

ECOLOGICAL NICHE MODELING: AN EMPIRICAL STUDY ON *Apis mellifera* POPULATION DISTRIBUTION

Ekolojik Niş Modelleme: *Apis mellifera* Popülasyon Dağılımı Üzerine Deneysel Çalışma

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ÖZ

Ekosistem çeşitliliğinde en önemli türlerden olan bal arısı, Apis mellifera türü dünya genelinde birçok bölgeye yayılım göstermiştir fakat iklim değişikliği sebebiyle yakın gelecekte sayılarının azalma tehdidi ile karşı karşıyadır. Bu nedenle iklimsel değişkenlerin bal arıları üzerindeki etkileri daha detaylı incelenmeli ve potansiyel negatif etki faktörleri belirlenmelidir. Bu çalışmada Birleşik Krallık, Hollanda, Fransa, Almanya ve Zambiya'da bulunduğu kaydedilen A. mellifera verileri iki farklı izdüşümü modeli yardımıyla şimdiki zaman ve gelecek tahminlerine yansıtıldı. Gelecek tahmininde Avrupa genelinde bal arılarında gözle görülür bir nüfus azalışı kaydedilirken Kuzey Amerika'da değişim, günümüze göre, çok azdı. Daha sonra PCA analiz yöntemi kullanarak 19 iklimsel değişken bir arada değerlendirildi ve günümüzden geleceğe büyüme oranları hesaplandı. Bu çalışma doğrultusunda genel olarak Avrupa'da gelecekte en çok değişiklik gösteren iklimsel değişkenlerin Kuzey Amerika'da gelecekte kritik bir değişikliğe uğramayacağı sonucuna ulaşıldı. Sonuç olarak, bu tür için yüksek orandaki nüfus azalışında etkili olan ve etkilerini yakın gelecekte Avrupa'da gösterecek olan değişkenler kışların şiddeti, en soğuk bölgenin ortalama sıcaklığı, yağış ve sıcaklık mevsimselliği olarak belirlendi.

Anahtar Kelimeler; Apis mellifera, iklim değişikliği, PCA, iklimsel değişkenler, ekolojik niş modelleme.

ABSTRACT

Apis mellifera is one of the species that aid in the maintenance of ecosystem diversity and spread all around the world, yet their numbers are subjected to a decline in the near future. In this study, *A. mellifera* species' occurrence data obtained from the United Kingdom, Netherlands, France, Germany, Zambia was studied by using the present and future projection models generated by using principal component analysis (PCA) on 19 bioclimatic variables. Regarding the future projections, the honey bee species will be significantly decreased in number in Europe, whereas in North America, the change from current to future was somewhat ambiguous. Therefore, the growth rates of the bioclimatic variables from present to the future for both Europe and North America were compared with each other to conclude the most effective bioclimatic variables on the species' occurrences. In conclusion, the most effective bioclimatic variables that caused the major decline in European clades of this species were assessed as the severity of winters, precipitation seasonality, temperature seasonality, and the mean temperature of the wettest quarter.

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Keywords; *Apis mellifera*, climate change, PCA ecological niche modeling, projections, bioclimatic variables, occurrences.

GENİŞLETİLMİŞ ÖZET

Amaç: Bu çalışmada Birleşik Krallık, Hollanda, Fransa, Almanya ve Zambiya'da bulunduğu kaydedilen *A. mellifera* verileri Gbif veri tabanından alındı ve iki farklı izdüşümü modeli kullanarak şimdiki zaman ve gelecek tahminlerine yansıtıldı.

Giriş: Polen taşıyıcı türler biyolojik çeşitliliğin sağlanması ve devamlılığını sağlayan en önemli etkenlerdendir. Ekosistem çeşitliliğinde en önemli türlerden olan *Apis mellifera*, arıcılık faaliyetleri başlıca olmak üzere insan etkisi ile dünya genelinde birçok bölgeye yayılım göstermiştir fakat yine de insan etkisi ile yakın gelecekte nüfuslarında bir azalma beklenmektedir. Bal arısı türleri için en önemli olumsuz etken faktörlerinden biri de bünyesindeki birçok değişkenin etkisi ile birlikte, bütün halinde ekosisteme zarar veren iklim değişikliğidir. Bu nedenle iklimsel değişkenlerin bal arıları üzerindeki etkileri daha detaylı incelenmeli ve potansiyel negatif etki faktörleri belirlenmelidir.

Yöntem ve Gereç: Gelecek tahminleri için, daha gerçekçi bir gelecek üzerine, araştırılan tür için tahminde bulunulması amacı ile en olası senaryo koşullarını içeren yakın gelecekteki iklimsel değişkenleri ifade eden WorldClim veri tabanı modeli tercih edildi. *A. mellifera* türünün potansiyel nüfus dağılımını analiz edebilmek amacıyla kullanılan iki model random forest (RF) ve generalized linear model (GLM) olarak belirlendi ve şimdiki zaman projeksiyonları için kullanıldı. Ayrıca genetik ve coğrafi olarak 3'e ayrılan, *A. mellifera* türüne ait, Avrupa, Afrika ve Büyük Britanya nesilleri ayrı ayrı GLM modeli kullanarak günümüze ve geleceğe yansıtıldı.

Bulgular: Gelecek tahmininde *A. mellifera* türündeki nüfus azalışı, Avrupa genelinde gözle görülür düzeyde, yakın gelecekteki tür kaybının ciddiyet düzeyini belirtebilecek ölçüde iken Kuzey Amerika'da kaydedilen değişim günümüze göre çok azdı. Daha sonra tahmin analizinde belirleyici olarak kullanılan iklim değişkenlerinin veri boyutu ve doğrusallığı değişkenler arasında düşürüp aynı zamanda bilgi kaybından en az miktarda etkilenmek amacıyla PCA analiz yöntemi kullanarak 19 iklimsel değişken bir arada değerlendirildi ve günümüzden geleceğe büyüme oranları hesaplandı. Tüm iklimsel değişkenler için hesaplanan büyüme oranları, gelecekte en çok değişime uğrayacak Avrupa

bölgesi, en az değişikliğe uğrayacak Kuzey Amerika Bölgesi ve dünya geneli arasında karşılaştırma yöntemi ile araştırıldı. Bu çalışma doğrultusunda, yakın gelecekte Avrupa'da en çok değişikliğe uğrayacak olan iklimsel değişkenlerin Kuzey Amerika'da gelecekte kritik bir değişikliğe uğramayacağı sonucuna ulaşıldı.

Sonuç: Bu tür için yüksek orandaki nüfus azalışında etkili olan ve etkilerini yakın gelecekte Avrupa'da gösterecek olan değişkenler kışların şiddeti, en soğuk bölgenin ortalama sıcaklığı, yağış ve sıcaklık mevsimselliği olarak belirlendi. Büyüme oranları doğrultusunda en çok farkı yaratacağı tespit edilen değişkenlerin Avrupa'da, Kuzey Amerika'dan ve dünyanın geri kalanından fark edilir derecede artış veya azalış gösterdiği analizler sonucunda doğrulanmış ve literatür bilgileri ile karşılaştırılarak bu değişkenlerin araştırılan tür üzerinde nüfus ve ekolojik niş korumada hâlihazırda yüksek tesirli olduğu tespit edilmiştir.

INTRODUCTION

Apis mellifera is the western honey bee species that are spread across the world mostly as a result of beekeeping activities due to its environmental, agricultural, and economical importance (Han et al., 2012). Honey bee species are a prerequisite for the maintenance of the ecosystem and diversity of many field crops of flowering plants, fruits, nuts, and vegetables as being one of the most important pollinators on Earth. However, honey bees are facing various threats as a result of the exclusively human effect of habitat destruction, pesticides, loss of genetic diversity, parasites, and climate change (Paudel et al., 2015). As a result of the decrease in the numbers of this species, the world's economy is affected negatively due to the decrease in ecological services. As a result of the beekeeping activities, *A. mellifera* species are spread across the world and diverged over time in Africa, the Middle East, and Europe, yet their numbers are decreasing with the changing climatic conditions and human activities (Arias and Sheppard, 2005). In addition to the direct effect of climate change, the honey bee populations are in decline worldwide also due to the indirect effects such as the infestations of pests and pathogens that cause honey bee loss (Sharif et al., 2021). Therefore, comprehensive research should

be focusing on the future projections of quantitative analysis on the *A. mellifera* species and the possible sources of decline response; in order to protect the colonies from the current degradation more importantly in the rather sensitive regions to the climatic changes such as Mediterranean zones (Flores et al., 2019).

Due to the diversity of the species' population that followed their globalization, the genetic difference between different lineage groups should also be considered for the population studies. In accordance with the comparisons of recent mtDNA and nuclear diversity data of honey bee species from distinct regions, several lineage groups were identified for this species that consist of mainly African and European clades.

With regard to the previous studies, the African origin of *A. mellifera* and the early colonization of west Europe has followed a regional differentiation during the intermediate Pleistocene glaciation. As a result, the extant haplotype frequency and distribution were influenced at a regional scale following the adaptations to local climatic conditions, along with the local beekeeping practices during the last decades (Jaffé et al, 2019). The significant evolutionary events that affected the genetic structure of *A. mellifera* species are; dispersal and differentiation after their divergence from the other cavity-nesting honeybee species, and differentiation of different clades from their native ranges of Europe, Africa, and the Middle East followed by the further dispersal and differentiation by human activities. The population size is further increased in Africa while European colonies were restricted in lower densities (Cánovas et al, 2008).

As shown by the previous studies, the 19 bioclimatic variables are highly correlated in terms of informativeness. Therefore, the linear combination of the 19 bioclimatic variables can be used more efficiently as the indicators for species' distribution, instead of selecting all separately (Makori et al., 2017).

The distribution modeling of species is carried out by utilizing a special package for programming in R. The biomod2 package illustrates larger areas than the initial occurrence data distribution provided by random sampling of the distribution and is used for ensemble forecasting of species distributions (Thuiller et al., 2009). According to the inquired data and the required output, various predictors are used in this package, such as Random forest (RF) and generalized linear model (GLM), and can be used

together to assess the fitness of the environmental conditions of the species occurrences to the projection model and for their comparisons. RF is an ensemble learning algorithm that can be applied only to decision trees. Since decision trees are likely to overfit, RF aims to increase the prediction through random subsampling of rows and columns by introducing a bias to the training phase. This bias results generally in higher test accuracy (Breiman, 2001). GLM, on the other hand, assumes the linear relationship between the expected response and the explanatory variables (PennState, 2022).

In this study, the present and the future projection models were applied to *A. mellifera* occurrence data by using one of the dimensional reduction methods, principal component analysis (PCA), on 19 bioclimatic variables. Here the aim was to explain more than 90% of the 19 bioclimatic variables by excluding multicollinearity. Additionally, based on the genetic information of difference and the distribution based on the location, the occurrence data of the *A. mellifera* species was classified as representing three lineage groups; African clade, Great Britain clade, and European clade.

METHODS

Acquiring the occurrence data of *Apis mellifera*

The occurrence data of *A. mellifera* is downloaded from the Gbif database (Global Biodiversity Information Facility, 2022). The date was restricted from 1981 to 2021, and the countries were restricted to the United Kingdom, Netherlands, France, Germany, and Zambia.

Distribution of the lineages on the occurrence data based on genetic information

The African species occurrence data was considered as a distinct clade from the European occurrences. Accordingly, the lineages were decided based on the geographical occurrence data and the genetic background of the species. In this study, the data were taken and classified based on the countries of origin as follows;

Clade 1: Great Britain

Clade 2: Germany, Belgium, France, and the Netherlands

Clade 3: South Africa

The distribution map of the *A. mellifera* species is plotted by using R studio based on the occurrence data obtained from Gbif and the 3 different lineages

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are colored differently as shown below by the world map (Figure 1). The African and European clades are focused in figures (Figure 2 and 3) respectively

with the European clade having 2 distinct clades also that were colored differently.

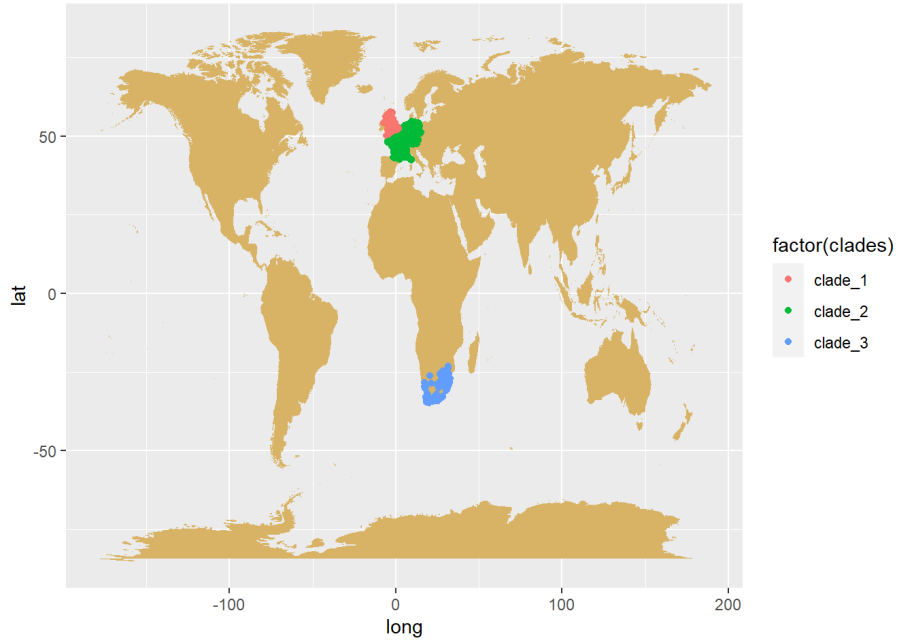


Figure 1. The distribution map of the *A. mellifera* shows the occurrences in Great Britain –as clade_1 in pink color, Germany, Belgium, France, and Netherlands –as clade_2 in green, and Africa –as clade_3 in blue.

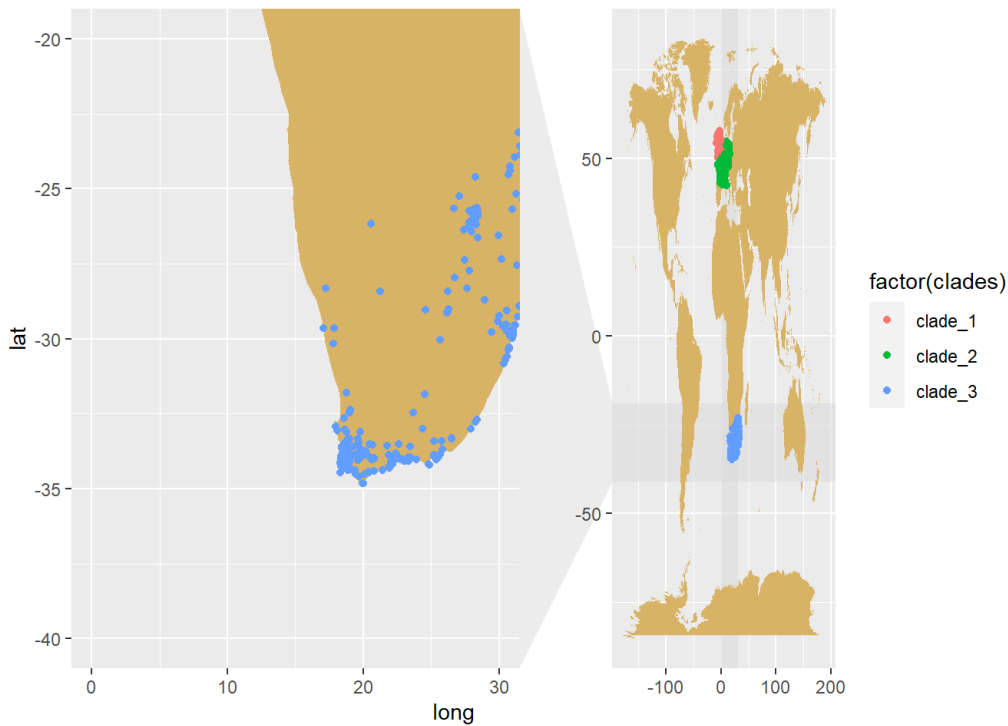


Figure 2. The focused picture of African clade_3.

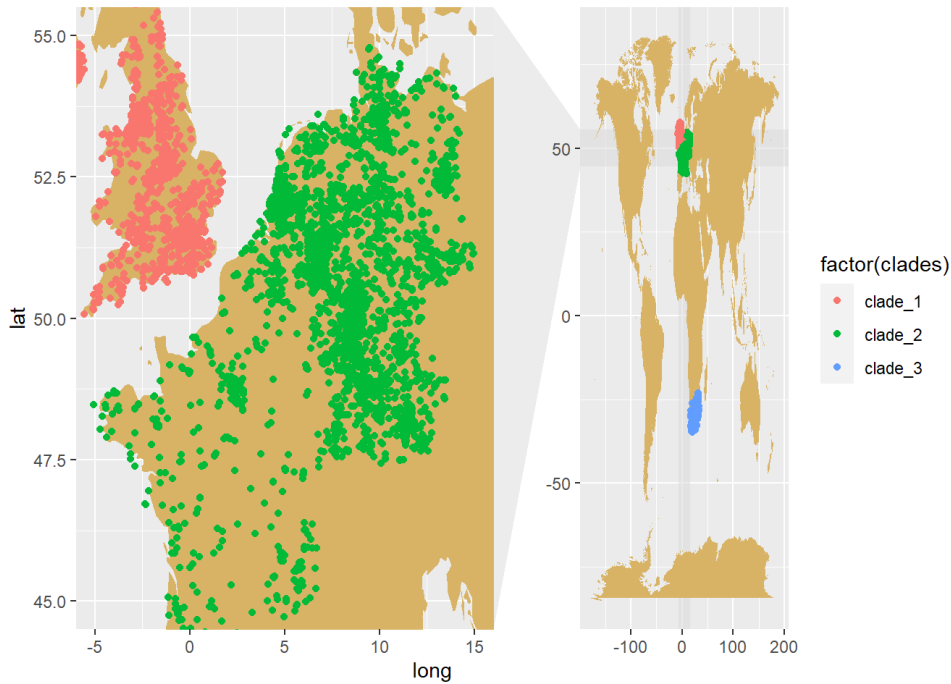


Figure 3. Focus on the European clades, clade_1, and clade_2, depicting the occurrences in Great Britain, Germany, Belgium, France, and the Netherlands.

Acquiring the historical and future bioclimatic variables

The data for each of the 19 bioclimatic variables, BIO 1 to 19, for 5-minute spatial resolutions were obtained manually from the WorldClim database for the historical bioclimatic variables (WorldClim, 2020). The future bioclimatic variables were also acquired from the WorldClim database for longitude/latitude degree of 5-minute spatial resolutions about 9 km at the equator future (2021-2040), and for CNRM-CM6-1 estimations of ssp370 (World Climate Research Programme, 2016). SSP370 scenario was selected because it is the closest to the current CO₂ emissions, due to the assumption that in the near future the climatic conditions will not be able to change drastically in 20 years of the time period. Also, because of the small lifespan of honey bees, a closer future scenario was selected to accomplish more realistic results from the projections. **Performing principal component analysis (PCA) on the bioclimatic variables**

In this study, for the utilization of the honey bee ecological niche model, PCA was performed on all of the 19 bioclimatic variables and the resulting linear

combination was used as the indicator variables. As a result, 4 dimensions were used instead of 19, since 4 eigenvectors were obtained having the eigenvalue greater than 1, meaning that they can explain more variability than what they are supposed to explain. The original space of 19 dimensions was reduced to 4 because the previous dimensions were highly correlated with each other since they are all coming from the same family namely the bioclimatic variable; thus, they all are linear combinations of each other. The reduced dimension space of 4 provided adequate information by explaining 90% variability. In terms of interpretability, here, computational cost and multicollinearity problems have been excluded along with the problem of biased results in the algorithm that were used for the current and future projections. Then, the current and the future projection models were constructed by using the 4 dimensions of the explanatory variables. Figure 4 shows the eigenvalues where the red line is 1 which is the limit for eigenvalues and the cumulative variance that was explained by the PCA respectively in the left and right scree diagrams.

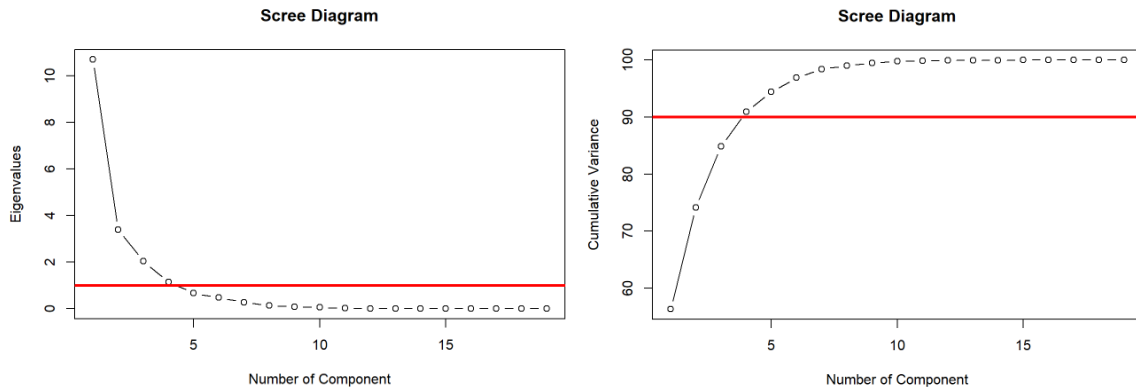


Figure 4. The eigenvalues are shown with the red line showing the limit for eigenvalues, 1 in the left plot. The cumulative variance is shown in the right plot with the red line showing 90% of the variability.

Additionally, PCA was performed on the future environmental variables, as well as the historical bioclimatic variables both by transforming data of the raster-layer object into a raster-stack object in order for BIOMOD species distribution models to work and to perform the current and future projections.

Species distribution modeling and projections

For forecasting of *A. mellifera* species distribution, initially, two model classes were used as part of the biomod2 package processing of modelling in order to test the fitness of the environmental conditions of the species occurrences to the projection model. Also, the pseudo-absence data was generated by using biomod2 projection models since the occurrence data acquired for *A. mellifera* was presence-only, and the undefined locations in the map were excluded by this way, otherwise, they cause manipulations in the projection and decrease the accuracy of the results.

Even if discussing all the details of such algorithms is beyond the scope of this paper, we can mention the bias-variance trade-off in machine learning algorithms. In general, when one is higher the latter is lower and vice versa. RF tries to find a good balance between them by introducing bias through random subsampling. The strength of the individual trees and the correlation between them cause

generalization errors in tree classifiers (Thuiller et al., 2009). Thus, GLM was also used as a model in the projection.

Analysis of some of the differences between the present and the future projections

Based on the changes observed for the present and the future projections for the species, analysis was carried out by using the bioclimatic variables. Firstly, the mean values of the bioclimatic variables for each location of the presence data were calculated. Then the comparisons for the calculated growth rate of each bioclimatic variable from present to future projections were done between North America, namely Mexico, and Europe in order to further study the underlying climatic reasons for the major declines that were observed for the European lineages by comparisons done with the regions that showed no observable change in the near future.

RESULTS

Present and future projections for *Apis mellifera*

The occurrence status map in Figure 5 illustrates both current and future distributions of *A. mellifera* species, generated by using both RF and GLM models.

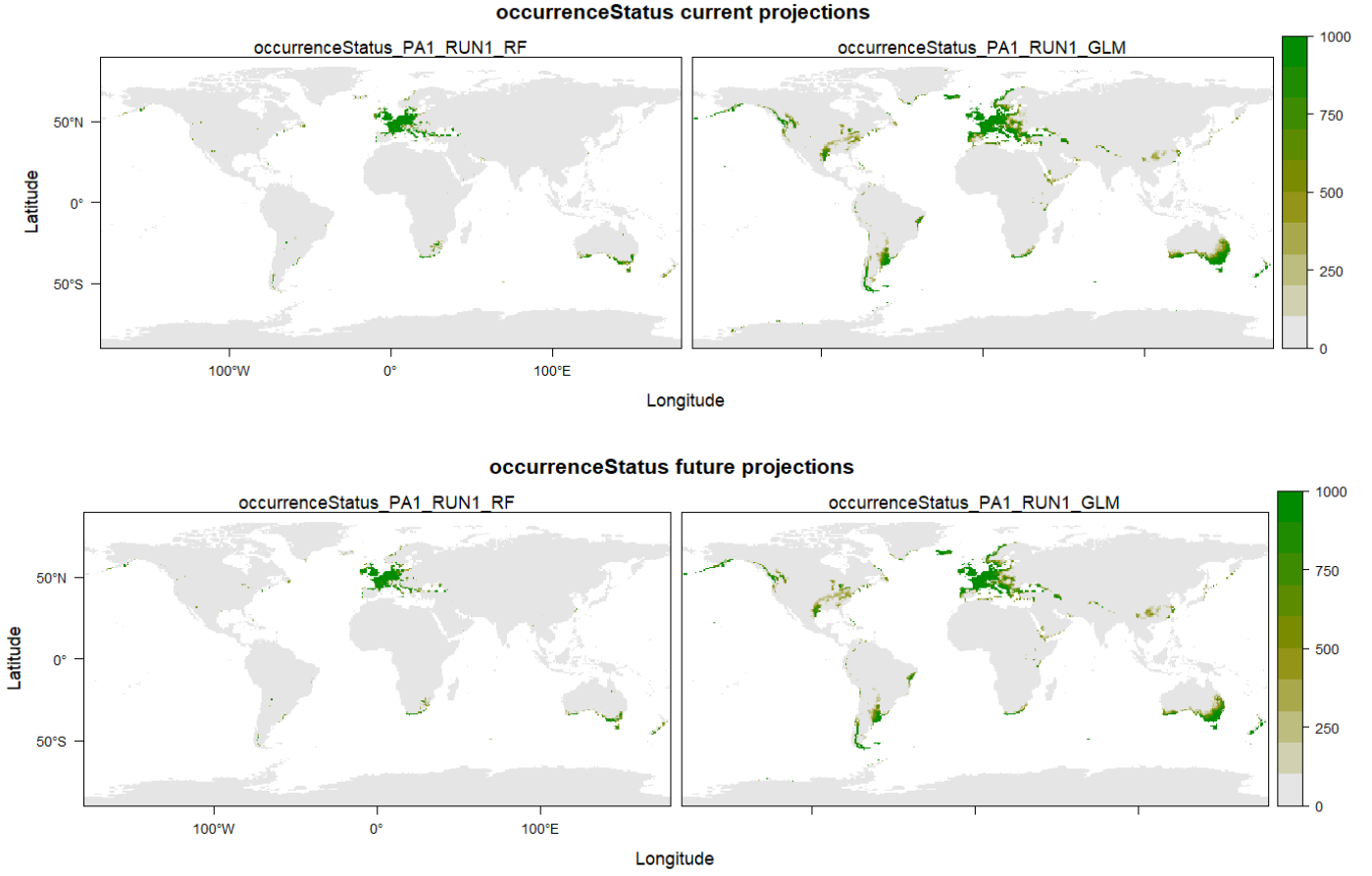


Figure 5. The distribution maps of the present projection of the species are shown above, and that of the future projection of the species are shown in the below pictures. Each projection was generated by using RF and GLM models as labeled RUN1_RF and RUN1_GLM.

Firstly, the GLM model used for both current and future projections projected the occurrences over a larger area than the RF model. Secondly, for both of the model projections, a significant decrease in occurrences was observed worldwide for the future projections. Especially, the major decrease was observed in the locations where the species were found less abundant than the locations where more abundance is projected.

Present and future projections for the different lineages of *Apis mellifera*

The GLM model was used for the present and future projections of the 3 lineages separately. Initially, the present and current projections of the first lineage of Great Britain are shown below (Figure 6).

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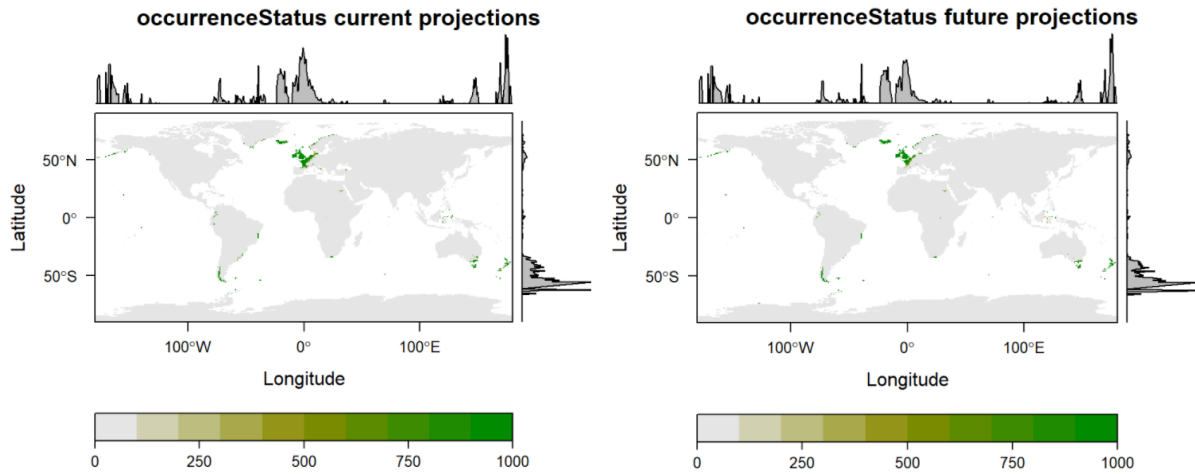


Figure 6. The distribution maps of the present projection of the species were generated by using the GLM model for the first lineage, clade_1.

For the clade_1, some slight changes in distribution from present to future were obtained. Again for the locations where the species are more abundant, no change in occurrence was observable, yet in the locations where the species are found less abundant, the future projections showed less occurrence especially around coastal regions of

southeast America, Italy, and Turkey Black Sea region.

Secondly, the present and the future projections for the second lineage of the occurrences in Germany, Belgium, France, and the Netherlands are depicted on the map (Figure 7).

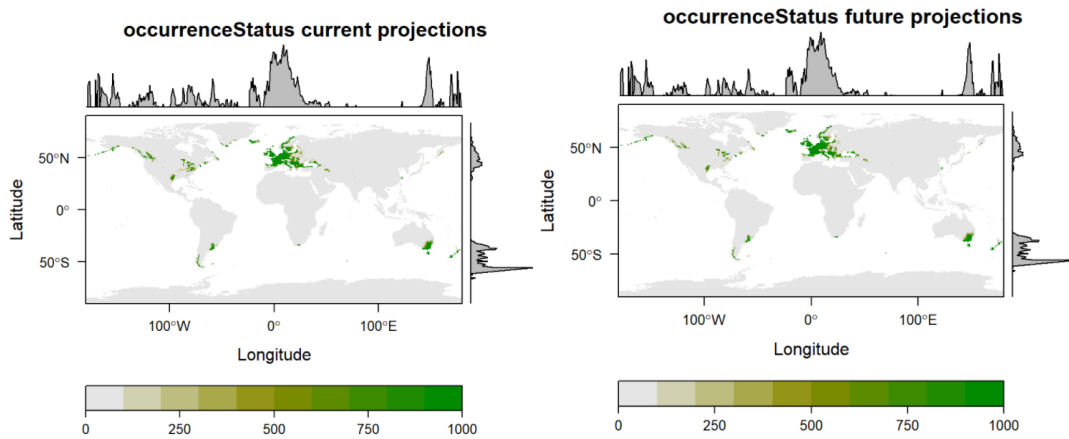


Figure 7. The distribution maps of the present projection of the species were generated by using the GLM model for the second lineage, clade_2.

For the second clade (Figure 7), a significant decrease was observed in the future projection compared to the present around the eastern coastal region of North America whereas the changes in the rest of the world were somewhat ambiguous.

Lastly, the third lineage of South Africa is shown below in Figure 8 as projected by the GLM model to the present and the future.

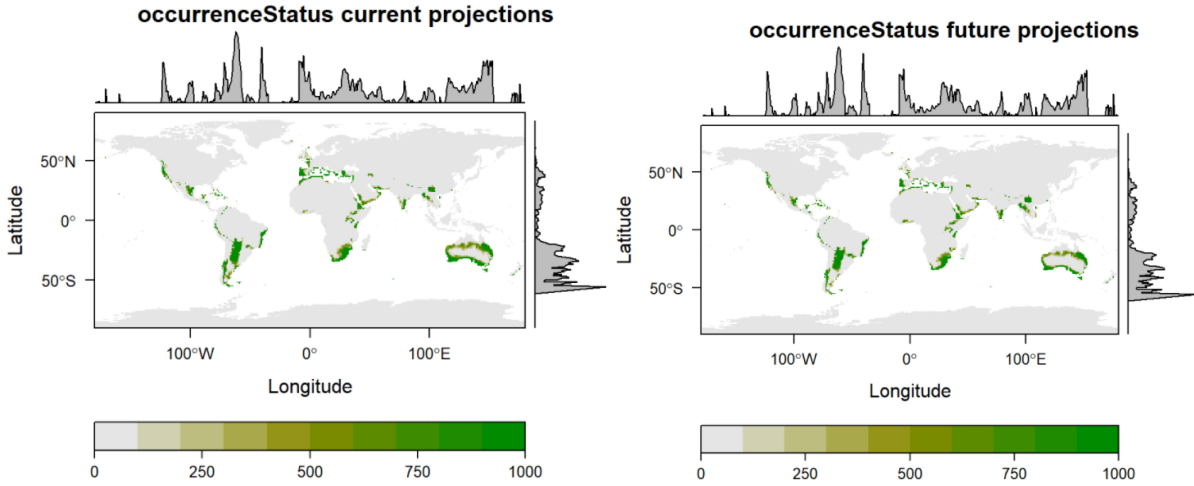


Figure 8. The distribution maps of the present projection of the species were generated by using the GLM model for the first lineage, clade_3.

For the 3rd lineage group, a slight increase in the occurrences in Argentina, Ghana, Nigeria, and Mozambique was observed in the future projection compared to the present, whereas the decrease was observed in the midland regions of Australia, South Africa, Mexico, and Europe.

Analysis on the bioclimatic variables that lie on the locations of the lineages

The mean values of the bioclimatic variables of present and future that are calculated for each location are shown below in Table 1.

Table 1. The mean values for current and future bioclimatic variables for each location in the presence data.

	means_current	means_future
BIO1	10.3136025664475	11.4260536559162
BIO2	8.12932007065567	8.23656814539118
BIO3	36.0917182126033	35.5872033440604
BIO4	553.814401011695	571.786200171954
BIO5	23.0217727425183	24.554102847215
BIO6	0.206130673364563	1.10327672907893
BIO7	22.8156420571953	23.4508261379741
BIO8	11.9309419711625	13.2118662566453
BIO9	7.76488228768998	8.77732713429388
BIO10	17.2515062962582	18.6451892693464
BIO11	3.73434130250618	4.73332450768689
BIO12	760.742233880989	775.627674945988
BIO13	84.7117216622946	87.1066431822113
BIO14	44.5579179897832	44.8745800569606
BIO15	21.0383202996386	21.8114940604337
BIO16	238.510561921856	245.029821884364
BIO17	147.859036310921	149.315166361207
BIO18	198.466519398039	201.801785625609
BIO19	190.357586635372	195.477184878682

Table 1 showed the mean values of the bioclimatic variables for both present and future. According to

Table 1, the Annual Mean Temperature will be increased by 1.1 degrees (BIO1), Mean Diurnal

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Range (BIO2) will not change remarkably, (BIO3) isothermality, will decrease by 0.5 points, (BIO4) temperature seasonality will increase by almost 28 points, Max Temperature of Warmest Month (BIO5) will increase by 1.5 points, Min Temperature of Coldest Month (BIO6) will increase by 0.9 points, Temperature Annual Range (BIO7) will increase by 0.6 points, Mean Temperature of Wettest Quarter (BIO8) will increase by 1 point, Mean Temperature of Driest Quarter (BIO9) will increase by 1 point, Mean Temperature of Warmest Quarter (BIO10) will increase by 1.4 points, Mean Temperature of Coldest Quarter (BIO11) will increase by 1 points, Annual Precipitation (BIO12) will increase by 15 points, Precipitation of Wettest Month (BIO13) will increase over 2 points, Precipitation of Driest Month (BIO14) and Precipitation Seasonality (BIO15) will be almost identical, Precipitation of Wettest Quarter (BIO16) will increase by 6.5 points, Precipitation of Driest Quarter (BIO17) will increase by 1.5 points, Precipitation of Warmest Quarter (BIO 18) will

increase by almost 3 points, and Precipitation of Coldest Quarter (BIO19) will increase over 5 points.

Analysis on the differences between present and future projections

The reasons behind the certain differences in the certain locations were searched by comparing the growth rates of the bioclimatic variables in such regions due to the expectation that they differ significantly. In Europe, there is a visible difference in the distribution of honey bees therefore, the analysis was focused in there to conclude whether they make any difference from present to future. On the other hand, in North America the change between the present and future projections was somewhat ambiguous, the comparisons were done between the Europe and the North America growth rates –percentage change. Table 2 shows the growth rates of Europe and North America, namely Mexico.

Table 2. The means calculated for the current, and the future bioclimatic variables along with the growth rates for Europe and North America, Mexico.

	means_europe_current	means_future	growth_rate		means_mexica_current	means_future	growth_rate
BIO1	10.8418817653946	12.2636349510256	11.5932445095494	BIO1	21.2794842010401	22.6086139103462	5.87886420006423
BIO2	9.00521080189194	9.06274363948366	0.634828037516847	BIO2	9.85852981587287	9.86313929034231	0.0467343543850897
BIO3	31.7373581274422	31.1618018660173	-1.84699287897233	BIO3	44.6733844362456	44.3597974318558	-0.706917124388466
BIO4	745.662088198472	768.72410220004	3.00003784655199	BIO4	503.715544421963	509.941685536379	1.22095158937002
BIO5	26.3403537017054	28.2765418924246	6.84733019364696	BIO5	32.4455969450478	33.8370765687766	4.11229268255634
BIO6	-2.51988145970525	-1.22012367564396	-106.526724299099	BIO6	9.13348229702168	10.4436592651183	12.54519067347
BIO7	28.8602351615028	29.4966655818685	2.15763513539957	BIO7	23.3121146515363	23.3934173168591	0.34754505603658
BIO8	11.881519628254	12.9270631148142	8.08802028174513	BIO8	26.4151459549386	27.9140879921818	5.36984062550416
BIO9	11.1298639062733	13.0459083642299	14.6869378847561	BIO9	17.9666572097155	19.3600442166121	7.19723049858009
BIO10	20.0183582609496	21.7974579238216	8.16195938576725	BIO10	27.2069105444283	28.6150868376024	4.92109739581015
BIO11	1.82852994269513	3.0926703327782	40.8753683405845	BIO11	14.8921839345767	16.1823395490646	7.97261490266094
BIO12	678.735606651858	681.715615077802	0.437133661021393	BIO12	1090.4224137931	1096.7277679928	0.574924277811894
BIO13	90.5038722459026	91.9474845392017	1.5700400076563	BIO13	160.376588021779	163.690865130693	2.02471720475545
BIO14	29.178843729363	29.2231644337408	0.151662919593282	BIO14	46.4460072595281	45.4166666561646	-2.26643802627857
BIO15	41.7415474941302	42.2321388960643	1.16165416850316	BIO15	46.7948444062699	47.8607001828195	2.22699578668575
BIO16	248.402353364952	250.771527479453	0.944754031015557	BIO16	412.872050816697	420.377646742196	1.78544125351697
BIO17	99.6213003542054	100.138640412219	0.516623808635956	BIO17	164.409255898367	164.65237459297	0.147655747573708
BIO18	151.975745932641	149.756073538114	-1.4821919018613	BIO18	369.714609800363	369.734800473748	0.00546085284890373
BIO19	184.982169658402	187.802915693467	1.50197137496495	BIO19	190.533121597096	190.288377313562	-0.128617568234835

From the above table, it was concluded that more drastic changes were observed from the present to future bioclimatic variables in Europe, than North America. For example, the Mean Temperature of Coldest Quarter (BIO11) increases over 40% in Europe whereas that increases almost 8% in North America, and the Min Temperature of Coldest Month (BIO6) decreases by 106% in Europe whereas that increases 12% in North America in the future.

Accordingly, the comparisons of the growth rates were done between North America, Europe, and the world as shown below in Table 3.

Table 3. The comparison of the growth rates of Europe, the world, and North America respectively.

	EU_Growth	World_Growth	NA_Growth
BIO1	11.5932445095494	12.7544732551088	5.87886420006423
BIO2	0.634828037516847	-1.18264984163205	0.0467343543850897
BIO3	-1.84699287897233	-2.41309437332736	-0.706917124388466
BIO4	3.00003784655199	-0.672934445273483	1.22095158937002
BIO5	6.84733019364696	5.88263420049868	4.11229268255634
BIO6	-106.526724299099	-532.499634244125	12.54519067347
BIO7	2.15763513539957	-0.474435526128063	0.34754505603658
BIO8	8.08802028174513	8.51412271860269	5.36984062550416
BIO9	14.6869378847561	17.7520395422023	7.19723049858009
BIO10	8.16195938576725	7.56957335204494	4.92109739581015
BIO11	40.8753683405845	32.5500125543644	7.97261490266094
BIO12	0.437133661021393	1.55001518849285	0.574924277811894
BIO13	1.5700400076563	3.1035018628058	2.02471720475545
BIO14	0.151662919593282	-0.169734199429162	-2.26643802627857
BIO15	1.16165416850316	1.36669412550563	2.22699578668575
BIO16	0.944754031015557	2.32598070054787	1.78544125351697
BIO17	0.516623808635956	0.755622928510687	0.147655747573708
BIO18	-1.4821919018613	0.0820956787201721	0.00546085284890373
BIO19	1.50197137496495	2.05168091391371	-0.128617568234835

The above table showed how drastic the changes will take place in the future for Europe, from the comparison that the changes are close to the world growth rates or exceed them even if the regional changes are in question.

DISCUSSION

From the present and future projections generated of *Apis mellifera* species and the 3 lineages of the species, by both RF and GLM models, overall a significant decrease in the occurrences was observed. However, by using the GLM model for the projections, 3 different lineages were also projected separately from each other and the whole species occurrences. From the separate projection models of each 3 lineages, the changes in the occurrences were observed more clearly since a limited region was in question and the projections were more realistic by working with a smaller group of occurrences. Additionally, since the lineages were decided based on the genetic information, for the ecological niche modeling of the species the genetic background and the different clade groups should also be considered alongside the occurrence only information. The comparative analysis of the changes in the bioclimatic variables for the least affected and the most affected regions provided detailed information on the possible sources of the major declines within the distinct lineages and revealed the most vulnerable regions to the climatic changes in the near future. Also, while performing PCA on the bioclimatic variables enabled collective assessment of the effects in the future, the separate

comparisons of each variable enabled to identify which variable results in more severe effects in the future.

Regarding the bioclimatic variables used for the projections, PCA was performed for each of the 19 bioclimatic variables, so that 90% of the variability was explained by 4 dimensions, instead of using 19 bioclimatic variables separately. As a result, the projections were done by using the information from all of the bioclimatic variables as well as using them all for the research of the factors that caused the changes between the projections, without facing the multicollinearity problem or dealing with the computational problems in terms of interpretability.

The GLM model was preferred over the RF model for the present and future projections of the 3 lineages since the model projected the occurrence data over a larger area than the RF model. Even if the size of the projected area does not necessarily reflect the accuracy of the method used, since the distribution of the *A. mellifera* species was recorded as they spread all around the world (Techer et al., 2017), and regardless of the model used, in this study, the differences in the occurrence projections over a large area was preferred for comparability of the results.

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By the bioclimatic variables' growth rate comparisons done for Europe, North America, and the whole world, the reason behind the significant decrease in this species' occurrences in Europe was investigated. Overall, more drastic changes were calculated in the bioclimatic variables from present to future projections for Europe; thus, it was concluded that climate change will be affecting Europe more than North America which in turn appeared to affect the species distribution negatively. Although Europe lineage (clade_2) accounts for the occurrences in North America, as a result of the severity of the difference between the climatic conditions, the same genetic lineage group responds differently in different locations.

For Europe, some of the bioclimatic variables were changed severely and predicted as the main causes of the decreases in the occurrences of the species. Although the *A. mellifera* species spread all around the world and shows great adaptive potential in all those diverse climates, the evidence demonstrated that climate change is directly affecting the honey bee development, behavior, physiology, and distribution (Le Conte and Navajas, 2008). In the past, high mortality rates were explained by longer cold, rainy, and hot weather periods (Kauffeld et al., 1976), also severe winter weather is reported to be the most important factor in the winter mortality rates of honey bees by the direct effect of the weather on colony productivity (VanEngelsdorp et al., 2008). This effect is also assessed in this study that the Min Temperature of Coldest Month (BIO6) decreases by 106% in Europe whereas 12% increase is seen for North America, also the Mean Temperature of Coldest Quarter (BIO11) increases over 40% in Europe whereas that increases almost 8% in North America. Therefore, Europe will have more severe winters in the future and this will be observable in the decrease of the numbers of *A. mellifera* species.

The other effect is the high temperatures and precipitation effects that are positively related to nectar production, accordingly colony productivity and increase in numbers in honey bees (Shuel, 1992). Therefore, insufficient precipitation at inappropriate times is expected to affect the numbers negatively in the future (Meixner, 2010). However, this precipitation effect is barely seen in the results, since a minor change is observed in the precipitation-related bioclimatic variables or it can be also concluded that, honey bees are vulnerable to minor changes in precipitation amounts and seasonality.

According to previous studies, the Temperature Seasonality (BIO4), and the Mean Temperature of Wettest Quarter (BIO8) affect the numbers of honey bees negatively, whereas the effect of the Precipitation of Wettest Month (BIO13) is positive (Delgado et al., 2012). In conjunction with the results of this study, it can be said that the major decrease in honey bee occurrences in Europe is also correlated with the effects of the changes on BIO4 and BIO8. Temperature seasonality is changed by 3 points for Europe, and the mean temperature of the wettest quarter was increased by 8 points both are remarkably high in Europe compared to North America and the world whereas precipitation of the wettest month increased by 1.5 points less than North America and the world. Another study showed that the most effective bioclimatic variables are mean temperature in the wettest quarter and mean annual temperature in honey bee numbers (Peil and Aranda, 2021); for which the severity of the effects was explained as the reasons for the future decrease in honey bee occurrences.

Other than the effects of the climatic condition variations solely on the *A. mellifera* species itself, expectedly, these changes will also influence the other interacting species with honey bees and influence the honey bee occurrences indirectly. Such an effect can be observed with the changes in the annual mean temperature, mean diurnal range, minimum temperature of the coldest month, and the mean temperature of the warmest quarter. Even if the population distribution was assessed based only on the bioclimatic variables in this study, further decline effects will be much more likely in the future. For instance, in the population distribution of invasive species such as parasitic flies the major contributions belong to the BIO1, BIO2, BIO6 and BIO10 variables in the Mediterranean region (Abou-Shaara and Darwish, 2021). As a result, since these variables already showed a higher growth rate in the European clades and contributed to the major decline in the distribution within the scope of this study, due to the interconnected effects, these bioclimatic variables will appear to be more disruptive in the future.

Regarding the regional future occurrence changes, whereas the major declines are likely to be observed in the coastal regions in the future, the South Africa region was assessed as if the population size there will be increased in the near future. *A. mellifera* species prefer warmer, fewer variable climates and mainland rather than island sites for visitation (Hung,

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2018) since the species response to temperature increase are increasing flight departures (Burrill and Dietz, 1981). This may explain the higher decrease in numbers around coastal regions and a slight increase in the numbers of the mainland for the African clade.

Lastly, step declines are the problem of North America for a long time as well as Europe and the risk factors are still affecting the populations' occurrences (Watanabe, 1994). Thus, in this study, the severity of the effects was compared between Europe and North America, yet the changes in North America cannot be assessed that might cause by the model performances the fitness to the data, as well as lack of repetition of the projections while using the models, and the insufficiency of the data.

Conclusions

Honey bees are one of the most important species in maintaining biodiversity as pollinators. The *Apis mellifera* species has great adaptive potential since they are spread all around the world mostly by human activities. However, the numbers of these species are decreasing mostly because of climate change, and again mostly because of human activities. In conclusion, conservation measures should be taken in order to decrease the loss of this species that in turn cause the disruption of ecotypes that are highly dependent on world biodiversity which is maintained by honey bees all around the world.

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