ISTANBUL TECHNICAL UNIVERSITY ★ GRADUATE SCHOOL

EXPLORING THE BIODIVERSITY PATTERNS OF ANATOLIA UNDER CHANGING CLIMATIC CONDITIONS

M.Sc. THESIS

Batuhan Atıf TUNÇ

Department of Climate and Marine Sciences

Earth System Science Programme

JUNE 2025

ISTANBUL TECHNICAL UNIVERSITY ★ GRADUATE SCHOOL

EXPLORING THE BIODIVERSITY PATTERNS OF ANATOLIA UNDER CHANGING CLIMATIC CONDITIONS

M.Sc. THESIS

Batuhan Atıf TUNÇ

(601221005)

Department of Climate and Marine Sciences

Earth System Science Programme

Thesis Advisor: Assist. Prof. Dr. Emrah ÇORAMAN

JUNE 2025

İSTANBUL TEKNİK ÜNİVERSİTESİ ★ LİSANSÜSTÜ EĞİTİM ENSTİTÜSÜ

DEĞİŞEN İKLİMSEL KOŞULLAR ALTINDA ANADOLU'NUN BİYOÇEŞİTLİLİK ÖRÜNTÜLERİNİN ARAŞTIRILMASI

YÜKSEK LİSANS TEZİ

Batuhan Atıf TUNÇ

(601221005)

İklim ve Deniz Bilimleri

Yer Sistem Bilimi Programı

Tez Danışmanı: Dr. Öğr. Üyesi Emrah ÇORAMAN

HAZİRAN 2025

Batuhan Atıf Tunç, a M.Sc. student of ITU Graduate School student ID 601221005, successfully defended the thesis entitled "EXPLORING THE BIODIVERSITY PATTERNS OF ANATOLIA UNDER CHANGING CLIMATIC CONDITIONS", which he prepared after fulfilling the requirements specified in the associated legislations, before the jury whose signatures are below.

Thesis Advisor: **Assist. Prof. Dr. Emrah ÇORAMAN** ……...
Istanbul Technical University

Jury Members: **Assoc. Prof. Dr. Demet BİLTEKİN** ……...
Istanbul Technical University

Assist. Prof. Dr. Fatih DİKMEN ……...
Istanbul University

Date of Submission : 29.04.2025

Date of Defense : 02.06.2025

FOREWORD

I would like to express my thanks to my supervisor, Assist. Prof. Dr. Emrah ÇORAMAN, for the invaluable guidance provided for this thesis, and for the continuous support and encouragement during my research journey.

I also extend my gratitude to the founders of the Eurasia Institute of Earth Sciences for establishing, and to its faculty, staff, and students for fostering an inclusive environment that encourages creativity and promotes rational inquiry.

This study is supported by the National Center for High Performance Computing (UHeM) (Grant Number: 4018472024).

June 2025 Batuhan Atıf TUNÇ

TABLE OF CONTENTS

Page

ABBREVIATIONS

AIC : Akaike Information Criterion

AICc : Corrected Akaike Information Criterion

AoH : Area of Habitat

AUC : Area Under the Receiver Operating Characteristic Curve

BRT : Boosted Regression Trees

CMIP6 : Coupled Model Intercomparison Project Phase 6

GBIF : Global Biodiversity Information Facility

GIS : Geographic Information System

IUCN : International Union for Conservation of Nature

km : Kilometer

MESS : Multivariate Environmental Similarity Surfaces

mm : Millimeter

RF : Random Forests

ROC : Receiver Operating Characteristic

SA : Spatial Autocorrelation

SDM : Species Distribution Model

SSP : Shared Socioeconomic Pathway

TSS : True Skill Statistic

WGS84 : World Geodetic System 1984

SYMBOLS

E : Novel Environments matrix

h : Hinge Maxent feature

l : Linear Maxent feature

lr : Learning rate

mtry : The number of variables to randomly sample as candidates at each split

nt : The number of trees

P : The matrix of committee average model predictions

p : Product Maxent feature

q : Quadratic Maxent feature

t : Threshold Maxent feature

tc : Tree complexity

α : The matrix of standard deviations among models

°C : Degree Celsius

° : Degree

LIST OF TABLES

Page

LIST OF FIGURES

Page

EXPLORING THE BIODIVERSITY PATTERNS OF ANATOLIA UNDER CHANGING CLIMATIC CONDITIONS

SUMMARY

Global change poses an unprecedented threat to Earth's biosphere. Global change induced ecological crises—often described as the sixth mass extinction—have become the most urgent issues for the fields of ecology and conservation science. Particularly, rapidly changing climatic conditions exerts disrupting pressures on global biodiversity. Spatially explicit assessments of biodiversity patterns occupy important roles in the immense challenge facing researchers in understanding and mitigating the effects of climate change on Earth's biosphere. Anatolia, an environmentally complex peninsula characterized by diverse climates and heterogeneous topography, hosts rich biodiversity with high endemism and intersects three biodiversity hotspots. Multiple reports highlight the underprotected status of Anatolian biodiversity and habitats. Furthermore, research on biodiversity patterns in Anatolia remains limited, particularly in terms of spatial assessments, with little to no comprehensive studies available. This study primarily aimed to assess the biodiversity patterns of Anatolia, in the context of climate change. To achieve these goals, species distribution modeling—a widely applied tool in ecology—was employed.

Species distribution modeling is a group of mathematical frameworks that relate species occurrences to environmental conditions, thereby allowing researchers to quantify and project species' niches under certain assumptions. These models require predictor variables that are relevant to species' environmental niches. This study focuses on climate change, therefore the 19 bioclimatic variables were utilized as environmental predictors. Bioclimatic variables are various derivations of precipitation and temperature that carry higher biological meaning. The bioclimatic data were sourced from WorldClim 2, an open-access climatic data repository. In order to project biodiversity patterns under climate change, future climate data were obtained from the sixth phase of Coupled Model Intercomparison Project. The averages of the outputs of six different climate models were used to project species distributions for the time periods 2041-2060 and 2081-2100 under the shared socio-economic pathways, SSP1-2.6, SSP2-4.5, SSP3-7.0, and SSP5-8.5.

Biodiversity data were sourced from the Global Biodiversity Information Facility, an open-access repository that integrates datasets from various sources, including field studies, museum specimens, and citizen science observations. The dataset used in the study consisted of presence-only species occurrence records for Türkiye, covering amphibians, birds, insects, mammals, and plants. A large portion of these records originated from citizen science observations. Following an extensive data filtering and preparation phase, species distributions were modeled one by one and grouped by higher taxa.

To model species distributions, various machine learning and statistical methods were employed. The approaches applied consisted of Maxent, random forests, and

boosted regression trees which have been placed as the top performing methods in multimodel benchmarks. Maxent is a Bayesian inference method that utilizes information theoretic concepts to provide the least biased probability distribution of the outcome variable given specified constraints set by the modeler. Random forests are decision-tree based methods, in which multiple trees, that are fitted to bootstrapped subsamples of training data with random subsamples of predictor variables, are combined into an ensemble model. Similarly, boosted regression trees are also decision-tree based models. However, in this approach, simpler trees are iteratively fitted, with each subsequent tree focusing on the remaining unexplained variance. Model fitting process involved a predictor selection phase tailored to each species, split sample cross-validation phase, and a parameter tuning phase before moving on to the fitting of the models. The models were validated on the test sets by their true skill statistics and areas under the receiver operating characteristic curves. Following the calculations of the uncertainty measures, the models were combined into ensembles. Their outputs and projections were utilized to produce biodiversity metrics indicating relative biodiversity and change in biodiversity under different climate scenarios. The spatial assessments of the biodiversity patterns were based on these metrics. Modeling the distributions of large numbers of species from varying taxa opened possibilities for complementary analyses. These included cohabitation analyses in which niche overlap metrics were calculated for pairs of species from different levels of ecological interactions and descriptive analyses of the bioclimatic conditions of areas with varying levels of biodiversity.

The results included the distributions of 519 species. By taxa, these species comprised of 5 amphibians, 118 birds, 126 insects, 5 mammalians, and 265 plants. Each taxa displayed their own idiosyncratic biodiversity patterns at finer scales across the study area. Though, the broad patterns shared among the taxa placed the coastal regions of Türkiye as high biodiversity areas. These included the Mediterranean, Aegean, Marmara, and Black Sea regions. At finer scales, Çukurova Delta emerged as one of the areas with the highest levels of biodiversity. The inner Anatolia and southeastern Anatolia were among the regions that exhibited relatively low biodiversity. When the study results were compared to the biodiversity range maps from the International Union for Conservation of Nature (IUCN)—despite fundamental differences in their objectives and methodologies—the two approaches showed considerable agreement. Although each taxon exhibited its own variations, insects showed the greatest deviations from the broad biodiversity patterns shared among taxa. Insect biodiversity was distributed more uniformly across the study area compared to other taxa, with relatively high biodiversity in northeastern Anatolia, where other taxa did not exhibit similar patterns. From a geographic perspective, the findings demonstrated strong associations between high biodiversity patterns and environmental features such as water bodies, forested areas, and topographical complexity. Avian diversity, in particular, exhibited a strong affinity for water bodies. While plants also shared this association, theirs was to a lesser extent. From the bioclimatic perspective, high biodiversity areas showed associations with lower temperature seasonality, higher precipitation, and higher precipitation seasonality.

The projections under future climatic conditions indicated general northward and northeastward shifts in biodiversity patterns, with notable inter-taxon variations at finer scales. These shifts intensified and expanded over successive time periods

and climate scenarios with increasing radiative forcing. Such findings align with global expectations for biodiversity shifts based on past ecological research. The southern and southwestern coastal regions of Türkiye exhibited declining biodiversity across climate scenarios. The Çukurova Delta, in particular, stood out, showing significant biodiversity losses that became more pronounced under successive climate scenarios. Conversely, the Black Sea region consistently exhibited increasing biodiversity across all taxa, with these patterns intensifying and expanding under successive scenarios. Moreover, complex biodiversity patterns emerged around elevation gradients, water bodies, and forest cover, highlighting the critical roles these features play in shaping biodiversity patterns under changing climatic conditions. These patterns varied considerably depending on taxon, geographic feature, location, and climate scenario. Elevational biodiversity shifts toward higher altitudes were common, congruent with past research. These patterns were often not simple, but rather nuanced. For example, the projections for plant biodiversity showed increases across the Taurus Mountains, except at the highest peaks, where biodiversity declined. Among the uncertainty measures, multivariate environmental similarity surfaces analysis identified southeastern Anatolia as the region that will host novel environmental conditions in the future. The degree of model agreements among themselves varied across taxa. However, broad patterns indicated relatively lower model agreement along the coastal regions, particularly in the southern and southwestern coasts.

This study employed species distribution models to map the spatial biodiversity patterns of Türkiye, addressing a notable gap in spatial approaches to biodiversity analyses in Anatolia. The results highlighted the coastal regions of Türkiye as high biodiversity areas and the inner Anatolia and southeastern Anatolia as low biodiversity areas across different taxa. The projections under future climate scenarios indicated biodiversity shifts toward the north and northeast. Additionally, geographical features such as elevation gradients, water bodies, and forest cover were identified as playing critical roles in shaping biodiversity patterns, particularly under changing climatic conditions. Species distribution models have proven to be indispensable tools in ecological research. However, they are not without limitations. Species' responses to environmental change are often complex and multifaceted, yet species distribution models capture only a single aspect of this complexity. This study underscored the need for multidisciplinary approaches that integrate multiple aspects of the issue for a deeper understanding of biodiversity patterns under climate change. In conclusion, this thesis provided a comprehensive spatial assessment of biodiversity patterns in Anatolia in the context of climate change, contributing to our understanding of the biodiversity in Anatolia. This study is expected to support future research, enhance biodiversity assessments, and inform conservation decision-making processes in Türkiye.

DEĞİŞEN İKLİMSEL KOŞULLAR ALTINDA ANADOLU'NUN BİYOÇEŞİTLİLİK ÖRÜNTÜLERİNİN ARAŞTIRILMASI

ÖZET

Küresel değişim, yeryüzü biyosferi için benzeri görülmemiş bir tehdit oluşturmaktadır. Küresel değişimin neden olduğu ve sıklıkla altıncı kitlesel yok oluş olarak adlandırılan küresel ekolojik kriz, özellikle koruma bilimi ve ekoloji alanları için en acil ve en kritik meselelerden biri hâline gelmiştir. Hızla değişen iklim koşulları, küresel biyoçeşitlilik üzerinde büyük baskılar oluşturarak ekosistemleri tahrip etmekte ve birçok türün yaşam alanlarını tehdit etmektedir. İklim değişikliğinin Dünya'nın biyosferi üzerindeki etkilerini anlamak ve bu etkileri hafifletmek konusunda yürütülen araştırmalarda, biyoçeşitlilik örüntülerinin mekansal açıdan ayrıntılı bir şekilde değerlendirilmesi büyük bir önem arz etmektedir. Çok çeşitli iklimsel bölgelere ve karmaşık bir topoğrafyaya sahip olan Anadolu, zengin biyoçeşitliliği ve görece yüksek endemizmi ile ekolojik açıdan dikkat çeken bir yarımadadır. Anadolu, aynı zamanda, küresel ölçekte yüksek koruma önceliğine sahip üç biyoçeşitlilik sıcak noktasına ev sahipliği yapmaktadır. Ancak, farklı raporlar Anadolu'daki biyoçeşitliliğin ve doğal habitatların yeterince korunmadığını ortaya koymaktadır. Buna ek olarak, Anadolu'daki biyoçeşitlilik örüntüleri üzerine yapılan araştırmalar özellikle mekansal değerlendirmeler açısından oldukça sınırlıdır ve bütüncül yaklaşıma sahip, kapsamlı çalışmalar neredeyse yok denecek kadar azdır. Bu tez, öncelikle Anadolu'nun biyoçeşitlilik örüntülerini iklim değişikliği bağlamında değerlendirmeyi hedeflemektedir. Bu doğrultuda, ekolojide yaygın olarak kullanılan etkili bir analiz yöntemi olan ekolojik niş modelleme yöntemi uygulanmıştır.

Ekolojik niş modelleme, türlerin çevresel koşullarla olan ilişkilerini matematiksel çerçeveler aracılığıyla tanımlayan bir modelleme yöntemidir. Bu yaklaşım sayesinde, belirli varsayımlar altında türlerin ekolojik nişleri nicel olarak değerlendirilebilir ve geleceğe yönelik dağılım projeksiyonları oluşturulabilir. Bu modeller, türlerin çevresel nişleriyle ilişkili olan yordayıcı değişkenlere ihtiyaç duyar. Bu çalışmanın odağı iklim değişikliği olduğundan, analizlerde bağımsız değişkenler olarak 19 biyoiklimsel değişken kullanılmıştır. Biyoiklimsel değişkenler, sıcaklık ve yağış gibi temel iklim parametrelerinin türevleri olup biyolojik açıdan daha anlamlı göstergeler sunar. Biyoiklimsel veriler, açık erişimli bir küresel iklim veri deposu olan WorldClim 2'den elde edilmiştir. Biyoçeşitlilik örüntülerinin değişen iklim koşulları altındaki durumlarını yansıtabilmek amacıyla, gelecek iklim verileri Birleştirilmiş Model Karşılaştırma Projesi'nin altıncı fazından (CMIP6) temin edilmiştir. 2041-2060 ve 2081-2100 dönemleri için farklı Ortak Sosyo-Ekonomik Rotalarını (Shared Socioeconomic Pathways - SSP) temel alan dört farklı senaryo (SSP1-2.6, SSP2-4.5, SSP3-7.0 ve SSP5-8.5) üzerine projeksiyonlar hedeflenmiştir. Geleceğe yönelik tür dağılım projeksiyonları oluşturulurken, altı farklı iklim modelinin çıktılarının ortalamaları alınarak, sadece tek model çıktısının getireceği belirsizlikten arındırılmış sonuçlar üretilmiştir.

Biyoçeşitlilik verileri, farklı kaynaklardan gelen tür gözlem kayıtlarını bir araya getiren ve açık erişimli bir veri deposu olan Küresel Biyoçeşitlilik Danışma Tesisi (GBIF) üzerinden temin edilmiştir. Bu veri tabanı; arazi çalışmaları, müze örnekleri ve vatandaş bilimi gözlemleri gibi farklı kaynaklardan gelen kayıtları tek çatı altında toplamaktadır. Bu çalışmada kullanılan veri seti, yalnızca mevcudiyet (presence-only) temelli tür gözlem kayıtlarından oluşmaktadır ve Türkiye'deki amfibi, kuş, böcek, memeli ve bitki türlerini kapsamaktadır. Çalışmada yer alan tür kayıtlarının önemli bir kısmı vatandaş bilimi gözlemleri aracılığıyla derlenmiştir, bu da geniş ölçekli veri sağlamanın yanı sıra, dikkatli bir veri filtreleme ve hazırlama sürecini gerektirmiştir. Veri setinin kullanılabilirliğini ve hassasiyetini artırmak amacıyla, kapsamlı bir veri filtreleme ve ön işleme süreci uygulanmıştır. Bu aşamalar tamamlandıktan sonra, üst taksonomik sınıflara göre gruplandırılarak, türlerin nişleri tek tek modellenmiştir.

Türlerin modellemelerinin gerçekleştirilmesi için, makine öğrenme ve istatistiksel yöntemlerden oluşan çeşitli yaklaşımlardan yararlanılmıştır. Bu çalışmada uygulanan yöntemler arasında Maxent, rastgele orman (random forests), ve artırılmış regresyon ağaçları (boosted regression trees) bulunmaktadır. Bu yöntemler, çoklu model karşılaştırmalarında en yüksek performans gösteren yaklaşımlar arasında yer almaktadır. Maxent, Bayesçi çıkarım prensiplerine dayanan ve enformasyon kuramı kavramlarını kullanarak, modelci tarafından belirlenen kısıtlamalar altında, hedef değişkeninin en az yanlı olasılık dağılımını hesaplayan bir modelleme yöntemidir. Rastgele ormanlar ise karar ağaçlarına dayalı bir makine öğrenme tekniğidir; bu yöntemde, eğitim verisinin bootstrap örnekleme yöntemiyle alınan alt örneklemlerine dayalı olarak üretilen çok sayıda karar ağacı, rastgele seçilen bağımsız değişkenlerle oluşturulur ve ardından bir topluluk modeli hâlinde birleştirilir. Benzer şekilde, artırılmış regresyon ağaçları da karar ağaçlarına dayalıdır. Ancak bu yöntemde daha basit ağaçlar yinelemeli olarak eğitilir ve her yeni ağaç, hedef değişkendeki model tarafından açıklanamayan varyansa odaklanarak modeli geliştirip, daha iyi tahminler üretmeyi hedefler. Model oluşturma süreci, her bir tür için özel olarak belirlenen bağımsız değişken seçim aşaması, eğitim-test veri ayrımı ile çapraz doğrulama süreci ve model parametrelerinin optimize edildiği bir aşama içermektedir. Modellerin doğruluğu, gerçek beceri istatistiği (true skill statistic) ve alıcı işletim karakteristik eğrisi altındaki alan (area under the receiver operating characteristic curve) ölçütleriyle değerlendirildi. Belirsizlik ölçümleri hesaplandıktan sonra modeller bir araya getirilerek topluluk modellerine dönüştürüldü. Bu modellerin çıktıları ve projeksiyonlar kullanılarak, farklı iklim senaryoları altında görece biyoçeşitliliği ve biyoçeşitlilik değişimini gösteren metrikler üretildi. Farklı taksonomik gruplardan gelen, yüksek sayıda türün dağılımlarının modellenmiş olması, ek tamamlayıcı analizlerin gerçekleştirilmesine olanak sağlamıştır. Bu analizler arasında, ekolojik etkileşimlerin farklı seviyelerinde bulunan türlerin çift olarak niş örtüşme ölçümlerinin hesaplandığı yaşam alanı paylaşma analizleri ve farklı biyoçeşitlilik seviyelerine sahip alanların biyoiklimsel koşullarının karşılaştırılması ve betimsel analizleri yer almaktadır.

Çalışmanın sonuçları, toplamda 519 türün mekansal dağılımlarını kapsamaktadır. Taksonomik gruplara ayrılmış şekilde bu türler; 5 amfibi, 118 kuş, 126 böcek, 5 memeli, ve 265 bitki türünden oluşmaktadır. Her takson, çalışma alanı genelinde kendine özgü biyoçeşitlilik örüntüleri sergilemiş olsa da tüm taksonlar arasında paylaşılan geniş ölçekli eğilimler belirli örüntüler oluşturmuştur. Bu eğilimler

doğrultusunda, Türkiye'nin kıyı bölgeleri yüksek biyoçeşitliliğe sahip alanlar olarak belirlenmişlerdir. Özellikle Akdeniz, Ege, Marmara ve Karadeniz bölgeleri yüksek biyoçeşitlilik değerleriyle öne çıkan alanlar arasında yer almaktadır. Daha ince ölçeklerde incelendiğinde, Çukurova Deltası çalışma alanındaki en yüksek biyoçeşitlilik seviyelerinden birine sahip bölgelerden biri olarak belirlenmiştir. Buna karşılık, İç Anadolu ve Güneydoğu Anadolu nispeten daha düşük biyoçeşitlilik seviyeleri sergilemişlerdir. Çalışmanın sonuçları, Uluslararası Doğa Koruma Birliği'ne (IUCN) ait biyoçeşitlilik dağılım haritaları ile karşılaştırılmıştır. Bu iki yaklaşım, amaçları ve metodolojileri açısından temel farklılıklar içermesine rağmen, sonuçlar arasında önemli ölçüde uyum gözlemlenmiştir. Her takson kendi farklı varyasyonlarını sergilese de geniş ölçekli biyoçeşitlilik örüntülerinden en büyük sapmayı böcekler göstermiştir. Böcek biyoçeşitliliği, diğer taksaya kıyasla çalışma alanı genelinde daha tekdüze bir dağılım sergilemiş ve ayrıca Kuzeydoğu Anadolu'da, diğer taksanın göstermediği görece yüksek biyoçeşitlilik seviyeleri sergilemiştir. Coğrafi açıdan değerlendirildiğinde, biyoçeşitlilik seviyelerinin yüksek olduğu alanlar ile bazı coğrafi faktörler arasında güçlü ilişkiler tespit edilmiştir. Su kaynakları, ormanlık alanlar ve topoğrafik karmaşıklık biyoçeşitlilik örüntülerin şekillenmesinde belirleyici faktörler olarak öne çıkmışlardır. Özellikle kuş çeşitliliği su kaynaklarıyla güçlü bir ilişki göstermiştir. Bitkiler de benzer eğilimler göstermiş olsa da kuşlara kıyasla bu ilişkiler daha zayıf kalmıştır. Biyoiklimsel açıdan incelendiğinde, yüksek biyoçeşitlilik gösteren alanların belirli iklimsel özelliklerle ilişkilendiği görülmüştür. Bu bölgelerin, daha düşük sıcaklık mevsimselliği, daha yüksek yıllık yağış miktarı, daha yüksek yağış mevsimselliği ile karakterize edildiği görülmüştür.

Gelecekteki iklim koşullarına yönelik projeksiyonlar, biyoçeşitlilik örüntülerinde, ince ölçekte taksa arası farklılıklar gözlemlense de genel olarak kuzeye ve kuzeydoğuya doğru bir kayma olduğunu ortaya koymuştur. Ayrıca, iklim senaryolarında artan ışınımsal zorlama ve ilerleyen zaman dilimleri ile birlikte, bu değişimlerin giderek daha da belirginleştiği ve genişlediği görülmüştür. Bu bulgular, geçmiş ekoloji ve iklim araştırmalarında ortaya çıkan biyoçeşitlilik değişimlerine dair küresel beklentilerle uyumludur. Türkiye'nin güney ve güneybatı kıyı bölgelerinde biyoçeşitliliğin, iklim senaryolarını takiben daha da yoğunlaşarak, azalma eğilimi gösterdiği tespit edilmiştir. Bu bölgeler arasında, Çukurova Deltası, yüksek biyoçeşitlilik kayıpları ile dikkat çekici bir örnek olarak öne çıkmıştır. Buna karşın, Karadeniz bölgesi, tüm taksa için, biyoçeşitliliğin arttığı bir bölge olarak belirlenmiş, ve bu artışlar sırasıyla iklim senaryoları ve zaman dilimlerini takiben yoğunlaşma ve genişleme göstermişlerdir. Bunların yanı sıra, topografik gradyentler, su kaynakları, ve orman örtüsü gibi faktörler etrafında karmaşık biyoçeşitlilik örüntüleri ortaya çıkmıştır. Bu bulgular, değişen iklim koşulları altında, bu çevresel faktörlerin biyoçeşitliliğin şekillenmesinde kritik roller oynadıklarına işaret etmektedir. Ancak, bu örüntülerin; taksona, coğrafi faktöre, konuma ve iklim senaryosuna bağlı olarak önemli ölçüde değişiklikler gösterdiği gözlemlenmiştir. Biyoçeşitliliğin topografik gradyentler etrafında yüksek rakımlara doğru kaydığı tespit edilmiştir ki bu durum, geçmiş ekolojik araştırmaların bulguları ile tutarlıdır. Ancak, bu değişimler her zaman basit, doğrusal eğilimler sergilememekte, aksine zaman zaman daha karmaşık ve nüanslı örüntüler ortaya çıkarmaktadır. Örneğin, bitkilere ilişkin projeksiyonlar, genel olarak Toros Dağları boyunca biyoçeşitlilik artışı gösterirken, en yüksek zirvelerde biyoçeşitliliğin azaldığını ortaya çıkarmıştır. Belirsizlik analizleri arasında, çok değişkenli çevresel benzerlik yüzeyleri (multivariate environmental similarity

surfaces) analizleri, Güneydoğu Anadolu'nun gelecekte, günümüzde çalışma alanı kapsamında yaşanmamış, yeni biyoiklimsel koşullara ev sahipliği yapacağını ortaya koymuştur. Model çıktılarının kendi aralarındaki uyuşma dereceleri taksaya göre değişiklikler göstermiştir. Ancak, geniş ölçekli eğilimler incelendiğinde, kıyı bölgelerinde, özellikle güney ve güneybatı kıyılarında, modeller arası uyuşmanın daha düşük olduğu görülmüştür.

Bu çalışma, ekolojik niş modellerini kullanarak Türkiye'nin mekansal biyoçeşitlilik örüntülerini haritalamış ve Anadolu'da biyoçeşitliliğe yönelik mekansal yaklaşımlar konusundaki önemli bir boşluğun doldurulması yönünde adım atmıştır. Elde edilen sonuçlar, Türkiye'nin kıyı bölgelerini yüksek biyoçeşitliliğe sahip alanlar olarak öne çıkarırken, İç Anadolu ve Güneydoğu Anadolu'yu görece düşük biyoçeşitliliğe sahip alanlar olarak belirlemiştir. Gelecekteki iklim senaryolarına yönelik projeksiyonlar, biyoçeşitliliğin kuzeye ve kuzeydoğuya doğru kayma eğilimi gösterdiğini tespit etmişlerdir. Bunun yanı sıra, topoğrafik gradyentler, su kaynakları ve orman örtüsü gibi coğrafi unsurların biyoçeşitliliğin şekillenmesinde önemli roller oynadıkları belirlenmiştir. Özellikle değişen iklim koşulları altında, bu unsurların biyoçeşitlilik dağılımını güçlü bir şekilde etkiledikleri görülmüştür. Ekolojik niş modelleme bir araç olarak, global değişim araştırmalarındaki önemini bir kez daha vurgulamıştır. Ancak, bu modellerin belirli limitleri olduğunu unutmamak gerektiği belirtilmelidir. Türlerin çevresel değişimlere verdiği tepkiler çoğu zaman çok yönlü, dinamik ve karmaşıktır. Buna karşın, ekolojik niş modelleri bu karmaşıklığın yalnızca bir yönünü ele alabilmektedir. Dolayısıyla, biyoçeşitlilik örüntülerinin değişen iklim koşulları altındaki dinamiğini daha kapsamlı bir şekilde anlamak için bütüncül, çok disiplinli yaklaşımlara ihtiyaç duyulduğu açıktır. Sonuç olarak, bu tez çalışması, iklim değişikliği bağlamında Anadolu'nun biyoçeşitlilik örüntülerine yönelik kapsamlı bir mekansal değerlendirme sunmuş ve bölgenin biyoçeşitliliği üzerine önemli bilgiler sağlamıştır. Bu çalışmanın, gelecekteki araştırmalara destek olması, biyoçeşitlilik değerlendirmelerine katkıda bulunması, ve Türkiye'deki doğa koruma politikalarının şekillendirilmesine bilimsel bir dayanak olması beklenmektedir.

1. INTRODUCTION

1.1 Global Change and Ecological Crises

The impacts of global change on Earth's biodiversity are among the most pressing issues in contemporary ecology (Pereira et al., 2012). The ongoing biodiversity crisis, often referred to as the sixth mass extinction, demands urgent attention (Barnosky et al., 2011). Unlike previous mass extinction events primarily driven by geological or astronomical events, the current biodiversity crisis is unprecedented in its rapid rate of biodiversity loss and its causation by human activities, including habitat destruction, climate change, and global resource exploitation. Biodiversity loss can trigger complex ecological cascades, where the extinction of a single species can disrupt entire ecosystem functions, leading to potential collapse of food webs, reduced ecosystem resilience, and diminished capacity for critical ecosystem services. Climate change, which is at the focus of this study, is one of the most significant drivers of this crisis. Its impacts, as well as the responses of Earth's biosphere to these impacts, are each multifaceted, adding layers of complexity to the problem (Bellard et al., 2012). The problem lies in understanding and predicting how biodiversity patterns will change under changing climatic conditions (Barnard & Thuiller, 2008). This is a highly active and dynamic area of research with diverse approaches and innovative ideas (Bektaş et al., 2024; Chevalier et al., 2024; Zurell, Schifferle, et al., 2024). To inform better decision-making in implementing preventative measures against the threats posed by global change, a deeper understanding of the mechanisms shaping biodiversity under changing climatic conditions is essential. One of the greatest challenges researchers face in addressing this question is uncertainty, which manifests at multiple levels. Climate change is human-driven, and the extent of climatic shifts depends on human action—a practically unpredictable factor. Additional uncertainty arises from the diverse ways species may respond to changing climate, including spatial, temporal, physiological, or adaptive changes (Bellard et al., 2012). To address these challenges, one path forward is to build knowledge around the problem. Species distribution modeling is a widely used tool in ecology that

contributes to this effort. These models form the core of this study's methodology, and the following section introduces them.

1.2 Species Distribution Models

Species distribution models (SDMs) are sets of mathematical equations that relate occurrence records of species or other biological systems to predictor variables presumed to influence their distributions (Guisan & Thuiller, 2005). Within the scientific community, SDMs are known by various names, including ecological niche models, habitat suitability models, and range maps, each with subtle differences in their intended meanings. Although similar modeling approaches have historical roots going back, SDMs as they are recognized today emerged in the late 20th century, driven by advancements in statistical methods that accommodate non-linearity and the development of geographic information systems (GIS), which provided enhanced data capabilities (Elith & Leathwick, 2009). Their popularity has further increased with the growing accessibility of computational resources and educational materials.

SDMs are versatile tools employed to answer a wide range of questions, including species distributions under paleoclimatic change (Gür, 2013), range dynamics of mutualist species (Adedoja et al., 2024), and population dynamics of invasive species (Maduna et al., 2024). More pertinently, they have become ubiquitous for investigating biodiversity patterns in the context of climate change (Gür, 2022; Lawler et al., 2009; Zurell et al., 2018). In a similar fashion, this study examines shifting biodiversity patterns in response to changing climatic conditions under the assumption that species track their niches.

SDMs often require considerable amounts of data to effectively model species distributions. In recent years, biodiversity databases have amassed a vast number of species occurrence records. A review of these databases revealed that spatially unique plant records have been growing at an exponential rate, a trend researchers have likened to 'Moore's Law' (Feng et al., 2022). The abundance of biodiversity data, coupled with the wide availability of environmental predictors, has significantly lowered the barriers to the effective application of SDMs. As data becomes more abundant and widely available, it brings promising potential for

scientific discovery, but it is crucial to uphold good data practices and standards, particularly in the age of big data.

While SDMs are powerful tools for ecological research, they inherently face several methodological limitations. A primary constraint is their reliance on the assumption of species-environment equilibrium, which may not always reflect the dynamic nature of ecological systems. Non-equilibrium states can introduce significant inaccuracies in model predictions. Another constraint for SDMs is the difficulty in accounting for biotic interactions. Although joint species distribution modeling techniques have been developed to address some of these challenges (Pichler & Hartig, 2021), their applicability is often limited, particularly in broad-scope studies like this one.

Extrapolative applications, such as projections, pose additional challenges for SDMs. In these contexts, the use of distal predictors—those that indirectly influence species distributions—can introduce significant biases. To mitigate this, it is generally advised to use predictors with direct effects on species distributions, especially when projecting beyond the temporal or spatial extent of the training data (Araújo et al., 2019).

The limitations of SDMs are discussed more extensively in the Discussion section. The common aphorism of British statistician George Box states, "All models are wrong, but some are useful." (Box, 1976). Similarly, while SDMs have their limitations, their utility and power as one of the few practical methods to forecast species distributions remain undeniable (Elith & Leathwick, 2009).

1.3 Biodiversity Patterns

Investigating the mechanisms that shape biodiversity patterns has long been a foundational focus in ecological research (Hutchinson, 1959; Macarthur & Wilson, 1967). Anatolia, a peninsula with intriguing biodiversity dynamics, is home to three biodiversity hotspots and hosts immense species richness with high levels of endemism. Moreover, it has experienced remarkable biodiversity shifts driven by paleoclimatic cycles (Gür, 2017; Médail & Diadema, 2009), providing climatic refugia within its environmentally complex areas and highlighting its value as a critical site for ecological research.

Climate change threatens Anatolia's biodiversity, including its hotspots (Trew & Maclean, 2021), high levels of endemism and rare species (Ohlemüller et al., 2008). Türkiye does not seem prepared for this challenge, ranking 178th out of 180 countries in the 'Biodiversity & Habitat' category of the Environmental Performance Index (Block et al., 2024). Biodiversity in Anatolia appears to be not only underprotected but underexplored as well. Spatial approaches are particularly lacking in examining biodiversity patterns. Improved knowledge of Anatolia's biodiversity patterns can guide policymakers and enhance efforts to protect and conserve its biodiversity.

Answers to the question what shapes biodiversity patterns are rather partial, contextual, and complex. Many mechanisms contribute; spanning evolutionary, ecological, and environmental processes. Among these, climate plays a prominent role; whether through water-energy dynamics (Hawkins et al., 2003) or environmental heterogeneity (Udy et al., 2021), it acts as a determinant of biodiversity gradients. This study centers on climate to spatially assess biodiversity patterns, which naturally couples the study to geographic axes. Topography is frequently discussed in relation to biodiversity gradients, particularly at smaller scales, where it is often associated with these gradients—and Anatolia, with its complex topography, is relevant to such discussions. However, topography is correlated with multiple different factors, including temperature and precipitation gradients and environmental isolation. These correlations can lead to confusion when attempting to understand causal mechanisms, and they can cause further problems under extrapolative applications, such as future projections. Therefore, it is as important as ever to ground statistical associations in causal models.

1.4 Scope and Aims of the Study

To the best of the author's knowledge, comprehensive broad-scale spatial biodiversity assessments of Anatolia remain absent in the current scientific literature. Consequently, an exploration of spatial biodiversity patterns to fill this apparent gap has been the first and foremost motivation of this study. This exploratory work was implemented through SDMs based on climatic variables. While a variety of factors influence species distributions, such as biotic interactions and landcover, this study focused solely on the climatic component.

The scientific community assesses biodiversity along multiple axes, including genetic, taxonomic, ecosystemic, and functional dimensions. This study's concept of biodiversity is limited to species richness, specifically that of amphibians, birds, insects, mammals and plants, with occurrence data sourced from the Global Biodiversity Information Facility (GBIF) (Figure 1.1).

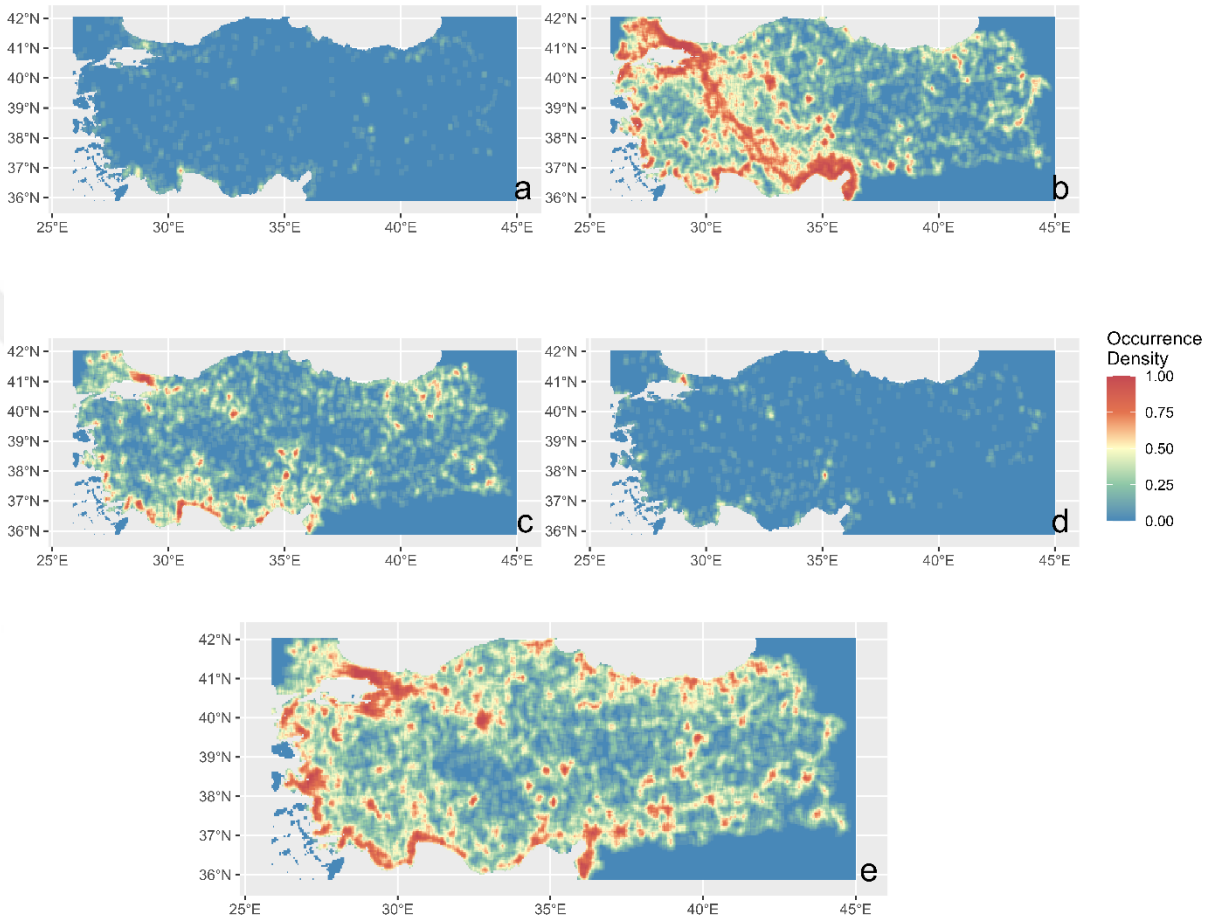

Figure 1.1: Occurrence records from GBIF grouped by taxa plotted as density maps; a) amphibians, b) birds, c) insects, d) mammals, e) plants.

In the context of climate change, species distributions were projected to future time periods under different climate scenarios, with the aim of assessing shifts in biodiversity patterns associated with changing climatic conditions. These results aim to provide high-resolution biodiversity maps that reveal both broad-scale and fine-scale biodiversity patterns and guide better decision-making in conservation and protection efforts.

Anatolia is a climatically complex region, making it a suitable candidate for studying biodiversity-climate relations. An additional aim of this study is to

explore the dynamics between climate and biodiversity, providing insights into the climatic patterns that influence biodiversity gradients.

To summarize, this study aims: i) to explore the spatial biodiversity patterns of Anatolia; ii) to assess potential biodiversity shifts under changing climatic conditions; iii) to provide high-resolution maps describing biodiversity patterns to inform conservation practices; and iv) to examine the relationship between climate and biodiversity patterns.

2. METHODS

2.1 Study Area

The study area encompasses Anatolia, extending from 35.90°N to 42.03°N latitude and from 25.90°E to 45.00°E longitude (Figure 2.1).

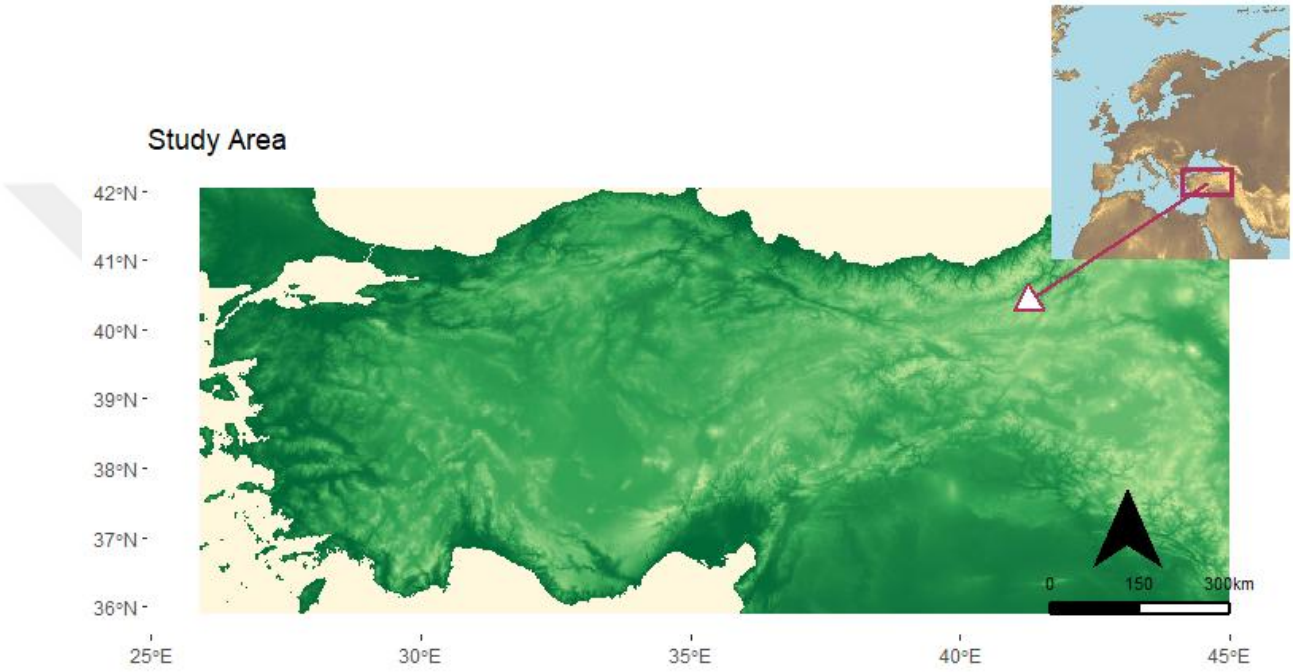

Figure 2.1: Map of the study area, Anatolia. Smaller map on the top right locates the study area within the broader scale of Western Palearctic.

Anatolia is environmentally complex. It is topographically heterogeneous, with an elevation gradient starting from sea level and going over 5,000 meters. Climatic diversity is another factor that contributes to this complexity. Anatolia is a region with a multitude of climates and microclimates. All this heterogeneity, richness, and complexity endow Anatolia with diverse habitats and microhabitats, which in turn promote biodiversity. Anatolia hosts multiple biodiversity hotspots which makes it a compelling subject of ecological study.

2.2 Climate Data

Every living being has ranges of climatic conditions within which they survive, grow and reproduce (Ecology: From individuals to ecosystems, 2020, p. 33), (Begon & Townsend, 2020, Chapter 2). Ecologists have been using climate to explain species' distributions ever since the field has been established (Grinnell, 1917). It has been projected that Earth's climate will change in the upcoming years and the extent of this change will depend on the socioeconomic pathway humankind will take (Calvin et al., 2023). Ecologic theory posits numerous and complex ways for individual species to react to these climatic changes. One striking prediction is that species' distributions will change with climatic conditions (Wiens et al., 2010). It is for these reasons, this study bases its environmental predictors on climate.

Bioclimatic parameters were deemed more appropriate for the particular purposes of the study. These are variables that are derived from temperature and precipitation and have more precise biological meaning (Table 2.1). Bioclimatic variables have been used widely in species distribution modeling (Dumlupinar et al., 2023; Oeser et al., 2024).

Bioclimatic data were sourced from WorldClim 2 (Fick & Hijmans, 2017) as the averages for the years 1970-2000 at 2.5 arc-minutes resolution. These are the data used in the modeling procedure.

Two future time periods were chosen as 2041-2060 and 2081-2100, mainly due to convention and data availability. As the mid-century and the end of century have been popular periods for projections among climate scientists and ecologists. Model outputs from the sixth phase of Coupled Model Intercomparison Project (CMIP6) were the source for future bioclimatic data. Six models were chosen from CMIP6 with the aim of representing different climate modeling approaches (Boucher et al., 2018; Peano et al., 2020; Shiogama et al., 2019; Tang et al., 2019; Volodin et al., 2019; von Storch et al., 2017). Among these modeling approaches are earth system models which take an holistic outlook to modeling and include many processes such as biogeochemical cycles, and global circulation models which model how air moves through the atmosphere, focusing on the physics of vortices. Mean averages of the outputs of these six models, again at 2.5 arc-minutes

resolution, were used as the final bioclimate product for species distribution projections. This climate ensemble, as opposed to a single model outputs, was preferred to remedy the uncertainty that comes from using model projections as source for analysis (Palmer, 2022).

Table 2.1: Bioclimatic variables and their descriptions.

Variable	Description
Bio1	Annual Mean Temperature
Bio2	Mean Diurnal Range (Mean of monthly (max temp – min temp))
Bio3	Isothermality (BIO2/BIO7) (×100)
Bio4	Temperature Seasonality (standard deviation ×100)
Bio5	Maximum Temperature of Warmest Month
Bio6	Minimum Temperature of Coldest Month
Bio7	Temperature Annual Range (BIO5-BIO6)
Bio8	Mean Temperature of Wettest Quarter
Bio9	Mean Temperature of Driest Quarter
Bio10	Mean Temperature of Warmest Quarter
Bio11	Mean Temperature of Coldest Quarter
Bio12	Annual Precipitation
Bio13	Precipitation of Wettest Month
Bio14	Precipitation of Driest Month
Bio15	Precipitation Seasonality (Coefficient of Variation)
Bio16	Precipitation of Wettest Quarter
Bio17	Precipitation of Driest Quarter
Bio18	Precipitation of Warmest Quarter
Bio19	Precipitation of Coldest Quarter

Another type of uncertainty comes from the fact that future climatic conditions depend on the socioeconomic output of human civilization. Because one can not model human behavior, various shared socioeconomic pathways (SSPs) were taken as different scenarios. These scenarios are SSP1-2.6, SSP2-4.5, SSP3-7.0 and SSP5-8.5 from the proposed pathways of IPCC (Calvin et al., 2023), ordered from the least greenhouse gas emitting scenario to the most greenhouse gas emitting scenario. By combining two future time periods with these four pathways, 8 different projections are produced. Including the predictions for contemporary climatic conditions, this study generates 9 different distributions for each species.

2.3 Biodiversity Data

Species occurrences data were obtained from Global Biodiversity Information Facility (GBIF). GBIF combines various datasets from different sources such as expert designed surveys, museum specimens or citizen science observations. It is an open access data repository available to all researchers.

To gather the biodiversity data for the study, species occurrences in the study area were filtered to include presence-only observations that have coordinates and have no geospatial issues (GBIF.org, 2024a, 2024b, 2024c, 2024d, 2024e). Taxonomic grouping of the study were set to Plants (Plantae), Birds (Aves), Mammals (Mammalia), Amphibians (Amphibia), and Insects (Insecta). Taxonomic breakdown of the dataset for species and observations are given in Table 2.2. The majority of the species had single or a few observations which are unfit for SDM purposes.

Table 2.2: Number of species and observations in the data organized by taxa.

Taxa	Species	Observations
Amphibians	43	1,990
Birds	540	2,334,283
Insects	6,948	132,450
Mammals	287	4,159
Plants	7,671	147,657

While the data used in the study is an amalgamation of various datasets from different surveying efforts, the majority of the data points come from citizen science observations.

2.4 Data Preparation

In the context of SDMs, species occurrence data often reveal a particular set of problems. These are spatial autocorrelation, sampling bias and lack of sufficient observations (Araújo et al., 2019; Segurado et al., 2006; Soley-Guardia et al., 2024). This section reports the methods applied to reduce and remedy their effects to model biases.

2.4.1 Evaluating the sufficiency of sample sizes

The law of large numbers implies that, in a stochastic system, as sample size increases, expected deviation from the true distribution decreases (Probability and Measure, 2012, p. 5), (Billingsley, 2012, Chapter 1). Implication of this for species distribution modeling is a notion of a sample size threshold below which the deviation of modeled distribution from true distribution is unacceptably large for the standards of scientific establishment. Determining of this threshold of minimum required observations for SDMs has lead to lengthy discussions and analyses (Collart & Guisan, 2023; Moudrý et al., 2023; Santini et al., 2021; Stockwell & Peterson, 2002; Thibaud et al., 2014; van Proosdij et al., 2016). Taxonomically broad scope of this study requires a generally applicable threshold. A weak consensus seems to be that a minimum of 30 observations is an appropriate cutoff for SDMs (Habitat Suitability and Distribution Models, 2017, p. 116), (Guisan et al., 2017, Chapter 7).

A cutoff of 30 is applied to the biodiversity data where species with less than 30 observations have been removed from the dataset. After this procedure, numbers of species left by higher taxa were 22 for mammals, 410 for birds, 10 for amphibians, 738 for plants and 575 for insects.

2.4.2 Spatial autocorrelation

Lack of sampling design in surveying efforts can lead to biases in species occurrence records. One way this can cause problems for SDMs is spatial autocorrelation. Spatial autocorrelation (SA) is when values of a variable are spatially dependent on one another. SDMs with spatial autocorrelation will perform poorer relative to ones without SA. SA is common in ecology; so, effects and remedies of it have been discussed extensively (Dormann, 2007; Guélat & Kéry, 2018; Segurado et al., 2006).

Occurrence data involved in this study is heavily weighted towards undesigned sampling. Therefore, it is necessary to reduce the effects of SA to build accurate models. One common way of addressing the issue of SA is spatial thinning of occurrence records (Segurado et al., 2006). Spatial thinning is systematic removal of occurrence records in a way that keeps a single record within a specified distance. This thinning distance is usually decided based on expert knowledge

about the species or higher taxa that are the foci of their corresponding studies (Gür, 2022; Oeser et al., 2024). Given that this study involves multiple higher level taxa that are different from each other, deciding on a thinning distance for each species is impractical. Therefore another approach is taken where appropriate thinning distances are calculated for each species (Assis, 2020; Boavida et al., 2016). For each species, their occurrence coordinates, with their corresponding georeferenced bioclimatic values, were extracted using R package raster (Hijmans, Etten, et al., 2023). Then, Euclidean distances between occurrence records have been calculated using R package ecodist (Goslee & Urban, 2023). For each bioclimatic variable and with 5 km increments up to 500 km, correlations of bioclimatic values with geographic distances have been calculated using linear models. These calculations resulted in minimum distances that did not have statistically significant autocorrelation[1] for each variable. Mean averages of these 19 distances were taken as thinning distance and species occurrence records were thinned using R package spThin (Aiello-Lammens et al., 2019). This process is repeated for each species.

2.4.3 Pseudo-absences

When building SDMs from presence-only occurrence data, many modeling approaches require there to be pseudo-absences included with species presence records (Barbet-Massin et al., 2012). These are intended to take the role of records of locations where species are absent. Pseudo-absences are sometimes called background samples as well.

To generate pseudo-absences, random samples are taken from the whole study area except the locations with species presence records (Barbet-Massin et al., 2012), using the R package terra (Hijmans, Bivand, et al., 2024). Number of pseudo-absences should be high enough to sample the whole range of environmental conditions in the study area. Increasing the number of pseudo-absences seems to improve model performances up to a point but also comes with increasing computational burden (Valavi et al., 2022). Taking into account the bioclimatic heterogeneity and complexity of Anatolia, a relatively large number of 30,000 pseudo-absences are sampled for each species in the dataset in order to cover the

[1] The threshold for statistical significance is set at 0.05.

entire range of bioclimatic conditions in the study area. Large numbers of pseudo-absences can cause class overlap problems in some SDM techniques such as random forests which are a type of modeling algorithm this study implements in its analyses. This problem is handled in section 2.5.3.

2.5 Model Building

Machine learning methods have been popular tools for building SDMs. They perform well in modeling species' relations to their environment and similar tasks. In addition, they have become more accessible due to increasing availability of computational resources, big data and educational resources. This study takes advantage of machine learning methods in building SDMs.

Valavi et al. (2022) performed a multi-model comparison on SDM benchmarks. Methods that performed the best were boosted regression trees, maxent and a modified version of random forests. These three machine learning methods were used in building the SDMs of the study. An ensemble approach is taken where models built by different algorithms are combined in order to reduce the uncertainty that can come from the outputs of a single model.

2.5.1 Predictor selection and multicollinearity

As elaborated before in section 2.2, bioclimatic variables are all different derivations of precipitation and temperature. This makes it likely that they have multicollinearity among each other. Multicollinearity is when multiple predictor variables of a model have linear relations among themselves (Alin, 2010). It is a problem that can cause all sorts of trouble such as unreliable predictor coefficients or inaccurate predictions during extrapolations. Since the SDMs of the study are needed to project onto future time periods, change in relations with time between collinear predictors would bias the projections and result in inaccurate species distributions for the future time periods. Therefore, it is made sure that the predictors used in modeling have less than 0.7 Spearman correlation among themselves (Dormann et al., 2013).

To determine which predictors explain the species occurrences the best, univariate generalized additive models were fitted and bioclimatic variables were ranked according to their Akaike Information Criterion (AIC) scores (Akaike, 1974). This

process is repeated for each species in the dataset. For each species, among the combinations of predictors that do not have multicollinearity, the combinations with the best AIC scores were selected to be the predictors for that particular species using the R package mecofun (Zurell, 2020).

2.5.2 Maxent

Maxent stands for maximum entropy. It describes the states of a system with the highest entropy which is often associated with disorder, randomness or uncertainty in different fields. Edwin Jaynes appropriated this descriptive concept into a statistical inference method called maximum-entropy inference (Jaynes, 1957a, 1957b). He postulated that the best approximation of a probability distribution that one has incomplete information of, is the least biased one, conditional on the partial information one has about the distribution. And this approximation is the probability distribution that maximizes the entropy[2].

Finding the maximum entropy distribution can be arduous mathematical work. Fortunately, machine learning algorithms have been developed that are proven to converge to maximum entropy probability distributions. Phillips et al. (2006) adapted maximum-entropy inference to species distribution modeling with the name Maxent. Maxent excels at SDMs with presence-only data (Elith et al., 2011) and has been used extensively and successfully to model species' distributions (Gür, 2022; Maduna et al., 2024).

First, data were partitioned into 75% training set and 25% test set. Before fitting the models, hyperparameter tuning processes were put in place to determine the optimal parameter settings for the best performing models. Using R packages maxnet (S. Phillips, 2021) and enmSdmX (Smith, 2024), different models were fitted with a range of regularization parameters and combinations of different Maxent features. Regularization is essentially smoothing of the fitted curves; it decreases the complexity of the model and increases its generalizability (Elith et al., 2011). Maxent features are different ways of modeling relationships between predictor and response variables. These are briefly; linear (l) models the means of predictors, quadratic (q) models the variances of predictors, product (p) models the

[2] The entropy being discussed here is Shannon entropy from Information theory (Shannon, 1948).

interactions between predictors, threshold (t) models immediate responses below or above some predictor thresholds and hinge (h) is a combination of t and l that can use l features between different predictor thresholds (Elith et al., 2011; S. J. Phillips et al., 2006; S. J. Phillips & Dudík, 2008). Among these different models, the best one was selected according to their scores on the corrected Akaike Information Criterion (AICc). AICc is a correction on AIC that penalizes complexity more harshly at small sample sizes and as sample sizes increase AICc gets closer to AIC (Burnham & Anderson, 2004). If the model passed the evaluation criteria which is elaborated on section 2.6.1, then the model training process was repeated with 100% of the data as training set. The resulting model was picked as the final model. If the model failed the evaluation criteria, then it was discarded.

2.5.3 Random forests

Random forests are ensembles of decision trees that bring many trees together to model the relationship between response variable and predictors (Breiman, 2001). One of the defining features of random forests is that they use a new subsample of the data when building each tree (Breiman, 1996). Similarly, at every branch split, only a random subsample of the available predictors is used. These features force individual trees in random forests to be substantially different from each other. Random forests are unlikely to overfit to training data as correlation between trees are broken due to these features. Random forests can be built as categorical classification trees or regression trees. Interpreting the response variable of this study as species' presences and absences categories or as 0s and 1s for absences and presences are both valid. For this study, 0s and 1s are selected since regression tends to perform better (Malley et al., 2012) and aligns more suitably with the structure of the study.

Large number of pseudo-absences have been generated in this study due to the reasons given in section 2.4.3. A common problem faced when building random forest SDMs with high pseudo-absences is class overlap. Class overlap problem shows itself when deep trees struggle separating presence and absence records with very similar environmental values. It can have a major negative effect on model performance (Valavi et al., 2022). Among the available remedies to this problem,

this study went with the shallow tuning process (Valavi et al., 2021). Shallow-tuned random forests (henceforth RF) allow presence and absence records with similar environmental values to be branched together by reducing the depth of the trees and performing broader splits.

Before starting the model building process, data were partitioned into 75% training and 25% test set. To tune the tree depth, models with a range of different depths have been fitted using R package ranger (Wright et al., 2023). These models had tree numbers of 5000 and numbers of predictors to be sampled (mtry) as the square root of total number of predictors. Models were then tested with a 5-fold cross validation and ranked according to their areas under the receiver operating characteristic curves (Konowalik & Nosol, 2021). The best scoring model was tested against the initially separated test set. If the model passed the evaluation criteria (section 2.6.1), the training process was repeated with 100% of the data as training set. If it failed the criteria, the model was discarded.

2.5.4 Boosted regression trees

Boosted regression trees (BRT) combine multiple simple regression trees, utilizing boosting techniques from machine learning (Schapire, 2003), to infer relationships between variables in the data. For BRT, tree fitting is a stagewise process unlike RF where tree fitting processes are in parallel and independent of each other. In BRT models, each tree is dependent on the trees fitted prior to itself. BRT iteratively fit trees on bootstrapped subsamples of data where each new tree focuses on the unexplained variance by the former trees (Elith et al., 2008). This iterative improvement of the model is done on a loss function by gradient descent.

In order to build a BRT model, a number of parameter values have to be decided, such as number of trees (nt), learning rate (lr) and tree complexity (tc). Number of trees is the total number of trees at the end of the modeling phase and lr is the weight of each tree's contribution to the model. It is preferable to have low lr and high nt, going down the loss function in smaller steps is often better (Elith et al., 2008). Although, this comes with a computational cost. Tree complexity refers to the number of branches meaning splits of the data. Heuristic at the root of BRT is that many broad rules of thumb are better than few intricate, complex models. That's why BRT design principles dictate simple trees. So, the options considered

are tc of 1 or 2. A tc of 2 allows interactions between predictors to be modeled at the cost of increased complexity. Since it is reasonable to assume interactions between bioclimatic parameters affecting species occurrences, a tc of 2 was used throughout the study.

After data were partitioned into 75% training and 25% test set, hyperparameter tuning phases have been processed to determine optimal nt at fixed low lr. Increasing number of trees at steps of 50 trees were iteratively fitted using R package dismo (Hijmans, Phillips, et al., 2023). These models were trained and tested on 10-fold cross validation folds. Number of trees that minimizes the holdout deviance was set as optimal nt as higher nt would not have increased model performances. Models with optimal parameters were evaluated against the previously left-out test set. Those that passed the evaluation criteria (section 2.6.1) were re-trained with 100% of data. Models that failed the evaluation criteria were discarded.

2.6 Model Evaluation and Assessment of Uncertainty

2.6.1 Model performance criteria

Models fitted with optimal parameters were tested against previously separated test sets and expected to perform above thresholds on two different evaluation criteria (Araújo et al., 2019). These two criteria are true skill statistic (TSS) and area under the receiver operating characteristic curve (AUC) as they seem to perform well in a wide variety of settings with presence-only data (Konowalik & Nosol, 2021). TSS is calculated by subtracting 1 from the sum of sensitivity and specificity (Allouche et al., 2006). Sensitivity refers to the probability that a model will correctly predict a presence. It is the number of true positives divided by the sum of true positives and false negatives. Inversely, specificity refers to the probability that the model will correctly predict an absence. So, it is the number of true negatives divided by the sum of true negatives and false positives (Fielding & Bell, 1997). All three modeling techniques of the study output probabilistic predictions. In order to evaluate model performance using TSS, conversion of model outputs to binary predictions of presence and absence was required. Using a threshold that maximizes sum of sensitivity and specificity, all probabilistic predictions were

converted to binary presence and absence predictions. This particular threshold was chosen as it is one of the best performing ones (Liu et al., 2005). After the conversions, TSSs of the models were calculated with R package mecofun (Zurell, 2020).

Unlike TSS, AUC is a threshold independent metric. All possible thresholds are used to create a receiver operating characteristic (ROC) curve. ROC curve is plotted on sensitivity at vertical axis and 1 – specificity on horizontal axis (Fielding & Bell, 1997). A 45 degree straight line in this plot would be equivalent to random predictions. Area under the ROC curve (AUC) is interpreted as the performance score of models. AUCs of the study models were calculated using R package mecofun (Zurell, 2020). Both AUC and TSS have been shown to be prevalence independent metrics (Allouche et al., 2006). But these notions have been challenged as well (Leroy et al., 2018). Although imperfect, they seem to be popular choices within studies that use SDMs (Farashi et al., 2017; Gillespie et al., 2024; Ke et al., 2024; Zurell et al., 2018). Models that performed both above 0.7 on AUC (Araújo et al., 2005) and above 0.4 on TSS (Landis & Koch, 1977) were kept, the rest were discarded.

2.6.2 Dealing with uncertainty

Projecting SDMs to future climatic scenarios involves going outside of training data to new environmental conditions. Leaving domain of interpolation in to extrapolation comes with all sorts of uncertainty that challenge projections and their interpretability (Chevalier et al., 2024; Santini et al., 2021; Soley-Guardia et al., 2024; Wolpert & Macready, 1997; Yates et al., 2018; Zurell et al., 2020). Fortunately, there are ways to handle uncertainty and clarify the limitations it imposes on projections. Following subsections are elaborations on the methods applied to engage with uncertainty.

2.6.2.1 Ensemble modeling

Ensembles are integrations of different models or ranges of different conditions to circumvent possible downfalls that might come about due to an unforeseen idiosyncrasy of a single model or a single set of initial conditions. Ensemble approach is particularly common in modeling of complex phenomena, especially

if extrapolation is involved in corresponding study. A standard way to build an ensemble of SDMs is combining outputs of different modeling methods. Although recently, there have been more sophisticated ensemble efforts such as merging SDMs with genomics (Barratt et al., 2024) or stacking SDMs and expert range maps together (Oeser et al., 2024), the ensemble of this study is limited to combining outputs of the models mentioned in section 2.5.

Study models Maxent, RF and BRT produce probabilistic predictions which are difficult to interpret. In addition, one of the evaluation criteria TSS had been calculated with binary present/absent predictions. Therefore, it would make sense to use the type of predictions that the models have been evaluated on. For these reasons, the probabilistic outputs of the models were converted into binary present/absent predictions using the threshold from before (see section 2.6.1) that maximizes the sum of specificity and sensitivity (Liu et al., 2005). Then, mean averages of the binary predictions among models were calculated and taken as the final outputs for analyses (Dormann et al., 2018). These model-averaged ensemble predictions are referred to as committee averages hereafter.

2.6.2.2 Variation of agreement between models

Whether different models agree or disagree on predictions provide useful insights on uncertainty of outputs. Agreement of models can vary with changing environmental inputs that are used to produce predictions. To quantify this variation of agreement between models, standard deviations among different model predictions for each species were calculated for all environmental conditions included in the different climate scenarios of the study (Habitat Suitability and Distribution Models, 2017, p. 234), (Guisan et al., 2017, Chapter 14). Species' standard deviations were combined by higher taxa for each climate scenario. The results for different climate scenarios then combined together to broadly assess how agreement between models change with different bioclimatic conditions for each higher taxa.

$$\sum_{j=1}^{m}\sum_{i=1}^{n} a_{ij} \tag{2.1}$$

Equation 2.1 demonstrates the process where a_{ij} is the standard deviations matrix of species *i* for the climate scenario *j*. Since this analysis is grouped by higher taxa, *n* refers to the set of species in a particular higher taxa and *m* is the set of different climate scenarios. After the calculations, the results were mapped for the study area by each taxa using R packages ggplot2 (Wickham et al., 2024) and tidyterra (Hernangómez et al., 2024) to assess the geographical distribution of model agreements.

2.6.2.3 Novel environments

Novel environments are environmental conditions that are not included in model training data but are realized in data used for projections. For the case in this study, projection data consist of the 8 future bioclimatic scenarios. Novel environments are calculated with multivariate environmental similarity surfaces (MESS) method (Elith et al., 2010) using R package predicts (Hijmans, Phillips, et al., 2024). Model outputs projected to these environments should be interpreted with extra care. Because models extrapolate out of the dataset in those environments and this may bring about an additional layer of uncertainty to the projections.

Since every species' training data possess different sets of bioclimatic predictors that best explain the corresponding species' occurrences, an overall assessment of novel environments that is valid for every species is not a straightforward act. An approach was taken where each species' novel environments were combined by taxa for every climate scenario. The process is given in equation 2.2 where E_i is the novel environments matrix for *i*th species and *n* is the set of species in the higher taxa.

$$\sum_{i=1}^{n} E_i \tag{2.2}$$

This process was repeated for each taxon and each climate scenario. The results were plotted using R package ggplot2 (Wickham et al., 2024).

2.7 Biodiversity Metrics

Biodiversity is an equivocal term in natural sciences. It can be used to refer to different concepts such as taxonomic diversity, phylogenetic diversity, functional

diversity or ecosystemic diversity. In this study, species richness is taken as the notion of biodiversity due to taxonomic perspective and data structure of the study. Henceforward, biodiversity refers to species richness unless otherwise is stated. Following subsections articulate the methods used to quantify biodiversity in order to assess biodiversity patterns in changing climate.

2.7.1 Total species richness

For each species, predictions were made over the study area using SDMs. Then this process was repeated for each climate scenario. Grouped by higher taxa and separately grouped by each climate scenario, committee average predictions (section 2.6.2.1) were summed over for each geographic cell in the study area. This way, the total species richness of specific geographic cells was attained.

$$\frac{\sum_{i=1}^{n} P_i}{n} \tag{2.3}$$

Equation 2.3 outlines the process where P_i is the matrix of committee average predictions for the ith species within the set of species n, representing a particular higher taxon. Total species richness was divided by n to account for the different numbers of species each taxon has in the dataset. The process in equation 2.3 was repeated for every higher taxon and every climate scenario. These calculations resulted in geographic distributions of species richness which are then plotted using R package ggplot2 (Wickham et al., 2024). The consequent maps exhibit the relative biodiversity of different regions.

2.7.2 Difference in total species richness

The methods in section 2.7.1 resulted in biodiversity values for both the baseline climate period 1970-2000 and the different future climate scenarios for every taxa. This brings about the possibility of assessing changes in biodiversity patterns with changing climate. In order to realize this possibility, the biodiversity matrices of 1970-2000 climate were subtracted from the biodiversity matrices of each future climate scenario one by one.

$$\frac{\sum_{i=1}^{n} {}_{f}P_i}{n} - \frac{\sum_{i=1}^{n} {}_{b}P_i}{n} \tag{2.4}$$

Equation 2.4 clarifies the process where ${}_{f}P_i$ is the matrix of committee average predictions of the ith species within the set of species n representing higher taxa for the future climate scenario, and likewise ${}_{b}P_i$ is the matrix of committee average predictions of the ith species within the set of species n representing higher taxa for the baseline climate scenario of 1970-2000. For each taxa, baseline predictions were subtracted from each of the future climate predictions one by one. Resulting matrices were mapped over the study area. These difference maps indicate the future changes in biodiversity from the baseline climate of 1970-2000.

2.8 Ecological Cohabitation Analyses

Modeling the distributions of hundreds of species from diverse higher taxa unlocks possibilities for gaining insights into ecological communities. To explore these possibilities, an approach of pairwise niche similarity assessments were taken. Pairs of insects/plants and birds/plants were selected due to relatively higher potential community relations such as forming trophic levels or pollination interactions (Galiana et al., 2024). For each bird and insect species, pairwise niche similarities with each plant species were calculated one by one using Warren's I statistic (Warren et al., 2008). I statistic calculates the differences between each prediction for two species using Hellinger distances and combines these differences into a single statistic ranging between 0 and 1 where 1 means identical distributions; 0 means no overlap.

It is not clear at what level of niche similarity or range overlap it becomes valid to infer that two species cohabitate. Therefore, multiple thresholds were used while cohabitation analyses were being conducted. For each bird and insect species, the number of plant species with which they have an I statistic above 0.66 and 0.33 were calculated separately. In addition, mean averages of their I statistics above the two thresholds are calculated as well. Although overlaps in geographical range or environmental space do not imply biotic interactions or community formation, they highlight species that coexist with the highest and lowest number of other species. These numbers, in turn, create a particular gradient from generalist to specialist species.

2.9 The Climatic Perspective on Biodiversity

Biodiversity maps from Section 2.7.1 facilitated the exploration of bioclimatic conditions that govern high-biodiversity areas. Biodiversity matrices from the baseline period (1970-2000) were filtered to isolate high-biodiversity quantiles, grouped by taxon. Rather than a single threshold, multiple cut-offs were applied, corresponding to top 5%, 10%, and 20% of the biodiversity metric[3] (Lu & Jetz, 2023). The bioclimate corresponding to these high-biodiversity intervals were then extracted and summary statistics were produced for each bioclimatic parameter grouped by taxa and intervals. Then the distributions of each bioclimatic parameter were plotted comparing the different taxa and different biodiversity thresholds, using R package ggridges (Wilke, 2024). All statistical analyses were conducted on R programming language version 4.3.1 (R Core Team, 2023) unless otherwise is stated.

[3] Due to the low sample size of mammals, top 3%, 10%, and 20% cut-offs were used, in order to differentiate the high-biodiversity intervals of mammals.

3. RESULTS

After applying the filters from the section 2.4 and discarding the models that failed the evaluation criteria (section 2.6.1), a total number of 519 species left in the study for further analyses. Taxonomic breakdown of the remaining species is given in table 3.1, and the full species list is given in table E.1 of Appendix E.

Table 3.1: The final number of species left after data processes and modeling, organized by taxa.

Taxa	Species
Amphibians	5
Birds	118
Insects	126
Mammals	5
Plants	265

3.1 Biodiversity Patterns of Anatolia in a Changing Climate

3.1.1 Maps

3.1.1.1 Amphibians

For amphibians, the coasts appear as high-biodiversity areas (Figure 3.1), encompassing the Mediterranean, Aegean, Marmara, and to a lesser extent Black Sea regions. Inland transitions generally correspond to reduced biodiversity, although high biodiversity persists further inland for the Aegean region. Pockets of high biodiversity also occur around water bodies such as lakes and river basins. In addition, certain high-elevation forest covers exhibit increased biodiversity due to the presence of *Rana macrocnemis*, a species with contrasting bioclimatic preferences to other amphibians in the dataset. Given the limited number of species in the amphibian dataset, individual species' effects on biodiversity patterns can be more distinguishable.

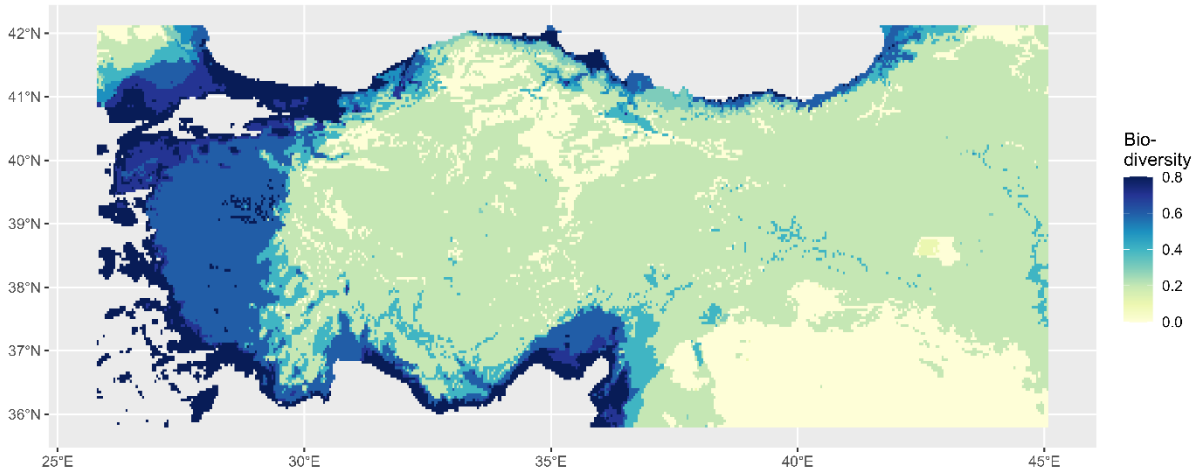

Figure 3.1: Amphibian biodiversity of Anatolia according to SDMs based on 1970-2000 bioclimate.

Biodiversity projections under future climate scenarios indicate a general biodiversity shift toward the north and northeast (Figures A.1a through A.1h). Certain patches in the coastal regions of Mediterranean and Aegean exhibit reduced biodiversity. These reductions expand under increasing radiative forcing in different Shared Socioeconomic Pathways (SSPs) and over successive time periods. Similarly, the increases in biodiversity expand under SSPs with higher radiative forcing and over successive time periods.

To visualize the change in biodiversity, difference maps (section 2.7.2) are presented in Figures 3.2a through 3.2h. Increases in biodiversity, along with expansions of areas with high biodiversity are evident in the coastal Black Sea region. This pattern consistently expands and intensifies under higher radiative forcing with successive time periods. The region around the city of Ordu is where the increase in biodiversity is the largest in terms of area. The pockets of high biodiversity around water bodies and high-elevation forest covers that were previously discussed show declining biodiversity. In their stead, patches of increased biodiversity emerge further inland in Aegean region and in southeastern Marmara region. For high radiative forcing scenarios in 2081-2100 periods, the Çoruh River basin and region around Lake Van exhibit significant increases in amphibian biodiversity (Figures 3.2g, 3.2h). For Thrace, patches in the northern

end, off the coast of İğneada show increased biodiversity for high radiative forcing SSPs. Conversely, areas around Lake Gala exhibit reduced biodiversity for high radiative forcing SSPs.

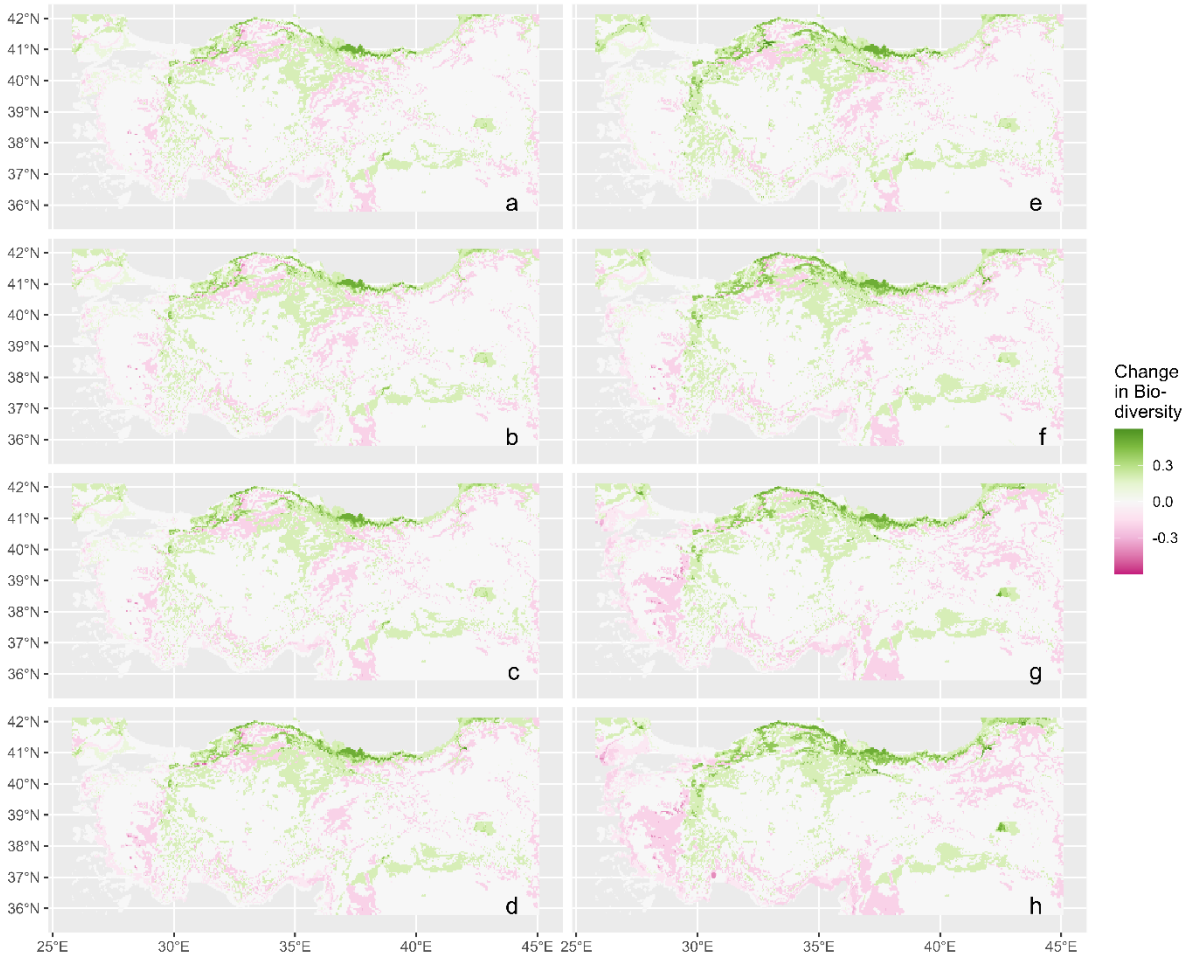

Figure 3.2: Change in amphibian biodiversity patterns under different future climate scenarios according to SDMs; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

3.1.1.2 Birds

Bird biodiversity is positively associated with water bodies such as lakes, river basins, and streams (Figure 3.3). Coastal areas of the Mediterranean, Aegean, Marmara, and Black Sea regions again exhibit high biodiversity. Where steep elevation gradients occur, high biodiversity sharply declines at higher elevations.

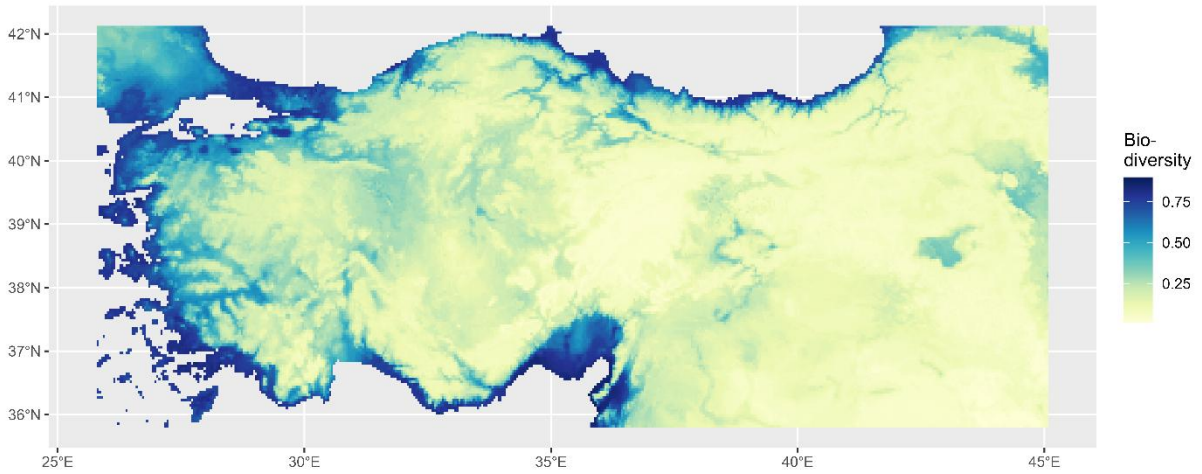

Figure 3.3: Bird biodiversity of Anatolia according to SDMs based on 1970-2000 bioclimate.

The projections under future climate scenarios generally display high bird biodiversity for the northern coastal areas (Figures A.2a through A.2h). While complex patterns occasionally do emerge among different future scenarios, the biodiversity trends generally align with successive SSPs and time periods. The apparent broad pattern of change from the difference maps is that of a shift in biodiversity from the south and southwest to the north and northeast (Figures 3.4a through 3.4h). The Black Sea region exhibits significant increases in biodiversity, which expand and intensify under higher radiative forcing SSPs and over successive time periods. However, certain areas within the Black Sea region, such as the Bafra plain and the Sinop peninsula, do not display biodiversity increases and remain neutral. The Çukurova Delta consistently shows reductions in biodiversity across all SSPs and time periods. Similarly, avian biodiversity decreases in the Mediterranean and Aegean coastal regions, as well as in river basins. In contrast to the biodiversity reductions observed in the Mediterranean, Aegean and Marmara regions, high-elevation areas and forest covers emerge as refuges, exhibiting higher biodiversity values that increase with successive SSPs. This biodiversity pattern is exemplified in a portion of Aegean region, including the Boz and Aydın mountains and parts of the Menderes Rivers basins, where biodiversity changes are projected under successive SSPs for the end of the century (Figure 3.5). Although avian biodiversity generally increases across the Taurus

Mountains, the highest peaks of Tauruses remain neutral in biodiversity, even under the highest-radiative-forcing SSPs.

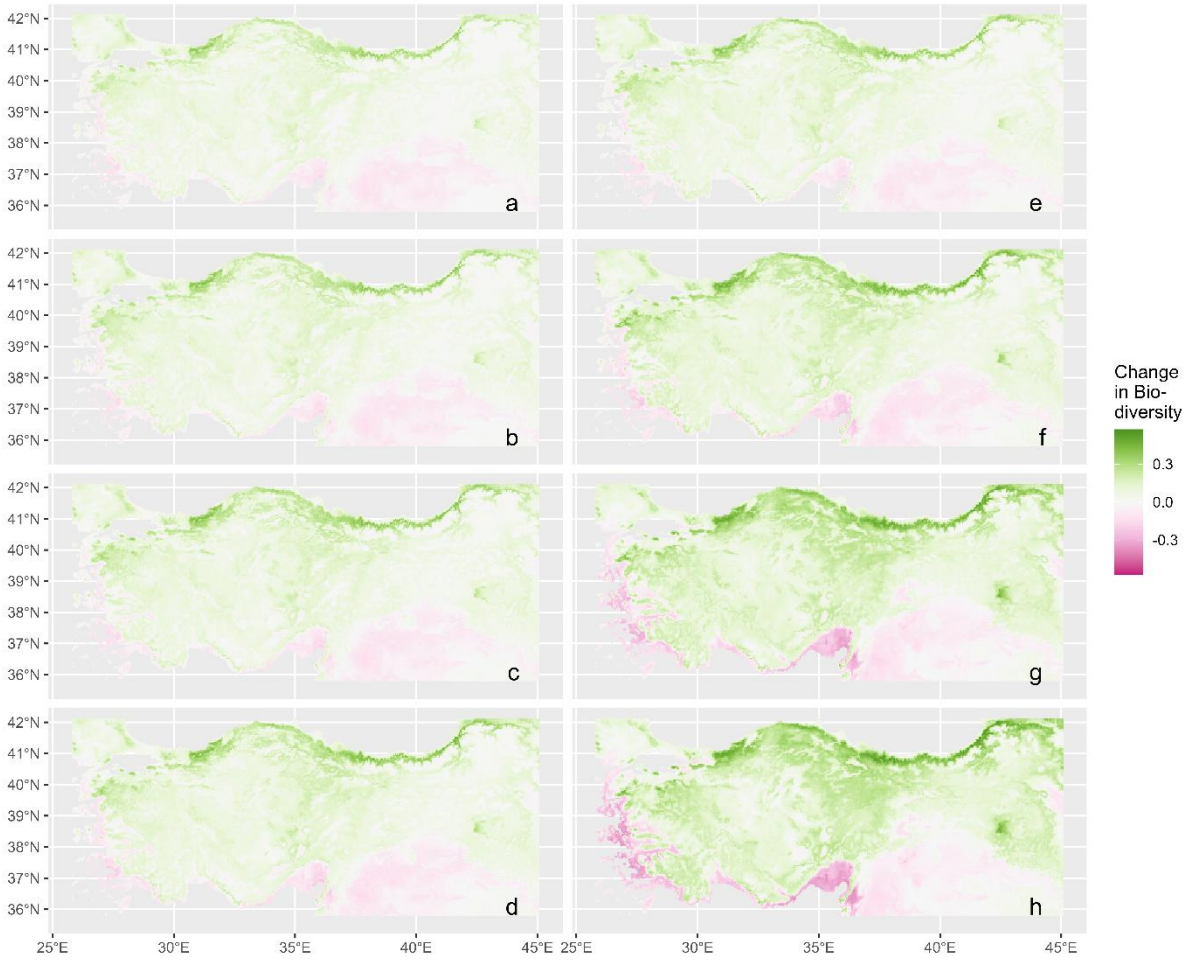

Figure 3.4: Change in avian biodiversity patterns under different future climate scenarios according to SDMs; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

Water bodies and change in biodiversity appear to have complex relationships. While Lake Van exhibits substantial increases, Lakes Beyşehir, Eğirdir, and Kovada are mostly neutral in biodiversity change. Moreover, Lakes Ulubat and İznik show reductions in biodiversity in higher radiative forcing SSPs. In addition, certain high-biodiversity refuges emerge in locations close in distance to Lake Ulubat such as Ihlamur Forests and Kapıdağ Peninsula. The Marmara region encompasses several relatively high-elevation forested areas that show increasing biodiversity. The northern Euphrates basin, a relatively high-biodiversity area under baseline bioclimatic conditions, contracts and eventually disappears as a

high-biodiversity pocket under SSPs with increasing radiative forcing by the end of the century (Figures A.2e, A.2f, A.2g, A.2h).

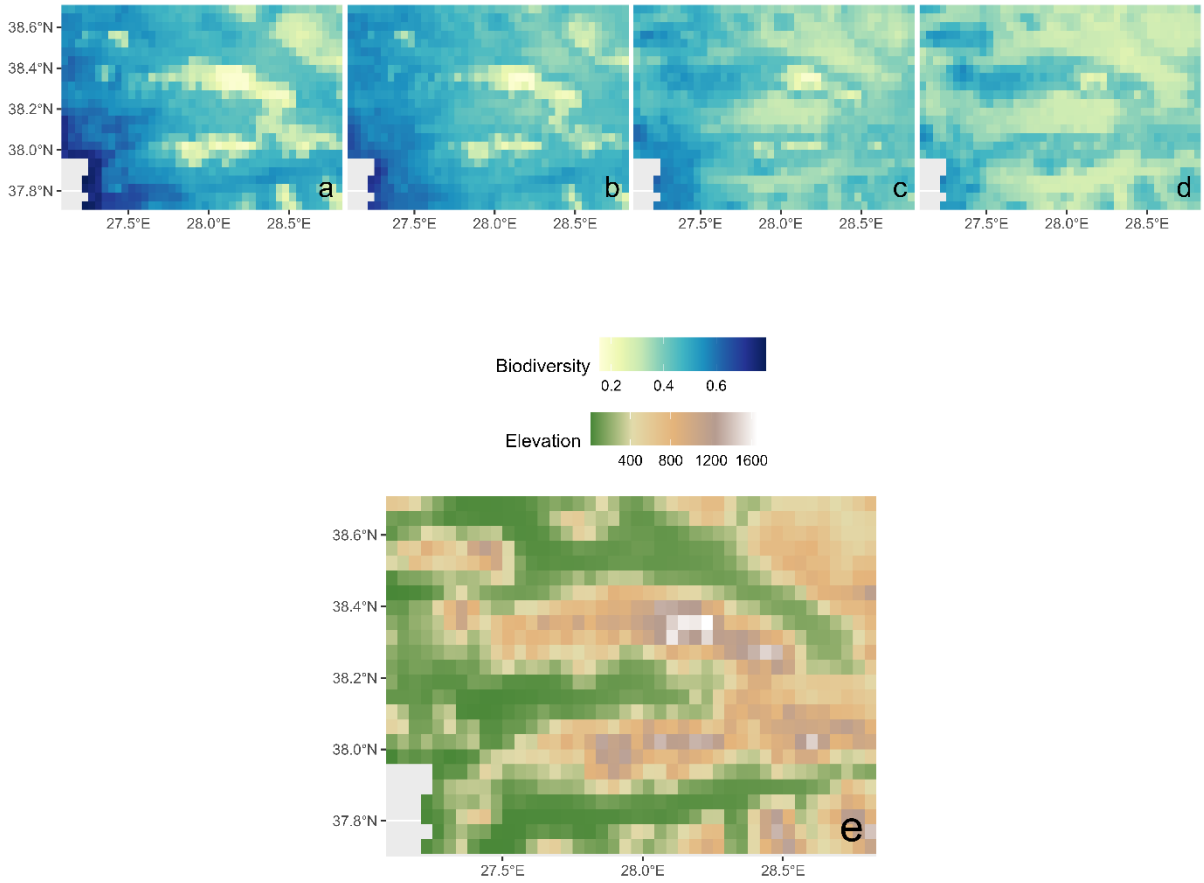

Figure 3.5: Change in avian biodiversity patterns and elevation map for the region of the Boz and Aydın Mountains and parts of Menderes Rivers system basin under different future climate scenarios for the 2081-2100 time period; a) SSP1-2.6, b) SSP2-4.5, c) SSP3-7.0, d) SSP5-8.5, e) Elevation map of the area in meters at 2.5 arc-minute resolution (Fick & Hijmans, 2017).

3.1.1.3 Insects

Insect biodiversity displays a broader distribution relative to the other taxa in the study (Figure 3.6). The southern coastal areas exhibit the highest levels of biodiversity, with the Aegean and Marmara regions following at noticeably lower levels than the south. In the Aegean region, biodiversity gradually decreases moving inland, with a sharp decline upon reaching inner Anatolia. This sharp decline appears to be delineated by several mountains and hills. With the exception

of the southeast and inner Anatolia which exhibit low levels of biodiversity, a large portion of the study area displays medium levels of biodiversity. Pockets of high biodiversity occur throughout the study area, often corresponding to forest covers, water bodies, and high elevation areas.

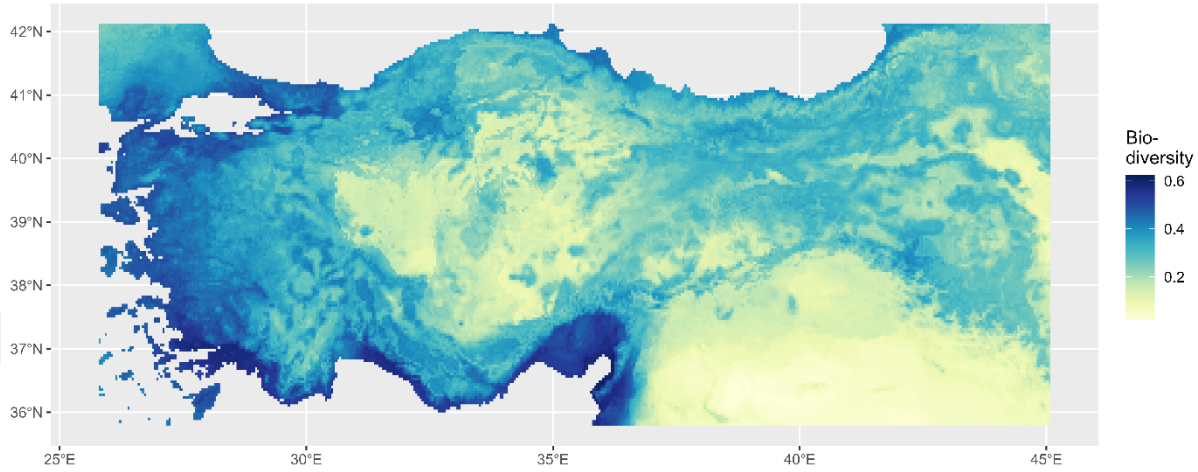

Figure 3.6: Insect biodiversity of Anatolia according to SDMs based on 1970-2000 bioclimate.

The projections under future climate scenarios present a general shift of biodiversity from the south to the north (Figures A.3a through A.3h). Beyond the northern shift, broad patterns of biodiversity distributions remain relatively stable.

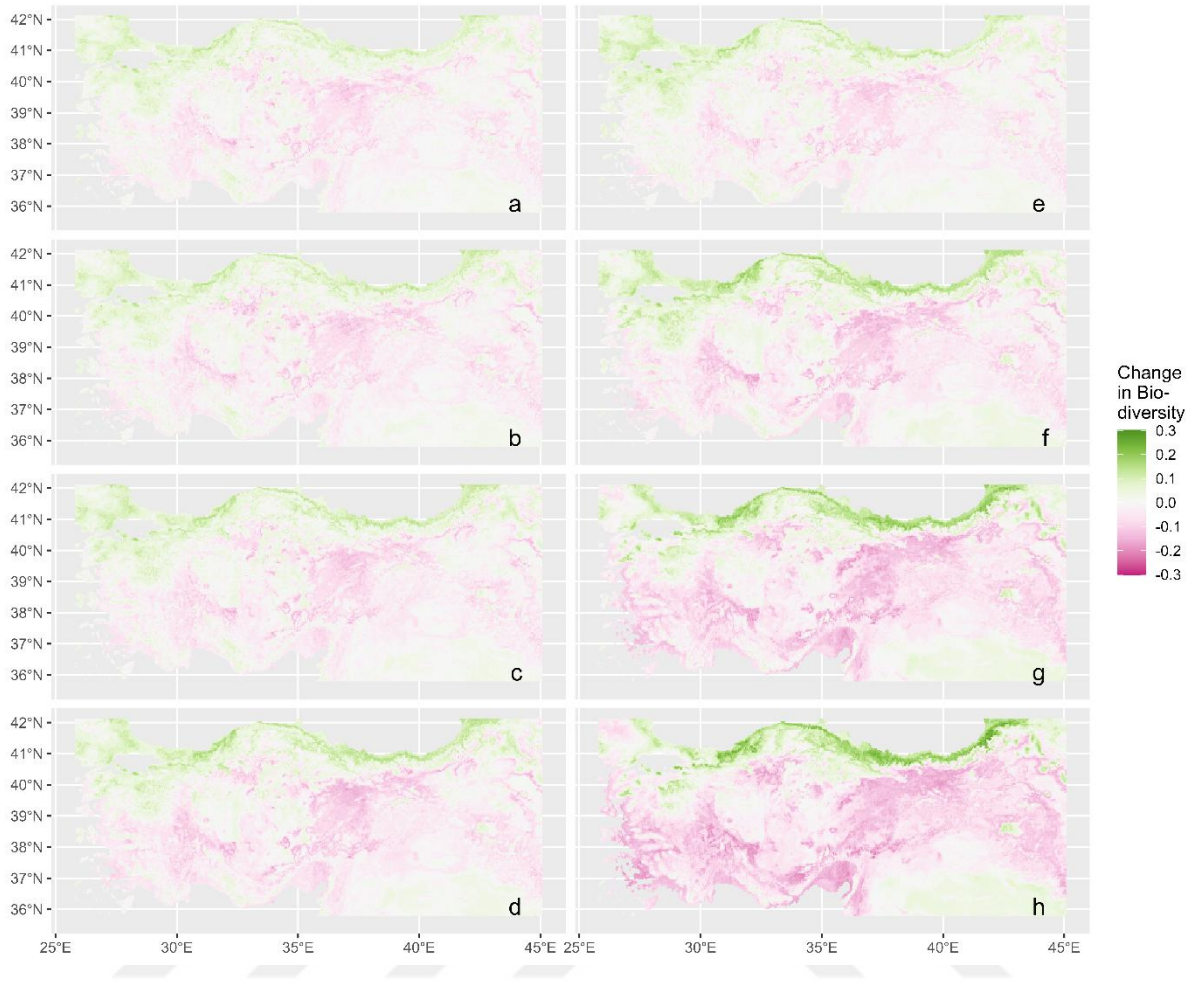

Figure 3.7: Change in insect biodiversity patterns under different future climate scenarios according to SDMs; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

The northern Black Sea region displays biodiversity increases which intensify and expand under higher-radiative-forcing SSPs and over successive time periods (Figures 3.7a through 3.7h). The Marmara region, extending into the northern Aegean, also exhibits increased biodiversity, particularly in high-elevation areas and forest covers. Outside of the Marmara and Black Sea regions, large portions of Anatolia show reductions in biodiversity. Amid these widespread reductions across the study area, certain pockets act as biodiversity refuges. These refuges are generally associated with high-elevation areas, forest covers, and water bodies. The relationships between these refuges and biodiversity patterns can be complex. The Taurus Mountains, in part, exhibit biodiversity increases under lower-forcing SSPs but these gains contract to smaller areas under higher-forcing SSPs. A similar biodiversity pattern emerges around Lake Beyşehir, where the initial biodiversity

increases are not only lost but shift to reductions under the highest-forcing SSPs. In contrast, Lake Van retains its biodiversity increases and even gains further with successive SSPs. Pockets of high biodiversity within inner Anatolia gradually contract and vanish under higher-forcing SSPs by the end of the century (Figures A.3e through A.3h). In a similar fashion, Eastern Anatolia gradually decreases in biodiversity under successive SSPs. High mountains are generally able to retain their biodiversity levels, though these areas contract toward the peaks under higher-forcing SSPs.

3.1.1.4 Mammals

While mammal biodiversity is high in coastal areas, particularly along the Mediterranean, Aegean and Marmara regions, the highest levels of biodiversity are generally located slightly inland in forested areas at low to medium elevations, but not at high elevations (Figure 3.8). Biodiversity gradually drops moving further inland to inner Anatolia and it is the lowest in the southeast. Inland Anatolia contains fragmented pockets of relatively high biodiversity, often associated with forest covers and river basins.

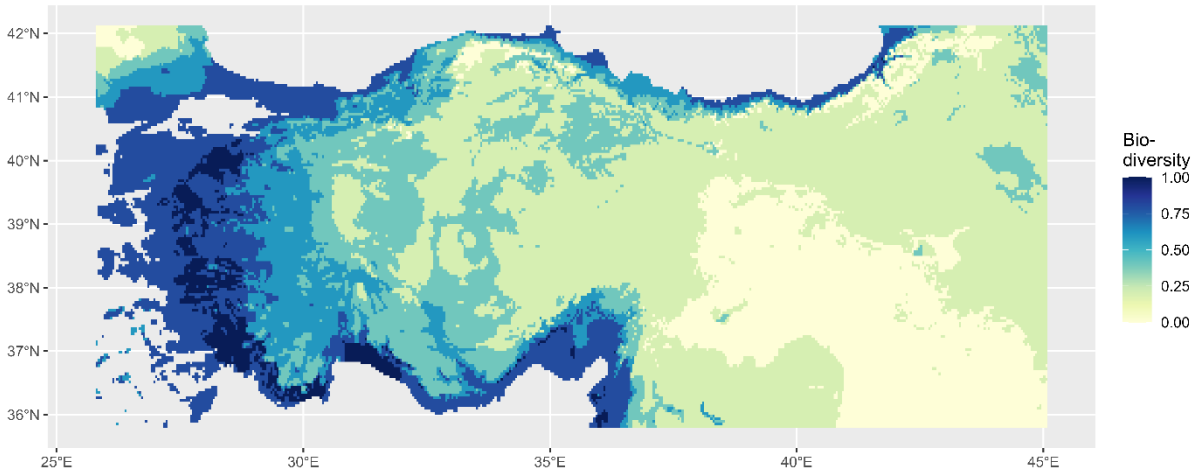

Figure 3.8: Mammal biodiversity of Anatolia according to SDMs based on 1970-2000 bioclimate.

Biodiversity distributions under future climate scenarios exhibit expansions of high biodiversity areas in the Black Sea region, along with contractions in the

Aegean and Mediterranean (Figures A.4a through A.4h). These patterns expand and intensify over successive SSPs and time periods; particularly in the Aegean and Mediterranean, and, to a lesser extent, in the Black Sea regions.

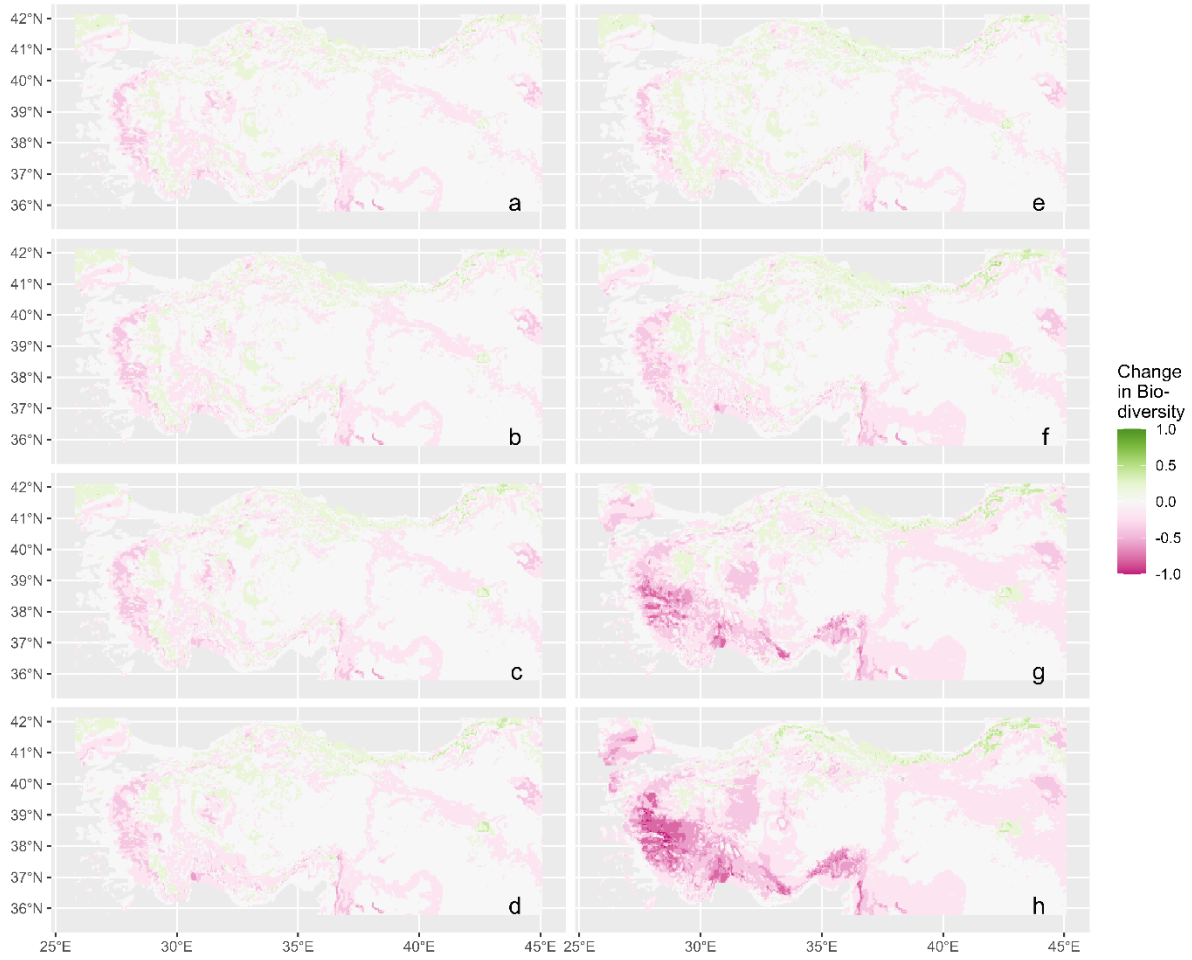

Figure 3.9: Change in mammal biodiversity patterns under different future climate scenarios according to SDMs; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

Difference maps reveal biodiversity reductions in the areas previously identified as high-biodiversity zones within the Aegean and Mediterranean regions (Figures 3.9a through 3.9h). Complementarily, biodiversity increases occur in higher-elevation forest covers and plateaus, extending toward the Tauruses in the Mediterranean and further inland to the east in the Aegean. In the highest radiative-forcing climate scenarios, most of these biodiversity increases vanish, besides a few small pockets in the Tauruses, Kaz Mountains, and the forested areas in the northeastern Aegean near Kütahya (Figures 3.9g, 3.9h). The Black Sea region

mostly exhibits biodiversity increases, along with decreases in a few patches. Çoruh River basin shows the largest increase in biodiversity. Thrace splits into two; the northern part with increases and the southern with decreases. Under the highest forcing SSPs, biodiversity decreases expand into the northern Thrace, leaving only small patches with biodiversity increases. Lake Van consistently displays increases, while pockets of increased biodiversity within the inner Anatolia gradually contract and vanish under SSPs with increasing forcings. One exception to this pattern is an environmentally complex area near Yozgat which displays increased biodiversity even under the SSP 5-8.5 for the 2081-2100 period (Figure 3.9h).

3.1.1.5 Plants

For plants, the coastal areas exhibit the highest levels of biodiversity, which gradually decline as one moves inland (Figure 3.10). In the Aegean region, however, high biodiversity extends further inland compared to the other regions. Along elevation gradients, biodiversity decreases with increasing altitude. Additionally, biodiversity demonstrates a positive association with water bodies such as river basins and lakes. Eastern Anatolia and the southeast display the lowest levels of biodiversity.

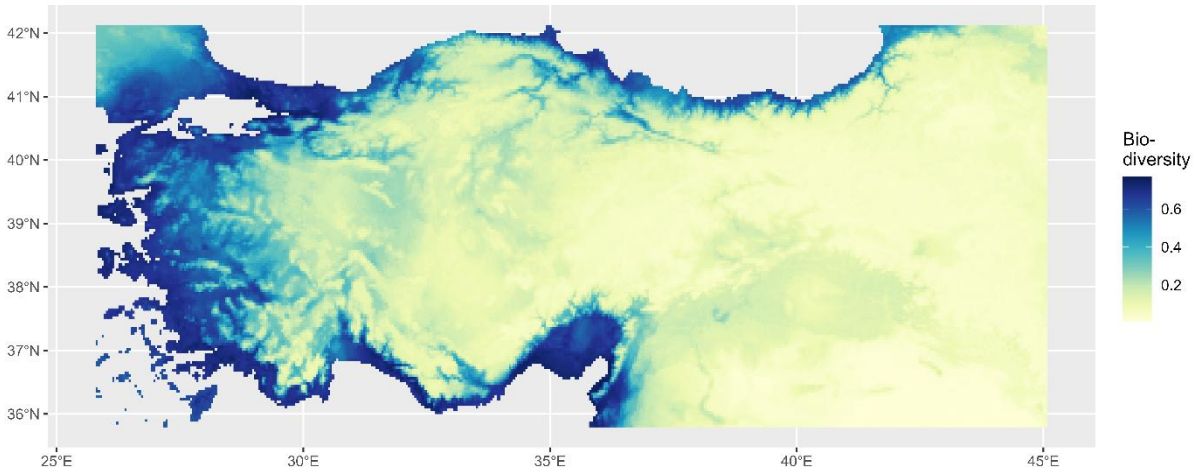

Figure 3.10: Plant biodiversity of Anatolia according to SDMs based on 1970-2000 bioclimate.

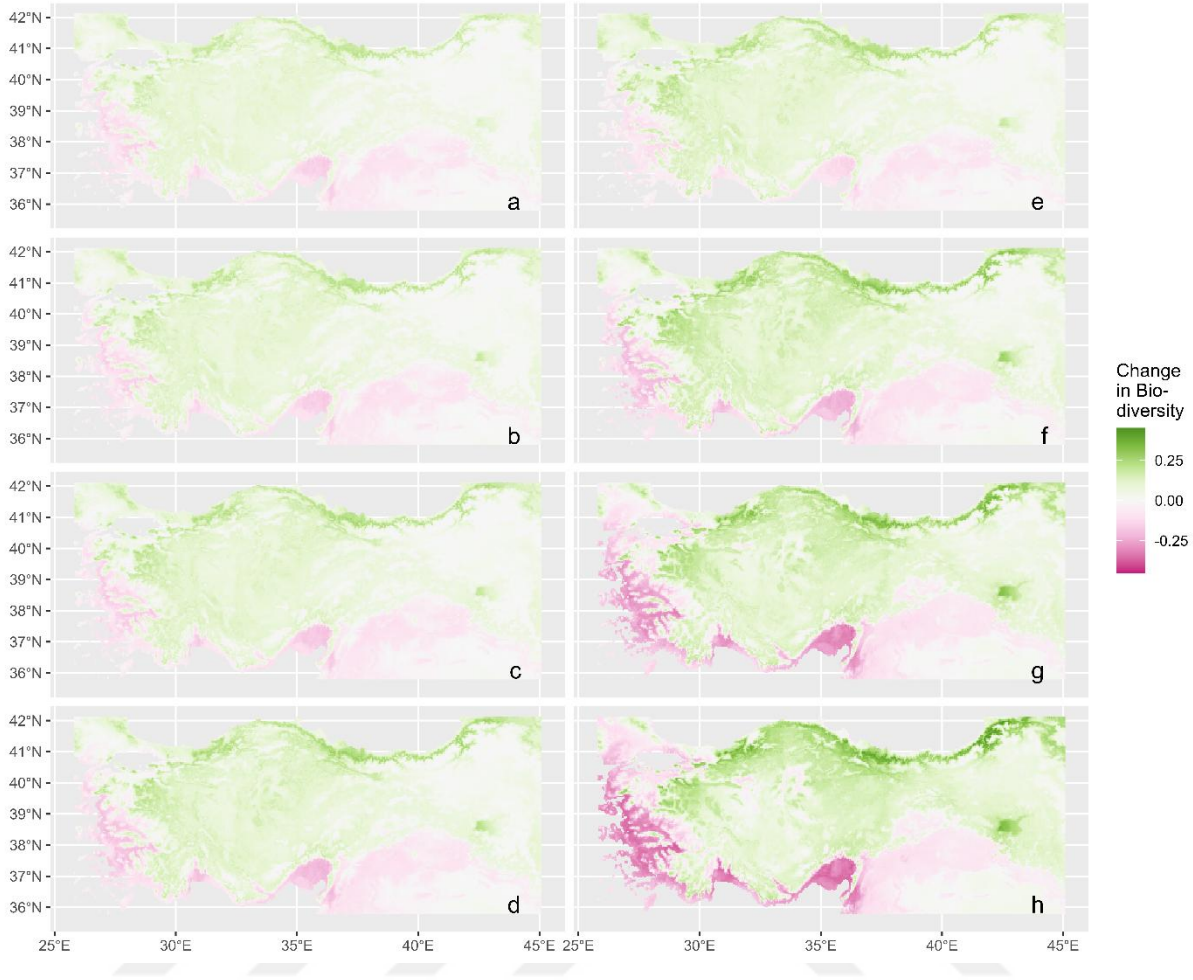

Figure 3.11: Change in plant biodiversity patterns under different future climate scenarios according to SDMs; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

Under future climate scenarios, plant biodiversity shifts toward the north and northeast, away from the south and southwest (Figures A.5a through A.5h). From another perspective, biodiversity transitions from lower to higher elevations. These trends generally expand and intensify under successive SSPs and across successive time periods.

The Black Sea region exhibits the highest biodiversity increases (Figures 3.11a through 3.11h). Significant biodiversity reductions appear along the coastal areas, deltas, and river basins of the Mediterranean and Aegean regions. Complementarily, plant biodiversity increases in higher-elevation areas, as one moves inland in the Mediterranean and Aegean regions. The Taurus Mountains display biodiversity increases, except at the highest peaks where biodiversity

slightly decreases. Similarly for the Aegean region, high-elevation areas show increased biodiversity such as the Aydın Mountains, Boz Mountains, and Mount Kaz. Additionally, the northeastern portion of the Aegean region exhibits widespread biodiversity increases across SSPs. Inner Anatolia also shows biodiversity increases, though these gains contract and become concentrated around refuges such as Lake Tuz and higher-elevation areas and plateaus around the Kızılırmak Basin under higher-radiative-forcing SSPs. Northeastern Anatolia generally displays biodiversity increases, except in the highest elevation areas, which mostly remain neutral. In contrast, southeastern Anatolia displays biodiversity reductions throughout, except for Mount Karaca where biodiversity increases. For the 2081-2100 time period, the northern part of the Euphrates-Tigris Rivers Basin exhibits biodiversity reductions, which expand under successive SSPs. Lake Van consistently displays significant biodiversity increases. Plant biodiversity increases in northern Thrace across future climate scenarios. Conversely, biodiversity remains mostly neutral in southern Thrace, except for the highest-forcing SSPs, where southern Thrace exhibits biodiversity reductions.

3.1.2 Uncertainty

The maps of novel environments are provided in Figures B.1 through B.5 of Appendix B. The southeast emerges as the region hosting novel environmental conditions on the largest scale. These areas of novel environments expand under successive SSPs and over successive time periods. Ağrı hosts novel bioclimatic conditions that expand in area under successive climate scenarios. Under the highest-forcing SSPs, the Aras and Kura River Basins in the northeast become home to novel climatic conditions. Similarly, novel environments emerge in the southwest of the study area under the highest-forcing SSPs, with additional occurrences in the southern regions around Antalya and the Çukurova Delta.

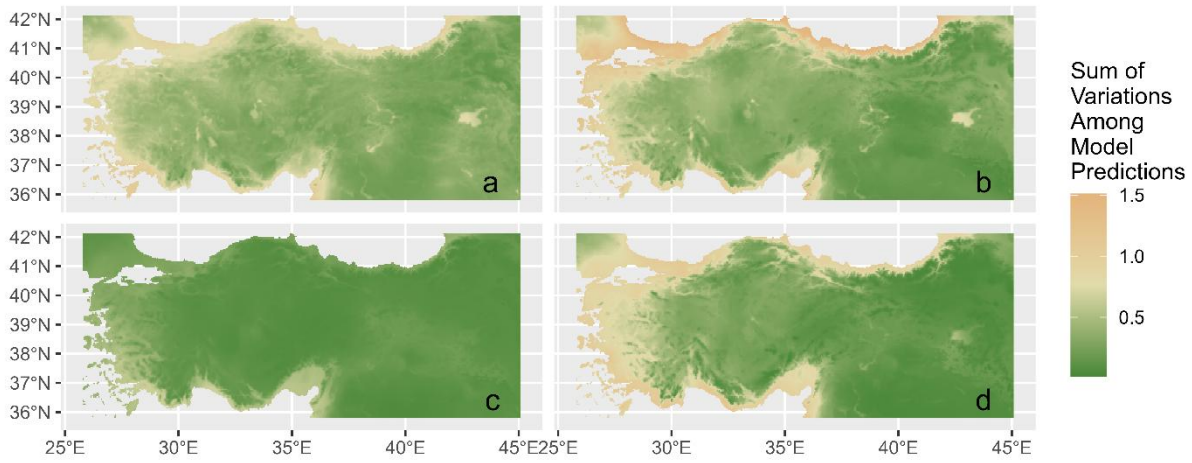

Figure 3.12: Sum of standard deviations among the model predictions divided by the number of species in the taxa grouped by taxa; a) Amphibians, b) Birds, c) Insects, d) Plants.

Generally, variations among models are highest in environmentally complex areas such as the coastal regions and areas near water bodies (Figure 3.12). The same cannot be said about elevation gradients, as higher-elevation areas mostly exhibit low variations. Amphibians models follow these general variation patterns (Figure 3.12a). For birds, the northern regions, The Black Sea and Marmara exhibit the highest variations (Figure 3.12b). In contrast, Insects models display higher variations in the southern and western coastal areas (Figure 3.12c). For plants, variations are high across all coastal areas. Additionally, the high variations among plants models extend further inland in the Aegean region (Figure 3.12d). Due to the limited number of models, variation maps could not be created for the mammals. Changes in variations across different climate scenarios are given in Appendix B (Figures B.6 through B.9). The variations remain mostly stable throughout different scenarios. Although, there are tendencies for certain areas near water bodies such as the Çukurova Delta and Euphrates-Tigris Basins to decrease in variations under the highest-forcing SSPs. For Insects, the variations increase in the northern Aegean and southern Marmara regions as the radiative forcing of SSPs becomes stronger (Figures B.8e, B.8f, B.8g, B.8h). Conversely for plants, the variations in the southern Aegean river basins decrease under the highest-forcing SSPs (Figure B.9h).

3.2 Bioclimate of Biodiversity

Annual mean temperature distributions in high-biodiversity areas exhibit increasingly distinctive bimodal patterns as biodiversity quantiles rise (Figure 3.13). The more pronounced double peaks at higher biodiversity quantiles indicate a possible association between temperature seasonality and Anatolian biodiversity. For the highest biodiversity quantiles, birds and insects show higher peaks at elevated temperatures, suggesting an association between higher temperatures and biodiversity.

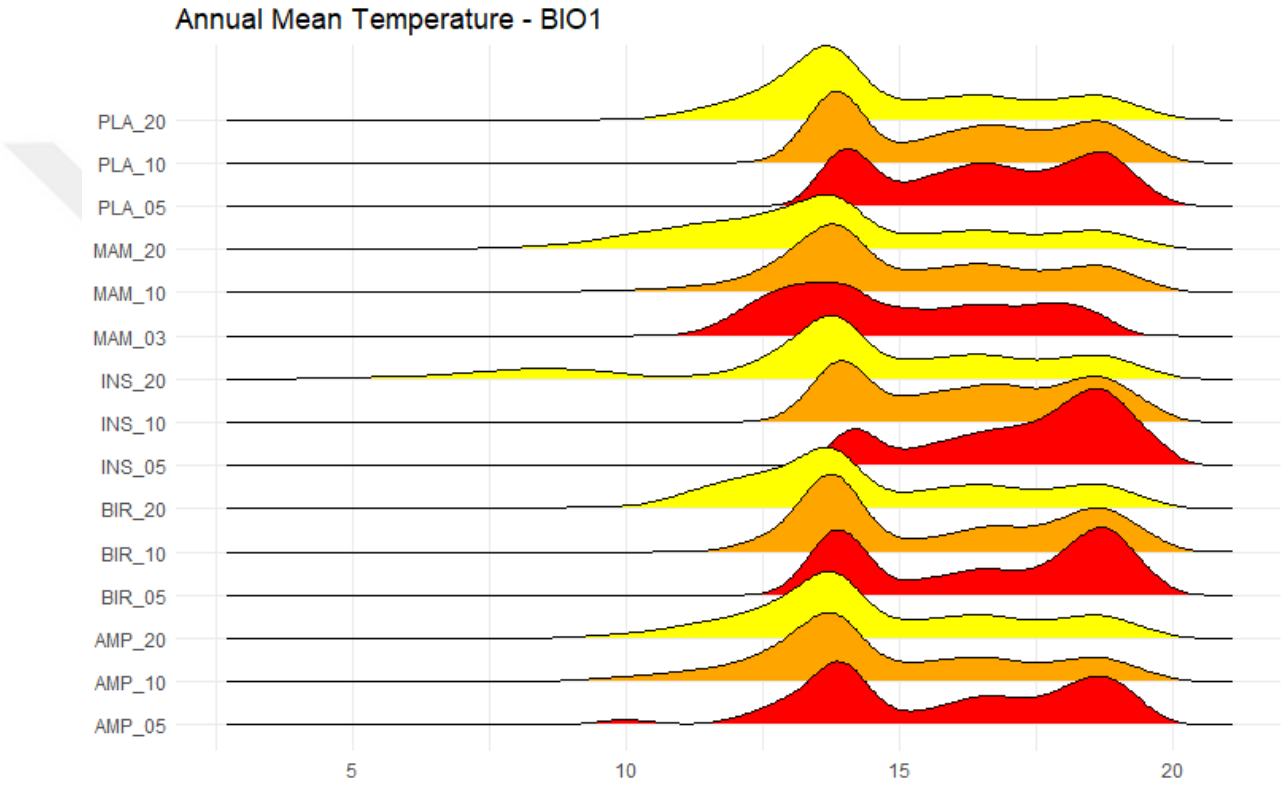

Figure 3.13: Distributions of annual mean temperature (BIO1) in °C of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

Annual precipitation distributions shift toward the right as biodiversity quantiles rise, indicating an association between higher precipitation and biodiversity (Figure 3.14). A secondary, smaller peak emerges around 1000 mm of precipitation with increasing biodiversity quantiles, across all taxa.

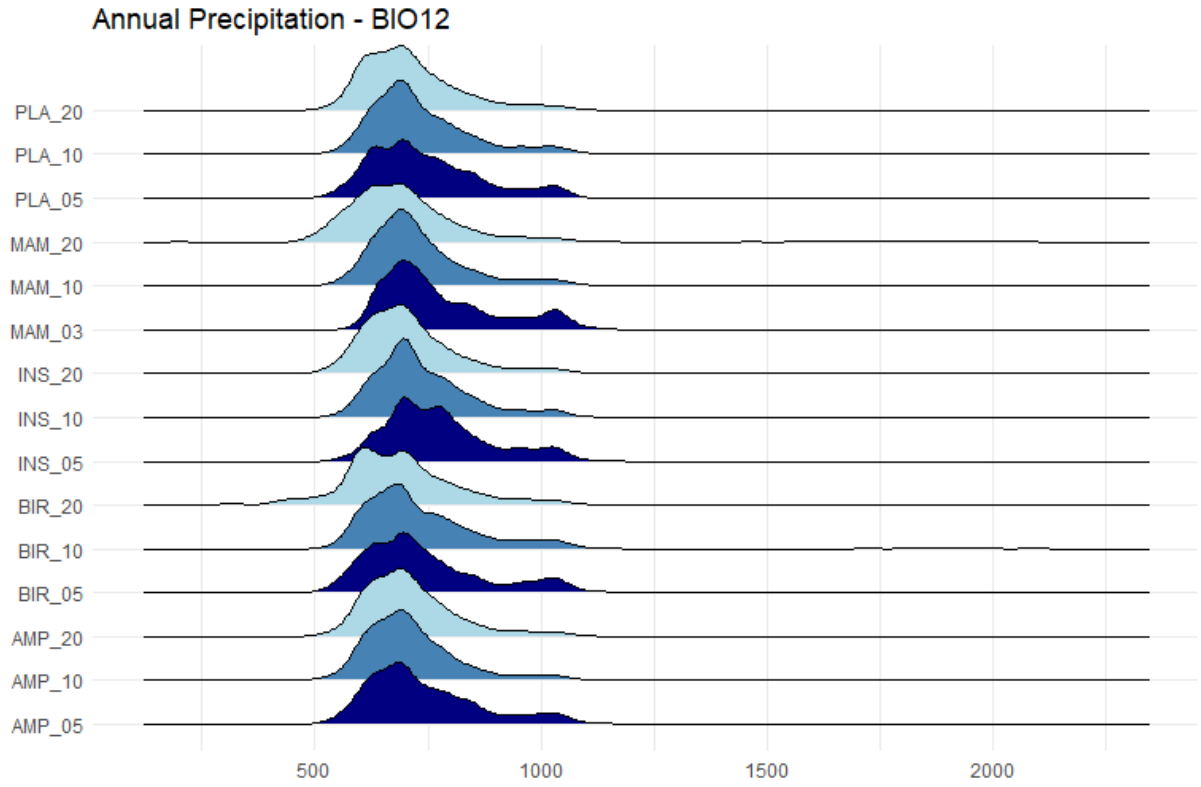

Figure 3.14: Distributions of annual precipitation (BIO12) in mm of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

Distributions of other bioclimatic variables are presented in Figures C.1 through C.17 and their summary statistics in Tables C.1 through C.15 of Appendix C. The distributions of temperature seasonality (BIO4; Figure C.3) generally decreases, shifting toward the left as biodiversity quantiles rise. This, interpreted together with annual temperature distributions (Figure 3.13), point to a picture of high biodiversity conditions in which multiple climates, with low intraclimatic temperature variations, occur. Jetz et al. (2004) found similar patterns for avian diversity. In contrast to temperature seasonality, precipitation seasonality increases as biodiversity quantiles rise (Figure C.13).

3.3 Niche Similarities of Cohabitating Species

Among the bird-plant pairs, *Curruca cantillans* (Subalpine Warbler) tops the niche similarity list, scoring over 0.66 in I statistic with 145 different plant species (Table D.1). The Warbler's average I statistic with these 145 plant species is 0.80, indicating a high level of bioclimatic niche similarity. *Curruca cantillans* has a

wide range across the Western Palearctic and predominantly prefers the western and southern coastal regions of Anatolia (Figure 3.15).

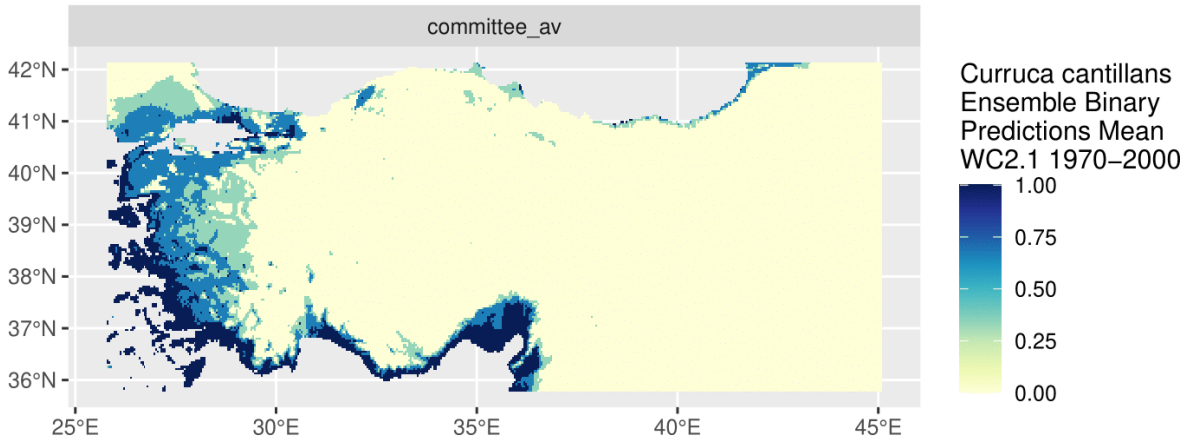

Figure 3.15: The distribution of *Curruca cantillans* (Subalpine Warbler), according to SDMs based on 1970-2000 bioclimate.

When a Warren's I threshold of 0.33 is considered instead of 0.66, *Emberiza cirlus* (Cirl Bunting) and *Dendrocoptes medius* (Middle Spotted Woodpecker) share the top spot in bird-plant pairs list with 247 plant species each. The mean averages of I statistics with these 247 species is 0.62 for the Bunting and 0.61 for the Woodpecker.

The niche similarity list features *Carpocoris mediterraneus* (Red Shield Bug) at the top for the insect-plant pairs (Table D.2). Red Shield Bug shares similar bioclimatic niches with 147 different plant species, scoring above 0.66 in I statistic with each of them. Average I statistic for these 147 pairs is 0.79. The Red Shield Bug is a polyphagous vegetarian, capable of feeding on a variety of plant species (Koçakoğlu & Candan, 2023). For the 0.33 threshold, *Calopteryx virgo* (Beautiful demoiselle) is at the top of the niche similarity list, scoring above 0.33 I statistic with 247 different plant species. Average I statistic, for the 247 pairs, is 0.60. The full niche similarity tables for both bird-plant and insect plant pairs are given in Appendix D.

4. DISCUSSION

4.1 Anatolian Biodiversity

This study utilized SDMs to analyze and evaluate biodiversity patterns in Anatolia from a bioclimatic perspective. The results revealed the spatial distributions of biodiversity across different timeframes and potential climate scenarios, while also providing insights into biodiversity patterns from an environmental perspective. The findings displayed general patterns of high biodiversity concentrated along the coastal regions, with considerable deviations among different taxa (Figures 3.1, 3.3, 3.6, 3.8, 3.10). Among these, insects exhibited the greatest deviation, displaying significant biodiversity across northeastern Anatolia (Figure 3.6). Water bodies, forested areas, and elevation gradients consistently appeared among the high-biodiversity patterns.

There is a notable lack of research adopting spatial or bioclimatic approaches to the study of species richness in Anatolia. However, there have been previous studies with similar scopes such as the designation of 'important areas' for specific taxa such as birds and plants (Magnin & Yarar, 1997; Özhatay et al., 2008). In these studies, designation of important areas involves multiple criteria that extend beyond biodiversity alone. Despite this conceptual difference, there is considerable overlap between the high biodiversity areas identified in this study and the important areas for both birds and plants. Nevertheless, discrepancies exist, such as Yüksekova, which is deemed an important bird and plant area but does not display particularly high species richness according to the results of this study. A possible explanation for this disagreement is the use of different criteria such as conservation status, species rarity, and threat levels, in the identification of important areas. Another study, focusing on the species richness of forest-dependent birds on a global scale (Buchanan et al., 2011), presents a biodiversity pattern that shows notable similarities to the avian biodiversity patterns observed in this study. However, the focus on the forest-dependent birds limits the extent of comparability between the two studies. Many of the highest avian biodiversity areas identified throughout the thesis, such as the Çukurova Delta—deemed one

of the most ornithologically exciting places in Anatolia (The Birds of Turkey, 2008, p. 39), (Kirwan & Aydemir, 2008)—fall outside the scope of the latter study. These conceptual mismatches further underscore the need for more spatial biodiversity analyses with broader scopes.

The International Union for Conservation of Nature (IUCN) publishes distribution maps for the taxa it evaluates for extinction threat. These are broad maps, created with the intention to provide quick references for where the taxa occur. They are also helpful for assessing species richness patterns. In this study, a combination of IUCN maps, representing species richness (IUCN, 2024) were compared to the biodiversity results generated here (Figure 4.1). The biodiversity map from this study combines the results of amphibians, birds, insects, mammals and plants. Whereas, the IUCN dataset consists of amphibians, birds, mammals, and reptiles.

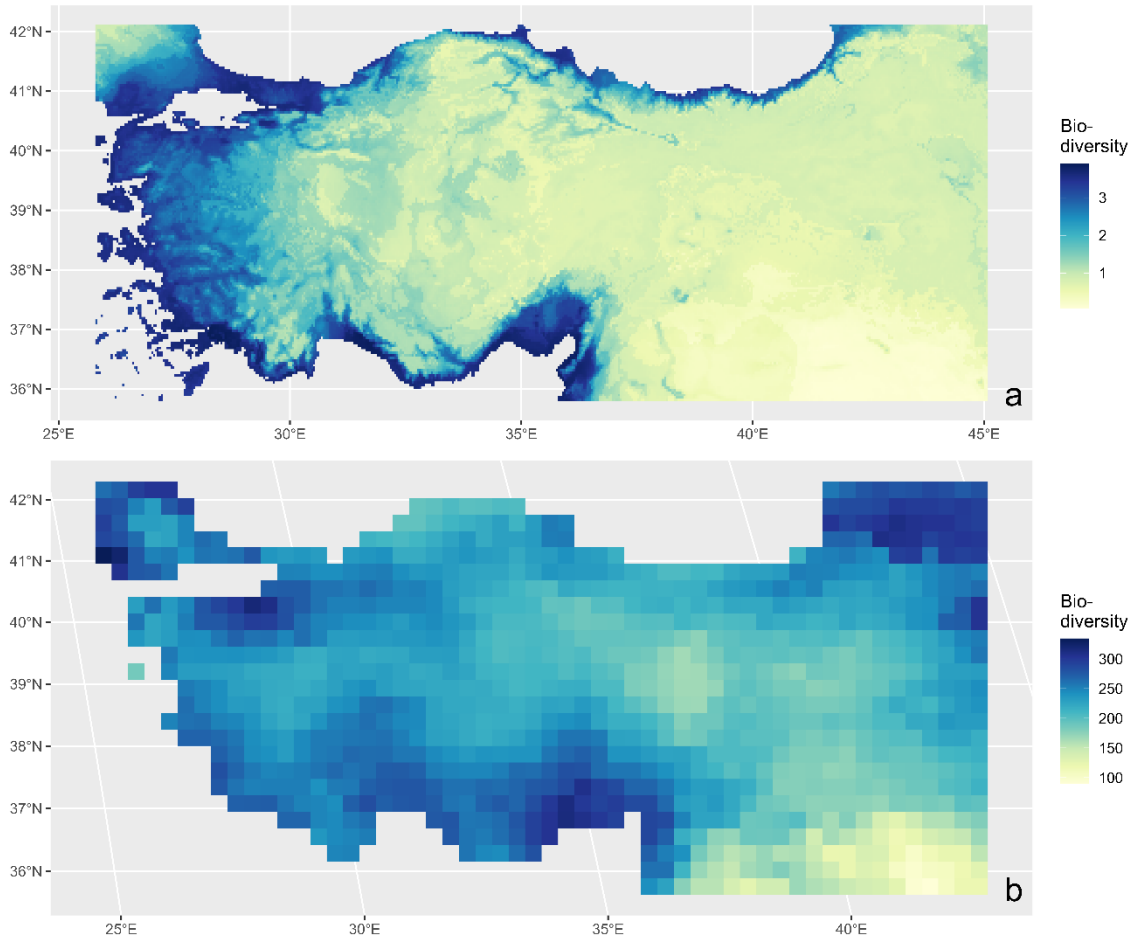

Figure 4.1: Species richness biodiversity patterns of Anatolia according to a) the SDMs for the taxa of amphibians, birds, insects, mammals, reptiles; and b) IUCN maps for the taxa of amphibians, birds, mammals, reptiles. Note the differences in the coordinate systems; WGS84 for this study, and Mollweide for IUCN.

Figure 4.1 shows a broad alignment in biodiversity patterns between the two maps. Both maps display high diversity in the southern coastal areas such as the Çukurova Delta, and again display high diversity around the water bodies in the southern Marmara region. Conversely, Inner Anatolia and the southeast exhibit relatively low biodiversity on both maps. In addition, IUCN offers Area of Habitat (AoH) maps which are created with refinements on the standard IUCN maps using habitat and elevation data. AoH maps are only available for the 2021 datasets of birds and mammals (IUCN, 2021). Comparisons were made once more, this time separately for birds and mammals, between the maps from this study and the IUCN AoH maps (Figure 4.2; Figure 4.3).

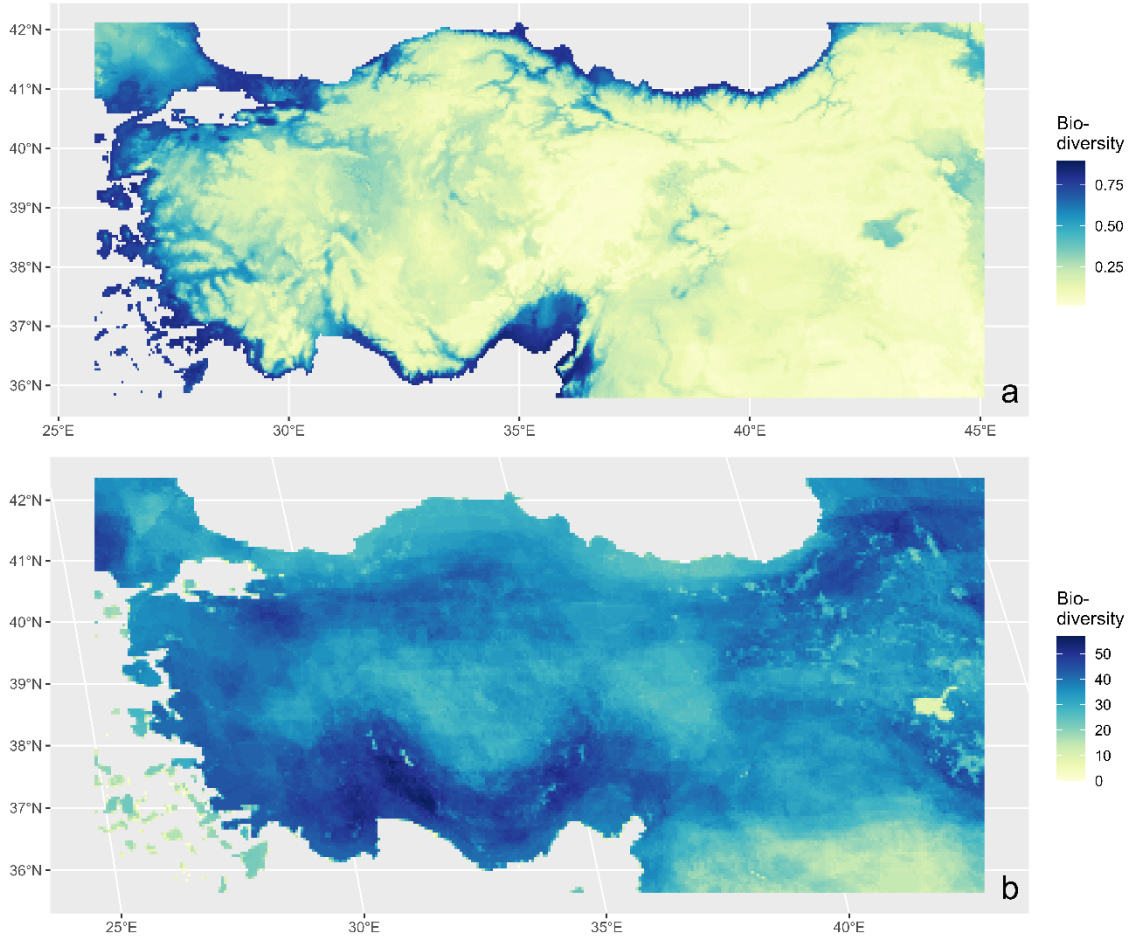

Figure 4.2: Avian species richness patterns of Anatolia according to a) the SDMs and b) the IUCN AoH maps. Note the differences in the coordinate systems; WGS84 for this study, and Mollweide for IUCN.

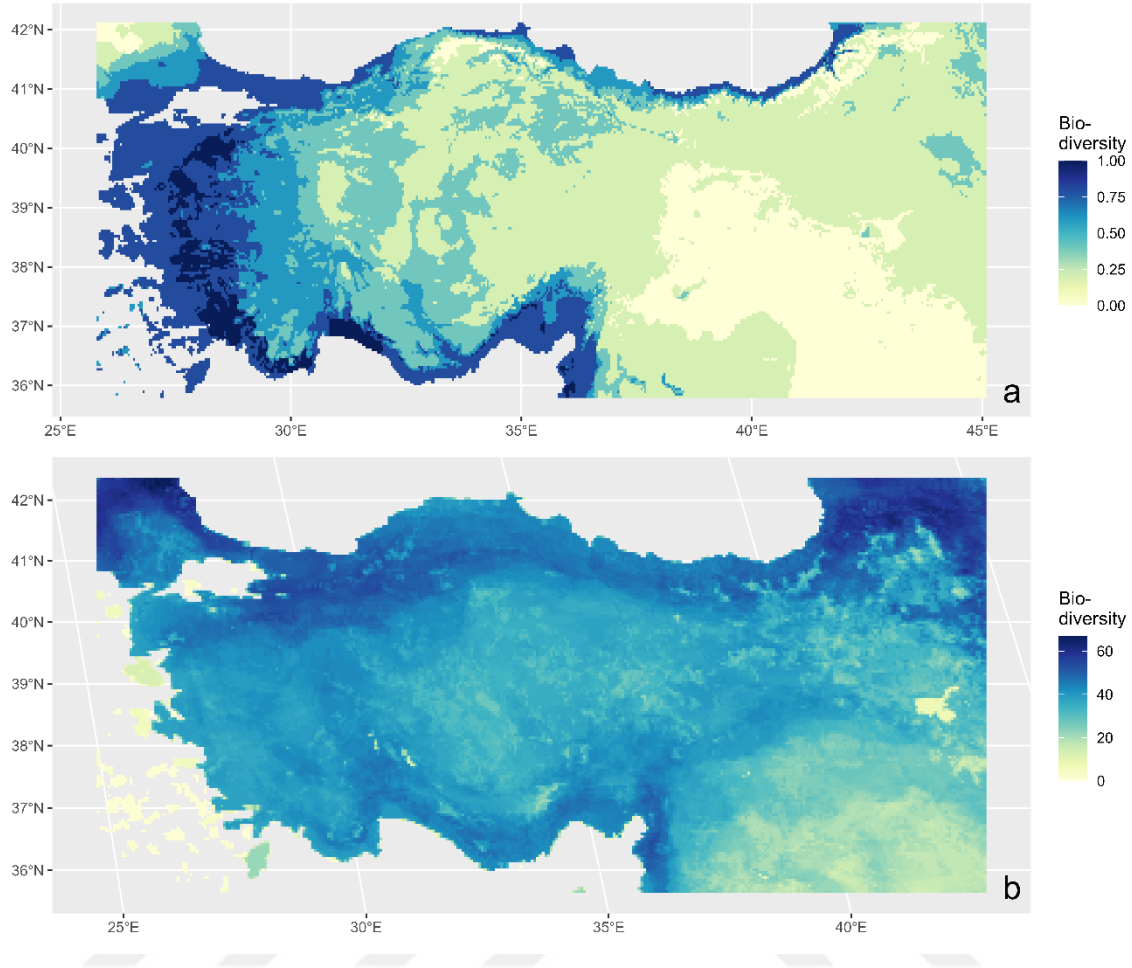

Figure 4.3: Mammal species richness patterns of Anatolia according to a) the SDMs and b) the IUCN AoH maps. Note the differences in the coordinate systems; WGS84 for this study, and Mollweide for IUCN.

For birds and mammals, the agreements between the maps are much less pronounced. Possible explanations for these low alignments could be the migratory dynamics of the taxa and the different modeling approaches adopted by the methods which require different interpretations of the results. These issues are further discussed in section 4.2.3. In addition, the low species count and sample sizes for the mammalian dataset pose a handicap for this study.

4.2 Biodiversity Projections, Uncertainty and the Limitations

The biodiversity projections of the study displayed a general poleward shift, consistent with established expectations (Parmesan et al., 1999; Parmesan & Yohe, 2003). Shifts in biodiversity patterns were particularly prominent around elevation gradients. Altitudinal shifts are a common ecological response to temperature warming and they have been well-documented in previous studies (Sekercioglu et

al., 2008; Sun et al., 2021; Telwala et al., 2013). Water bodies and forested areas also played significant roles in shaping the projected changes in biodiversity patterns. Similarly, precipitation gradients which are strongly influenced by topography, were closely associated with biodiversity patterns. Water-energy dynamics have been studied previously as key predictors of species richness patterns (Hawkins et al., 2003).

The reliability of SDMs in projecting climate change impacts has been extensively questioned (Santini et al., 2021; Sinclair et al., 2010). Biological responses to climatic changes can be complex and multifaceted; involving combinations of spatial, physiological, phenological, or genetic adaptations (Bellard et al., 2012). Although novel approaches have been proposed for integrating phenological or genetic dimensions (Barratt et al., 2024; Zurell, Zimmermann, et al., 2024), SDMs by themselves focus solely on the spatial extent of possible responses. There are several factors that can cause problems for SDM projections; these problems are discussed in the following subsections.

4.2.1 Temperature as a proximal predictor and the divergence between statistical and causal models

SDMs should be based on proximal predictors or those with well-understood surrogate relations to avoid unexpected biases and inaccuracies (Araújo et al., 2019). Temperature is one of the most frequently used predictors in ecological climate change studies. The effects of temperature on species distributions and biodiversity have several proposed explanations; two are explored here. First, as the energy in the environment: temperatures can be either too hot or too cold for a species to sustain necessary biological processes (Humboldt, 1850), which in turn shapes biodiversity patterns (Menéndez et al., 2006). Second, as free energy for plant productivity: as temperatures rise with increasing solar radiation in the photosynthetic wavelengths, plant productivity increases, which in turn promotes biodiversity (Hutchinson, 1959). Both mechanisms likely play roles in shaping biodiversity patterns. However, the greenhouse effect—the primary driver of the temperature increases—affects only radiation in infrared wavelengths. So, while temperatures rise, plant productivity remains relatively stable, not taking into account the minor positive effect of higher CO_2 concentrations in the atmosphere.

This disparity creates a complex causal mechanism concerning temperature and biodiversity (Figure 4.4), which most statistical models fail to account for. This limitation could lead to inaccuracies in SDM projections, particularly for energy-limited ecosystems such as those found in the Karadeniz region.

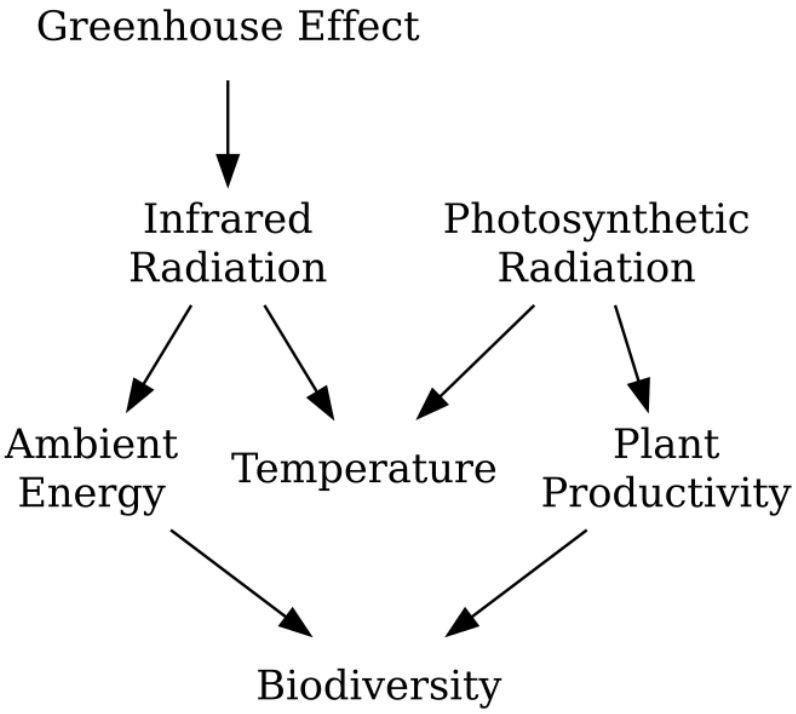

Figure 4.4: Causal graph illustrating the proposed temperature-biodiversity mechanism. Arrows represent one-way directional causal relations.

4.2.2 Niche truncation and Anatolia as the study extent

National borders might not represent the most appropriate spatial extent for addressing certain research questions or focusing on specific taxa when building SDMs. If the species whose niche is being modeled continues to occur beyond the borders of the study area—and the external area contains novel environmental conditions not represented within the study area—then the resulting species' niche is truncated. This issue, known as niche truncation, is a common problem in SDMs (Araújo et al., 2019). A similar issue arises when unsampled areas within the study borders contain novel environmental conditions where the taxon of interest occurs, unbeknownst to the modeler. In such cases, the modeler is once again confronted with a truncated niche. Niche truncation can lead to inaccurate projections because full range of environmental tolerances are not included in model training.

When a study centers around a region as opposed to a particular taxon, avoiding niche truncation becomes highly unlikely. No matter how the extent is defined, some species' niches are likely to extend beyond the environmental conditions of the study area. Anatolia is unique in this context, as it encompasses a wide range of climatic conditions and is bordered by natural boundaries. Consequently, it is reasonable to assume that Anatolia contains fairly large portions of the climatic niches of most species it hosts. In addition, Anatolia is bordered by large seas within its latitudinal range, throughout which climate changes more sharply. Species inhabiting both sides of the sea may exhibit local climatic adaptations. In such cases, modeling the full niche corresponds to an average of multiple local niches, potentially leading to inaccuracies. Whereas, modeling the truncated niche in those cases corresponds to the climatic niche of a particular population within the species, which is arguably more meaningful in certain contexts such as studies prioritizing regional biodiversity where colonization from outside the region is discounted.

4.2.3 Further issues in species distribution modeling

Biodiversity data is a crucial component of species distribution modeling. This study relied on the GBIF repository for species occurrence records, which include numerous citizen science observations. Citizen science data is likely to contain more errors than data collected through scientifically designed sampling. Another issue associated with this type of data is biased sampling, which can occur spatially, temporally, or along other axes. For example, 'interesting' species may be sampled more frequently, while elusive species may be undersampled. Remedies for spatial oversampling are discussed in the Methods section. While not applicable to this study, methods for partially addressing spatial undersampling have been proposed recently (Bracho-Estévanez et al., 2024). These advancements are promising for improving the performance and broader applicability of SDMs. Regarding temporal sampling biases, assuming milder weather conditions are sampled more frequently, a weighted samples approach could help mitigate these biases. However, determining appropriate weights presents its own challenges, and many observations lack the necessary date information. Date information introduces another consideration: taking tailored actions for specific taxa with

migratory dynamics, such as filtering bird records to include only observations from the breeding season, which could potentially enhance SDM performances. Another consideration regarding occurrence record dates is that the climate data used in the modeling corresponds to the 1970-2000 period (Fick & Hijmans, 2017), whereas species observation dates may not align with this timeframe. While this discrepancy may pose minimal issues in the early 21st century, it could become more problematic later in the century as species increasingly fall out of equilibrium with their niches due to the accelerated rate of climate change. Since SDMs fundamentally assume that species are in equilibrium with their niches, this misalignment could considerably impact model performances.

Another point of consideration is species' dispersal limitations. This study did not impose spatial constraints on species' future distributions. It is unclear how to determine the accurate distances given the immense dispersal variability within the taxa. A common approach involves estimating an average dispersal distance per unit time for a particular species and using this to calculate a buffer around the current distribution based on the projected time frame (Guisan & Thuiller, 2005). However, this approach is likely to underestimate species' dispersal distances, because dispersal patterns are better described by fat-tailed distributions (Maximum Entropy and Ecology, 2011, p. 66), (Harte, 2011, Chapter 3). In these types of distributions, probabilities of extreme values decay much more slowly and statistics like mean averages become less meaningful (Statistical Consequences of Fat Tails, 2022, p. 22), (Taleb, 2022, Chapter 3). Furthermore, selection bias can lead to an underestimation of dispersal capability. For example, seeds that disperse the furthest from the origin may fail to germinate because areas further away from the origin are more likely to be environmentally unsuitable, meaning that these long-distance dispersal events often go undetected, leading to an underestimation of dispersal capability. More sophisticated methods for integrating dispersal into SDMs using custom probability distributions exist (Engler et al., 2012), though they require more detailed information about the taxa.

SDMs tend to perform better when modeling specialist species compared to generalist species (Goedecke et al., 2020). This is because, with the same amount of data, occurrence records of specialist species, confined to narrow environmental conditions, carry a stronger signal, whereas those of generalist species are more

prone to statistical noise. This imbalance can introduce bias into overall biodiversity assessments, such as those conducted in this study. Nevertheless, the assumption that generalist species, on average, have more occurrence records than specialist species suggests that the impact of this bias may be less significant than initially anticipated.

Missing predictors that determine species' niches can negatively impact SDM performances. Although this study may have omitted other important predictors beyond climate, it is also unclear whether the full influence of climate on species distributions has been incorporated into the modeling process. For instance, climate change is expected to increase the frequency of extreme events such as wildfires, hurricanes, droughts, and floods, all of which can notably affect species distributions (Bellard et al., 2012). These types of events are difficult to fully account for in SDMs because the climate data used in modeling mostly consists of averages. While SDMs may indirectly capture some aspects of extreme events, their full impacts are absent from projections.

One particular limitation of SDMs is their susceptibility to misinterpretation. It is important to recognize that SDMs are built upon observations that would make up the realized niche. However, species often do not fill their niches for many different reasons, and in some cases, they may even occupy niches that extend beyond their fundamental niches. An example of the latter is sink populations—populations that persist in unsuitable environments by relying on immigration from other populations that are within their fundamental niche to sustain their numbers. While SDMs are trained on these realized niches, their outputs are not exactly the extensions of those realized niches. Nor can it be said that they infer the fundamental niches in their outputs. In the ecology community, SDMs are referred to by various names, including ecological niche models, habitat suitability models, climate envelopes, range maps, and spatial models (Elith & Leathwick, 2009). Although all of these terms come close, none fully encapsulates the meaning of SDM outputs. Because SDMs do not fully correspond to existing ecological terms, their outputs should be interpreted with careful consideration of their capabilities and limitations.

4.3 Biodiversity Assessments in the Age of Global Change

Biodiversity is a multidimensional concept, conventionally assessed through three components; genetic, species, and ecosystem diversity (Burgess et al., 2024). SDMs provide only a narrow window into the problem of biological response to environmental change, focusing only on a single species at a time. There appears to be no privileged biological level upon which all aspects of the issue supervene. That is why global change ecology should embrace diverse methodologies (Enquist et al., 2024). Collaborative and integrative approaches represent important paths forward. The emerging transdisciplinary field of macrogenetics is a good example, combining genetics and ecology to analyze biodiversity for conservation implications (Schmidt et al., 2023). Promising approaches also leverage concepts from diverse disciplines, such as applying machine learning to integrate incompatible models (Oeser et al., 2024) or using ecological niche theory to spatially incorporate intraspecific variation for conservation purposes (Hanson et al., 2020). Accounting for variation both within and among biological systems is a recurring theme in contemporary scientific challenges. Hierarchical Bayesian modeling may be an underutilized tool in such challenges, as it is inherently capable of incorporating variation across multiple levels (Statistical Rethinking, 2020, p. 400), (McElreath, 2020, Chapter 13).

Conservation biology is confronted with major challenges of the Anthropocene (Bellard et al., 2012). The results of this study suggest major asynchronous shifts in species' distributions, which could have important implications for conservation. While ecosystems are known to be resilient to certain perturbations (Holling, 1973), the response of ecosystems to interventions that alter the compositions of ecological communities is much less understood. Communities as wholes tracking niches together in sync is a naïve assumption. The projections of this study imply that most ecological communities or ecosystems will encounter new species, lose existing species, or often experience both, to varying extents, depending on different climate scenarios. This problem highlights the need for a complementary approach to the traditional habitat conservation perspective. In addition to identifying existing habitats and communities for conservation, it is also necessary to determine environmental conditions that promote biodiversity as a complementary environmental approach and incorporate these insights into

conservation practices. The future of Earth's biosphere is vast and filled with uncertainties, emphasizing the importance of adopting diverse and comprehensive conservation strategies.

This study utilized SDMs to assess biodiversity patterns in Anatolia under a changing climate. SDMs, while not without their limitations, have been and continue to be one of the most valuable tools in ecological studies. By emphasizing the importance of spatial and environmental approaches to biodiversity assessments, this study employed diverse tools to project changes in biodiversity patterns across Anatolia, offering insights that could inform future conservation efforts.

REFERENCES

Adedoja, O. A., Dormann, C. F., Coetzee, A., & Geerts, S. (2024). Moving with your mutualist: Predicted climate-induced mismatch between Proteaceae species and their avian pollinators. *Journal of Biogeography*, *51*(6), 992–1003. https://doi.org/10.1111/jbi.14804

Aiello-Lammens, M. E., Boria, R. A., Radosavljevic, A., Vilela, B., Anderson, R. P., Bjornson, R., & Weston, S. (2019). *spThin: Functions for Spatial Thinning of Species Occurrence Records for Use in Ecological Models* (Version 0.2.0) [Computer software]. https://cran.r-project.org/web/packages/spThin/index.html

Akaike, H. (1974). A new look at the statistical model identification. *IEEE Transactions on Automatic Control*, *19*(6), 716–723. https://doi.org/10.1109/TAC.1974.1100705

Alin, A. (2010). Multicollinearity. *WIREs Computational Statistics*, *2*(3), 370–374. https://doi.org/10.1002/wics.84

Allouche, O., Tsoar, A., & Kadmon, R. (2006). Assessing the accuracy of species distribution models: Prevalence, kappa and the true skill statistic (TSS). *Journal of Applied Ecology*, *43*(6), 1223–1232. https://doi.org/10.1111/j.1365-2664.2006.01214.x

Araújo, M. B., Anderson, R. P., Márcia Barbosa, A., Beale, C. M., Dormann, C. F., Early, R., Garcia, R. A., Guisan, A., Maiorano, L., Naimi, B., O'Hara, R. B., Zimmermann, N. E., & Rahbek, C. (2019). Standards for distribution models in biodiversity assessments. *Science Advances*, *5*(1), eaat4858. https://doi.org/10.1126/sciadv.aat4858

Araújo, M. B., Pearson, R. G., Thuiller, W., & Erhard, M. (2005). Validation of species–climate impact models under climate change. *Global Change Biology*, *11*(9), 1504–1513. https://doi.org/10.1111/j.1365-2486.2005.01000.x

Assis, J. (2020). *R Pipelines to reduce the spatial autocorrelation in Species Distribution Models. theMarineDataScientist* [Computer software]. https://github.com/jorgeassis/spatialAutocorrelation

Barbet-Massin, M., Jiguet, F., Albert, C. H., & Thuiller, W. (2012). Selecting pseudo-absences for species distribution models: How, where and how many? *Methods in Ecology and Evolution*, *3*(2), 327–338. https://doi.org/10.1111/j.2041-210X.2011.00172.x

Barnard, P., & Thuiller, W. (2008). Introduction. Global change and biodiversity: Future challenges. *Biology Letters*, *4*(5), 553–555. https://doi.org/10.1098/rsbl.2008.0374

Barnosky, A. D., Matzke, N., Tomiya, S., Wogan, G. O. U., Swartz, B., Quental, T. B., Marshall, C., McGuire, J. L., Lindsey, E. L., Maguire, K. C., Mersey, B., & Ferrer, E. A. (2011). Has the Earth's sixth mass extinction already arrived? *Nature*, *471*(7336), 51–57. https://doi.org/10.1038/nature09678

Barratt, C. D., Onstein, R. E., Pinsky, M. L., Steinfartz, S., Kühl, H. S., Forester, B. R., & Razgour, O. (2024). Life on the edge: A new toolbox for population-level

climate change vulnerability assessments. *Methods in Ecology and Evolution*, *n/a*(n/a). https://doi.org/10.1111/2041-210X.14429

Begon, M., & Townsend, C. R. (2020). *Ecology: From individuals to ecosystems* (Fifth edition). Wiley.

Bektaş, B., Chisholm, C., Egelkraut, D., Lynn, J., Block, S., Deola, T., Dommanget, F., Enquist, B. J., Goldberg, D. E., Haider, S., Halbritter, A. H., He, Y., Jaunatre, R., Jentsch, A., Klanderud, K., Kardol, P., Lachmuth, S., Loucougaray, G., Münkemüller, T., … Alexander, J. M. (2024). Colonization and extinction lags drive non-linear responses to warming in mountain plant communities across the Northern Hemisphere. *Ecography*, *n/a*(n/a), e07378. https://doi.org/10.1111/ecog.07378

Bellard, C., Bertelsmeier, C., Leadley, P., Thuiller, W., & Courchamp, F. (2012). Impacts of climate change on the future of biodiversity. *Ecology Letters*, *15*(4), 365–377. https://doi.org/10.1111/j.1461-0248.2011.01736.x

Billingsley, P. (2012). *Probability and measure* (Anniversary edition). Wiley.

Block, S., Emerson, J. W., Esty, D. C., De Sherbinin, A., & Wendling, Z. A. (2024). *2024 Environmental Performance Index*.

Boavida, J., Assis, J., Silva, I., & Serrão, E. A. (2016). Overlooked habitat of a vulnerable gorgonian revealed in the Mediterranean and Eastern Atlantic by ecological niche modelling. *Scientific Reports*, *6*(1), 36460. https://doi.org/10.1038/srep36460

Boucher, O., Denvil, S., Levavasseur, G., Cozic, A., Caubel, A., Foujols, M.-A., Meurdesoif, Y., Cadule, P., Devilliers, M., Ghattas, J., Lebas, N., Lurton, T., Mellul, L., Musat, I., Mignot, J., & Cheruy, F. (2018). *IPSL IPSL-CM6A-LR model output prepared for CMIP6 CMIP* [Dataset]. Earth System Grid Federation. https://doi.org/10.22033/ESGF/CMIP6.1534

Box, G. E. P. (1976). Science and Statistics. *Journal of the American Statistical Association*, *71*(356), 791–799. https://doi.org/10.1080/01621459.1976.10480949

Bracho-Estévanez, C. A., Arenas-Castro, S., González-Varo, J. P., & González-Moreno, P. (2024). Spatially explicit metrics improve the evaluation of species distribution models facing sampling biases. *Ecological Informatics*, *84*, 102916. https://doi.org/10.1016/j.ecoinf.2024.102916

Breiman, L. (1996). Bagging predictors. *Machine Learning*, *24*(2), 123–140. https://doi.org/10.1007/BF00058655

Breiman, L. (2001). Random Forests. *Machine Learning*, *45*(1), 5–32. https://doi.org/10.1023/A:1010933404324

Buchanan, G. M., Donald, P. F., & Butchart, S. H. M. (2011). Identifying Priority Areas for Conservation: A Global Assessment for Forest-Dependent Birds. *PLOS ONE*, *6*(12), e29080. https://doi.org/10.1371/journal.pone.0029080

Burgess, N. D., Ali, N., Bedford, J., Bhola, N., Brooks, S., Cierna, A., Correa, R., Harris, M., Hargey, A., Hughes, J., McDermott-Long, O., Miles, L., Ravilious, C., Rodrigues, A. R., Van Soesbergen, A., Sihvonen, H., Seager, A., Swindell, L., Vukelic, M., … Butchart, S. H. M. (2024). Global Metrics for Terrestrial Biodiversity. *Annual Review of Environment and Resources*, *49*(1), 673–709. https://doi.org/10.1146/annurev-environ-121522-045106

Burnham, K. P., & Anderson, D. R. (2004). Multimodel Inference: Understanding AIC and BIC in Model Selection. *Sociological Methods & Research*, *33*(2), 261–304. https://doi.org/10.1177/0049124104268644

Calvin, K., Dasgupta, D., Krinner, G., Mukherji, A., Thorne, P. W., Trisos, C., Romero, J., Aldunce, P., Barrett, K., Blanco, G., Cheung, W. W. L., Connors, S., Denton, F., Diongue-Niang, A., Dodman, D., Garschagen, M., Geden, O., Hayward, B., Jones, C., … Péan, C. (2023). *IPCC, 2023: Climate Change 2023: Synthesis Report. Contribution of Working Groups I, II and III to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change [Core Writing Team, H. Lee and J. Romero (eds.)]. IPCC, Geneva, Switzerland.* (First). Intergovernmental Panel on Climate Change (IPCC). https://doi.org/10.59327/IPCC/AR6-9789291691647

Chevalier, M., Broennimann, O., & Guisan, A. (2024). Climate change may reveal currently unavailable parts of species' ecological niches. *Nature Ecology & Evolution*, *8*(7), 1298–1310. https://doi.org/10.1038/s41559-024-02426-4

Collart, F., & Guisan, A. (2023). Small to train, small to test: Dealing with low sample size in model evaluation. *Ecological Informatics*, *75*, 102106. https://doi.org/10.1016/j.ecoinf.2023.102106

Dormann, C. F. (2007). Effects of incorporating spatial autocorrelation into the analysis of species distribution data. *Global Ecology and Biogeography*, *16*(2), 129–138. https://doi.org/10.1111/j.1466-8238.2006.00279.x

Dormann, C. F., Calabrese, J. M., Guillera-Arroita, G., Matechou, E., Bahn, V., Bartoń, K., Beale, C. M., Ciuti, S., Elith, J., Gerstner, K., Guelat, J., Keil, P., Lahoz-Monfort, J. J., Pollock, L. J., Reineking, B., Roberts, D. R., Schröder, B., Thuiller, W., Warton, D. I., … Hartig, F. (2018). Model averaging in ecology: A review of Bayesian, information-theoretic, and tactical approaches for predictive inference. *Ecological Monographs*, *88*(4), 485–504. https://doi.org/10.1002/ecm.1309

Dormann, C. F., Elith, J., Bacher, S., Buchmann, C., Carl, G., Carré, G., Marquéz, J. R. G., Gruber, B., Lafourcade, B., Leitão, P. J., Münkemüller, T., McClean, C., Osborne, P. E., Reineking, B., Schröder, B., Skidmore, A. K., Zurell, D., & Lautenbach, S. (2013). Collinearity: A review of methods to deal with it and a simulation study evaluating their performance. *Ecography*, *36*(1), 27–46. https://doi.org/10.1111/j.1600-0587.2012.07348.x

Dumlupinar, İl., Gür, H., & Özüdoğru, B. (2023). Distributional ecology of Noccaea vesicaria in relation to the Anatolian Diagonal. *Turkish Journal of Botany*, *47*(4), 267–277. https://doi.org/10.55730/1300-008X.2765

Elith, J., Kearney, M., & Phillips, S. (2010). The art of modelling range-shifting species. *Methods in Ecology and Evolution*, *1*(4), 330–342. https://doi.org/10.1111/j.2041-210X.2010.00036.x

Elith, J., & Leathwick, J. R. (2009). Species Distribution Models: Ecological Explanation and Prediction Across Space and Time. *Annual Review of Ecology, Evolution, and Systematics*, *40*(Volume 40, 2009), 677–697. https://doi.org/10.1146/annurev.ecolsys.110308.120159

Elith, J., Leathwick, J. R., & Hastie, T. (2008). A working guide to boosted regression trees. *Journal of Animal Ecology*, *77*(4), 802–813. https://doi.org/10.1111/j.1365-2656.2008.01390.x

Elith, J., Phillips, S. J., Hastie, T., Dudík, M., Chee, Y. E., & Yates, C. J. (2011). A statistical explanation of MaxEnt for ecologists. *Diversity and Distributions*, *17*(1), 43–57. https://doi.org/10.1111/j.1472-4642.2010.00725.x

Engler, R., Hordijk, W., & Guisan, A. (2012). The MIGCLIM R package – seamless integration of dispersal constraints into projections of species distribution models. *Ecography*, *35*(10), 872–878. https://doi.org/10.1111/j.1600-0587.2012.07608.x

Enquist, B. J., Kempes, C. P., & West, G. B. (2024). Developing a predictive science of the biosphere requires the integration of scientific cultures. *Proceedings of the National Academy of Sciences*, *121*(19), e2209196121. https://doi.org/10.1073/pnas.2209196121

Farashi, A., Shariati, M., & Hosseini, M. (2017). Identifying biodiversity hotspots for threatened mammal species in Iran. *Mammalian Biology*, *87*, 71–88. https://doi.org/10.1016/j.mambio.2017.06.002

Feng, X., Enquist, B. J., Park, D. S., Boyle, B., Breshears, D. D., Gallagher, R. V., Lien, A., Newman, E. A., Burger, J. R., Maitner, B. S., Merow, C., Li, Y., Huynh, K. M., Ernst, K., Baldwin, E., Foden, W., Hannah, L., Jørgensen, P. M., Kraft, N. J. B., … López-Hoffman, L. (2022). A review of the heterogeneous landscape of biodiversity databases: Opportunities and challenges for a synthesized biodiversity knowledge base. *Global Ecology and Biogeography*, *31*(7), 1242–1260. https://doi.org/10.1111/geb.13497

Fick, S. E., & Hijmans, R. J. (2017). WorldClim 2: New 1-km spatial resolution climate surfaces for global land areas. *International Journal of Climatology*, *37*(12), 4302–4315. https://doi.org/10.1002/joc.5086

Fielding, A. H., & Bell, J. F. (1997). A review of methods for the assessment of prediction errors in conservation presence/absence models. *Environmental Conservation*, *24*(1), 38–49. https://doi.org/10.1017/S0376892997000088

Galiana, N., Arnoldi, J.-F., Mestre, F., Rozenfeld, A., & Araújo, M. B. (2024). Power laws in species' biotic interaction networks can be inferred from co-occurrence data. *Nature Ecology & Evolution*, *8*(2), 209–217. https://doi.org/10.1038/s41559-023-02254-y

GBIF.org. (2024a). *Occurrence Download* (p. 700210415) [Darwin Core Archive,text/tab-separated-values,application/zip]. The Global Biodiversity Information Facility. https://doi.org/10.15468/DL.QXYMSD

GBIF.org. (2024b). *Occurrence Download* (p. 34842630) [Darwin Core Archive,text/tab-separated-values,application/zip]. The Global Biodiversity Information Facility. https://doi.org/10.15468/DL.XN3HKN

GBIF.org. (2024c). *Occurrence Download* (p. 52998736) [Darwin Core Archive,text/tab-separated-values,application/zip]. The Global Biodiversity Information Facility. https://doi.org/10.15468/DL.QAMGT7

GBIF.org. (2024d). *Occurrence Download* (p. 1184042) [Darwin Core Archive,text/tab-separated-values,application/zip]. The Global Biodiversity Information Facility. https://doi.org/10.15468/DL.9ZFWTY

GBIF.org. (2024e). *Occurrence Download* (p. 823197540) [Darwin Core Archive,text/tab-separated-values,application/zip]. The Global Biodiversity Information Facility. https://doi.org/10.15468/DL.Q7GTGJ

Gillespie, L. E., Ruffley, M., & Exposito-Alonso, M. (2024). Deep learning models map rapid plant species changes from citizen science and remote sensing data. *Proceedings of the National Academy of Sciences*, *121*(37), e2318296121. https://doi.org/10.1073/pnas.2318296121

Goedecke, F., Marcenò, C., Guarino, R., Jahn, R., & Bergmeier, E. (2020). Reciprocal extrapolation of species distribution models between two islands – Specialists perform better than generalists and geological data reduces prediction accuracy. *Ecological Indicators*, *108*, 105652. https://doi.org/10.1016/j.ecolind.2019.105652

Goslee, S., & Urban, D. (2023). *ecodist: Dissimilarity-Based Functions for Ecological Analysis* (Version 2.1.3) [Computer software]. https://cran.r-project.org/web/packages/ecodist/index.html

Grinnell, J. (1917). The Niche-Relationships of the California Thrasher. *The Auk*, *34*(4), 427–433. https://doi.org/10.2307/4072271

Guélat, J., & Kéry, M. (2018). Effects of spatial autocorrelation and imperfect detection on species distribution models. *Methods in Ecology and Evolution*, *9*(6), 1614–1625. https://doi.org/10.1111/2041-210X.12983

Guisan, A., & Thuiller, W. (2005). Predicting species distribution: Offering more than simple habitat models. *Ecology Letters*, *8*(9), 993–1009. https://doi.org/10.1111/j.1461-0248.2005.00792.x

Guisan, A., Thuiller, W., & Zimmermann, N. E. (2017). *Habitat Suitability and Distribution Models: With Applications in R*. Cambridge University Press. https://doi.org/10.1017/9781139028271

Gür, H. (2013). The effects of the Late Quaternary glacial–interglacial cycles on Anatolian ground squirrels: Range expansion during the glacial periods? *Biological Journal of the Linnean Society*, *109*(1), 19–32. https://doi.org/10.1111/bij.12026

Gür, H. (2017). Geç Kuvaterner Buzul Buzullararası Döngülerinin Anadolu'nun Biyolojik Çeşitliliği Üzerine Etkileri. *Türkiye Jeoloji Bülteni / Geological Bulletin of Turkey*. https://doi.org/10.25288/tjb.363813

Gür, H. (2022). The future impact of climate and land-use changes on Anatolian ground squirrels under different scenarios. *Ecological Informatics*, *70*, 101693. https://doi.org/10.1016/j.ecoinf.2022.101693

Hanson, J. O., Rhodes, J. R., Butchart, S. H. M., Buchanan, G. M., Rondinini, C., Ficetola, G. F., & Fuller, R. A. (2020). Global conservation of species' niches. *Nature*, *580*(7802), 232–234. https://doi.org/10.1038/s41586-020-2138-7

Harte, J. (2011). *Maximum entropy and ecology: A theory of abundance, distribution, and energetics* (1. publ). Oxford University Press.

Hawkins, B. A., Field, R., Cornell, H. V., Currie, D. J., Guégan, J.-F., Kaufman, D. M., Kerr, J. T., Mittelbach, G. G., Oberdorff, T., O'Brien, E. M., Porter, E. E., & Turner, J. R. G. (2003). Energy, Water, and Broad-Scale Geographic

Patterns of Species Richness. *Ecology*, *84*(12), 3105–3117. https://doi.org/10.1890/03-8006

Hernangómez, D., code), D. D. (for ggspatial, & code), ggplot2 authors (for contour). (2024). *tidyterra: "tidyverse" Methods and "ggplot2" Helpers for "terra" Objects* (Version 0.6.1) [Computer software]. https://cran.r-project.org/web/packages/tidyterra/index.html

Hijmans, R. J., Bivand, R., Dyba, K., Pebesma, E., & Sumner, M. D. (2024). *terra: Spatial Data Analysis* (Version 1.7-78) [Computer software]. https://cran.r-project.org/web/packages/terra/index.html

Hijmans, R. J., Etten, J. van, Sumner, M., Cheng, J., Baston, D., Bevan, A., Bivand, R., Busetto, L., Canty, M., Fasoli, B., Forrest, D., Ghosh, A., Golicher, D., Gray, J., Greenberg, J. A., Hiemstra, P., Hingee, K., Ilich, A., Geosciences, I. for M. A., … Wueest, R. (2023). *raster: Geographic Data Analysis and Modeling* (Version 3.6-26) [Computer software]. https://cran.r-project.org/web/packages/raster/index.html

Hijmans, R. J., Phillips, S., Barbosa, M., Brunsdon, C., & Rowlingson, B. (2024). *predicts: Spatial Prediction Tools* (Version 0.1-16) [Computer software]. https://cran.r-project.org/web/packages/predicts/index.html

Hijmans, R. J., Phillips, S., & Elith, J. L. and J. (2023). *dismo: Species Distribution Modeling* (Version 1.3-14) [Computer software]. https://cran.r-project.org/web/packages/dismo/index.html

Holling, C. S. (1973). Resilience and Stability of Ecological Systems. *Annual Review of Ecology and Systematics*, *4*, 1–23.

Humboldt, A. von. (1850). *Views of Nature: Or Contemplations on the Sublime Phenomena of Creation* (E. C. Otté & H. G. Bohn, Trans.). Cambridge University Press. https://doi.org/10.1017/CBO9781139095983

Hutchinson, G. E. (1959). Homage to Santa Rosalia or Why Are There So Many Kinds of Animals? *The American Naturalist*, *93*(870), 145–159.

IUCN (International Union for Conservation of Nature). (2021). *The IUCN Red List version 2021-3 Species Richness from AoH maps. (Spatial data)* [Dataset]. https://www.iucnredlist.org

IUCN (International Union for Conservation of Nature). (2024). *The IUCN Red List version 2024-2 Species Richness. (Spatial data)* [Dataset]. https://www.iucnredlist.org

Jaynes, E. T. (1957a). Information Theory and Statistical Mechanics. *Physical Review*, *106*(4), 620–630. https://doi.org/10.1103/PhysRev.106.620

Jaynes, E. T. (1957b). Information Theory and Statistical Mechanics. II. *Physical Review*, *108*(2), 171–190. https://doi.org/10.1103/PhysRev.108.171

Jetz, W., Rahbek, C., & Colwell, R. K. (2004). The coincidence of rarity and richness and the potential signature of history in centres of endemism. *Ecology Letters*, *7*(12), 1180–1191. https://doi.org/10.1111/j.1461-0248.2004.00678.x

Ke, C., Gong, L., Geng, Y., Wang, Z., Zhang, W., Feng, J., & Jiang, T. (2024). Patterns and correlates of potential range shifts of bat species in China in the context of

climate change. *Conservation Biology*, e14310. https://doi.org/10.1111/cobi.14310

Kirwan, G. M., & Aydemir, G. (Eds.). (2008). *The birds of Turkey: The distribution, taxonomy, and breeding of Turkish birds*. Christopher Helm.

Koçakoğlu, N. Ö., & Candan, S. (2023). Morphology of the Female Reproductive System in Carpocoris mediterraneus Tamanini, 1958 (Heteroptera: Pentatomidae). *Transactions of the American Entomological Society*, *149*(1). https://doi.org/10.3157/061.149.0103

Konowalik, K., & Nosol, A. (2021). Evaluation metrics and validation of presence-only species distribution models based on distributional maps with varying coverage. *Scientific Reports*, *11*(1), 1482. https://doi.org/10.1038/s41598-020-80062-1

Landis, J. R., & Koch, G. G. (1977). The Measurement of Observer Agreement for Categorical Data. *Biometrics*, *33*(1), 159–174. https://doi.org/10.2307/2529310

Lawler, J. J., Shafer, S. L., White, D., Kareiva, P., Maurer, E. P., Blaustein, A. R., & Bartlein, P. J. (2009). Projected climate-induced faunal change in the Western Hemisphere. *Ecology*, *90*(3), 588–597. https://doi.org/10.1890/08-0823.1

Leroy, B., Delsol, R., Hugueny, B., Meynard, C. N., Barhoumi, C., Barbet-Massin, M., & Bellard, C. (2018). Without quality presence–absence data, discrimination metrics such as TSS can be misleading measures of model performance. *Journal of Biogeography*, *45*(9), 1994–2002. https://doi.org/10.1111/jbi.13402

Liu, C., Berry, P. M., Dawson, T. P., & Pearson, R. G. (2005). Selecting thresholds of occurrence in the prediction of species distributions. *Ecography*, *28*(3), 385–393. https://doi.org/10.1111/j.0906-7590.2005.03957.x

Lu, M., & Jetz, W. (2023). Scale-sensitivity in the measurement and interpretation of environmental niches. *Trends in Ecology & Evolution*, *38*(6), 554–567. https://doi.org/10.1016/j.tree.2023.01.003

Macarthur, R. H., & Wilson, E. O. (1967). *The Theory of Island Biogeography* (REV-Revised). Princeton University Press. https://www.jstor.org/stable/j.ctt19cc1t2

Maduna, S. N., Aspholm, P. E., Hansen, A. B., Klütsch, C. F. C., & Hagen, S. B. (2024). Ecological niche modelling and population genomics provide insights into the geographic and demographic 'explosion' of a non-indigenous salmonid. *Diversity and Distributions*, ddi.13811. https://doi.org/10.1111/ddi.13811

Magnin, G., & Yarar, M. (1997). *Important bird areas in Turkey*. Doğal Hayati Koruma Derneği.

Malley, J. D., Kruppa, J., Dasgupta, A., Malley, K. G., & Ziegler, A. (2012). Probability Machines: Consistent Probability Estimation Using Nonparametric Learning Machines. *Methods of Information in Medicine*, *51*(01), 74–81. https://doi.org/10.3414/ME00-01-0052

McElreath, R. (2020). *Statistical rethinking: A Bayesian course with examples in R and Stan* (Second edition). CRC Press.

Médail, F., & Diadema, K. (2009). Glacial refugia influence plant diversity patterns in the Mediterranean Basin. *Journal of Biogeography*, *36*(7), 1333–1345. https://doi.org/10.1111/j.1365-2699.2008.02051.x

Menéndez, R., Megías, A. G., Hill, J. K., Braschler, B., Willis, S. G., Collingham, Y., Fox, R., Roy, D. B., & Thomas, C. D. (2006). Species richness changes lag behind climate change. *Proceedings of the Royal Society B: Biological Sciences*, *273*(1593), 1465–1470. https://doi.org/10.1098/rspb.2006.3484

Moudrý, V., Bazzichetto, M., Remelgado, R., Devillers, R., Lenoir, J., Mateo, R., Consortium, S., Sillero, N., Lecours, V., Cord, A., Barták, V., Balej, P., Rocchini, D., Torresani, M., Arenas-Castro, S., Man, M., Prajzlerova, D., Gdulova, K., Prošek, J., … Šímová, P. (2023). *Optimising Species Distribution Models: Sample size, positional error, and sampling bias matter*. https://doi.org/10.32942/X2JS5D

O**eser, J., Zurell, D., Mayer, F., Çoraman, E., Toshkova, N., Deleva, S., Natradze, I., Benda, P., Ghazaryan, A., Irmak, S., Hasanov, N., Guliyeva, G., Gritsina, M., & Kuemmerle, T.** (2024). The Best of Two Worlds: Using Stacked Generalisation for Integrating Expert Range Maps in Species Distribution Models. *Global Ecology and Biogeography*, *n/a*(n/a), e13911. https://doi.org/10.1111/geb.13911

Ohlemüller, R., Anderson, B. J., Araújo, M. B., Butchart, S. H. M., Kudrna, O., Ridgely, R. S., & Thomas, C. D. (2008). The coincidence of climatic and species rarity: High risk to small-range species from climate change. *Biology Letters*, *4*(5), 568–572. https://doi.org/10.1098/rsbl.2008.0097

Özhatay, N., Byfield, A., & Atay, S. (2008). *Türkiye'nin 122 önemli bitki alanı* (2. baskı). WWF Türkiye (Doğal Hayatı Koruma Vakfı).

Palmer, T. (2022). *The primacy of doubt: From quantum physics to climate change, how the science of uncertainty can help us understand our chaotic world* (First edition). Basic Books.

Parmesan, C., Ryrholm, N., Stefanescu, C., Hill, J. K., Thomas, C. D., Descimon, H., Huntley, B., Kaila, L., Kullberg, J., Tammaru, T., Tennent, W. J., Thomas, J. A., & Warren, M. (1999). Poleward shifts in geographical ranges of butterfly species associated with regional warming. *Nature*, *399*(6736), 579–583. https://doi.org/10.1038/21181

Parmesan, C., & Yohe, G. (2003). A globally coherent fingerprint of climate change impacts across natural systems. *Nature*, *421*(6918), 37–42. https://doi.org/10.1038/nature01286

Peano, D., Lovato, T., & Materia, S. (2020). *CMCC CMCC-ESM2 model output prepared for CMIP6 LS3MIP* [Dataset]. Earth System Grid Federation. https://doi.org/10.22033/ESGF/CMIP6.13165

Pereira, H. M., Navarro, L. M., & Martins, I. S. (2012). Global Biodiversity Change: The Bad, the Good, and the Unknown. *Annual Review of Environment and Resources*, *37*(1), 25–50. https://doi.org/10.1146/annurev-environ-042911-093511

Phillips, S. (2021). *maxnet: Fitting "Maxent" Species Distribution Models with "glmnet"* (Version 0.1.4) [Computer software]. https://cran.r-project.org/web/packages/maxnet/index.html

Phillips, S. J., Anderson, R. P., & Schapire, R. E. (2006). Maximum entropy modeling of species geographic distributions. *Ecological Modelling*, *190*(3), 231–259. https://doi.org/10.1016/j.ecolmodel.2005.03.026

Phillips, S. J., & Dudík, M. (2008). Modeling of species distributions with Maxent: New extensions and a comprehensive evaluation. *Ecography*, *31*(2), 161–175. https://doi.org/10.1111/j.0906-7590.2008.5203.x

Pichler, M., & Hartig, F. (2021). A new joint species distribution model for faster and more accurate inference of species associations from big community data. *Methods in Ecology and Evolution*, *12*(11), 2159–2173. https://doi.org/10.1111/2041-210X.13687

R Core Team. (2023). *R: A Language and Environment for Statistical Computing* (Version 4.3.1) [Computer software]. R Foundation for Statistical Computing. https://www.R-project.org/

Santini, L., Benítez-López, A., Maiorano, L., Čengić, M., & Huijbregts, M. A. J. (2021). Assessing the reliability of species distribution projections in climate change research. *Diversity and Distributions*, *27*(6), 1035–1050. https://doi.org/10.1111/ddi.13252

Schapire, R. E. (2003). The Boosting Approach to Machine Learning: An Overview. In D. D. Denison, M. H. Hansen, C. C. Holmes, B. Mallick, & B. Yu (Eds.), *Nonlinear Estimation and Classification* (Vol. 171, pp. 149–171). Springer New York. https://doi.org/10.1007/978-0-387-21579-2_9

Schmidt, C., Hoban, S., & Jetz, W. (2023). Conservation macrogenetics: Harnessing genetic data to meet conservation commitments. *Trends in Genetics*, *39*(11), 816–829. https://doi.org/10.1016/j.tig.2023.08.002

Segurado, P., Araújo, M. B., & Kunin, W. E. (2006). Consequences of spatial autocorrelation for niche-based models. *Journal of Applied Ecology*, *43*(3), 433–444. https://doi.org/10.1111/j.1365-2664.2006.01162.x

Sekercioglu, C. H., Schneider, S. H., Fay, J. P., & Loarie, S. R. (2008). Climate Change, Elevational Range Shifts, and Bird Extinctions. *Conservation Biology*, *22*(1), 140–150. https://doi.org/10.1111/j.1523-1739.2007.00852.x

Shannon, C. E. (1948). A Mathematical Theory of Communication. *Bell System Technical Journal*, *27*(3), 379–423. https://doi.org/10.1002/j.1538-7305.1948.tb01338.x

Shiogama, H., Abe, M., & Tatebe, H. (2019). *MIROC MIROC6 model output prepared for CMIP6 ScenarioMIP* [Dataset]. Earth System Grid Federation. https://doi.org/10.22033/ESGF/CMIP6.898

Sinclair, S. J., White, M. D., & Newell, G. R. (2010). How Useful Are Species Distribution Models for Managing Biodiversity under Future Climates? *Ecology and Society*, *15*(1). https://www.jstor.org/stable/26268111

Smith, A. B. (2024). *enmSdmX: Species Distribution Modeling and Ecological Niche Modeling* (Version 1.1.6) [Computer software]. https://cran.r-project.org/web/packages/enmSdmX/index.html

Soley-Guardia, M., Alvarado-Serrano, D. F., & Anderson, R. P. (2024). Top ten hazards to avoid when modeling species distributions: A didactic guide of assumptions, problems, and recommendations. *Ecography*, *2024*(4), e06852. https://doi.org/10.1111/ecog.06852

Stockwell, D. R. B., & Peterson, A. T. (2002). Effects of sample size on accuracy of species distribution models. *Ecological Modelling*, *148*(1), 1–13. https://doi.org/10.1016/S0304-3800(01)00388-X

Sun, Y., Sun, Y., Yao, S., Akram, M. A., Hu, W., Dong, L., Li, H., Wei, M., Gong, H., Xie, S., Aqeel, M., Ran, J., Degen, A. A., Guo, Q., & Deng, J. (2021). Impact of climate change on plant species richness across drylands in China: From past to present and into the future. *Ecological Indicators*, *132*, 108288. https://doi.org/10.1016/j.ecolind.2021.108288

Taleb, N. N. (2022). *Statistical Consequences of Fat Tails: Real World Preasymptotics, Epistemology, and Applications* (arXiv:2001.10488). arXiv. https://doi.org/10.48550/arXiv.2001.10488

Tang, Y., Rumbold, S., Ellis, R., Kelley, D., Mulcahy, J., Sellar, A., Walton, J., & Jones, C. (2019). *MOHC UKESM1.0-LL model output prepared for CMIP6 CMIP* [Dataset]. Earth System Grid Federation. https://doi.org/10.22033/ESGF/CMIP6.1569

Telwala, Y., Brook, B. W., Manish, K., & Pandit, M. K. (2013). Climate-induced elevational range shifts and increase in plant species richness in a Himalayan biodiversity epicentre. *PloS One*, *8*(2), e57103. https://doi.org/10.1371/journal.pone.0057103

Thibaud, E., Petitpierre, B., Broennimann, O., Davison, A. C., & Guisan, A. (2014). Measuring the relative effect of factors affecting species distribution model predictions. *Methods in Ecology and Evolution*, *5*(9), 947–955. https://doi.org/10.1111/2041-210X.12203

Trew, B. T., & Maclean, I. M. D. (2021). Vulnerability of global biodiversity hotspots to climate change. *Global Ecology and Biogeography*, *30*(4), 768–783. https://doi.org/10.1111/geb.13272

Udy, K., Fritsch, M., Meyer, K. M., Grass, I., Hanß, S., Hartig, F., Kneib, T., Kreft, H., Kukunda, C. B., Pe'er, G., Reininghaus, H., Tietjen, B., Tscharntke, T., van Waveren, C.-S., & Wiegand, K. (2021). Environmental heterogeneity predicts global species richness patterns better than area. *Global Ecology and Biogeography*, *30*(4), 842–851. https://doi.org/10.1111/geb.13261

Valavi, R., Elith, J., Lahoz-Monfort, J. J., & Guillera-Arroita, G. (2021). Modelling species presence-only data with random forests. *Ecography*, *44*(12), 1731–1742. https://doi.org/10.1111/ecog.05615

Valavi, R., Guillera-Arroita, G., Lahoz-Monfort, J. J., & Elith, J. (2022). Predictive performance of presence-only species distribution models: A benchmark study with reproducible code. *Ecological Monographs*, *92*(1), e01486. https://doi.org/10.1002/ecm.1486

van Proosdij, A. S. J., Sosef, M. S. M., Wieringa, J. J., & Raes, N. (2016). Minimum required number of specimen records to develop accurate species distribution models. *Ecography*, *39*(6), 542–552. https://doi.org/10.1111/ecog.01509

Volodin, E., Mortikov, E., Gritsun, A., Lykossov, V., Galin, V., Diansky, N., Gusev, A., Kostrykin, S., Iakovlev, N., Shestakova, A., & Emelina, S. (2019). *INM INM-CM5-0 model output prepared for CMIP6 ScenarioMIP* [Dataset]. Earth System Grid Federation. https://doi.org/10.22033/ESGF/CMIP6.12322

von Storch, J.-S., Putrasahan, D., Lohmann, K., Gutjahr, O., Jungclaus, J., Bittner, M., Haak, H., Wieners, K.-H., Giorgetta, M., Reick, C., Esch, M., Gayler, V., de Vrese, P., Raddatz, T., Mauritsen, T., Behrens, J., Brovkin, V., Claussen, M., Crueger, T., … Roeckner, E. (2017). *MPI-M MPIESM1.2-HR model output prepared for CMIP6 HighResMIP* [Dataset]. Earth System Grid Federation. https://doi.org/10.22033/ESGF/CMIP6.762

Warren, D. L., Glor, R. E., & Turelli, M. (2008). Environmental Niche Equivalency Versus Conservatism: Quantitative Approaches to Niche Evolution. *Evolution*, *62*(11), 2868–2883. https://doi.org/10.1111/j.1558-5646.2008.00482.x

Wickham, H., Chang, W., Henry, L., Pedersen, T. L., Takahashi, K., Wilke, C., Woo, K., Yutani, H., Dunnington, D., Brand, T. van den, Posit, & PBC. (2024). *ggplot2: Create Elegant Data Visualisations Using the Grammar of Graphics* (Version 3.5.1) [Computer software]. https://cran.r-project.org/web/packages/ggplot2/index.html

Wiens, J. J., Ackerly, D. D., Allen, A. P., Anacker, B. L., Buckley, L. B., Cornell, H. V., Damschen, E. I., Jonathan Davies, T., Grytnes, J., Harrison, S. P., Hawkins, B. A., Holt, R. D., McCain, C. M., & Stephens, P. R. (2010). Niche conservatism as an emerging principle in ecology and conservation biology. *Ecology Letters*, *13*(10), 1310–1324. https://doi.org/10.1111/j.1461-0248.2010.01515.x

Wilke, C. O. (2024). *ggridges: Ridgeline Plots in "ggplot2"* (Version 0.5.6) [Computer software]. https://cran.r-project.org/web/packages/ggridges/index.html

Wolpert, D. H., & Macready, W. G. (1997). No free lunch theorems for optimization. *IEEE Transactions on Evolutionary Computation*, *1*(1), 67–82. IEEE Transactions on Evolutionary Computation. https://doi.org/10.1109/4235.585893

Wright, M. N., Wager, S., & Probst, P. (2023). *ranger: A Fast Implementation of Random Forests* (Version 0.16.0) [Computer software]. https://cran.r-project.org/web/packages/ranger/index.html

Yates, K. L., Bouchet, P. J., Caley, M. J., Mengersen, K., Randin, C. F., Parnell, S., Fielding, A. H., Bamford, A. J., Ban, S., Barbosa, A. M., Dormann, C. F., Elith, J., Embling, C. B., Ervin, G. N., Fisher, R., Gould, S., Graf, R. F., Gregr, E. J., Halpin, P. N., … Sequeira, A. M. M. (2018). Outstanding Challenges in the Transferability of Ecological Models. *Trends in Ecology & Evolution*, *33*(10), 790–802. https://doi.org/10.1016/j.tree.2018.08.001

Zurell, D. (2020). *mecofun: Useful functions for macroecology and species distribution modelling.* Ecology & Macroecology lab, University of Potsdam. https://gitup.uni-potsdam.de/macroecology/mecofun

Zurell, D., Franklin, J., König, C., Bouchet, P. J., Dormann, C. F., Elith, J., Fandos, G., Feng, X., Guillera-Arroita, G., Guisan, A., Lahoz-Monfort, J. J., Leitão, P. J., Park, D. S., Peterson, A. T., Rapacciuolo, G., Schmatz, D. R., Schröder, B., Serra-Diaz, J. M., Thuiller, W., … Merow, C. (2020). A standard protocol for reporting species distribution models. *Ecography*, *43*(9), 1261–1277. https://doi.org/10.1111/ecog.04960

Zurell, D., Graham, C. H., Gallien, L., Thuiller, W., & Zimmermann, N. E. (2018). Long-distance migratory birds threatened by multiple independent risks from

global change. *Nature Climate Change*, *8*(11), 992–996. https://doi.org/10.1038/s41558-018-0312-9

Zurell, D., Schifferle, K., Herrando, S., Keller, V., Lehikoinen, A., Sattler, T., & Wiedenroth, L. (2024). Range and climate niche shifts in European and North American breeding birds. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *379*(1902), 20230013. https://doi.org/10.1098/rstb.2023.0013

Zurell, D., Zimmermann, N. E., & Brun, P. (2024). The niche through time: Considering phenology and demographic stages in plant distribution models. *Journal of Ecology*, *112*(9), 1926–1939. https://doi.org/10.1111/1365-2745.14361

APPENDICES

APPENDIX A: Biodiversity Distributions According to the Future Climate Scenarios.

APPENDIX B: The Measures of Uncertainty.

APPENDIX C: Bioclimate of High Biodiversity Areas.

APPENDIX D: Species Cohabitation Statistics Tables.

APPENDIX E: The Names of the Species Included in the Analyses.

APPENDIX A

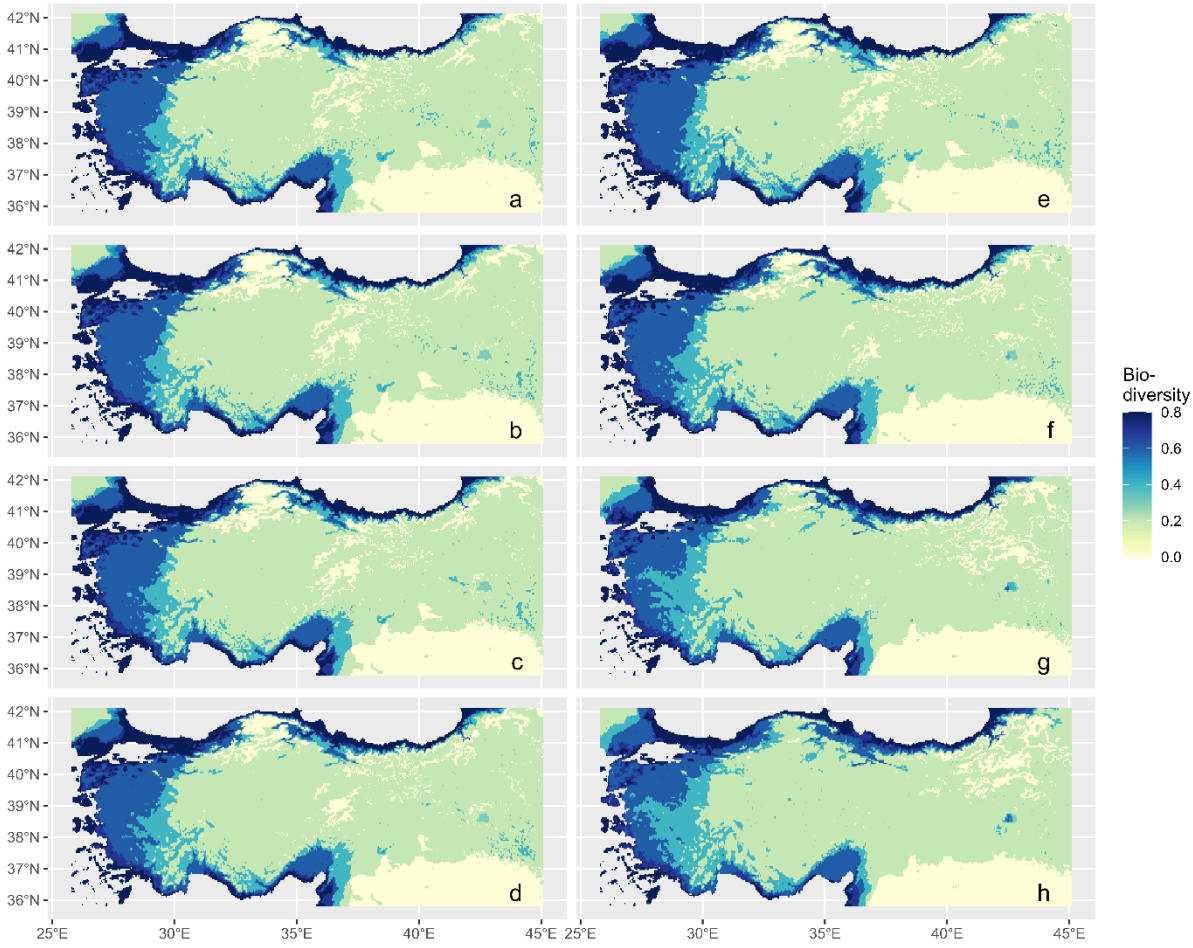

Figure A.1: Amphibian biodiversity projections of Anatolia according to SDMs based on future climate scenarios; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

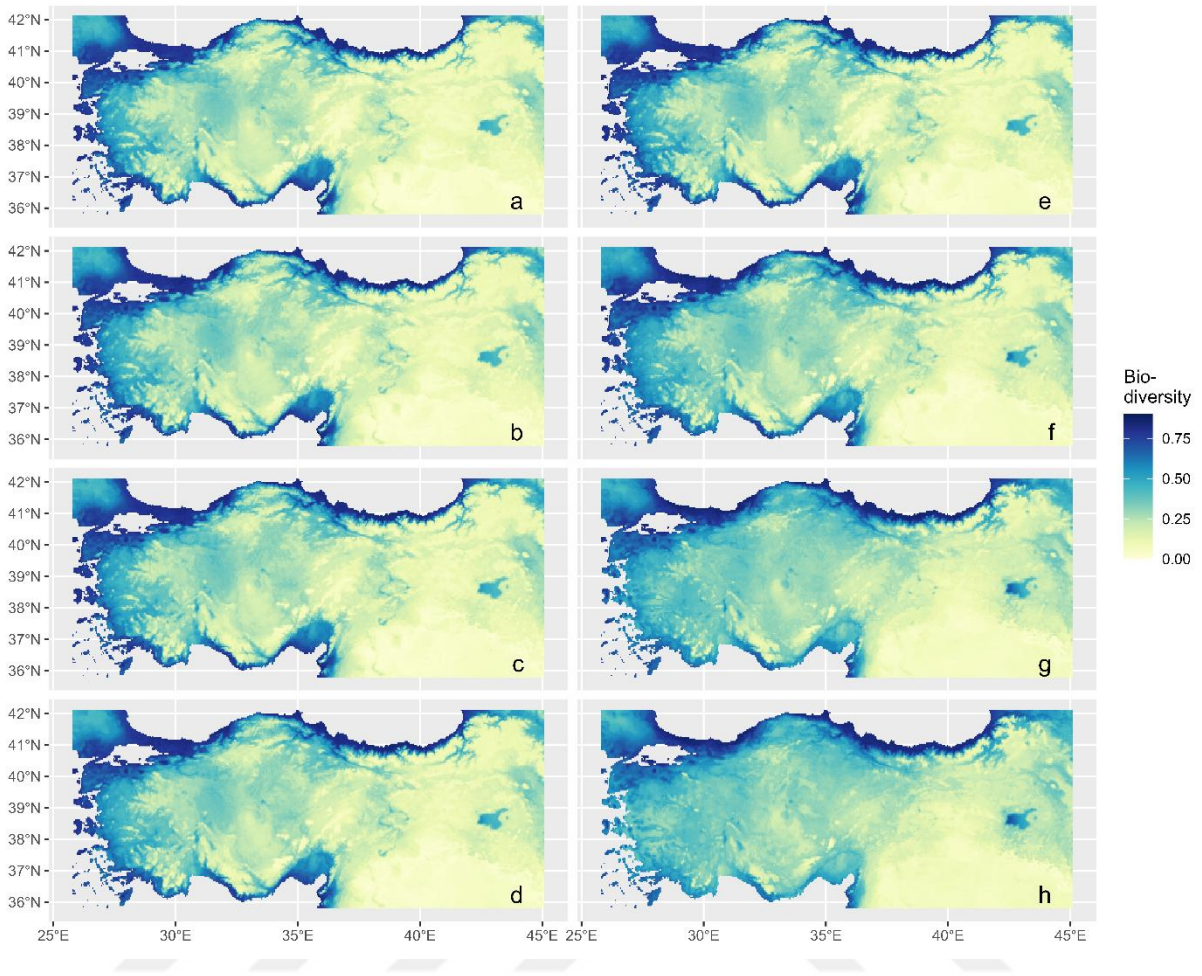

Figure A.2: Bird biodiversity projections of Anatolia according to SDMs based on future climate scenarios; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

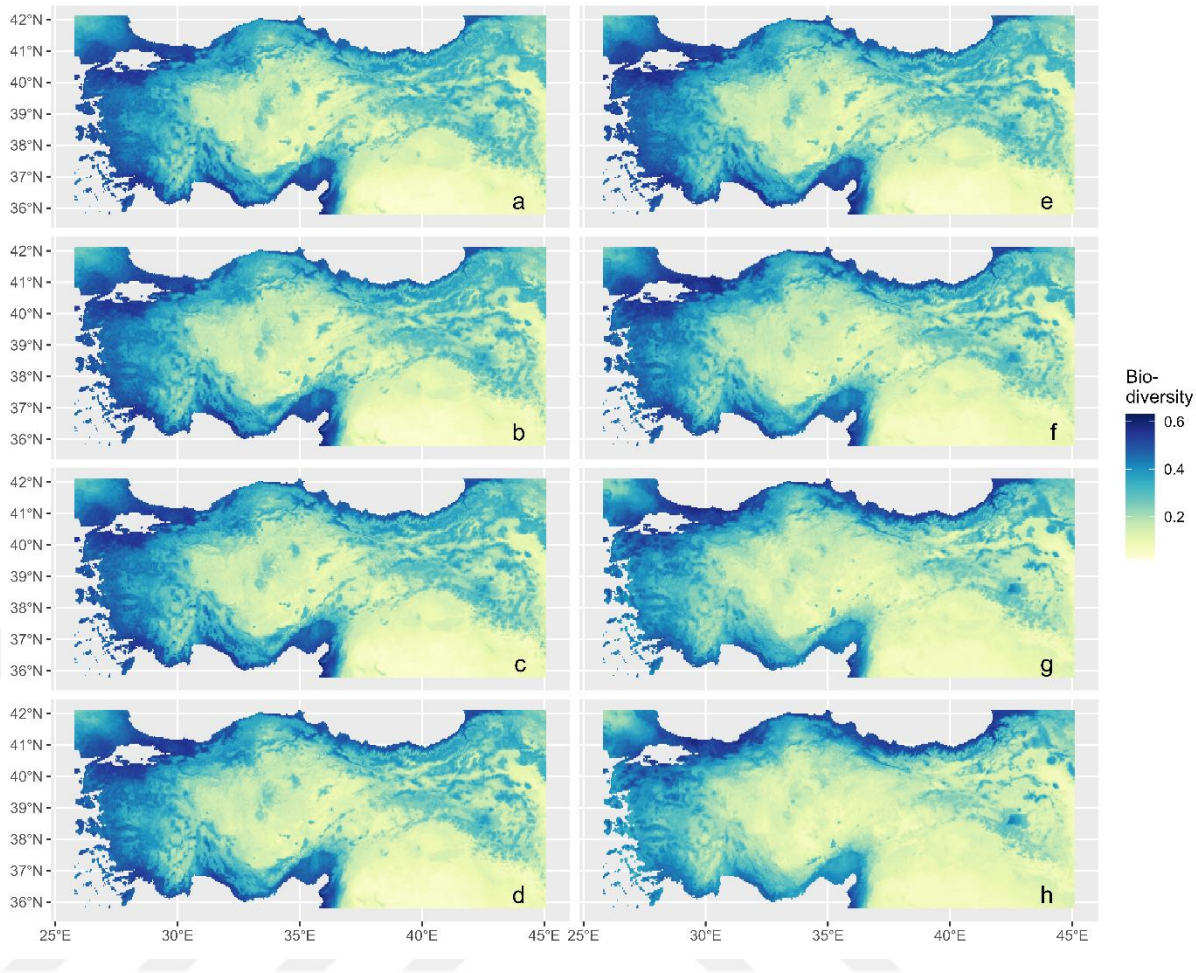

Figure A.3: Insect biodiversity projections of Anatolia according to SDMs based on future climate scenarios; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

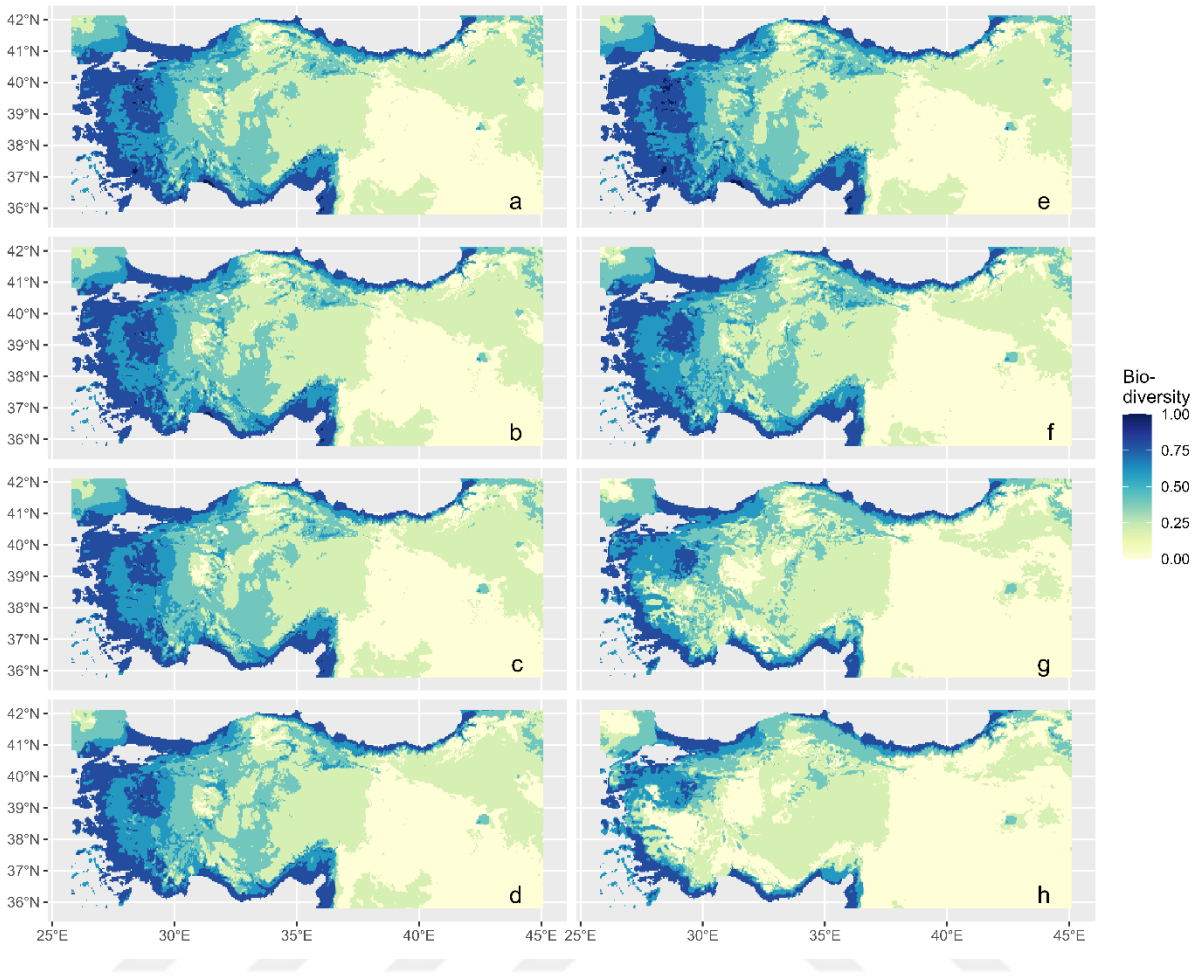

Figure A.4: Mammal biodiversity projections of Anatolia according to SDMs based on future climate scenarios; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

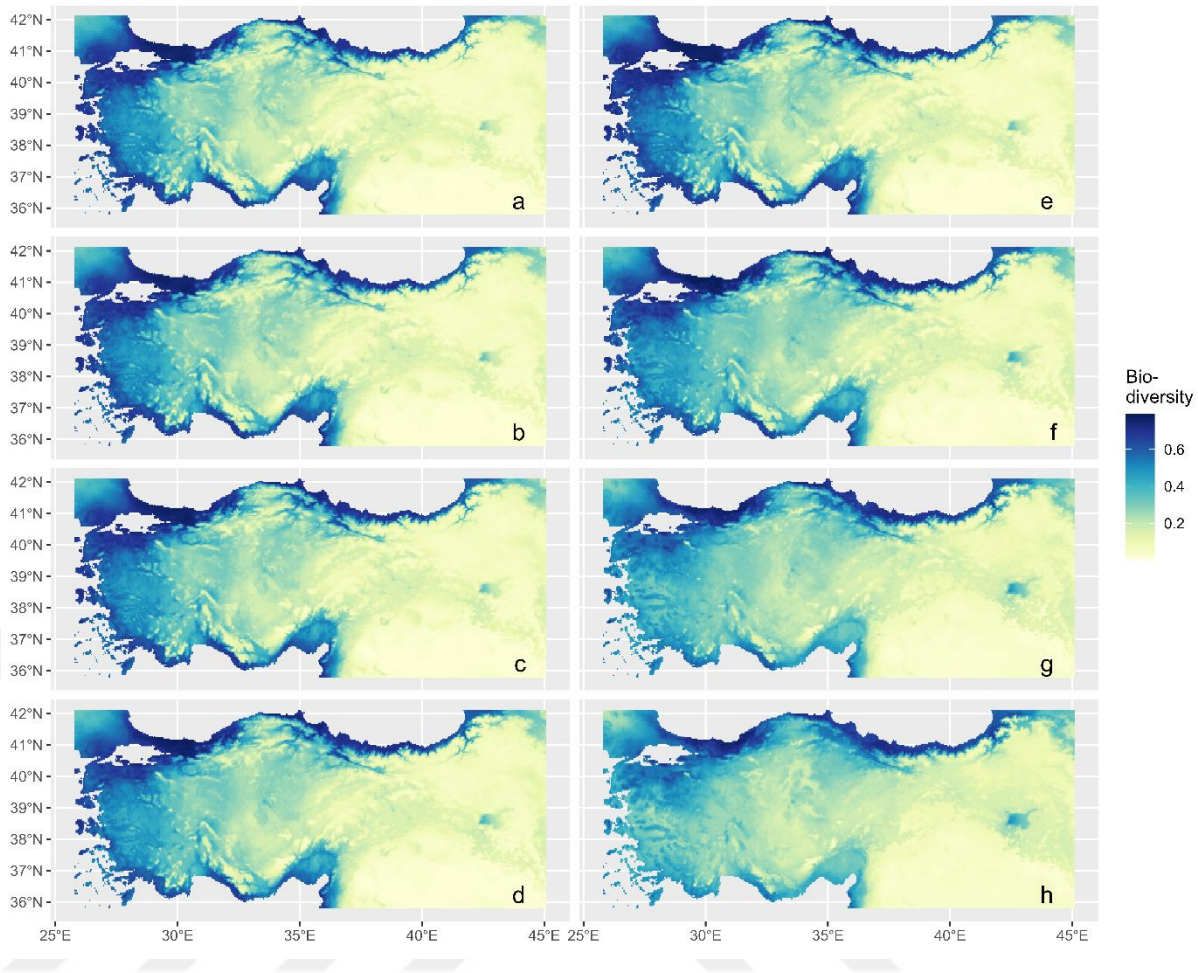

Figure A.5: Plant biodiversity projections of Anatolia according to SDMs based on future climate scenarios; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

APPENDIX B

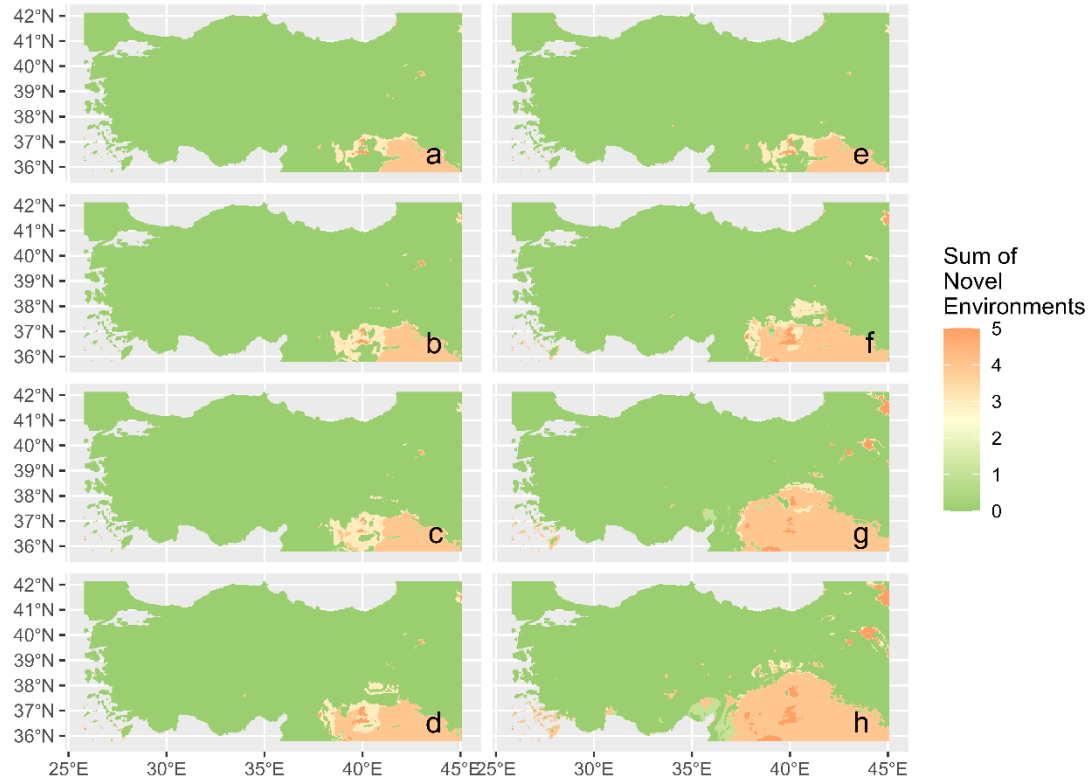

Figure B.1: Novel environments for amphibians according to MESS based on future climate scenarios; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

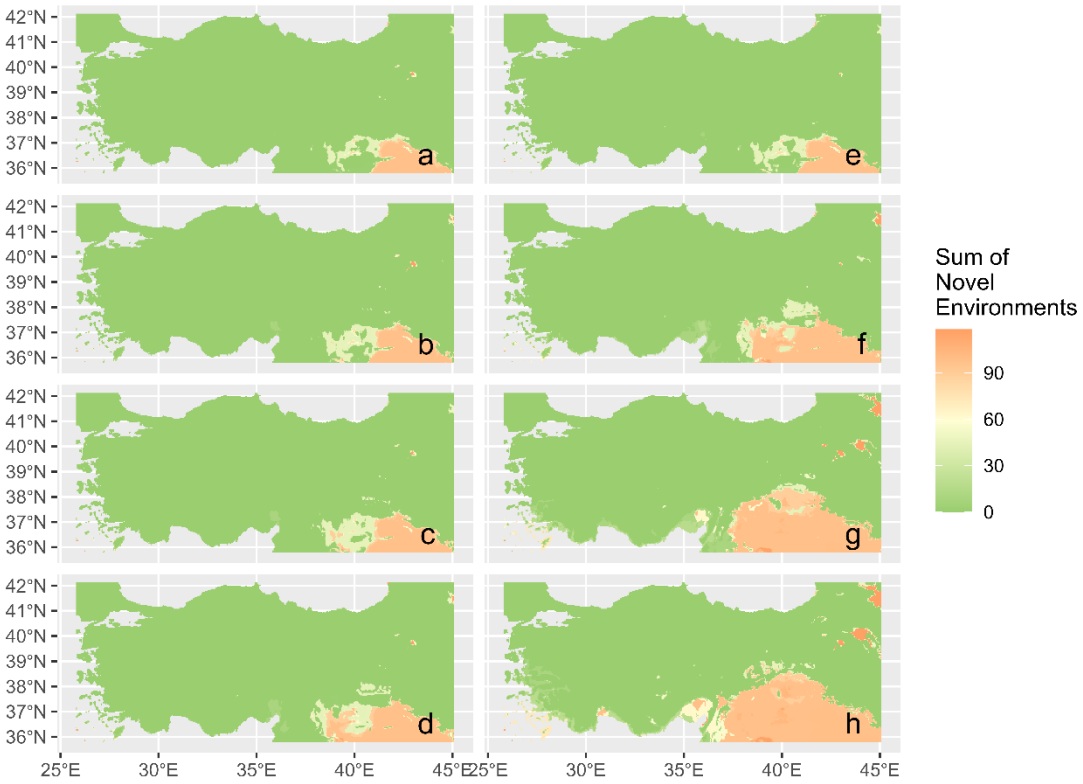

Figure B.2: Novel environments for birds according to MESS based on future climate scenarios; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

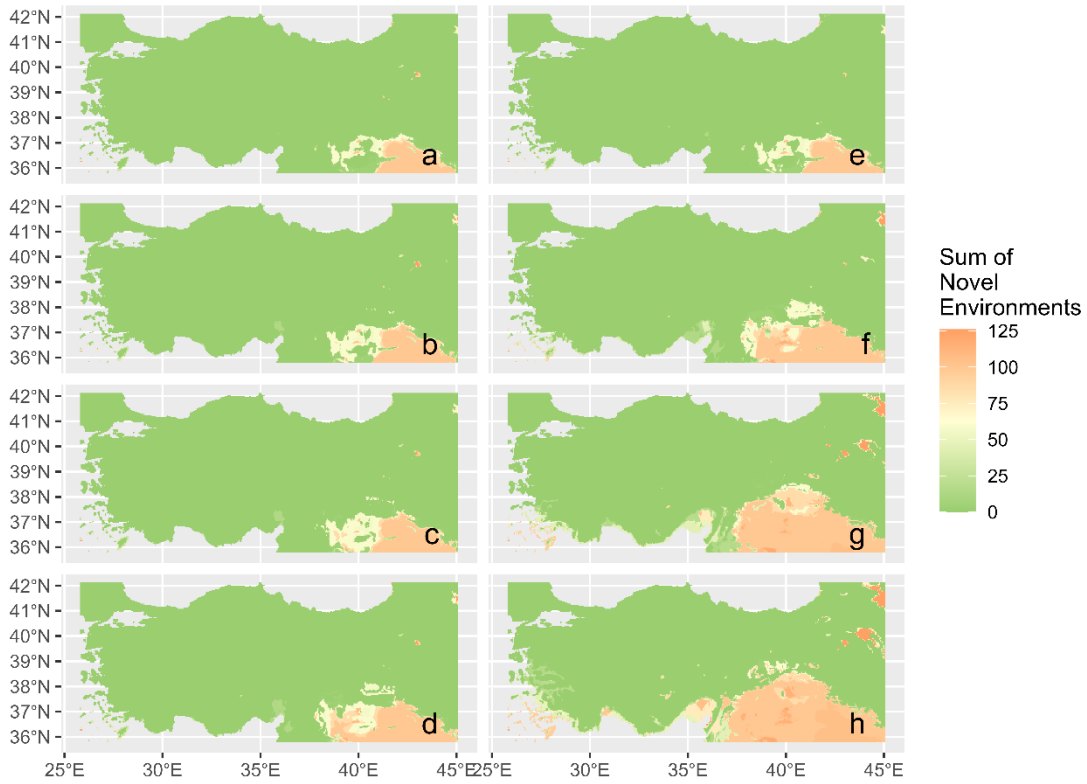

Figure B.3: Novel environments for insects according to MESS based on future climate scenarios; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

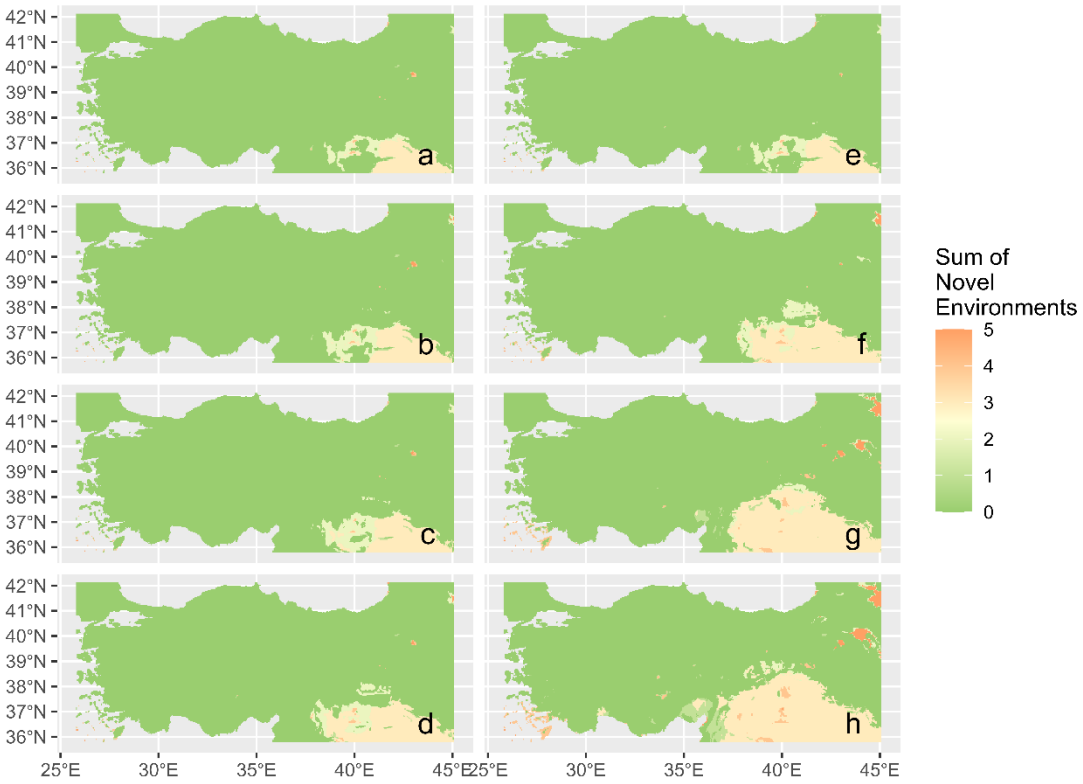

Figure B.4: Novel environments for mammals according to MESS based on future climate scenarios; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

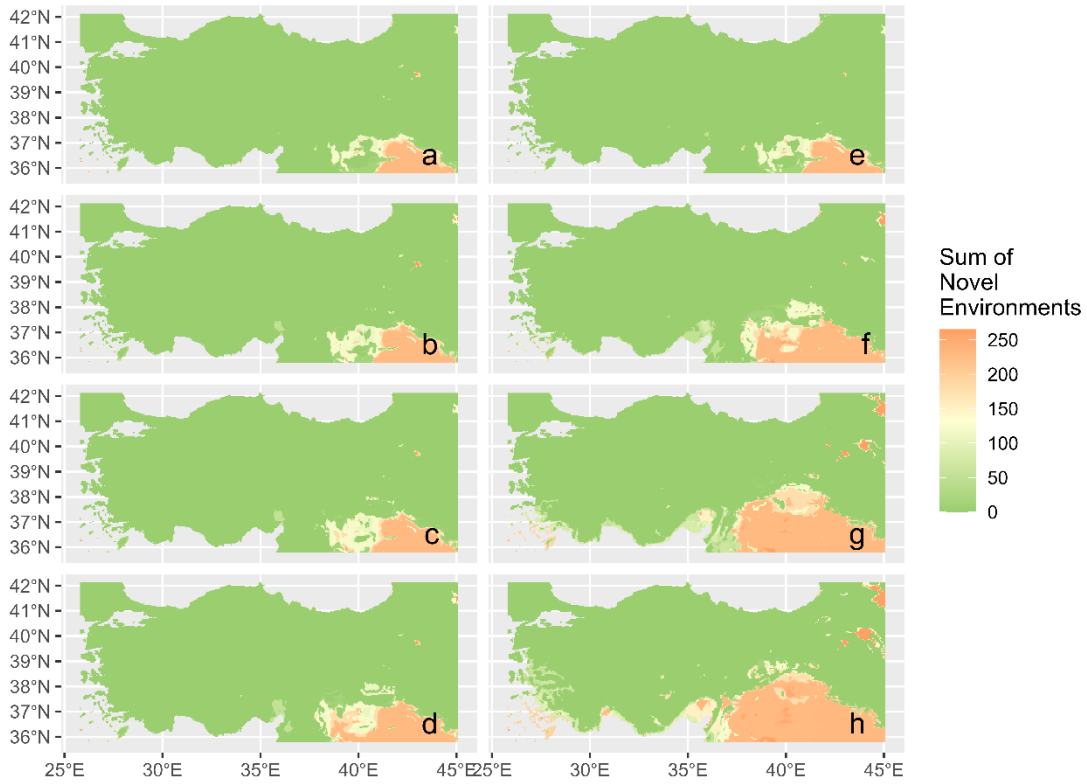

Figure B.5: Novel environments for plants according to MESS based on future climate scenarios; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period.

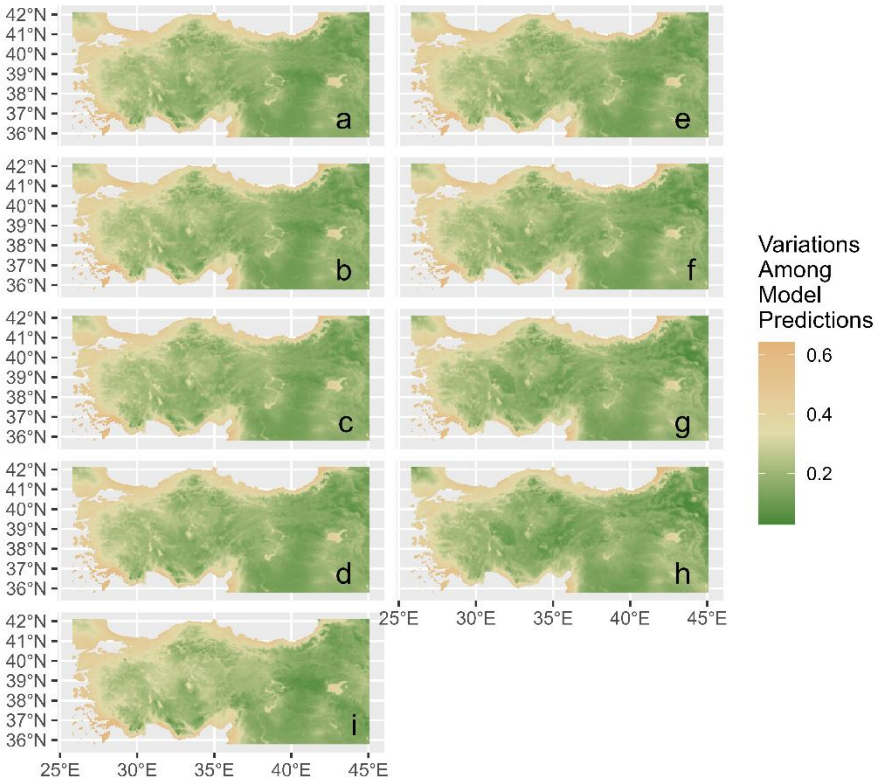

Figure B.6: Sum of standard deviations among the amphibian model predictions grouped by future climate scenarios and the baseline climate; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period, i) The historical bioclimate values for the 1970-2000 period.

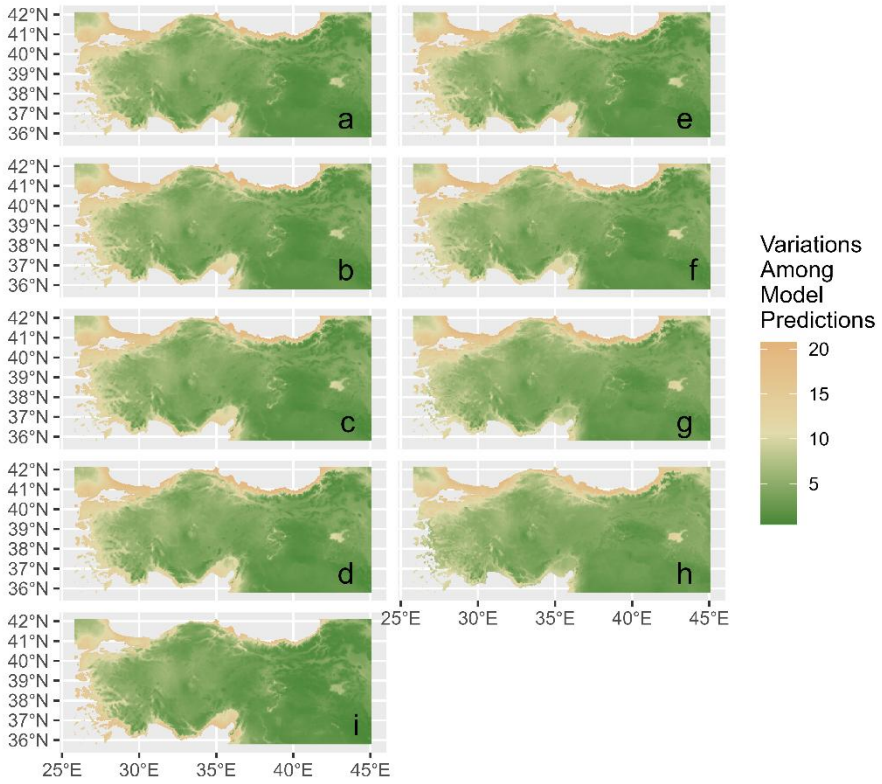

Figure B.7: Sum of standard deviations among the bird model predictions grouped by future climate scenarios and the baseline climate; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period, i) The historical bioclimate values for the 1970-2000 period.

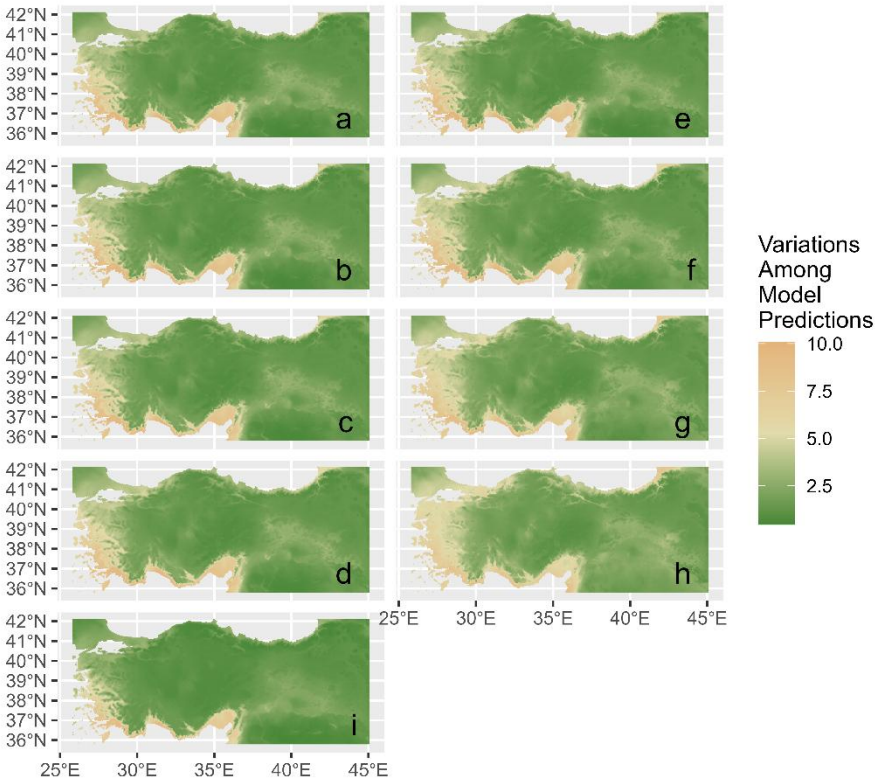

Figure B.8: Sum of standard deviations among the insect model predictions grouped by future climate scenarios and the baseline climate; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period, i) The historical bioclimate values for the 1970-2000 period.

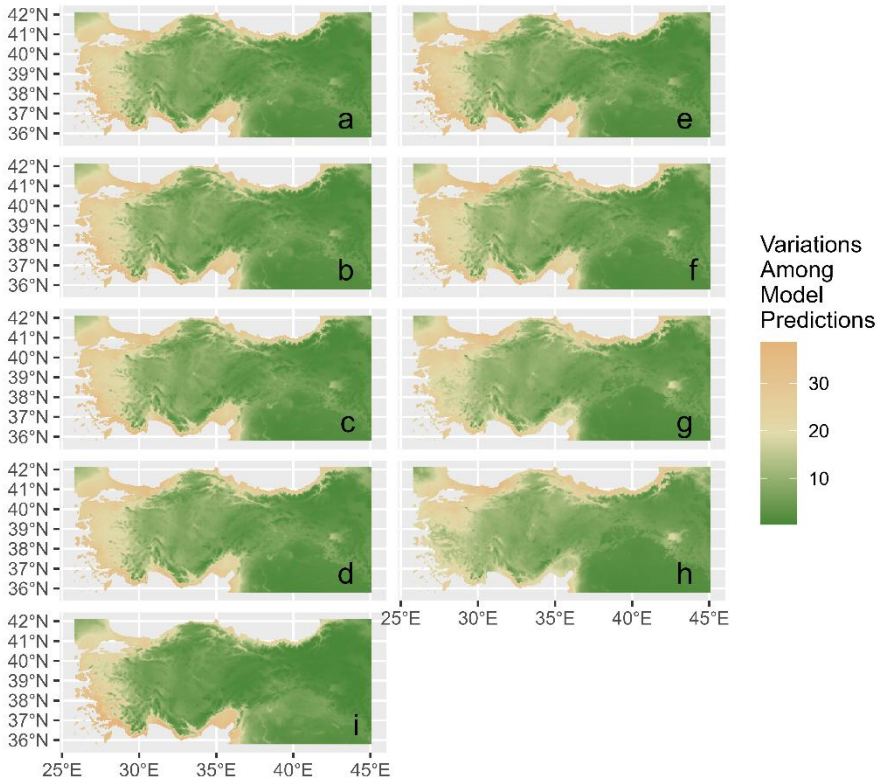

Figure B.9: Sum of standard deviations among the plant model predictions grouped by future climate scenarios and the baseline climate; a) SSP1-2.6 for 2041-2060 period, b) SSP2-4.5 for 2041-2060 period, c) SSP3-7.0 for 2041-2060 period, d) SSP5-8.5 for 2041-2060 period, e) SSP1-2.6 for 2081-2100 period, f) SSP2-4.5 for 2081-2100 period, g) SSP3-7.0 for 2081-2100 period, h) SSP5-8.5 for 2081-2100 period, i) The historical bioclimate values for the 1970-2000 period.

APPENDIX C

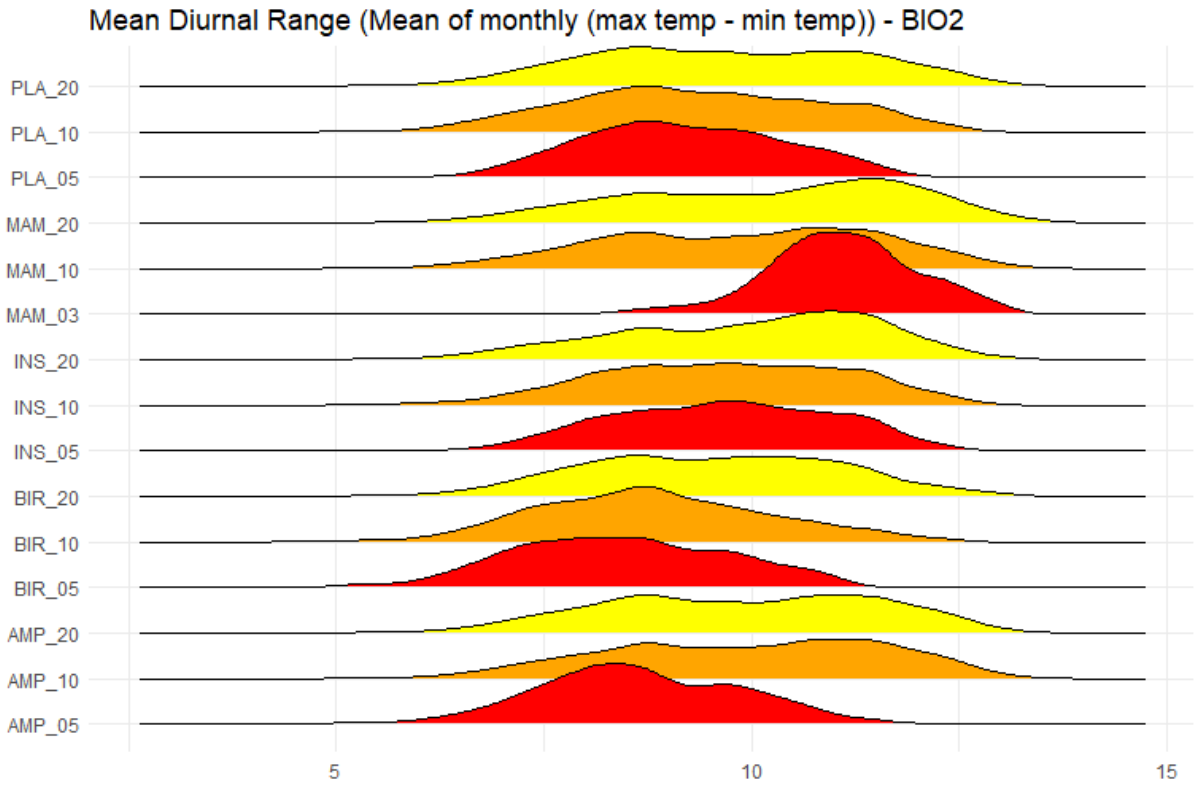

Figure C.1: Distributions of Mean Diurnal Ranges (BIO2) in °C of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

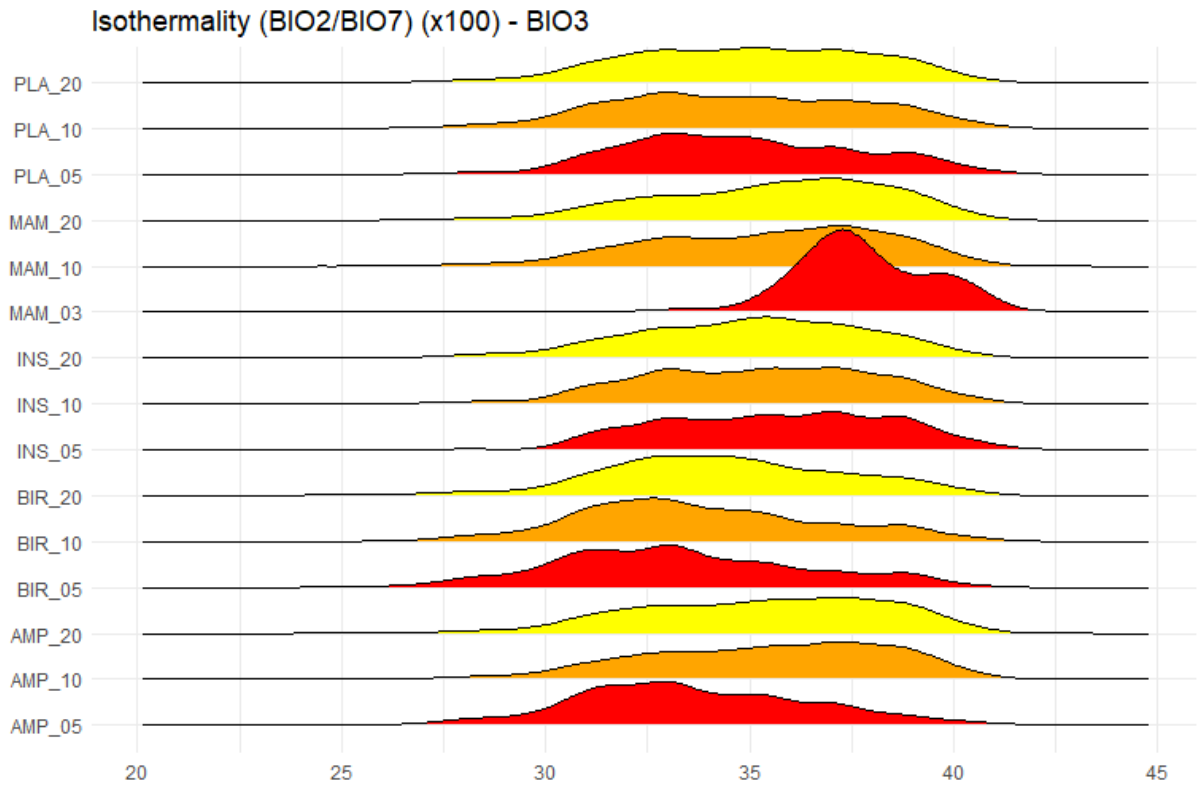

Figure C.2: Distributions of Isothermalities (BIO3) of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

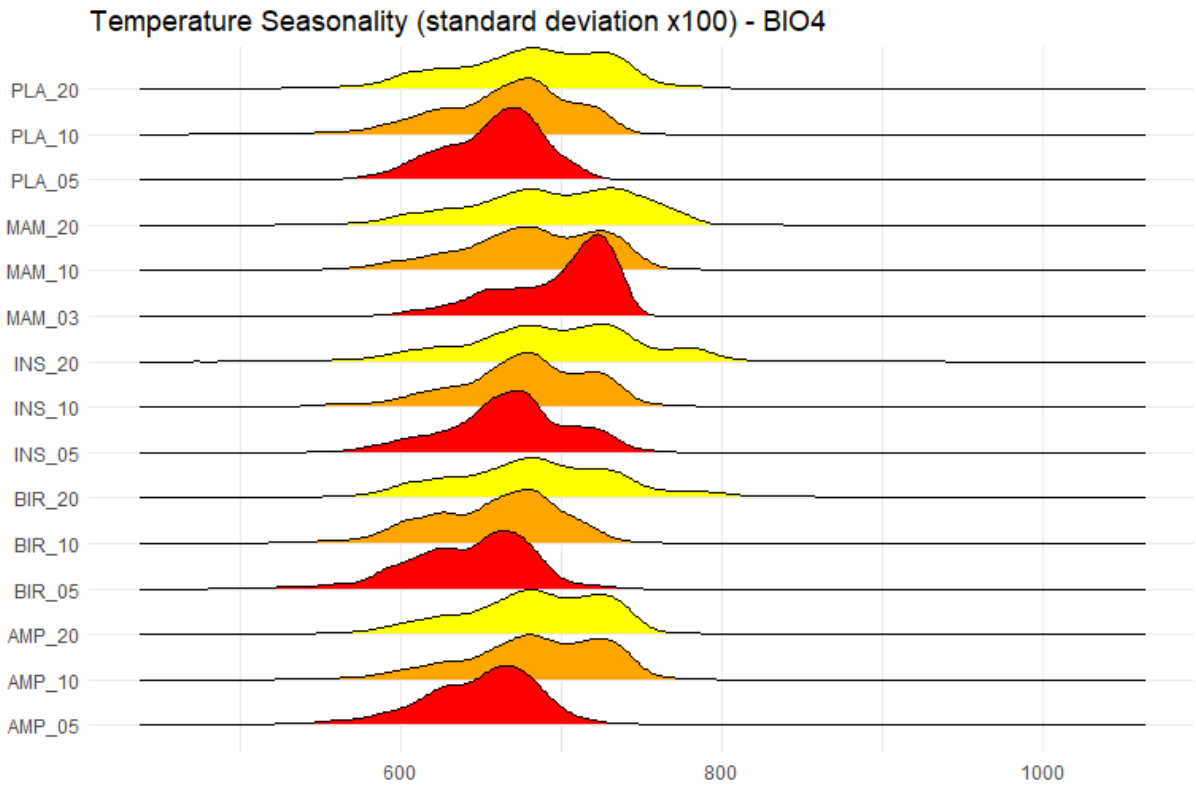

Figure C.3: Distributions of temperature seasonalities (BIO4) of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

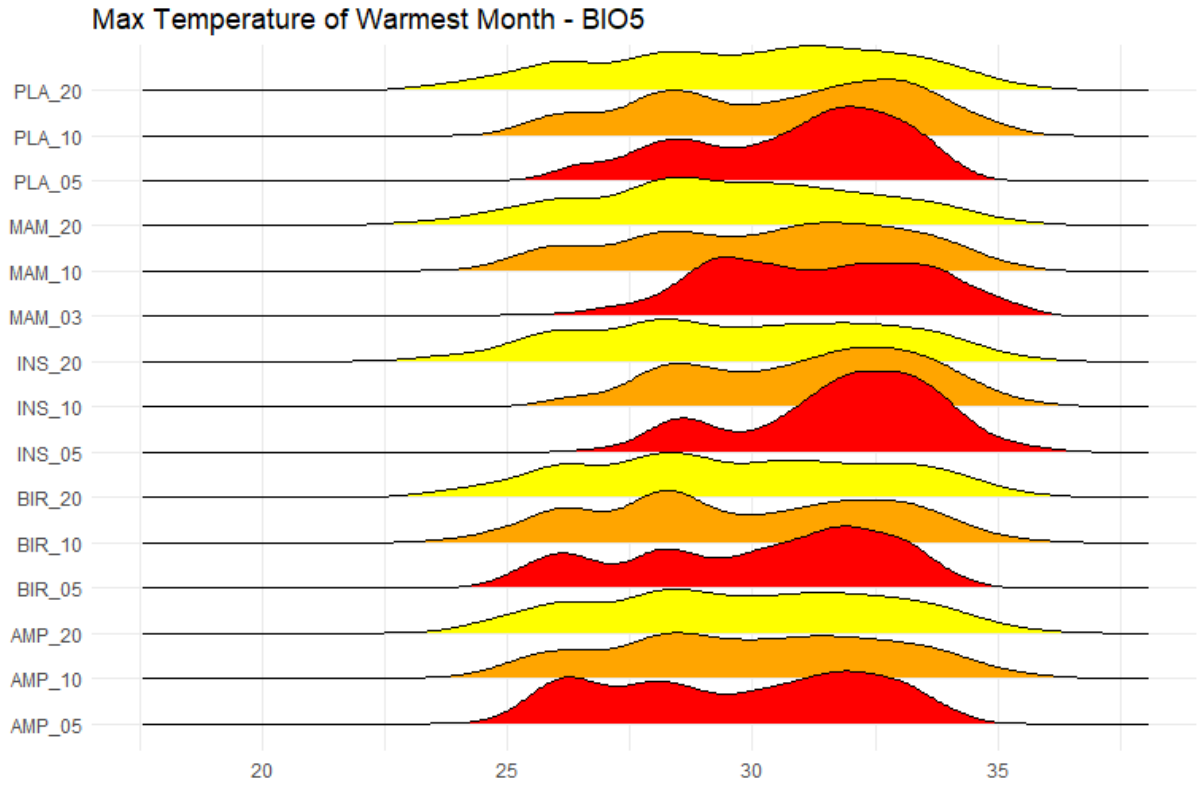

Figure C.4: Distributions of maximum temperatures of warmest months (BIO5) in °C of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

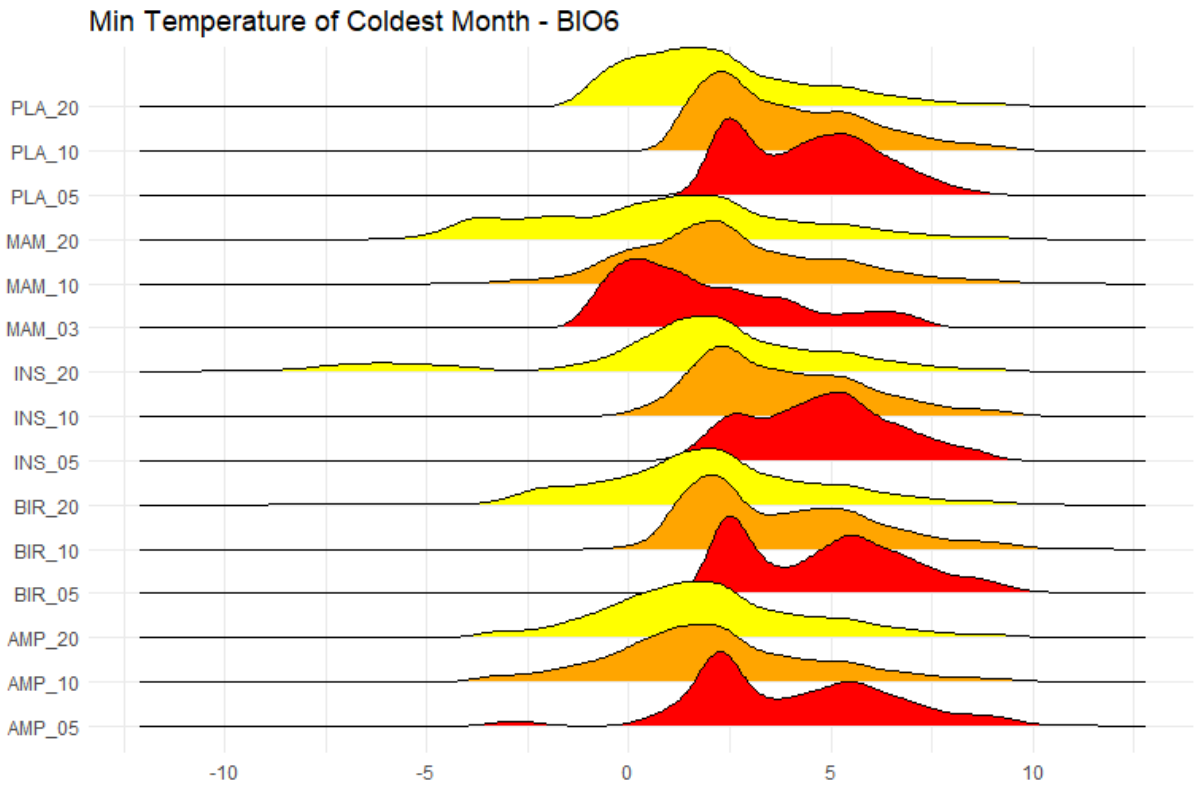

Figure C.5: Distributions of minimum temperatures of coldest months (BIO6) in °C of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

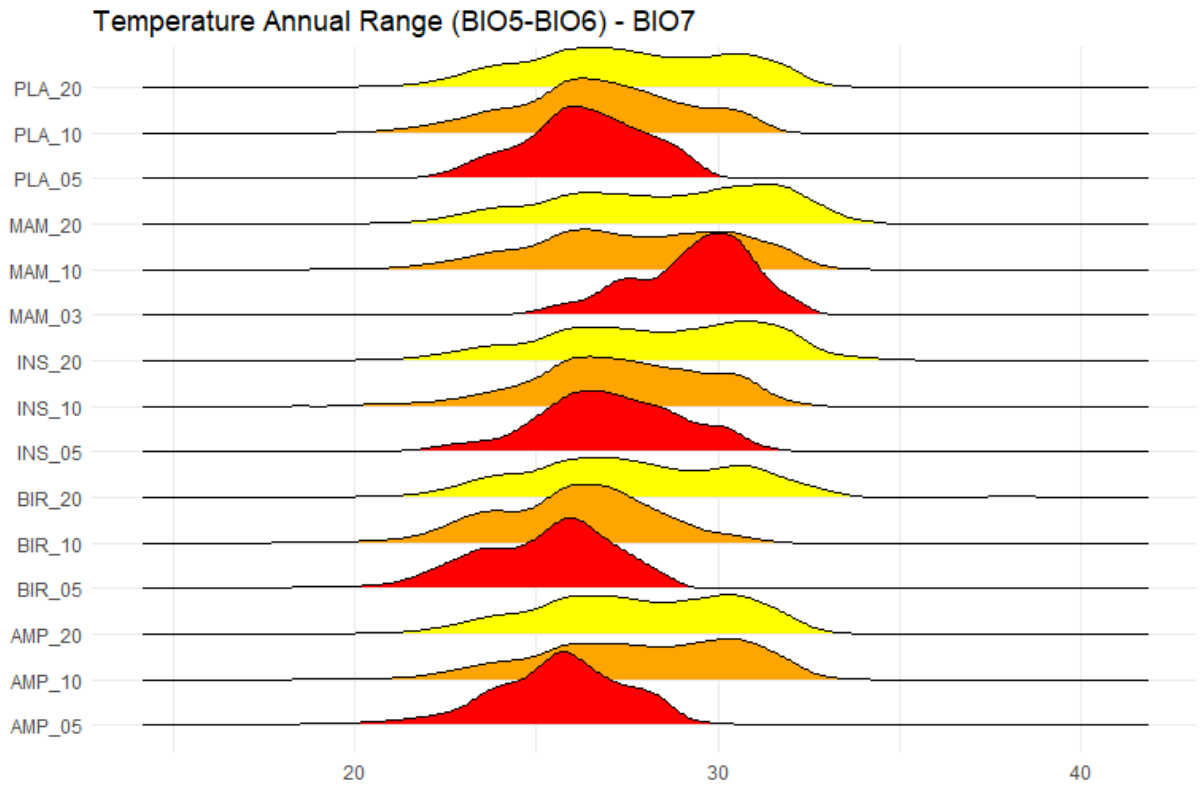

Figure C.6: Distributions of temperature annual range (BIO7) in °C of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

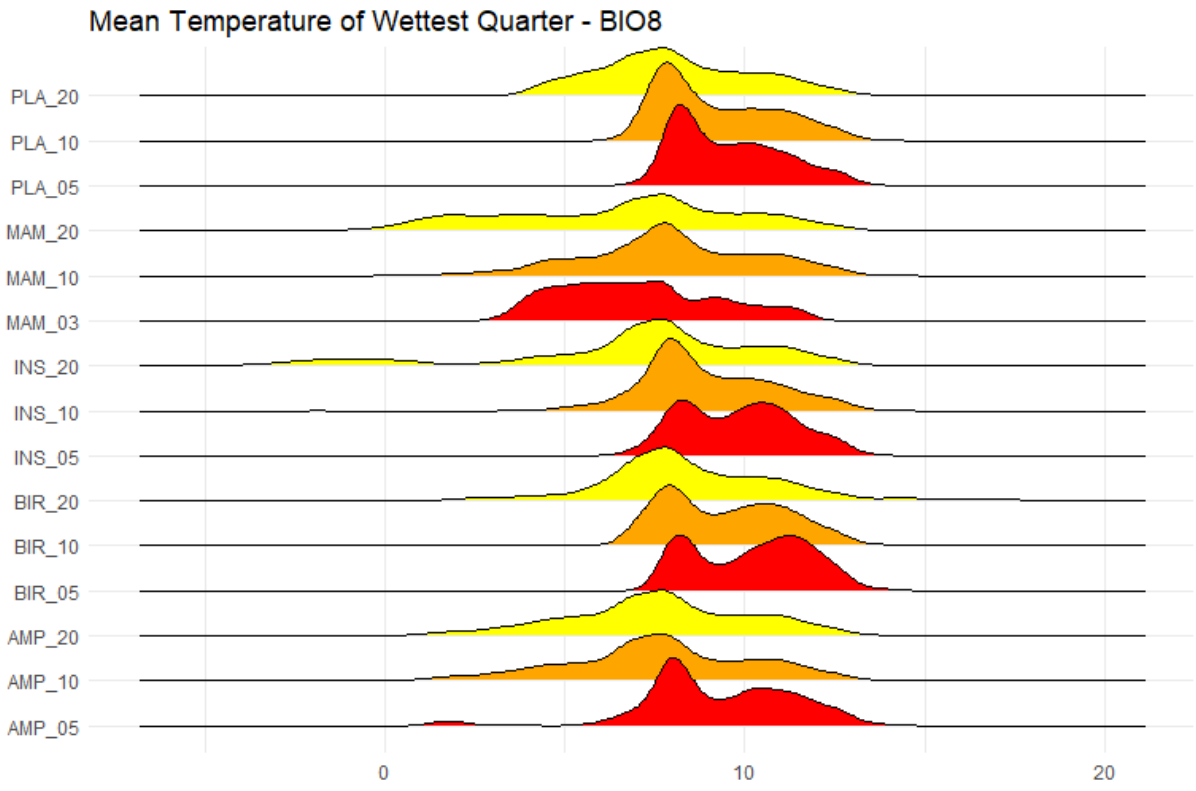

Figure C.7: Distributions of mean temperatures of wettest quarters (BIO8) in °C of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

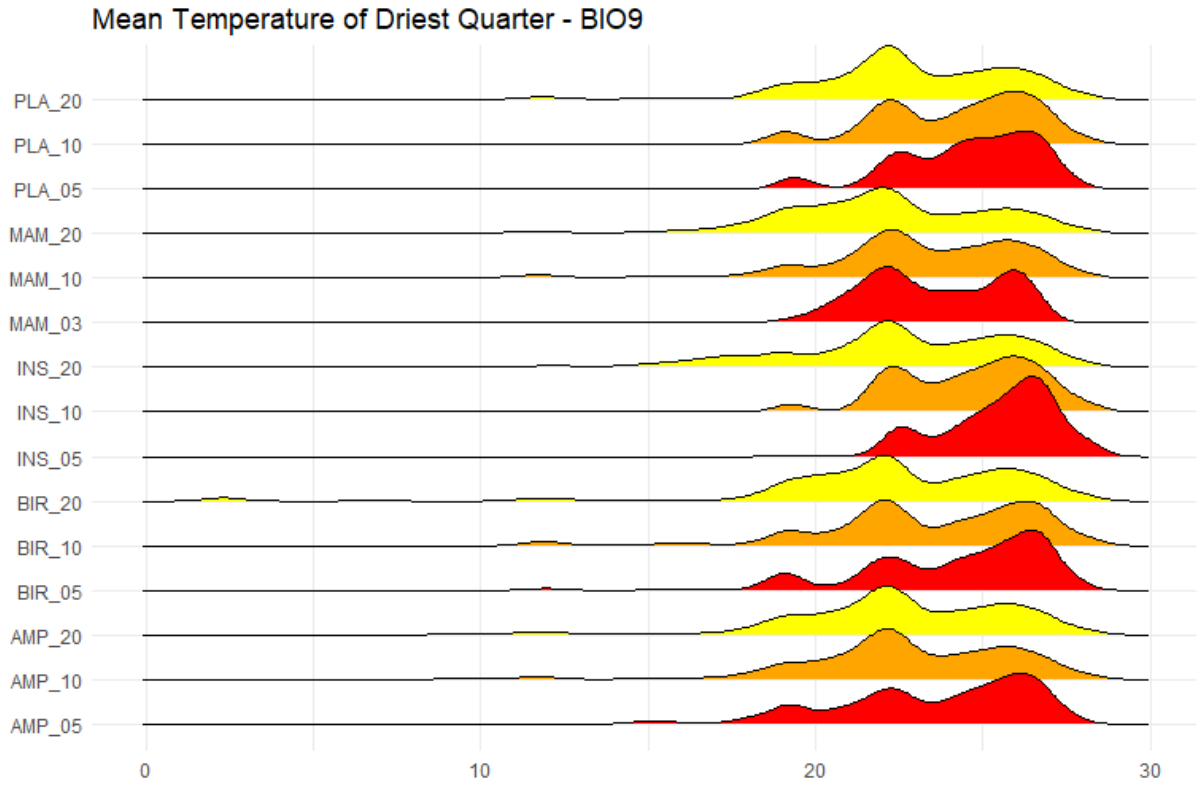

Figure C.8: Distributions of mean temperatures of driest quarters (BIO9) in °C of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

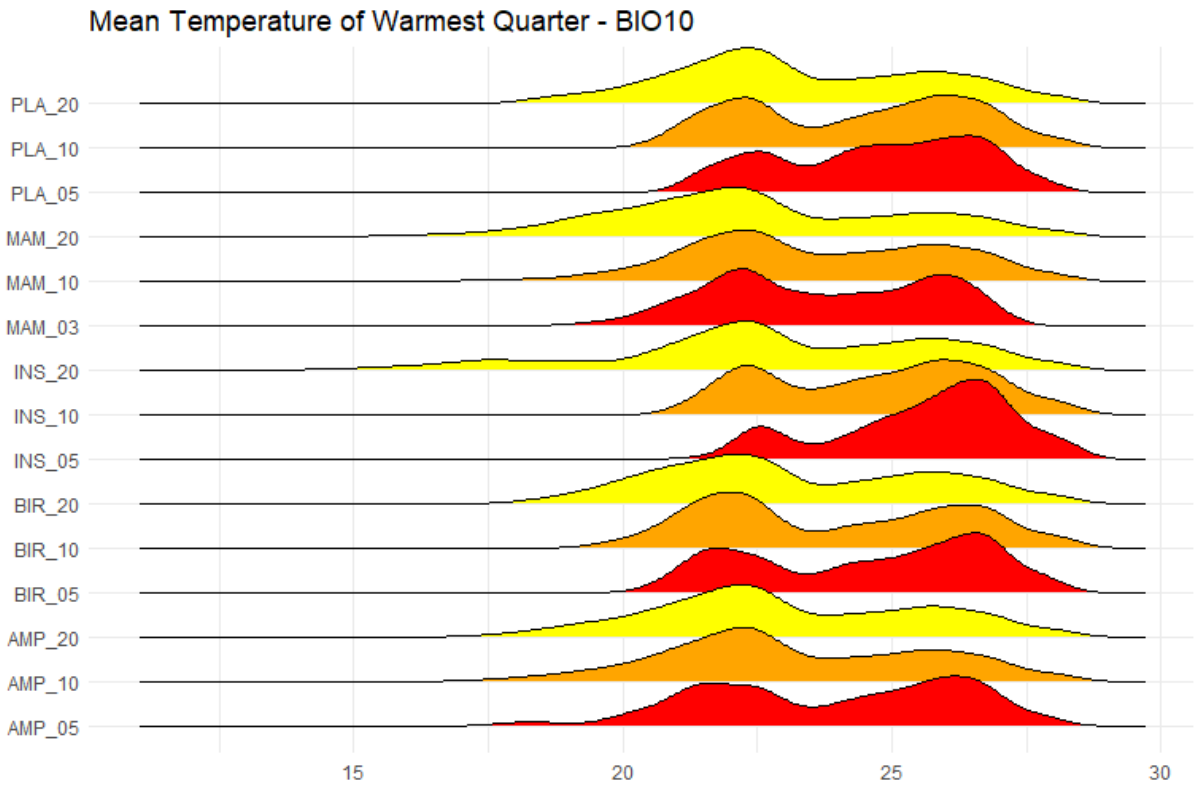

Figure C.9: Distributions of mean temperatures of warmest quarters (BIO10) in °C of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

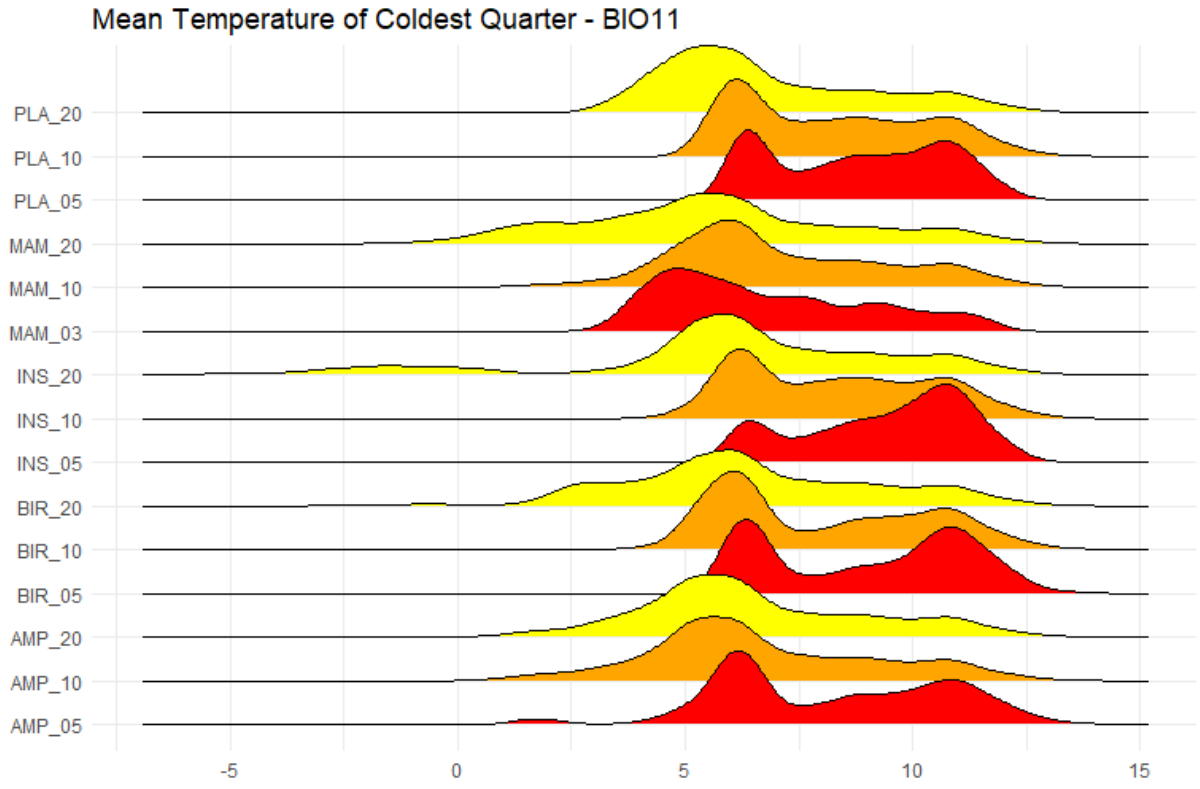

Figure C.10: Distributions of mean temperatures of coldest quarters (BIO11) in °C of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

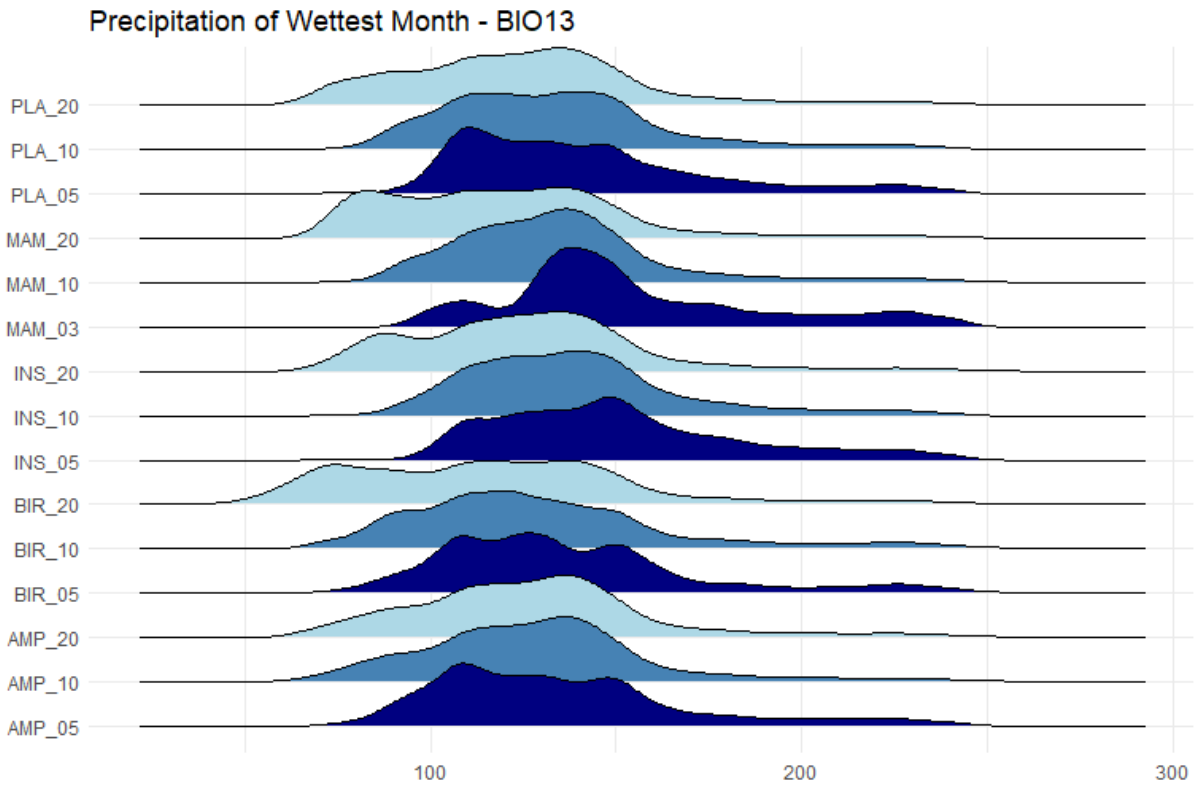

Figure C.11: Distributions of precipitation of wettest months (BIO13) in mm of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

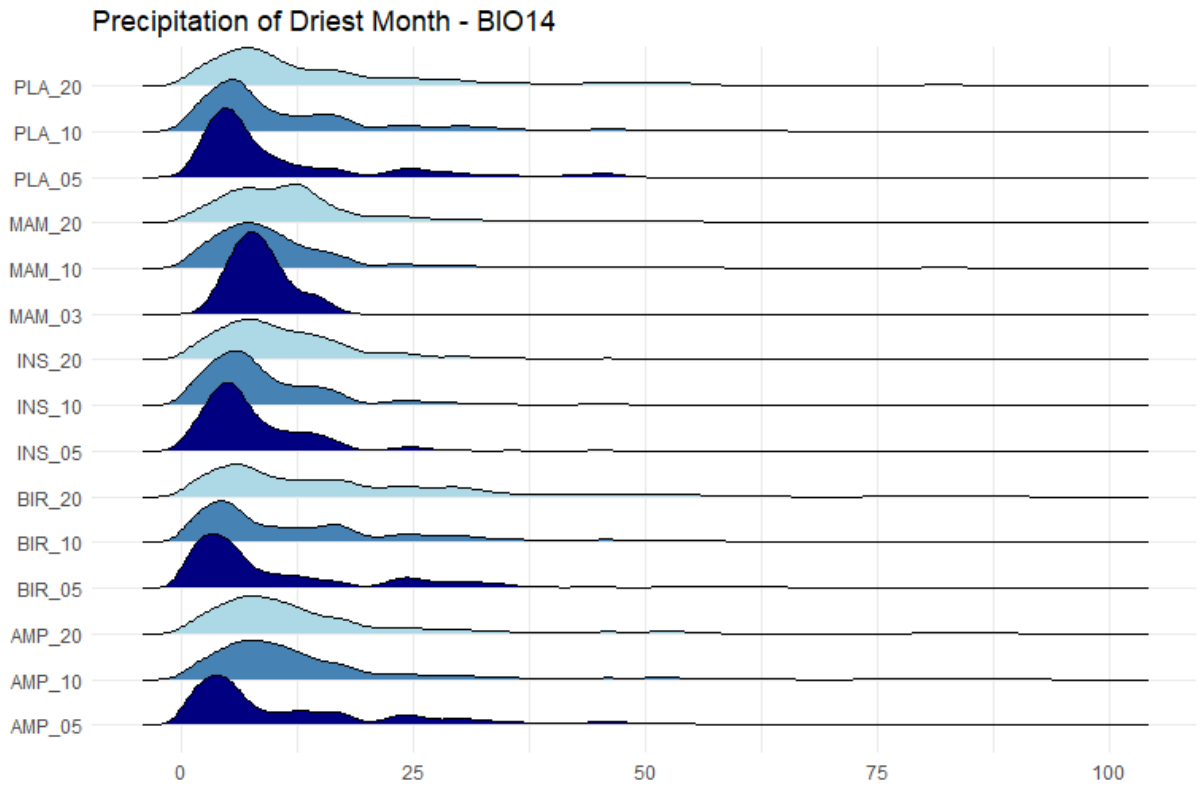

Figure C.12: Distributions of precipitation of driest months (BIO14) in mm of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

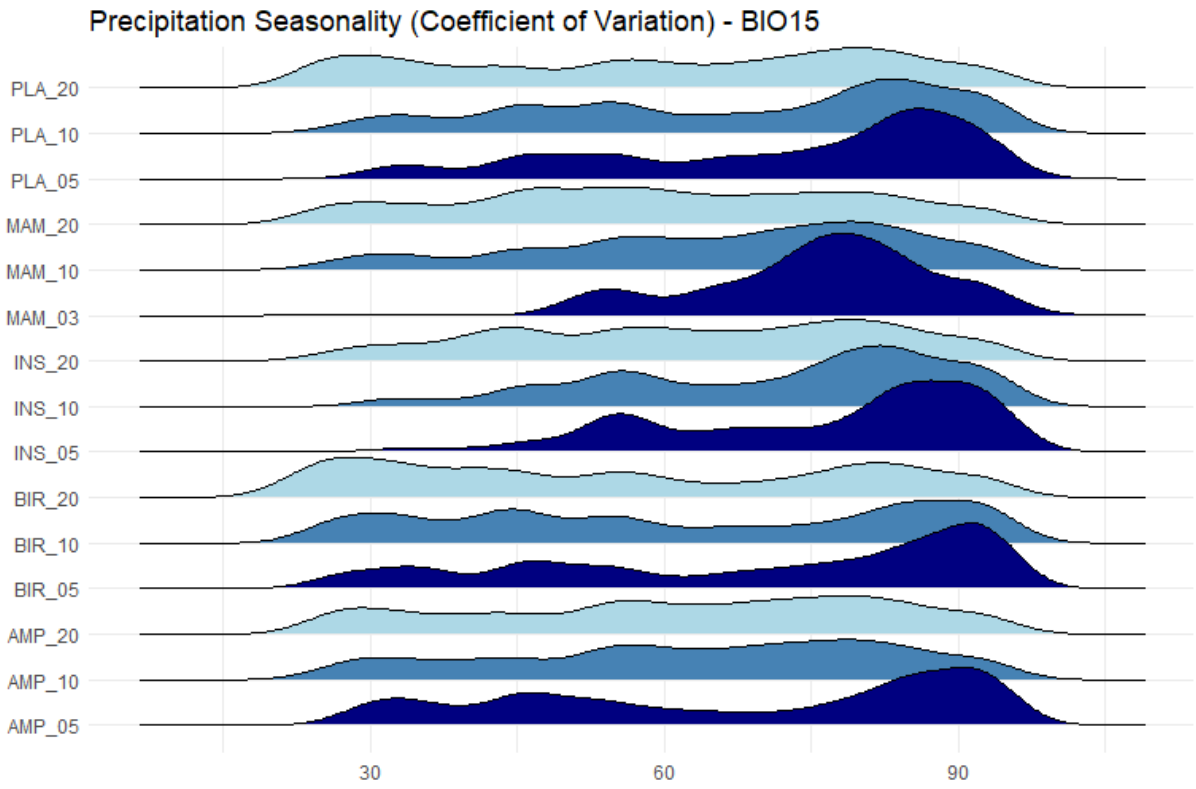

Figure C.13: Distributions of precipitation seasonalities (BIO15) of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

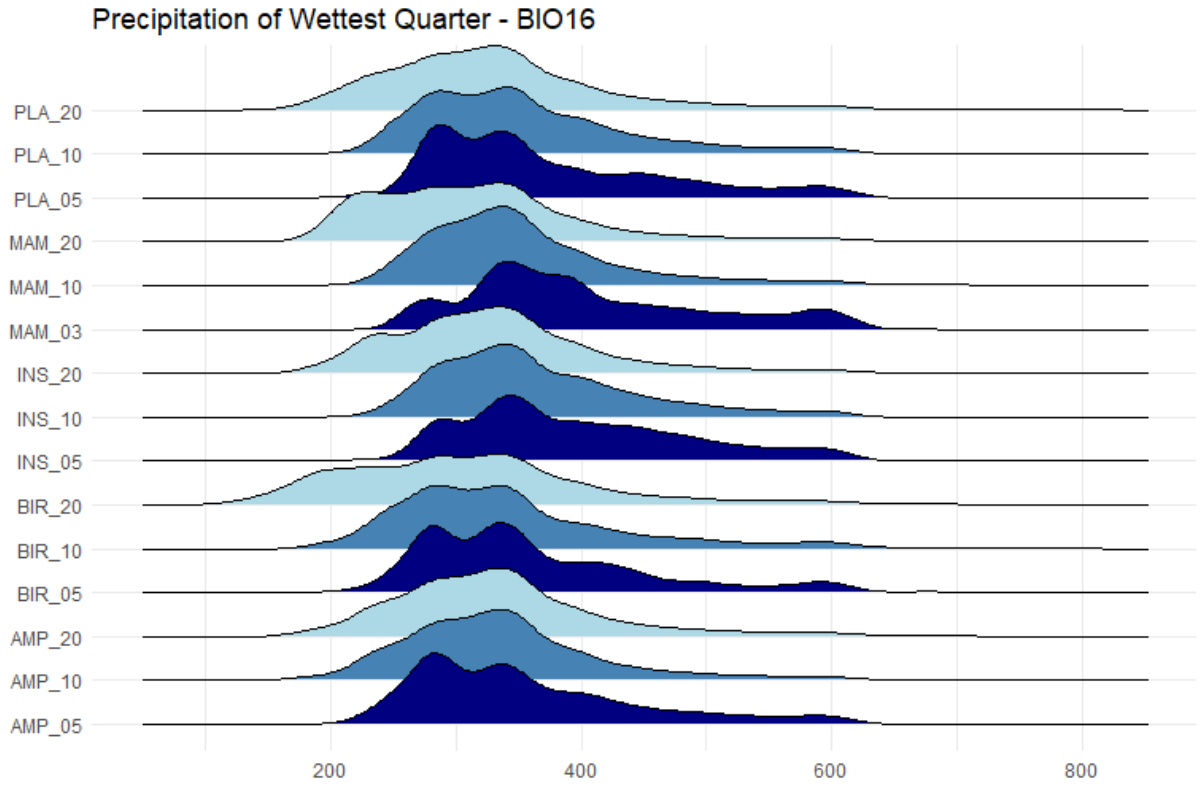

Figure C.14: Distributions of precipitation of wettest quarters (BIO16) in mm of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

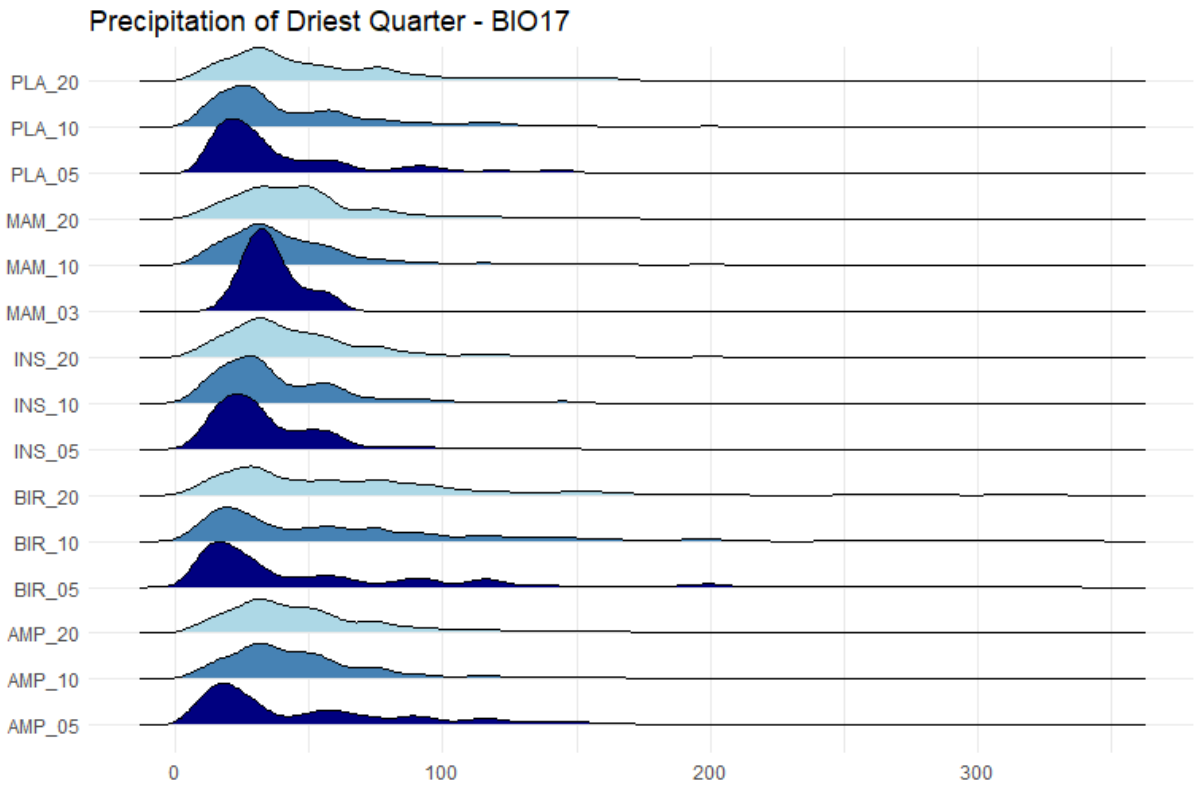

Figure C.15: Distributions of precipitation of driest quarters (BIO17) in mm of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

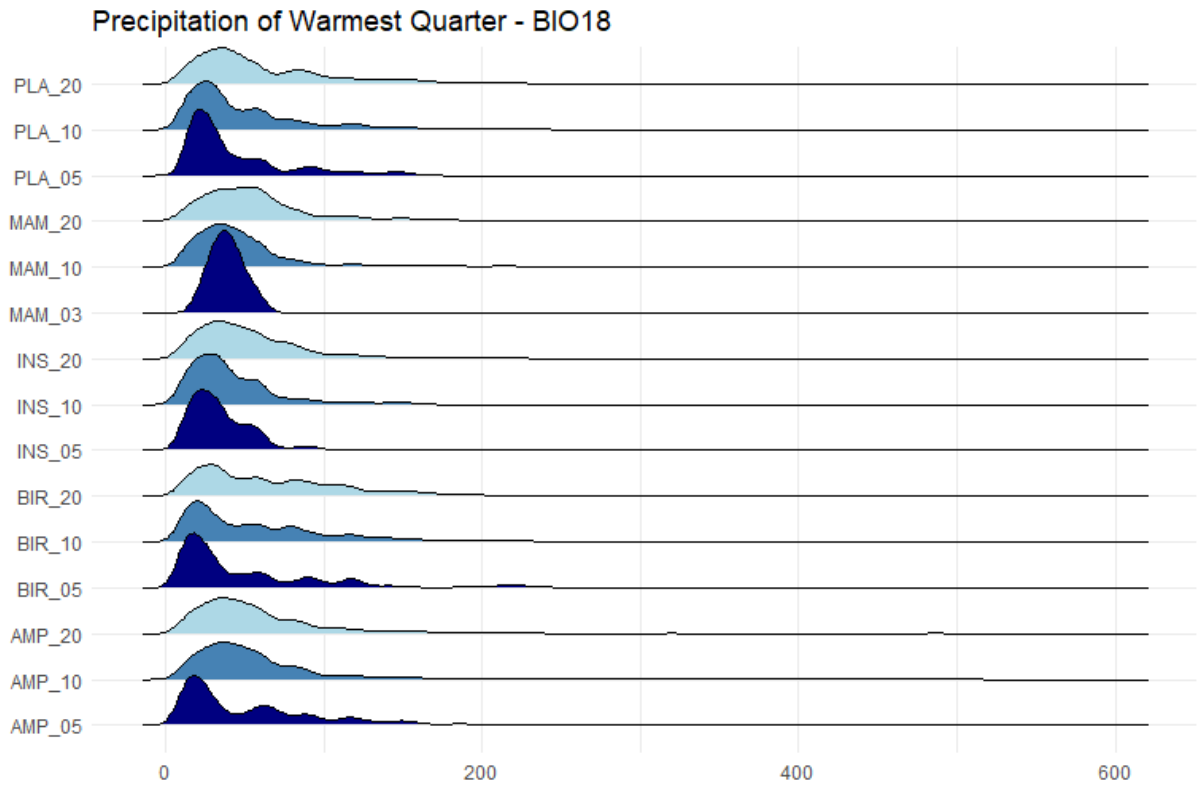

Figure C.16: Distributions of precipitation of warmest quarters (BIO18) in mm of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

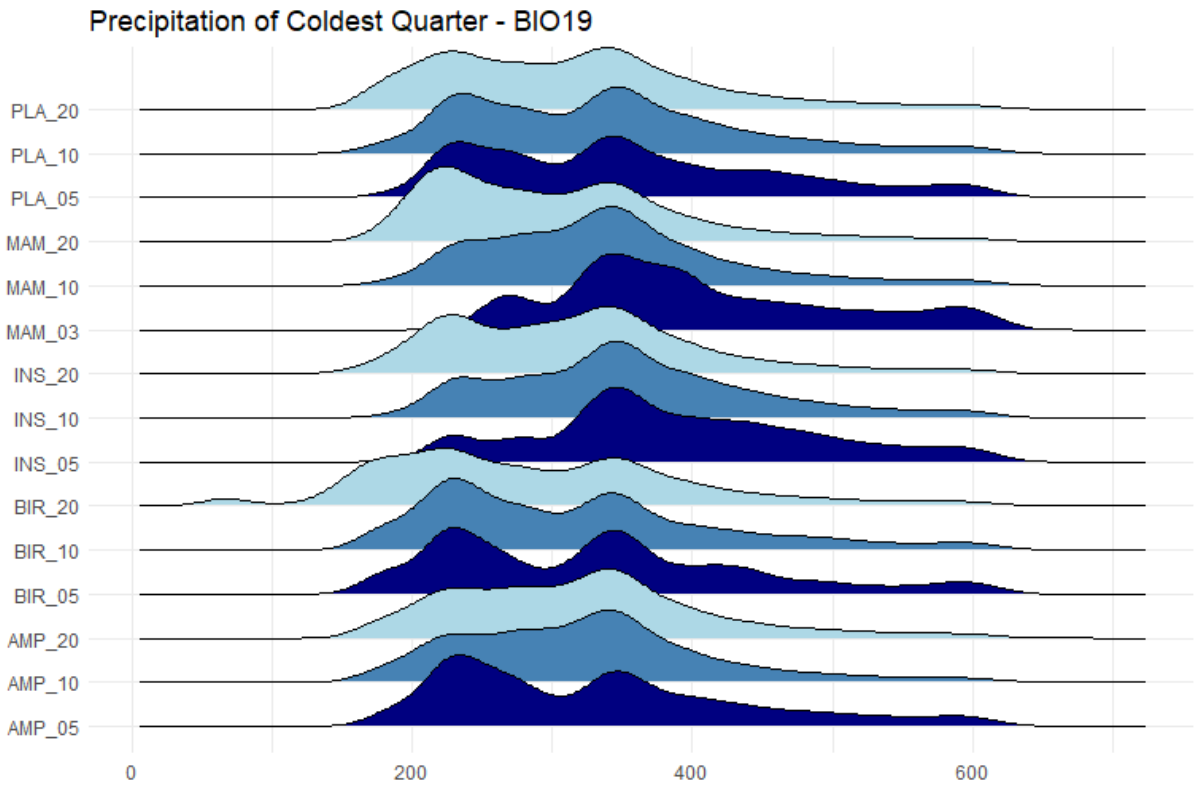

Figure C.17: Distributions of precipitation of coldest quarters (BIO19) in mm of high biodiversity areas grouped by taxa. On the left, three letters represent the taxa and the numbers following them indicate the top 20%, 10%, and 5% of the biodiversity values, corresponding to the (100 – number)th quantile.

Table C.1: Summary statistics of bioclimatic variables corresponding to the 95% quantile of amphibian biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	9.340	13.828	15.921	15.805	18.146	20.010
bio2	3.308	7.813	8.579	8.642	9.589	12.373
bio3	21.483	31.587	33.339	33.661	35.640	43.391
bio4	457.649	626.012	654.538	648.333	675.054	757.496
bio5	24.160	27.348	29.817	29.646	31.924	34.700
bio6	-3.668	2.240	3.920	4.082	5.840	11.700
bio7	15.300	24.428	25.712	25.564	26.900	30.728
bio8	1.222	7.933	9.083	9.270	10.872	14.450
bio9	11.134	21.695	24.133	23.493	25.927	28.135
bio10	17.299	21.828	24.161	23.881	25.983	28.256
bio11	1.222	6.139	8.182	8.214	10.489	14.067
bio12	480.000	651.000	711.000	745.334	811.000	2,236.000
bio13	72.000	109.000	130.000	135.441	151.000	272.000
bio14	0.000	4.000	7.000	13.976	22.000	93.000
bio15	25.425	46.502	72.462	67.000	87.390	99.976
bio16	200.000	286.000	337.000	357.757	405.000	783.000
bio17	4.000	19.000	33.000	53.192	77.000	341.000
bio18	4.000	20.000	36.000	56.108	78.000	486.000
bio19	163.000	243.000	325.000	333.929	397.000	663.000

Table C.2: Summary statistics of bioclimatic variables corresponding to the 90% quantile of amphibian biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	7.774	13.212	14.084	14.762	16.610	20.010
bio2	3.308	8.640	10.019	9.902	11.262	13.866
bio3	21.483	33.129	35.655	35.367	37.754	43.391
bio4	457.649	655.813	686.051	682.497	718.404	810.591
bio5	22.532	27.878	30.002	29.968	32.179	36.828
bio6	-4.440	0.492	1.911	2.149	3.655	11.700
bio7	15.300	25.859	27.956	27.819	30.100	34.500
bio8	-0.305	6.179	7.643	7.656	9.465	14.450
bio9	7.052	21.166	22.619	22.740	25.239	28.629
bio10	15.894	21.516	22.776	23.230	25.334	28.629
bio11	-0.305	5.041	6.165	6.676	8.442	14.067
bio12	478.000	644.000	699.000	737.316	769.000	2,292.000
bio13	60.000	109.000	128.000	129.478	144.000	278.000
bio14	0.000	6.000	10.000	14.961	17.000	100.000
bio15	18.993	48.016	65.092	63.009	79.024	99.976
bio16	159.000	283.000	329.000	340.300	375.000	813.000
bio17	4.000	29.000	44.000	57.205	66.000	348.000
bio18	4.000	31.000	47.000	62.750	70.000	508.000
bio19	158.000	258.000	322.000	324.908	370.000	677.000

Table C.3: Summary statistics of bioclimatic variables corresponding to the 80% quantile of amphibian biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	6.617	13.064	14.000	14.643	16.509	20.010
bio2	3.308	8.576	9.890	9.844	11.212	13.866
bio3	21.483	33.005	35.535	35.277	37.637	43.391
bio4	457.649	653.343	684.951	681.127	716.830	1,006.276
bio5	20.304	27.612	29.772	29.782	32.066	36.828
bio6	-8.820	0.348	1.800	2.054	3.540	11.700
bio7	15.300	25.772	27.780	27.728	30.028	40.696
bio8	-0.305	6.086	7.633	7.651	9.457	20.117
bio9	7.052	20.858	22.481	22.550	25.121	28.629
bio10	14.433	21.342	22.660	23.089	25.231	28.629
bio11	-2.307	4.924	6.082	6.568	8.249	14.067
bio12	323.000	642.000	698.000	741.503	771.000	2,292.00
bio13	56.000	107.000	127.000	128.373	144.000	278.000
bio14	0.000	7.000	11.000	16.072	18.000	100.000
bio15	18.993	44.970	63.494	61.515	78.544	99.976
bio16	138.000	280.000	327.000	337.706	373.000	813.000
bio17	4.000	29.000	45.000	60.710	73.000	348.000
bio18	4.000	31.000	49.000	67.019	77.000	605.000
bio19	59.000	251.000	319.000	321.739	368.000	677.000

Table C.4: Summary statistics of bioclimatic variables corresponding to the 95% quantile of avian biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	12.668	14.159	16.847	16.513	18.568	20.010
bio2	3.383	7.464	8.399	8.419	9.402	11.381
bio3	21.970	31.092	33.039	33.304	35.410	41.359
bio4	457.733	618.216	649.111	642.732	670.396	746.500
bio5	23.700	28.005	30.547	30.037	32.133	34.700
bio6	1.600	2.800	4.986	4.886	6.371	11.700
bio7	15.400	23.800	25.500	25.152	26.540	28.920
bio8	7.177	8.549	10.383	10.198	11.491	20.117
bio9	11.289	22.367	24.869	24.116	26.335	28.283
bio10	19.995	22.419	24.937	24.524	26.413	28.283
bio11	5.338	6.636	9.405	8.995	10.912	13.967
bio12	480.000	645.000	711.000	752.637	810.000	2,224.00
bio13	71.000	112.000	131.000	137.471	152.000	269.000
bio14	1.000	3.000	6.000	13.499	19.750	87.000
bio15	23.234	48.139	75.698	68.831	89.027	99.578
bio16	194.000	293.000	341.000	364.233	411.000	792.000
bio17	5.000	17.000	29.000	52.027	72.750	331.000
bio18	6.000	18.000	31.000	55.662	73.000	605.000
bio19	162.000	240.000	332.000	334.809	399.000	627.000

Table C.5: Summary statistics of bioclimatic variables corresponding to the 90% quantile of avian biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	11.358	13.719	15.273	15.747	18.066	20.010
bio2	3.308	7.823	8.753	8.827	9.762	12.614
bio3	21.483	31.624	33.388	33.782	35.740	43.391
bio4	457.649	628.150	663.949	657.397	686.736	776.425
bio5	23.068	27.580	29.592	29.758	32.200	36.556
bio6	-0.812	2.000	3.300	3.768	5.284	11.700
bio7	15.300	24.496	26.168	25.990	27.476	31.924
bio8	6.078	7.952	9.390	9.500	10.861	20.117
bio9	7.443	21.670	23.739	23.343	25.994	28.629
bio10	18.880	21.870	23.759	23.921	26.065	28.629
bio11	3.309	6.012	7.471	8.020	10.142	14.067
bio12	480.000	646.000	703.000	758.420	801.000	2,292.00
bio13	66.000	106.000	124.000	130.630	147.000	278.000
bio14	0.000	5.000	11.000	17.086	24.000	92.000
bio15	21.845	42.453	60.532	61.977	84.519	99.976
bio16	181.000	280.000	327.000	346.973	387.000	813.000
bio17	4.000	22.000	48.000	64.161	87.000	348.000
bio18	4.000	22.000	49.000	69.658	87.000	605.000
bio19	158.000	234.000	303.000	320.335	374.000	677.000

Table C.6: Summary statistics of bioclimatic variables corresponding to the 80% quantile of avian biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	8.956	12.870	13.954	14.646	16.627	20.010
bio2	3.308	8.367	9.545	9.522	10.702	13.524
bio3	21.483	32.317	34.221	34.295	36.445	43.391
bio4	457.649	649.506	685.272	689.429	723.704	1,043.345
bio5	22.084	27.372	29.536	29.640	32.056	36.828
bio6	-9.080	0.304	1.908	1.977	3.624	11.700
bio7	15.300	25.567	27.472	27.662	29.996	40.356
bio8	0.449	7.023	8.135	8.553	10.083	20.117
bio9	1.193	20.585	22.370	22.261	25.265	28.629
bio10	16.759	21.285	22.691	23.174	25.359	28.629
bio11	-3.555	4.704	6.131	6.437	8.410	14.067
bio12	245.000	608.000	681.000	713.408	764.000	2,292.00
bio13	41.000	86.000	115.000	117.217	140.000	278.000
bio14	0.000	6.000	13.000	18.454	25.000	94.000
bio15	15.534	33.884	53.819	55.627	78.587	99.976
bio16	104.000	236.000	302.000	311.265	361.000	813.000
bio17	4.000	29.000	55.000	67.611	89.000	348.000
bio18	4.000	30.000	58.000	75.893	100.000	605.000
bio19	51.000	207.000	273.000	288.797	355.000	677.000

Table C.7: Summary statistics of bioclimatic variables corresponding to the 95% quantile of insect biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	13.504	16.066	17.783	17.279	18.695	20.010
bio2	6.031	8.658	9.689	9.664	10.686	12.796
bio3	25.772	33.365	35.688	35.628	37.812	43.391
bio4	527.898	645.813	668.902	667.268	690.259	780.408
bio5	26.175	30.764	32.136	31.825	33.252	36.556
bio6	0.828	3.432	4.812	4.796	5.940	10.050
bio7	20.300	25.730	26.984	27.029	28.432	32.296
bio8	5.313	8.444	9.855	9.808	10.969	14.217
bio9	19.086	24.505	25.861	25.460	26.745	28.629
bio10	21.135	24.602	25.949	25.560	26.785	28.629
bio11	5.313	8.050	9.789	9.386	10.839	13.225
bio12	539.000	692.000	757.000	775.392	836.000	1,172.00
bio13	73.000	125.000	146.000	150.571	168.000	245.000
bio14	1.000	4.000	6.000	8.230	11.000	47.000
bio15	29.045	62.446	82.021	75.812	88.907	99.976
bio16	206.000	331.000	378.000	397.128	456.000	627.000
bio17	7.000	20.000	29.000	34.764	46.000	149.000
bio18	7.000	21.000	30.000	36.100	47.000	158.000
bio19	184.000	329.000	376.000	390.095	455.000	627.000

Table C.8: Summary statistics of bioclimatic variables corresponding to the 90% quantile of insect biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	7.306	14.235	16.340	16.260	18.106	20.010
bio2	4.200	8.562	9.683	9.648	10.813	13.055
bio3	24.000	33.011	35.319	35.168	37.372	43.391
bio4	488.418	652.462	679.002	675.944	707.161	811.485
bio5	24.528	29.100	31.417	31.110	32.960	36.828
bio6	-6.364	2.212	3.460	3.811	5.204	11.250
bio7	17.400	25.763	27.284	27.299	29.110	32.684
bio8	-1.941	7.757	8.557	8.948	10.244	14.342
bio9	15.446	22.733	24.838	24.513	26.147	28.629
bio10	16.617	22.768	24.945	24.679	26.249	28.629
bio11	-1.941	6.393	8.170	8.301	10.083	13.967
bio12	509.000	667.000	714.000	738.266	790.000	1,172.00
bio13	72.000	118.000	136.000	139.301	152.000	245.000
bio14	1.000	5.000	7.000	10.056	13.000	49.000
bio15	28.210	56.947	76.686	71.551	84.832	99.976
bio16	203.000	309.000	349.000	366.463	408.000	627.000
bio17	5.000	22.000	32.000	40.630	53.000	158.000
bio18	5.000	23.000	35.000	42.088	54.000	171.000
bio19	163.000	288.000	347.000	354.734	405.000	627.000

Table C.9: Summary statistics of bioclimatic variables corresponding to the 80% quantile of insect biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	3.762	13.055	14.060	14.254	16.606	20.010
bio2	3.308	8.752	10.188	9.933	11.178	13.631
bio3	21.483	32.967	35.168	34.973	37.123	43.391
bio4	457.649	661.294	696.988	696.602	732.608	977.657
bio5	20.564	27.428	29.700	29.703	32.132	36.828
bio6	-11.040	0.312	1.876	1.428	3.616	11.700
bio7	15.300	26.080	28.463	28.274	30.713	37.308
bio8	-5.827	5.747	7.559	6.889	9.307	15.507
bio9	11.362	20.750	22.561	22.506	25.241	28.629
bio10	13.067	21.283	22.726	22.873	25.338	28.629
bio11	-5.827	4.924	6.142	5.965	8.389	14.067
bio12	471.000	636.000	692.000	724.161	760.000	2,292.00
bio13	65.000	105.000	125.000	126.647	143.000	278.000
bio14	0.000	6.000	10.000	13.851	16.000	92.000
bio15	18.817	46.892	64.187	63.199	79.105	99.976
bio16	162.000	277.000	325.000	333.974	371.000	813.000
bio17	4.000	28.000	40.000	52.910	61.000	348.000
bio18	4.000	30.000	46.000	59.515	71.000	519.000
bio19	123.000	244.000	317.000	319.541	367.000	677.000

Table C.10: Summary statistics of bioclimatic variables corresponding to the 97% quantile of mammal biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	11.080	13.301	14.580	15.022	16.794	19.095
bio2	7.740	10.526	11.077	11.082	11.653	13.204
bio3	32.313	36.714	37.546	37.776	38.919	43.391
bio4	585.581	672.915	708.554	697.136	724.098	750.987
bio5	24.740	29.548	31.304	31.274	33.050	35.924
bio6	-1.340	0.236	1.400	1.961	3.346	8.100
bio7	22.800	28.286	29.584	29.314	30.508	32.884
bio8	2.949	5.379	6.878	7.064	8.644	13.783
bio9	10.858	21.944	23.367	23.531	25.540	27.336
bio10	18.695	22.109	23.579	23.715	25.588	27.336
bio11	2.949	4.905	6.257	6.798	8.533	12.200
bio12	565.000	683.000	736.000	778.070	843.000	1,916.00
bio13	92.000	133.000	146.000	154.536	173.000	245.000
bio14	2.000	6.000	8.000	8.659	10.000	94.000
bio15	27.843	69.181	77.134	75.639	83.375	99.976
bio16	251.000	334.000	382.000	402.689	461.500	668.000
bio17	17.000	29.000	34.000	36.370	41.000	307.000
bio18	17.000	31.000	38.000	39.669	46.000	443.000
bio19	246.000	333.000	382.000	401.263	461.500	627.000

Table C.11: Summary statistics of bioclimatic variables corresponding to the 90% quantile of mammal biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	7.163	13.488	14.409	15.101	16.908	20.010
bio2	3.308	8.593	9.990	9.869	11.193	13.866
bio3	21.483	33.197	35.734	35.399	37.666	43.391
bio4	457.649	652.930	683.691	681.076	717.942	820.534
bio5	21.804	28.118	30.532	30.241	32.451	36.384
bio6	-5.440	0.920	2.225	2.534	4.020	11.700
bio7	15.300	25.776	27.792	27.707	29.959	34.500
bio8	-1.208	6.517	7.855	7.953	9.693	15.507
bio9	7.285	21.658	23.138	23.044	25.487	28.527
bio10	15.191	21.817	23.286	23.562	25.566	28.527
bio11	-1.208	5.414	6.480	7.051	8.801	14.067
bio12	483.000	659.000	708.000	753.517	780.000	2,278.00
bio13	70.000	116.000	133.000	135.717	147.000	278.000
bio14	1.000	6.000	9.000	14.015	15.000	97.000
bio15	22.994	54.137	69.703	66.389	80.717	99.976
bio16	188.000	300.000	340.000	355.828	388.000	800.000
bio17	5.000	27.000	38.000	54.098	58.000	348.000
bio18	6.000	29.000	42.000	59.498	61.000	516.000
bio19	172.000	277.000	335.000	340.097	384.000	677.000

Table C.12: Summary statistics of bioclimatic variables corresponding to the 80% quantile of mammal biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	3.879	12.095	13.618	13.919	15.850	20.010
bio2	3.308	8.816	10.424	10.181	11.568	14.059
bio3	21.483	33.506	35.889	35.550	37.724	43.391
bio4	457.649	660.243	696.507	693.662	733.746	846.308
bio5	18.780	27.532	29.472	29.489	31.650	36.828
bio6	-8.416	-1.284	1.116	1.028	2.860	11.700
bio7	15.300	26.196	28.760	28.460	30.992	34.760
bio8	-4.514	3.971	7.012	6.566	8.873	20.117
bio9	3.695	20.047	22.005	21.999	24.520	28.629
bio10	12.093	20.671	22.184	22.493	24.617	28.629
bio11	-4.514	3.665	5.497	5.642	7.473	14.067
bio12	173.000	616.000	680.000	712.554	753.000	2,292.00
bio13	36.000	94.000	118.000	120.737	139.000	278.000
bio14	0.000	7.000	12.000	15.701	17.000	100.000
bio15	20.927	45.358	58.975	59.496	75.666	99.976
bio16	89.000	254.000	308.000	318.600	357.000	813.000
bio17	1.000	31.000	46.000	58.795	66.000	348.000
bio18	1.000	34.000	52.000	66.770	74.000	605.000
bio19	89.000	231.000	291.000	305.217	354.000	677.000

Table C.13: Summary statistics of bioclimatic variables corresponding to the 95% quantile of plant biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	13.344	14.532	16.585	16.515	18.271	20.010
bio2	6.031	8.294	9.133	9.191	10.064	12.185
bio3	25.772	32.750	34.579	34.791	36.930	42.062
bio4	527.898	637.656	662.731	657.854	679.331	726.716
bio5	25.500	28.968	31.246	30.778	32.482	34.892
bio6	1.500	2.790	4.476	4.442	5.694	9.417
bio7	20.650	25.268	26.344	26.335	27.551	30.408
bio8	6.469	8.260	9.286	9.559	10.645	14.217
bio9	15.949	23.050	24.845	24.543	26.178	28.231
bio10	20.967	23.051	24.931	24.724	26.247	28.256
bio11	5.708	6.783	8.925	8.808	10.500	13.217
bio12	509.000	653.000	721.000	745.708	814.500	1,147.00
bio13	72.000	115.000	135.000	141.604	158.000	245.000
bio14	1.000	4.000	6.000	10.581	12.000	47.000
bio15	29.045	55.998	78.661	71.994	86.700	99.578
bio16	203.000	298.500	345.000	372.200	428.000	627.000
bio17	10.000	20.000	29.000	42.325	54.500	151.000
bio18	10.000	21.000	30.000	43.619	56.000	164.000
bio19	172.000	266.000	343.000	355.846	426.500	627.000

Table C.14: Summary statistics of bioclimatic variables corresponding to the 90% quantile of plant biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	12.453	14.006	16.103	16.066	17.947	20.010
bio2	4.492	8.223	9.252	9.327	10.498	12.821
bio3	24.725	32.444	34.633	34.702	37.154	43.391
bio4	475.363	640.506	671.604	666.199	694.012	757.709
bio5	24.500	28.410	30.964	30.576	32.751	35.696
bio6	0.700	2.254	3.396	3.850	5.218	11.500
bio7	17.000	25.265	26.716	26.726	28.358	32.036
bio8	5.905	7.828	8.720	9.206	10.490	14.450
bio9	11.647	22.324	24.605	24.106	26.024	28.517
bio10	20.050	22.397	24.679	24.369	26.119	28.517
bio11	4.950	6.322	8.015	8.238	9.987	14.067
bio12	509.000	656.000	707.000	735.219	788.000	1,206.00
bio13	70.000	112.000	131.000	134.479	149.000	245.000
bio14	1.000	5.000	8.000	12.725	16.000	66.000
bio15	23.057	51.313	72.962	67.659	84.667	99.976
bio16	198.000	293.000	340.000	354.608	397.000	627.000
bio17	6.000	22.000	33.000	49.415	63.000	217.000
bio18	7.000	23.000	36.000	51.293	63.000	266.000
bio19	163.000	256.000	334.000	336.380	392.000	627.000

Table C.15: Summary statistics of bioclimatic variables corresponding to the 80% quantile of plant biodiversity.

Variable	Min	1st Qu.	Median	Mean	3rd Qu.	Max
bio1	10.230	13.297	14.097	14.872	16.608	20.010
bio2	3.308	8.427	9.645	9.683	11.017	13.866
bio3	21.483	32.748	35.015	34.940	37.271	43.391
bio4	457.649	648.460	684.336	680.582	718.243	829.767
bio5	22.640	27.652	30.093	29.862	32.200	36.828
bio6	-1.948	0.588	1.908	2.322	3.624	11.700
bio7	15.300	25.556	27.464	27.540	29.888	34.500
bio8	3.014	6.603	7.854	8.114	9.657	20.117
bio9	6.359	21.302	22.629	22.777	25.243	28.629
bio10	17.657	21.636	22.843	23.313	25.341	28.629
bio11	2.543	5.084	6.164	6.808	8.403	14.067
bio12	480.000	636.000	696.000	738.680	774.000	2,292.00
bio13	60.000	102.000	124.000	125.882	143.000	278.000
bio14	0.000	6.000	11.000	17.187	22.000	95.000
bio15	19.015	39.835	61.686	59.811	79.084	99.976
bio16	162.000	272.000	322.000	332.567	371.000	813.000
bio17	4.000	29.000	46.000	64.226	79.000	348.000
bio18	4.000	31.000	48.000	69.947	87.000	605.000
bio19	152.000	236.000	308.000	314.372	366.000	677.000

APPENDIX D

Table D.1: Birds/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Curruca cantillans	0.612	0.804	145	0.718	215
Pelecanus crispus	0.594	0.757	139	0.671	224
Falco eleonorae	0.609	0.807	138	0.703	220
Curruca melanocephala	0.623	0.770	132	0.661	243
Tyto alba	0.602	0.776	130	0.676	226
Larus canus	0.604	0.779	128	0.673	229
Cygnus olor	0.597	0.764	124	0.663	229
Cisticola juncidis	0.584	0.806	122	0.690	212
Puffinus yelkouan	0.597	0.794	122	0.669	229
Phalacrocorax aristotelis	0.587	0.788	121	0.662	227
Strix aluco	0.595	0.745	118	0.639	241
Ficedula hypoleuca	0.577	0.732	116	0.632	231
Microcarbo pygmaeus	0.581	0.724	116	0.625	237
Sylvia melanocephala	0.593	0.746	112	0.633	240
Luscinia luscinia	0.578	0.751	111	0.639	231
Calidris alba	0.576	0.759	109	0.643	227
Hippolais icterina	0.569	0.786	109	0.649	224
Ichthyaetus audouinii	0.547	0.796	107	0.667	204
Tringa erythropus	0.561	0.752	106	0.639	222
Mergus serrator	0.555	0.779	98	0.631	224
Emberiza cirlus	0.591	0.758	95	0.621	247

Table D.1 (continued): Birds/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Psittacula krameri	0.572	0.733	94	0.610	239
Sylvia borin	0.545	0.744	93	0.615	224
Dendrocoptes medius	0.589	0.752	92	0.616	247
Hydrocoloeus minutus	0.542	0.761	92	0.617	223
Thalasseus sandvicensis	0.525	0.780	85	0.625	208
Calidris ferruginea	0.503	0.755	80	0.610	201
Pluvialis apricaria	0.516	0.757	80	0.606	211
Lymnocryptes minimus	0.511	0.761	78	0.605	210
Numenius arquata	0.526	0.741	78	0.601	219
Limosa lapponica	0.505	0.752	76	0.597	210
Calidris alpina	0.537	0.704	75	0.593	227
Rallus aquaticus	0.536	0.699	74	0.590	229
Arenaria interpres	0.500	0.752	73	0.596	206
Crex crex	0.513	0.729	73	0.589	218
Hydroprogne caspia	0.507	0.739	72	0.589	215
Regulus ignicapilla	0.549	0.720	72	0.589	240
Calidris canutus	0.487	0.750	71	0.584	206
Certhia brachydactyla	0.552	0.738	70	0.588	240
Chroicocephalus genei	0.522	0.716	70	0.591	221
Scolopax rusticola	0.514	0.712	70	0.586	220

Table D.1 (continued): Birds/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Phasianus colchicus	0.550	0.723	69	0.578	242
Calonectris diomedea	0.455	0.752	67	0.586	192
Stercorarius parasiticus	0.494	0.745	66	0.584	207
Regulus regulus	0.549	0.735	65	0.579	242
Larus cachinnans	0.497	0.724	63	0.577	212
Numenius phaeopus	0.471	0.740	63	0.569	203
Asio flammeus	0.514	0.706	62	0.578	222
Sitta krueperi	0.541	0.731	62	0.576	239
Ficedula albicollis	0.541	0.749	59	0.566	244
Hippolais olivetorum	0.529	0.722	58	0.594	223
Larus fuscus	0.485	0.742	56	0.578	202
Phylloscopus orientalis	0.496	0.721	56	0.602	203
Gavia arctica	0.481	0.724	55	0.561	212
Sylvia ruppeli	0.499	0.723	52	0.600	207
Calidris temminckii	0.521	0.686	46	0.568	230
Cygnus columbianus	0.498	0.725	46	0.543	223
Platalea leucorodia	0.525	0.726	43	0.574	229
Charadrius alexandrinus	0.512	0.723	42	0.558	229
Halcyon smyrnensis	0.496	0.710	41	0.581	212
Picus canus	0.481	0.721	41	0.545	217

Table D.1 (continued): Birds/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Pluvialis squatarola	0.445	0.736	41	0.544	197
Pelecanus onocrotalus	0.519	0.704	40	0.574	225
Porzana parva	0.527	0.703	40	0.569	232
Pycnonotus xanthopygos	0.441	0.710	40	0.569	193
Bucephala clangula	0.455	0.712	39	0.550	198
Erythropygia galactotes	0.479	0.735	37	0.573	205
Burhinus oedicnemus	0.502	0.718	36	0.546	228
Dendrocopos leucotos	0.509	0.720	36	0.558	230
Glareola pratincola	0.510	0.732	35	0.549	231
Mergellus albellus	0.485	0.696	34	0.564	210
Anser albifrons	0.493	0.716	32	0.536	227
Emberiza caesia	0.481	0.742	31	0.581	206
Falco columbarius	0.488	0.695	27	0.535	226
Lanius excubitor	0.468	0.698	27	0.521	219
Certhia familiaris	0.354	0.725	25	0.499	148
Netta rufina	0.483	0.695	24	0.535	218
Panurus biarmicus	0.458	0.718	24	0.501	221
Loxia curvirostra	0.419	0.737	23	0.500	188
Haematopus ostralegus	0.445	0.684	21	0.518	203
Poecile palustris	0.378	0.747	21	0.508	168

Table D.1 (continued): Birds/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Apus affinis	0.385	0.744	20	0.514	179
Haliaeetus albicilla	0.494	0.696	20	0.535	231
Phoenicopterus roseus	0.458	0.709	19	0.512	220
Chlidonias niger	0.486	0.677	16	0.549	218
Gallinago media	0.441	0.674	16	0.520	197
Pyrrhula pyrrhula	0.316	0.717	15	0.494	115
Dryocopus martius	0.345	0.741	14	0.485	148
Gavia stellata	0.387	0.714	14	0.496	172
Prinia lepida	0.358	0.737	13	0.488	172
Ceryle rudis	0.332	0.742	11	0.458	159
Buteo lagopus	0.394	0.715	10	0.494	192
Ichthyaetus ichthyaetus	0.397	0.711	10	0.492	184
Acrocephalus melanopogon	0.465	0.683	9	0.523	215
Tringa stagnatilis	0.466	0.674	9	0.518	219
Aythya marila	0.377	0.703	8	0.484	174
Calidris falcinellus	0.463	0.686	7	0.486	237
Passer moabiticus	0.306	0.728	7	0.439	137
Tetraogallus caspius	0.257	0.747	7	0.496	76
Carpodacus erythrinus	0.257	0.744	6	0.480	72
Merops persicus	0.310	0.696	5	0.430	137

Table D.1 (continued): Birds/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Oenanthe pleschanka	0.411	0.677	5	0.493	193
Phylloscopus nitidus	0.202	0.709	5	0.474	51
Perdix perdix	0.152	0.746	4	0.493	47
Phylloscopus sindianus	0.136	0.679	3	0.473	26
Rhodospiza obsoleta	0.226	0.700	3	0.493	43
Linaria flavirostris	0.092	0.702	2	0.508	22
Vanellus spinosus	0.463	0.669	2	0.538	209
Cygnus cygnus	0.427	0.674	1	0.505	199
Sylvia mystacea	0.211	0.714	1	0.459	40
Carpospiza brachydactyla	0.086		0	0.440	30
Charadrius leschenaultii	0.252		0	0.371	54
Charadrius morinellus	0.280		0	0.373	95
Elanus caeruleus	0.209		0	0.411	38
Oenanthe xanthoprymna	0.088		0	0.396	20
Oxyura leucocephala	0.392		0	0.445	203
Porphyrio porphyrio	0.416		0	0.481	200
Sitta tephronota	0.079		0	0.457	30

Table D.2: Insects/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Carpocoris mediterraneus	0.630	0.790	147	0.698	231
Mantis religiosa	0.625	0.781	144	0.684	235
Nezara viridula	0.629	0.812	144	0.709	227
Libellula fulva	0.621	0.769	141	0.671	238
Orthetrum coerulescens	0.622	0.780	141	0.686	231
Zelus renardii	0.621	0.805	139	0.698	228
Onychogomphus forcipatus	0.617	0.780	137	0.682	231
Charaxes jasius	0.585	0.772	136	0.684	215
Vespa orientalis	0.589	0.799	136	0.708	209
Polyphylla fullo	0.597	0.800	132	0.692	218
Pelopidas thrax	0.581	0.786	127	0.682	214
Gonepteryx cleopatra	0.556	0.755	126	0.666	210
Leptotes pirithous	0.582	0.732	126	0.638	232
Empusa fasciata	0.578	0.728	124	0.640	228
Pararge aegeria	0.568	0.757	121	0.657	216
Epallage fatime	0.562	0.742	115	0.642	220
Chalcolestes parvidens	0.598	0.750	112	0.632	243
Rhaphigaster nebulosa	0.579	0.736	110	0.630	234
Nemoptera sinuata	0.533	0.746	108	0.649	203
Nomophila noctuella	0.559	0.771	108	0.640	222
Gegenes pumilio	0.519	0.738	106	0.650	198

Table D.2 (continued): Insects/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Erythromma viridulum	0.551	0.787	104	0.655	210
Anacridium aegyptium	0.543	0.798	101	0.659	205
Mustha spinosula	0.539	0.704	93	0.613	218
Trithemis arteriosa	0.504	0.727	93	0.625	199
Zerynthia cerisy	0.536	0.723	92	0.622	215
Aeshna mixta	0.554	0.724	89	0.604	236
Coccinella septempunctata	0.575	0.742	87	0.604	246
Sympetrum meridionale	0.543	0.720	87	0.614	221
Anax imperator	0.572	0.738	84	0.604	245
Calopteryx virgo	0.576	0.742	84	0.604	247
Orthetrum chrysostigma	0.487	0.741	84	0.625	191
Ceriagrion georgifreyi	0.557	0.722	79	0.598	236
Graphosoma italicum	0.569	0.750	79	0.598	246
Anax parthenope	0.491	0.742	75	0.592	203
Coreus marginatus	0.545	0.730	69	0.576	238
Spilostethus pandurus	0.467	0.753	69	0.594	193
Orthetrum taeniolatum	0.479	0.722	68	0.610	196
Aeshna isoceles	0.500	0.714	64	0.579	213
Trithemis festiva	0.457	0.736	64	0.604	187
Gomphus schneiderii	0.473	0.718	61	0.600	193

Table D.2 (continued): Insects/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Iris oratoria	0.545	0.715	61	0.579	240
Zizeeria karsandra	0.513	0.707	60	0.589	216
Hipparchia algirica	0.530	0.755	52	0.564	236
Erythromma lindenii	0.529	0.721	51	0.575	229
Coenagrion scitulum	0.511	0.736	50	0.551	231
Oxythyrea cinctella	0.525	0.752	50	0.565	234
Cordulegaster picta	0.530	0.735	49	0.563	241
Diplacodes lefebvrii	0.434	0.739	49	0.578	185
Trithemis annulata	0.432	0.739	49	0.581	182
Polistes dominula	0.528	0.687	48	0.580	228
Polyommatus ottomanus	0.492	0.719	30	0.512	242
Orthetrum sabina	0.403	0.748	29	0.549	178
Bombus terrestris	0.424	0.705	28	0.534	183
Brachythemis fuscopalliata	0.451	0.715	26	0.555	197
Carabus scabrosus	0.377	0.727	25	0.522	143
Maniola telmessia	0.423	0.721	25	0.524	196
Platycnemis kervillei	0.390	0.746	24	0.506	183
Aglais io	0.382	0.712	22	0.508	156
Coenagrion puella	0.395	0.710	20	0.482	171
Fabriciana adippe	0.438	0.717	19	0.493	209

Table D.2 (continued): Insects/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Platycnemis dealbata	0.448	0.714	19	0.521	205
Nymphalis antiopa	0.331	0.704	18	0.500	123
Pyrrhocoris apterus	0.460	0.695	18	0.518	215
Hipparchia mersina	0.460	0.724	17	0.541	211
Cordulegaster insignis	0.374	0.700	14	0.482	146
Onychogomphus lefebvrii	0.382	0.732	14	0.513	180
Hipparchia fatua	0.477	0.714	13	0.555	208
Melanargia galathea	0.331	0.701	13	0.484	131
Argynnis paphia	0.429	0.703	12	0.492	203
Speyeria aglaja	0.280	0.729	11	0.489	87
Orthetrum albistylum	0.418	0.709	10	0.515	197
Coenonympha arcania	0.312	0.701	9	0.472	116
Eristalis tenax	0.466	0.668	9	0.536	214
Polyommatus menalcas	0.292	0.717	9	0.484	93
Anax ephippiger	0.372	0.730	8	0.491	165
Melitaea athalia	0.306	0.735	7	0.465	114
Chazara persephone	0.150	0.758	6	0.506	42
Plebejus argus	0.163	0.719	6	0.482	46
Melitaea collina	0.319	0.705	5	0.437	135
Sympecma fusca	0.408	0.704	5	0.452	208

Table D.2 (continued): Insects/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Agrodiaetus admetus	0.178	0.689	4	0.487	53
Brenthis daphne	0.338	0.691	4	0.440	140
Episyrphus balteatus	0.416	0.664	4	0.506	191
Eumedonia eumedon	0.103	0.709	4	0.489	31
Lycaeides idas	0.106	0.732	4	0.488	32
Parnassius apollo	0.145	0.740	4	0.487	41
Pseudochazara mniszechii	0.125	0.725	4	0.492	40
Polyommatus poseidon	0.122	0.707	3	0.480	28
Zerynthia deyrollei	0.184	0.712	3	0.449	61
Arethusana arethusa	0.111	0.693	2	0.476	33
Hipparchia parisatis	0.126	0.666	2	0.438	23
Leptoglossus occidentalis	0.416	0.669	2	0.486	201
Lycaena thetis	0.084	0.723	2	0.504	19
Lycaena virgaureae	0.073	0.672	2	0.486	21
Parnassius mnemosyne	0.169	0.668	2	0.456	36
Polyommatus carmon	0.095	0.740	2	0.489	24
Polyommatus firdussii	0.062	0.753	2	0.517	16
Polyommatus ripartii	0.086	0.680	2	0.474	23
Polyommatus wagneri	0.069	0.678	2	0.494	17
Pseudochazara beroe	0.077	0.742	2	0.509	20

Table D.2 (continued): Insects/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Pseudochazara mamurra	0.136	0.693	2	0.468	34
Syrichtus poggei	0.185	0.762	2	0.438	52
Agriades corydonius	0.040	0.669	1	0.450	10
Coenonympha saadi	0.081	0.732	1	0.441	33
Erebia aethiops	0.110	0.761	1	0.488	26
Kirinia climene	0.049	0.776	1	0.498	11
Lycaena alciphron	0.056	0.780	1	0.500	14
Palaeochrysophanus candens	0.071	0.670	1	0.496	20
Plebejus amanda	0.116	0.751	1	0.478	22
Pseudochazara geyeri	0.053	0.793	1	0.536	13
Pseudochazara thelephassa	0.100	0.715	1	0.473	33
Agrodiaetus iphigenia	0.038		0	0.407	12
Brenthis hecate	0.028		0	0.399	9
Clossiana euphrosyne	0.101		0	0.444	29
Glaucopsyche astraea	0.058		0	0.405	8
Melitaea arduinna	0.160		0	0.429	35
Melitaea persea	0.079		0	0.446	19
Nymphalis xanthomelas	0.294		0	0.375	84
Onychogomphus assimilis	0.449		0	0.504	210
Orthetrum cancellatum	0.419		0	0.478	209

Table D.2 (continued): Insects/Plants cohabitation values according to pairwise Warren's I statistics. uWI_0 is mean I statistic, uWI_66 mean I statistic of species that scored above 0.66, no_66 is number of species with I statistic over 0.66, uWI_33 is mean I statistic of species that scored above 0.33, no_33 is number of species with I statistic over 0.33. Sorted by no_66 in descending order.

species	uWI_0	uWI_66	no_66	uWI_33	no_33
Polyommatus hopfferi	0.099		0	0.439	18
Pontia chloridice	0.269		0	0.379	90
Pseudochazara pelopea	0.077		0	0.438	21
Quercusia quercus	0.145		0	0.405	39
Sympetrum flaveolum	0.151		0	0.455	29

APPENDIX E

Table E.1: The names of the species, included in the analyses, sorted alphabetically.

Species	Taxa	Species	Taxa	Species	Taxa
Abutilon theophrasti	Plantae	*Allium rotundum*	Plantae	*Asio flammeus*	Aves
Acer negundo	Plantae	*Amaranthus retroflexus*	Plantae	*Asparagus acutifolius*	Plantae
Acrocephalus melanopogon	Aves	*Anacamptis papilionacea*	Plantae	*Asphodelus ramosus*	Plantae
				Asplenium ceterach	Plantae
Aegilops biuncialis	Plantae	*Anacamptis pyramidalis*	Plantae	*Astragalus hamosus*	Plantae
Aegilops caudata	Plantae	*Anacridium aegyptium*	Insecta	*Avena barbata*	Plantae
Aegilops cylindrica	Plantae	*Anagyris foetida*	Plantae	*Avena fatua*	Plantae
Aegilops geniculata	Plantae	*Anax ephippiger*	Insecta	*Avena sativa*	Plantae
Aegilops neglecta	Plantae	*Anax imperator*	Insecta	*Aythya marila*	Aves
Aegilops tauschii	Plantae	*Anax parthenope*	Insecta	*Ballota nigra*	Plantae
Aesculus hippocastanum	Plantae	*Anemone blanda*	Plantae	*Bellis perennis*	Plantae
Aeshna isoceles	Insecta	*Anemone coronaria*	Plantae	*Beta lomatogona*	Plantae
Aeshna mixta	Insecta	*Anser albifrons*	Aves	*Bituminaria bituminosa*	Plantae
Agave americana	Plantae	*Apus affinis*	Aves	*Bombus terrestris*	Insecta
Aglais io	Insecta	*Arbutus andrachne*	Plantae	*Brachythemis fuscopalliata*	Insecta
Agriades corydonius	Insecta	*Arbutus unedo*	Plantae		
Agrodiaetus admetus	Insecta	*Arenaria interpres*	Aves	*Brenthis daphne*	Insecta
Agrodiaetus iphigenia	Insecta	*Arethusana arethusa*	Insecta	*Brenthis hecate*	Insecta
Ailanthus altissima	Plantae	*Argynnis paphia*	Insecta	*Briza maxima*	Plantae
Albizia julibrissin	Plantae	*Arisarum vulgare*	Plantae	*Bucephala clangula*	Aves
Alcea rosea	Plantae	*Arum italicum*	Plantae	*Bufotes viridis*	Amphibia
Alkanna tinctoria	Plantae	*Arundo donax*	Plantae	*Burhinus oedicnemus*	Aves

Species	Taxa	Species	Taxa	Species	Taxa
Buteo lagopus	Aves	*Centaurea calcitrapa*	Plantae	*Citrullus lanatus*	Plantae
Calendula arvensis	Plantae	*Ceratonia siliqua*	Plantae	*Clematis cirrhosa*	Plantae
Calepina irregularis	Plantae	*Cercis siliquastrum*	Plantae	*Clematis vitalba*	Plantae
Calidris alba	Aves	*Ceriagrion georgifreyi*	Insecta	*Clinopodium vulgare*	Plantae
Calidris alpina	Aves	*Certhia brachydactyla*	Aves	*Clossiana euphrosyne*	Insecta
Calidris canutus	Aves	*Certhia familiaris*	Aves	*Coccinella septempunctata*	Insecta
Calidris falcinellus	Aves	*Ceryle rudis*	Aves		
Calidris ferruginea	Aves	*Chalcolestes parvidens*	Insecta	*Coenagrion puella*	Insecta
Calidris temminckii	Aves	*Chamaenerion angustifolium*	Plantae	*Coenagrion scitulum*	Insecta
Calonectris diomedea	Aves			*Coenonympha arcania*	Insecta
Calopteryx virgo	Insecta	*Charadrius alexandrinus*	Aves	*Coenonympha saadi*	Insecta
Campanula glomerata	Plantae	*Charadrius leschenaultii*	Aves	*Colchicum variegatum*	Plantae
Campanula rapunculoides	Plantae	*Charadrius morinellus*	Aves	*Conium maculatum*	Plantae
		Charaxes jasius	Insecta	*Cordulegaster insignis*	Insecta
Capparis spinosa	Plantae	*Chazara persephone*	Insecta	*Cordulegaster picta*	Insecta
Capsella bursa-pastoris	Plantae	*Chelidonium majus*	Plantae	*Coreus marginatus*	Insecta
Carabus scabrosus	Insecta	*Chlidonias niger*	Aves	*Cornus mas*	Plantae
Carpocoris mediterraneus	Insecta	*Chroicocephalus genei*	Aves	*Cornus sanguinea*	Plantae
		Chrozophora tinctoria	Plantae	*Coronilla varia*	Plantae
Carpodacus erythrinus	Aves	*Cichorium intybus*	Plantae	*Corylus avellana*	Plantae
Carpospiza brachydactyla	Aves	*Cirsium vulgare*	Plantae	*Cotinus coggygria*	Plantae
Carthamus tinctorius	Plantae	*Cisticola juncidis*	Aves	*Crataegus monogyna*	Plantae
Cedrus libani	Plantae	*Cistus creticus*	Plantae	*Crex crex*	Aves
Celtis australis	Plantae	*Cistus laurifolius*	Plantae	*Crithmum maritimum*	Plantae
		Cistus salviifolius	Plantae	*Cucumis melo*	Plantae

Species	Taxa	Species	Taxa	Species	Taxa
Cupressus sempervirens	Plantae	*Echium plantagineum*	Plantae	*Falco eleonorae*	Aves
Curruca cantillans	Aves	*Echium vulgare*	Plantae	*Felis catus*	Mammalia
Curruca melanocephala	Aves	*Elanus caeruleus*	Aves	*Ficaria verna*	Plantae
Cydonia oblonga	Plantae	*Emberiza caesia*	Aves	*Ficedula albicollis*	Aves
Cygnus columbianus	Aves	*Emberiza cirlus*	Aves	*Ficedula hypoleuca*	Aves
Cygnus cygnus	Aves	*Empusa fasciata*	Insecta	*Ficus carica*	Plantae
Cygnus olor	Aves	*Epallage fatime*	Insecta	*Filipendula vulgaris*	Plantae
Cynanchum acutum	Plantae	*Epilobium hirsutum*	Plantae	*Foeniculum vulgare*	Plantae
Cynodon dactylon	Plantae	*Episyrphus balteatus*	Insecta	*Fraxinus angustifolia*	Plantae
Cynoglossum creticum	Plantae	*Erebia aethiops*	Insecta	*Galega officinalis*	Plantae
Cytinus ruber	Plantae	*Erica arborea*	Plantae	*Galium aparine*	Plantae
Daphne sericea	Plantae	*Erinaceus concolor*	Mamma	*Gallinago media*	Aves
Datura stramonium	Plantae	*Eristalis tenax*	Insecta	*Gavia arctica*	Aves
Daucus carota	Plantae	*Eryngium maritimum*	Plantae	*Gavia stellata*	Aves
Dendrocopos leucotos	Aves	*Erythromma lindenii*	Insecta	*Gegenes pumilio*	Insecta
Dendrocoptes medius	Aves	*Erythromma viridulum*	Insecta	*Geranium dissectum*	Plantae
Digitalis ferruginea	Plantae	*Erythropygia galactotes*	Aves	*Glareola pratincola*	Aves
Diplacodes lefebvrii	Insecta	*Eumedonia eumedon*	Insecta	*Glaucium flavum*	Plantae
Dracunculus vulgaris	Plantae	*Euphorbia characias*	Plantae	*Glaucopsyche astraea*	Insecta
Dryocopus martius	Aves	*Euphorbia helioscopia*	Plantae	*Glebionis coronaria*	Plantae
Ecballium elaterium	Plantae	*Euphorbia peplus*	Plantae	*Gomphus schneiderii*	Insecta
Echinops ritro	Plantae	*Euphorbia rigida*	Plantae	*Gonepteryx cleopatra*	Insecta
Echinops spinosissimus	Plantae	*Fabriciana adippe*	Insecta	*Graphosoma italicum*	Insecta
Echium italicum	Plantae	*Falco columbarius*	Aves	*Gundelia tournefortii*	Plantae

Species	Taxa	Species	Taxa	Species	Taxa
Haematopus ostralegus	Aves	*Ilex aquifolium*	Plantae	*Linaria flavirostris*	Aves
Halcyon smyrnensis	Aves	*Iris oratoria*	Insecta	*Loxia curvirostra*	Aves
Haliaeetus albicilla	Aves	*Juniperus communis*	Plantae	*Luscinia luscinia*	Aves
Hedera helix	Plantae	*Kirinia climene*	Insecta	*Lycaeides idas*	Insecta
Heliotropium europaeum	Plantae	*Lactuca serriola*	Plantae	*Lycaena alciphron*	Insecta
		Lagurus ovatus	Plantae	*Lycaena thetis*	Insecta
Hibiscus trionum	Plantae	*Lamium amplexicaule*	Plantae	*Lycaena virgaureae*	Insecta
Hipparchia algirica	Insecta	*Lamium purpureum*	Plantae	*Lymnocryptes minimus*	Aves
Hipparchia fatua	Insecta	*Lanius excubitor*	Aves	*Lysimachia arvensis*	Plantae
Hipparchia mersina	Insecta	*Lantana camara*	Plantae	*Lythrum salicaria*	Plantae
Hipparchia parisatis	Insecta	*Larus cachinnans*	Aves	*Malva sylvestris*	Plantae
Hippolais icterina	Aves	*Larus canus*	Aves	*Maniola telmessia*	Insecta
Hippolais olivetorum	Aves	*Larus fuscus*	Aves	*Mantis religiosa*	Insecta
Hordeum bulbosum	Plantae	*Lathyrus aphaca*	Plantae	*Marrubium vulgare*	Plantae
Hordeum spontaneum	Plantae	*Lathyrus cicera*	Plantae	*Medicago arabica*	Plantae
Hydrocoloeus minutus	Aves	*Lathyrus inconspicuus*	Plantae	*Medicago orbicularis*	Plantae
Hydroprogne caspia	Aves	*Lathyrus oleraceus*	Plantae	*Medicago polymorpha*	Plantae
Hyla orientalis	Amphib	*Laurus nobilis*	Plantae	*Medicago radiata*	Plantae
Hypericum androsaemum	Plantae	*Lavandula stoechas*	Plantae	*Medicago rigidula*	Plantae
Hypericum perforatum	Plantae	*Leptoglossus occidentalis*	Insecta	*Melampyrum arvense*	Plantae
Hypericum triquetrifolium	Plantae	*Leptotes pirithous*	Insecta	*Melanargia galathea*	Insecta
				Melia azedarach	Plantae
Ichthyaetus audouinii	Aves	*Libellula fulva*	Insecta	*Melissa officinalis*	Plantae
Ichthyaetus ichthyaetus	Aves	*Limodorum abortivum*	Plantae	*Melitaea arduinna*	Insecta
		Limosa lapponica	Aves		

Species	Taxa	Species	Taxa	Species	Taxa
Melitaea athalia	Insecta	*Oenanthe xanthoprymna*	Aves	*Pallenis spinosa*	Plantae
Melitaea collina	Insecta	*Olea europaea*	Plantae	*Pancratium maritimum*	Plantae
Melitaea persea	Insecta	*Onychogomphus assimilis*	Insecta	*Panurus biarmicus*	Aves
Mentha pulegium	Plantae			*Papaver rhoeas*	Plantae
Mercurialis annua	Plantae	*Onychogomphus forcipatus*	Insecta	*Pararge aegeria*	Insecta
Mergellus albellus	Aves	*Onychogomphus lefebvrii*	Insecta	*Parentucellia latifolia*	Plantae
Mergus serrator	Aves			*Parnassius apollo*	Insecta
Merops persicus	Aves	*Ophrys speculum*	Plantae	*Parnassius mnemosyne*	Insecta
Microcarbo pygmaeus	Aves	*Ophrys sphegodes*	Plantae	*Passer moabiticus*	Aves
Morus nigra	Plantae	*Opuntia ficus-indica*	Plantae	*Peganum harmala*	Plantae
Muscari comosum	Plantae	*Orchis anatolica*	Plantae	*Pelecanus crispus*	Aves
Muscari neglectum	Plantae	*Orchis italica*	Plantae	*Pelecanus onocrotalus*	Aves
Mustha spinosula	Insecta	*Orthetrum albistylum*	Insecta	*Pelophylax bedriagae*	Amphibia
Myrtus communis	Plantae	*Orthetrum cancellatum*	Insecta	*Pelophylax ridibundus*	Amphibia
Nemoptera sinuata	Insecta	*Orthetrum chrysostigma*	Insecta	*Pelopidas thrax*	Insecta
Nerium oleander	Plantae	*Orthetrum coerulescens*	Insecta	*Perdix perdix*	Aves
Netta rufina	Aves	*Orthetrum sabina*	Insecta	*Phalacrocorax aristotelis*	Aves
Nezara viridula	Insecta	*Orthetrum taeniolatum*	Insecta		
Nomophila noctuella	Insecta	*Osyris alba*	Plantae	*Phasianus colchicus*	Aves
Numenius arquata	Aves	*Oxalis pes-caprae*	Plantae	*Philadelphus coronarius*	Plantae
Numenius phaeopus	Aves	*Oxythyrea cinctella*	Insecta	*Phillyrea latifolia*	Plantae
Nymphalis antiopa	Insecta	*Oxyura leucocephala*	Aves	*Phlomis herba-venti*	Plantae
Nymphalis xanthomelas	Insecta	*Palaeochrysophanus candens*	Insecta	*Phoenicopterus roseus*	Aves
Oenanthe pleschanka	Aves			*Phragmites australis*	Plantae
		Paliurus spina-christi	Plantae	*Phylloscopus nitidus*	Aves

Species	Taxa	Species	Taxa	Species	Taxa
Phylloscopus orientalis	Aves	*Polyommatus firdussii*	Insecta	*Pseudochazara mniszechii*	Insecta
Phylloscopus sindianus	Aves	*Polyommatus hopfferi*	Insecta	*Pseudochazara pelopea*	Insecta
Phytolacca americana	Plantae	*Polyommatus menalcas*	Insecta	*Pseudochazara thelephassa*	Insecta
Picnomon acarna	Plantae	*Polyommatus ottomanus*	Insecta	*Psittacula krameri*	Aves
Picus canus	Aves	*Polyommatus poseidon*	Insecta	*Pteridium aquilinum*	Plantae
Pinus brutia	Plantae	*Polyommatus ripartii*	Insecta	*Ptilostemon chamaepeuce*	Plantae
Pinus nigra	Plantae	*Polyommatus wagneri*	Insecta	*Puffinus yelkouan*	Aves
Pinus sylvestris	Plantae	*Polyphylla fullo*	Insecta	*Punica granatum*	Plantae
Pistacia lentiscus	Plantae	*Pontia chloridice*	Insecta	*Pycnonotus xanthopygos*	Aves
Pistacia terebinthus	Plantae	*Populus alba*	Plantae	*Pyracantha coccinea*	Plantae
Pistacia vera	Plantae	*Porphyrio porphyrio*	Aves	*Pyrrhocoris apterus*	Insecta
Plantago major	Plantae	*Portulaca oleracea*	Plantae	*Pyrrhula pyrrhula*	Aves
Platalea leucorodia	Aves	*Porzana parva*	Aves	*Pyrus communis*	Plantae
Platanus orientalis	Plantae	*Prinia lepida*	Aves	*Pyrus spinosa*	Plantae
Platycnemis dealbata	Insecta	*Prosopis farcta*	Plantae	*Quercus cerris*	Plantae
Platycnemis kervillei	Insecta	*Prospero autumnale*	Plantae	*Quercus coccifera*	Plantae
Plebejus amanda	Insecta	*Prunella vulgaris*	Plantae	*Quercus ithaburensis*	Plantae
Plebejus argus	Insecta	*Prunus cerasifera*	Plantae	*Quercus petraea*	Plantae
Pluvialis apricaria	Aves	*Prunus laurocerasus*	Plantae	*Quercus pubescens*	Plantae
Pluvialis squatarola	Aves	*Prunus persica*	Plantae	*Quercusia quercus*	Insecta
Poecile palustris	Aves	*Prunus spinosa*	Plantae	*Rallus aquaticus*	Aves
Polistes dominula	Insecta	*Pseudochazara beroe*	Insecta	*Rana macrocnemis*	Amphibia
Polygonum aviculare	Plantae	*Pseudochazara geyeri*	Insecta		
Polyommatus carmon	Insecta	*Pseudochazara mamurra*	Insecta		

Species	Taxa	Species	Taxa	Species	Taxa
Raphanus raphanistrum	Plantae	*Sherardia arvensis*	Plantae	*Sympecma fusca*	Insecta
Regulus ignicapilla	Aves	*Silybum marianum*	Plantae	*Sympetrum flaveolum*	Insecta
Regulus regulus	Aves	*Sitta krueperi*	Aves	*Sympetrum meridionale*	Insecta
Reseda lutea	Plantae	*Sitta tephronota*	Aves	*Syrichtus poggei*	Insecta
Rhaphigaster nebulosa	Insecta	*Smilax aspera*	Plantae	*Tetraogallus caspius*	Aves
Rhododendron luteum	Plantae	*Solanum nigrum*	Plantae	*Thalasseus sandvicensis*	Aves
Rhodospiza obsoleta	Aves	*Solanum villosum*	Plantae	*Thinopyrum intermedium*	Plantae
Ricinus communis	Plantae	*Sonchus oleraceus*	Plantae		
Robinia pseudoacacia	Plantae	*Sorghum bicolor*	Plantae	*Tilia tomentosa*	Plantae
Rosa canina	Plantae	*Spartium junceum*	Plantae	*Tordylium apulum*	Plantae
Ruscus aculeatus	Plantae	*Spermophilus xanthoprymnus*	Mamma	*Trachystemon orientale*	Plantae
Salvia sclarea	Plantae			*Tribulus terrestris*	Plantae
Salvia verbenaca	Plantae	*Speyeria aglaja*	Insecta	*Trifolium campestre*	Plantae
Salvia verticillata	Plantae	*Spilostethus pandurus*	Insecta	*Trifolium cherleri*	Plantae
Salvia viridis	Plantae	*Stachys cretica*	Plantae	*Trifolium fragiferum*	Plantae
Sambucus ebulus	Plantae	*Stachys lavandulifolia*	Plantae	*Trifolium hirtum*	Plantae
Santolina chamaecyparissus	Plantae	*Stercorarius parasiticus*	Aves	*Trifolium purpureum*	Plantae
		Sternbergia lutea	Plantae	*Trifolium resupinatum*	Plantae
Sarcopoterium spinosum	Plantae	*Strix aluco*	Aves	*Trifolium spumosum*	Plantae
Scandix pecten-veneris	Plantae	*Styrax officinalis*	Plantae	*Trifolium stellatum*	Plantae
Sciurus anomalus	Mamma	*Sus scrofa*	Mamma	*Tringa erythropus*	Aves
Scolopax rusticola	Aves	*Sylvia borin*	Aves	*Tringa stagnatilis*	Aves
Scolymus hispanicus	Plantae	*Sylvia melanocephala*	Aves	*Trithemis annulata*	Insecta
Sedum album	Plantae	*Sylvia mystacea*	Aves	*Trithemis arteriosa*	Insecta
Senecio vulgaris	Plantae	*Sylvia ruppeli*	Aves	*Trithemis festiva*	Insecta

Species	Taxa	Species	Taxa	Species	Taxa
Tyto alba	Aves	*Viburnum tinus*	Plantae	*Vinca major*	Plantae
Urtica dioica	Plantae	*Vicia eriocarpa*	Plantae	*Viscum album*	Plantae
Urtica urens	Plantae	*Vicia ervilia*	Plantae	*Vitex agnus-castus*	Plantae
Vanellus spinosus	Aves	*Vicia faba*	Plantae	*Vitis vinifera*	Plantae
Verbascum sinuatum	Plantae	*Vicia hybrida*	Plantae	*Xanthium spinosum*	Plantae
Veronica cymbalaria	Plantae	*Vicia lutea*	Plantae	*Zelus renardii*	Insecta
Veronica multifida	Plantae	*Vicia narbonensis*	Plantae	*Zerynthia cerisy*	Insecta
Veronica persica	Plantae	*Vicia orientalis*	Plantae	*Zerynthia deyrollei*	Insecta
Vespa orientalis	Insecta	*Vicia peregrina*	Plantae	*Zizeeria karsandra*	Insecta
Viburnum lantana	Plantae	*Vicia sativa*	Plantae	*Ziziphus jujuba*	Plantae
Viburnum opulus	Plantae	*Vicia villosa*	Plantae		

CURRICULUM VITAE

PHOTO

Name Surname : Batuhan Atıf Tunç

EDUCATION :

• **B.A. :** 2020, Anadolu University, Faculty of Business Administration, Department of Business Administration.