in populations” (Ahas et al., 2002; Vliet & Schwartz, 2002). As the changes in consistent seasonal activities of animals are relatively simple to track due to many directly observable patterns such as timing and geographical direction, there has been significant attention to this topic. Walther et al. (2002) concludes that spring activities in various taxa have occurred progressively earlier since 1960s and more importantly, they link this shift to change in spring temperatures. They summarize common effects as earlier breeding or first singing of birds, earlier arrival of migrants, earlier appearance of butterflies, earlier choruses and spawning in amphibians, and earlier shooting and flowering of plants. In bats specifically, it has been observed that a specific bat species’ reproductive cycles has moved from autumn to winter in Southern Spain (Ibáñez, 1997).

Second possible adaptation is evolutionary. In some cases, the climate change could also have an impact on the evolution of some species, through the organism's genes. Bradshaw & Holzapfel (2001) conclude that rapid climate warming also penetrated to the level of the gene in different organisms. They also conclude that small animals with shorter life cycles and large population size will be able to survive, while large animals with long life cycles and small population size will either face a decline in population size or be replaced by other (in this case southern) species. On this specific point, it should be noted that evolutionary adaptation is highly debated in the literature. For example, it has also been suggested that the first adaptation after a change in the environment is geographical and an evolutionary change is a result of adapting to the new geographical environment (Peterson et al., 1999) rather than first change being evolutionary.

Third and last form of adaptation is in the form of moving to more suitable geographical habitats. We already know with very high confidence that climate change is already affecting living systems (Parmesan & Yohe, 2003). In bats specifically, it has been detected that some bats (namely *Pipistrellus kuhlii*) have been observed to change and expand their distribution in Eastern Europe (Sachanowicz et al., 2006).

As mentioned earlier, results of a study by Root et al. (2003) had indicated that around 80% of analyzed species had a temperature related shift in the expected direction, which would be a unique direction forecasted by the model incorporating each situation's specific variables into account. They conclude that wild animals and plants are all responding to climate change and that a significant impact of climate change is already discernable in animal and plant populations. As part of the same analysis, they also looked at phenological changes for five groups of species (invertebrates, amphibians, birds, non-trees and trees) and found out that all five had experienced shifts. The shifts are observed even in minor (<1°C) temperature changes (Root et al., 2003).

There are theories to suggest that the rate of climate change might be too fast for many species to adapt continuously (Lynch & Lande, 1995; Burger & Lynch, 1995). Moreover, not every species can adapt adequately or on time. Theoretically, the population of a species that is unable to adapt to changes in environment is expected to decrease up to level of extinction. There is empirical evidence that supports this theory, such as the observed decreases in some migratory bird populations due to their inability to adapt to climate change (Møller et al., 2008).

Ecosystems are extremely complex in nature, and the observed dynamics are understood only partially. Also, a particular challenge is to build causal relationships between observed changes. Genotypic variation is important to survival, as in theory the more variation a species has, the more potential of change are at its disposal during the course of its evolution (Landweber & Dobson, 1999; Young & Clarke, 2000). In line with this theory, it has been shown that in environments and species where genetic variation is low, such as montane small mammals, climate induced reductions may increase probability of extinction (Ditto & Frey, 2007). To make matters more complicated, some species of amphibians and reptiles are modelled to expand their distributions (with unlimited dispersal assumptions), due to warming creating more favourable environmental conditions for the mentioned species (Araújo et al., 2006). Similar to amphibians and reptiles, in bat species it has been suggested that although there are major extinctions predicted in Europe, northern parts of the continent are likely to harbour suitable climatic conditions for an increasing number of species (Rebelo et al., 2010). Both these expansion examples demonstrate the complicated nature of anticipating the impact of climate change in species distributions.

The key determinant of the success of evolutionary adaptation is the rate of rescue mutations, and this figure remains completely unknown. What is known is that the current adaptation has been more on survival efficiency than on reproductive success (Bell & Collins, 2008). Improving survival efficiency at the expense of reproductive capacity will protect total population of a species only in the short term, as this will likely cause number of births not being able to match or exceed number of deaths in the future. This fact might cause extinction in some cases and thus damage the ecosystem the species are in. A damaged ecosystem might result in significantly reduced economic output thus costing damage to the economy. Moreover, the economical investment required to re-create an ecosystem after damage or extinction is extremely high (Millennium Ecosystem Assessment, 2005). On the other hand, there are other proven precautions that can be taken before extinction or biodiversity damage happens, if this damage can be anticipated beforehand. For example, it has been proven that there is a positive correlation between proportion of protected land and species richness in a region (Evans et al. 2006). As it can be seen, the field of biodiversity conservation within the context of global climate change is extremely complicated and encompasses different levels from understanding the current changes, including assessing the impact of these changes, to taking action to prevent them if required. Therefore, the first step in the preventive or corrective action is the identification of potential direction of the changes ahead of us.

One major barrier standing in the way of identifying future changes and thus consideration of preventive actions is the availability of data in some parts of the world, such as the area that this study focuses. Ferrier (2002) has suggested three strategies to lessen the negative impact of lack of data: “(1) more closely integrating biological and environmental data through predictive modelling, with increased emphasis on modelling collective properties of biodiversity rather than individual entities; (2) making more rigorous use of remotely mapped surrogates in conservation planning by incorporating knowledge of heterogeneity within land-classes, and of varying levels of distinctiveness between classes, into measures of conservation priority and achievement; and (3) using relatively data-rich regions as test-beds for evaluating the performance of surrogates that can be readily applied across data-poor regions.” This study aims at delivering on the first of these suggested strategies and consequently taking a step towards understanding the very complicated dynamics of the upcoming environmental changes.

Last, it is worth mentioning that although the methodologies that this study utilized have been used extensively in other parts of the world as referenced in the above paragraphs, to our knowledge there are no studies covering the same region using a climate change perspective. On one hand this highlights the fact that the study is a novel one for the region, on the other hand it also implies a large gap in possible studies and thus points to an opportunity. Besides lack of accumulated know-how of such techniques and an arguably low public awareness of the study field that would have decreased the interest, there are other clear reasons which are likely to have made the execution of such studies very challenging. These issues will also be touched upon in the following sections of this study.

3. MATERIALS AND METHODOLOGY

The primary objective of the study was to create bat species' richness maps for different future time periods and to withdraw conclusions from these results. The main steps of the modelling are explained below:

3.1. Geographical Area, Species and Time Horizon

The geographical area selected for the study was Eastern Mediterranean including Turkey, Cyprus and Levant area (Israel, Jordan, Lebanon, Syria and Sinai Peninsula). Overall, the Mediterranean region consists of 18 countries and its climate is characterized by mild temperatures, winter dominated rainfall, and dry summer (Wigley, 1992). These countries can be grouped into two based on their climate and socio-economical characteristics: northern basin (Spain, France, Monaco, Italy, Former Yugoslavia, Albania, and Greece) and southern basin (Turkey, Cyprus, Syria, Lebanon, Israel, Egypt, Libya, Malta, Tunisia, Algeria, and Morocco) countries. Southern regions are warmer and drier, due to low seasonal rainfall and high evapotranspiration rates (Rosenzweig & Tubiello, 1996). In order to make climatic characteristics that form the basis of the modelling even more similar, this study focused on the non-African (thus eastern) part of the southern basin.

The study was completed using presence records of different bat species, because the modelling technique allows records from any animal or plant species for use. A major limitation, however, was the availability of presence data for sufficient number of species to create meaningful species richness maps.

Some of the distinct advantages of using bats are the following: i) Bats have been observed in detail in the selected area, thus it was relatively easy to acquire presence data; ii) They have numerous sub-species with different habitat requirements and presence conditions. Typically, a study observing bats covers several of these sub-species. This coverage offered a strong base of unique species that resulted in more comprehensive biodiversity analysis. In the literature scanned, the study identified presence data for 49 different bat species; iii) Bats have high dispersal ability (unlike e.g. amphibians), which is an important factor, as the model predicts occurrences in areas with no observed presence. If the studied species had low dispersal abilities, then occurrence in such areas would have lower probabilities.

In terms of time horizon, the study covered four different periods: current (average of 1950-2000), 2020, 2050, and 2080.

3.2. Input Data

3.2.1. Species presence data

All species presence data were obtained from existing research in the literature or databases (Benda & Horacek, 1998; Benda, et al., 2006; Benda, et al., 2008; Benda, et al., 2007; Benda, et al., 2009; Horacek, et al., 2008; Furman & Özgül, 2002; Furman & Ozgul, 2004; The Hebrew University of Jerusalem (BioGIS Project). The geographical plot of all presence records is given in Figure 3.1.

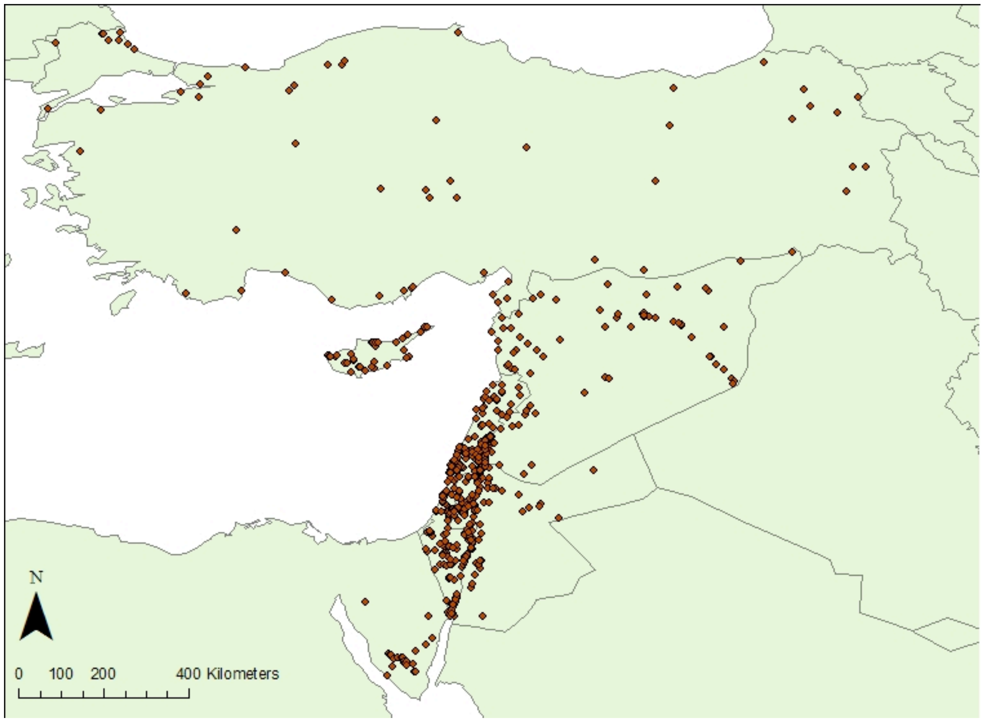

Figure 3.1. Geographical plot of all presence records (circles) included in the study. Multiple observations in the same spot are marked with a single circle.

All of these resources included at least the following data: species name, name of location observed, and latitude and longitude of location observed. After the analysis was performed, a total of 49 species' presence records in 891 unique locations were obtained (Appendix A). The matching of unique species and location records resulted in 2022 combinations.

In order to reduce modelling biases, any species with less than 25 unique presence records has been excluded from the study (Hernandez et al., 2006). Also, eight species, which had limited presence records in the required resolution compared to previous observations (Benda & Horacek, 1998), have been excluded from the modelling. These species were *Miniopterus schreibersii, Myotis blythii, Myotis myotis, Pipistrellus pipistrellus, Rhinolophus* *euryale, Rhinolophus ferrumequinum, Rhinolophus hipposideros,* and *Tadarida teniotis*. This resulted in a final list of 18 unique species and 1147 presence records (Table 3.1).

Table 3.1. Species included in the final modelling (ranked by number of presence records)

Species	Presence records	Species	Presence records
Pipistrellus kuhlii	272	*Myotis emarginatus*	51
Rhinopoma hardwickei	90	*Otonycteris hemprichii*	45
Rousettus aegyptiacus	82	*Plecotus austriacus*	40
Myotis capaccinii	70	*Rhinopoma microphyllum*	39
Myotis nattereri	64	*Rhinolophus blasii*	39
Asellia tridens	58	*Pipistrellus bodenheimeri*	39
Eptesicus bottae	56	*Taphozous nudiventris*	38
Eptesicus serotinus	55	*Rhinolophus clivosus*	30
Hypsugo savii	53	*Hypsugo ariel*	26

3.2.2. Climatic data (current and forecasts)

Climate data were obtained from worldclim.org for both past and future time periods. The website provides 19 bioclimatic variables for current conditions (Annual Mean Temperature, Mean Diurnal Range (Mean of monthly (max temp - min temp)), Isothermality (Mean Diurnal Range/Temperature Range) (* 100), Temperature Seasonality (standard deviation *100), Max Temperature of Warmest Month, Min Temperature of Coldest Month, Temperature Annual Range (maximum temperature of the warmest month minus minimum temperature of the coldest month), Mean Temperature of Wettest Quarter, Mean Temperature of Driest Quarter, Mean Temperature of Warmest Quarter, Mean Temperature of Coldest Quarter, Annual Precipitation, Precipitation of Wettest Month, Precipitation of Driest Month, Precipitation Seasonality (Coefficient of Variation), Precipitation of Wettest Quarter, Precipitation of Driest Quarter, Precipitation of Warmest Quarter, Precipitation of Coldest Quarter).

Future bioclimatic data were derived using documented methodology (Ramírez & Bueno-Cabrera, 2009) for 2020, 2050, and 2080. During this procedure, three climatic variables available from worldclim website (average, minimum, and maximum temperatures (all monthly in ºC)) were used as source and were processed with the following two software: DIVA-GIS 7.1.2.3 and ArcGIS 9.3.

Two different scenarios for future data calculated with Hadley Centre Coupled Model, version 3 (HadCM3) model were used in the study. These were based on IPCC's different scenarios-A2A and B2A. All climatic data had a resolution of 2.5 arc-minutes (~4.5km) in order to match the resolution of the presence data.

3.3. Modelling

The modelling was performed with a "presence-only" method due to the lack of reliable absence data. Obtaining reliable absence data for bats is very challenging due to their elusive nature and nocturnal behaviour. A "maximum entropy modelling" (Maxent 3.3.1), approach was used, because it proved to be among the best available techniques (Elith et al., 2006; Hernandez et al., 2006).

Maximum entropy modelling technique and Maxent software are designed to take a set of environmental variables as input to produce a model of given species' range. Maxent uses a machine learning approach to estimate the geographical range of species by finding the maximum entropy distribution with the constraint that expected value of the output matches the empirical average of occurrence data provided (Phillips et al., 2004; Phillips et al., 2006).

15% of the presence data chosen randomly was used to test the model while the remaining 85% was used in training the model. Models were run with a maximum of 1000 iterations in auto features. Receiver Operating Characteristics (ROC) plots were produced to estimate model predictive ability. Subsequently, the overall success of the modelwas assessed by using the "accuracy measure area under curve for ROC plots (AUC)" technique within a range of 0.5 (randomness) to 1.0 (perfect discrimination).

Maxent software performs a "jackknife" analysis of the average gain with training and test data, and also with AUC. During this calculation, Maxent works iteratively over the set of bioclimatic variables and calculates three separate models: 1) a model excluding a bioclimatic variable in turn and including all others; 2) a model using only each individual variable, and 3) a model using all variables. The results are presented in html format and include these three models' gain. The gain is a measure of the likelihood of the samples; for example, if the gain is 2, it means that the average sample likelihood is exp (2) ≈ 7.4 times higher than that of a random modelled area. The uniform distribution has a gain value of 0, so the higher the gain, the better is the model's predictive power (Phillips et al., 2006).

Using the results from Maxent as explained above, the relationship between the occurrence of bats and bioclimatic variables was determined first by an analysis of gains provided by different variables. This process helped eliminate non-relevant bioclimatic variables from the model. In order to do this, the model was first run with all of 19 variables. As the model output includes summary of gains as a result of the use of different variables, some variables that were easily identified as irrelevant. Using a step by step approach, batch of variables were excluded from the model and the model was re-run. This process continued until six variables were left. The chosen bioclimatic models had the highest indicated gain in the overall modelling: in 16 out of 18 models, the combination of the variables (calculation 3 above) had better gain than any individual variable (calculation 1 above) or the sole use of an individual one (calculation 2 above). On the remaining two models, the increase in gains with different calculations made by excluding some variables would have not been material. In both of the incremental gain cases (*Hypsugo ariel* and *Myotis nattereri* models) gain would have been only 0.0001 higher than the combined gains of 2.0708 and 1.8516, respectively. Details for each model's gain can be found in Appendix B.

This process identified the six most important variables (Temperature Annual Range, Precipitation of Driest Quarter, Precipitation Seasonality (Coefficient of Variation), Mean Temperature of Coldest Quarter, Annual Mean Temperature, Mean Temperature of Warmest Quarter) with which the model was run for all of the 18 initial species using the settings mentioned above.

Maxent software predicts future distribution of the species by projecting a model calculated with current conditions to the future bioclimatic variables. This is how species distribution models for 2020, 2050, and 2080 were generated. For comparability, the same settings were used during the entire modelling process.

3.4. Combining the Models

The output of Maxent assigns a presence probability value (between 0 and 1) for the modelled species to each pixel of the geographic area. This continuous data were reclassified into a binary format using the "10 percentile training presence" value calculated by Maxent. This value assumes that up to 10% of presence data had errors related to species identification or geographical coordinates which is highly likely when dealing with data collected by several researchers over a wide time span (Raes et al., 2009). Any probability below this value was considered a signal of absence and vice versa.

The converted binary presence map was calculated for all modelled four time periods and for 18 species. The 18 maps in each time period belonging to different species were added in order to produce species richness maps, highlighting the existence of a higher number species at one location by darker colour. Therefore, the range for possible values in a modelled location lies between 0-18, 0 indicating presence of no species and 18 indicating potential presence of all of them.

This step of combining maps was completed in ArcGIS 9.3 with the help of scripts prepared in Python programming language. These scripts can be found in Appendix D. The scripts were used to obtain threshold output values from Maxent result files and feed them into ArcGIS automatically.

3.5. Analyzing Data

Additional data analyses to interpret the data further were performed, such as visualization of species richness turnover and plotting presence overlaps over time periods.

3.5.1. Visualize species richness turnover

In order to obtain species richness change maps, combined presence figures for each location in current species richness maps were subtracted from projected ones. This produced an estimate of the loss or gain of species richness over time for the same location. These results were calculated and mapped in ArcGIS.

3.5.2. Chart presence overlaps over time

After reclassification of the output data, presence is indicated by 1 and absence by 0. Presence overlap maps were calculated by multiplying the current data with the forecasted data. In these calculated maps, the locations marked by 1 indicated areas where a species was present both in current and forecasted time frames. The number of locations marked by 1 in the presence overlap maps was divided by the number of locations marked by 1 in the current maps to estimate percentage presence overlap. Python scripts in ArcGIS and Microsoft Excel software were used during this process. These results were presented in charts, and analyses were performed based on this information.

4. RESULTS

AUC values for ROC plots, which indicate the accuracy of the model, were all higher than 0.86 with an average of 0.94±0.04 across 18 models (0.5 indicates randomness, 1.0 indicates a perfect match). This indicates a very strong predictive power of the model. Additionally, the average training AUC of the model excluding one of the six variables was found to be lower than the model with all six variables. This means that removing any of the variables reduces the predictive ability of the model relative to that using all six variables.

The most relevant variable in all models based on sum of contribution to models was annual temperature variation, which also proved to be as such for six species. Precipitation of driest quarter was the most relevant variable for eight species, while in aggregate having a lower contribution than temperature annual range. The other variables kept in the model in the order of relevance were: precipitation seasonality, precipitation of driest quarter, mean temperature of coldest quarter, annual mean temperature, and mean temperature of warmest quarter. Model outputs showing the relevance and relative significance of the variables are summarized in Table 4.1.

Table 4.1. Summary of variable contributions, AUC scores for each variable and indication of the number of times each variable was the most relevant for a species.

Variable	Sum of contribution	Average AUC without	St. Dev. AUC without	Times most relevant
Temperature Annual Range	545.04	0.93	0.094	6
Precipitation of Driest Quarter	471.72	0.93	0.094	8
Precipitation Seasonality	381.58	0.92	0.095	2
Mean Temperature of Coldest Quarter	260.58	0.93	0.094	2
Annual Mean Temperature	89.38	0.93	0.091	0
Mean Temperature of Warmest Quarter	51.69	0.93	0.094	0
Sum	1,800			18

Based on these variables, Maxent produced current and future distribution maps of each species. Example distribution map for current time period for *Rousettus aegyptiacus* can be found in Figure 4.1, and output for all species can be found in Appendix C.

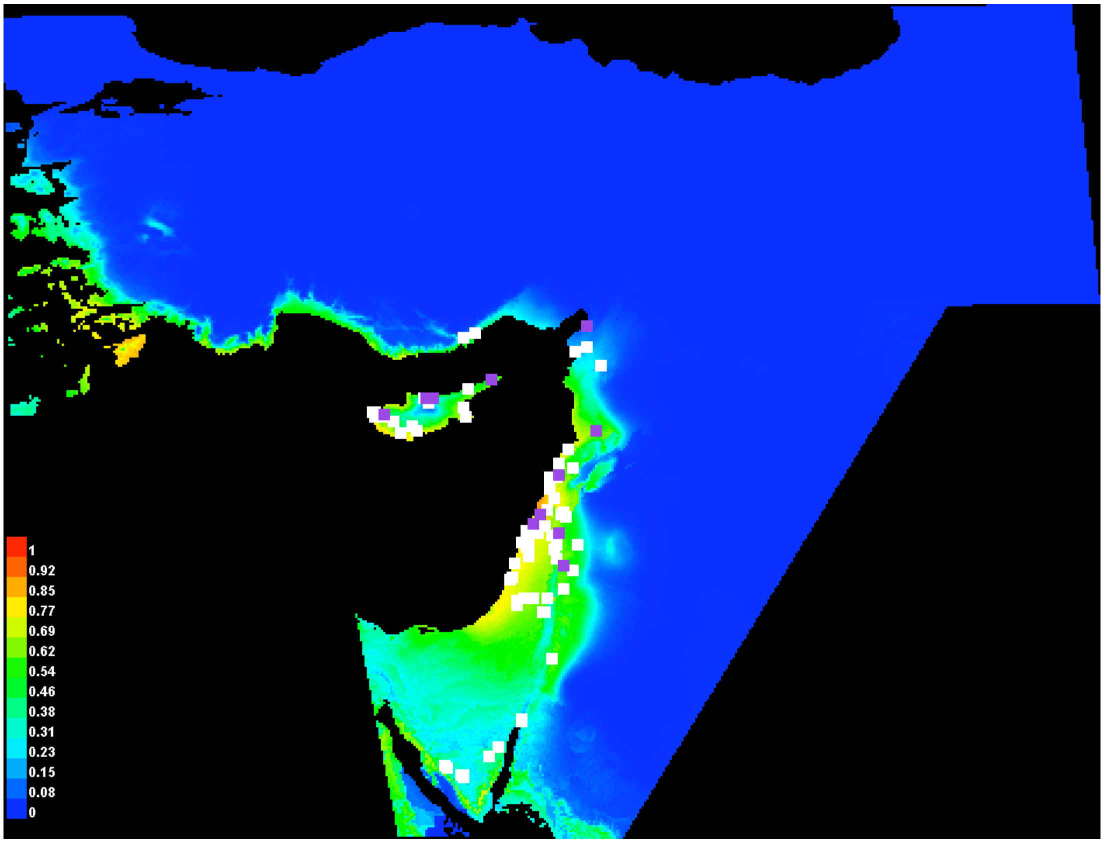

Figure 4.1. *Rousettus aegyptiacus* Maxent model output. Legend is of probability of occurrence, squares are actual observed locations.

The outputs for individual species were analyzed by aggregating the results under the species richness map (Figure 4.2), which gives a quick overview of today's species distribution patterns. There is a very strong presence of different species in Sinai, Israel and Jordan area, and in general species are concentrated in the sea shores. The only areas with no modelled presence are central Turkey and eastern Jordan. When the results were charted, 16% of the studied area was seen to have no modelled presence of studied species; 48% of the area is modelled to contain 1-3 of modelled species (Figure 4.3).

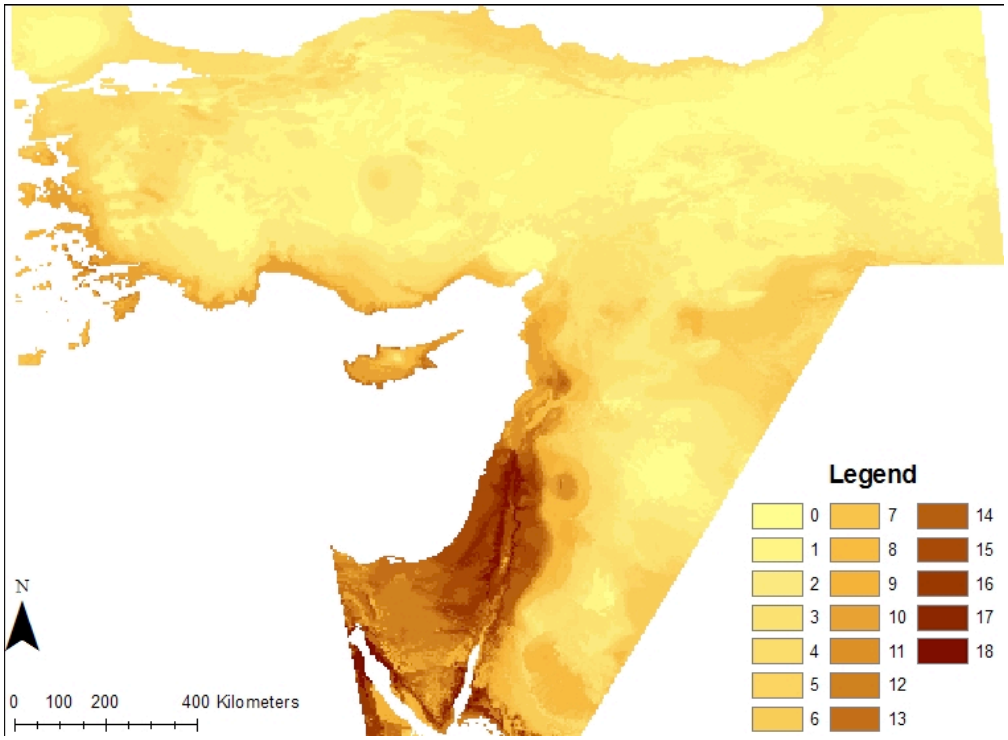

Figure 4.2. Current species richness map of modelled species

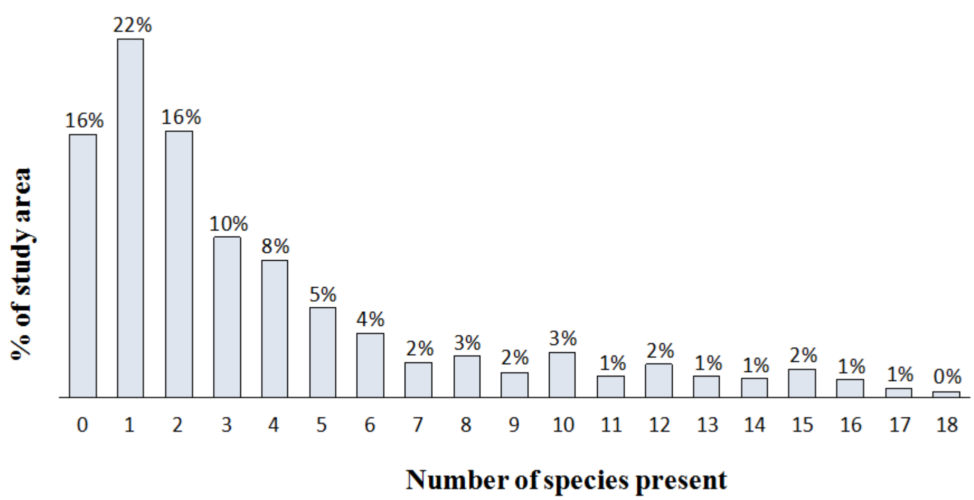

Figure 4.3. Current species richness chart

In both of the future climate scenarios (A2A and B2A), the predicted distribution maps (Figure 4.4) show a visible decreasing pattern in future modelled species richness. Cyprus, Mediterranean islands and the area around Sinai, Israel, Lebanon and West Jordan always remain rich in terms of number of species present.

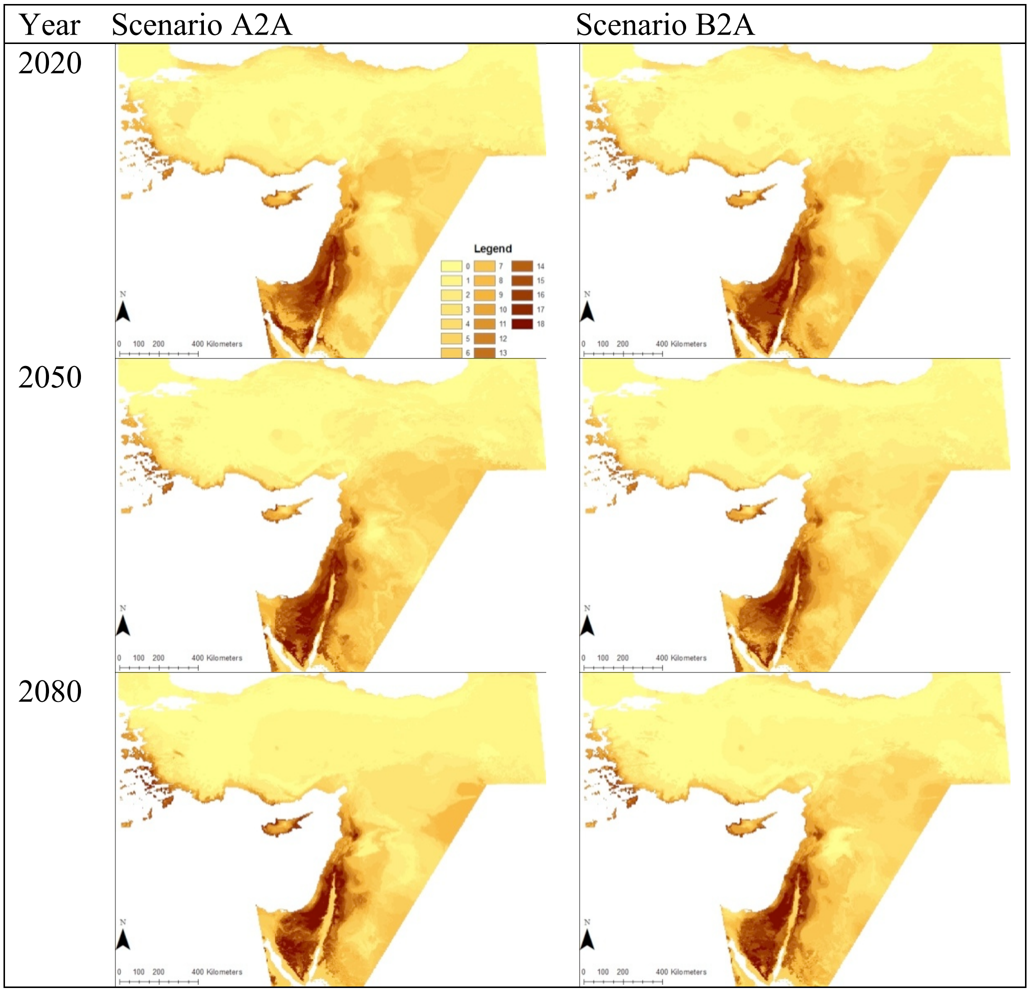

Figure 4.4. Modelled species richness maps by period and forecast scenarios

Representation of species distribution maps numerically is depicted in Table 4.2. The data show that there is an increase in areas with no presence between the current period and 2020, from 16% today to 26% in scenario A2A and 20% in scenario B2A. After 2020, the two scenarios are following a different pattern but reach a similar outcome in 2080. To visualize these patterns, total number of pixels (part of a map in constant defined area size, in rectangular or polygonal form) occupied by all modelled species have been calculated. Total modelled area consists of 82,472 pixels and every pixel can contain zero, one or multiple species. If all presences in every pixel are summed, an indicative summary of total presence in the area can be obtained. This value could have been smaller or larger than the total number of pixels in studied area depending on the richness in different parts of the area. In the current scenario, total number of pixels with various presences is 310,051. In scenario A2A, this figure in years 2020, 2050 and 2080 are 277,513, 304,492, and 290,872, respectively. Same calculation for scenario B2A yields values of 290,904, 270,615, and 292,601, respectively. These mean that in both scenarios there is deterioration in species richness in 2020 then a recovery in scenario A2A and a further deterioration in scenario B2A. Then in 2080 both scenarios reach similar levels, below current values, even though this means deterioration compared to 2050 in scenario A2A and recovery in scenario B2A.

Another way of analyzing species distribution is through clustering areas by number of modelled species present. The results of this analysis can be found in Table 4.2, where percentages refer to the percentage of area covered.

Table 4.2. Presence summary of species distribution maps

Scenario	Year	% Area with no modelled presence	% Area with 1-3 species	% Area with 4-10 species	% Area with 11+ species
Current		16%	48%	27%	10%
A2A	2020	26%	39%	26%	9%
A2A	2050	29%	32%	29%	10%
A2A	2080	20%	50%	20%	10%
B2A	2020	29%	37%	23%	10%
B2A	2050	31%	37%	24%	8%
B2A	2080	29%	31%	31%	9%

The above presented presence summary of species distribution against time is plotted in Figure 4.5 for Scenario A2A (a) and B2A (b). It was found that in scenario A2A, only areas containing less than four species increased in number, signifying a decrease in the overall species richness that is consistent with previous findings. In scenario B2A there is a more significant increase in areas with no modelled presence (from 16% to 29%). Also areas with 4-10 species present increases in 2080 by four percentage points in scenario B2A. As the numbers of pixels mentioned earlier indicate, the net result of these changes is a decrease in species richness in both scenarios.

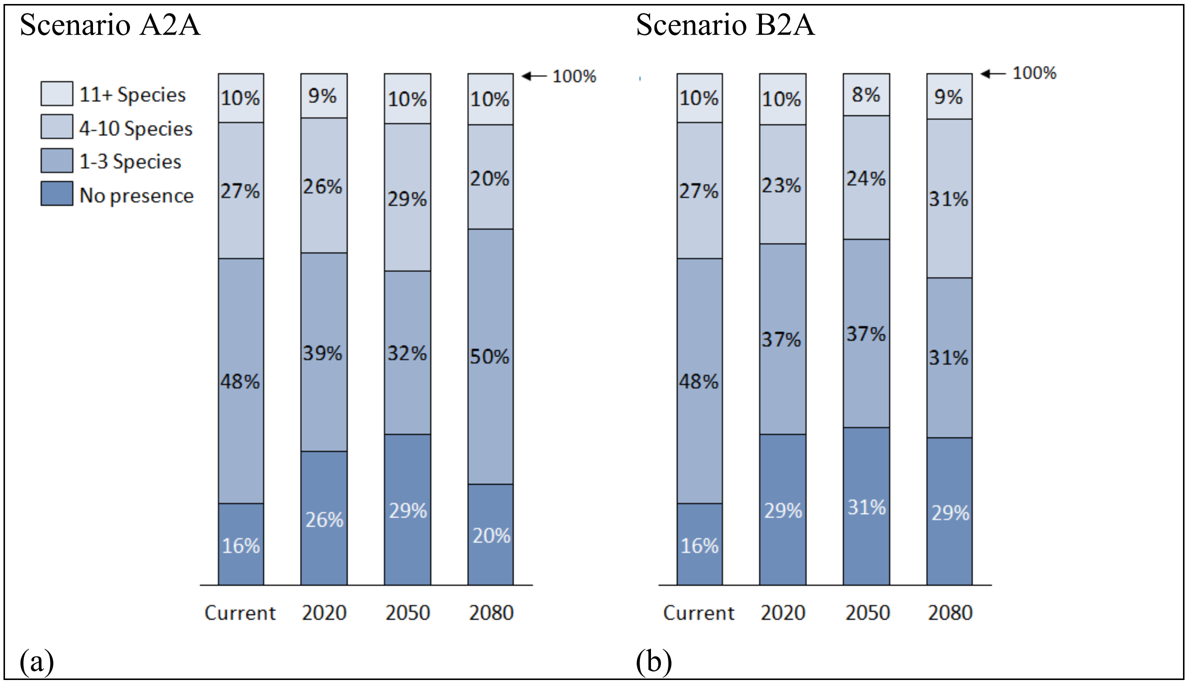

Figure 4.5. Relative distribution of species richness in time for scenarios A2A (a) and B2A (b).

Another way of visualizing the models is to calculate the species richness change by area and then map it. The maps in Figure 4.6 show these changes.

Year Scenario A2A Scenario B2A

2020

2050

2080

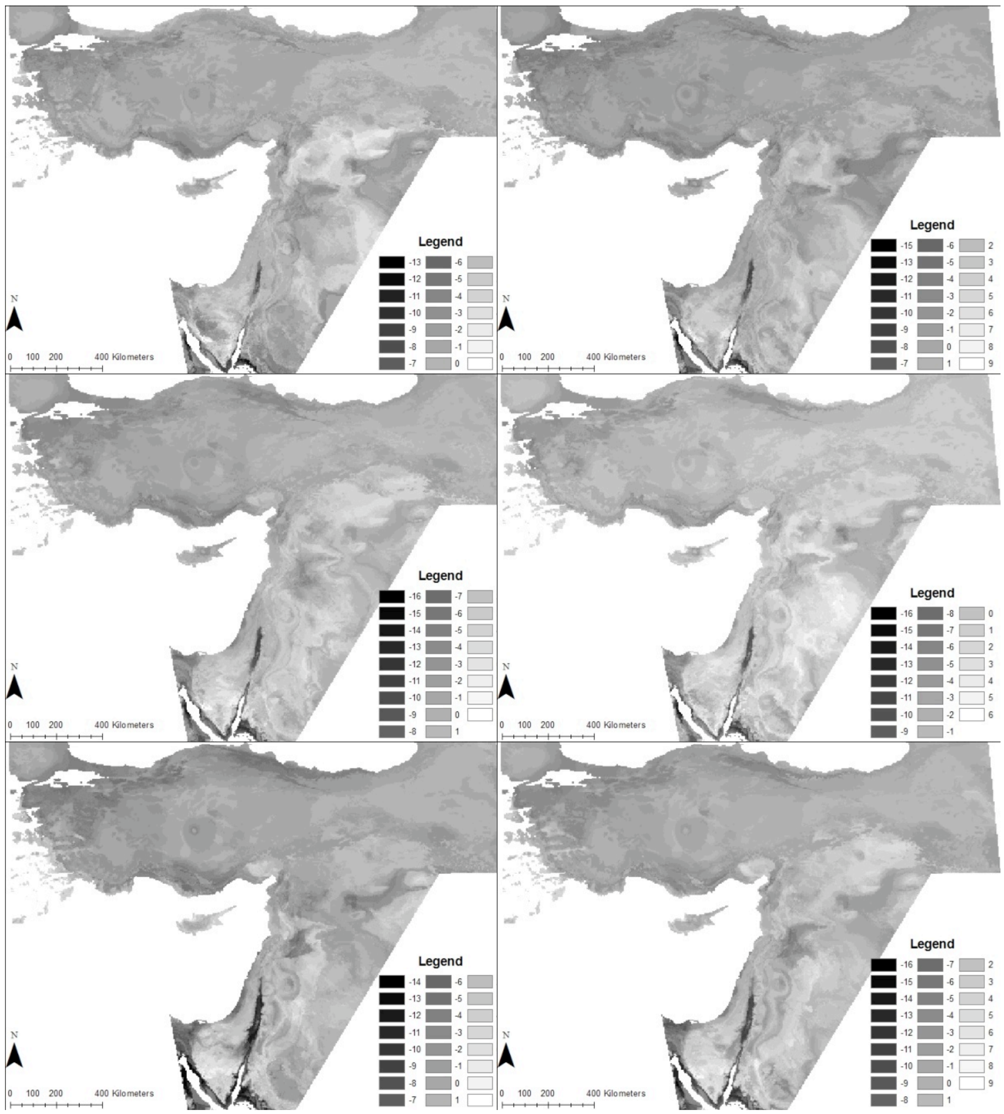

Figure 4.6. Maps of species richness change (forecasted period – current)

These maps also show that in 2020 there will be a deterioration in species richness compared to current conditions whereby the sea shores including a large part of Turkey face the largest loss of species richness. As not all areas are modelled to deteriorate in species richness, the net gain or loss in species richness should be checked to make better conclusions.

Table 4.3 shows changes in both area and average species richness over time calculated by the difference of [total area multiplied by the number of species in that area] values in the model of future period and in the model of current period.

Table 4.3. Summary of species richness change

Scenario	Period	% area with decreased species richness	% net Gain/Loss in Species Richness
A2A	2020	49%	-7%
A2A	2050	41%	-1%
A2A	2080	39%	-4%
B2A	2020	43%	-4%
B2A	2050	46%	-8%
B2A	2080	42%	-4%

Values in Table 4.3 indicate that in scenario A2A 39% of the modelled area will experience a decrease in species richness. In scenario B2A, this figure is 42%. However, it is worth mentioning that this also means that 61% and 58% of the modelled area, for scenarios A2A and B2A respectively, will have stable or increased specie richness. Hence it is important to look at net gains or losses in species richness, also presented in Table 4.3, which consistently point out to a net loss throughout the modelled periods.

So far the aggregate outcomes of the scenarios have been analyzed. A visualization of species by species data will be the last step of the analysis of modelling outcome by checking any trends. Figure 4.7 summarizes the expansion or contraction pattern of species in the modelled area. Bar lengths are estimated by calculating the total area that a species might occupy during both the current and future time periods. The percentage increase or decrease for the current period relative to the future indicates the expansion or contraction of the species.

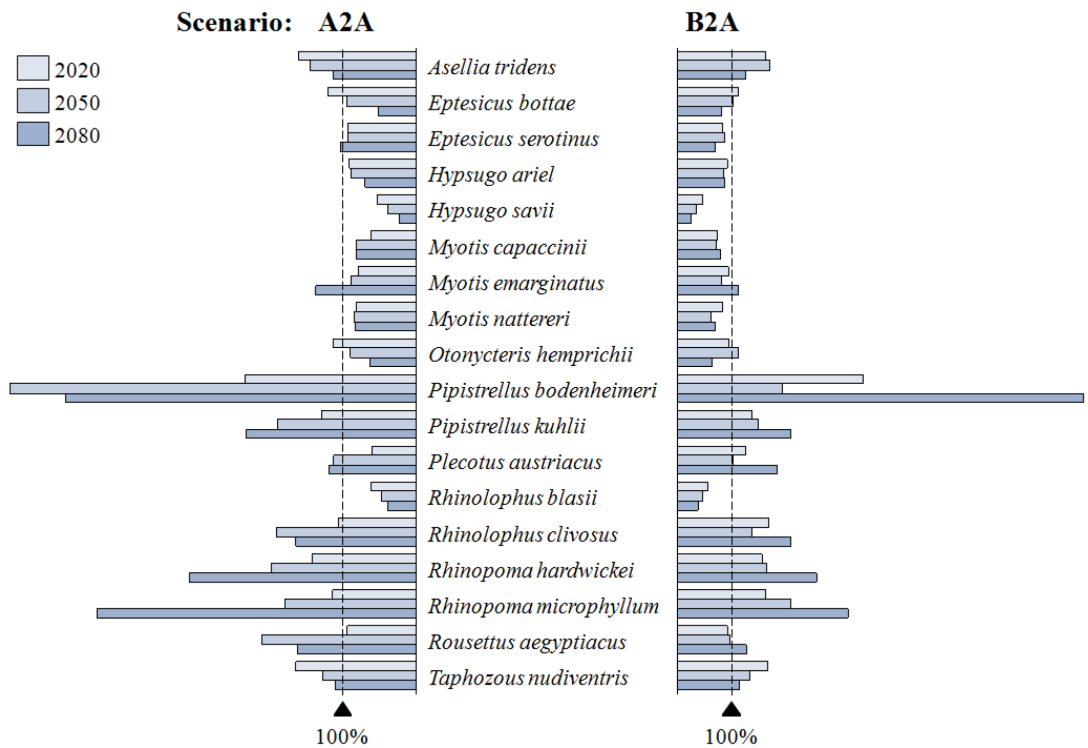

Figure 4.7. Expansion/contraction pattern of species by year and scenario vs. current time period. (100% is stable distribution, <100% is contraction)

In 2080, seven and eight (in scenarios A2A and B2A respectively) species are modelled to face contraction in their area of presence (most contracting species are *Rhinolophus blasii* and *Hypsugo savii*). The exact figures are summarized in Table 4.4. The rest of the species (11 species in scenario A2A and ten species in scenario B2A) are modelled to expand (most expanding species are *Pipistrellus bodenheimeri, Rhinopoma microphyllum, Rhinopoma hardwickei*). Overall, the net result is a contraction in total area occupied by the species, as explained in the previous section (Table 4.3).

Table 4.4. Number of species modelled to face area contractions vs. current time period (<100% in Figure 4.7)

Time Period	Scenario A2A	Scenario B2A
2020	9	9
2050	9	8
2080	7	8

With our current technologies and modelling capabilities, it is extremely difficult (if not impossible) to have a comprehensive model that takes into account all variables necessary for a species presence. So the modelling exercise partly assumes that climatic variables define a wide range of other environmental factors. On the other hand, we can still analyze one more aspect of the model results to check how serious of a threat the environmental factors other than climatic variables can be: this is "range shifts" of species.

The underlying logic behind analyzing range shifts is that if a species does not change its current range, it is less exposed to threats posed by absence of non-environmental necessary conditions but more exposed to changes in the environment of their current distribution. Figure 4.8 shows the expected percentage of area that will continue to host the same species.

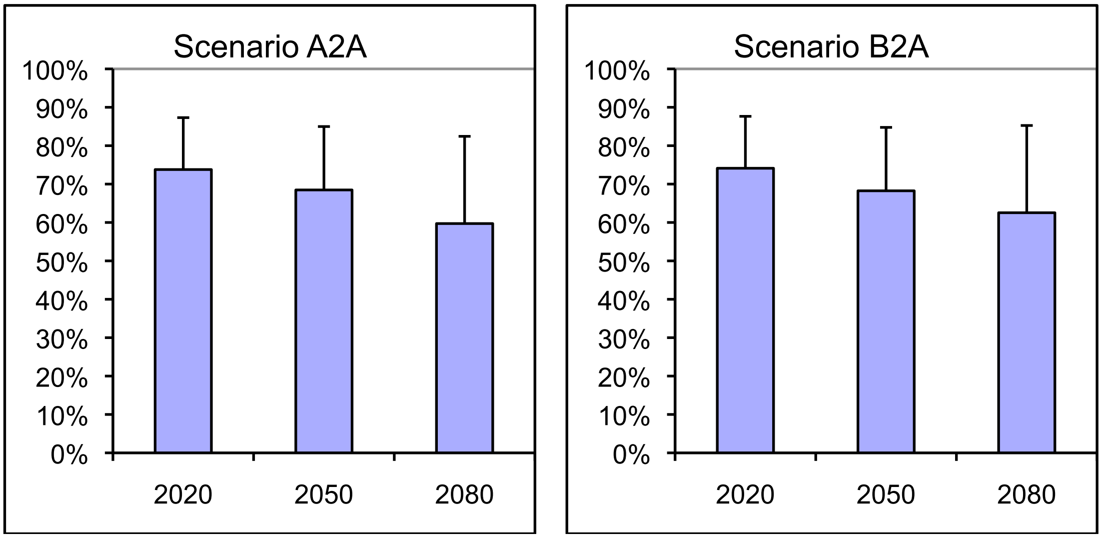

Figure 4.8. Modelled average range shifts of species by scenario and period of model (lines indicate standard deviation)

The figures show that 60% and 63% of the areas will be inhabited by same species in 2080 according to scenarios A2A and B2A, respectively. In other words scenario A2A predicts that 40% of expected presence in 2080 will occur in an area that is not currently inhabited by the same species.

5. DISCUSSION

To the best of our knowledge, this is the first species distribution modelling study covering the eastern Mediterranean region from a climate change perspective. The results suggest that bats will suffer from climate change throughout the 21st century in the studied area on two fronts: i) species richness will deteriorate, and ii) the total area occupied by bats will decline. These impacts will be more severely observed in Turkey's coastal areas, northwest Turkey, Red Sea coasts, Israel, and west of Syria and Jordan.

As Martínez-Meyer et al. (2004), who had applied this modelling to past data to accurately forecast today's biodiversity conditions, and Waltari et al. (2007), who compared genetic analysis to ecological modelling to find converging results in both approaches, have shown, the modelling techniques used in this analysis are proven to have strong predictive abilities.

The results of the study delineate the most important factors that affect bat presence in the region. These factors turned out to be i) temperature annual range, ii) precipitation of driest quarter, iii) precipitation seasonality, and iv) mean temperatures (that of coldest quarter, annual mean, and that of warmest quarter). Previous studies indicate that thermal conditions of roosts have a strong influence on bats' survival because metabolic rate, evaporative water loss and gestation time are adversely affected when temperatures lay outside the optimum conditions (Webb et al., 1995; Racey et al., 1987). Thus, the results of the study are in line with those in available literature, which also indicate that temperature and water availability have great relevance on bat hysiology and survival (Baken & Kunz, 1988).

As far as the species richness is concerned, the results of the study have shown a downward trend in species richness within current-to-2080 period. Specifically, the models of future species richness indicate the following: i) there will be an increase in the area with no modelled presence (from 16% today to 20% in scenario A2A and to 29% in scenario B2A in 2080), ii) ~40% of the studied area is expected to have a decrease in species richness coupled with a net loss of ~4% in average species per area, iii) 7 and 8 (in scenarios A2A and B2A respectively) of 18 studied species will contract in total occupied area, and iv) 37-40% of future modelled presence will occur in an area that does not contain the same species today. The outcome is consistent across the two analyzed scenarios, which are based on different but increasing economic activity levels. These results suggest that multiple bat species will have to go through habitat changes in order to continue their existence. These changes might have various phenological implications such as earlier births and lack of hibernation.

Although the analysis has produced consistent results, it had some limitations. The main one was the limitation of the study to the use of only bioclimatic variables. For example, the study could not make use of any land cover (or habitat) variables. These limitations make the models best case scenarios as the models implicitly assume that any variable other than bioclimatic ones will be similar to those where known presence had been observed. Thus, almost all the results analyzed in this study are more optimistic in terms of species richness than actual, albeit it is not known how much more optimistic. This finding is observed in the actual presence data (Figure 3.1). In the southern coast of Turkey (Mediterrannean), there are observed occurences of bats. However, although the climatic conditions are mostly similar and thus the modelling predicts similar presence (Figure 4.2), the western coast of Turkey (Aegean) does not host nearly as many bats as the modelled results according to the actual presence data. This is likely to be a result of lack of caves and/or other habitat requirements.

Moreover, the analysis focused on the total area of the study. Looking at the total area implicitly assumes that the species can move freely between different areas, as long as the forecasted bioclimatic variables are within a range that can accommodate those species. Similar to the limitations stated earlier, although we can confidently assume that if the climatic conditions are not met, a species will not be present in a certain area, the opposite is not necessarily true (i.e. an area that has all the required climatic conditions might lack other factors necessary for a species survival such as availability of food or lack of roosts being the most obvious ones). For instance, *Rousettus aegyptiacus,* who feeds on fruits, is not observed on the Aegean coast of Turkey even though the models gave a strong probability of existence based on climate conditions. This is probably due to lack of specific trees that are foraged heavily by *Rousettus aegyptiacus*, such as date trees, in the Aegean coast of Turkey. This is an example of how various factors other than climate influence the expected distribution of a species.

The results highlighted that climate change will not impact every species in the same way. There are two species with more than 50% modelled decrease in their presence area until 2080 (*Rhinolophus blasii, Hypsugo savii*). Combined with the above mentioned challenges and limitations of the model, it can be said that the actual decrease in presence areas are likely to be higher than the modelled ones, putting these species at a greater risk. On the other hand, four species (*Pipistrellus kuhlii, Rhinopoma hardwickei, Rhinopoma microphyllum, Pipistrellus bodenheimeri*) are modelled to have more than 200% increase in their presence area, and this effectively means they have a very low probability of extinction.

Thus, although the overall impact of climate change on species richness is negative, making generalizations such as “all species will suffer” is impossible. This variation is in line with the general agreement in available literature about the complexity of modelling and its use in understanding future dynamics (Elith et al., 2006; Pearson and Dawson, 2003). One way of interpreting this point is that as we do not know the exact impact of the modelled challenges in animal survival, the future trends forecasted in this study is not necessarily a cause for concern. At this point, an important point to emphasize is the complexity of assessing the economic impact of changes in an ecosystem (Millennium Ecosystem Assessment, 2005). For instance, the decrease in *Rousettus aegyptiacus* might be beneficial for the farmers' planting dates. On the other hand, the decrease on insectivorous bats is likely to increase the insect load of an area (Williams-Guillén et al., 2008), resulting in extra costs in terms of insecticides for farmers. Hence, it is extremely difficult to assess the long-term effects of these changes because of the very complex features of any ecosystem.

Moreover, if at some point we realize that the changes in biodiversity are economically damaging to us, the economical investment required to re-create the necessary balance will be extremely high (Millennium Ecosystem Assessment, 2005). Therefore, the results of this study should not be taken lightly. The summarized results indicate that whichever way we look at the results, there will be a significant decrease in total richness within the studied area. Worst of all, we are unable to assess the exact impact of this change.

6. RECOMMENDATIONS

The study faced three major challenges throughout the execution and some relatively easy steps might help any future studies in this field. The challenges could be summarized as follows:

- Obtaining presence data for many parts of the studied area: Unfortunately, although some data is available through past studies, there is no central database that holds these data, and this meant that all data had to be manually extracted from available papers. There are two potential solutions to this: i) including an awareness campaign to help researchers input more data to available databases, such as European Environment Agency website, ii) creating a regional database to standardize the sharing of the data.
- Obtaining and optimizing bioclimatic variables: The methodologies are widely documented but they require significant processing times in repetitive tasks. A standard set of data hosted in servers (e.g. university) would not only significantly ease future studies, but also set a framework for defining study areas and time periods to allow comparison of the literature.
- Manual nature of compiling results: This was actually the major challenge, which was overcome by the use of Python scripts, which require very specific knowledge that is not common to all that work in this field. The source of scripts used in this study is made available in the Appendix D to help researchers in the field and to facilitate future studies. It is important to note that had there been a central repository for this sort of tools, the know-how would have expanded much faster over time, thus providing a more complete setup for future studies.

The suggestions mentioned above would help shift the time spent on data manipulation to results analyses, and enable specialization in a field which seems to get global attention lately. With these improvements, the ecological modelling work can be simplified so that similar research can be undertaken for various groups of species within Turkey and surrounding regions. This would help build a significant information base for assessing the future changes in biodiversity and thus guide decision makers in making more informed decisions about the future of our environment in the region or globally. In addition, further research in this area including the following would strongly help achieve this goal: i) performing same analysis with other IPCC scenarios, ii) monitoring bat phenology in areas that suffer significant losses in species richness due to climate change, and iii) ground-truth current species richness observations. Consequently, it will be possible to build upon the results of this study, and also test its predictions.

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APPENDIX A: ALL SPECIES WITH PRESENCE RECORDS (ALPHABETICAL)

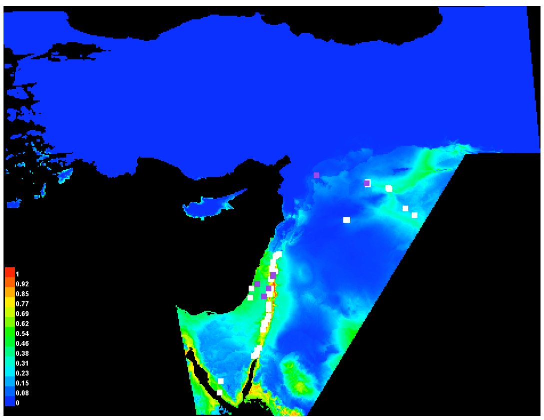
1	*Asellia tridens*
2	*Barbastella barbastellus*
3	*Barbastella leucomelas*
4	*Eptesicus anatolicus*
5	*Eptesicus bottae*
6	*Eptesicus serotinus*
7	*Hypsugo ariel*
8	*Hypsugo savii*
9	*Miniopterus schreibersii*
10	*Myotis aurascens*
11	*Myotis bechsteinii*
12	*Myotis blythii*
13	*Myotis capaccinii*
14	*Myotis daubentonii*
15	*Myotis emarginatus*
16	*Myotis myotis*
17	*Myotis mystacinus*
18	*Myotis nattereri*
19	*Nyctalus lasiopterus*
20	*Nyctalus leisleri*
21	*Nyctalus noctula*
22	*Nycteris thebaica*
23	*Otonycteris hemprichii*
24	*Pipistrellus ariel*
25	*Pipistrellus bodenheimeri*
26	*Pipistrellus kuhlii*
27	*Pipistrellus nathusii*
28	*Pipistrellus pipistrellus*
29	*Pipistrellus pygmaeus*
30	*Pipistrellus rueppellii*
31	*Plecotus auritus*
32	*Plecotus austriacus*

33	*Plecotus christii*
34	*Plecotus kolombatovici*
35	*Plecotus macrobullaris*
36	*Rhinolophus blasii*
37	*Rhinolophus clivosus*
38	*Rhinolophus euryale*
39	*Rhinolophus ferrumequinum*
40	*Rhinolophus hipposideros*
41	*Rhinolophus mehelyi*
42	*Rhinopoma cystops*
43	*Rhinopoma hardwickei*
44	*Rhinopoma microphyllum*
45	*Rousettus aegyptiacus*
46	*Tadarida teniotis*
47	*Taphozous nudiventris*
48	*Taphozous perforatus*
49	*Vespertilio murinus*

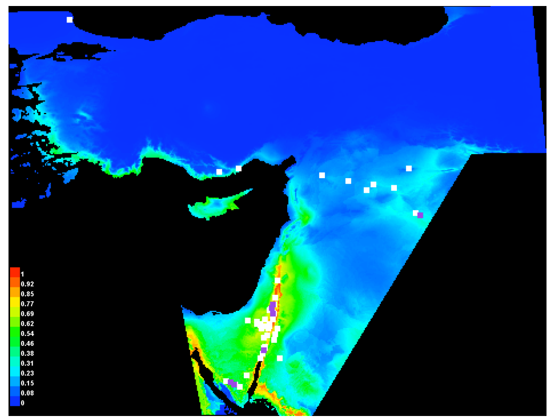
APPENDIX B: JACKKNIFE OF REGULARIZED GAINS IN DIFFERENT MODELS, AND POTENTIAL INCREASES BY INCLUSIONS OR EXCLUSIONS OF VARIABLES (IF ANY)

Species	Regularized Training Gain	Potential increase in gain
Pipistrellus bodenheimeri	3.1942	none
Rhinopoma hardwickei	3.0911	none
Rhinopoma microphyllum	2.9121	none
Rhinolophus clivosus	2.2203	none
Asellia tridens	2.0978	none
Taphozous nudiventris	2.0881	none
Hypsugo ariel	2.0708	0.0001
Rousettus aegyptiacus	1.9834	none
Myotis emarginatus	1.8555	none
Myotis nattereri	1.8516	0.0001
Plecotus austriacus	1.6563	none
Pipistrellus kuhlii	1.5385	none
Eptesicus bottae	1.5373	none
Hypsugo savii	1.4504	none
Rhinolophus blasii	1.4051	none
Otonycteris hemprichii	1.3262	none
Myotis capaccinii	1.2362	none
Eptesicus serotinus	0.8771	none

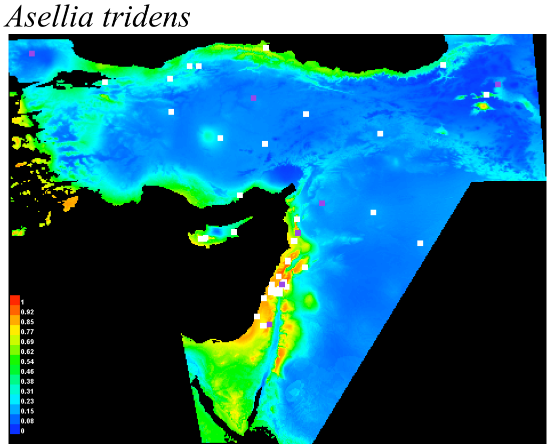
APPENDIX C: CURRENT DISTRIBUTION MAPS BY SPECIES, MAXENT OUTPUT



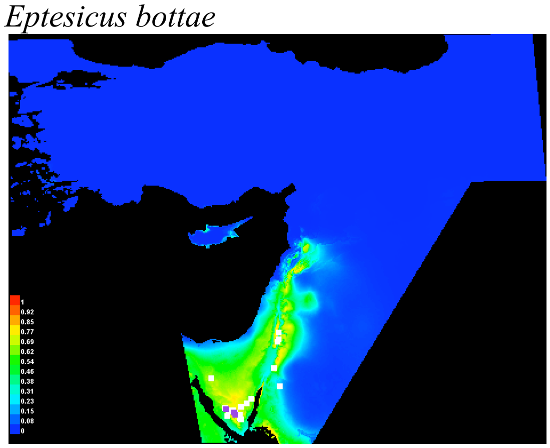
Asellia tridens



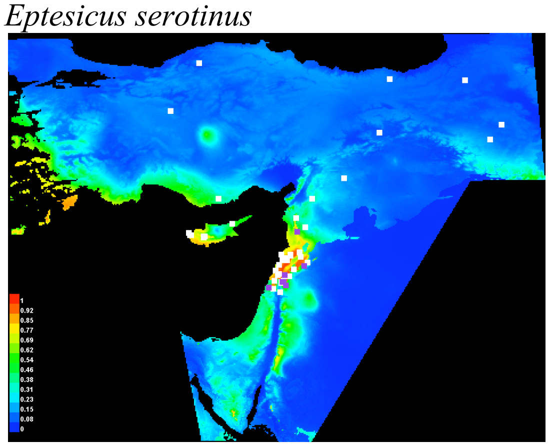
Eptesicus bottae



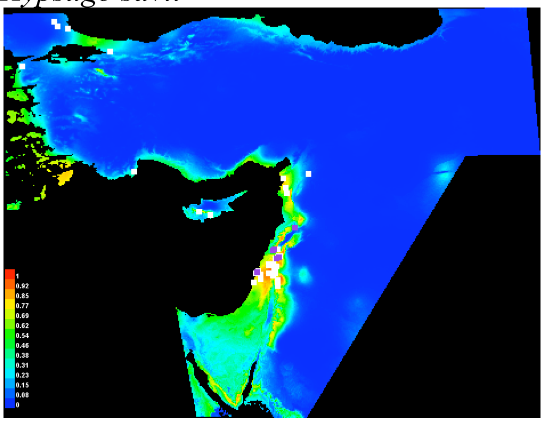
Eptesicus serotinus

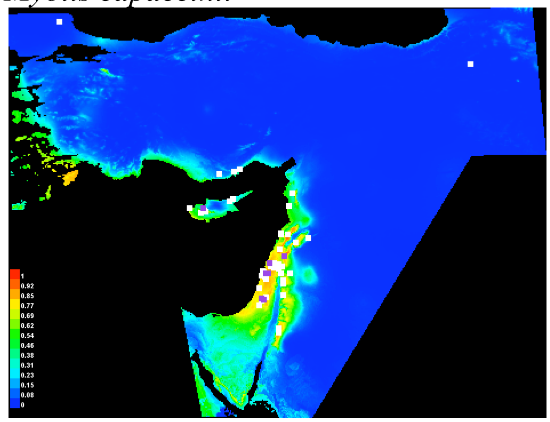


Hypsugo ariel

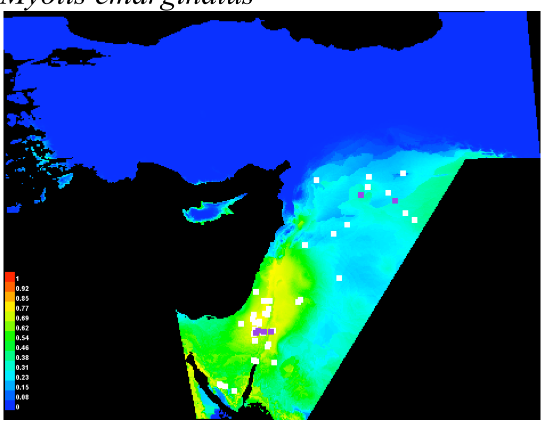


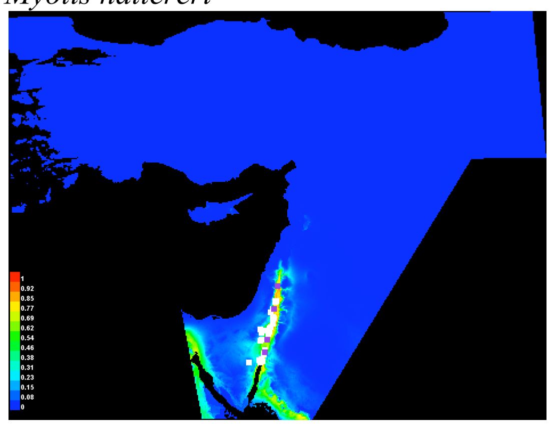
Hypsugo savii *Myotis capaccinii*



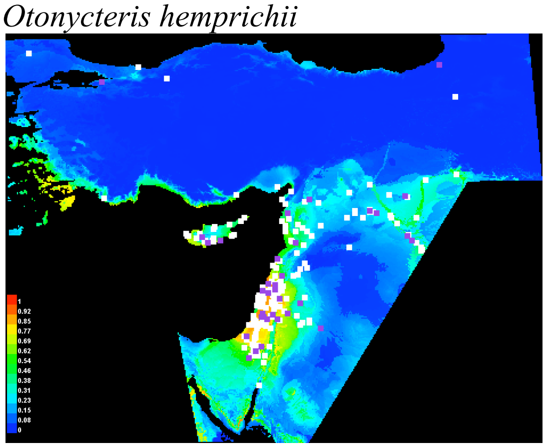


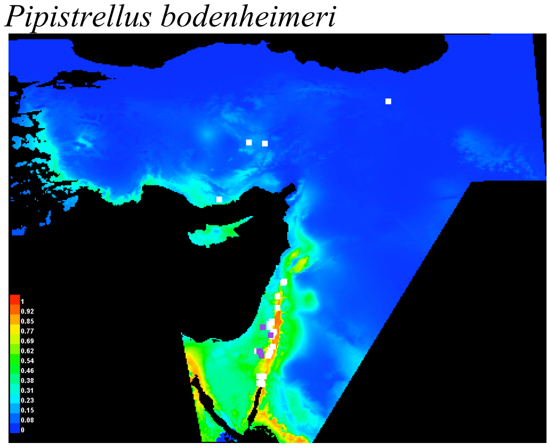
Myotis emarginatus *Myotis nattereri*



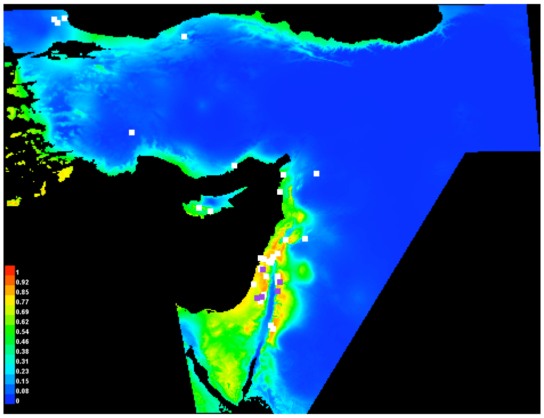


Otonycteris hemprichii *Pipistrellus bodenheimeri*

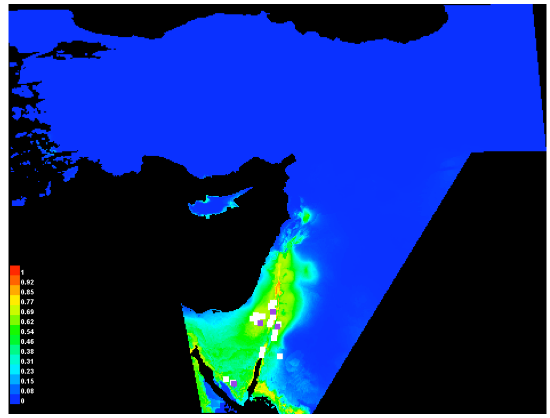




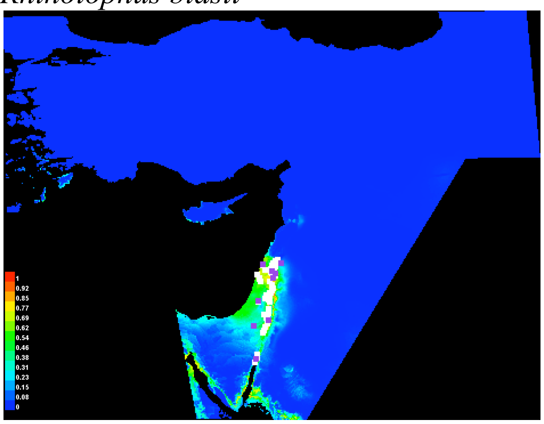
Pipistrellus kuhlii *Plecotus austriacus*



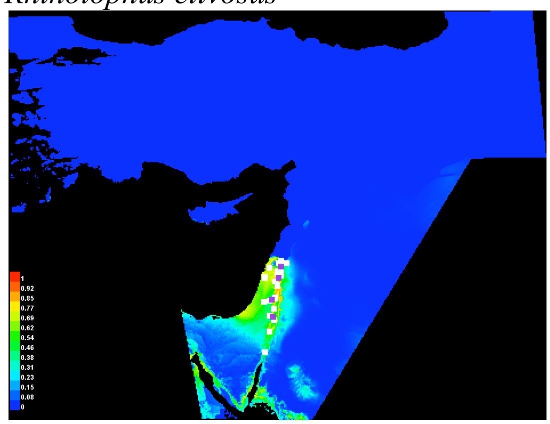
Rhinolophus blasii



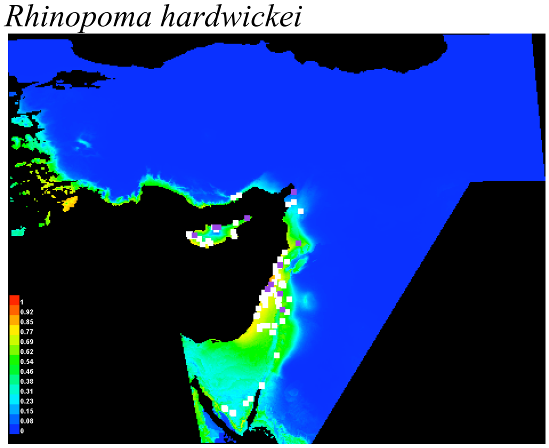
Rhinolophus clivosus



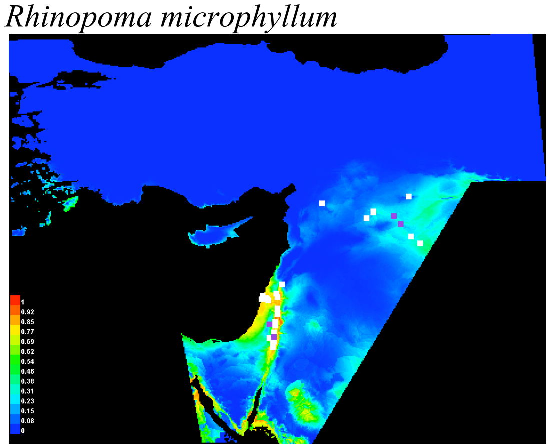
Rhinopoma hardwickei



Rhinopoma microphyllum



Rousettus aegyptiacus



Taphozous nudiventris

APPENDIX D: PYTHON SCRIPTS USED FOR AUTOMATIC PROCESSING OF RESULTS

```
# 10percentiles.py
# Author: Ari Kesisoglu
# Requirements: None
# Date: Dec 28, 2009
# Description:
# Extracts 10th percentile values from results.csv files in maxent output folder
# These values are later used in reclassification of presence probabilities (see Reclass(Folder).py)

import os, glob

f = glob.glob('*Results.csv')
new = open(os.curdir + "thresholds.txt", "w")
for asc in f:
	text = open(asc, "r")
	temp = text.readlines()
	print asc
	text.close()
	data = temp[1]
	data_array = data.split(",")
	species = data_array[0]
	threshold = data_array[80]
	combined = species + ";" + threshold + ";"
	print combined
	new.write(combined)
new.close()

# Reclass(Folder).py
# Author: Ari Kesisoglu
# Requirements: None, works within ArcMap
# Date: Dec 28, 2009
# Description:
# Reclassifies (or changes) the values in all rasters in a folder on a cell-by-cell basis within the analysis window.
# Can be used in conjunction with 10percentiles.py
```

```
# Import system modules
import sys, string, os, glob, arcgisscripting

# Create the Geoprocessor object
gp = arcgisscripting.create()

inFolder = sys.argv[1]
outFolder = sys.argv[2]

# thresholds should be written in .thresholds.txt under the same folder with the format: species1;0.0001;species2;0.0007;...

inputs_raw = open(inFolder + "\\.thresholds.txt", "r")
inputs_lines = inputs_raw.readlines()
inputs = inputs_lines[0]

inputlist = inputs.split(";")

if outFolder == "#":
outFolder = inFolder
theFiles = glob.glob(inFolder+"/*.aux")

counter = 0

for i in theFiles:
selector = (counter * 2) + 1
inFull = str(i).replace("\\","/")
justName = os.path.split(inFull)[1]
inRaster = (inFolder + "/" + str(justName)[:-4]).replace("\\","/")
outRaster = (outFolder + "/" + str(justName)[:-4]).replace("\\","/")
gp.AddMessage(selector)
gp.AddMessage("Converting: " + inRaster)
gp.AddMessage("Producing: " + outRaster)

  # Set the reclassify ranges
currentminrange_str = inputlist[selector]
currentminrange_float = float(currentminrange_str)
gp.AddMessage("Current min range: " + currentminrange_str)
currentmaxrange_float = currentminrange_float + 0.000001
currentmaxrange_str = str(currentmaxrange_float)
reclassifyRanges = "0.000000 " + currentminrange_str + " 0;" + currentmaxrange_str + " 1.000000 1"
gp.AddMessage("Current range: " + reclassifyRanges)
try:
            # Check out ArcGIS Spatial Analyst extension license
```

```
		gp.CheckOutExtension("Spatial")

		# Set the reclassify ranges

		# Process: Reclassify
		gp.Reclassify_sa(inRaster, "Value", reclassifyRanges, outRaster, "DATA")
except:
		# If an error occurred while running a tool, then print the messages
		print gp.GetMessages()
counter = counter + 1

# export_attributes_table.py
# Author: Ari Kesisoglu
# Requirements: None, works within ArcMap
# Date: Jan 6, 2010
# Description:
# Extracts the attributes table of all rasters in a folder
# It is customized to extract only rows with values '1', lines 31-35 should be customized to change this behavior

import os, sys, glob, arcgisscripting

gp = arcgisscripting.create()

#rasterPathList = gp.getparameterastext(0).split(';')
inFolder = sys.argv[1]
theFiles = glob.glob(inFolder+"/*.aux")

outputdir = str(inFolder).replace("\\","/")
outputfile = open(inFolder + "/counts.csv", "w")

for i in theFiles:
	inFull = str(i).replace("\\","/")
	justName = os.path.split(inFull)[1]
	inRaster = (inFolder + "/" + str(justName)[:-4]).replace("\\","/")
	gp.Addmessage(inRaster)
	rows = gp.searchcursor(inRaster)
	row = rows.next()

	while row:
		value = str(row.getvalue('VALUE'))
		count = str(row.getvalue('COUNT'))
		if value == "1":
			tobewritten = justName[:-4] + "," + value + "," + count + "\n"
			gp.addmessage(tobewritten)
			print tobewritten
```

```
                outputfile.write(tobewritten)
            row = rows.next()
outputfile.close()

# Multiply (Folder).py
# Author: Ari Kesisoglu
# Requirements: ArcGIS Spatial Analyst extension license, works within ArcMap
# Date: Jan 6, 2010
# Description:
# Multiplies all layers in two folders, files need to have the same names
# It is customized for the directory structure I used in my study so you need to customize lines 17-20
# Alternatively you can uncomment lines 18 and 20, and comment 19 and 21 to enter the folders manually to the script

# Import system modules
import os, sys, glob, arcgisscripting

# Create the Geoprocessor object
gp = arcgisscripting.create()

inFolder = sys.argv[1]
#currentFolder = sys.argv[2]
currentFolder = inFolder[:-8] + "current"
#outFolder = sys.argv[3]
outFolder = str(inFolder).replace("4_Output_Reclasses","5_Output_Multiplies")
theFiles = glob.glob(inFolder+"/*.aux")

for i in theFiles:
    inFull = str(i).replace("\\","/")
    justName = os.path.split(inFull)[1]
    inRaster = (inFolder + "/" + str(justName)[:-4]).replace("\\","/")
    currentRaster = (currentFolder + "/" + str(justName)[:-4]).replace("\\","/")
    outRaster = (outFolder + "/" + str(justName)[:-4]).replace("\\","/")
    gp.Addmessage(inRaster + " " + currentRaster + " " + outRaster)

    try:
        # Check out ArcGIS Spatial Analyst extension license
        gp.CheckOutExtension("Spatial")

        # Process: Times
        gp.Times_sa(inRaster, currentRaster, outRaster)

    except:
        # If an error occurred while running a tool, then print the messages.
        print gp.GetMessages()
```

```
# combinedcsvs.py
# Author: Ari Kesisoglu
# Requirements: None
# Date: Jan 10, 2009
# Description:
# Combines all results.csv files in maxent output folder into one file

import os, glob

f = glob.glob('*Results.csv')
new = open(os.curdir[:-1] + "combinedresults.csv", "w")
firsttime = 1
for asc in f:
	text = open(asc, "r")
	temp = text.readlines()
	print asc
	print firsttime
	text.close()
	if firsttime == 1:
		labels = temp[0]
		print labels
		new.write(labels)
		firsttime = 0
	data = temp[1]
	print data
	new.write(data)
new.close()
```