IMPACT OF CLIMATE CHANGE ON THE TEMPORAL AND SPATIAL DISTRIBUTION OF THE INDIAN PEAFOWL (*Pavo cristatus*) IN KERALA

by

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(2011 - 20 - 104)

THESIS

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DECLARATION

I, Sanjo Jose V. (2011 – 20 – 104) hereby declare that this thesis entitled **"Impact of climate change on the temporal and spatial distribution of the Indian Peafowl (*Pavo cristatus*) in Kerala"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

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Certified that this thesis entitled **"Impact of climate change on the temporal and spatial distribution of the Indian Peafowl (*Pavo cristatus*) in Kerala"** is a record of research work done independently by Mr. Sanjo Jose V., under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to him.

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Sanjo Jose V.

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SYMBOLS AND ABBREVATIONS

|r|	Pearson correlation matrix
AKN	Avian Knowledge Network
alt	Altitude
AUC	Area under the curve
bio1	Annual mean temperature
bio2	Mean diurnal range
bio3	Isothermality
bio4	Temperature seasonality
bio5	Maximum temperature of warmest month
bio6	Minimum temperature of coldest month
bio7	Temperature annual range
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

bio16	Precipitation of wettest quarter
bio17	Precipitation of driest quarter
bio18	Precipitation of warmest quarter
bio19	Precipitation of coldest quarter
BRT	Boosted Regression Trees
CIAT	The International Centre for Tropical Agriculture
DK-GARP	Desktop Genetic Algorithm for Rule-set Prediction
DMSP	Defence Meteorological Satellite Program
EEA	European Environment Agency
FAO	Food and Agriculture Organization of the United Nations
GAM	Generalised Additive Models
GARP	Genetic Algorithm for Rule-set Prediction
GCMs	General Circulation Model
GCMs	Global circulation models
GDM	Generalized Dissimilarity Models (GDM)
GHCN	Global Historical Climatology Network
GIS	Geographic Information System
GLM	Generalized Linear Model
HadGEM2-AO	Hadley Global Environment Model 2- Atmosphere-Ocean
IPCC	Intergovernmental Panel on Climate Change
landcover	Land cover

LCCS	Land Cover Classification System (LCCS)
MARS	Multivariate Adaptive Regression Splines (MARS)
MARS-COMM	Multivariate Adaptive Regression Splines-Community data
MaxEnt	Maximum Entropy Modelling
MM5	Mesoscale Model version 5
OM-GARP	Open-Modeller Genetic Algorithm for Rule-set Prediction
R^2	Coefficient of determination
RAMS	Regional Atmospheric Modelling System
RCPs	Representative Concentration Pathways
ROC	Receiver Operating Characteristic Curve
SD	Standard Deviation
SRTM	Shuttle Radar Topography Mission
UK	United Kingdom
wbint	Inland water bodies
wbpere	Perennial water bodies
wlint	Linear water inland
wlpere	Perennial rivers
WMO	World Meteorological Organization

INTRODUCTION

CHAPTER 1

INTRODUCTION

The world is worried about global warming and the impact it will have on the people and the ecosystems on which they depend. Climate change became one of the major challenges of our time and it adds enormous stress to our societies and to the environment. Prominent changes are reflected in the temperature and apparently these changes are a result of the increased levels of the greenhouse gases. According to IPCC AR5 synthesis report, in the Northern Hemisphere the period from 1983 to 2012 was likely the warmest 30 year period of the last 1400 years. Over the period 1880 to 2012, the globally averaged combined land and ocean surface temperature showed a warming of 0.85 °C (0.65 °C to 1.06 °C) (Allen *et al.*, 2014). Scientist assumes that there could be a further heat increase of at least 1.8 degrees during the 21st century, even if we take decisions for mitigation now. Also there would be changes in the precipitation patterns. The effects of these changes are vast challenges for mankind. The human activities and the related anthropogenic activities like fossil fuel combustion and the greenhouse gas emissions are the primary causes for climate change. Climate change intensifies other problems like loss of biodiversity and ecosystem services, water scarcity, floods and droughts, desertification and land degradation and intensified biogeochemical cycles. Adaptive mechanisms have to be practiced to combat the climatic changes experienced over the globe. The knowledge regarding these changes have to be updated and constantly reviewed. People have to be aware about the climate change and its penalties.

The effects of climate change on biodiversity are poorly understood compared to the physical dimensions of these changes. Climate change effects a number and variety of plant and animal species in a particular location. A sudden change in the climate requires larger and faster scales of adaptation than in the past. The species which fails to adapt are at a risk of extinction. A single loss of species will lead to cascading effects since each organisms are connected by food webs and other biological interactions.

The migration of animals are linked to climate factors such as temperature, moisture availability and amount of daylight. The natural patterns of various species are disrupted due to the changes in the climate. These in turn will affect the behavior and interactions of various species. Some may adjust their life cycle patterns to the changing weather conditions, but some may fail.

There are evidences which shows that the recent climatic changes have affected numerous organisms with diverse geographical distributions. Climatic regimes influences species distributions through species-specific physiological thresholds of temperature and precipitation tolerance. These climatic envelops are shifted due to the warming trends. Some animal and bird species will change their locations in search of a better place where the environmental conditions are favorable for their growth and reproduction. The stress condition imparted by the combined effect of temperature and humidity causes metabolic changes in the living species. For avoiding the stress they can alter the metabolic and physiological activity. The migration will lower the stress by maintaining their bodily functions same as before by finding ambient conditions outside. These migrations can be considered as a biological indicator of climate change which tells the society about the change happening in the environment. The species are expected to track the shifting climate.

In Kerala there is a change in the climate during recent years, which led to the species distributional change, especially causing migration changes in the avian species. The birds are best regarded as a good bio indicator of climate change. Also they can be easily understood by the public and policy makers, since birds are very popular and it have a recognizable and iconic status throughout the world. A slight change in the environment will be tracked by the bird and will rush to a safe place where the environment is quite favorable for their growth and reproduction. The biotic interactions are not static in spatial and temporal resolution and it can be linked with the impacts of the climatic changes.

There has been a considerable change in the distributional range of Peafowl (*Pavo cristatus*) in Kerala. One of the earliest bird survey in Kerala, (erstwhile Travancore-Cochin), was conducted by Salim Ali and Hugh Whistler (1935-36). However, Ali (1969) reports that he found the Indian Peafowl's from the deciduous forests of Peechi-Vazhani. Subsequent to that there are quite a few records of the Indian Peafowl from Kerala (eBird, 2016).

For the understanding of the distributional change with respective to the environment, species distribution models can be used. They are empirical models which relates the field observations to the environmental predictor variables using the statistical methods. These models are used to predict the changes in the distributions that would happen in the future by incorporating the climate model data.

In this project we are trying to model the distribution change happened to the Indian Peafowl in Kerala using appropriate model techniques. We are putting a hypothesis that, changes in the distribution of the Indian Peafowl was due to the recent changes in the climate of Kerala. This species can be used as a bio-indicator of climate change if the results obtained are good. So far by observational and traditional experiences we came to such a conclusion, but there is no scientific explanation to all these.

The primary objective of this study is to find out the reasons for the expansion of the distribution of the Indian Peafowl (*Pavo cristatus*) in Kerala and to find out the possible reasons for the change in the distribution pattern of the Indian Peafowl. Using modelling techniques we can develop an ecological niche model based on the current climate data and to project the regional shifts in the distribution pattern of the Indian

Peafowl based on the results of the model in the changing future climatic conditions under different scenarios.

The methodology followed can be used for further studies of various other species which are being changing its distributions. The study can reveal better about the physical changes happening in the environment whereas the statistical data analysis can just give the quantified changes which may not be ecologically significant. The models will be beneficial to predict the future distributional changes in the Indian Peafowl and in a similar way other significant species can also be studied. This study can provide a better idea about the impact of climate change on the geographical distribution of the Indian Peafowl.

REVIEW OF LITEREATURE

CHAPTER 2

REVIEW OF LITERATURE

2.1 SPECIES DISTRIBUTION: FACTORS

The strong relationship of the distributions of individual species and species richness with the climate of that region had been noted by bio geographers centuries back itself. Combinations of predictor's especially environmental factors had a significant correlation with the species distribution, but the effect was uncertain (Freedman, 1983; Graham, 2003; Whittingham *et al.*, 2006; Platts *et al.*, 2008; Murray and Conner, 2009). Factors affecting the species distribution was an unresolved issue in ecology (Araujo and Guisan, 2006). It was concluded that the decline in the population of *Turdus torquatus* (Ring Ouzel) in Northern Britain was due to the increase in summer temperature and decrease in summer rainfall (Beale *et al.*, 2006). Bird species distribution was affected by other factors like summer weather (Robinson *et al.*, 2007), food availability (Conrad *et al.*, 2006) and habitat distribution and quality (Fuller *et al.*, 2007). The bird population was also affected by trends in uniform crop land associated with the crop loss, margin and hedge foraging habitat and nest sites (Gregory *et al.*, 2007; Thaxter *et al.*, 2010). Climatic variables such as number of cold and wet days, length of winter frosts and snow periods, summer drought and spring temperatures affected the bird species demography leading to varying population trends over time (Robinson *et al.*, 2007). Due to increased winter temperature population of *Ardea cinerea* (Grey Heron) in Northern Italy has increased (Fasola *et al.*, 2010).

2.2 CLIMATE CHANGE IN KERALA

There were evidences which showed the decline of annual rainfall in the southern part of Kerala, whereas northern part doesn't showed similar trends (Soman *et al.*, 1988). An increase in the mean surface temperature (1.5°C) during monsoon season was predicted in the decade 2040-2049 with respect to 1980s (Saseendran *et al.*, 2000). Studies showed that southwest monsoon rainfall and annual rainfall was decreasing, but post monsoon rainfall as increasing (Krishnakumar *et al.*, 2008; 2009). Annual rainfall received in the Palakkad Gap in Western Ghats region varied with altitude and compared to the entire state annual rainfall was comparatively lower over these regions (Raj and Azeez, 2009; 2010).

The following results were released by India Meteorological Department in their monograph published on 2013. Increasing annual mean maximum (+0.01°C/year) and minimum temperature (+0.01°C/year) trend was significant (95%) over Kerala. Significant increase in annual mean diurnal temperature range DTR trends (+0.01°C/year) had been observed in Kerala. However annual average rainfall had decreased (-1.43mm/year) over Kerala. Winter mean maximum temperature trend was increasing (+0.01°C/year). In winter rainfall there observed a decreasing trend in Kerala (-0.4 mm/year). There showed an increasing trend in summer mean maximum temperature (+0.01°C/year) whereas no trend was observed in summer mean minimum temperature trends. But summer mean temperatures had significantly increased over Kerala (+0.01°C/year). State averaged summer mean DTR trend was increasing at the rate of +0.01°C/year. Maximum decline in summer mean rainfall trends had taken place over Kerala (-1.15 mm/year). The monsoon mean maximum (+0.02°C/year) and mean temperature (+0.01°C/year) was increasing. Monsoon season mean DTR trend also showed an increasing trend (+0.02°C/year). The monsoon rainfall trend showed a decreasing trend (-2.42 mm/year). The post monsoon mean maximum (+0.01°C/year), mean minimum (+0.01°C/year) and mean temperature (+0.01°C/year) was increasing. The post monsoon rainfall showed an increase of +1.68 mm/year (Rathore *et al.*, 2013).

2.3 IMPACTS OF CLIMATE CHANGE ON BIRDS

2.3.1 Birds as bio-indicators

The avian species had the capacity to be considered as important bio-indicators which was easily understood by the public and policy makers, since birds were very popular and it have a recognizable and iconic status throughout the world (Crick, 2004). Climate change was considered as one of the most dangerous and widespread threat to biological diversity (IPCC, 2007). According to Willis and Bhagwat (2009) anthropogenic activities were transforming ecological systems globally, changing the world's climate and reducing and fragmenting habitats. Birds were well known indicators of climate change having advantages of best known class of organisms in climate research (Wormworth and Sekercioglu, 2011) and birdwatchers across the globe make up an extensive datasets (www.ebird.org; www.worldbirds.org).

2.3.2 Effect of climate change on physiology of birds

The weather affects the metabolic rate of birds directly and indirectly, which influenced the bird behaviour. Important activities like feeding and breeding would be reduced when birds avoid places with unfavourable climates (Walsberg, 1993). Crick (2004) reported that the success of breeding depends upon the production of various hormones which would be fluctuated under various weather conditions. Indirect effect on bird activity and behaviour was induced by the temperature changes and humidity. Results by Gregory *et al*. (2009) showed that due to climate change a detectable continent-wide effect had already took place with negative and positive effects at the level of large species assemblage. Nevertheless, there were studies which hinted at the important role of physiological responses of birds to the climatic changes (McKechnie, 2008; McNab, 2009).

2.3.3 Responses of birds towards climate change

The responses done by the species to climate change was generally by three methods such as movement (if the species are mobile they will track the suitable environment niches), adaptation (if the species are able to adjust to the changing conditions and have high physiological tolerances) and extirpation (when both movement and adaptation fails) (Holt, 1990; Melillo *et al*., 1995). Apart from climatic factors, land-use and habitat change, biotic interactions and evolutionary adaptation also played a role in the species distribution (Huntley *et al*., 2006; La Sorte and Thompson, 2007; Beale *et al*., 2008). Thomas (2010) stated that climate can be considered as one of the major determinants of range boundaries. Endothermic birds were affected indirectly by climate change due to its impacts on vegetation in their communities rather than direct effects on physiology (Aragon *et al*., 2010a). Chen *et al*. (2011) argued that the majority of the shifts in distribution was due to climate warming and he showed evidences for range shifting towards the pole and upwards by many species (Chen *et al*., 2011).

2.3.4 Climate change and avian distributional range

Gibbons and Wotton (1996) showed that the distributional range expansion of Dartford Warbler (*Sylvia undata*) in the UK since the 1960s was due to the lack of severe winters. The studies that documented earlier revealed that, the shift in the distributional range in many regions was appeared to track changing temperatures and the interaction between temperature and precipitation also played a significant role in the range distributions (Hawkins *et al*., 2003). Temporal distributional study could be done to investigate how much change have happened for this interactions over the century (Hawkins *et al*., 2003). A different approach study by studying the community index rather than species range margins revealed that, in France northward shift in breeding bird assemblage was substantial but it was not a fast response to track the climate warming experienced there (Devictor *et al*., 2008). The shifting distribution of birds had been linked to climate change already (Gregory *et al*., 2009; Niven *et al*., 2009; Chen *et al*., 2011). A significant relation was found between predicted changes in the range extent and variations in population trend, of those bird species whose ranges were expanding showed an increase in population size and vice-versa (Gregory *et al*., 2009). A non-significant upward shift was detected in the breeding bird's distribution over Western Italian Alps (Popy *et al*., 2010). Considering the whole bird community, not much significant distributional change was observed, and scientists predicted using the models, based on current distribution and climatic variables that, the distribution would be substantially rearranged for a single bird species according to the predicted climate warming (Virkkala *et al*., 2010). Reif *et al*. (2010) found that, at higher latitude and altitude, range reduction was observed in some species due to the lack of habitat. Tropical bird species was increasingly recognized as most vulnerable species to climate change (La Sorte and Jetz, 2010; Harris *et al*., 2011; Sodhi *et al*., 2011; Wormworth and Sekercioglu, 2011). The findings of Bradbury *et al*. (2011) showed that, between 1974 and 2006, *Sylvia undata* expanded its range upward and northward in UK. The impacts of climate change on species distribution was important since it also affected the demographic rates of birds (Pautasso, 2012).

2.3.5 Importance of range distribution studies

A wide knowledge regarding the species ecological and geographic distribution was needed for the better understanding of ecological and evolutionary determinants of various spatial patterns of biodiversity (Rosenzweg, 1995; Ricklefs, 2004; Graham *et al*., 2006) and for the conservation planning and forecasting (Ferrier, 2002b; Funk and Richardson, 2002; Rushton *et al*., 2004). Indicators of the impact of climate change was in the developing stage and scientists and policy makers were looking forward for the further development to study the biological consequences of climatic warming and implementing adaptive and mitigative measures (Mace and Baillie, 2007; EEA, 2007).

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2.4 MODELLING OF SPECIES DISTRIBUTION

2.4.1 Importance of species distribution modelling

Root (1988a, 1988b) and Root and Schneider (1993) found strong statistical correlation between the distribution and abundance of 148 wintering land birds and six environmental factors which mainly included the climatic variables. Gates *et al.* (1994) used multivariate regression equations for modelling the species distribution in UK, with reference to the land use and climatic variables and the results showed that the climate had strong relationship with bird distribution and redistributions were happening with the predicted climate warming. By using climate envelops they described the spatial distribution and such predictions had to be tested against current distribution pattern for the change in the measurements of distribution. Additional factors like biotic interactions, geographic barriers and history were not included, which meant that species would be present rarely in the suitable environments (Anderson *et al.*, 2002; Svenning and Skov, 2004; Araujo and Pearson, 2005).

Species distribution models were used to study the spatial configuration and characteristics of habitats that permitted the continuity of species in landscapes (Araujo and Williams, 2000; Ferrier *et al.*, 2002b; Scotts and Drielsma; 2003), past species distribution (Hugall *et al.*, 2002; Peterson *et al.*, 2004), species distribution in future climatic conditions (Bakkenes *et al.*, 2002; Skov and Svenning, 2004; Araujo *et al.*, 2004; Thomas *et al.*, 2004; Thuiller *et al.*, 2005) and relationships between environmental parameters and species richness (Mac Nally and Fleishman, 2004).

Conservation practitioners depended upon distribution models for the estimation of most suitable areas for a species and could predict the probability of presence in areas where systematic surveys have not done (Elith, 2002). For the study of changing distributions the use of predictive modelling was used. The environmental variables, including climate could be possibly correlated with the absence or presence of a species if their distribution was accurately mapped (Crick, 2004).

Using the known distributional information of species, the environmental conditions were defined and thus identifying the geographical regions having similar environment and modelling the species distribution (Pearson and Dawson, 2003). The distribution of species abiotic niches in relation with the environmental data at the observed localities had been studied widely using bio-geographical analysing techniques (Guisan and Thuiller, 2005).The only way to test the hypothesis or scenarios foretelling the future was by watching the real future to unfold and to overcome this difficulty we could use past changes in the environment to test whether species and its ecosystems have responded in a similar way that the models predicted (Araujo *et al*., 2005). Species distribution models are trying to give the predictions of the species distribution using the presence or abundance of species in relation to a particular environment predictors. These models were widely used as a tool to explore the various arguments in ecology, evolution and conservation (Elith *et al*., 2006).

These models could also estimate the future species distribution under various climate change scenarios (Jeschke and Strayer, 2008; Sinclair *et al*., 2010), potential expansion in newly colonized areas by the introduced species (Jimenez-Valverde *et al*., 2011; Jeschke and Strayer, 2008) and could be used in reserve planning (Thorn *et al*., 2009). The study of these shifts in the distribution of bird species were essential for the management of protected area networks and conservation of endangered bird species (Aragón *et al*., 2010b; Araújo *et al*., 2011). Due to the shifts in distribution the current protected areas would become outdated, leading to the management of whole landscape for biodiversity conservation (Pautasso *et al*., 2011).

2.4.2. Process of species distribution modelling

2.4.2.1 Steps in species distribution modelling

The modelling of species distribution was done by several steps: (1) present day data of species in the form of point of occurrence (Peterson *et al.*, 1998; Peterson and Stockwell, 2001b); (2) ecological niche models are developed which is tested using the distributional data (Guisan and Zimmerman, 2000; Kobler and Adamic, 2000); (3) based on the general circulation models of climate change, the shift in the distribution is projected onto the landscape of interest; (4) onto the transformed landscapes distributional shifts are being modelled by projecting ecological niche models of particular species. In the environmental space models can estimate the suitable ecological niche by analysing the response of species to abiotic environmental factors (Soberon and Peterson, 2005) and using these, the model could derive the probability of presence of species for any given area or trace the specific environmental conditions which suits the particular species (Elith *et al.*, 2011).

2.4.2.2 Methods for testing accuracy

There were several methods used for the modelling of species distribution which varied in the steps of modelling; selecting the most suitable predictor variables, defined functions for each of the variable, weight variable contributions, the interactions of predictors and species and in predicting the geographic patterns of occurrence (Guisan and Zimmerman, 2000; Burgman *et al.*, 2005; Wintle and Bardos, 2006). The various rules in the models were made up of individual algorithms and based on it, the landscapes would be identified within and outside the ecological niche (Peterson, 2001a). Hierarchical portioning could be adopted in order to compare alternative models and to study the weight of evidence of different factors that were included in the model (Mac Nally, 2002). Concerns of the accuracy of prediction of future species distribution under varying climatic conditions were addressed by testing the climatic envelope models (Akcakaya *et al.*, 2006; Pearson *et al.*, 2006; Araujo and

Rahbek, 2006; Zimmer, 2007). The accuracy of model description about the range of conditions suitable for a species depended upon the degree of environmental dimensions that defined the species distributional limits (Pearson *et al.*, 2007). Models were built mainly on correlations between the variables and distribution patterns and this did not identified the causal relationship due to autocorrelation among the variables (Bahn and McGill, 2007; Currie, 2007; Beale *et al.*, 2008), but this method was limited due to the same data source used for all the different models. To reduce the misinterpretation of the responses of the species distribution, large geographical areas were examined and thus the correlation of environmental variables with climatic variables was reduced (Maclean *et al.*, 2008). It was used to resolve ambiguities due to correlated predictors, but it failed to find out the spurious correlations among the environmental factors which was used to define the spatial distribution (Ashcroft *et al.*, 2011). To improve the credibility of predictions of species distribution range generalized linear mixed models were applied (Swanson *et al.*, 2013).

2.4.3. Advancements in species distribution modelling

Over the terrestrial distribution of species, climate got a primary influence and it was the core idea of niche modelling. Even though predictive power of models have increased, the understanding of mechanisms lying behind was challenging (Shipley, 1999). Studies related to the modelling of future distribution over past distribution shifts were fewer, but the usage of climate envelope approach were used commonly to resolve this (Berry *et al.*, 2002; Thomas et al., 2004; Harrison *et al.*, 2006). For the prediction of species distribution from environmental data, usage of ecological niche modelling was appreciated (Pearson and Dawson, 2003). Advancements in science and technology led to the development of complex mathematical general circulation models (GCMs), which stimulated the global climate and associating with different greenhouse gas emission scenarios, future climate was also predicted (Raper and Giorgi, 2005). The correlation between climatic and non-climatic factors and shortage of data regarding the species-specific physiological parameters and processes still became an encounter (Kearney, 2006). The models were used to predict the current bird species distribution using the present climate data and likewise they could also be used to predict the future distribution based on predicted future climatic conditions (Huntley *et al.*, 2006). Predictive models had been developed using the association between climate and vertebrate distribution focusing on birds (Jetz *et al.*, 2007).

2.4.4. Species distribution studies

Species richness and distribution patterns of the animals could be explained according to environmental variables including climatic conditions (Kerr, 2001; Ricklefs, 2004; Ceballos and Ehrlich, 2006; Mittelbach, 2010). Numerous studies succeeded at predicting the species distribution using climate data (Pearson *et al.*, 2002; Bakkenes *et al.*, 2002; Burns *et al.*, 2003; Thuiller *et al.*, 2005; Calef *et al.*, 2005; Rehfeldt *et al.*, 2006; Hamann and Wang, 2006; McKenney *et al.*, 2007; Peterson *et al.*, 2008; Stankowski and Parker, 2010; Joyner *et al.*, 2010; Beever *et al.*, 2010). It was assumed in the studies of future distribution predictions that, the changes in the species ranges occurring at warmer conditions was mirrored by the changes in the colder extremities since both used the same climate-space (Berry *et al.*, 2002; Thomas *et al.*, 2004; Harrison *et al.*, 2006). There were studies which predicted the mass extinction of species over the next century (Peterson *et al.*, 2002; Bakkenes *et al.*, 2002; Thomas *et al.*, 2004; Thuiller *et al.*, 2005; Malcom *et al.*, 2006), and redistribution of species range (Iverson and Prasad, 1998; Pearson *et al.*, 2002; Burns *et al.*, 2003; Calef *et al.*, 2005; Rehfeldt *et al.*, 2006; Hamann and wang, 2006; McKenney *et al.*, 2007; Peterson *et al.*, 2008). As a result of devastating impacts on biodiversity due to climate change, numerous analytical techniques had developed to correlate quantifiable climatic variables with the known location of species (Heikkinen *et al.*, 2006; Elith *et al.*, 2006; Guisan *et al.*, 2007; Loiselle *et al.*, 2008; Graham *et al.*, 2008; Feeley and Silman, 2010; Beever *et al.*, 2010). The changes in distribution could be of range shifts or range expansion and the role of the temperature dependence had been studied (Maclean *et al.*, 2008). At various levels prediction of species richness had been explained by environmental variables (Coops *et al*., 2009; Hinsley *et al*., 2009; Hansen *et al*., 2011; BarMassada *et al*., 2012; Fitterer *et al*., 2012). It was observed that for forest bird richness temperature variables were strongly correlated and for open woodland bird richness it was precipitation variables (Goetz *et al*., 2014).

2.5 DATA USED FOR MODELLING

2.5.1 Type of data and performance of the model

Due to the biases in the geographic and environmental space, the presence only models failed to get a general test of model accuracy when used withheld data for predicting species distribution (Bojorquez *et al*., 1995, Hijmans *et al*., 2000; Soberon *et al*., 2000; Kadmon *et al*., 2004). Possibilities to check the performance of the model were done by including artificial data and checking the accuracy predicted responses or using both presence and presence-absence data for modelling and fitted functions were compared (Austin *et al*., 1995). More predictive success was there when the independent data was not used to build the model, which were called as ‘test” data and the ‘training’ data were those which were used for building the model (Fielding and Bell, 1997). Numerous test statistics or discrimination indexes was being used for the testing of model performance (Fielding and Bell, 1997; Pearce and Ferrier, 2000). The predictive performance of the models were more focused in the evaluation step and some known occurrences which are withheld (only presence data) from the development of model by splitting the data set, k-fold partitioning, or bootstrapping (Fielding and Bell, 1997; Hastie *et al*., 2001; Araujo *et al*., 2005).

The assessment of accuracy was based upon the wellness of prediction using the withheld data (Boyce *et al*., 2002; Hirzel and Guisan, 2002b). Kappa and the area under receiver operating characteristic curve (AUC) which were the commonly used indices, were not suitable for the evaluation of poorly sampled regions (Boyce *et al*., 2002; Phillips *et al*., 2006). Predicting higher proportion of test localities (low omission rate) and not predicting a large proportion of study area would provide informative predictions as the model was statistically identical from a random prediction. Chi-square test or upper-tailed binomial probability was used for assessing the statistical significance of model when data portioning was done for testing (Anderson *et al.*, 2002). Performance of the predicted model was dependent on the observed absence data available (Loiselle *et al.*, 2003). A 2-2 confusion matrix could be used for describing the frequency of predicting correctly and incorrectly about the absences and presences and test were limited that do not require absence data in presence only models (Anderson *et al.*, 2003).

According to theoretical grounds, it was suggested not to include absence data (which may occurred due to non-inclusion of data in the model), since it would judge false-positive predictions as failures when potential suitable habitat was modelled (Anderson *et al.*, 2003; Pearson and Dawson, 2003; Sobero´n and Peterson, 2005). Using a random or spatially stratified partition (Peterson and Shaw, 2003), was most common and simple, but the problems with these small records were, the data was too small while partitioning into test and training data sets and negative data was problematic (Anderson and Martinez-Meyer, 2004). Predictive performance was decreased when some studies had done using small samples (Stockwell and Peterson, 2002; Reese *et al.*, 2005). Since distribution models were widely used and advancement in data availability and modelling methods were increasing, it was the need of the hour for broad synthetic analyses of high predictive ability and accuracy of species distribution modelling methods for presence only data (Elith *et al.*, 2006). Using independent, well-structured presence-absence dataset for validation improved the evaluation of the model performance (Elith *et al.*, 2006).

By the development in the machine learning and statistical disciplines many methods had been produced which were capable to capture complex responses, even the data was very noisy. But it doesn't received any exposure in distribution modelling even though the work was promising (Phillips *et al.*, 2006, Leathwick *et al.*, 2006). Biases in the geographic and environmental space were also seen in resampling designs too (Elith *et al.*, 2006). When only few observed locality records were available, jack-knife approach could be used which enabled the assessment of predictive ability. Jack-knife ('leave-one-out') procedure was good in assessing the model having a small number of occurrences. The model excluded each observed locality (n) once and continued to build the model using the remaining n-1 localities. For testing the model, 'n' different models were built and the predictability was assessed by the model ability to predict the single locality from the training data (Pearson *et al.*, 2007). The modelling techniques and validation used presence data only because its absence data were rarely available and difficult to detect in surveys (Pearson *et al.*, 2007). Studies done by Algar *et al.*, (2009) showed that temporal prediction was quite accurate, but in order to reduce the biases spatial autocorrelation could be done by using regression models.

2.5.2 Presence and absence records

The research on the development of distribution modelling had focused on the creation of models using presence/absence or abundance data, where systematic sampling methods were done in the regions of interest (Austin and Cunningham, 1981; Hirzel and Guisan, 2002b; Cawsey *et al.*, 2002). In the past, the presence only data were analysed using the calculations of envelopes or distance-based measures which were developed specifically for that purpose (Silverman, 1986; Busby, 1991; Walker and Cocks, 1991; Carpenter *et al.*, 1993). In most presence/absence models, it was assumed that breeding habitats were saturated (Capen *et al.*, 1986). Only presence data were assessed as some methods suggested in the species distribution modelling (Nix, 1986; Carpenter *et al.*, 1993).

There was a chance for two types of errors such as false positives and false negatives while using presence/absence models (Fielding and Bell, 1997). Later on adaptation to model presence-only data from presence-absence methods (which used a binomial response for modelling) using the background environment samples (data developed by selecting random points over the study area) or using 'non-use' or 'pseudo absence' area (Stockwell and Peters, 1999; Boyce *et al.*, 2002; Ferrier *et al.*, 2002b; Zaniewski *et al.*, 2002; Keating and Cherry, 2004; Pearce and Boyce, 2006). Since absence data were rarely available due to poor sampling or missing species occurrences during surveys, methods which required both the data set uses 'pseudo-absences' instead of real absence data (Ferrier *et al.*, 2002a; Engler *et al.*, 2004) or some methods used background data for the entire study area (Hirzel *et al.*, 2002b).

Species occurrence data were widely available and more accessible, as they were available as environment data layers of high spatial resolution created using satellite imageries (Turner *et al.*, 2003) and through highly sophisticated climate data (Thornton *et al.*, 1997; Hijmans *et al.*, 2005). It was challenging to validate the absence data since wildlife-habitat connection was absent even though there existed a potential for a species to be seen at a site (MacKenzie *et al.*, 2004; Gu and Swihart, 2004).

Alternative methods of several kind were used for modelling ecological niches and most of them used both the presence and absence records (Bourg *et al.*, 2005). Predictions from each methods differed greatly, which in turn showed the importance of selection of methods and verification of results from different methods (Thuiller *et al.*, 2004; Pearson *et al.*, 2006). Most of the species occurrence data had been recorded without any specific sampling methods, and a high portion of these data were obtained from presence only records from museum or herbarium collections which were accessible electronically (Graham *et al.*, 2004; Huettmann 2005; Soberon and Peterson, 2005). Currently there were methods which used the presence information of others members of community, which supplemented the data regarding the modelled species and for rare species this method was promising since the wider community information helped in revealing the modelled relationships (Elith *et al.*, 2006). The problem with these type of presence data was that, the intent and methods employed for collecting the data were rarely known and the with certainty we could not infer the absence data (Elith *et al.*, 2006). Novel tactics had been introduced over the last decade which exploited only presence data, thus removing the necessity of absence locations (Baldwin, 2009).

2.6 ASSESSMENT OF CLIMATIC CHANGES

For the assessment of climate change on biodiversity, several tools were used which included global climate models, regional climate models, dynamic and equilibrium vegetation models, species bioclimatic envelope models and site-specific sensitivity analysis (Sulzman *et al.*,1995). Equilibrium simulations which used a step increase in CO2 showed the increasing temperatures in both hemispheres, but transient simulations showed both the ups and downs in the temperature distribution (Sulzman *et al.*, 1995). Regional models could be used along with the Global Circulation Models (GCMs) which gave more resolution. MM5 (Mesoscale Model version 5) and RAMS (Regional Atmospheric Modelling System) were the two major regional models that were widely used (Sulzman *et al.*, 1995). The climate dynamics of southern hemisphere and northern hemisphere were different, so models developed with primary focus for a particular hemisphere would not yield good results in the other hemisphere (Grassl, 2000).

For determining the local climate change, regional models was more useful than that of global models which depended on global forcings (Pitman *et al.*, 2000). These models could represent the land-use changes and its effect on cloud formation mechanisms. But the results of these models were not easily available for all regions. GCM and regional climate models were used by dynamic vegetation models, forest gap models, biome envelope models and species envelope models in order to give light into different aspects of the biogeography of future climate change (Cramer *et al.*, 2000).

General Circulation Models (GCMs), modelled the global climate provide projections at various resolutions and there were differences between the various models in projected climate change values for each grid cell and they were regarded as the entry points for the conservation assessments of climate change since only these models provides estimates of future climate change due to the greenhouse gas forcings (Hannah *et al*., 2002). The assessments were improved by opting results from transient (not equilibrium) simulations of CO2 increase and models which was completely coupled with ocean and atmosphere to the regions of interest (Hannah *et al*., 2002).

2.7 SPECIES DISTRIBUTION MODELLING TYPES AND TECHNIQUES

2.7.1 Modelling in relation to land scape and vegetation

Forest 'gap' models were used to simulate species-specific succession dynamics in an area less than 1 ha, but there were limitations for representing the landscape-level changes (Shugart, 1990). Global biome models projected the future distribution of current vegetation using the limiting climatic conditions. In these models vegetation was in equilibrium with climate and therefore it cannot model the transition dynamics of species. But dynamic global vegetation model incorporated dynamics but they cannot be used to obtain species-specific results (Woodward and Beerling, 1997). In a competitive and dynamic environment, prediction of species composition at a landscape scale cannot be done by models. Dynamic vegetation was lacking the character of species-specificity, dynamic and competitive elements were lacked by envelope models and gap models lacked the spatial resolution (Woodward and Beerling, 1997). Land use projection models showed the pattern of the habitat fragmentation and based on the projections of the parameters like population and consumption levels it modelled the future (Sala *et al*., 2000).

The projected land use model reduced the potential range shift of a species done by bioclimatic models. For example, when potential climate envelope of a species shifted into an area having agriculture or to an urban settlement, the species may be faced with extinction. Integrative and sensitivity analysis on the basis of the site ecology and individual species characteristics could be used as an essential supplement to the modelling purposes, even though it lacked the spatial specificity of models (Hannah *et al.*, 2002).

The species-specific interaction had to be studied in conservation planning measures and the best tool available for this were species bioclimatic envelope models. They shared the same principle of biome envelope models, in which the current distribution of species was used to 'train' a model for the future incorporating the predicted climatic conditions (Hannah *et al.*, 2002). Envelopes were constructed using the Geographic Information System (GIS) software's or by genetic algorithms or general additive modelling (Peterson *et al.*, 2001a; Berry *et al.*, 2002; Midgley *et al.*, 2002). But these models could not model dynamic transitions, interspecific competition, herbivory, dispersal or other factors. By coupling with land-use projection models, application of the results of the bioclimatic envelope models could be used in real world conservation (Hannah *et al.*, 2002).

2.7.2 Generalized Dissimilarity Models (GDM)

For the modelling of spatial turnover in a community composition among a pairs of sites as functions of environmental differences between these sites, Generalized Dissimilarity Models (GDM) were used. For the estimation of probability of occurrence of species distributions of a given species, kernel regression algorithm was used within the transformed environmental space produced by GDM (Lowe, 1995). Elements of matrix regression and generalized linear modelling were combined which allowed the user to model non-linear responses of the environment which captured the ecologically realistic relationships between dissimilarity and ecological distance (Ferrier, 2002, Ferrier *et al.* 2002c).

2.7.3 GLM and GAM models

Non-parametric and non-linear functions were used by Generalised Linear Models (GLM) whereas Generalised Additive Models (GAM) used parametric and combinations of linear, quadratic or cubic terms. GAMS can model complex ecological response shapes than GLM because of greater flexibility (Yee and Mitchell, 1991). GLM and GAM were widely used in species distribution modelling because ecological relationships were modelled realistically and they have strong statistical foundations (Austin, 2002).

2.7.4 Multivariate Adaptive Regression Splines (MARS)

For fitting non-linear responses, an alternative regression based method called Multivariate Adaptive Regression Splines (MARS) were used. It used piece wise linear fits rather than smooth functions. It was very easy to use in GIS applications for making prediction maps, faster to implement compared to GAMs and had the ability to analyse community data (MARS-COMM) which helped in relating the variation in occurrence of species to the environmental predictors in one analysis, and later estimating the individual model coefficients for each species simultaneously (Leathwick *et al.*, 2005).

2.7.5 Genetic Algorithm for Rule-set Prediction (GARP)

For the approximation of species fundamental ecological niches several approaches had been used such as BIOCLIM (Nix, 1986), logistic multiple regression (Austin *et al.*, 1990) and Genetic Algorithm for Rule-set Prediction (GARP). GARP was defined by heterogeneous rules that defined the polyhedrons in the ecological niche spaces that were assumed to be liveable by a particular species. The model quality was assessed by dividing the occurrence points into 'training data' used for training and 'test data' used for testing models (Fielding and Bell, 1997). GARP had having two versions: DK-GARP used widely for the modelling data from natural history collections and OM-GARP, a new open modeller implementation, where both these used a genetic algorithm for selecting a set of rules for adaptations of regression and range specifications, hence predicted the best species distribution (Stockwell and Peters, 1999). GARP is a machine-learning approach and also linked the occurrence records to the environment variables using envelope (variables are bounded to lower and upper bounds), atomic (values are assigned to each variable) and logistic regression rules. The algorithm used pseudo-absence localities since the model works on presence-absence data (Stockwell and Peters, 1999). GARP included the properties of both BIOCLIM and logistic multiple regression and it was based upon artificial-intelligence (Stockwell and Noble, 1992; Stockwell and Peters, 1999). The extensive testing done on GARP model showed that it have high predictive ability for species geographic distributions (Peterson and Cohoon, 1999; Peterson and Stockwell, 2001b; Peterson *et al.*, 2001a).

2.7.6 Maximum Entropy Modelling (MaxEnt)

MaxEnt uses the distribution of maximum entropy which was subjected to the constraint that the expected value of each environment variable (interactions) in the estimated distribution matched its empirical average for estimating the species distribution (Phillips *et al.*, 2006). Using the background locations and data derived constraints, it approximated the most uniform distribution (Philips *et al.*, 2004; Philips *et al.*, 2006). In this model the complexity of the fitted functions could be choose, if presence only species data were used. It was observed that Maximum entropy modelling (MaxEnt) had done better or as well than other modelling techniques (Elith *et al.*, 2006; Hernandez *et al.*, 2006; Philips *et al.*, 2006). Compared to other algorithms, MaxEnt achieved higher success rate and it marked the differences even at low sample sizes (Pearson *et al.*, 2007). MaxEnt models predicted broader area of suitable conditions and the MaxEnt projection had the ability to predict excluded areas also, but the model performance felt a negative impact when sample sizes were reduced artificially (Pearson *et al.*, 2007).

MaxEnt had used to investigate the distributional patterns of Geckos (*Uroplatus* spp.) for predicting the species distribution (Pearson *et al.*, 2007), American black bear (*Ursus americanus*) for the assessment of denning habitat (Baldwin and Bender, 2008), Bush dog (*Speothos venaticus*) to appraise the excellence of protection (DeMatteo and Loiselle, 2008), Little bustard (*Tetrax tetrax*) for modelling the seasonal distribution changes (Suárez-Seoane *et al.*, 2008), predicting and mapping of Sage grouse's (*Centrocercus urophasianus*) nesting habitat, Asian slow lorises (*Nycticebus* spp.) was assessed to threats and species distribution analysed to find conservation urgencies (Thorn *et al.*, 2009). MaxEnt can precisely build the model even there are less number of location points and it was an advantageous feature since frequently there are deficiency of dependable locations obtainable for mapping the spreading of species (Baldwin, 2009).

2.7.7 Boosted Regression Trees (BRT)

Boosting Regression Trees were developed in a forward stage-wise manner, where small modifications were done in the model at each step for better fitness of data (Friedman *et al.*, 2000). BRT used the combination of two algorithms: regression-tree algorithm also called as the boosting algorithm to construct a combination or "ensemble" of trees. The use of regression-trees helped in the good selection of relevant variables and it could model interactions. It was upon the weighted versions of data set where the observation that were poorly fitted in the preceding model and they were accounted by adjusting the weights (Elith *et al.*, 2006). Over fitting of data were avoided by using cross-validation in BRT, to grow the models progressively during the predictive accuracy testing on withheld portions of the data (Elith *et al.*, 2006).

2.8 FACTS ABOUT THE INDIAN PEAFOWL (*Pavo cristatus*)

The Indian Peafowl were mainly seen in tropical forest of the country (Mukharjee, 1979). Activity of birds were high during dawn and dark (Sharma, 1979) mainly during the time interval 6:30 A.M-9:30 A.M and 4:30 P.M-6:30 P.M. For breeding, roosting and foraging they select scrubs, huge trees and fields respectively (Johnsingh and Murali, 1980). They usually opt for scrubs and open areas for dust bathing and lekking, an action to attract the females (Yasmin and Yahva, 1996). They were preferred to seen in areas like scrub jungles, forest fringes, agricultural fields, stream sides (Padmanabhan P, 2007) and human habitation in semi-wild conditions where the climate was mostly humid, dry and semi-arid conditions (Ramesh and McGowan, 2009). Abundance of the Indian Peafowl depended upon three main factors: prey density, biomass (Ramesh and McGowan, 2009) and the habitat diversity resulting in availability of food (Ranjith and Jose, 2016). In areas where there was a lack of predators, competing species and awayness from anthropogenic activities increased the number of Indian Peafowl. Validating their affinity towards crop fields, more number of the Indian Peafowl are located nearby paddy fields. When the human interaction augmented by increased logging, clearing of bushes and construction work, the population dimished in those areas (Ranjith and Jose, 2016).

MATERIALS AND METHODS

CHAPTER 3

MATERIALS AND METHODS

3.1 POINT LOCALITIES OF THE INDIAN PEAFOWL

The Indian Peafowl presence data were obtained from the e-Bird reference data, an Internet-based checklist program which is freely available (www.eBird.org). These data are published in compliance with the Avian Knowledge Network (AKN) and it is run by the National Audubon Society and the Cornell Lab of Ornithology and the data is copyrighted with these organizations. The data consists of Breeding Bird Survey from 1966 onwards. It have advanced geo-referencing and broad user-base. The georeferenced data of the Indian Peafowl from the years 1979-2015 were retrieved from it. Duplicate records were avoided using the tools in Excel and a corresponding shape file was generated in ArcMap 10.3.

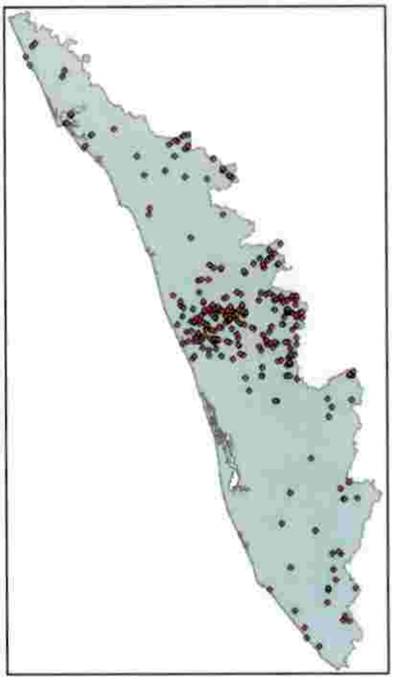


Figure 1. Occurrence points for the Indian Peafowl in Kerala

3.2 ENVIRONMENTAL VARIABLES

The bioclimatic variables were used for the current and future conditions from the WorldClim v1.4 database (http://www.worldclim.org/download) (Hijmans *et al.*, 2005) for each georeferenced presence locations. These variables were derived from the monthly rainfall and temperature values and generated 19 different variables which are more meaningful. These variables represent annual trends, seasonality and extreme or limiting environmental factors. They are coded under different names such as;

3.2.1 bio1 (Annual Mean Temperature): The average temperature of 12 months was used to acquire the annual mean temperature. This approximated the total energy inputs for an ecosystem.

3.2.2 bio2 (Mean Diurnal Range): Each month's diurnal range (difference between maximum and minimum temperature) was averaged for 12 months of a year. This provided information regarding the relevance of temperature fluctuation for different species.

3.2.3 bio3 (Isothermality): Isothermality was used to measure the oscillations of day to night temperatures relative to the annual oscillations ((bio2/bio7)x100). This could reveal the influence of larger or smaller variations in temperature of a month relative to that year.

3.2.4 bio4 (Temperature Seasonality): It is the temperature variation (SDx100) over a year (or averaged years) relative to the SD (variation) of monthly temperature averages. Greater variability in temperature is inferred from larger SD.

3.2.5 bio5 (Maximum Temperature of Warmest Month): It measures the maximum monthly temperature over a year which was useful in the determination of affects by warm temperature anomalies in species distribution.

3.2.6 bio6 (Minimum Temperature of Coldest Month): Measures the minimum temperature over a time period useful in the analysis of affects from cold temperatures.

3.2.7 bio7 (Temperature Annual Range): Quantifies the temperature variation over a period (bio5-bio6) and helps in the examination of species distribution and the effects of extreme temperature conditions on it.

3.2.8 bio8 (Mean Temperature of Wettest Quarter): Approximation of mean temperatures prevailing during the wettest season and its effect on species distribution can be studied.

3.2.9 bio9 (Mean Temperature of Driest Quarter): Mean temperature of driest quarter was measured to know the effects of it on species distribution.

3.2.10 bio10 (Mean Temperature of Warmest Quarter): Quantifies the mean temperature over warmest quarter and helps in the examination of species distribution.

3.2.11 bio11 (Mean Temperature of Coldest Quarter): Mean temperature of coldest quarter was measured to know the effects of it on species distribution.

3.2.12 bio12 (Annual Precipitation): It is the sum total of all the monthly precipitation and it evaluates the total water inputs which was useful in ascertaining the importance of water availability in determining the species distribution.

3.2.13 bio13 (Precipitation of Wettest Month): Precipitation of wettest month was measured and studies the species distribution when an extreme precipitation condition occurs.

3.2.14 bio14 (Precipitation of Driest Month): Total precipitation received during the driest month was measured to study the extreme conditions and its impacts on species distribution

3.2.15 bio15 (Precipitation Seasonality): Variation of monthly precipitation throughout the year was measured. It is the ratio of SD of monthly total precipitation to the mean monthly total precipitation.

3.2.16 bio16 (Precipitation of Wettest Quarter): Precipitation of wettest quarter was measured and studies the species distribution when an extreme precipitation condition occurs.

3.2.17 bio17 (Precipitation of Driest Quarter): Total precipitation received during the driest quarter was measured to study the extreme conditions and its impacts on species distribution

3.2.18 bio18 (Precipitation of Warmest Quarter): Precipitation of warmest quarter was measured and studies the species distribution when an extreme precipitation condition occurs.

3.2.19 bio19 (Precipitation of Coldest Quarter): Mean precipitation of coldest quarter wa s measured to know the effects of it on species distribution.

The unit of temperature is '^{0}Cx10' and that of precipitation is 'mm'. 30 arc-seconds (0.86 km^2 at the equator) data were used for both current and future conditions. They were in the latitude/longitude coordinate reference system under the datum WGS84. The bioclimatic variables were calculated from aggregated data such as monthly precipitation, minimum, mean and maximum temperature. The data layers were generated by interpolating average monthly data available from weather stations. This data had got its own advantages and disadvantages. According to World Meteorological Organization (WMO) climate is defined as the measurement of the mean and variability of relevant quantities of certain variables (such as temperature, precipitation or wind) over a period of time, ranging from months to thousands or millions of years. The classical period is 30 years.

H

The WorldClim interpolated climate layers were made by using major climate databases compiled by the Global Historical Climatology Network (GHCN), the Food and Agriculture Organization of the United Nations (FAO), World Meteorological Organization (WMO), the International Center for Tropical Agriculture (CIAT), R-HYdronet and numerous other databases for Australia, New-Zealand, the Nordic European Countries, Ecuador, Peru and Bolivia, The Shuttle Radar Topography Mission (SRTM) elevation database and using ANUSPLIN software which interpolates noisy multi-variate data using thin plate smoothing splines (Hutchinson and Xu, 2013). The current bioclimatic layers corresponds to the time period from 1950 to 2000. For ecological niche modelling the future prediction of distribution for the Indian Peafowl, the same current bioclimatic layers and future bioclimatic layers corresponding the climatic responses of Representative Concentration Pathways (RCPs) using the coupled model HadGEM2-AO of 30 seconds resolution were used, which is available in the WorldClim database. All the four scenarios such as RCP2.6, RCP 4.5, RCP 6.0 and RCP 8.5 were used.

Table 1. Different RCP's and its characteristics

Name	**Model used**	**Radiative forcing**	**CO2 equivalent (ppm)**	**Temperature anomaly (°C)**
RCP2.6	IMAGE	3.1 W/m^2 at mid-century, returning to 2.6 W/m^2 by 2100	490	1.5
RCP4.5	MiniCAM	4.5 W/m^2 post 2100	650	2.4
RCP6	AIM	6 W/m^2 post 2100	850	3.0
RCP8.5	MESSAGE	8.5 W/m^2 in 2100	1370	4.9

Besides the bioclimatic layers altitude (alt), inland water bodies (wbint), perennial water bodies (wbpere), linear water inland (wlint), perennial rivers (wlpere) and land cover (landcov) were also used for the ecological niche modelling. The world water bodies' datasets uses the source from DeLorme publishing company's 1:2,000,000 world data. The land cover data is sourced from SPOT VEGETATION, Defence Meteorological Satellite Program (DMSP) data under the name Land Cover Classification System (LCCS) having 85 percent accuracy with Forest Survey of India Report at a resolution of 1km. The altitude data was obtained from Shuttle Radar Topography Mission (SRTM) at a resolution of 3 arc-second or 90 meters.

3.3 MAXIMUM ENTROPY SPECIES DISTRIBUTION MODELLING (MaxEnt)

The species distribution of the Indian Peafowl was studied using MaxEnt 3.3.3k. The MaxEnt software is based upon the maximum-entropy principle and used for species habitat modelling. This software uses a set of georeferenced occurrence locations and environmental layers obtained from WorldClim database to create the species distribution model. MaxEnt is freely available online (https://www.cs.princeton.edu/~schapire/MaxEnt/). The data should be inputted into the software in the required format. Species data was made into '.csv' format and the bioclimatic layers should be of '.asc' format. Software was programmed to appropriate levels according to our requirements for the run under settings options (Philips *et al.*, 2004; 2006).

3.4 OPTIMIZATION OF REPLICATION RUN TYPE

The replication run in MaxEnt were done mainly using three types: cross-validate, bootstrap and subsampling.

Cross-validation is a form of replication in which the occurrence data were randomly split into numerous (k) groups ('folds') of equal size and leaving out a single part, it will fit the model to the other k-1 parts (combined), thus obtaining predictions for the left-out part. This procedure was repeated for each part and the results were combined. The advantage of using cross-validation was that it used all the data for the validation purpose which would be helpful in dealing with small number of data sets. It used the data efficiently for reporting the range and standard error. It simultaneously allowed to assess uncertainties in prediction which was useful in model evaluation. But since only a part of the data was used for model fitting, it was difficult to retrieve test data which was statistically (spatially) independent of training data (Hijmans, 2012; Wenger and Olden, 2012). Overestimation of model performance and under estimation of the standard error of predictions could occur while using spatially correlated folds. Bootstrap method lose statistical independence of the test and train data and the AUC values would end up slightly inflated.

The bootstrap method is a flexible and strongest statistical tool which could be used to quantify the uncertainty associated with a given estimator 'r' statistical method. It could provide the estimation of standard error of a coefficient or a confidence interval for that coefficient. In this method distinct data sets were prepared by repeated sampling observations from the original data set with replacement, rather than repeatedly obtaining independent data sets from the population. This method was most commonly used if the occurrence data are small. The 'bootstrap data sets' were created by sampling with replacement having the same size of the original data set. So some observations could appear more than once and some doesn't showed up at all in these data sets. In each bootstrap sample there was a significant overlap with the original data, about two-thirds of the original data points appears in each sample. This would lead the bootstrap to seriously underestimate the true prediction error.

In repeated subsampling the presence data sets were repeatedly split into random training and testing data sets. The number of replicates and the percentage to be withheld from each replicated run could be fixed. These method could be adopted if there was moderate to many occurrences of the species. One possible disadvantage of the subsampling was the selection of the weak effect variables. These variables have low inclusion frequencies due to the correlation between other variables (De Bin *et al.*, 2015).

Based on these three replication run types, 3 different models were done using similar conditions. Among them the best type was chosen and based on that further modelling steps have been forwarded.

3.5 VARIABLE CONTRIBUTION TO THE MODEL

Analysis had done to identify the contribution of each variable to the modelling of distribution for the Indian Peafowl, including all bioclimatic variables, altitude and water bodies. This was done for current distribution (no future projection), using the most suited sampling technique identified from previous analysis. 10 subsampling replicates were used, keeping 25 percent of the data for testing and the remaining data were used to build the model. The output was made in logistic format to get the probability of occurrence in the range of 0-1. In the determination of the percentage contribution, the increased regularized gain is added to the contribution of the corresponding variable, or subtracted from it if the change to the absolute value of lambda is negative in each repetition of the training algorithm. For the estimation of permutation importance, the values of each environmental variable on training presence and background data were randomly permuted.

3.6 VARIABLE OPTIMIZATION IN THE MODEL

For analysing the accuracy of model prediction, trials were done using a single sampling technique with 10 replicates and 25 test percentage. Only bioclimatic variables were used for optimization since they are going to be used for the future prediction. Other variables like altitude, land cover and water bodies cannot be predicted for future, so they were dropped in further modelling procedures. MaxEnt output had features that described the authenticity of the data and how fit was the predicted model. Omission curves and AUC curves both described the accuracy of the model (Fielding and Bell, 1997; Philips *et al.*, 2006; Elith *et al.*, 2011). The analysis of omission/commission graph revealed the omission rate and predicted area at different threshold levels. The orange and blue shading surrounding the lines on the graph represented its variability. The predicted omission rate was a straight line according to the definition of cumulative output format. The omission rate should be close to the predicted omission. The sensitivity vs. 1-specificity graph depicted the area under the Receiver Operating Characteristic (ROC) curve or area under the curve (AUC). This allowed easy comparison of the performance of one model with another and a most useful tool to evaluate multiple MaxEnt models. An AUC value of 0.5 indicated that the model performance was no better than random, while values close to 1.0 indicated better model performance. Using these features of MaxEnt output, the various models projected under different settings were analysed and the best fitted model based on the ROC curve and having high AUC value was selected (Philips *et al.*, 2006).

Variable optimization was a very important part in the model building process. Some variables may not be related to the outcome and even if all variables were related to the outcome, it was advised to remove some, having a small effect in order to increase the interpretability of the final model (epistemic sparsity) or to produce a model with better predictability (predictive sparsity) by reducing the variance (De Bin *et al.*, 2015). For interpreting the contributions of each environmental variable to the species distribution model, highly correlated variables should be removed to avoid autocorrelation. Many climatic variables were highly correlated among each other and including all these would not affect the quality of the MaxEnt model prediction but seriously limited the contribution of other correlated variables. If there was a highly correlated variable in the model, then it excluded all other correlated variable from being incorporated into the model which may have a significant importance in the prediction of species distribution (Brown, 2014). The response curves made from the presence could be misleading if the correlation exists. When there are highly correlated variables, the percent contributions should be taken with caution. If the test and training data were spatially auto correlated, the test omission line lied well below the predicted omission line which was not a good fit for the model. Spatially auto correlated data would inflate the accuracy measurement for presence only models (Veloz, 2009), so it was essential to eliminate spatially correlated variables prior to the modelling process.

The bioclimatic variables (bio1-bio19) for the current conditions (1950-2000) were statistically studied using correlation matrix (Pearson) and coefficients of determination (R^2). The variables were categorized based on the correlation values $|r| > 0.7$ and $|r| > 0.9$ and $R^2 > 0.9$. From these variables, those were selected having higher percentage contribution and permutation importance results based on MaxEnt model output were used for future predictions. The percentage contribution chart showed the relative contribution of each environment variables to the MaxEnt model. In each iteration of the training algorithm, the increase in regularized gain was added to the contribution of the corresponding variable or subtracted from it if the change to the absolute value of lambda is negative. They depended on the path taken by the MaxEnt code to get the solution and the contribution values changed when it took another way to get the same result. When there were highly correlated variables care should be taken in interpreting these values. The permutation importance depended on the MaxEnt model rather than the path it used to obtain the value. The importance was measured by randomly permuting the values of that variable among both the presence and background (training points) and by calculating the decrease in training AUC. Higher the decrease showed that the model heavily depended on that variable. The Jack-knife test of variable importance depicted the environment variable having the highest gain when used in isolation (having the most useful information) and the environment variable which decreased the gain the most when it is omitted (having the most information that isn't present in the other variables). The selected variables after removing the correlated ones were used for the further modelling.

3.7 FUTURE PREDICTIONS OF DISTRIBUTION FOR THE INDIAN PEAFOWL

Prediction of species distribution in the future could be done in MaxEnt by projecting the trained environment layers to another set of environment layers containing the future climatic data set. The projection layers should have trained layers which were mutually compatible but the conditions will be different. The name of the layers and the map projection should be the same as that of the trained data. A model was trained on the environmental variables which corresponded to the current climatic conditions and was projected into a separate layer based on the future environmental data. Models of different RCPs were done using a single sampling technique with 15 replicates and 25 test percentage. To know the role of different variables in determining the varying distribution patterns there, model trials were done corresponding to the number of variables used for the future prediction. In each trials one of the variable is excluded, to analyse the changes happening in the prediction without that variable. Through this method, impact of each variable in specific locations could be identified and concluded.

RESULTS

CHAPTER 4

RESULTS

4.1 DISTRIBUTION OF THE INDIAN PEAFOWL IN THE PAST

Salim Ali and Hugh Whistler had conducted one of the earliest bird survey of Kerala (erstwhile Travancore-Cochin), during the period 1935-1936. There were no reports of spotting of the Indian Peafowl in Kerala. It was on 1969, Ali reports that he found the Indian Peafowl's from the deciduous forests of Peechi-Vazhani. According to the e-Bird reference data, the first recorded sighting of the Indian Peafowl in Kerala was on 1979 from the district of Wayanad. This data proves the less abundance of the Indian Peafowl in Kerala. But during the subsequent periods the presence records of the Indian Peafowl showed an increasing trend. Also these data depicts the spreading of the Indian Peafowl to most parts of Kerala especially in the districts of Palakkad and Thrissur. Table 2 shows the number of presence records and Fig. 2 shows the increasing spatial distribution of the Indian Peafowl in Kerala over the past 37 years.

Table 2. Number of presence records of the Indian Peafowl in Kerala over the past 37 years

Time Period	No. of presence records
1980-1990	2
1991-2000	8
2001-2010	53
2011-2015	1451

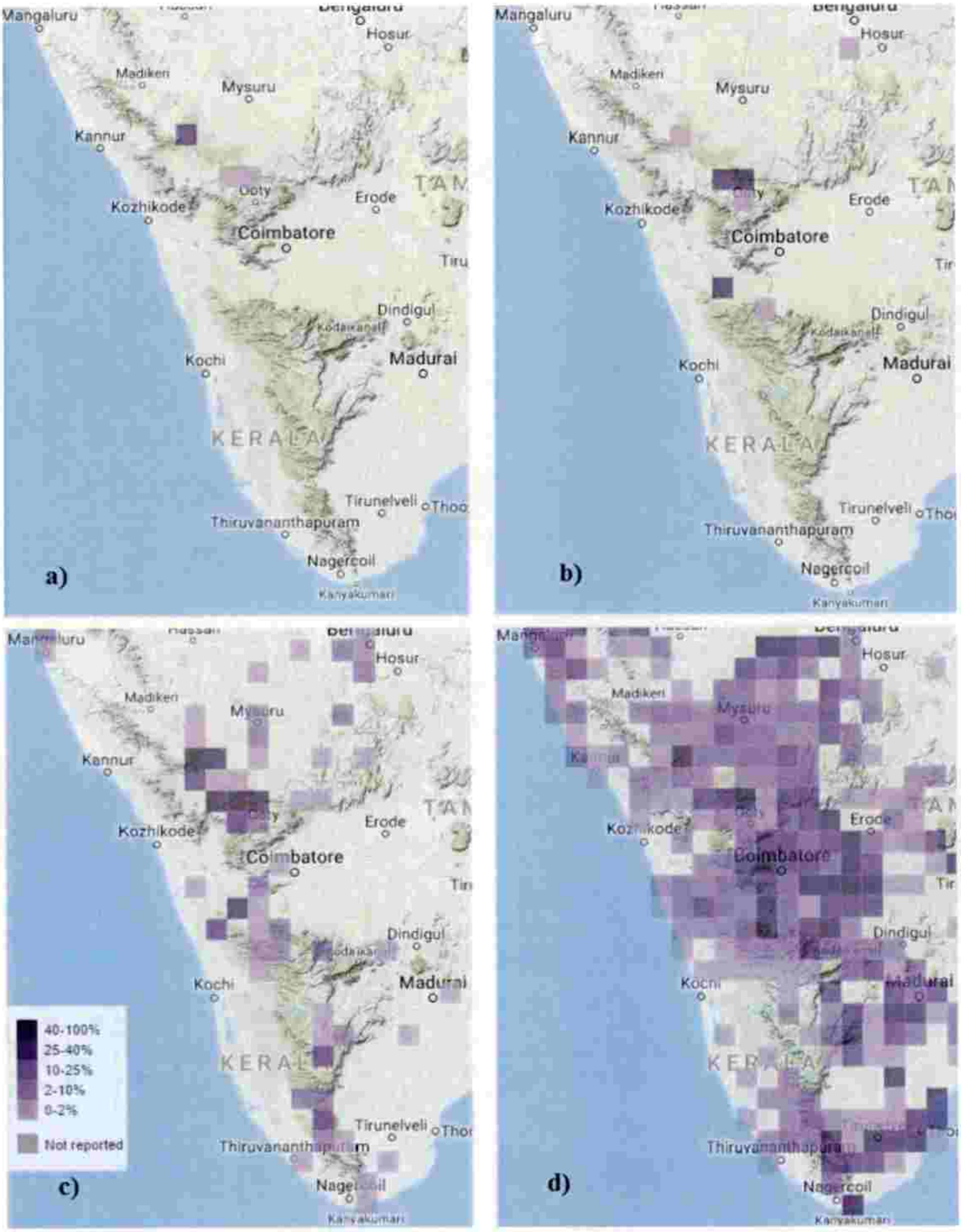


Figure 2. Spatial distribution of the Indian Peafowl in Kerala over the period a) 1980-1990 b) 1991-2000 c) 2001-2010 d) 2011-2015

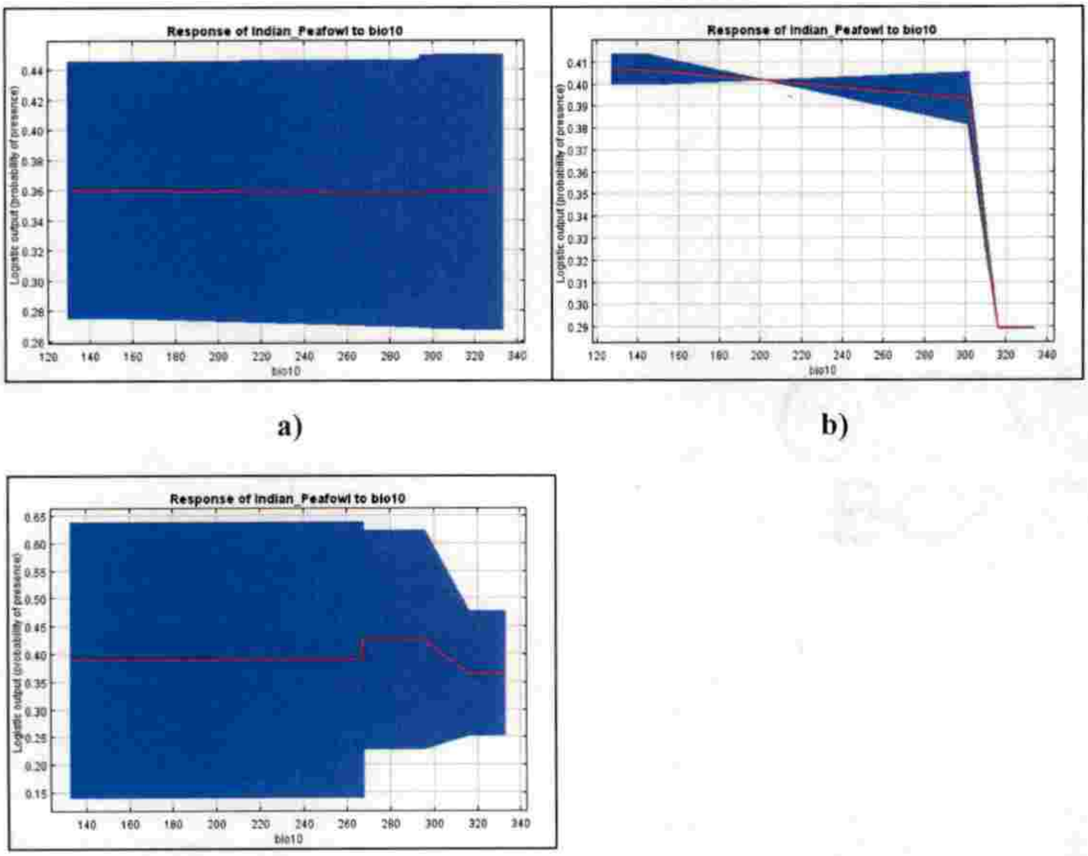
4.2 SELECTION OF REPLICATION RUN TYPE

Replication run types using bootstrap, cross-validate and subsampling showed different AUC values, omission/commission graphs, distribution patterns of species, response curves and variable contributions. Even in the same replication type there was variations in the above features except in cross-validate where every feature was exactly the same as other models.

In the Fig.2 the response curves of mean temperature of warmest quarter (bio10) is depicted. When bootstrap (Fig.2a) and cross-validate (Fig.2c) was used as a replication type for modelling, the SD was higher whereas the SD was lower for subsampling (Fig.2b). Higher the SD, higher was the variability leading to lower reliability on the model. Only one variable (bio10) was shown here and the Figures for the remaining 18 variables were given in Appendix 1.

Even though the standard deviation (SD) for the AUC curve was very much lower in bootstrap method (Table.1) compared to others, the SD for the response curves was higher (Fig.2a) and it was found lower in subsampling (Fig.2b). In cross-validate, all the model output showed the same result (Table.1).

In bootstrap (Fig. 2a) the omission on training line was too below the predicted omission line where as in subsampling (Fig. 2b) and cross-validate (Fig. 2c), both line were more or less close and parallel to each other. But the standard deviation in cross-validate (Fig. 2c) replication type was higher than that of subsampling (Fig. 2b). Thus it was concluded that the subsampling replication was more reliable in the modelling of distribution of the Indian Peafowl.



a)

b)

c)

Figure 3. Response of the Indian Peafowl to mean temperature of warmest Quarter (bio10) in a) bootstrap b) subsampling c) cross-validate replication type (blue colour indicates the SD).

Table 3. Output values from models using different replication run type

Replication run type	**Replication number**			**Test percentage**			**Average test AUC values**			**Standard Deviation (SD) for AUC curve**		
Model No.	1	2	3	1	2	3	1	2	3	1	2	3
Bootstrap	2	2	2	20	20	20	0.920	0.917	0.911	0.003	0.006	0.008
Subsampling	2	2	2	20	20	20	0.798	0.820	0.807	0.011	0.030	0.013
Cross-validate	2	2	2	0	0	0	0.820	0.820	0.820	0.030	0.030	0.030

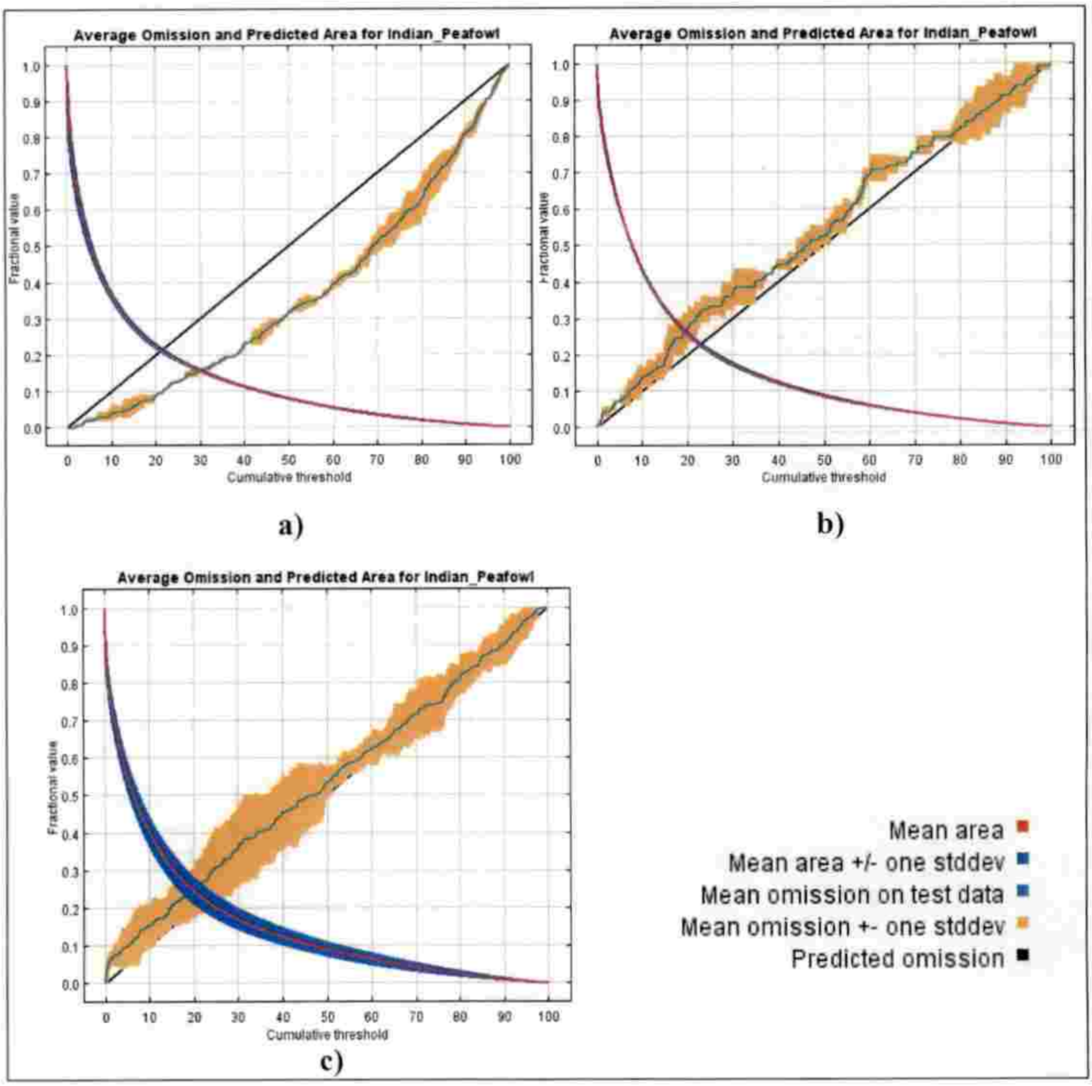


Figure 4. Analysis of omission rate of different replication types in the distribution model of the Indian Peafowl a) bootstrap b) subsampling c) cross-validate

4.3 VARIABLE CONTRIBUTION TO THE MODEL DISTRIBUTION OF THE INDIAN PEAFOWL

Table 4. Percent contribution and permutation importance of all environmental variables to the model

Environmental variables	Percent contribution	Permutation
bio4	28	2.6
bio12	8.1	0.7
wlint	7.9	23.1
wbpere	7.7	6.2
bio17	6.3	5.8
landcover	5.8	1.5
bio18	5.3	3.7
bio3	4.6	1.6
bio14	3.7	24.4
bio15	3.6	1.8
bio5	3.6	0
bio13	3.6	10.5
wlpere	2.9	4.2
bio10	2.1	0.1
bio2	1.7	1.2
wbint	1.2	1.2
bio19	1	2.5
alt	0.8	4
bio16	0.6	0.4
bio7	0.4	0.3
bio11	0.3	1.4
bio1	0.3	0.3
bio8	0.2	1.2
bio6	0.1	1.1
bio9	0	0.2

The MaxEnt output showed the percent contribution, permutation importance and Jackknife importance of all the environmental variables and it is shown in Table.3. The variable which showed higher percent contribution was temperature seasonality (bio4) and mean temperature of driest quarter (bio9) doesn't showed any contribution at all. Eight variables out of twenty five showed contribution lesser than 1.0. Considering the permutation importance, precipitation of driest month (bio14) and linear water inland (wlint) and shows higher importance with 24.4 and 23.1 percent respectively. Maximum temperature of warmest month (bio5) showed no importance at all and other variables like bio12, bio10, bio16, bio7, bio1 and bio9 showed importance lesser than 1.0.

The jackknife results shown in Fig.4 explains that, the precipitation of driest quarter (bio17) and temperature seasonality (bio4) had the highest gain when it was done using only that variable. Variables like altitude, bio11, bio6, wbint, wbpere and wlpere showed a gain lesser than 0.1. While looking into the gain without a variable, three water related variables (wbpere, wlint and wlpere) showed lesser gain. But this was not significant as it was much above than 0.8 and closest to the gain achieved with all variables.

The response curves from the MaxEnt output (Fig.5) showed how each environmental variable was affecting the distribution of the Indian Peafowl. The curves shown below are logistic prediction changes as each environmental variable was varied, keeping all other environmental variables at their average sample value. The variables which showed positive response in favour of the distribution at a particular location when the values were increased are bio6, bio8, bio11, bio15, bio18, wbint, wlint and wlpere. Whereas bio2, bio3, bio12, bio13, bio14, bio16, bio17, bio19, landcover, wlint and wbpere lowered the chance of survival of species in that area when the values were increased. Some variables like bio1, bio4, bio5, bio5, bio7, bio9, bio10 and altitude showed no significant change to the survival of species. The response curves created using only the corresponding variable are depicted in Fig.6.

6

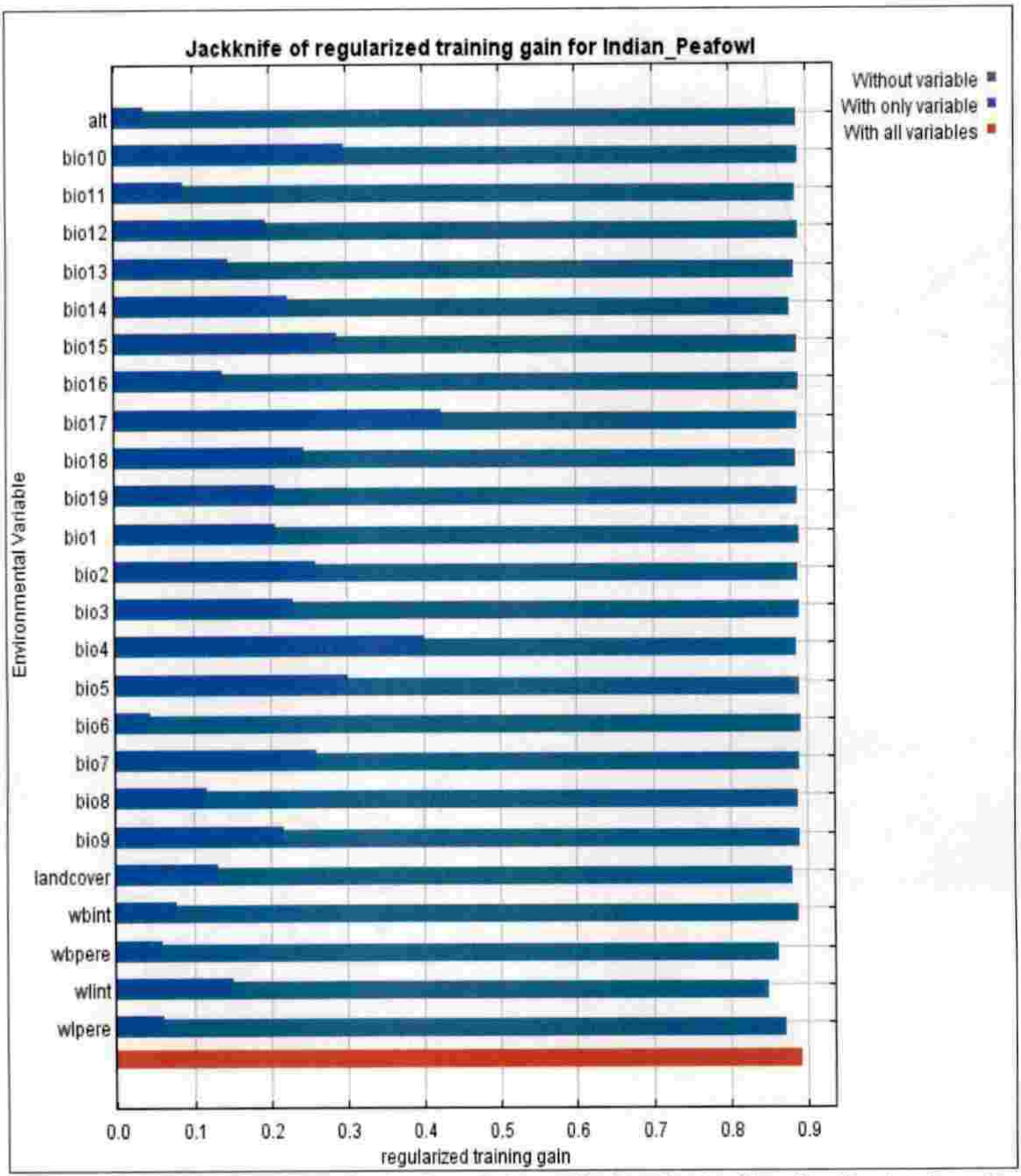


Figure 5. Jackknife of regularized training gain for the Indian Peafowl using all variables

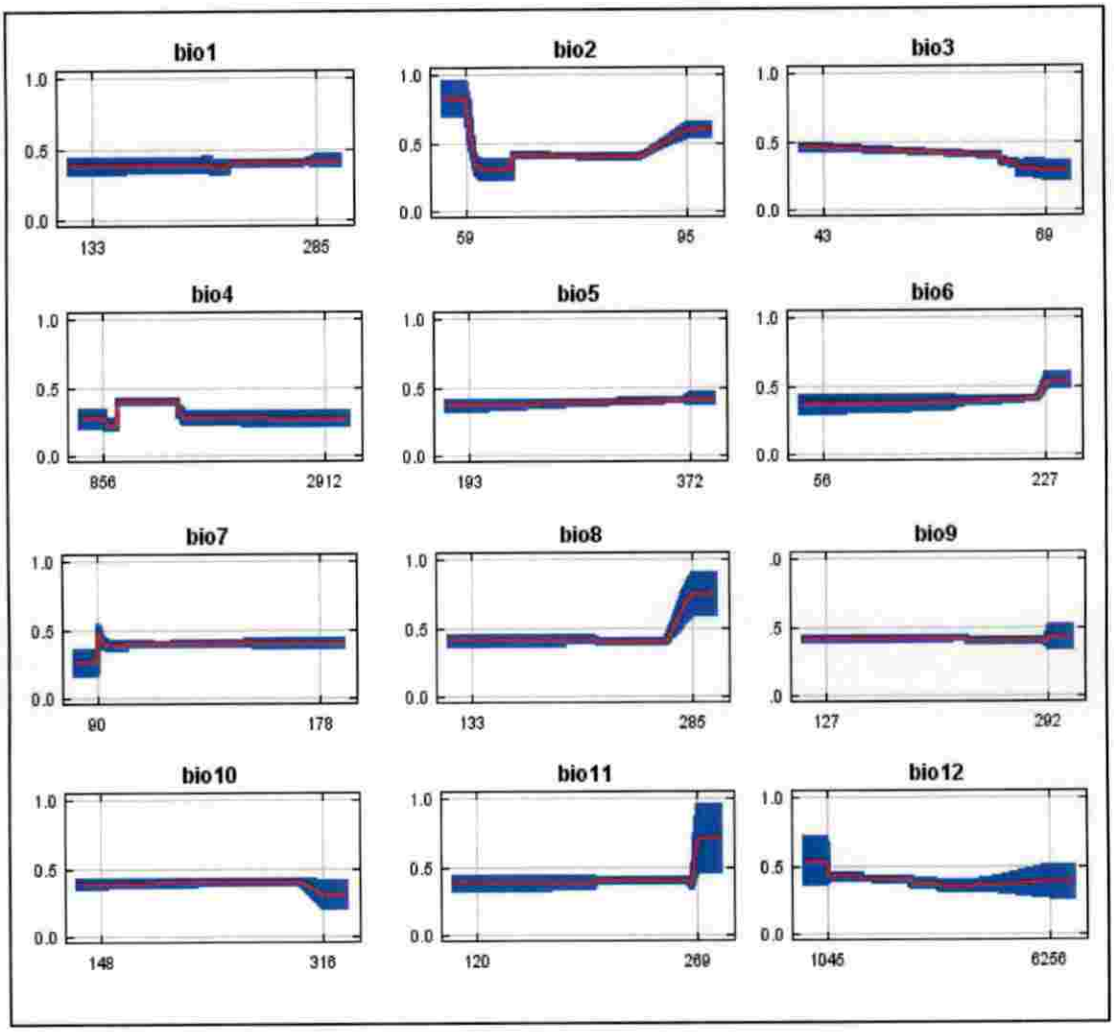


Figure 6. Response curves of each variable in the distribution of the Indian Peafowl keeping all other variables at their average values

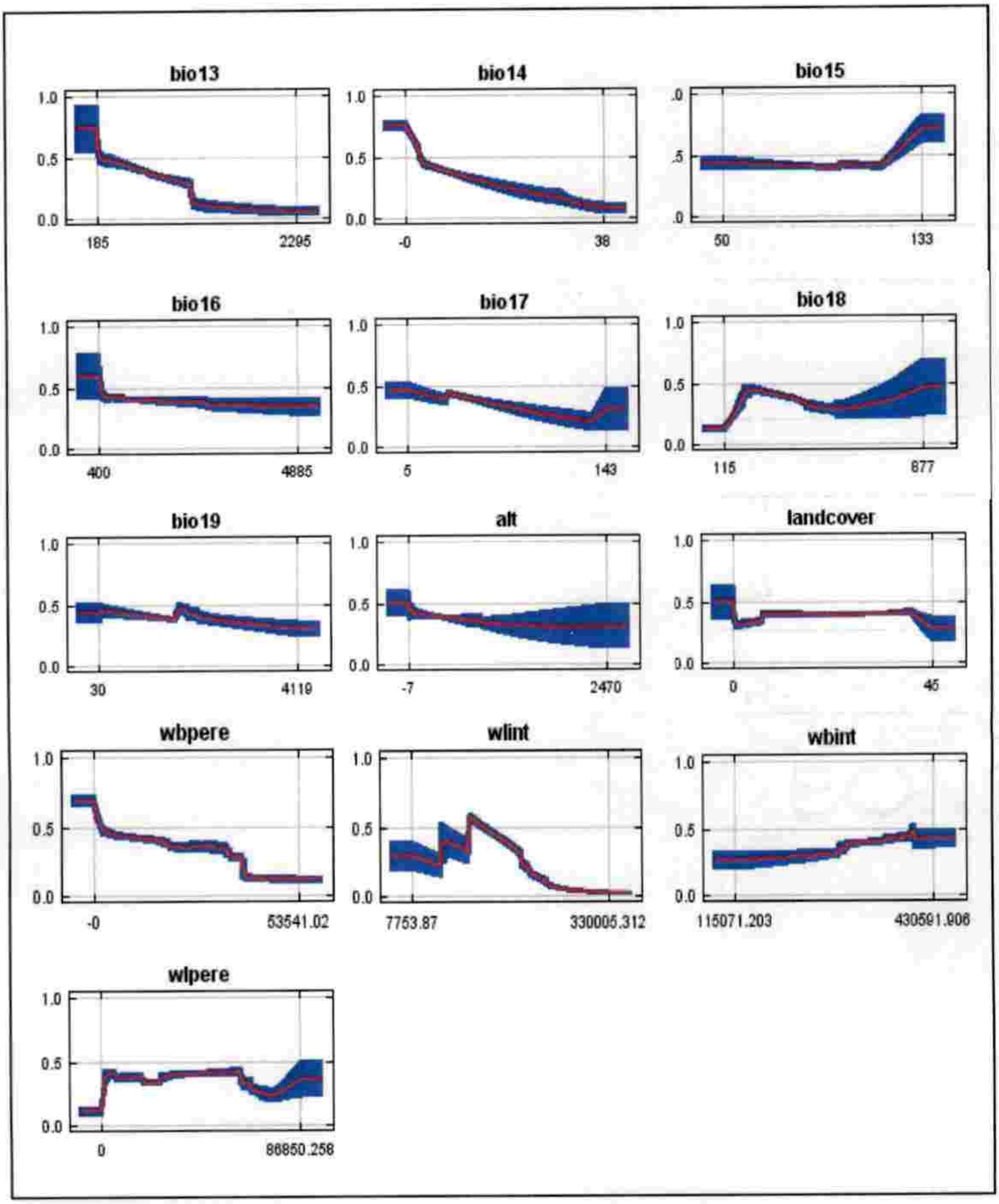


Figure 6. Response curves of each variable in the distribution of the Indian Peafowl keeping all other variables at their average values

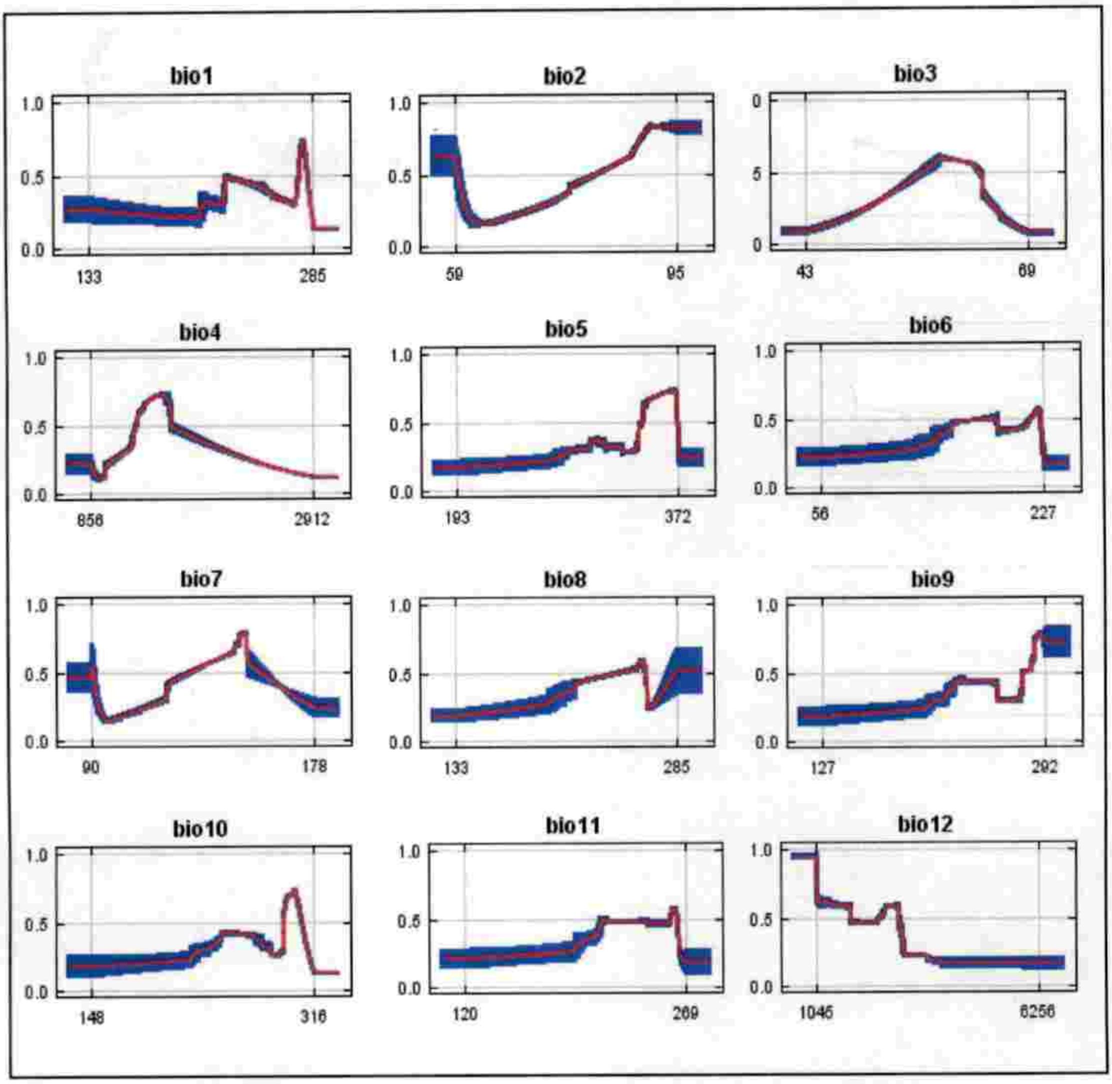


Figure 7. Response curves of each variable in determining the distribution of the Indian Peafowl created using only the corresponding variable

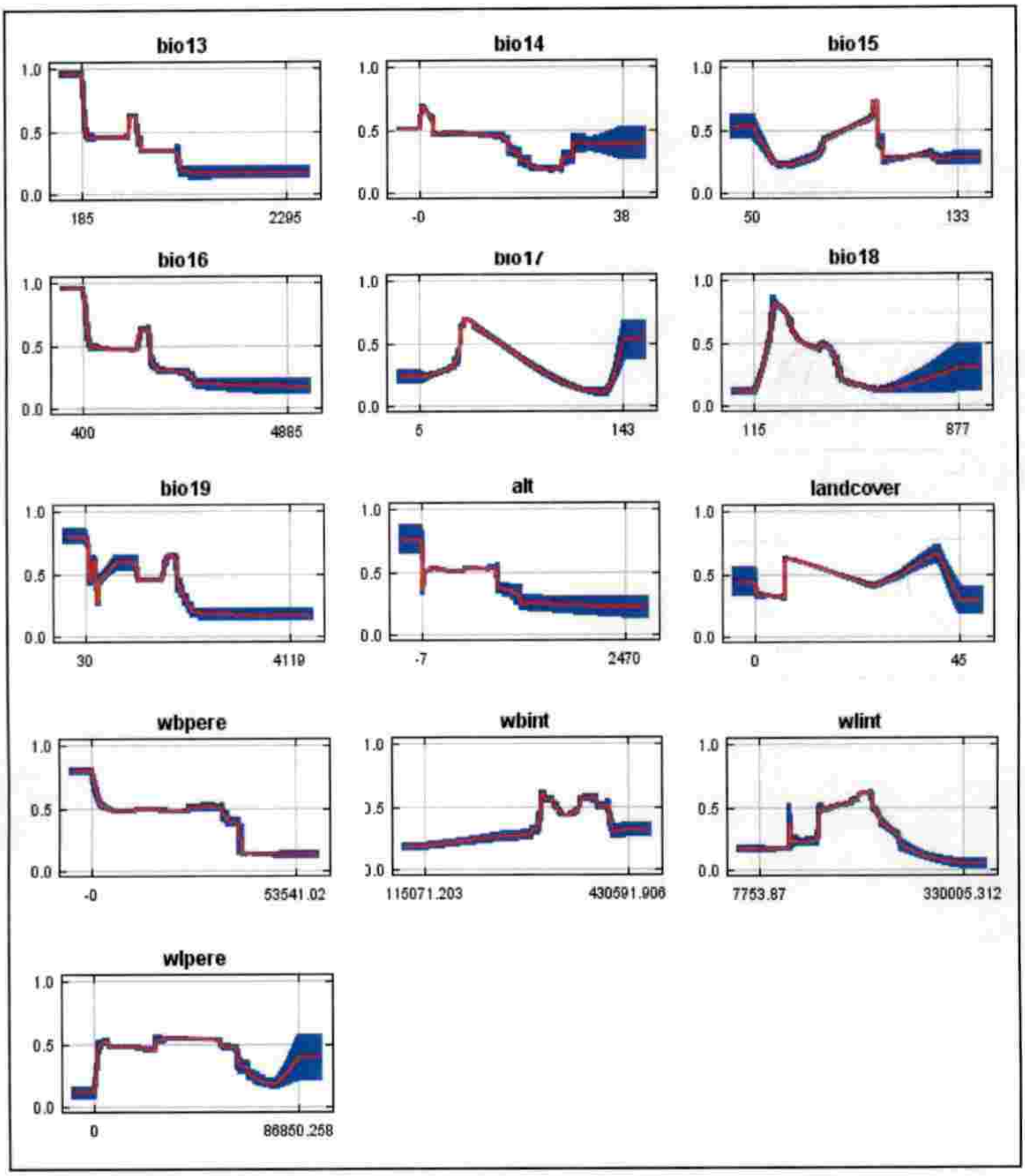


Figure 7. Response curves of each variable in determining the distribution of the Indian Peafowl created using only the corresponding variable

The analysis of the response curves using only the corresponding variables is given below. This explains the role of each variable, when they were used alone.

4.3.1 Annual mean temperature (bio1)

When the annual mean temperature (bio1) was low (<22.5°C) the probability on the occurrence of the Indian Peafowl was below 50 percent. However, when the annual mean temperature (bio1) was higher 27-28 °C, the probability on the occurrence of the Indian Peafowl increased.

4.3.2 Mean diurnal range of temperature (bio2)

There showed a 63 percent probability of presence for the Indian Peafowl when the mean diurnal range of temperature (bio2) was between 5.5 °C and 5.9 °C. An increasing trend was observed in probability of presence for the Indian Peafowl when the mean diurnal range of temperature went beyond 6.5 °C and reached 50 percent at 8.2 °C. The probability on the presence of the Indian Peafowl was the highest (83%) when the mean diurnal range of temperature was 9 °C and above.

4.3.3 Isothermality (bio3)

When the isothermality (bio3) was in the range 5.3 and 6.3, the probability of presence for the Indian Peafowl was greater than 50 percent. There was lower probability of presence for the Indian Peafowl (10%) when the isothermality was <4.3 and >6.7.

4.3.4 Temperature seasonality (bio4)

The favourable range of temperature seasonality (bio4) was between 12.5 °C and 16 °C. At <1200 and >2200 the probability of presence for the Indian Peafowl was lesser than 30 percent.

4.3.5 Maximum temperature of warmest month (bio5)

The distribution of the Indian Peafowl was found to be greater than 50 percent when the maximum temperature of warmest month was between 34 °C and 37 °C and beyond 37 °C the distribution of the Indian Peafowl dropped to 25 percent.

4.3.6 Minimum temperature of coldest month (bio6)

When the minimum temperature of coldest month (bio6) was 22 °C, the probability of presence for the Indian Peafowl was the highest (57%).

4.3.7 Temperature annual range (bio7)

The most suited temperature annual range (bio7) for the distribution of the Indian Peafowl was between 14 °C and 15.1 °C.

4.3.8 Mean temperature of wettest quarter (bio8)

As mean temperature of wettest quarter (bio8) increased from 12 °C, there was an increase in the probability distribution of the Indian Peafowl and reached the highest (60%) at 26 °C.

4.3.9 Mean temperature of driest quarter (bio 9)

Probability of presence for the Indian Peafowl was more than 50 percent when the mean temperature of driest quarter (bio9) was greater than 27 °C and was highest (80%) at 29 °C.

4.3.10 Mean temperature of warmest quarter (bio10)

As mean temperature of warmest quarter (bio10) increased, the probability of presence for the Indian Peafowl increased and reached 75 percent at 30 °C. But higher the mean temperature of warmest quarter (<30 °C) the distribution for the Indian Peafowl reduced drastically.

4.3.11 Mean temperature of coldest quarter (bio11)

The probability of presence for the Indian Peafowl was 50 percent when the mean temperature of coldest quarter (bio11) was between 21 °C and 26 °C. In all other mean temperature of coldest quarter (bio11) the probability of presence for the Indian Peafowl was lower.

4.3.12 Annual precipitation (bio12)

As annual precipitation (bio12) increased, the probability distribution of the Indian Peafowl decreased. The probability of presence for the Indian Peafowl was higher (0.95) when the annual precipitation (bio12) was below 1000mm. When annual precipitation increased above 3000mm the probability of presence for the Indian Peafowl dramatically touched the minimum point (15%).

4.3.13. Precipitation of wettest month (bio13)

The probability of presence for the Indian Peafowl was 97 percent when the precipitation of wettest month (bio1) was below 200mm. As precipitation of wettest month (bio1) increased probability of presence for the Indian Peafowl reduced considerably. When the precipitation of wettest month was greater than 1200mm, the probability of presence for the Indian Peafowl was at its minimum (18%).

4.3.14 Precipitation of driest month (bio14)

According to the model prediction the precipitation of driest month should be lower for the maximum probability of presence for the Indian Peafowl (68%). When precipitation of driest month increased the probability of presence for the Indian Peafowl was reduced.

4.3.15 Precipitation of seasonality (bio15)

When precipitation of seasonality (bio15) was below 50mm, the probability of presence for the Indian Peafowl was 54 percent which reduced to the minimum when precipitation increased. But the probability of presence for the Indian Peafowl increased when the precipitation of seasonality was greater than 60mm and reached maximum (74%) at 100mm and when precipitation of seasonality was greater than 100mm the probability of presence for the Indian Peafowl decreased to 28 percent.

4.3.16 Precipitation of wettest quarter (bio16)

When precipitation of wettest quarter (bio16) was below 400mm, the probability of presence for the Indian Peafowl was 98 percent and as bio16 increased, the probability distribution of the Indian Peafowl decreased and reached the minimum value (20%) at 2700mm.

4.3.17 Precipitation of driest quarter (bio17)

When precipitation of driest quarter (bio17) was between 30mm to 40mm, the probability of presence for the Indian Peafowl was 64 to 70 percent respectively. At lower (<30mm) and higher (>60mm) precipitation of driest quarter, the distribution of the Indian Peafowl was found low.

4.3.18 Precipitation of warmest quarter (bio18)

At lower (<180mm) and higher (>300mm) precipitation of warmest quarter (bio18), the probability of presence for the Indian Peafowl was lower than 50 percent.

4.3.19 Precipitation of coldest quarter (bio19)

When the precipitation of coldest quarter (bio19) increased from 0mm to 2200mm, the probability of presence for the Indian Peafowl decreased from 80 to 20 percent.

4.3.20 Altitude (alt)

At altitudes (alt) between 0m and 900m the probability of presence for the Indian Peafowl was found to be 50 percent. At higher altitudes (alt) the relation was negative.

4.3.21. Quantitative variables

Quantitative variables such as inland water bodies (wbint), perennial water bodies (wbpere), linear water inland (wlint), perennial rivers (wlpere) and land cover (landcover) also do had a role in the probability of distribution of the Indian Peafowl.

4.4 VARIABLE OPTIMIZATION IN THE MODEL

The six trial models produced by the MaxEnt was analysed for the average test AUC values and SD and among them the best was selected for further studies. The output showed varying average test AUC values and SD for each trials, even though the sampling type, number of replicates and test percentage of data used were same for every models.

Table 5. Average test AUC values and SD of each trial model of the distribution of the Indian Peafowl using subsampling replication

Model Trial No.	Average test AUC value	SD of AUC curve
1	0.813	0.029
2	0.809	0.022
3	0.807	0.017
4	0.820	0.020
5	0.807	0.026
6	0.810	0.025

The fourth model was selected as a typical one that can be used for further steps such as variable optimization and future prediction since it had highest AUC value and SD was lower as compared to the other 4 models. The third model had the lowest SD, but the AUC value of it was the lowest among them.

The test omission rate and receiver operating characteristic (ROC) curve (Fig.7) was found more fit in this model compared to others. The Fig.7a shows that the mean omission line on the test data was passing though the predicted omission line. In the Fig.7b the AUC line was passing through the left top of the random prediction.

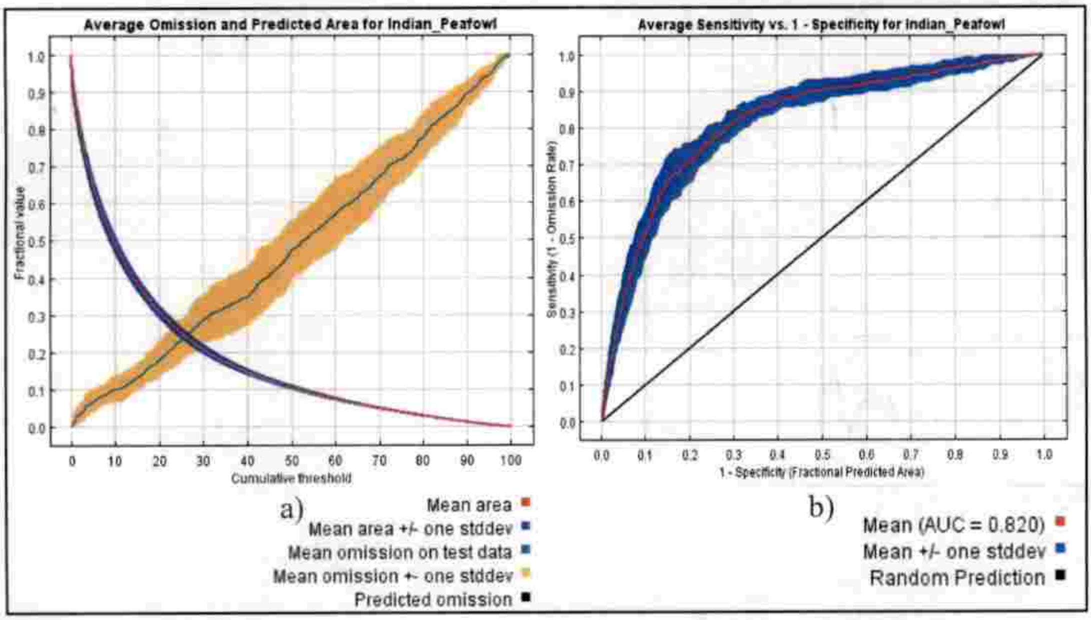


Figure 8. Test omission rate (a) and ROC curve (b) of variable optimization model of the Indian Peafowl

To find out the correlation among the environmental variables, they were tested by using Pearson correlation matrix and coefficients of determination (R^2). The results are depicted in the Table.5 and Table.6. Six variables were chosen in $|r|>0.7$ and 9 variables under $|r|>0.9$ prioritized on the basis of percent contribution and permutation importance. In the same manner twelve variables were selected under the criteria $R^2>0.9$. Only precipitation of warmest quarter (bio18) was having no correlation in all categories. The variable having more number of correlation between other variables was mean temperature of warmest quarter (bio10) (six correlations under $|r|$ and 5 correlations under R^2). In $|r|>0.9$ criteria variables like bio3, bio4, bio15, bio18 and bio19 are uncorrelated. Eight variables such as bio3, bio4, bio5 bio14, bio15, bio17, bio18 and bio19 are uncorrelated under $R^2>0.9$.

Table 6. Pearson correlation matrix of the environmental variables

🟧 |r|>0.9; 🟨 |r| 0.9-0.7

Variables	BIO10	BIO11	BIO12	BIO13	BIO14	BIO15	BIO16	BIO17	BIO18	BIO19	BIO1	BIO2	BIO3	BIO4	BIO5	BIO6	BIO7	BIO8	BIO9
BIO10	1	0.984	0.225	0.128	-0.522	0.209	0.222	-0.367	-0.006	0.680	0.994	-0.112	0.033	0.412	0.947	0.967	-0.099	0.945	0.983
BIO11	0.984	1	0.269	0.143	-0.430	0.169	0.245	-0.277	0.062	0.674	0.994	-0.239	0.173	0.250	0.888	0.984	-0.237	0.973	0.974
BIO12	0.225	0.269	1	0.931	-0.477	0.744	0.975	-0.347	0.632	0.777	0.259	-0.597	0.197	-0.176	0.046	0.336	-0.534	0.166	0.265
BIO13	0.128	0.143	0.931	1	-0.582	0.898	0.982	-0.548	0.388	0.668	0.133	-0.399	-0.083	-0.024	0.014	0.176	-0.298	0.012	0.153
BIO14	-0.522	-0.430	-0.477	-0.582	1	-0.814	-0.588	0.917	0.015	-0.662	-0.467	-0.172	0.501	-0.675	-0.584	-0.418	-0.266	-0.263	-0.527
BIO15	0.209	0.169	0.744	0.898	-0.814	1	0.858	-0.806	0.131	0.592	0.176	-0.090	-0.398	0.311	0.195	0.168	0.035	-0.002	0.222
BIO16	0.222	0.245	0.975	0.982	-0.588	0.858	1	-0.514	0.479	0.763	0.238	-0.476	0.026	-0.052	0.081	0.291	-0.391	0.121	0.256
BIO17	-0.367	-0.277	-0.347	-0.548	0.917	-0.806	-0.514	1	0.279	-0.481	-0.302	-0.288	0.610	-0.626	-0.452	-0.224	-0.387	-0.120	-0.368
BIO18	-0.006	0.062	0.632	0.388	0.015	0.131	0.479	0.279	1	0.436	0.058	-0.671	0.515	-0.402	-0.188	0.186	-0.675	0.050	0.037
BIO19	0.680	0.674	0.777	0.668	-0.662	0.592	0.763	-0.481	0.436	1	0.695	-0.396	0.106	0.214	0.557	0.730	-0.354	0.580	0.708
BIO1A	0.994	0.994	0.259	0.133	-0.467	0.176	0.238	-0.302	0.058	0.695	1	-0.201	0.133	0.320	0.912	0.986	-0.197	0.967	0.982
BIO2	-0.112	-0.239	-0.597	-0.399	-0.172	-0.090	-0.476	-0.288	-0.671	-0.396	-0.201	1	-0.707	0.690	0.197	-0.343	0.979	-0.290	-0.152
BIO3	0.033	0.173	0.197	-0.083	0.501	-0.398	0.026	0.610	0.515	0.106	0.133	-0.707	1	-0.780	-0.221	0.240	-0.831	0.290	0.070
BIO4	0.412	0.250	-0.176	-0.024	-0.675	0.311	-0.052	-0.626	-0.402	0.214	0.320	0.690	-0.780	1	0.649	0.212	0.758	0.146	0.372
BIO5	0.947	0.888	0.046	0.014	-0.584	0.195	0.081	-0.452	-0.188	0.557	0.912	0.197	-0.221	0.649	1	0.847	0.215	0.824	0.919
BIO6	0.967	0.984	0.336	0.176	-0.418	0.168	0.291	-0.224	0.186	0.730	0.986	-0.343	0.240	0.212	0.847	1	-0.338	0.962	0.963
BIO7	-0.099	-0.237	-0.534	-0.298	-0.266	0.035	-0.391	-0.387	-0.675	-0.354	-0.197	0.979	-0.831	0.758	0.215	-0.338	1	-0.308	-0.143
BIO8	0.945	0.973	0.166	0.012	-0.263	-0.002	0.121	-0.120	0.050	0.580	0.967	-0.290	0.290	0.146	0.824	0.962	-0.308	1	0.930
BIO9	0.983	0.974	0.265	0.153	-0.527	0.222	0.256	-0.368	0.037	0.708	0.982	-0.152	0.070	0.372	0.919	0.963	-0.143	0.930	1

Table 7. Coefficient of determination (R^2) of environmental variables

🟨 $R^2 > 0.9$

Variables	BIO10	BIO11	BIO12	BIO13	BIO14	BIO15	BIO16	BIO17	BIO18	BIO19	BIO1	BIO2	BIO3	BIO4	BIO5	BIO6	BIO7	BIO8	BIO9
BIO10	1	0.968	0.051	0.016	0.273	0.044	0.049	0.135	0.000	0.462	0.988	0.013	0.001	0.170	0.897	0.935	0.010	0.892	0.967
BIO11	0.968	1	0.072	0.020	0.185	0.029	0.060	0.077	0.004	0.454	0.988	0.057	0.030	0.063	0.788	0.968	0.056	0.947	0.949
BIO12	0.051	0.072	1	0.868	0.227	0.553	0.952	0.121	0.399	0.604	0.067	0.357	0.039	0.031	0.002	0.113	0.286	0.028	0.070
BIO13	0.016	0.020	0.868	1	0.339	0.806	0.964	0.301	0.150	0.446	0.018	0.159	0.007	0.001	0.000	0.031	0.089	0.000	0.023
BIO14	0.273	0.185	0.227	0.339	1	0.662	0.346	0.841	0.000	0.439	0.218	0.030	0.251	0.455	0.341	0.175	0.071	0.069	0.278
BIO15	0.044	0.029	0.553	0.806	0.662	1	0.735	0.649	0.017	0.350	0.031	0.008	0.158	0.097	0.038	0.028	0.001	0.000	0.049
BIO16	0.049	0.060	0.952	0.964	0.346	0.735	1	0.264	0.229	0.583	0.057	0.227	0.001	0.003	0.006	0.085	0.153	0.015	0.066
BIO17	0.135	0.077	0.121	0.301	0.841	0.649	0.264	1	0.078	0.231	0.091	0.083	0.372	0.392	0.204	0.050	0.150	0.014	0.135
BIO18	0.000	0.004	0.399	0.150	0.000	0.017	0.229	0.078	1	0.190	0.003	0.451	0.265	0.162	0.035	0.035	0.455	0.002	0.001
BIO19	0.462	0.454	0.604	0.446	0.439	0.350	0.583	0.231	0.190	1	0.483	0.157	0.011	0.046	0.311	0.533	0.125	0.337	0.501
BIO1A	0.988	0.988	0.067	0.018	0.218	0.031	0.057	0.091	0.003	0.483	1	0.040	0.018	0.103	0.831	0.972	0.039	0.935	0.964
BIO2	0.013	0.057	0.357	0.159	0.030	0.008	0.227	0.083	0.451	0.157	0.040	1	0.500	0.476	0.039	0.118	0.958	0.084	0.023
BIO3	0.001	0.030	0.039	0.007	0.251	0.158	0.001	0.372	0.265	0.011	0.018	0.500	1	0.609	0.049	0.058	0.690	0.084	0.005
BIO4	0.170	0.063	0.031	0.001	0.455	0.097	0.003	0.392	0.162	0.046	0.103	0.476	0.609	1	0.421	0.045	0.574	0.021	0.138
BIO5	0.897	0.788	0.002	0.000	0.341	0.038	0.006	0.204	0.035	0.311	0.831	0.039	0.049	0.421	1	0.717	0.046	0.680	0.844
BIO6	0.935	0.968	0.113	0.031	0.175	0.028	0.085	0.050	0.035	0.533	0.972	0.118	0.058	0.045	0.717	1	0.114	0.926	0.927
BIO7	0.010	0.056	0.286	0.089	0.071	0.001	0.153	0.150	0.455	0.125	0.039	0.958	0.690	0.574	0.046	0.114	1	0.095	0.020
BIO8	0.892	0.947	0.028	0.000	0.069	0.000	0.015	0.014	0.002	0.337	0.935	0.084	0.084	0.021	0.680	0.926	0.095	1	0.864
BIO9	0.967	0.949	0.070	0.023	0.278	0.049	0.066	0.135	0.001	0.501	0.964	0.023	0.005	0.138	0.844	0.927	0.020	0.864	1

The |r| and R^2 values in combination with percent contribution and permutation importance were used for selecting the most suitable variables, which determined the spatial distribution of the Indian Peafowl.

Table 8. Percent contribution and permutation importance of bioclimatic variables based on selected model trial

Variable	Percent contribution	Permutation importance
bio4	31.0	07.4
bio17	14.5	09.6
bio15	09.7	06.2
bio18	07.8	04.7
bio12	07.7	03.7
bio14	05.4	15.5
bio3	04.9	10.1
bio13	04.2	20.4
bio5	03.8	0.3
bio19	03.2	05.6
bio2	02.5	02.9
bio1	01.2	01.7
bio16	01.1	01.5
bio6	0.9	07.9
bio10	0.8	0.3
bio7	0.5	0.1
bio11	0.4	01.4
bio8	0.2	0.8
bio9	0.1	0

4.4.1. Model using variables of high percentage contribution having $|r| >0.7$

Variables were sorted out having high percentage contribution according to the correlation coefficient below 0.7 ($|r| >0.7$). Six variables were selected; bio4, bio17, bio18, bio15, bio5 and bio2. The average test AUC value was 0.799 with a SD of 0.028.

4.4.2. Model using variables of high permutation importance having $|r| >0.7$

Six variables having high permutation importance based on correlation coefficient below 0.7 ($|r| >0.7$) such as bio13, bio14, bio3, bio6, bio4 and bio18 were selected. The average test AUC value was 0.800 having a SD of 0.024.

4.4.3. Model using variables of high percentage contribution having $|r| >0.9$

The nine variables selected based on the high percentage contribution having $|r| >0.9$ are bio4, bio 17, bio15, bio18, bio12, bio3, bio5, bio19 and bio2. The average test AUC value was 0.811 and SD of it is 0.032.

4.4.4. Model using variables of high permutation importance having $|r| >0.9$

Based on the permutation importance, nine variables having $|r| >0.9$ were selected; bio13, bio14, bio3, bio6, bio4, bio15, bio19, bio18 and bio2. This model have got average test AUC value of 0.812 and a SD of 0.020.

4.4.5. Model using variables of high percentage contribution having $R^2 >0.9$

The twelve optimized variables having percentage contribution and $R^2 >0.9$ were bio4, bio17, bio15, bio18, bio12, bio14, bio3, bio1, bio5, bio19, bio2 and bio1. The average test AUC value was found to be 0.797 and SD was 0.033.

4.4.6. Model using variables of high permutation importance having $R^2 >0.9$

Twelve variables were selected based on high permutation importance and having $R^2 >0.9$. They were bio13, bio4, bio3, bio17, bio6, bio4, bio15, bio19, bio18, bio12, bio2 and bio5. The average test AUC value of this model was 0.823 and having a SD of 0.021.

From these models, the model based on variables having high permutation importance and |r| >0.7 was selected for the future prediction of the Indian Peafowl, since the variables were less and have a good AUC value of 0.8 and low SD value of 0.024.

4.5 Current and future predictions of the distribution of the Indian Peafowl

The current distribution pattern of the Indian Peafowl was depicted by MaxEnt software using the optimized variables. The current distribution of the Indian Peafowl using the presence records from 1979 to 2015 is given in Fig.7. The current distribution pattern showed abundance of Peafowl in central part of Kerala, mainly Palakkad, Thrissur and Malappuram districts. In the eastern slopes of Western Ghats (Chinnar, Wayanad and Parambikulam), there were presence of Peafowl having a probability greater than 50 percent.

Table 9. Percent contribution and permutation importance of optimized variables in the future prediction model for distribution of the Indian Peafowl

Environmental variable	Percent contribution	Permutation importance
bio4	41.88	11.43
bio13	19.90	30.18
bio18	13.03	03.68
bio14	11.78	19.29
bio3	09.43	24.63
bio6	04.18	10.83

The most contributing variable (41.9%) for the model construction was temperature seasonality (bio4) and the least (4.2%) was minimum temperature of coldest month (bio6). The variable having high permutation importance (30.18) were precipitation of wettest month (bio13) and isothermality (bio3) by 24.63 percent.

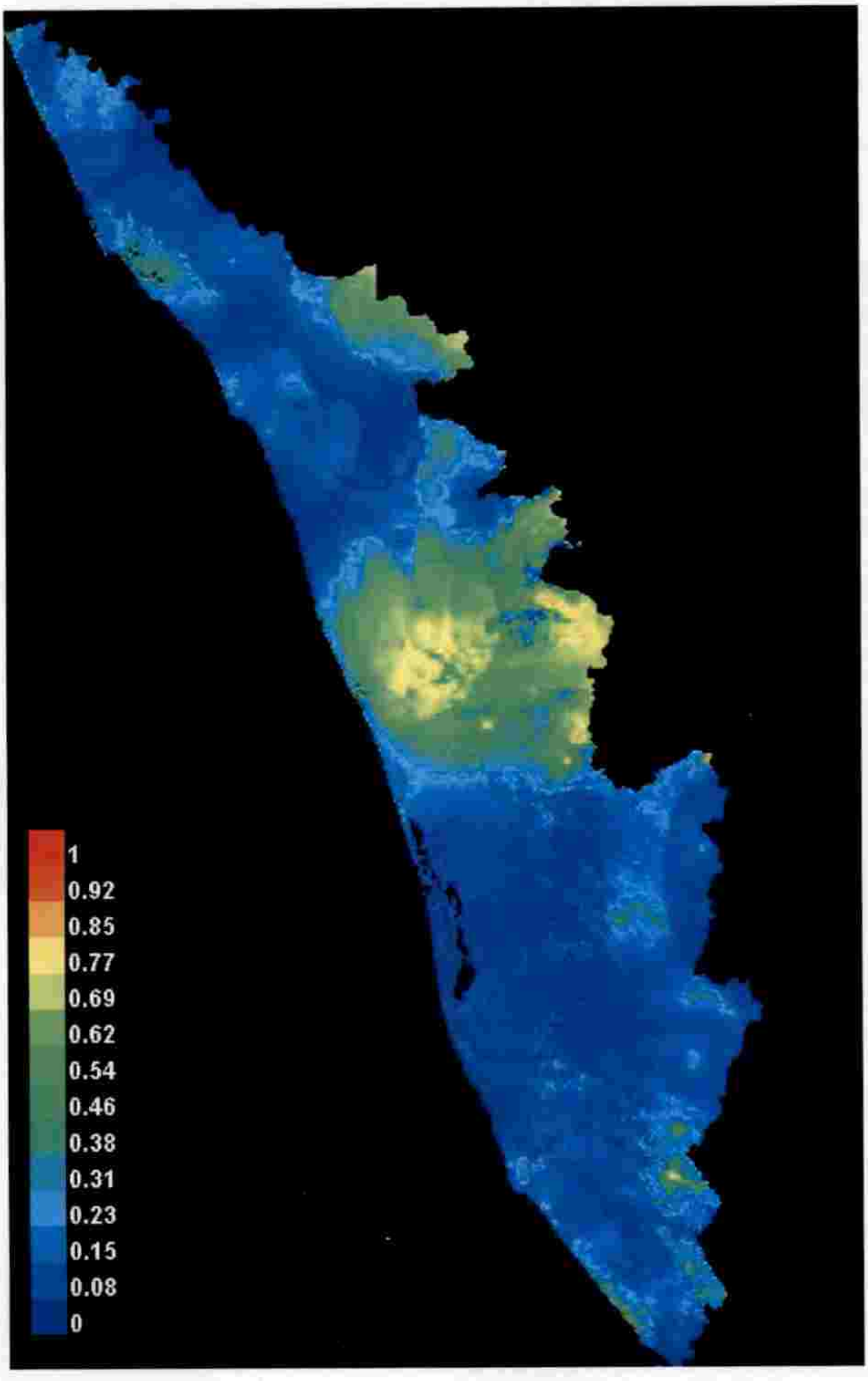


Figure 9. Current distribution of the Indian Peafowl in Kerala

The results of the Jackknife test of variable importance showed higher gain for temperature seasonality (bio4) when used in isolation and the environment variable that decreased the gain the most when it was omitted was precipitation of wettest month (bio13).

Figure 10. Jackknife of regularized training gain in the future prediction models of distribution for the Indian Peafowl, when optimized variables are used

Models prepared using the optimized variables under four different Representative Concentration Pathways (RCP) such as RCP2.6, RCP4.5, RCP6 and RCP8.5 gave the prediction for future distribution of the Indian Peafowl in Kerala for the years 2050 and 2070. The comparison of climate data of different RCPs are shown in appendix-2.

The predicted distribution of the Indian Peafowl in 2050 under the RCP2.6 model is given in Fig. 10. According to which the probability of the Indian Peafowl distribution would expand to the midlands of Thiruvananthapuram, Kollam, Kottayam, the midlands and low lands of Ernakulam, the low lands, midlands and the high lands in Thrissur, the mid and the high lands of Palakkad, low lands of Malappuram, Kozhikode, Kannur and Kasargode. The highlands of Wayanad, Idukki, Kottayam, Pathanamthitta, Kollam and Thiruvananthapuram also showed probability for the presence of the Indian Peafowl.

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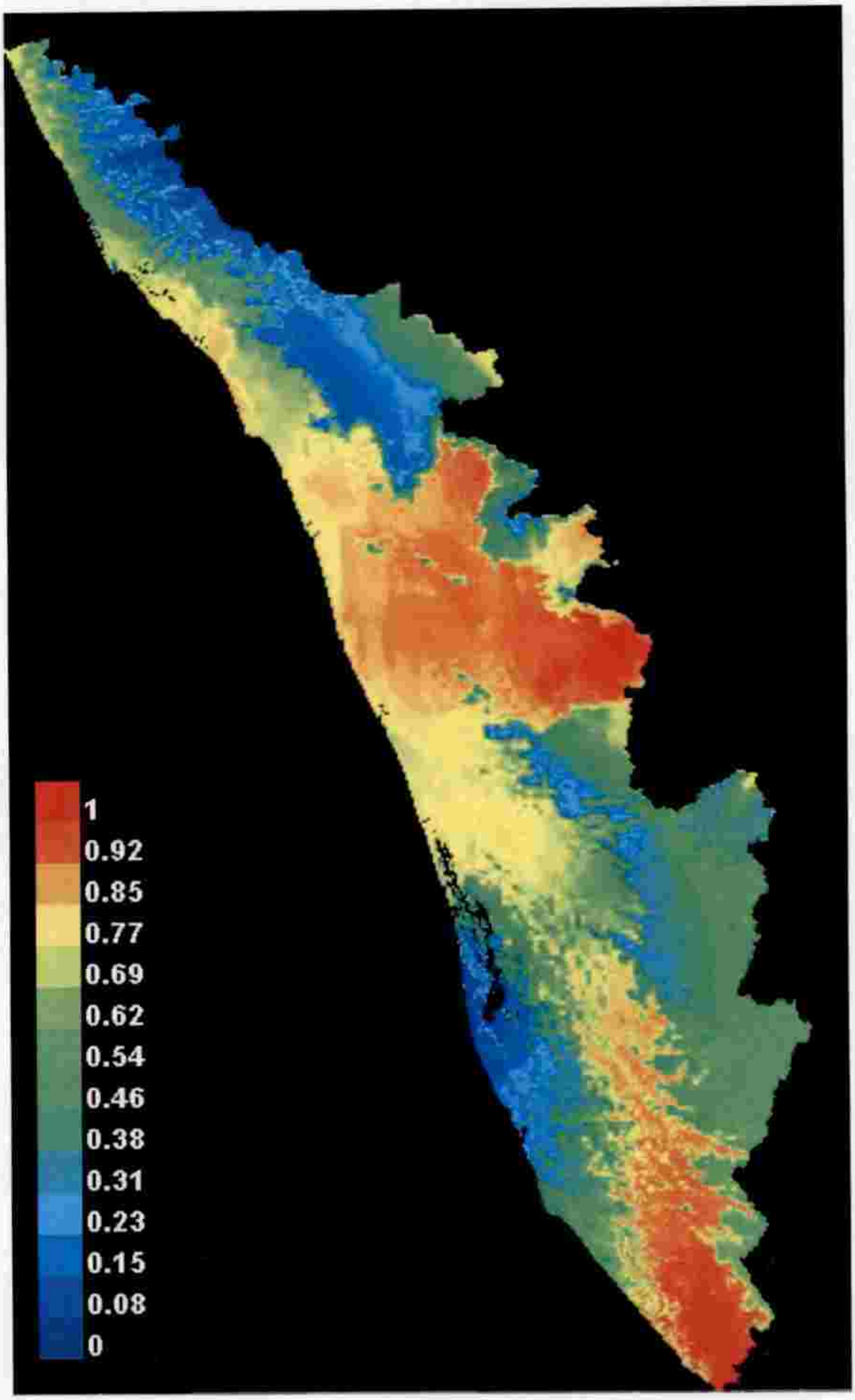

Figure 11. Prediction of the future distribution of the Indian Peafowl for 2050 under RCP2.6 prediction

The predicted distribution of the Indian Peafowl in 2050 under the RCP4.5 model is given in Fig. 11. According to which the probability of the Indian Peafowl would become stronger in the mid lands and low lands of Ernakulam, the low lands, mid lands and the high lands in Thrissur, the mid and the high lands of Palakkad, low lands of Malappuram, Kozhikode, Kannur and Kasargode. The Indian Peafowl, distribution would expand to the mid lands and high lands of Thiruvananthapuram, Kollam, and Kottayam. Also the high lands of Wayanad, Idukki and Pathanamthitta showed probability of presence for the Indian Peafowl.

The predicted distribution of the Indian Peafowl in 2050 under the RCP6 model is given in Fig. 12. A northward expansion of distribution of the Indian Peafowl was seen under RCP6 model predictions. Based on this model the probability of the Indian Peafowl would become stronger in the mid lands and low lands of Ernakulam, the low lands, mid lands and the high lands in Thrissur, the mid lands and the high lands of Palakkad, low lands and high lands of Malappuram, low lands of Kozhikode, Kannur and Kasargode and high lands of Wayanad. The Indian Peafowl distribution would expand to the high lands of Thiruvananthapuram and Kollam.

The predicted distribution of the Indian Peafowl in 2050 under the RCP8.5 model is given in Fig. 13. Similar to 2050 RCP6 model prediction, a northward expansion of distribution of the Indian Peafowl would be seen in RCP8.5 prediction. Based on this model prediction the probability of the Indian Peafowl would become rich in the low lands and mid lands in Thrissur, the mid lands and the high lands of Palakkad, low lands and high lands of Malappuram, low lands of Kozhikode and Kannur and high lands of Wayanad. Certain parts of the high lands of Kollam and Pathanamthitta shows probability for the distribution of the Indian Peafowl.

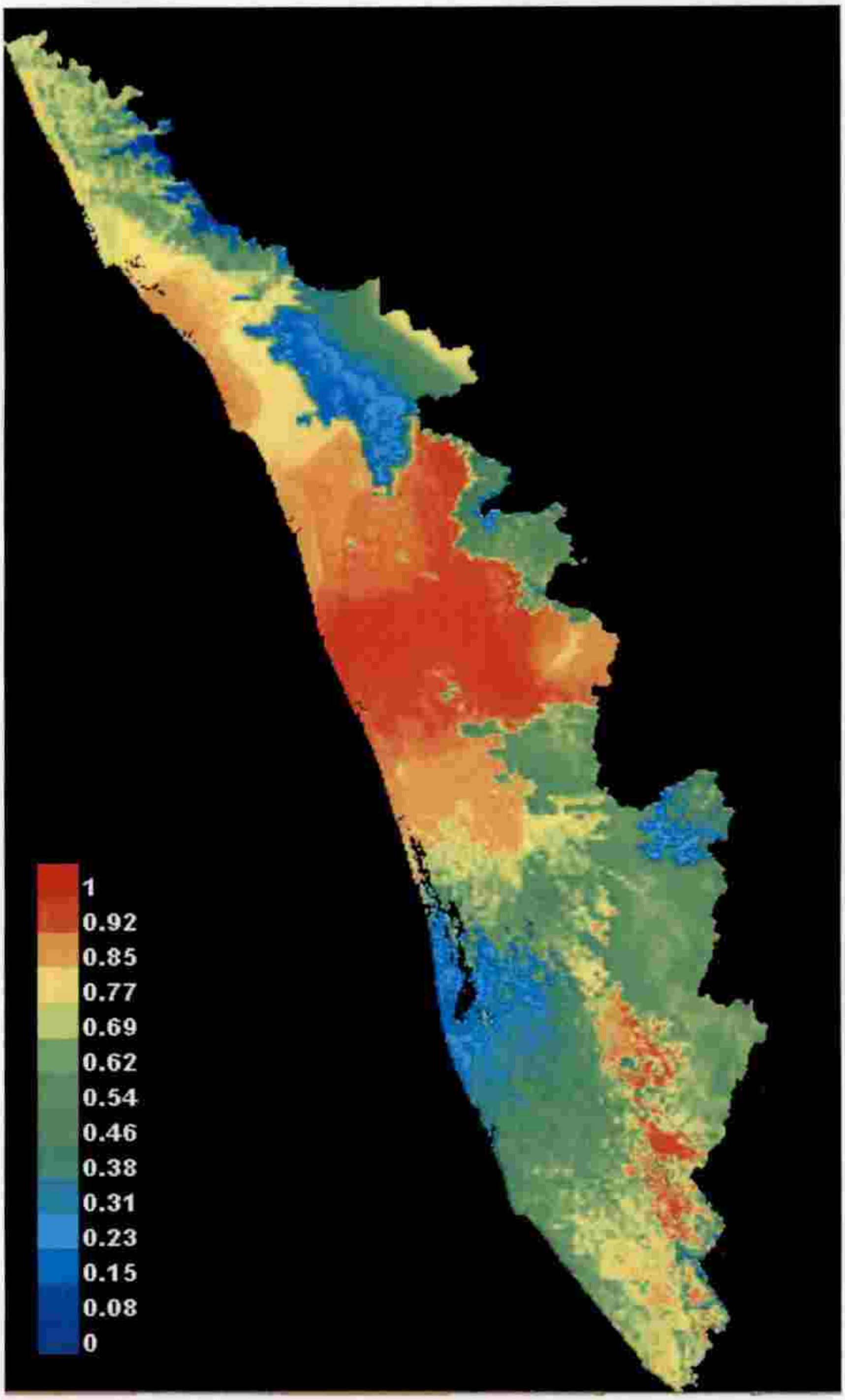

Figure 12. Prediction of the future distribution of the Indian Peafowl for 2050 under RCP4.5 prediction

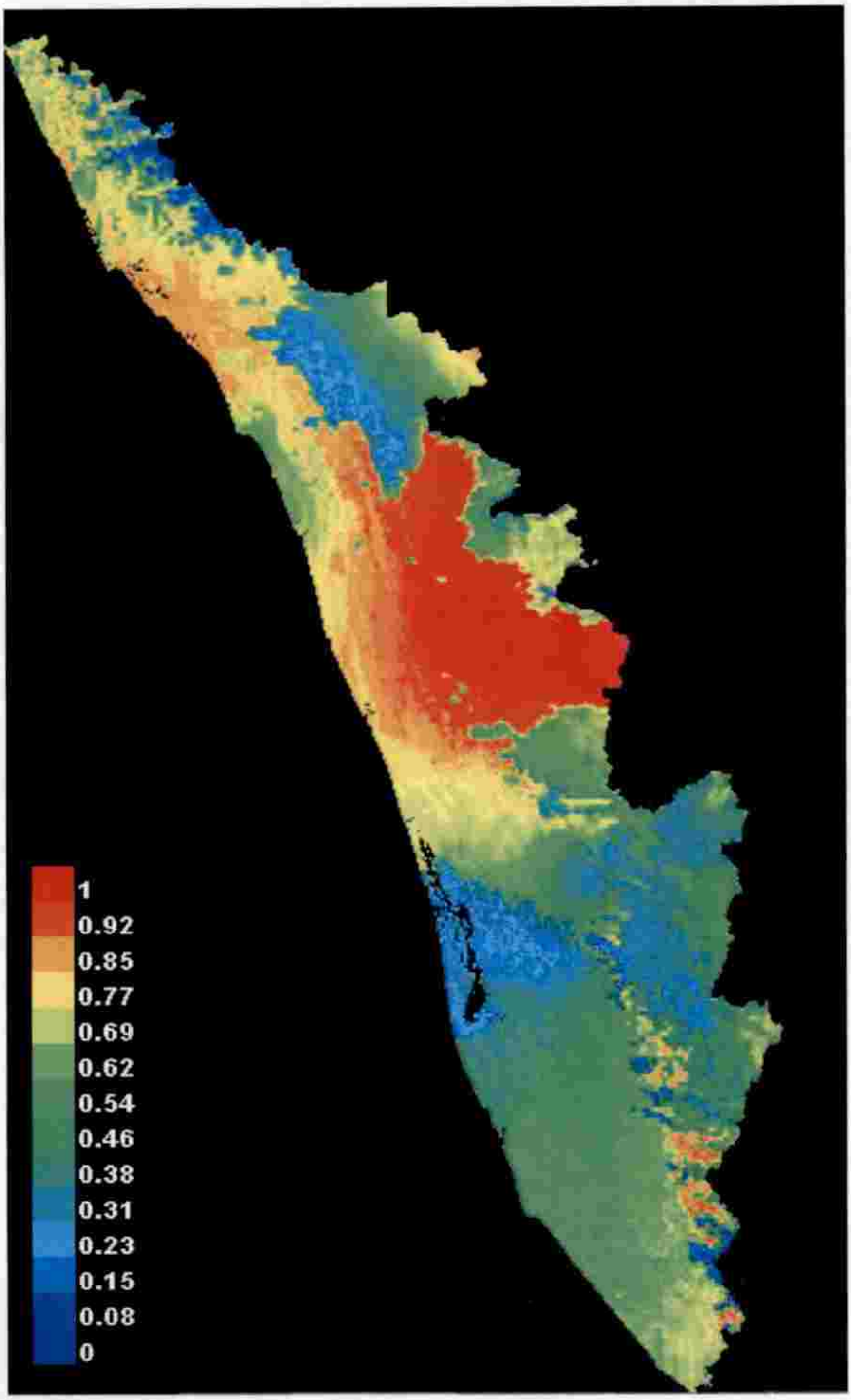

Figure 13. Prediction of the future distribution of the Indian Peafowl for 2050 under RCP6 prediction

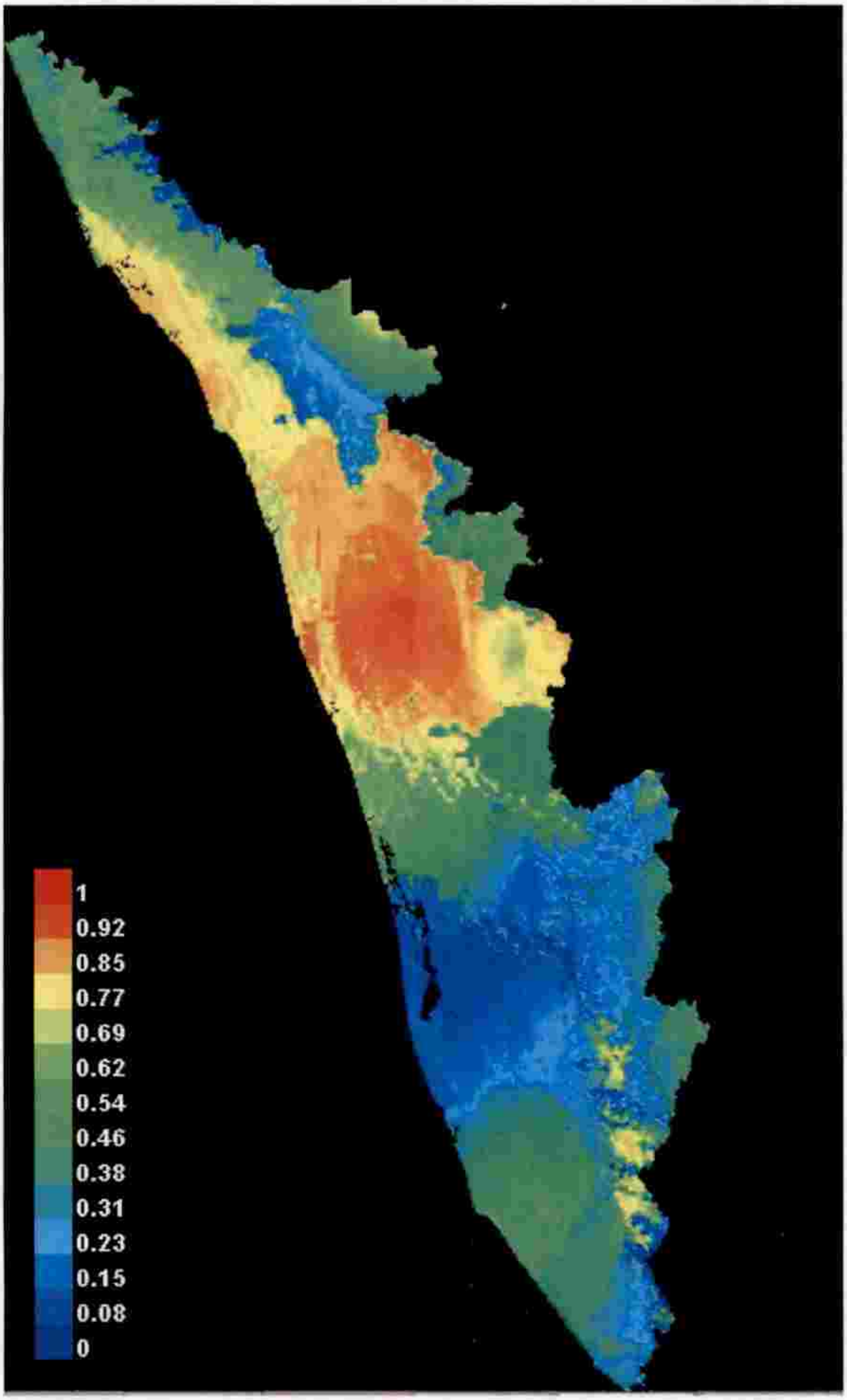

Figure 14. Prediction of the future distribution of the Indian Peafowl for 2050 under RCP8.5 prediction

The predicted distribution of the Indian Peafowl in 2070 under the RCP2.6 model is given in Fig. 14. The Indian Peafowl, distribution would expand to the low lands, mid lands and high lands of Thiruvananthapuram and Kollam, mid lands and high lands of Kottayam, low lands of Alappuzha, the mid lands and low lands of Ernakulam, the low lands, mid lands and the high lands in Thrissur, the mid lands and the high lands of Palakkad, low lands of Malappuram, Kozhikode and Kannur. The high lands of Wayanad, Idukki, Kottayam and Pathanamthitta, would also show probability for the presence of the Indian Peafowl.

The predicted distribution of the Indian Peafowl in 2070 under the RCP4.5 model is given in Fig. 15. Based on this model prediction, the probability of the Indian Peafowl would confine mainly to the mid lands and high lands of Palakkad and Malappuram. The low lands of Kozhikode and Kannur, high lands of Wayanad and Kollam and low lands and mid lands of Thrissur and Ernakulam shows probability for the distribution of the Indian Peafowl.

The predicted distribution of the Indian Peafowl in 2070 under the RCP6 model is given in Fig. 16. The Indian Peafowl, distribution would expand to the low lands, mid lands and highlands of Thiruvananthapuram, mid lands and high lands of Kollam, Kottayam, the low lands, midlands and the high lands in Ernakulam, Thrissur and Malappuram, the mid and the high lands of Palakkad, low lands of Kozhikode and Kannur.

The predicted distribution of the Indian Peafowl in 2070 under the RCP8.5 model is given in Fig. 17. Based on the RCP8.5 model prediction the probability of the Indian Peafowl would become rich in the low lands, mid lands and high lands in Thrissur and Malappuram, the mid lands and the high lands of Palakkad, low lands of Kozhikode and Kannur and high lands of Wayanad. Certain parts of the high lands of Idukki, Pathanamthitta and Kollam showed probability for the distribution of the Indian Peafowl.

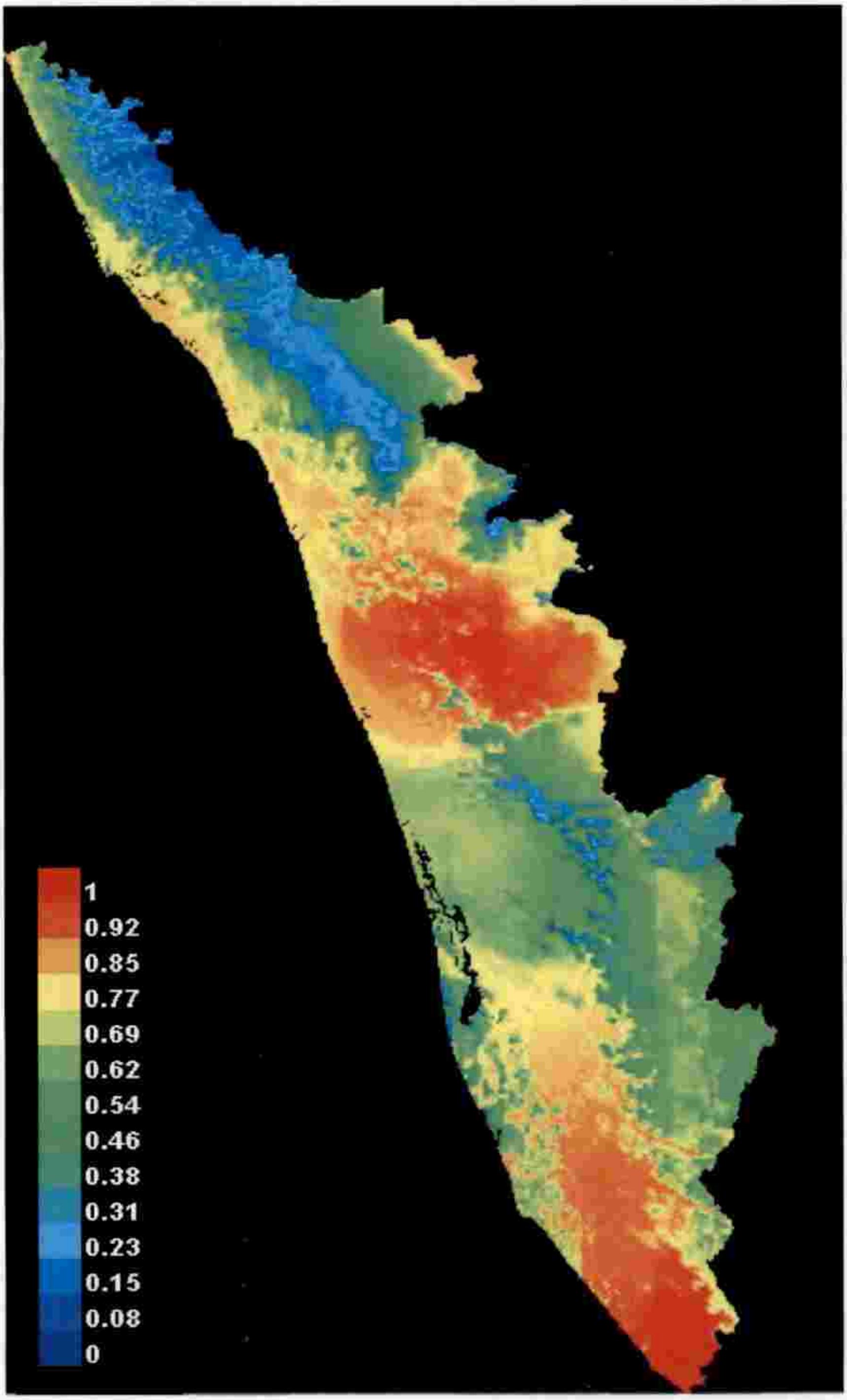

Figure 15. Prediction of the future distribution of the Indian Peafowl for 2070 under RCP2.6 prediction

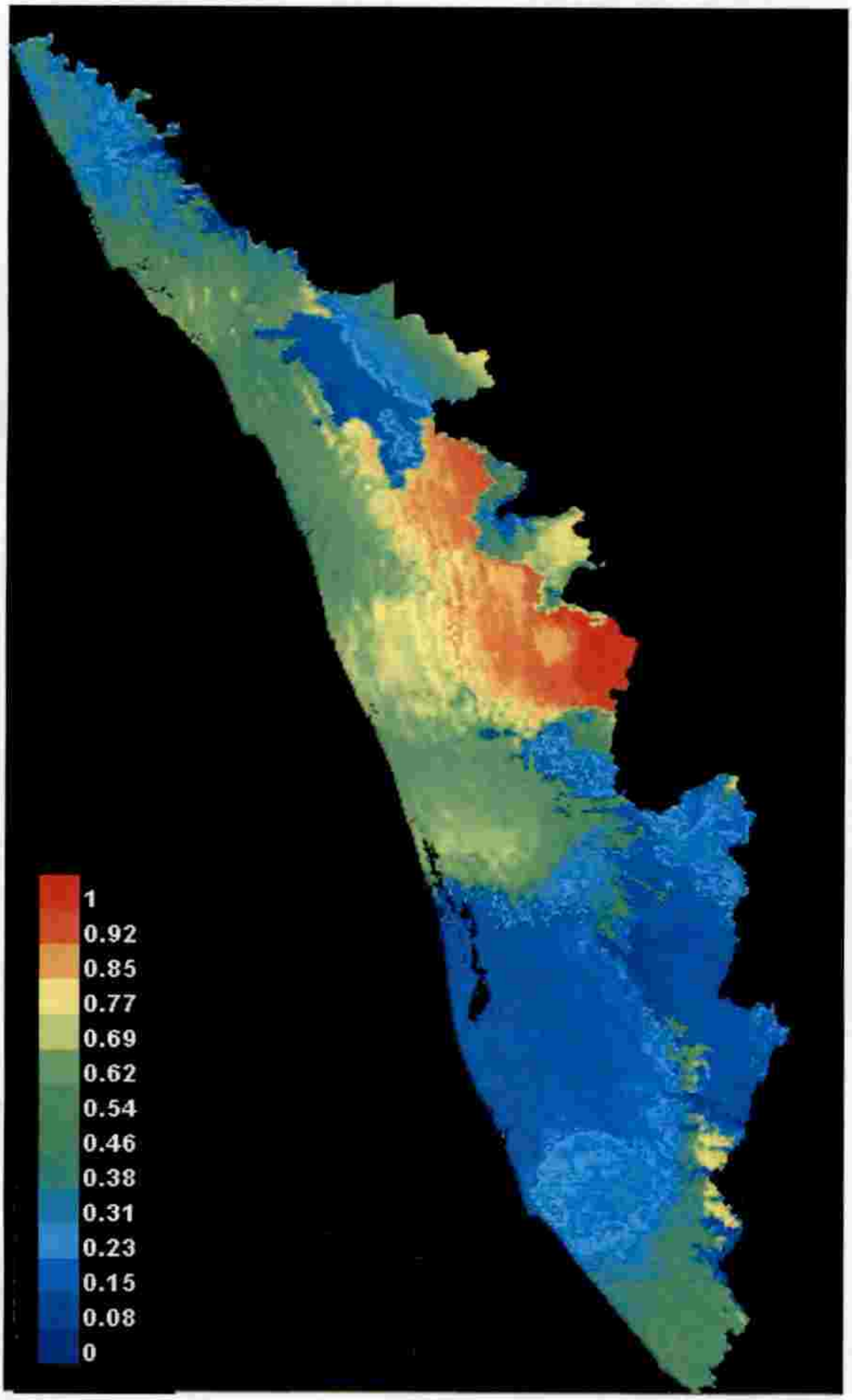

Figure 16. Prediction of the future distribution of the Indian Peafowl for 2070 under RCP4.5 prediction

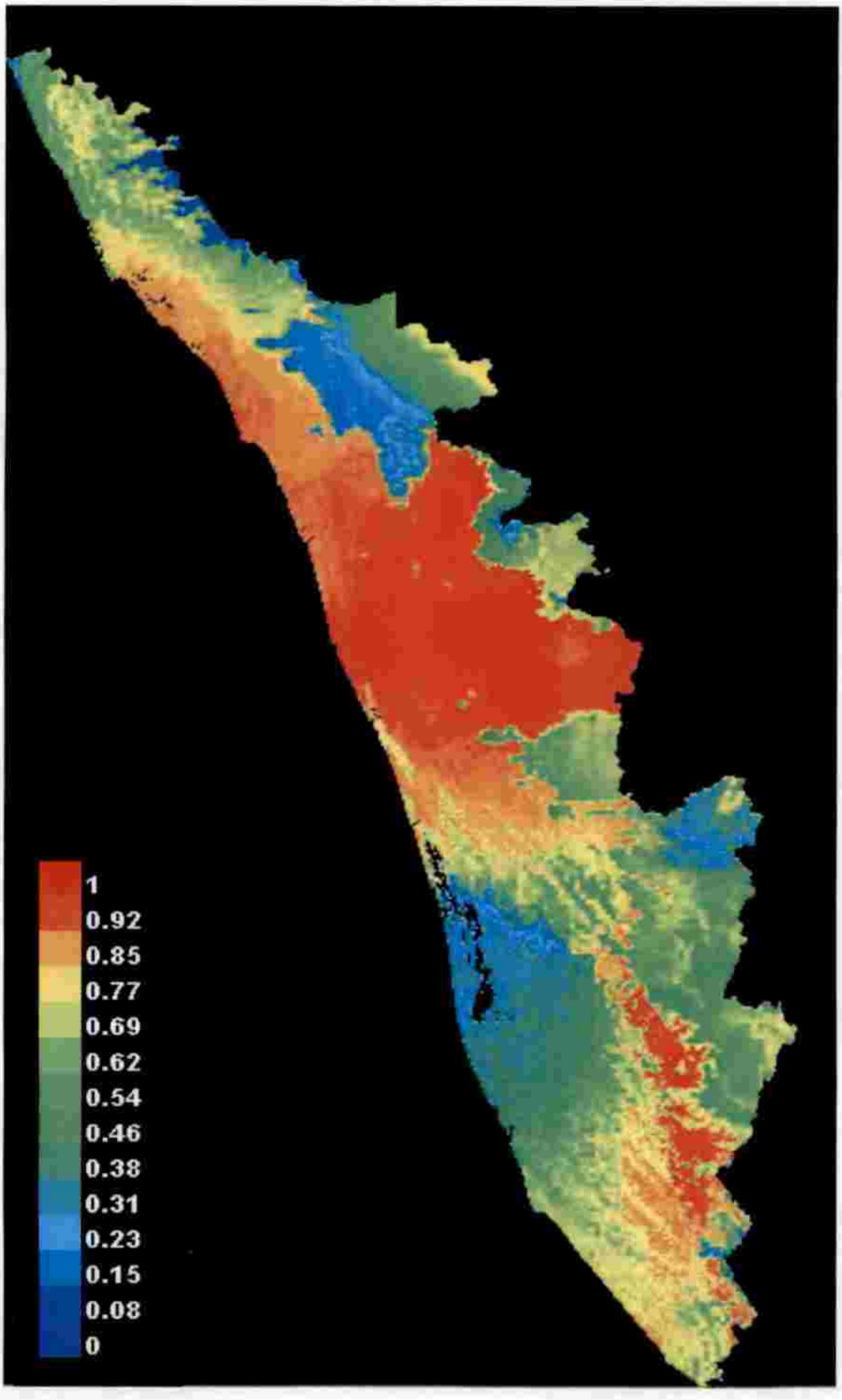

Figure 17. Prediction of the future distribution of the Indian Peafowl for 2070 under RCP6 prediction

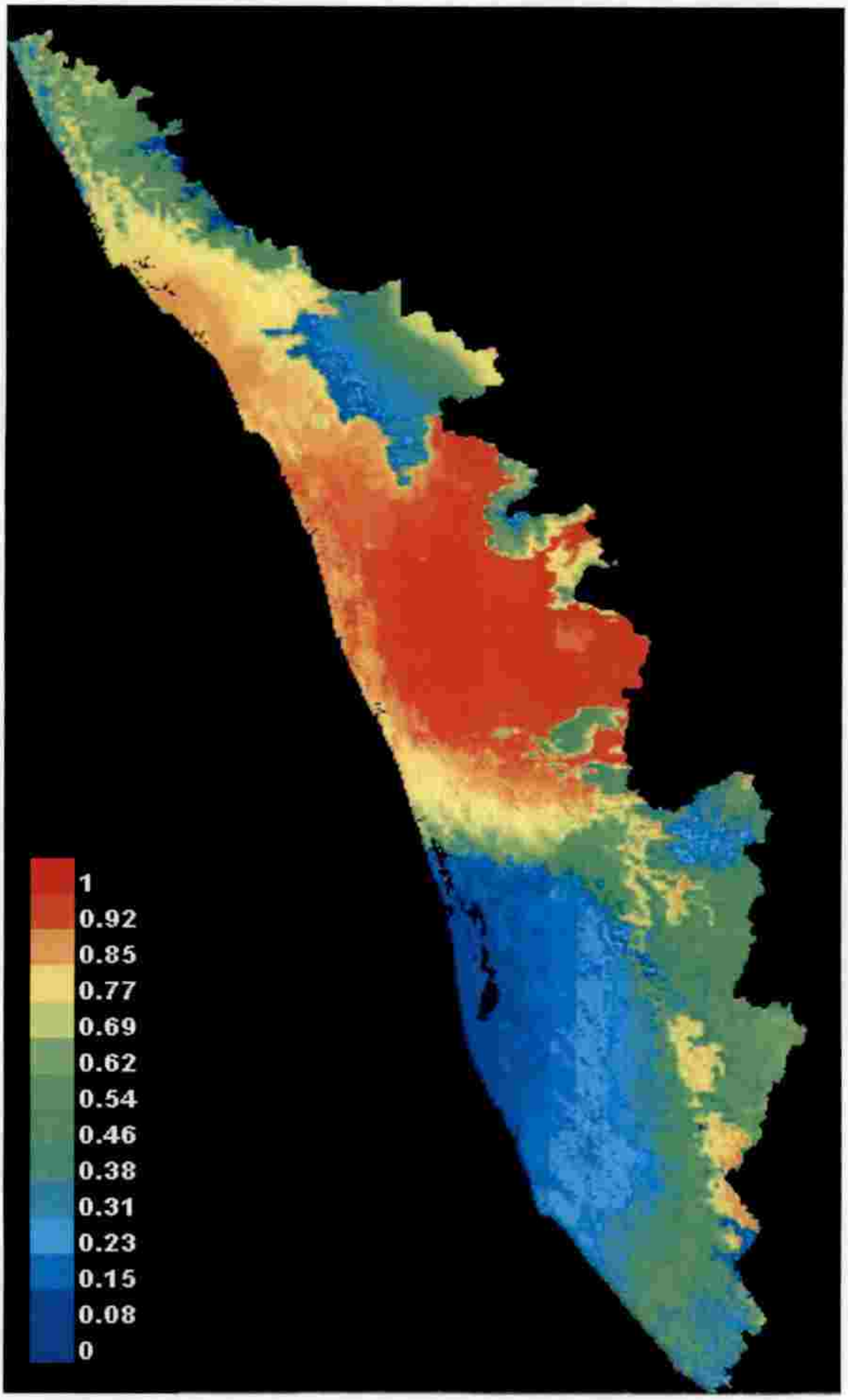

Figure 18. Prediction of the future distribution of the Indian Peafowl for 2070 under RCP8.5 prediction

DISCUSSION

CHAPETR 5

DISCUSSION

The effects of climate change are being spread in all sectors. The existence of life is being questioned and several species have become extinct due to the devastating incidents happened to nature. Intolerant species have been perished and some gone extinct when the habitat is changed drastically due to the extreme climatic events. Several other species changed their habitat to appropriate spaces or showed adaptive mechanisms. Among avian species, changes in distribution is widely seen since they are sensitive to small climatic shifts and due to their migration.

The Indian Peafowl was a sparsely distributed species in Kerala. This study was initiated because of the wide spread occurrence of the Indian Peafowl over the last one decade or so. For the last 10 years or so there have been widespread records of the Indian Peafowl from various habitats from across Kerala.

Thus the present study examines the current distribution patterns of the Indian Peafowl based on climatic variables and other physical variables and also the distribution of the Indian Peafowl is being projected for the years 2050 and 2070 under four Representative Concentration Pathways (RCP).

MaxEnt software was used to study the distributional changes of the Indian Peafowl by relating the presence data points to the climatic conditions prevailing there. The study used the occurrence data points of the Indian Peafowl from 1979 to 2015 and climate data from 1950-2000 for current conditions and for the years 2050 and 2070, climate was predicted by using the coupled model HadGEM2-AO of 30 second resolution under four different Representative Concentration Pathways (RCPs). In this chapter the results obtained are discussed and analysed in detail.

5.1 SELECTION OF REPLICATION RUN TYPE

The objective of replication run type is to assess generality, thereby achieving sense for the model in the identification of attributes of the species distribution and to evade noisy sampling procedures. MaxEnt provides three types of replication types for the evaluation of models such as cross-validation, bootstrapping and subsampling. In cross-validation, presence locations are alienated to training and test data, to fit the model and to evaluate the model respectively. It is preferred by some studies since it handles data efficiently and users can easily find the statistical results such as range and standard error (Merow *et al.*, 2013). But while using cross-validation, only one part of the data is used for model fitting which questions the statistical and spatial independency of test data from training data. This will lead to spatially correlated folds which overestimates the model performance and undervalues the standard error of prediction (Anderson and Raza, 2010). The model is taking test data in a self-manner, so automatically test percentage becomes to zero even the user decided to use some portion of data for testing. In all trial models based on cross-validation, the average test AUC value and SD (Table.2) and the result outputs are the same, telling the lack of independency of test data. So this method is not well suited for future predictions. The SD for the AUC curve (Fig.2c) was quite higher compared to other models.

The bootstrap technique produces pseudo samples which is disconcerted forms of the parent data (Efron, 1979). This is one of the popular resampling technique used for statistical approaches. Replacement of observations from original data is done which allows the creation of possible replications of some observation (De Bin *et al.*, 2016). Our study revealed that it have got high average test AUC value and low SD (Table.2) which can be regarded as best fit of the model. But the problems related to bootstrap is the propensity in choosing too many variables (Janitza *et al.*, 2015). High inclusion frequency for noise variables are prominent in bootstrap approaches (Rospleszcz *et al.*, 2014). The analysis of omission rate in Fig.3a shows clearly about the autocorrelation with test and training data. In both bootstrap and cross-validation the SD for the response curves were higher (Fig.2 a,c).

Subsampling is regarded as an effective substitute for bootstrap (Hartigan, 1969) and it was observed to produce a stable model (Meinshausen and Buhlmann, 2006; 2010). Even when bootstrap fails, it showed linear consistency (Davison *et al.*, 2003). Unlike bootstrap there is no replacement of observations. Subsampling does not encourage the inclusion of noise variables, which permits the acknowledgement of relevant variables. It uses all possible thresholds to discriminate relevant and noise variables (De Bin *et al.*, 2016). Selection of weak effect variables can be considered as a disadvantage to this technique. Even though average test AUC value of subsampling was lower compared to cross-validate and bootstrap (Table.2) and subsampling was selected as an effective replication type since it have lower correlation among variables than in cross-validate and does not include noisy variables like in bootstrap.

5.2 VARIABLE CONTRIBUTION TO THE MODEL DISTRIBUTION OF THE INDIAN PEAFOWL

MaxEnt model output gives the contributions of environmental variables which are used in the construction of distribution model of the Indian Peafowl. In each step of the MaxEnt algorithm, coefficient of a single feature is altered and the gain of the model is increased. At the end of training process these increased gain of each variable are converted into percentage, thus obtaining the percentage contribution. From the analysis of Table.3, temperature seasonality (bio4) showed highest percentage contribution (28%) in the construction of model, whereas mean temperature of driest quarter (bio9) have no contribution at all. Other than bioclimatic variables linear water inland (wlint), perennial water bodies (wbpere) and land cover variables have a significant role as they contribute 7.9, 7.7 and 5.8 percent respectively. Altitude have lower contribution (0.8%) in the distribution of the Indian Peafowl. But these percentage contributions are heuristically defined. They will differ when the path used to get the same solution changes according to different algorithms. Also due to the correlations among the variables, handling of percentage contributions should be made with caution.

The determination of permutation importance (Table.3) is path independent and it depends only on the final MaxEnt model. The decrease in training AUC in accordance with the random permuting values of each variable among both background and presence data is calculated and higher the decrease in AUC resembles the increased dependency of that particular variable. The resulting values are normalized to percentages. So it is more advisable for measuring the contribution of each variable. For the distribution of model precipitation of driest month (bio14) and linear water inland (wlint) shows higher importance. Among the other bioclimatic variables precipitation of wettest month (bio13), precipitation of driest quarter (bio17), precipitation of warmest quarter (bio18) and temperature seasonality (bio4) shows higher importance.

The Jackknife depicts (Fig.4) the training gain of each variable when the model was run in isolation and later it compares to the training gain of all variables. This is helpful in identifying the most contributed variable individually. The variables showing good fit to the training data are temperature annual range (bio7) and temperature seasonality (bio4) and appears to have the most useful information by itself. The environment variable that decreases the gain the most when it is omitted is linear water inland (wlint), which therefore appears to have the most information that isn't present in the other variables. But since it is of no considerable change when compared to others, it can be concluded that no variable contains substantial amount of useful information that is not already contained in other variables.

The responses of each variable is depicted in the graphs shown in Fig.5 and Fig.6. The Fig.5 shows the response of each curves when other variables are at their average values. The variables which have a positive effect on the distribution of the Indian Peafowl at a particular location are minimum temperature of coldest month (bio6), mean temperature of wettest quarter (bio8), mean temperature of coldest quarter (bio11), precipitation of seasonality (bio15), precipitation of warmest quarter (bio18), inland water bodies (wbint), and perennial rivers (wlpere), whereas Mean diurnal range (bio2), isothermality (bio3), temperature seasonality (bio4), Precipitation of wettest month (bio13), precipitation of driest month (bio14), precipitation of wettest quarter (bio16), precipitation of driest quarter (bio17), precipitation of coldest quarter (bio19), linear water inland (wlint) and perennial water bodies (wbpere) have a negative effect for the chance of survival of the Indian Peafowl in that area. Variables like annual mean temperature (bio1), maximum temperature of warmest month (bio5), temperature annual range (bio7), mean temperature driest quarter (bio9), mean temperature of warmest quarter (bio10), annual precipitation (bio12) and altitude (alt) showed no significant change to the survival of species. But these response curves depends on the values of other variables too. Interpreting these response curves are difficult, if there are strong correlation existing among variables. These curves show marginal effect of changing exactly one variable, whereas the model may take advantage of sets of variables changing together.

In contrast to the above marginal response curves, MaxEnt creates another set of response curves using only the corresponding variable (Fig.6). The dependence of predicted suitability both on the selected variable and on dependencies induced by correlations between the selected variable and other variables is reflected in these plots. If there is strong correlation between variables, it is easier to interpret using these curves.

The ideal annual mean temperature (bio1) for the presence of Peafowl is 27-28°C (Fig.5). During the maximum warmest period (bio5) the optimum range of temperature is 34 °C to 37 °C (Fig.6). But it can't prolong at this higher temperature for a longer time. Mean temperature greater than 30 °C during the warmest quarter (bio10) is negatively affecting the probability of presence (Fig.6). Higher the mean diurnal range (bio2), higher is the probability of presence and annually it ranges from 14 °C to

15 °C (Fig.6). When the minimum temperature of coldest month (bio6) and mean temperature of coldest quarter (bio11) are lower, the probability of presence for the Indian Peafowl decreased (Fig.6). Precipitation is negatively affecting the probability of presence. Annual precipitation (bio12) should be low (<1000mm) for higher probability of the Indian Peafowl (100%) and at regions receiving annual rainfall less than 3000mm have a probability of <60 percent for the presence of the Indian Peafowl (Fig.6). During wettest month (bio13), the Indian Peafowl are abundant (97%) in areas having <200mm rainfall and it can go upto <400mm while considering the whole wettest quarter (bio16). During the coldest quarter (bio19), lower precipitation is favouring the probability of presence (Fig.6).

5.3 VARIABLE OPTIMIZATION IN THE MODEL

The trials of model run for selecting the most fitted one showed the results as shown in Table.3. The average test AUC value is used as a selection criteria for this. Based on the ranking of locations it measures the predictive accuracy which is threshold independent. It can be interpreted as the probability of ranking higher a randomly chosen presence location than a randomly chosen background point (Merow *et al.*, 2013). In the case of presence only data, higher the AUC shows that, the model is well distinguished between presences and background locations. The model having higher AUC is more accurate. Table.4 shows the different trials and the average test AUC values. The fourth trial obtained high AUC value and it is taken as the reference model for further studies. Also in the Fig.7a it is seen that the omission on test samples is a very good match to the predicted omission rate. In the ROC curve (Fig.7b), the mean (red line) is above the random prediction line which shows the model is better in predicting the presences.

Climatic variables are well known for high correlation among each other (Brown, 2014). For the interpretation of the contribution of each input variable to the species distribution model, autocorrelation of the input have to be reduced by removing highly correlated variables. Inclusion of these variables will not affect the quality of the prediction, but can seriously limit the inference of the contribution of any correlated variable. When a highly correlated variable is included in the model, then all other highly correlated variables will be excluded from being incorporated. This will result in the improper representation of the 'analysis of variable contributions' in the model output. To find out the correlation among the environmental variables, they were tested by using Pearson correlation matrix |r| and coefficients of determination (R^2). The result is shown in the Table.5 and Table.6. Variables having |r| value >0.9 and >0.7 and R^2 value >0.9 are selected separately to draw out the important variables according to the percentage contribution and permutation importance (Table.7). Models based on these conditions are created and the most suitable one is selected based on the outputs produced my MaxEnt. Only bioclimatic variables are used for further analysis, because future projections for others is not predictable.

Model selection is based on the average test AUC value, SD, |r| and R^2 value and the number of variables used. Lesser the number of variables, more good is the model. It is considered that, if lesser variables explain the model, the correlation will be at its minimum, percent contribution can be effectively studied and it is easy to interpret the model. Model considering the |r|>0.7 will certainly have lesser amount of variables, since most of the variables have some sort of correlation with one another. |r|>0.9 will contain greater number of variables than |r|>0.7 since most of them have correlation lesser than 0.9. So number of variables are considered initially and the model using variables of high percentage contribution having |r| >0.7 and model using variables of high permutation importance having |r| >0.7 are selected. The AUC value of the first (0.799) was lower than the second (0.800). Also the SD was higher for the first (0.028) than the second (0.024). So it can be concluded that model using variables of high permutation importance having |r| >0.7 is better. The variables selected are isothermality (bio3), temperature seasonality (bio4), minimum temperature of coldest month (bio6), precipitation of wettest month (bio13), precipitation of driest month (bio14) and precipitation of warmest quarter (bio18). Based on this, the models are constructed for the current distribution and future distribution.

5.4 CURRENT AND FUTURE PREDICTIONS OF THE DISTRIBUTION OF THE INDIAN PEAFOWL

5.4.1 Current distribution

The current distribution of the Indian Peafowl based on the six variables in the selected model is shown in Fig.8. Most abundant distribution was seen in the central part of Kerala, especially in Palakkad and Thrissur districts. The high lands of Wayanad and Idukki also showed probability of distribution greater than 50 percent. In Chinnar region, Idukki the probability was almost 100 percent. Even the low lands of Thrissur had the potential for the survival of the Indian Peafowl. In districts such as Alappuzha, Kottayam, Kollam (except high lands) and Thiruvananthapuram, Kannur (except low lands) and Kasaragod had no probability of distribution for the Indian Peafowl in the current conditions. The abundance of the Indian Peafowl in Palakkad, Thrissur, Wayanad and Chinnar could be explained by temperature profile and amount of rainfall. The Indian Peafowl was a species which inhabited in dry conditions. They were commonly seen in North India and Tamil Nadu where low precipitation and moderate temperatures were experienced. Likewise the eastern slopes of Western Ghats in Kerala received lower rainfall resulting in dryness which favoured the habitual conditions of the Indian Peafowl. From there, they were spreading to the interiors of the Kerala. The existence of Palakkad gap made it easier for the establishment of the Indian Peafowl in central Kerala. But as a conventional thought, they should not be present in Kerala since it was an area receiving high amount of rainfall and mostly covered with tropical rain forest. This expanding distribution of the Indian Peafowl actually warns about the spreading of dryness in Kerala. The reduction in the amount of rainfall and hike in the temperature profile favoured the environmental conditions which was suitable for the Indian Peafowl distribution.

Using MaxEnt output analysis, the six bioclimatic variables used for modelling had been critically analysed for their role in determining the distribution pattern of the Indian Peafowl in Kerala. Table.8 shows the importance of temperature seasonality (bio4) in model construction. But the variables which was playing the key role in determining the probability of presence are precipitation of wettest month (bio13) and isothermality (bio3). The Jackknife test of variable importance (Fig.9) showed temperature seasonality (bio4) contained the most useful information by itself and precipitation of wettest month (bio13) contained most information that isn't present in the other variables.

5.4.2 Predicted future distribution of the Indian Peafowl

Models prepared using the optimized variables under four different Representative Concentration Pathways (RCP) such as RCP2.6, RCP4.5, RCP6 and RCP8.5 gave the prediction for future distribution of the Indian Peafowl in Kerala for the years 2050 and 2070. In every predictions the distribution of the Indian Peafowl would be spreading compared to current scenario. Generally three factors were considered for the abundance of species; suitable environment which favoured the conditions for growth, availability of food materials and the number of species. This study was mainly based on the environmental conditions. But the primary factor which favoured the species distribution was their pre-existence over there or number of population. If there was no population pre-existing, there won't be any future population. So keeping this as the primary factor, the environmental variables were studied. The availability of food was also a key factor in determining the distribution. Off late the Indian Peafowl was even considered as a pest species by the farmers. They either fed upon or destroyed various crops including the vegetables and paddy.

In the analysis of distribution of the Indian Peafowl in Kerala, the six bioclimatic variables were critically analysed. A single variable cannot determine the distribution of the Indian Peafowl. The analysis was done by considering the combined effects of all the variables. The precipitation during the wettest month (bio13) was found to be increasing all over Kerala in all the RCP predictions and the decreased abundance in some RCP predictions could be explained by this. The predicted distribution of the Indian Peafowl under different scenarios when each variable is excluded in each run is shown in appendix-3. This would clearly depicts the areas where each variable has its influence. The meteorological data shown in appendix-2 and the modelled distribution figures of the Indian Peafowl is used for analysing each RCP prediction.

5.4.2.1 Distribution of the Indian Peafowl for 2050 under RCP2.6 prediction

Fig.10 shows that the distribution of the Indian Peafowl would increase over central, northern low lands and southern mid lands and high lands of Kerala. The increase or decrease in probability of presence could be explained by the response curves of the variables (Fig.6). In all parts of Kerala, there would be an increase in the minimum temperature of coldest month (bio6) and in the temperature seasonality (bio4). The abundance in central and southern parts was due to the decrease in isothermality (bio3) and precipitation of driest month (bio14). In northern Kerala apart from the variation in above given variables, there would be a decrease in precipitation during warmest quarter (bio18).

5.4.2.2 Distribution of the Indian Peafowl for 2050 under RCP4.5 prediction

The result (Fig.11) was almost similar to RCP 2.6 (Fig.10) prediction but would show a decrease in the probability of Indian Peafowl in the mid lands of southern parts of Kerala and in high lands of Palakkad region due to the increase in precipitation during the wettest month (bio13). A widespread increase would be seen in low lands of northern Kerala, high lands of Wayanad and low lands and mid lands of central Kerala due to the increase in minimum temperature of coldest month (bio6) and decrease in precipitation of driest month (bio14), precipitation of warmest quarter (bio18) and temperature seasonality (bio4). In the low lands of Kannur and Kasaragod and high lands of Thiruvananthapuram the precipitation of wettest month (bio13) would be decreasing.

5.4.2.3 Distribution of the Indian Peafowl for 2050 under RCP6 prediction

Distribution of the Indian Peafowl for 2050 under RCP6 prediction (Fig.12) showed that, the low lands and mid lands of northern part of Kerala, low lands, mid lands and high lands of central part of Kerala and high lands of southern part of Kerala would show an increase in probability of presence due to the decrease in the temperature seasonality (bio4), precipitation of driest month (bio14) and precipitation of warmest quarter (bio18) and increase in the minimum temperature of coldest month (bio6). In mid lands of central part of Kerala and high lands of Kollam, Pathanamthitta, Idukki and Palakkad the distribution will be minimized due to the increasing precipitation during wettest month (bio13).

5.4.2.4 Distribution of the Indian Peafowl for 2050 under RCP8.5 prediction

The probability of presence of the Indian Peafowl under RCP8.5 prediction (Fig.13) was similar to RCP2.6 scenario (Fig.10), except the decrease seen in low lands and mid lands of southern Kerala and high lands of Palakkad. This decrease was explained by the increasing precipitation during wettest month (bio13). There would be an increase in temperature seasonality (bio4) except in high lands of Kollam, a decrease in precipitation during driest month (bio14) and warmest quarter (bio18) and an increase of minimum temperature during coldest month (bio6) which resulted in the increased distribution in the Indian Peafowl.

5.4.2.5 Distribution of the Indian Peafowl for 2070 under RCP2.6 prediction

During 2070 under RCP2.6 prediction (Fig.14) due to the increase in the minimum temperature of coldest month (bio6) and in the temperature seasonality (bio4) and decrease in the isothermality (bio3) and precipitation of driest month (bio14), the probability of presence of the Indian Peafowl will increase compared to current conditions (similar to 2050 RCP2.6). The distinguishing characteristics of this prediction was that Alappuzha would become a favourable environment for the growth of the Indian Peafowl due to the increase in the minimum temperature of coldest month (bio6). The increased distribution of the Indian Peafowl in lowlands and midlands of central Kerala and low lands of Kasargode was due to the decreased precipitation of warmest quarter (bio18). The high lands of Wayanad would have high abundance of the Indian Peafowl due to the increased minimum temperature of coldest month (bio6) and decreased precipitation of warmest quarter (bio18).

5.4.2.6 Distribution of the Indian Peafowl for 2070 under RCP4.5 prediction

The probability of presence of the Indian Peafowl during 2070 under RCP4.5 prediction (Fig.15) would decrease throughout Kerala compared to other RCP predictions for the years 2050 and 2070. Only the mid lands and high lands of Thrissur and Palakkad would show more probability for the distribution of the Indian Peafowl due to the increased minimum temperature of coldest month (bio6). The lower probability of presence for the Indian Peafowl was due to the increasing precipitation during wettest month (bio13), driest month (bio14) and warmest quarter (bio18) and increased isothermality (bio3) and decreased temperature seasonality (bio4).

5.4.2.7 Distribution of the Indian Peafowl for 2070 under RCP6 prediction

The distribution of the Indian Peafowl for 2070 under RCP6 prediction (Fig.16) would be similar to the prediction made by RCP4.5 for the year 2050 (Fig.11). The low lands of Kannur and Kozhikode, the low lands and mid lands of Malappuram and Thrissur, mid lands and high lands of Palakkad and high lands of Kottayam, Pathanamthitta, Kollam and Thiruvananthapuram would show high probability for the distribution of the Indian Peafowl due to the decrease in isothermality (bio3) and decreased precipitation during driest month (bio14) and warmest quarter (bio18) and increase in minimum temperature of coldest month (bio6). The abundance would be decreasing in the low lands of Kasargode and high lands of Idukki due to the decreased temperature seasonality (bio4) over there.

5.4.2.8 Distribution of the Indian Peafowl for 2070 under RCP8.5 prediction

During 2070 under RCP8.5 prediction (Fig.17) the low lands and mid lands of southern Kerala and high lands of Idukki would show decrease in the probability of distribution of the Indian Peafowl due to the decreased temperature seasonality (bio4) and increased precipitation during wettest month (bio13) and driest month (bio14). The mid lands and high lands of Palakkad, low lands, mid lands and high lands of Malappuram and Thrissur would be showing high probability in the distribution of the Indian Peafowl due to the increase in the minimum temperature of coldest month (bio6) and decreased precipitation during wettest month (bio13) and warmest quarter (bio18).

SUMMARY AND CONCLUSION

CHAPETR 6

SUMMARY AND CONCLUSION

Climate change can have broad effects on biodiversity and ecosystems. Several studies have been undertaken to study the effects of climate change on both plant and animal species and it revealed the changes occurring in the phenology, distribution and abundance of species. Birds are considered as an important bio-indicators, which reflects the changes happening in their environment. These changes can affect the bird distribution and it is the field where predictive modelling can be applied. Accurate mapping of presence records can be used for correlating it with environmental variables, so that prediction for the future distribution of that species can be mapped. This is used especially in the conservation practices, where the potential places of occurrences can be identified and measures can be taken to protect them in the changed habitat.

This study was emphasized on the impacts of climate change on the temporal and spatial distribution of the Indian Peafowl in Kerala. Using modelling techniques, the distribution for the same is projected for the years 2050 and 2070 under various climate change scenarios. The occurrence data for the Indian Peafowl was collected for a 37 year period from 1979-2015. Using the current climatic conditions (1950-2000) obtained from WorldClim as bioclimatic layers, correlation and probability was calculated for current distribution using MaxEnt software using Maximum Entropy method. Using the results obtained from these, future prediction is being made. By analyzing the current and projected future distribution, following results have been obtained.

- In determining the distribution of the Indian Peafowl using MaxEnt, subsampling method was selected as an effective replication type since it have lower correlation among variables than in cross-validate method and does not include noisy variables like in bootstrap method.

- The variable which showed highest percentage contribution in the construction of model for the distribution of Indian Peafowl was temperature seasonality (bio4), while the mean temperature of driest quarter had little contribution at all (bio9).
- Altitude had no significant role in determining the distribution of the Indian Peafowl.
- The permutation importance in determining the probability of the Indian Peafowl was higher for the precipitation of driest month and linear water inland (wlint) when all variables were used for analysis.
- Temperature annual range (bio7) and temperature seasonality (bio4) appeared to have the most useful information by itself and linear water inland (wlint) have the most information that isn't present in other variables, when all variables were used for modelling the distribution of the Indian Peafowl.
- The variables which had a positive effect on the distribution of the Indian Peafowl at a particular location were mean temperature of coldest quarter (bio11), precipitation of seasonality (bio15), precipitation of warmest quarter (bio18), minimum temperature of coldest month (bio6), mean temperature of wettest quarter (bio8), inland water bodies (wbint), and perennial rivers (wlpere).
- Precipitation of wettest month (bio13), precipitation of driest month (bio14), precipitation of wettest quarter (bio16), precipitation of driest quarter (bio17), precipitation of coldest quarter (bio19), mean diurnal range (bio2), isothermality (bio3), temperature seasonality (bio4), linear water inland (wlint) and perennial water bodies (wbpere) had a negative effect for the chance of survival of the Indian Peafowl in that area.
- Some variables such as altitude, mean temperature of warmest quarter (bio10), annual precipitation (bio12), annual mean temperature (bio1), maximum temperature of warmest month (bio5) and mean temperature of driest quarter (bio9) showed no significant change to the distribution of the Indian Peafowl.
- It cannot prolong during high temperatures (>37 °C) during summer season (bio5).

- Higher the precipitation, lower the probability of presence of the Indian Peafowl. Regions receiving annual precipitation (bio12) lesser than 1000mm favours the probability of presence for the Indian Peafowl by 100 percent and lesser than 3000mm rainfall shows probability of 60 percent and more in sighting the Indian Peafowl in that region.
- During driest period (bio14), no rainfall is good for achieving probability of presence for the Indian Peafowl greater than 50 percent.
- When precipitation of warmest quarter (bio18) was decreased (<300mm) the probability of presence for the Indian Peafowl increased to 50 percent.
- As isothermality (bio3) ranged between 53 and 63 the probability of presence for the Indian Peafowl was greater than 50 percent.
- When temperature seasonality (bio4) was between 12.5 °C and 16 °C, the probability of presence for the Indian Peafowl was greater than 50 percent.
- As the minimum temperature of coldest month (bio6) increased the probability of presence for the Indian Peafowl increased and reached maximum (57%) at 22.5°C.
- Model construction using variables of high permutation importance having $|r| > 0.7$ was better when compared to other models.
- Most abundant distribution of the Indian Peafowl in the current scenario was seen in the central part of Kerala, especially in Palakkad and Thrissur districts. The high lands of Wayanad and Idukki also shows probability of distribution greater than 50 percent. The low lands of Thrissur and North Kerala had the potential for the habitation of peafowl.
- The expanding distribution of the Indian Peafowl may be considered as a warning about the spreading of dryness in Kerala.
- The most contributing variable for the future prediction model construction of the Indian Peafowl using the optimized variables was temperature seasonality (bio4) by 41.9 percent and the least was minimum temperature of coldest month (bio6) by 4.2 percent. But the most heavily depended variable (permutation importance)

in the model for distribution of the Indian Peafowl were precipitation of wettest month (bio13) by 30.18 percent and isothermality (bio3) by 24.63 percent.

- Probability for the presence for the Indian Peafowl would be increasing throughout Kerala in all future projections except in low lands of Alappuzha and high lands of Wayanad. Only in 2070 RCP2.6 projection there showed abundance of the Indian Peafowl in Alappuzha and high lands of Wayanad.
- The probability of presence for the Indian Peafowl increased to 100 percent in the central parts of Kerala (Palakkad, Thrissur, and Malappuram).
- In 2070 RCP4.5, the probability of presence for the Indian Peafowl would be lower compared to other projections throughout Kerala.
- Especially in southern parts of Kerala, the probability of distribution for the Indian Peafowl would reduce in 2050 RCP8.5, 2070 RCP4.5 and 2070 RCP8.5 projections.
- The increasing distribution of the Indian Peafowl over Kerala in the future prediction was associated with the increase in minimum temperature of coldest month (bio6) and decrease in precipitation of warmest quarter (bio18).
- If the precipitation of wettest month (bio13) wouldn't have increased the probability for presence of the Indian Peafowl would have been increased considerably all over Kerala. So precipitation of wettest month could be considered as a controlling factor in the presence of the Indian Peafowl.

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CHAPTER 7

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ABSTRACT

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IMPACT OF CLIMATE CHANGE ON THE TEMPORAL AND SPATIAL DISTRIBUTION OF THE INDIAN PEAFOWL (*Pavo cristatus*) IN KERALA

by

SANJO JOSE V.

(2011 - 20 - 104)

THESIS ABSTRACT
Submitted in partial fulfilment of the
requirements for the degree of

B.Sc. – M.Sc. (Integrated) Climate Change Adaptation
Faculty of Agriculture
Kerala Agricultural University

ACADEMY OF CLIMATE CHANGE EDUCATION AND RESEARCH
VELLANIKKARA, THRISSUR – 680 656
KERALA, INDIA
2016

CHAPTER 8

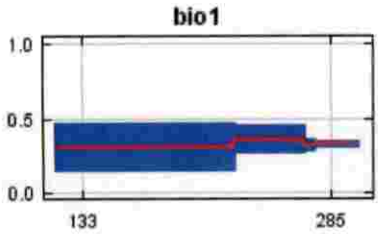
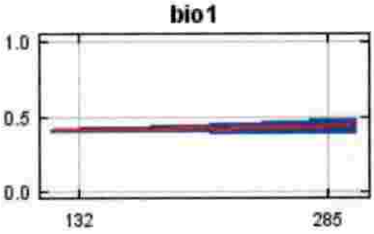
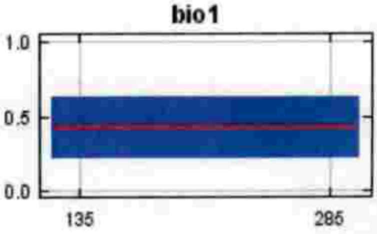
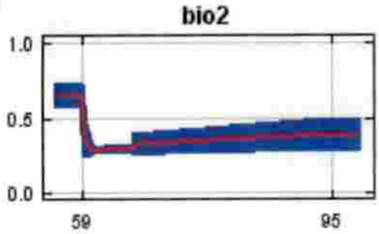
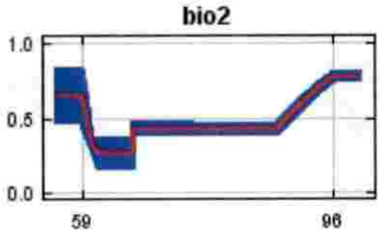
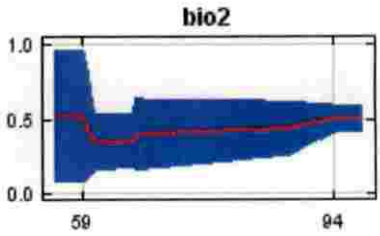
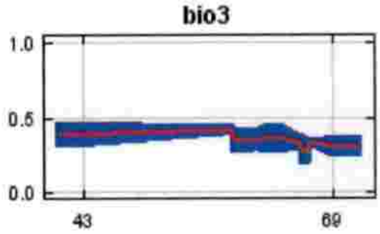
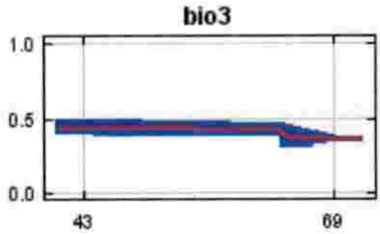
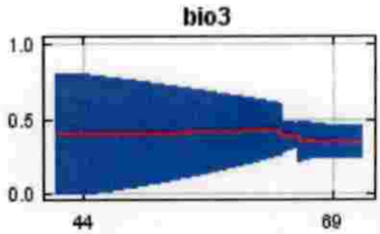
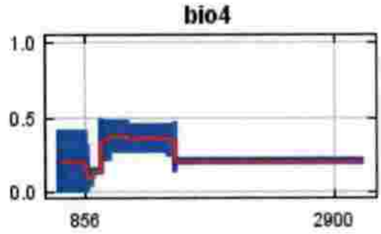
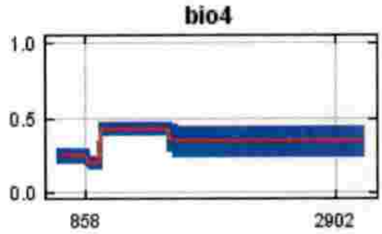
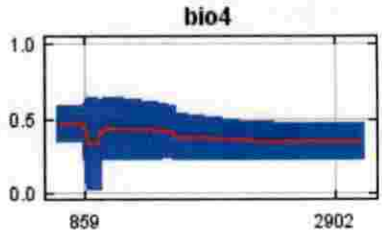
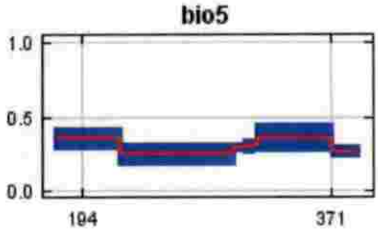
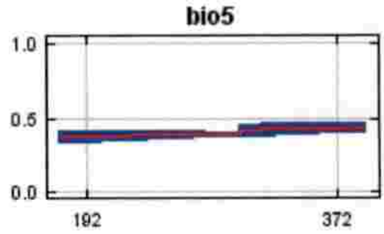
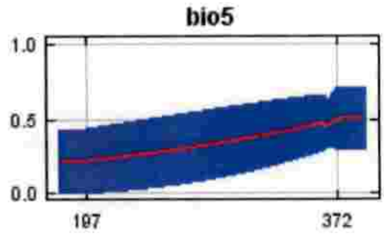
ABSTRACT

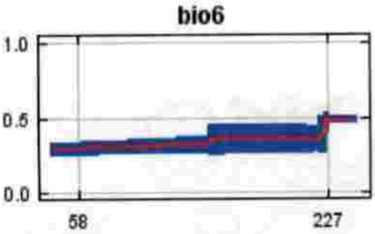
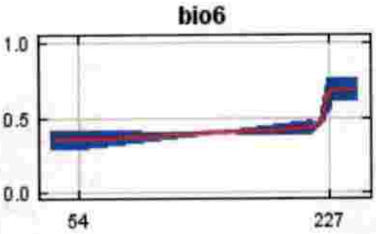
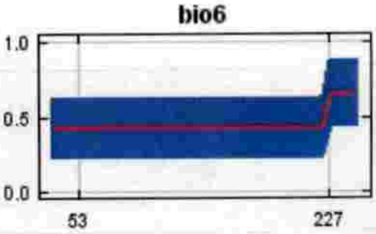
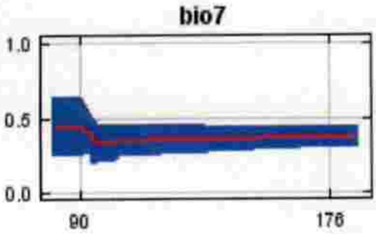
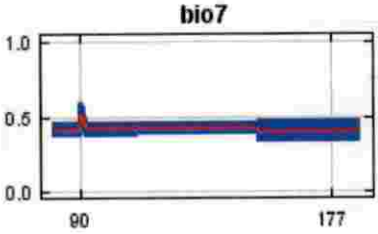
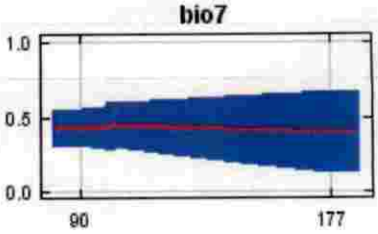
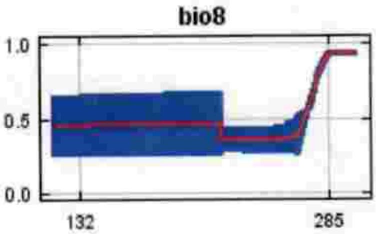
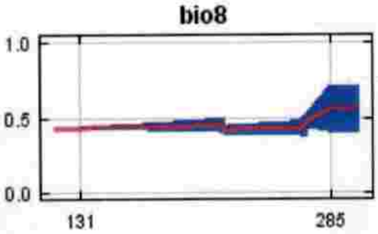
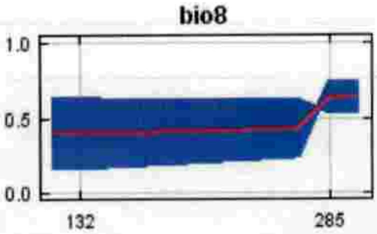
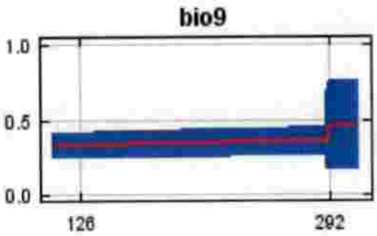
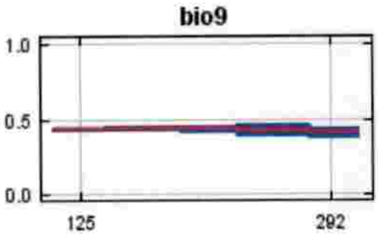
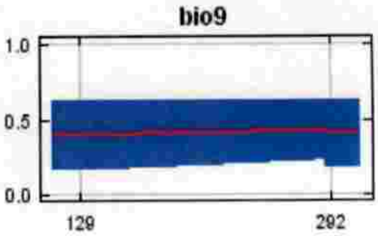
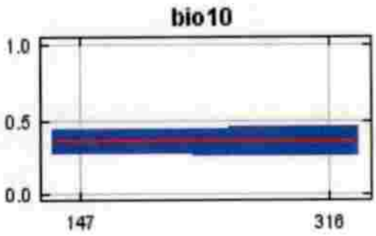
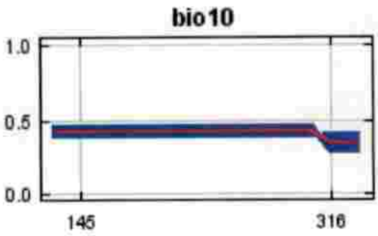
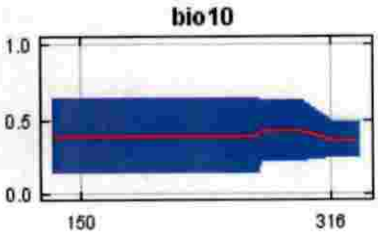
It has been of great importance for the researchers in finding the factors which influenced the species distributions. They are keen to know the current and future distribution patterns of endangered species for implementing the conservation strategies. Some invasive species are expanding their territory into new areas and it have to identify accurately. Avian species are regarded as a good bio-indicator of these devastating changes in the environment. This study was done based on the spatial and temporal distribution of the Indian Peafowl in Kerala, which would be supportive to establish the changes happening in the environment at various places. During the recent decades, rapid expansion in the distribution of the Indian Peafowl was occurred. The hypothesis of this study was that, this expansion is due to the climatic changes. To delineate species distributions and habitat associations, MaxEnt program was used. Using the current presence data acquired from e-Bird data source and 19 bioclimatic variables from WorldClim v1.4 the distribution of the Indian Peafowl had been modelled. Using the current distribution analysis, it would project the distribution of Indian Peafowl into the future by converging it to the maximum entropy probability distribution. Only the uncorrelated variables were used for the study, selected by checking for its percent contribution, permutation importance and R^2 value. The study revealed the current (1950-2015) and projected distribution pattern of the Indian Peafowl for the years 2050 and 2070 under different RCP projections. The projected models tells about the increasing spatial distribution of the Indian Peafowl throughout Kerala except in Alappuzha and western slopes of Wayanad. The central part of Kerala is the hotspot of the Indian Peafowl currently and it will be the same in the future. The combined effects of precipitation and temperature variation have an indispensable role in this projected distribution of the Indian Peafowl.

APPENDICES

APPENDIX-I

Response curves of each variable using bootstrap, subsampling and cross-validate replication types

Bootstrap	Subsampling	Cross-validate
 	 	
 	 	
 	 	
 	 	
 	 	

Bootstrap	Subsampling	Cross-validate
 bio6 	 bio6 	 bio6
 bio7 	 bio7 	 bio7
 bio8 	 bio8 	 bio8
 bio9 	 bio9 	 bio9
 bio10 	 bio10 	 bio10

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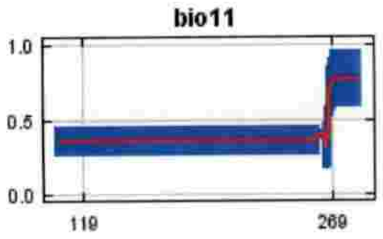
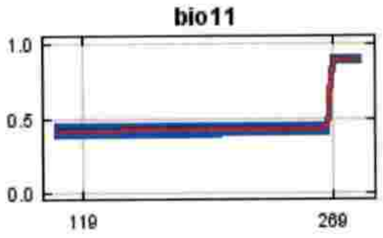
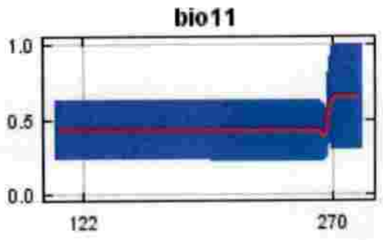
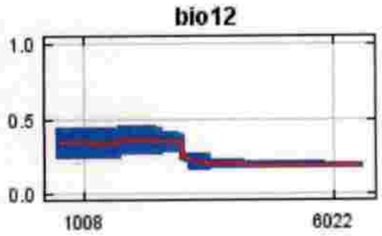
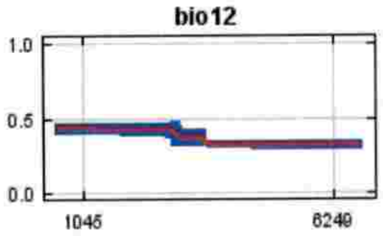
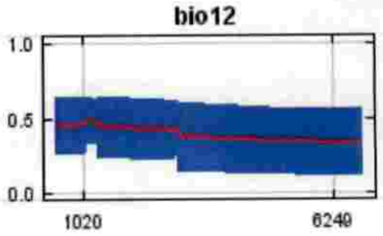
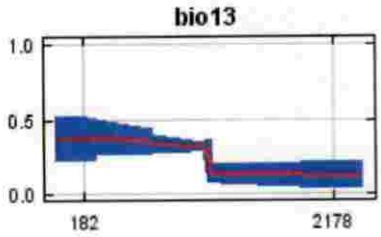
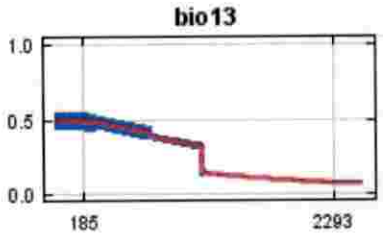
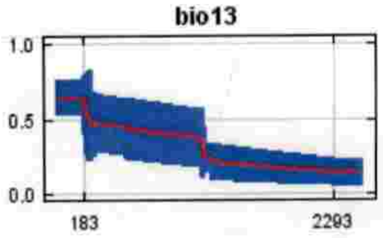
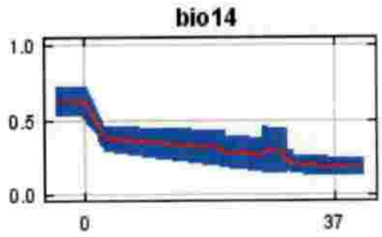
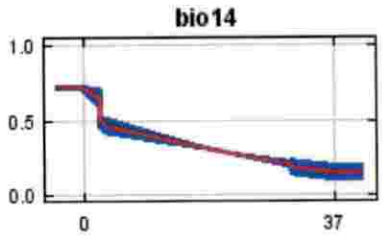
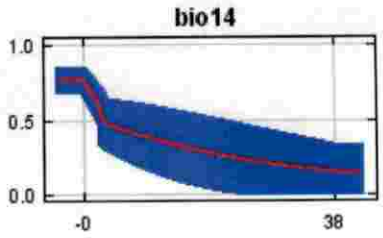
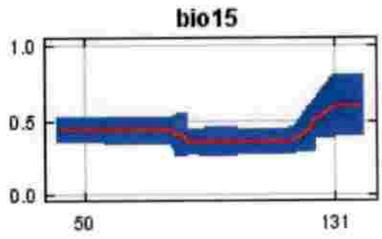
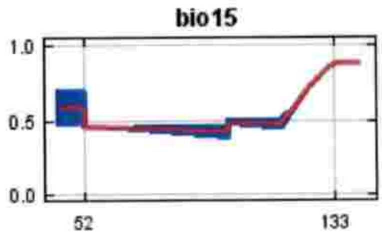
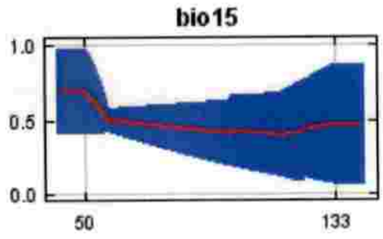
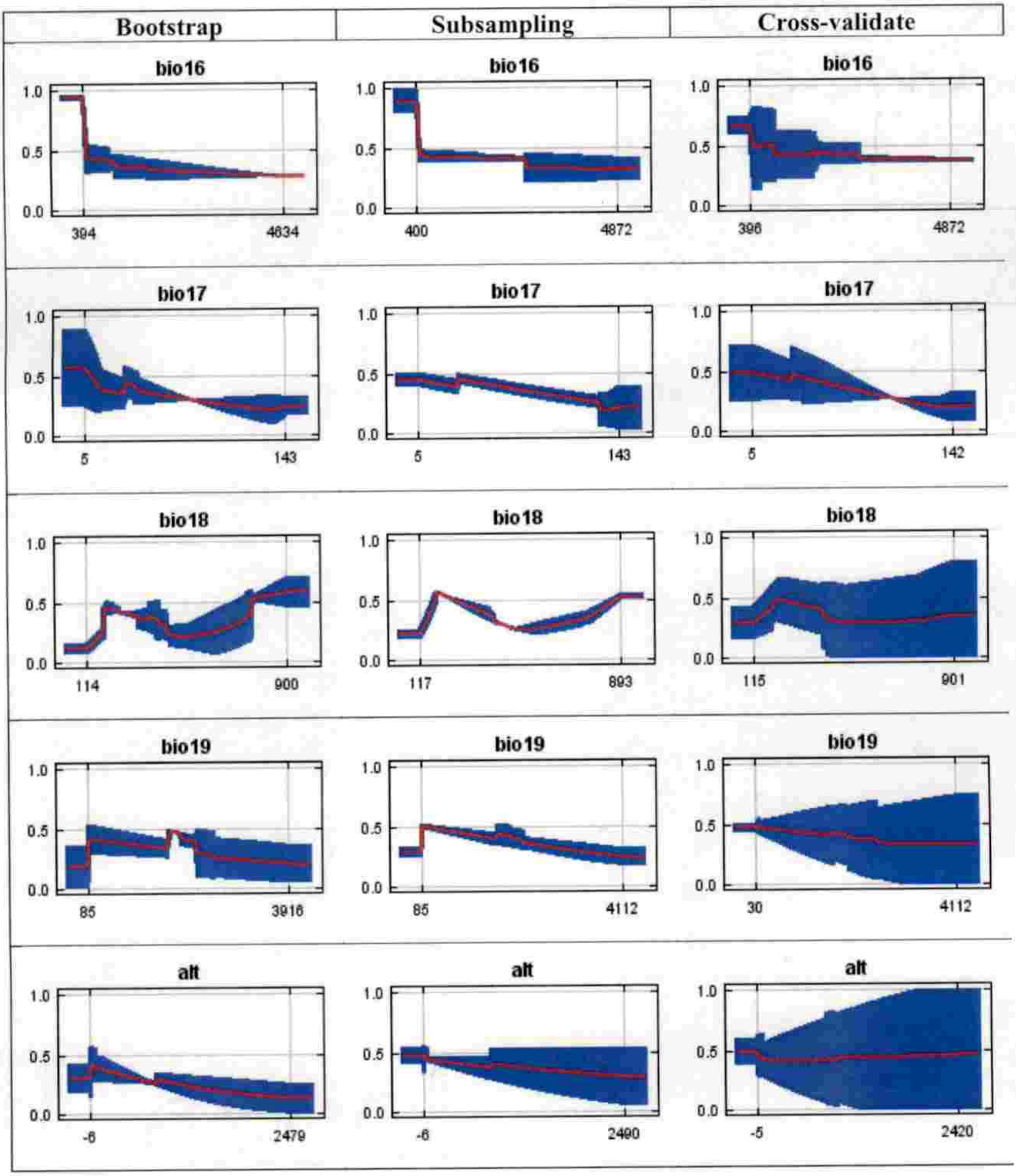
 bio11 	 bio11 	 bio11
 bio12 	 bio12 	 bio12
 bio13 	 bio13 	 bio13
 bio14 	 bio14 	 bio14
 bio15 	 bio15 	 bio15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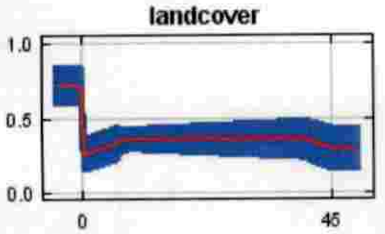
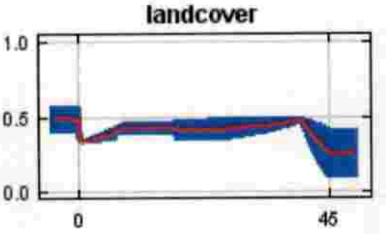
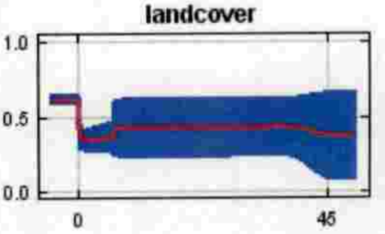
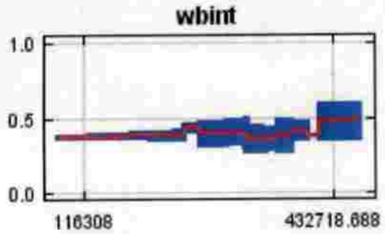
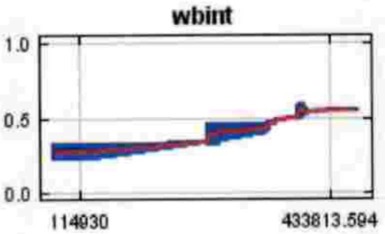
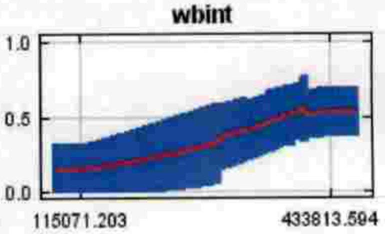
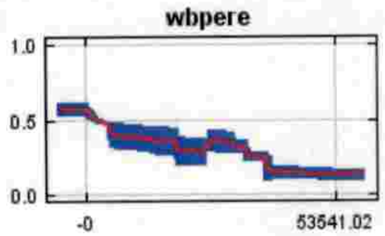
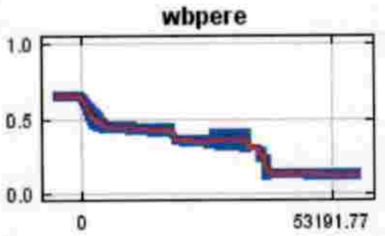
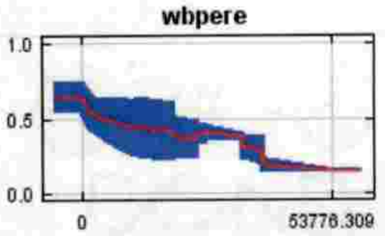
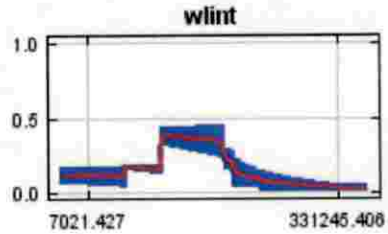
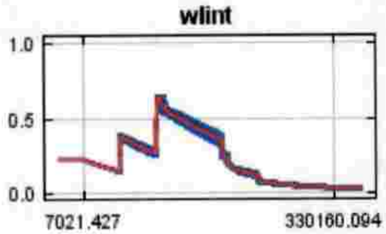
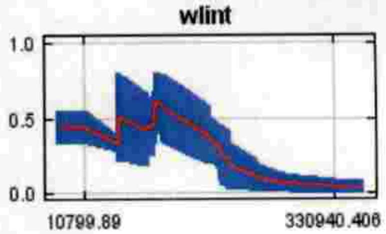
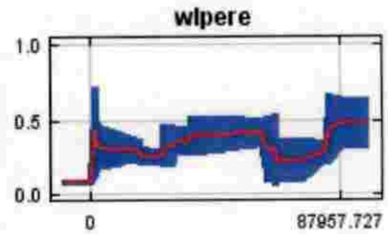
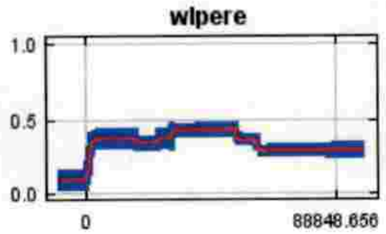
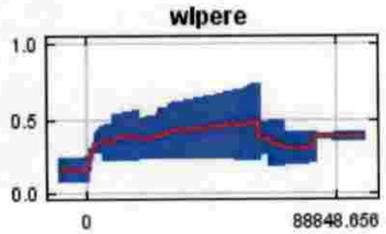
		
		
		
		
		

APPENDIX-II

Precipitation of wettest month (bio13) in mm

Sl. No	Place	1950 - 2000	2050				2070			
			RCP 2.6	RCP 4.5	RCP 6	RCP 8.5	RCP 2.6	RCP 4.5	RCP 6	RCP 8.5
1	Achankovil, Kollam	233	313	328	314	306	297	319	366	384
2	Adat, Thrissur	360	384	417	390	345	366	399	446	511
3	Bekal, Kasargode	360	384	417	390	345	366	399	446	511
4	Chettuva, Thrissur	475	569	531	453	557	531	501	532	435
5	Chinnar, Idukki	702	797	751	618	748	733	708	748	592
6	Choolanur, Palakkad	568	672	634	532	651	620	598	630	514
7	Fort St.Angelo, Kannur	583	700	642	563	691	673	605	654	531
8	Muthanga, Wayanad	675	772	698	590	742	696	685	727	622
9	Palode, Thiruvananthapuram	286	341	333	272	339	306	315	323	317
10	Parambikulam, Palakkad	678	729	617	534	621	673	603	650	695
11	Shendurney, Kollam	378	432	407	356	417	443	380	425	342
12	Thattekkad bird sanctuary, Idukki	1294	1364	1204	1021	1292	1261	1224	1290	1084
13	Thavanoor, Malappuram	1266	1341	1213	1056	1332	1283	1290	1320	1189
14	Veli, Thiruvananthapuram	741	841	782	652	782	788	736	789	604
15	Vellanikkara, Thrissur	726	832	774	649	780	778	730	781	605
	All Kerala average	652	741	690	583	702	689	660	701	574

Precipitation of driest month (bio14) in mm

Sl. No	**Place**	**1950 - 2000**	**2050**				**2070**			
			RCP 2.6	**RCP 4.5**	**RCP 6**	**RCP 8.5**	**RCP 2.6**	**RCP 4.5**	**RCP 6**	**RCP 8.5**
1	Achankovil, Kollam	24	18	17	14	24	17	26	16	31
2	Adat, Thrissur	9	7	6	6	8	5	8	6	11
3	Bekal, Kasargode	1	1	1	1	1	1	1	1	1
4	Chettuva, Thrissur	2	2	1	2	2	1	2	1	4
5	Chinnar, Idukki	29	24	22	18	24	20	36	21	28
6	Choolanur, Palakkad	2	2	1	2	2	1	2	1	3
7	Fort St.Angelo, Kannur	3	2	2	3	2	2	3	3	3
8	Muthanga, Wayanad	4	3	3	3	4	3	4	3	5
9	Palode, Thiruvananthapuram	14	11	10	10	12	9	15	9	16
10	Parambikulam, Palakkad	22	19	16	13	22	14	26	14	28
11	Shendurney, Kollam	2	2	1	2	2	1	2	1	3
12	Thattekkad bird sanctuary, Idukki	3	3	2	3	2	2	4	2	6
13	Thavanoor, Malappuram	25	21	18	19	24	20	30	15	39
14	Veli, Thiruvananthapuram	18	14	14	12	19	12	20	12	22
15	Vellanikkara, Thrissur	1	1	1	1	1	1	1	1	2
	All Kerala average	6	5	5	4	6	4	7	4	8

Precipitation of warmest quarter (bio18) in mm

Sl. No	Place	1950 - 2000	2050				2070			
			RCP 2.6	**RCP 4.5**	**RCP 6**	**RCP 8.5**	**RCP 2.6**	**RCP 4.5**	**RCP 6**	**RCP 8.5**
1	Achankovil, Kollam	347	661	204	451	333	643	530	438	295
2	Adat, Thrissur	207	217	146	170	130	182	242	146	164
3	Bekal, Kasargode	314	315	314	315	314	312	316	313	314
4	Chettuva, Thrissur	255	243	193	216	176	223	272	191	222
5	Chinnar, Idukki	293	312	170	200	150	328	271	151	152
6	Choolanur, Palakkad	380	445	260	297	224	390	524	264	265
7	Fort St.Angelo, Kannur	362	358	328	346	320	351	389	232	348
8	Muthanga, Wayanad	280	328	186	223	164	265	370	187	194
9	Palode, Thiruvananthapuram	283	354	186	227	165	280	408	188	190
10	Parambikulam, Palakkad	386	420	239	263	210	480	359	214	221
11	Shendurney, Kollam	374	443	255	294	220	380	520	257	260
12	Thattekkad bird sanctuary, Idukki	282	266	218	241	206	249	291	217	250
13	Thavanoor, Malappuram	542	675	330	378	294	643	723	329	314
14	Veli, Thiruvananthapuram	738	823	402	611	415	778	709	581	394
15	Vellanikkara, Thrissur	353	392	251	284	219	342	450	252	261
	All Kerala average	338	385	236	273	210	342	433	241	244

Isothermality (bio3) ([bio2/bio7] x100)

Sl. No	Place	1950 - 2000	2050				2070			
			RCP 2.6	**RCP 4.5**	**RCP 660**	**RCP 8.5**	**RCP 2.6**	**RCP 4.5**	**RCP 6**	**RCP 8.5**
1	Achankovil, Kollam	65	61	61	64	64	59	65	61	64
2	Adat, Thrissur	61	58	56	60	58	56	61	57	58
3	Bekal, Kasargode	62	61	63	64	63	61	65	63	63
4	Chettuva, Thrissur	59	56	55	58	57	55	59	56	56
5	Chinnar, Idukki	65	60	63	65	65	60	66	63	64
6	Choolanur, Palakkad	63	61	60	63	63	60	65	61	62
7	Fort St.Angelo, Kannur	61	59	60	61	61	59	63	61	60
8	Muthanga, Wayanad	61	60	58	61	61	57	63	58	59
9	Palode, Thiruvananthapuram	63	60	60	63	62	58	64	60	62
10	Parambikulam, Palakkad	65	63	65	67	66	60	68	64	66
11	Shendurney, Kollam	62	61	60	63	62	59	64	61	62
12	Thattekkad bird sanctuary, Idukki	59	56	56	58	56	55	59	56	56
13	Thavanoor, Malappuram	67	65	66	68	69	63	69	67	69
14	Veli, Thiruvananthapuram	62	58	5959	61	60	57	63	58	60
15	Vellanikkara, Thrissur	61	61	60	62	61	59	63	60	60
	All Kerala average	62	60	60	62	61	59	64	60	61

Maximum temperature of warmest month (bio13) in °C

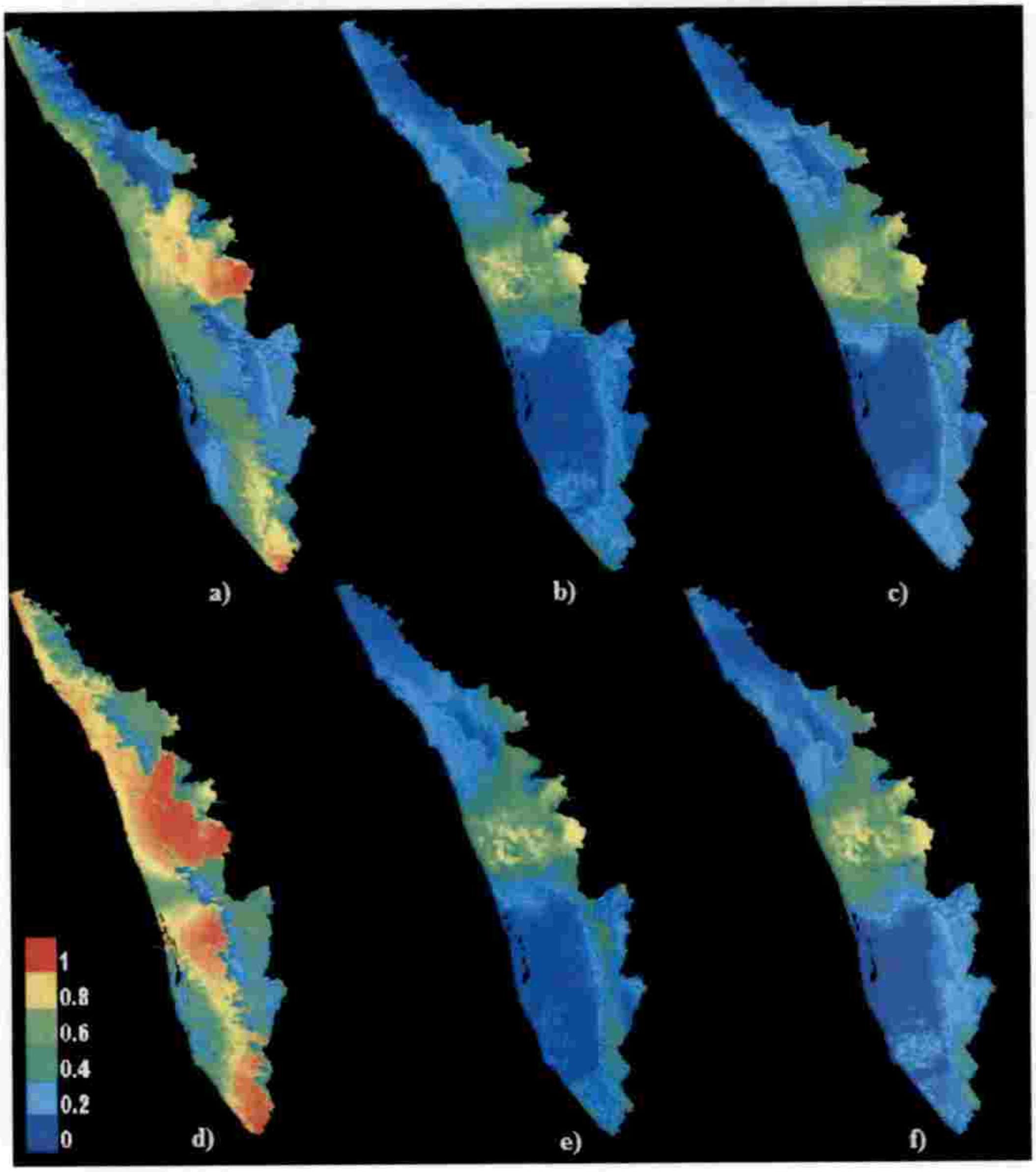
Sl. No	Place	1950 - 2000	2050				2070			
			RCP 2.6	RCP 4.5	RCP 6	RCP 8.5	RCP 2.6	RCP 4.5	RCP 6	RCP 8.5
1	Achankovil, Kollam	11.0	12.2	11.4	11.0	11.0	12.4	10.7	11.4	11.0
2	Adat, Thrissur	13.3	14.1	14.5	13.4	13.9	14.8	13.3	13.9	13.8
3	Bekal, Kasargode	11.1	10.9	10.8	10.3	10.4	11.1	10.8	10.5	10.1
4	Chettuva, Thrissur	13.3	14.1	14.3	13.4	13.9	14.6	13.3	13.8	13.6
5	Chinnar, Idukki	10.3	10.9	10.2	9.9	9.9	11.5	9.7	10.2	9.9
6	Choolanur, Palakkad	13.2	13.4	13.5	12.7	13.4	13.5	13.1	13.1	12.5
7	Fort St.Angelo, Kannur	12.2	12.4	12.3	11.6	11.9	12.6	11.8	11.8	11.6
8	Muthanga, Wayanad	14.5	14.7	15.4	14.4	14.9	15.1	14.5	14.7	14.4
9	Palode, Thiruvananthapuram	11.7	12.4	12.7	11.6	12.0	13.1	11.7	12.1	11.7
10	Parambikulam, Palakkad	8.7	9.8	8.7	8.5	8.5	9.8	8.5	8.6	8.1
11	Shendurney, Kollam	13.2	13.4	13.6	12.8	13.4	13.6	13.2	13.2	12.8
12	Thattekkad bird sanctuary, Idukki	13.5	13.9	14.1	13.1	13.9	14.3	13.2	13.6	13.5
13	Thavanoor, Malappuram	9.4	9.7	9.6	9.4	9.5	10.2	9.5	9.4	8.6
14	Veli, Thiruvananthapuram	11.5	12.8	12.6	12.1	11.8	13.4	11.3	12.3	12.0
15	Vellanikkara, Thrissur	13.9	13.9	14.3	13.5	14.4	14.2	13.8	14.2	13.6
	All Kerala average	13.0	13.4	13.4	12.7	13.2	13.7	12.9	13.1	12.7

Table.6 Minimum temperature of coldest month (bio6) in ^{0}C

Sl. No	**Place**	**1950 - 2000**	**2050**				**2070**			
			RCP 2.6	**RCP 4.5**	**RCP 6**	**RCP 8.5**	**RCP 2.6**	**RCP 4.5**	**RCP 6**	**RCP 8.5**
1	Achankovil, Kollam	16.5	17.6	18.5	18.4	19.2	17.2	19.7	19.0	20.6
2	Adat, Thrissur	18.0	19.3	19.9	29.8	21.0	18.5	21.3	20.5	22.8
3	Bekal, Kasargode	21.4	22.5	23.4	22.9	23.4	22.5	24.3	23.5	24.6
4	Chettuva, Thrissur	15.7	17.0	17.7	17.5	18.6	16.3	18.9	18.2	20.2
5	Chinnar, Idukki	21.6	22.6	23.5	23.3	24.0	22.3	24.5	23.9	25.3
6	Choolanur, Palakkad	22.2	23.4	24.1	23.9	24.8	22.9	25.2	24.5	26.3
7	Fort St.Angelo, Kannur	21.3	22.5	23.3	22.9	23.6	22.2	24.2	23.6	24.9
8	Muthanga, Wayanad	22.0	23.2	23.9	23.8	24.9	22.6	25.2	24.4	26.5
9	Palode, Thiruvananthapuram	18.8	20.0	20.7	20.7	21.7	19.4	22.0	21.2	23.3
10	Parambikulam, Palakkad	22.5	23.5	24.4	24.2	24.9	23.2	25.4	24.8	26.1
11	Shendurney, Kollam	22.2	23.4	24.1	24.0	24.9	22.9	25.2	24.5	26.4
12	Thattekkad bird sanctuary, Idukki	16.6	17.9	18.6	18.4	19.3	17.3	19.8	19.1	20.9
13	Thavanoor, Malappuram	22.5	23.6	24.4	24.3	25.0	23.3	25.5	24.8	26.3
14	Veli, Thiruvananthapuram	12.9	14.0	14.9	14.9	15.7	13.6	16.2	15.4	17.3
15	Vellanikkara, Thrissur	22.1	23.3	24.0	23.8	24.8	22.7	25.1	24.4	26.3
	All Kerala average	20.7	21.9	22.6	22.5	23.4	21.4	23.8	23.1	24.9

APPENDIX-III

The prediction of distribution of the Indian Peafowl for the year 2050 under RCP 2.6 prediction when variables a) bio3 b) bio4 c) bio6 d) bio13 e) bio14 f) bio18



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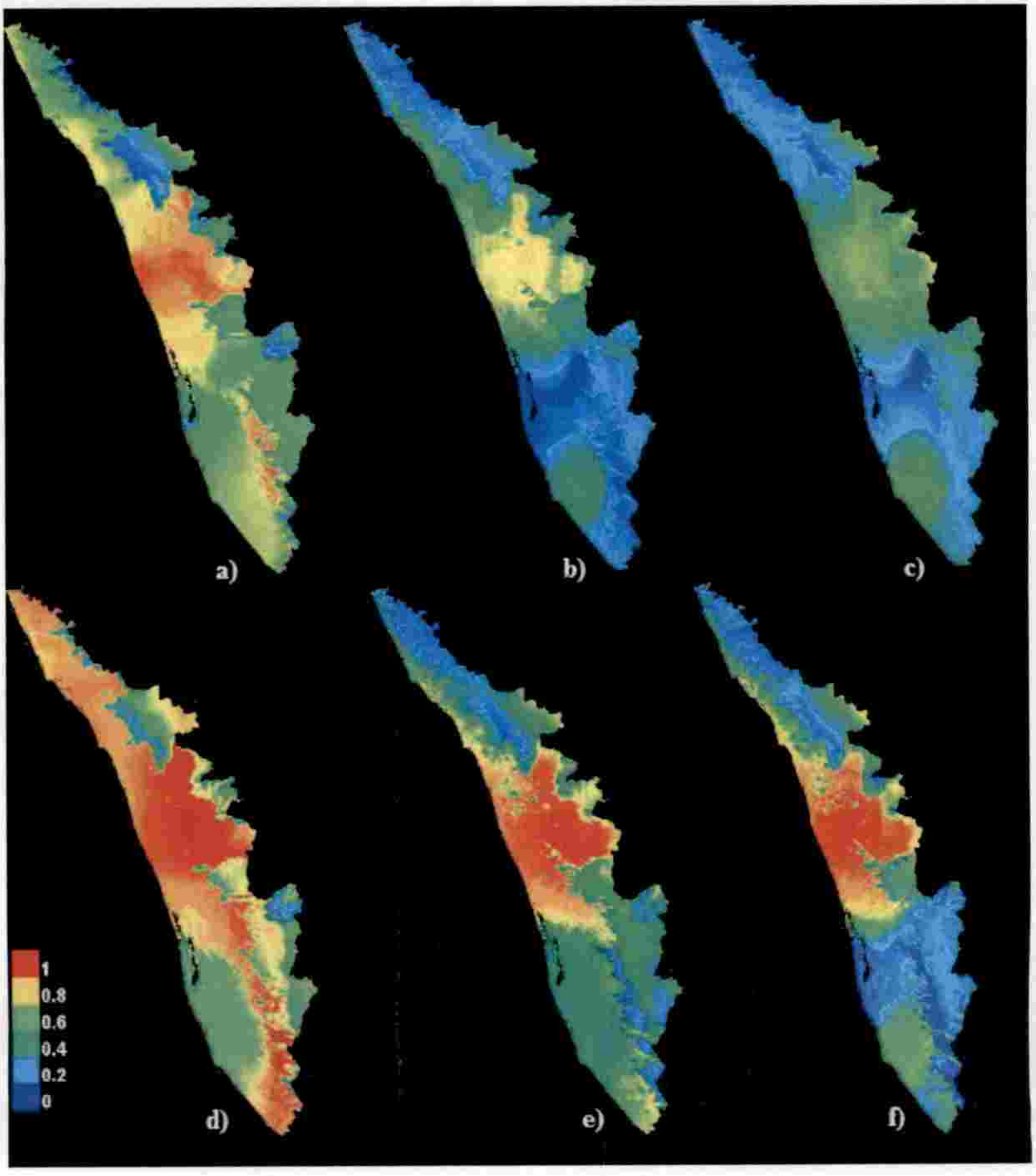
The prediction of distribution of the Indian Peafowl for the year 2050 under RCP 4.5 prediction when variables a) bio3 b) bio4 c) bio6 d) bio13 e) bio14 f) bio18



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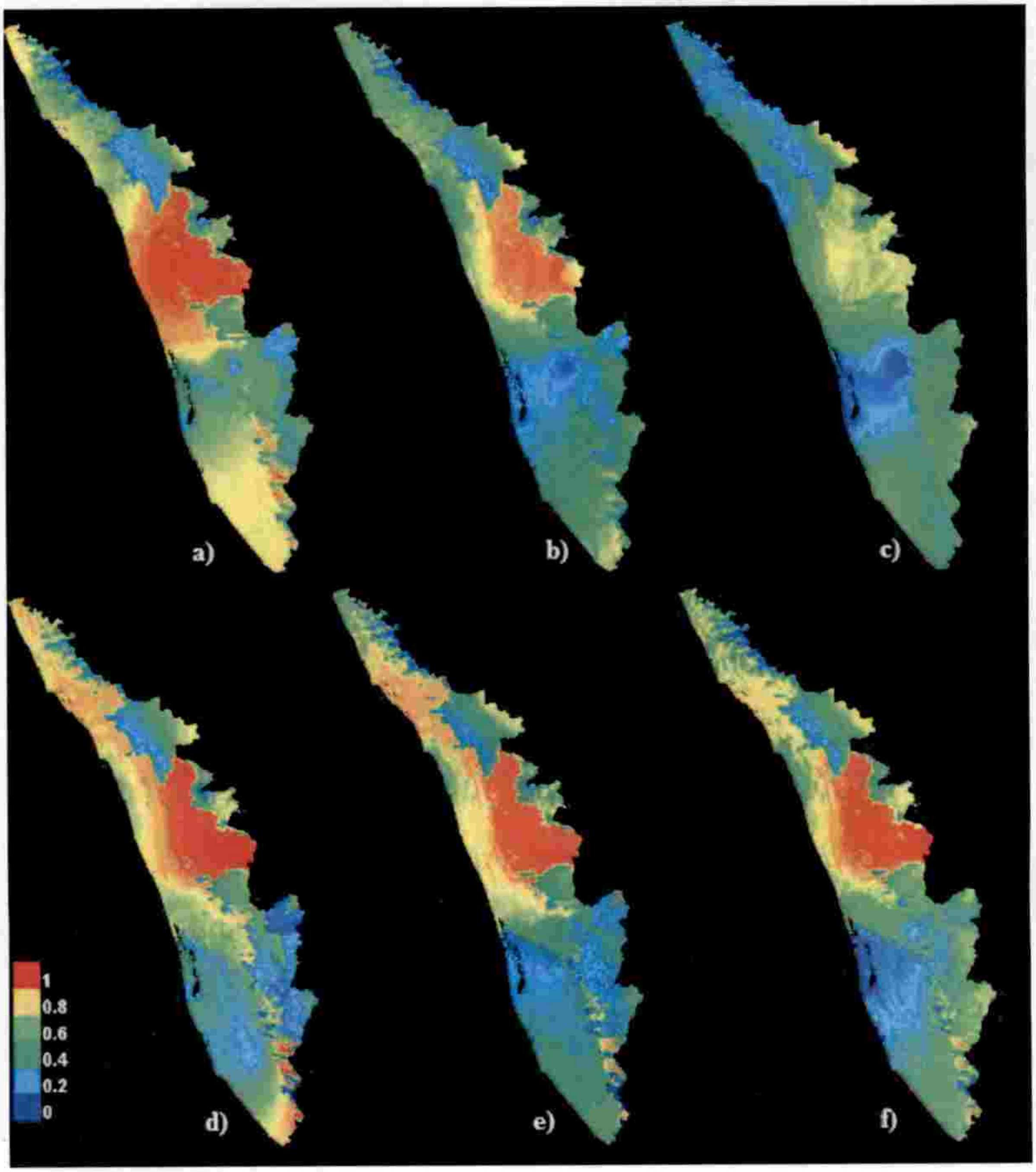
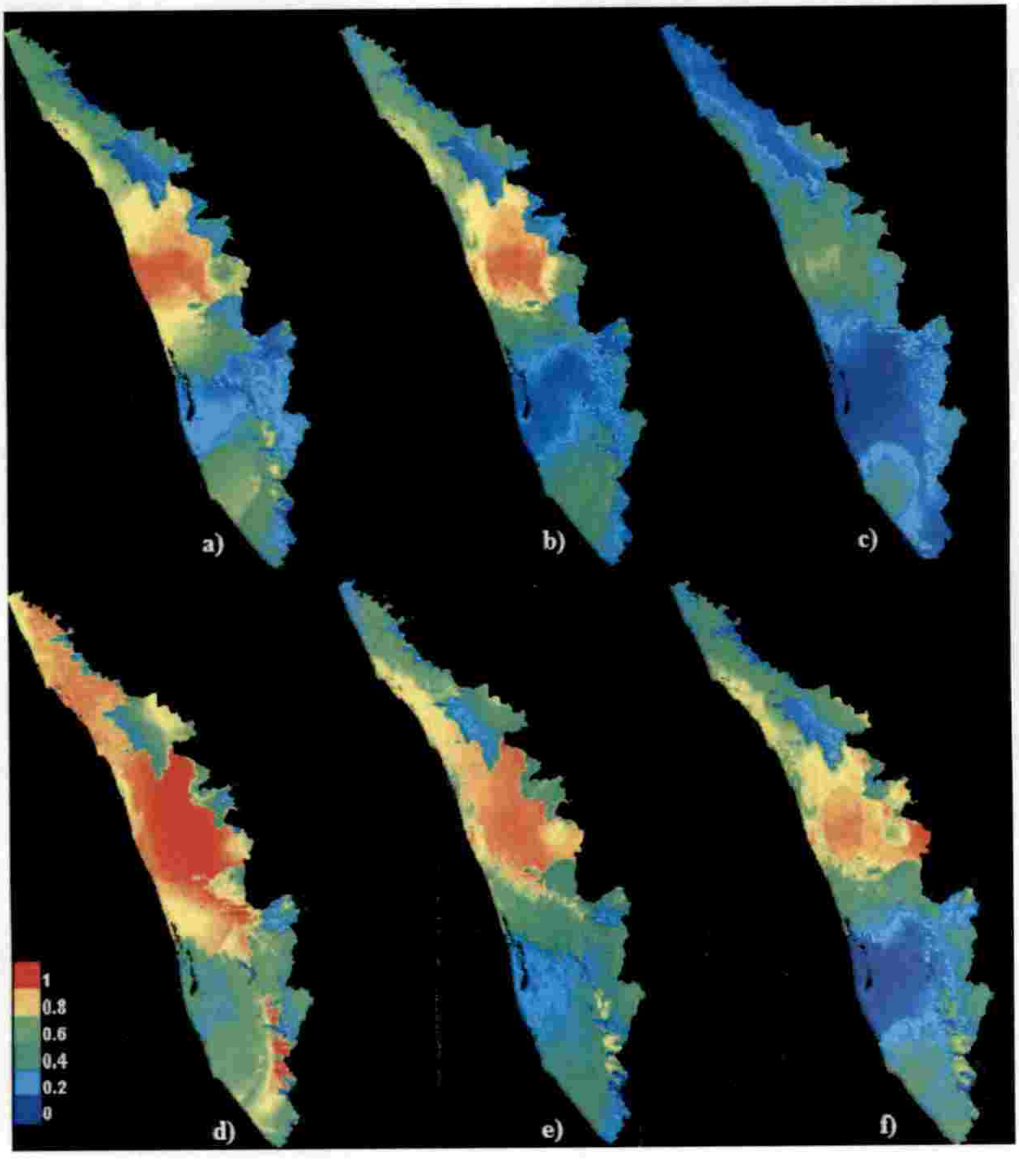


The prediction of distribution of the Indian Peafowl for the year 2050 under RCP8.5 prediction when variables a) bio3 b) bio4 c) bio6 d) bio13 e) bio14 f) bio18



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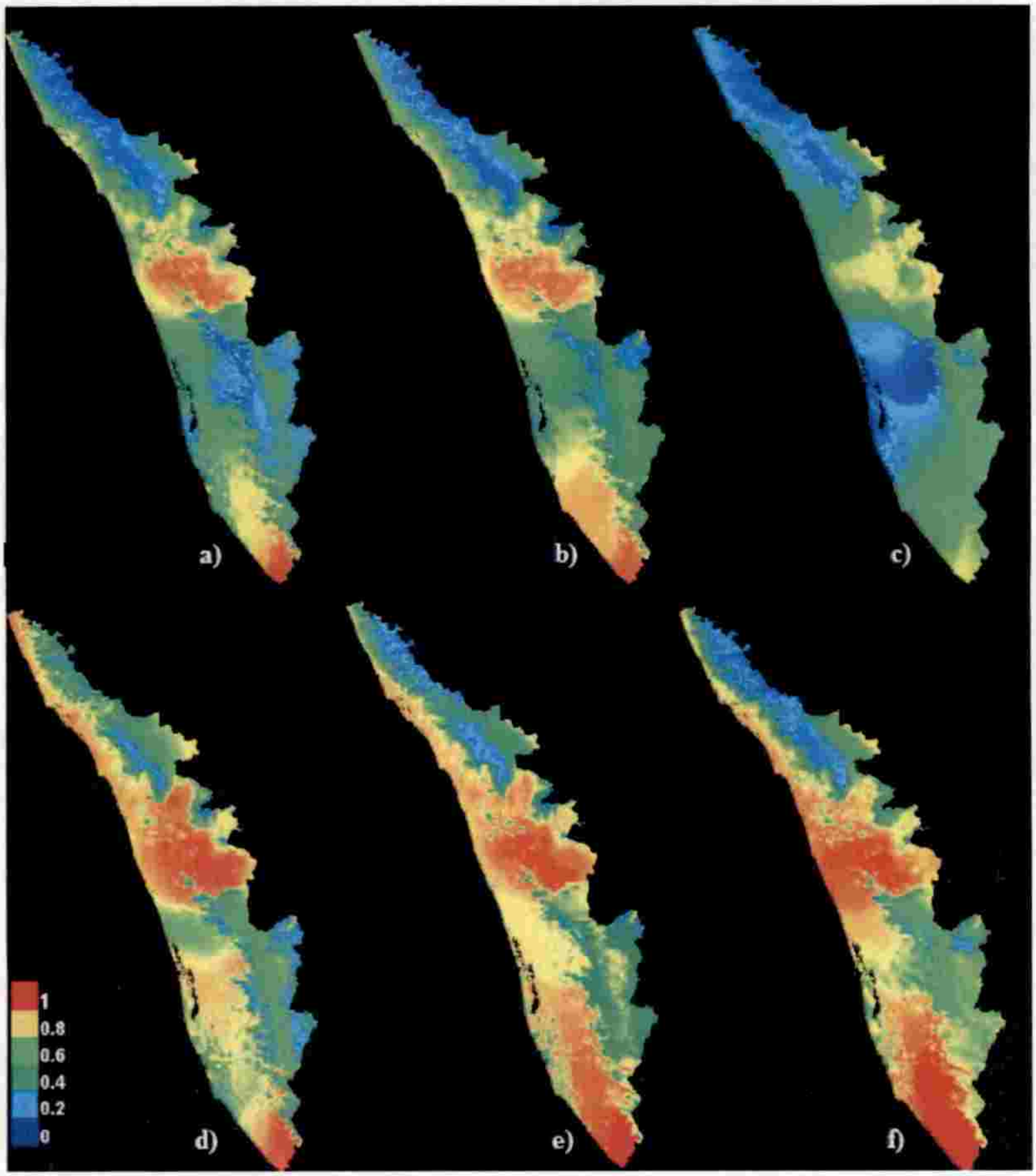

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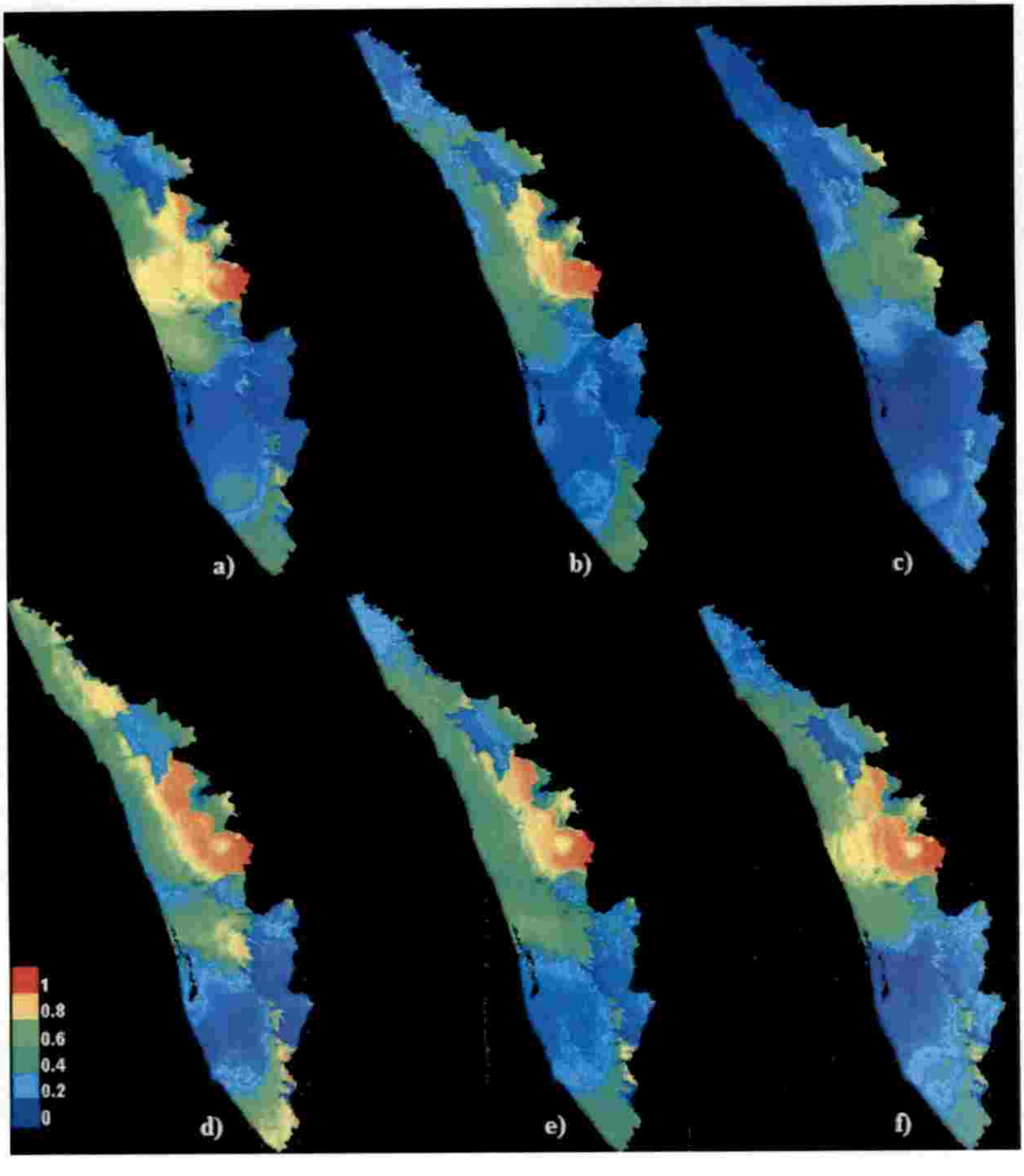

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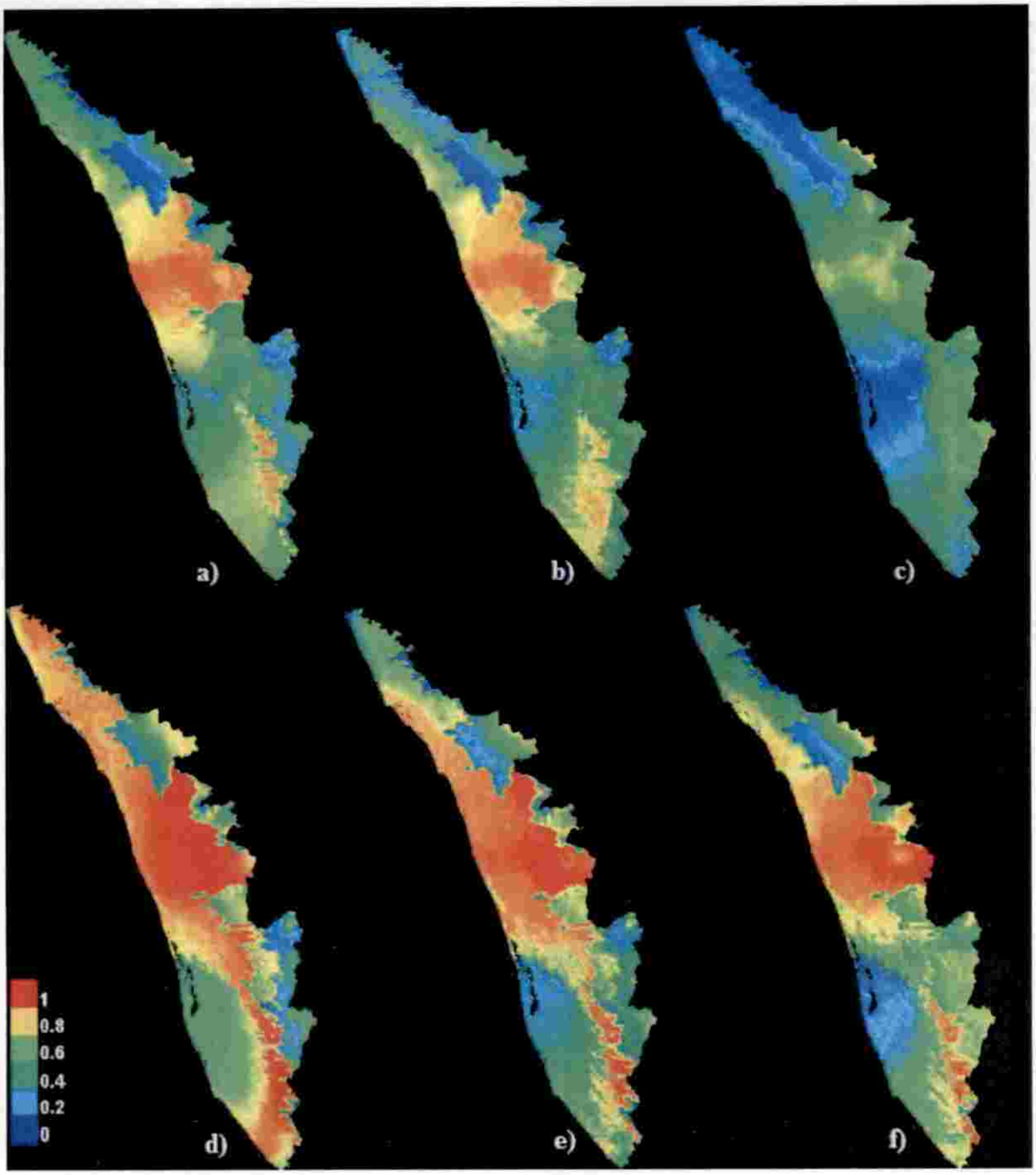
The prediction of distribution of the Indian Peafowl for the year 2070 under RCP6 prediction when variables a) bio3 b) bio4 c) bio6 d) bio13 e) bio14 f) bio18



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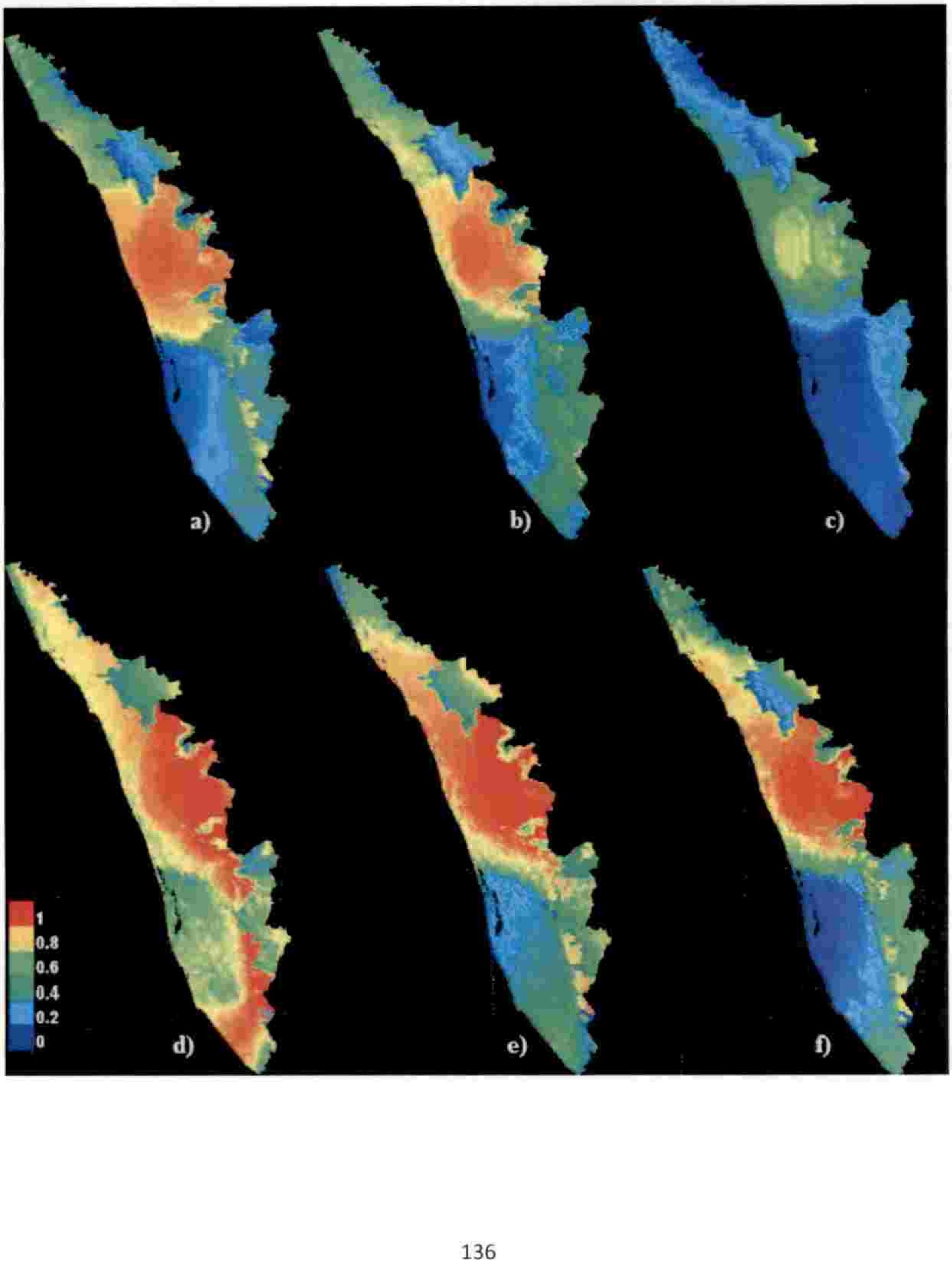
The prediction of distribution of the Indian Peafowl for the year 2070 under RCP8.5 prediction when variables a) bio3 b) bio4 c) bio6 d) bio13 e) bio14 f) bio18



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REVIEW
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Modeling of Greenhouse Gas Emission from Livestock

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The effects of climate change on humans and other living ecosystems is an area of on-going research. The ruminant livestock sector is considered to be one of the most significant contributors to the existing greenhouse gas (GHG) pool. However, there are opportunities to combat climate change by reducing the emission of GHGs from ruminants. Methane (CH_4) and nitrous oxide (N_2O) are emitted by ruminants via anaerobic digestion of organic matter in the rumen and manure, and by denitrification and nitrification processes which occur in manure. The quantification of these emissions by experimental methods is difficult and takes considerable time for analysis of the implications of the outputs from empirical studies, and for adaptation and mitigation strategies to be developed. To overcome these problems, computer simulation models offer substantial scope for predicting GHG emissions. These models often include all farm activities while accurately predicting the GHG emissions, including both direct as well as indirect sources. The models are fast and efficient in predicting emissions and provide valuable information on implementing the appropriate GHG mitigation strategies on farms. Further, these models help in testing the efficacy of various mitigation strategies that are employed to reduce GHG emissions. These models can be used to determine future adaptation and mitigation strategies, to reduce GHG emissions thereby combating livestock induced climate change.

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Keywords: GHG, IFSM, livestock methane, mitigation, modeling, nitrous oxide

INTRODUCTION

Global warming, the rise in the average surface temperature of Earth has been attributed to greenhouse gases (GHGs) like carbon dioxide (CO_2), methane (CH_4), water vapor (H_2O), nitrous oxide (N_2O) and hydroflurocarbons (HFCs) through the "*greenhouse effect*" and is an alarming issue worldwide (Smit et al., 2014; Li et al., 2016). The increasing atmospheric concentrations of GHGs in recent years are primarily due to the anthropogenic activities involving fossil fuel burning, application of nitrogen fertilizers in farming and the rearing and breeding of large ruminants. In actuality GHG's are necessary for human survival. Over millennium GHGs have stabilized in the atmosphere resulting in an average surface temperature of 15°C. Without the heat retention capacity of GHG the Earth would likely be uninhabitable. Natural processes are contributing to increasing levels of atmospheric GHG; however, the aforementioned anthropogenic activities are now contributing to additional warming, leading to rapid climate change (IPCC-Intergovernmental Panel on Climate Change, 2013; Quaghebeur et al., 2015).

According to the IPCC-Intergovernmental Panel on Climate Change (2013), over the period 1880–2012 the average land and ocean temperature increased by 0.85°C (0.65 to 1.06°C), and the last three decades were warmer than any other decade before 1850. The number of cold days and nights have decreased and warm days and night have increased. In addition, the frequency of heat waves has increased over Asia, Europe and Australia (IPCC-Intergovernmental Panel on Climate Change, 2013). The sea surface temperature over the Northern Hemisphere increased compared to the Southern Hemisphere. Over the period 1971 to 2010 the upper ocean (0 to 75 m depth) warmed by 0.11°C (0.09 to 0.13°C). Increasing temperature has resulted in the melting of glaciers and Arctic sea ice. Melting of the Greenland ice sheet has increased from 34Gt yr^{-1} to 215Gt yr^{-1} over the period 1992 to 2011 and Antarctic ice sheet melting increased from 30Gt yr^{-1} to 147Gt yr^{-1} (IPCC-Intergovernmental Panel on Climate Change, 2013). Due to the melting of ice the sea level has increased by 0.19 m (0.017 to 0.21 m) over the period 1901 to 2010 (IPCC-Intergovernmental Panel on Climate Change, 2013). Rainfall distribution has shown high variability in both the hemispheres. Averaged over the mid-latitudes the Northern Hemisphere has experienced increased in rainfall, whereas the Southern Hemisphere has experienced decreased rainfall. Furthermore, extreme weather events appear to be increasing in frequency globally.

Based on data from 2004, CO_2 contributed 77%, CH_4 14%, N_2O 8%, and HFCs 1% of global GHG emissions (IPCC-Intergovernmental Panel on Climate Change, 2007). The current concentrations of CO_2, CH_4, and N_2O are 395.4 ppm, 1893 ppb, and 326 ppb respectively, having a lifetime of 100–300, 12, and 121 years, respectively. Atmospheric concentrations of CO_2 have increased by 16 times between 1900 and 2008 (Le Quéré et al., 2014; Beyzavi et al., 2015). The intensity of warming for each gas is referred to as the Global Warming Potential (GWP). The GWP of each gas is determined relative to the GWP of CO_2 which is given a value of one. The GWP of CH_4, N_2O, and hydroflurocarbons are 23, 296, and 12000 respectively (UNEP, 2012). These gases are naturally occurring, but the increasing concentration due to the anthropogenic effects is of concern. GHG emissions have been determined for the industrial/agricultural sector. Energy generation contributes 26% of total global emissions, industries 19%, land use, land change and forestry 17%, agriculture 14%, residential and commercial buildings 8%, and waste and wastewater contribute 3% (IPCC-Intergovernmental Panel on Climate Change, 2007).

The livestock sector is considered to be a major contributor to climatic change (Steinfeld et al., 2006). FAO (2006) presented an aggregated view about the impacts of livestock on climate change. The direct and indirect effects of animal agriculture on climate change were espoused. The sources of GHG from livestock production systems were determined to be from land use and land change, feed production, animal production, manure management, and processing and transportation. A US Environmental Protection Agency report which was also published in 2006 suggested that by 2020 global enteric CH_4 emission would be 2344 Mt CO_2–eq/yr and CH4 emissions from manure storage to be at 523 Mt CO_2–eq/yr (EPA-US Environmental Protection Agency, 2006). Emissions of N_2O from cropping practices were estimated to reach 2937 Mt CO_2–eq/yr by 2020 (EPA-US Environmental Protection Agency, 2006).

It is clear that climate change is real and that the forces behind this change are GHG emissions. It is inevitable that renewable energy will form a component of, any attempts to reduce GHG emissions from the livestock sector. However, using renewable energy in livestock production is not enough. The livestock sector needs to focus emissions reduction strategies on management approaches that can be applied to livestock in the field. It has been estimated that approximately 12.5% of the total global GHG emission are from the livestock sector (Steinfeld et al., 2013) and 80% of the total emission from agriculture is from the livestock sector. Approximately 9% of CO_2, 36% of CH_4, and 64% of N_2O is contributed to the livestock production process and 75% of the CO_2 emitted from livestock is from ruminants (Prasad et al., 2015). Methane and N_2O have a GWP of 23 and 296 with a lifetime of 12 and 114 years, respectively, whereas CO_2 has a lifetime of 100–300 years (Le Quéré et al., 2014). Mitigating the emission of CO_2 in the livestock sector will be less effective in reducing the effects of GHGs compared to the mitigation of short living gases like CH_4 and N_2O which are the major GHG from the livestock sector. This review is an attempt to highlight the role of livestock in contributing to climate change through enteric fermentation and manure management. Special emphasis has been given to highlighting the difficulties in conducting on farm mitigation studies and signifying the importance of modeling as an alternative for finding solution in curtaining livestock related climate change.

SOURCES OF GHGs IN LIVESTOCK FARMS

According to Steinfeld et al. (2006), global livestock agriculture was responsible for 7516 Mt per year of CO_2 equivalents (CO_2 eq) or 18% of the anthropogenic GHG emissions annually. It is from the animal and manure emissions that 37% of global agricultural CH_4 and N_2O arise and the remainder is associated with cropping and deforestation (EPA-US Environmental Protection Agency, 2006). The various sources of GHGs from livestock farms are described in **Figure 1**. Globally dairy animals, including cull cows and dual purpose beef cattle account for approximately 4% of anthropogenic GHG emissions (FAO-Food and Agriculture Organization of the United Nations, 2010). In developed countries the GHG emissions from dairy production are generally lower than in developing countries due to the higher productivity (Hagemann et al., 2011), and better feed quality. According to the EEA (2011), beef and dairy cattle are estimated to contribute 2.1 and 1.2% respectively to anthropogenic GHG inventories in the European Union (EU) whereas in the United States (US) the contributions are 2.75 and 0.55% respectively (EPA-US Environmental Protection Agency, 2006). However, in developed countries where pastoral agriculture is a significant portion of the economy, such as Ireland and New Zealand or developing countries like Brazil and India, the emission contribution from dairy production to the national inventory

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FIGURE 1 | Different sources of GHGs from livestock farms (Adopted from Sejian et al., 2015).

will be higher (FAO-Food and Agriculture Organization of the United Nations, 2010). It is misleading if the CH_4 emissions from the livestock sector are examined only as a proportion of total anthropogenic GHG emission (Knapp et al., 2014). Methane emissions are dependent upon the population size of the ruminants, their productivity, and manure handling system. Reducing CH_4 and N_2O emissions from livestock production are focused on because they are less expensive to mitigate than CO_2 emissions (EPA-US Environmental Protection Agency, 2006; FAO-Food and Agriculture Organization of the United Nations, 2010; Shafer et al., 2011; Gerber et al., 2013).

Enteric fermentation causes the emission of CH_4, which is a by-product of the breaking down of carbohydrate molecules into soluble particles by methanogens residing within the rumen. Thus, formed CH_4 is eructated by the animal and becomes a GHG. Feed quality is a major determinant of CH_4 production. High fiber content (cellulose) in the feed will increase CH_4 emission. Methane is also produced, as is N_2O via the breakdown of manure. When manure is managed in a liquid form the organic matter contained in it are exposed to anaerobic bacteria that decompose the manure and in the process GHGs are formed and liberated. The formation of N_2O is by nitrifying and denitrifying bacteria which reside in the soil. The emission of N_2O from manure depends upon the nitrogen and carbon content of manure, and for the duration of the storage and type of treatment (IPCC-Intergovernmental Panel on Climate Change, 2006). The oxidation of ammonia nitrogen to nitrate nitrogen (nitrification) is a necessary prerequisite for the emission of N_2O from stored animal manures. Nitrification happens in aerobic condition, whereas denitrification occurs in anaerobic conditions in which the nitrites and nitrates are transformed to N_2O and dinitrogen (N_2). In order for N_2O to be produced from manure, nitrites and nitrates are required (under anaerobic conditions) which then allow the formation of the oxidized forms under aerobic conditions (IPCC-Intergovernmental Panel on Climate Change, 2006).

Nitrogen fertilizer, animal manure applications to land and urine deposition by grazing animals are the main sources of emitted N_2O (Brown et al., 2001). Unlike CH_4, N_2O production can only take place if specific conditions are met, i.e., the combined processes of anaerobic and aerobic bacteria: (1) Nitrification, transformation of ammonium to nitrate (aerobic); and (2) Denitrification, formation of nitrogen gas from nitrate reduction (anaerobic). Oxygen content, moisture content and soil conditions will influence N_2O emission. Normally due to the anaerobic conditions prevailing in manure, nitrification and denitrification doesn't occur. But when forced and controlled aeration of liquid manure or solid manure for removing organic matter (OM), nitrogen and water (drying) then denitrification occurs after aeration (nitrification). A mixture of manure and straw/litter, results in partial compaction and this forms favorable conditions for passive aeration, resulting in uncontrolled nitrification and denitrification (Groenestein and Van Faassen, 1996). The other sources of GHG emission from livestock farms are, livestock related land use change, feed production, on farm fossil fuel use and post-harvest emission (Steinfeld et al., 2006).

SIGNIFICANCE OF REDUCING GHG FROM THE LIVESTOCK SECTOR

From the above discussion, it is evident that livestock act as an important source of GHG emissions and any attempt to develop mitigation strategies to reduce emissions may be beneficial in slowing climate change. Furthermore, CH_4 production through enteric fermentation also contributes to the dietary energy loss. In addition, nutrient use efficiency decreases due to CH_4 synthesis. Any factor (feed or management) that reduces nutrient use efficiency will result in greater CH_4 emissions. Deficiencies in nutrient requirements for rumen microorganisms reduce microbial growth efficiency, which further reduces microbial biomass resulting in reduced digestibility of foodstuffs and reduced feed intake. In order to combat this, as a consequence of the interspecies hydrogen transfer, the bacteria which are syntrophic to the methanogens produce 1 ATP per molecule of glucose which they utilize for growth and biomass production. It is important to note that this energy is not utilized by the animal. Hence, any attempt to reduce livestock related GHG emissions, apart from the goal of reducing their impact on climate change, may also improve production efficiency of livestock by preventing the dietary energy loss.

DIFFICULTIES ASSOCIATED WITH EXPERIMENTAL REDUCTION

The production of GHGs through enteric fermentation and manure management is a complex process. The quantification of these gases often requires complex and expensive equipment. Additionally the collection and measurement of GHGs are time consuming. Further, the mitigation strategies designed for a particular ecological zone will not necessarily be suitable in another zone due to the complexities in the rumen microbial population. In addition, the feeding habits of the animals and the feed resources available may not be the same across agro-ecological zones. Furthermore, the climatic conditions prevailing in a particular locality are a crucial factor influencing GHG production. All these factors are involved in livestock's contribution to GHG emissions and hence climate change. The complexity of various farming systems makes it difficult to identify appropriate mitigation strategies that can be universally applied. There is every chance that even if a strategy is identified by conventional experiments, by the time the work is completed other components of this complex might influence the gas production in a different way. This means that expensive studies need to be repeated numerous times. Hence, research efforts are needed to identify strategies that may be cost effective, less time consuming and with wider applicability.

SIGNIFICANCE OF MODELING

Projections indicate that by 2050 animal production is expected to increase by 80% compared to 2005 (Alexandratos and Bruinsma, 2012). There is an increasing global demand for milk and meat, and this demand is being met with increased production from pasture based systems (Fiala, 2008; Thornton, 2010). Projections show that the global annual growth rate of beef to 2050 will be 1.2%, which is very close to the annual growth rate of 1.3% for total meat production to 2050 (Alexandratos and Bruinsma, 2012). Hence there is an urgent need to identify simpler cost effective technologies to quantify GHG emissions and to find appropriate solutions for climate change. Computer simulation models are valuable tools for the study of feedback and feed forward interactions between mitigation of GHG emissions and adaptation to climate change in ruminant based production systems. These models offer substantial scope for identifying solutions to livestock related climate change. The models will also provide strategic direction for Government policies related to climate change and food security. It is inevitable that the models will have complex interactions among farm components and climate systems. Tools and models are being developed to estimate GHG emission from livestock systems in the form of process-based simulation (Schils et al., 2007b), emission factor calculations (Amani and Schiefer, 2011; Colomb et al., 2012), and life cycle assessments (LCA)-based approaches (De Vries and de Boer, 2010; De Boer et al., 2011; Cowie et al., 2012). These models have wide acceptance in the scientific community due to the efforts made to improve the understanding of the effect of various systems and changes in farm performance. Further, these models may serve as an alternative for the expensive, time consuming and technically difficult experimentation in a field and farm scale (Bryant and Snow, 2008).

MODELING OF GHGs IN LIVESTOCK FARMS

The primitive models which used the prediction equations corresponding to the nutrient uptake of the animals and the subsequent emission of gases were evaluated. These models are commonly referred to as Empirical/Statistical models. They use simple and uncomplicated regression equations based on feed characteristics. However, these models were used in very costly extensive experiments. The environmental changes and the microbial populations residing in the rumen are not included in these models. No factors other than the feed characteristics are studied. The interactions of various other systems are not evaluated. Further, these models cannot be used to predict the changes in CH_4 emissions outside the range they were developed for. Hence, to overcome these drawbacks, mechanistic/dynamic models which simulate CH_4 emissions based on a mathematical description of ruminal fermentation biochemistry were developed. These models are not costly and they evaluate the complexities associated with enteric CH_4 emission. Mitigation measures can be assessed for their effectiveness under varying scenarios of climate and feed intake at field level. The information pertaining to the climate of the particular ecological zone and the routine management practices being followed in livestock farms is also included in these models (Del Prado et al., 2009; Cullen and Eckard, 2011; Graux et al., 2011, 2012; Bell et al., 2012). These models also take into account the information on microbial population and their efficiency in CH_4 production rate. However, the complexity of the systems involved in a mechanistic model makes it difficult to operate. The rapid dynamic changes in metabolic flux during lactation, especially in late pregnancy and early lactation are also difficult to quantify using these models. The models use empirical equations derived from statistical analysis to simulate the enteric CH_4 emission. These equations have limitations in their ability to quantify the characteristics of the animals and diets they use (Ellis et al., 2010). The success rate for accurately predicting the GHG emission using these models relies heavily on the quality of the input data, such as the chemical composition of the diet, degradation rates of feed components, and passage rates.

Components of Modeling

Input flows and output flows in the livestock sector depends upon the management practices and the environmental conditions prevailing at the site. For each gas the emission mechanism is different. Carbon dioxide emissions depend on C intake and the fixation processes linked with respiration and the direct energy use. Methane emission occurs due to the enteric fermentation in the rumen and the manure management under anaerobic conditions. Denitrification and nitrification processes in manure storages and soils, and the leaching of NO_3 and volatilization of NH_3 results in N_2O emission. Although these are all the primary pathways by which the models predict the GHGs that are being produced from livestock farms, emissions from other sectors beyond the boundaries of the farm have been considered in few models. The models have used different approaches to incorporating all of the components into a single system. The objectives of each model differ: such as GHG emission estimates, GHG mitigation measures and implications of various adaptation and mitigation strategies in on the farm. The various components in the models have to be interrelated effectively if the objective (correct output from the model) is to be achieved. To adequately analyze animal productivity, emission estimates, feeding practices, and animal type the models need to be quantified based on metabolic parameters. Manure management is incorporated into the model by quantifying the flows transformations of manure on the farm and the emission are simulated. Further, information pertaining to housing of the animals, manure storage facilities, treatment of manure and application of manure in the field is programmed into these models. The different livestock related activities and their contribution to existing GHG pool are described in **Figure 2**.

In addition, the dry matter (DM) volume and the liquid content of manure is dynamically tracked for the C and N fractions (Olesen et al., 2006; Chardon et al., 2012; Rotz et al., 2012). Often CH_4 is modeled using the IPCC Tier 2 approach (IPCC-Intergovernmental Panel on Climate Change, 2006) while NH_3 and N_2O emissions are modeled by volatilization and aerobic condition of manure respectively (Rotz et al., 2012).

For the estimation of N_2O emission and C sequestration management practices and their interactions between soil, animal, plant and weather conditions are evaluated. The process based models look into the various interactions and dynamic changes happening to the N pathway (Li et al., 2012) such as denitrification and nitrification processes where N intermediates for N_2O and N_2 production (Firestone and Davidson, 1989). Temporal variability of N_2O depends upon the temperature, rainfall pattern and the amount of N substrate availability and by proper modeling of climate and management practices it is evaluated.

For grazing animals the pasture availability is very important and it can be modeled as the function of soil water, N availabilities and weather condition. From the empirical equations (Foley et al., 2011) mechanistic models are developed by incorporating soil characteristics, ambient temperature and solar radiation as the driving factors (Del Prado et al., 2011; Rotz et al., 2012). Different grazing systems can be included in the model (rotational grazing being the most difficult one to simulate; Graux et al., 2011). Spatial variability of the pastures is incorporated in some models, while others assume uniform distribution over the whole field. The variations in GHG emission with soil properties can be analyzed accurately using this simulation (Linn and Doran, 1984; Ruser et al., 2006).

Soil C constitutes the other component in the field. Soil is the third largest global C pool (Lal, 2008). Improved management of grasslands for increased forage production has the potential to increase C stocks (Freibauer et al., 2004; Rees et al., 2005). The C stock and GHG emission are interrelated, and by modifying the quality and composition of manure, land use changes, variability in feed intake and wider variations in the microbial activity will change the metabolic functions and thereby emission quantity (Vellinga and Hoving, 2011). Natural sources and sinks are not included in the models as they are insignificant contributors to CO_2 changes in the atmosphere. During long term analyses C sequestration is not considered because C assimilated equals C stored and emitted C from the farm (Del Grosso et al., 2002; Matthews et al., 2010).

Many models have been developed to analyze animal productivity in different environmental conditions and the associated GHG emission. MITERRA- (a Europen model) is an environmental assessment model used to assess the effects of the implementation of NH_3 and NO_3 measures and policies on the GHG emissions such as CH_4, N_2O, and CO_2. The MITERRA-Europe model is partly based on the models GAINS (Greenhouse Gas and Air Pollution Interactions and Synergies) and CAPRI (Common Agricultural Policy Regionalised Impact), complemented with an N leaching module, a soil C module and a module for mitigation (Lesschen et al., 2011). It measures the emission from enteric fermentation, manure management, N_2O

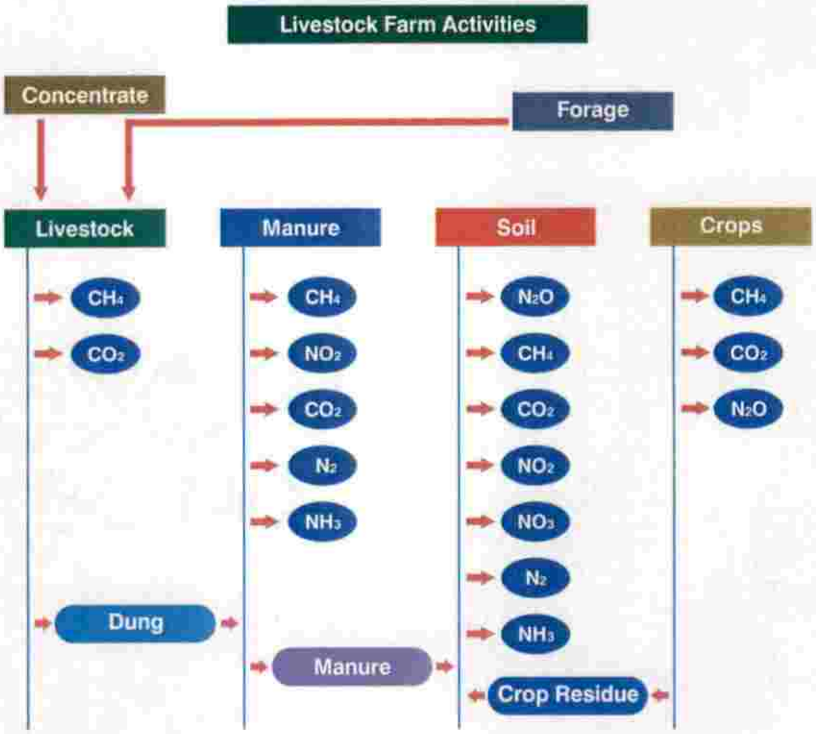

FIGURE 2 | Pictorial representation of different livestock related activities and their contribution to GHG pool.

emission, fertilizer production, organic soil cultivation, liming, and fossil fuel use. The data for livestock numbers, crop areas, and animal production are inputted from the databases of FAO and Eurostat and for emission factors from IPCC, GAINS and spatial environmental data. This model is able to simulate nitrogen and GHG emissions however, at the global scale further validation and model comparisons are needed to increase the confidence intervals for the model. The feed intake parameter needs to be further tested and parameterized. **Table 1** describes the different models available and their merits and demerits.

The Integrated Model to Assess the Global Environment (IMAGE) model studies the long term effects of human activities on the environment. The regional production of food, animal production, timber harvest, local climatic conditions and terrain the evaluation are incorporated within the model. The land use and cover are efficiently simulated in this model (Kram and Stehfest, 2006; Neumann et al., 2011). The model evaluates the efficient population needed in a region and estimates the feed requirement by the animals (Bouwman et al., 2005; Neumann et al., 2011). IMAGE distinguishes the pastoral livestock systems based on the grazing ruminants and mixed and landless (industrial) production systems, integrating crop and livestock production where animals are fed with a mixture of crops, grasses, and fodder and crop residues.

The LEITAP model which is based upon the Global Trade Analysis Project (GTAP) model was developed to evaluate the changes associated with GHG emission based on the number of animals on a national level. It is formulated based on the neoclassical microeconomic theory multiregional, multisectorial, static, and the applied general equilibrium model. Projections for livestock numbers and agricultural land use were calculated for the EU for 2010, 2020, and 2030 (Neumann et al., 2011). For the estimation of GHG emissions from livestock farms within the EU a model named FarmGHG was created. This model evaluates the emission of CH_4 and N_2O released from farms and the CO_2, CH_4, and N_2O emission from feed, fertilizer and imported energy. This model was developed to quantify the effects of management practices on emissions of GHGs. The model proposed that by increasing N use, efficiency the emission of GHG can be reduced.

The DairyWise model was developed to estimate GHG emissions from dairy farms. This empirical model integrates all the major systems in the dairy into a whole farm model. Inputs such as farm management, herd type, cropping plan, soil characteristics, grass and feed management, buildings and equipment are quantified in this model (Schils et al., 2007a). The CH_4 emission is calculated from the enteric fermentation and N_2O is calculated from the manure management. Both direct and indirect N_2O emissions are simulated where direct emissions for N inputs through fertilizers, manure application, biological fixation, and urine excreted during grazing, crop residues, and peat oxidation (Schils et al., 2007b).

The Sustainable and Integrated Management Systems for Dairy Production (SIMS-Dairy) model simulates biodiversity,

TABLE 1 | Various types of models, components, merits and demerits.

Model	Components	Merits	Demerits	References
MITERRA- Europe	Livestock numbers, crop areas, animal production, enteric fermentation, manure management, N2O emission, fertilizer production, organic soil cultivation, liming and fossil fuel use	Effects of mitigation measures	At a global scale more validation is needed	Lesschen et al., 2011
IMAGE	Animal productivity, Feed conversion, Livestock rations, Production system Mix, Livestock production, Management intensity livestock, Grass requirement, Animal stocks, Feed crop requirement	Environmental consequences of human activities worldwide can be evaluated	Values of animal, plant life, health and diversity are difficult to quantify, highly complex, large and chaotic	Kram and Stehfest, 2006
LEITAP	Land allocation, productivity of marginal land, land supply function	Population of animal stock can be calculated	No climate module	Neumann et al., 2011
FarmGHG	Feed, fertilizer, energy imported	Quantifying GHG emission	Based on feed	Olesen et al., 2006
DairyWise	Farm management, herd type, cropping plan, soil characteristics, grass and feed management, buildings and equipments	Whole farm model, direct and indirect emissions can be calculated	No climate module	Schils et al., 2007b
SIMS-Dairy	Biodiversity, landscape, animal welfare, soil quality and product quality	Emphasis on management strategies and sustainable development	No climate module	Del Prado and Scholefield, 2006
FarmSim	The area and type of crop and grassland and herd types and number, the grasslands, the crops and the feeding and waste management systems	Got nine interacting modules. Integrated with IPCC tier 1 and 2 methodology	No climate module	Saletes et al., 2004
IFSM	Crop production, feed intake, manure amount, animal respiration and microbial respiration	Integrates biological and physical process of crop and animals	Metabolic fluxes are not considered	Chianese et al., 2009
GLEAM	Herd, manure, and feed	Simulate environmental implications on the production system	No climate module	Gerber et al., 2013

IMAGE, Integrated Model to Assess the Global Environment; SIMS-Dairy, Sustainable and integrated Management Systems for Dairy Production Model; FarmSim, FARM SIMulation Model; IFSM, Integrated Farm System Model; GLEAM, Global Livestock Environmental Assessment Model.

landscape, animal welfare, soil quality and product quality (Del Prado and Scholefield, 2006). It focuses on the management practices in the livestock sector and aims to obtain a sustainable system. The possible impacts of mitigation strategies on the emission of GHG are studied in this model. Emission from soil, animal excreta as manure, or urine and emissions from the rumen are analyzed (Schils et al., 2007b).

The FARM SIMulation (FarmSim) model simulates GHG emission from nine interacting modules. The flow of product among various components of the farm system is included in this model. PASIM model where GHGs exchanged over the different grassland types on the farm are integrated with IPCC Tier 1 and Tier 2 methodology, where emissions from cropland and cattle housing are evaluated and included in the FarmSim model. The structure of the farm, including the area, type of crop(s), grassland and herd type, the number of herd per type, the area of grasslands, the crops and the feeding and waste management systems are inputted into the model.

The Integrated Farm System Model (IFSM) integrates the biological and physical processes of a crop, beef or dairy farm in order to simulate crop production, feed use and manure output over a period of time while at the same time incorporating the weather parameters (Rotz et al., 2009). The crop production of alfalfa, grass, corn, soybean, and small grain crops can be predicted based on daily soil and weather conditions. The feed consumed by an animal and the response (e.g., average daily gain) are related to the nutrient content of the feed. The manure quality and quantity is based upon the nutrient content of the feed consumed. When simulating GHG emission modules for the balance of C will need to be based upon processes like crop production, animal respiration and microbial respiration plus manure management. Certain criteria have been formulated for the potential evaluation of the models The models should (i) simulate the processes by which CO_2 emissions will be affected when farm management practices change; (ii) represent every process influencing GHG emissions; (iii) predict the observed data in the past for its accuracy under different potential conditions; and (iv) accurate data should be available for the accurate simulation.

The Global Livestock Environmental Assessment Model (GLEAM) explores the environmental implications of on farm production practices (Gerber et al., 2013). Its development is based upon five modules which reproduce the main elements of livestock supply chains: (1) *Herd module*; this module evaluate the number of animals per GIS grid cell, where they have been managed with different farming systems; the herd characteristics and structure of each cell are studied under this module; (2) *Manure module*; evaluates the manure production from the GIS cell from each animal type; (3) *Feed module*; calculates the various components in the feed, nutrient content and the emissions per kg of feed given; (4) *System module*; incorporates the herd, manure and feed modules to determine the energy requirement by each animal type, the annual production from each GIS cell, emissions produced from manure management, enteric fermentation and feed production, and (5) *Allocation module*; calculates the total GHG emission from the farm incorporating all the direct, indirect and post farm emissions. GLEAM uses geo-referenced data to calculate the GHG emissions from the farm. The information regarding the productivity and the practices undertaken to increase livestock production is collected at various levels of aggregation such as at a country level, agro-ecological zones, or a combination of these. The main data sources are Gridded Livestock of the World (FAO-Food and Agriculture Organization of the United Nations, 2007), National Inventory Reports of Annex I countries (UNFCCC-United Nations Framework Convention on Climate Change., 2009), International Food Policy Research Institute (IFPRI), Life Cycle Inventory data from SIK, International Agricultural Research (CGIAR) and statistics from FAO (FAOSTAT, 2009).

ADVANTAGES OF MODELING OVER CONVENTIONAL EXPERIMENTS

The models outlined above are being used for simulating and predicting the GHG emission from the livestock sector. However, further development is required to improve the accuracy of the model outputs. Components of the model must include modules which are comprised of animal, crop, soil, and climate data. Models need to be developed based upon the various animal characteristics, their feeding habits, metabolic fluxes, microbial population, manure management, farm management, and climatic conditions. These models should be region specific rather than global as the components of model may be different for different regions. Furthermore, the parameters that are standardized for one agro-ecological zone may not be the same for another. In addition, the climatic conditions will also differ between regions. For example the body weight of a cow in Europe will be different from that of Asia. Any differences will result in errors if the same standardized values made for another region are used. The model assumptions have to be changed according to the conditions prevailing in respective regions. These regionalized models can be effectively used to simulate and predict the GHG emissions from livestock enterprises. These models could become an alternative solution for livestock related climate change by initiating quick actions to mitigate such emissions. Doing experiments in the field may take years to quantify the emissions and to analyze the implications of various mitigation strategies employed for the reduction of emission. However, through modeling each variation in any of the targeted parameters can be identified real time. Using simulation models we can vary conditions at the farm level that affect the metabolic mechanism of animals and fermentation processes. The model outputs can then be used to evaluate potential mitigation strategies. Projection of emissions from the animals can be projected into the future. This is not possible in experimental conditions. The projections can be used to formulate the appropriate mitigation strategies for the future, thus making management strategies more systematic and efficient.

CONCLUSION

Livestock undoubtedly need to be a priority focus as the global community seeks to address the challenge of climate change. The magnitude of the discrepancy between the estimates illustrates the need to provide the climate change community and policy makers with accurate GHG emission estimates and information about the link between agriculture and climate. Improving the global estimates of GHG attributed from livestock systems is of paramount importance. This is not only to define the magnitude of the impact of livestock on climate change, but to understand their contribution relative to other sources of GHG. Estimates of GHG emission through experiments under different production system is practically impossible and with growing awareness of global warming and its continuous negative impact on agricultural production systems, attention should be directed toward immediate mitigation strategies to curtail such emissions.

The complexity of various farming systems makes it difficult to identify appropriate mitigation strategies that can be universally applied. Hence simulation models offer huge scope as these models may serve as an alternative for the expensive, time consuming and technically difficult experimentation in a field and farm scale. Such information will enable effective mitigation options to be designed to reduce emissions and improve the sustainability of the livestock sector, while continuing to provide livelihoods and food for a wide range of people.

A synthesis of the available literature suggests that the mechanistic models are superior to empirical models in accurately predicting the CH_4 emission from farms. The latest development in prediction model is the IFSM which is a process-based whole-farm simulation technique. The IFSM takes into account the entire livestock farm operations, including breed of animal, production stage, available feed resources, grazing information, pasture management, manure handling, and local weather condition. It is possible through these models to evaluate the variations in GHG emission by altering any of the targeted parameters in real time mode. Thus, these models could become an alternative solution for livestock related climate change by initiating quick actions to mitigate such emissions.

FUTURE PERSPECTIVES

Farmers typically adopt the most cost-effective and easy-to-adapt options. The services provided by the models have currently no market value among the farming community, but may become valuable in the future. Although many modeling studies are being undertaken, they do not have the capability to quantify the potential interactions among ecosystem services. The rapid dynamic changes in metabolic flux during lactation, especially in late pregnancy and early lactation have to be rectified in future models. There is also a need to integrate the effects of climate change on plant protection issues, pollination and risks from pathogens. Because this can affect the safety of the feed quality given to the animals and the microbial population is affected badly by the pesticide actions within the rumen. A balanced systems-based approach to quantify synergies and trade-offs is still lacking in current models because of the inherent complexity of some of these relationships. Multifunctionality in farms implies greater levels of heterogeneity in farming systems, and hence increase the complexity of the farm scenarios to be modeled.

AUTHOR CONTRIBUTIONS

VJ-Literature collection and introduction preparation; VS-Preparation of outline and editing manuscript; MB-Collected information and prepared write up on sources of GHGs in livestock farms; AR-Collected information and prepared write up on significance of reducing GHG from the livestock sector; AL-Collected information and prepared write up on difficulties associated with experimental reduction; YA-Collected information and prepared write up on significance of modeling; MS-Collected information and prepared write up on modeling of GHGs in livestock farms; RB-Collected information and prepared write up on advantages of modeling over conventional experiments; JG-Prepared conclusion and future perspectives.

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