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# Distribution modelling and climate change risk assessment strategy for rare Himalayan Galliformes species using archetypal data abundant cohorts for adaptation planning

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ABSTRACT

In a macroecological approach, we have used the data abundant species or archetypal cohorts as proxies for the data deficient species, to model their distributions. Upon successful modelling, we assessed climate change impacts on their distribution in the Himalayan arc extending from the Indian borders in the west to the hills in Myanmar. Out of 34 Galliformes species occurring in the Himalayan arc, 21 species were retained in this study, rest were dropped due to very low occurrences. Best performing variables from the set of environmental variables (n = 36) consisting of topography, vegetation, soil, anthropogenic indices and bioclimatic factors were tested for collinearity. Ordination (PCA and NMDS) and clustering (hierarchical clustering, agnes, partitioning around medoids and k–means clustering) and Species Archetype Modelling (SAM) methods were performed for finding the archetypal cohorts among the species. The clusters were used for two different modelling frameworks- Species Distribution Models (SDMs) with a combination of biophysical and topographical parameters; and Bioclimatic Envelope Models (BEMs) with only bioclimatic variables. Predicted climate-driven changes in species ranges (year 2070, RCP 4.5 and 8.5) were assessed. The 21 species were clustered in four groups. Precipitation emerged as the overall significant driving factor for all the three clusters. Random Forest was the highest performing model across the clusters. Two cluster restricted to the eastern Himalayas were found to be the most affected in a climate change scenario. Cluster belonging to the western Himalayas was predicted to lose about 70% of its bioclimatic habitats in both the scenarios. In a first attempt, this study presents a novel approach towards distribution and climate change modelling for the rare Galliformes, using abundant Galliformes over a pan Himalayan scale.

## 1. Introduction

Habitat selection by the species, factors governing the selection and thereby, distribution of the species in space, are research subjects that transcend both classical ecology and conservation biology (Morris, 2003). Understanding of species habitat association is

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pivotal for making informed conservation and management actions. This has consequently resulted in the evolution of methodologies for studying habitat utilization by species from its primitive form (Hildén, 1965) to the most advanced form (Boyce et al., 2003). However, studying habitat utilization by cryptic and elusive species in remote areas is a difficult task to comprehend (Valerio et al., 2020). Hence, in modern ecology, ecological patterns are often expected to be generalized over large geographic realms, based on local patterns (Wiens and Rotenberry, 1981). This ability to generalize patterns and information from ecological investigations has contributed towards effective conservation planning (Borges et al., 2017). The landscape-level habitat-species association predictors can be projected over the large scale to identify conservation priority areas for the species (Borges et al., 2017). For example, the spatial distribution of a species is associated with several factors, including spatial distribution of food resources, movement paths (Hildén, 1965), vegetation structure (Lack, 1933), topographic heterogeneity (Besnard et al., 2013), climatic factors (Morris et al., 2012) etc., among many other factors. Therefore, information on species associations with such habitat characteristics can be computed with the use of a single model or a combination of several modelling techniques. These methods are commonly known as Species Distribution Models (SDM) (Elith & Leathwick, 2009) and Ensemble Species Distribution Models (ESDM) which is a pluralistic SDM model. Moreover, these models are also widely used in projecting the climate change impacts on the species distribution (Bagaria et al., 2020).

The Himalayan region (Fig. 1), deemed as the water tower of Asia (Singh & Singh, 1987), is the youngest mountain system and possesses a high level of endemism, which resulted from its topographic and climatic variability (Xu et al., 2009). Its variability has also resulted in enhanced biodiversity, and hence, it is one of the hotspots (Mittermeier, 2004; Appendix Text S1.1). The mountain ecosystem of the Himalayas is vulnerable to climate change, as a number of studies have projected that the species and ecosystem of the Himalayan Range are susceptible to global warming which is largely anthropogenic (Xu et al., 2009; Chettri et al., 2020). Furthermore, the impacts are visible in the form of habitat loss (Bagaria et al., 2020; Harrison, 2020) and receding glaciers (Parry et al., 2020).

The Galliformes, commonly referred to as 'gallinaceous', is a group of birds which has evolved as terrestrial birds, inhabit a variety of habitats including forests, deserts, cultivated lands, bamboo thickets, alpine meadows and are widely distributed (Coles, 2009). In India, 45 species of Galliformes, having oriental affinities have been reported, of which seven are endemic to India. The highest diversity of Galliformes is reported from the Himalayan region (n = 34) out of which 29 species are range-restricted within the Himalayas (Sathyakumar & Sivakumar, 2007). The Galliformes are threatened because of habitat loss, anthropogenic disturbance, global warming and poaching throughout their distribution range (Sathyakumar & Sivakumar, 2007). In spite of their beautiful plumage and their role as indicators of habitat quality, these birds are among the least studied animals. Although there have been efforts to estimate the status and distribution of a few species, most of them are restricted in small areas not covering the entire range in the Himalayas (Appendix Text S1.2). Moreover, the available knowledge on these species is largely old and may be obsolete in the current anthropogenic scenario. Further, a recent study on Galliformes pointed out the incompleteness of information on geographic ranges of many species (Gupta et al. (2020)).

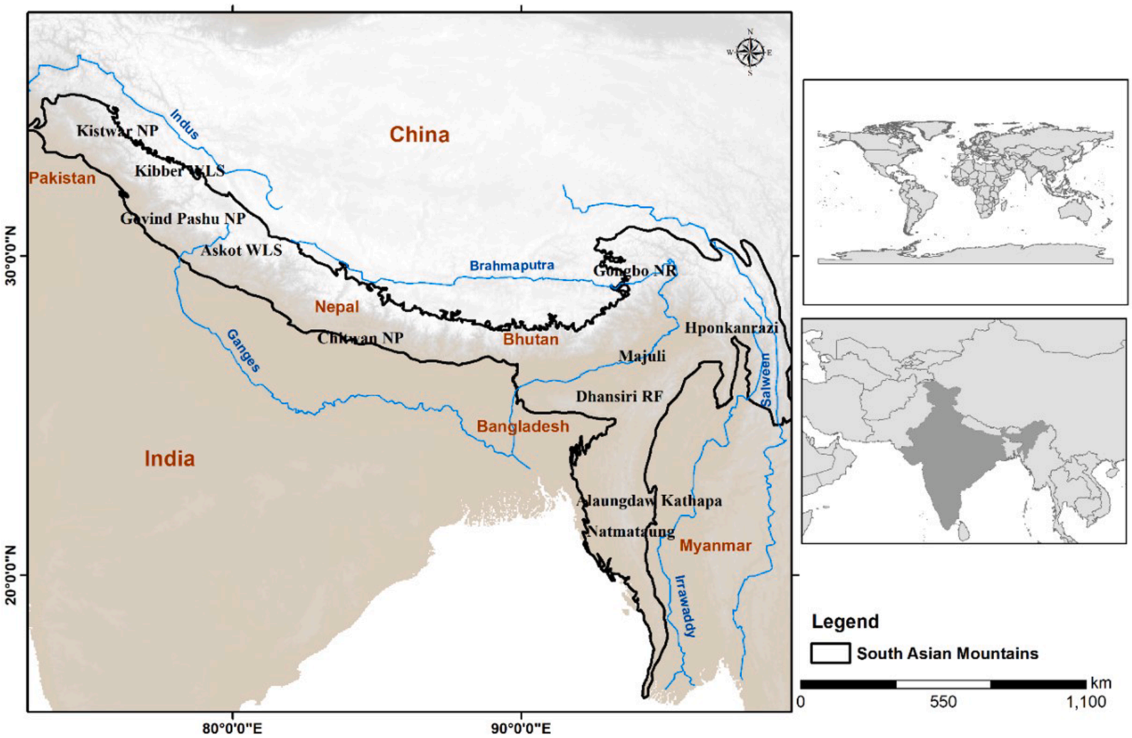


**Fig. 1.** The study area – the Himalayan arc. The Himalayan arc in India, cutting through its neighbouring countries and important rivers flowing across the study area. The base map is a Digital Elevation Model (DEM) from Shuttle Radar Topographic Mission (SRTM), NASA.

Hence, in recognition of the threats posed by climate change to habitats in the Himalayan Range, we attempted to generate information on the current distribution of these species which is a prerequisite for developing any conservation and management strategy (Morris, 2003). Out of the Himalayan Range restricted species (n = 29), information on 15 species is poor because of their elusive nature and remote distribution. Through the present study, we also attempted to find occurrence proxies for such data deficient species using data abundant species, which share similar habitat and environment. We formed the archetypal data abundant cohorts by clustering and using their occurrence records in SDM frameworks by adopting the macroecological principals (Marquet, 2009) to understand the cohort relationship with environment at large scale (Himalayan Range). These archetypal cohorts are groups of species that share common habitat characteristics (Dunstan et al., 2011) and henceforth, we refer to them as archetypal cohorts. Further, we explored the potential consequences of future climate change on the distribution of these Himalayan Range restricted species with bioclimatic variables based Bioclimatic Envelope Models (BEMs).

## 2. Methods

### *2.1. Species occurrence records*

Occurrence records of all the Galliformes species were collected through primary data (camera trap, sign survey), secondary data (Appendix Table S2.1) and open source data repositories (Global Biodiversity Information Facility (GBIF)). The primary data was collected during 2018 to 2019 from six different study landscapes distributed in the entire Indian Himalayan Region (Lahaul & Spiti, Uttarkashi, Darjeeling, East Sikkim, East Seang and West Kameng). Occurrences from all sources were collated and extracted according to the boundary of the Himalayan Range (Appendix Text S1.1). Among the 29 Himalayan Range restricted species, sufficient occurrences were not available for 9 species (Appendix Text S2.3), having less than five occurrences each. A generalist species, Black Francolin *Francolinus francolinus* which has a presence in the foothills and Terai region too, was also considered due to its abundant presence in the high-altitude region (2500–5000 m) of the Himalayas. In total 21 species represented by 5888 occurrence records, were compiled (Table 1). There were few data deficient species for which the number of occurrence records was less than 30 counts and individual distribution modelling for them was difficult (Table 1). Hence, to assess the distribution range and suitable habitat for these species, using the environmental parameters, we grouped all the species into clusters with similar environmental affinities. To date, no study is available which has attempted SDM for these species covering the entire range. Due to lack of information on the home range of these species, a home range of 2 $km^2$ was considered based on published information on home ranges of other Galliformes species (Appendix Text S2.4), for generating pseudo-absences. The occurrences were also tested for spatial autocorrelations and filtered through a window of 2 $km^2$.

### *2.2. Habitat variables*

For implementing the SDM, we used a set of 35 explanatory variables (data sources in Appendix Text S2.2). These variables were agriculture expansion index, development threat index, urban expansion index, gridded population, distance from rivers, distance from roads, elevation, slope, mean Normalised Difference Vegetation Index (NDVI) For pre-monsoon, monsoon and post monsoon, soil

**Table 1**
A list of the 21 Galliformes species, 20 of which were range-restricted within the Himalayas, were considered in this study. Six of these species had less than 30 counts of occurrences hence not modelled individually.

| common name | scientific name | IUCN status | No. of occurrence records | No. of occurrence records after spatial filtering |
|---|---|---|---|---|
| Black Francolin | *Francolinus francolinus* | Least Concern | 2511 | 649 |
| Blood Pheasant | *Ithaginis cruentus* | Least Concern | 12 | 10 |
| Blyth's Tragopan | *Tragopan blythii* | Vulnerable | 218 | 55 |
| Cheer Pheasant | *Catreus wallichii* | Vulnerable | 33 | 26 |
| Chestnut-breasted Partridge | *Arborophila mandellii* | Vulnerable | 256 | 36 |
| Grey Peacock | *Polyplectron bicalcaratum* | Least Concern | 599 | 106 |
| Hill Partridge | *Arborophila torqueola* | Least Concern | 59 | 29 |
| Himalayan Snowcock | *Tetraogallus himalayensis* | Least Concern | 10 | 2 |
| Hume's Pheasant | *Syrmaticus humiae* | Near Threatened | 76 | 11 |
| Kalij Pheasant | *Lophura leucomelanos* | Least Concern | 179 | 106 |
| Koklass Pheasant | *Pucrasia macrolopha* | Least Concern | 18 | 9 |
| Himalayan Monal Pheasant | *Lophophorus impejanus* | Least Concern | 46 | 39 |
| Mountain-bamboo Partridge | *Bambusicola fytchii* | Least Concern | 406 | 75 |
| Rufous-throated Partridge | *Arborophila rufogularis* | Least Concern | 899 | 120 |
| Satyr Tragopan | *Tragopan satyra* | Near Threatened | 22 | 17 |
| Sclater's Monal | *Lophophorus sclateri* | Vulnerable | 34 | 4 |
| Snow Partridge | *Lerwa lerwa* | Least Concern | 12 | 10 |
| Temnick's Tragopan | *Tragopan temminckii* | Least Concern | 38 | 7 |
| Tibetan Partridge | *Perdix hodgsoniae* | Least Concern | 10 | 2 |
| Western Tragopan | *Tragopan melanocephalus* | Vulnerable | 45 | 30 |
| White-cheeked Partridge | *Arborophila atrogularis* | Near Threatened | 360 | 30 |

Adapted from Sathyakumar and Sivakumar (2007).

nutrient retention, soil rooting, soil oxygen availability for roots, soil workability index, soil toxicity index and bioclimatic variables (n = 19). The values of the explanatory variables were extracted for the species occurrence locations using ESRI ArcGIS 10.6. The variables were first tested for collinearity by computation of their Variance Inflation Factors (VIFs, Marquaridt, 1970). Variable responses were generated for identifying variables of importance, using the R package 'caret' (Kuhn, 2008, Fig. S3.1) and correlations among variables were tested for removing collinearity (Fig. S3.2). Finally, ten variables were retained -agriculture, aspect, precipitation of driest month (bio_14), precipitation seasonality (bio_15), precipitation of driest quarter (bio_17), mean NDVI of pre-monsoon months, mean NDVI of monsoon months, population density, distance from river and slope; for ordination, clustering and distribution modelling for the SDMs.

### 2.3. Species clustering and cohort formation

We clustered the species and made cohorts by grouping species based on variables which are found to be of significance in predicting the group for each entity. The ideal number of clusters were determined using the within-sum of squares method (Kassambara, 2017) in R environment v 3.6.2 (R Core Team, 2019), with package 'cluster' (Kaufman & Rousseeuw, 2009). Further, for ascertaining the clusters based on ordination methods, we used the selected variables and ordinated them in R package 'FactoMineR' (Lê et al., 2008) using Principle Component Analysis (PCA, Comon, 1994) and Non-Metric Dimensional Scaling (NMDS, Kruskal, 1964). Species were clustered using hierarchical clustering method (Hartigan, 1975), agnes method (Struyf et al., 1997), partitioning around medoids (PAM) method (Struyf et al., 1997) and k-means clustering method (Hartigan & Wong, 1979). Lastly, we have also implemented the Species Archetype Modelling (SAM) framework which is an analytical framework that uses mixtures of Generalised Linear Models for identifying archetypes in the data (Dunstan et al., 2011; Appendix Text S4.5; Fig. S4.8–9).

### 2.4. Climatic predictors

For the purpose of BEMs, the 19 bioclimatic variables alone were tested for collinearity using VIF, retaining variables with VIF value lower than 5 (Akinwande et al., 2015). The selected bioclimatic variables for the BEMs modelling procedure were mean diurnal range (bio_2) (2.006), isothermality (bio_3) (3.059), bio_14 (4.365), bio_15 (3.053) and precipitation of coldest quarter (bio_19) (4.754). A number of General Circulation Models (GCMs) for future climate are available under the four Representative Concentration Pathway (RCP) assumptions (2.6, 4.5, 6.0 and 8.5), based on the Assessment Report 5 (AR5) of the Intergovernmental Panel for Climate Change (IPCC, 2014). To avoid bias from a single GCM, a mean (Weiland et al., 2012; Venkataraman et al., 2016) of three different GCMs were used based on their ranking (Das et al., 2018) – Goddard Institute for Space Studies E2-H (GISS-E2-H), Model for Interdisciplinary Research on Climate 5 (MIROC5), and Max Planck Institute-Earth System Model (MPI-ESM). We used this ensemble of GCMs for the year 2070 at two emission scenarios (RCPs 4.5 and 8.5).

### 2.5. Modelling procedure

The selection and calibration of models were performed using two separate modes. In the first mode, an SDM was developed with

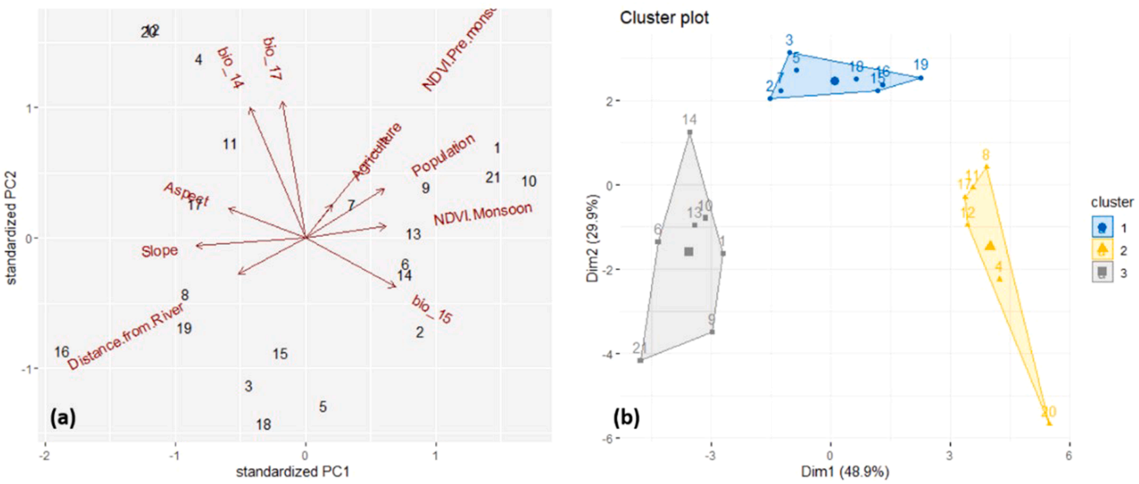


**Fig. 2.** Ordination and clustering of the Galliformes dataset. (a) Principal Component Analysis based ordination of the species with respect to the attached environmental variables showing associations among groups of species (b) Euclidean distance based K-means clustering of the species. Note: 1-Black Francolin, 2-Blood Pheasant, 3-Blyths Tragopan, 4-Cheer Pheasant, 5-Chestnut-breasted Partridge, 6-Grey Peacock, 7-Hill Partridge, 8-Himalayan Snowcock, 9-Humes Pheasant, 10-Kalij Pheasant, 11-Koklass Pheasant, 12-Himalayan Monal Pheasant, 13-Mountain Bamboo Partridge, 14-Rufous-throated Partridge, 15-Satyr Tragopan, 16-Sclater's Monal, 17-Snow Partridge, 18-Temnick's Tragopan, 19-Tibetan Partridge, 20-Western Tragopan, 21-White-cheeked Partridge.

the use of both bioclimatic and biophysical variables. Whereas, in the second mode, the BEMs were made using bioclimatic variables only. The BEMs were developed to project the climate change-driven impacts in the climatically suitable habitat of the species clusters. An ensemble modelling approach, was used for developing both SDMs and BEMs, using r package 'biomod2′ (Thuiller et al., 2016). The key steps in the modelling procedure were data-formatting, model selection and parameterization. These key steps remained consistent through the different modelling modes and clusters (Appendix Text S3.3). To test whether the species considered in this study for archetype cluster formation could be modelled individually, and if there was overlap between the clustered models and individual models, we also applied the BEM framework on the individual species that had over 30 occurrence points (Table 1). The model parameters applied to the individual species models were the same as the archetype cluster to which they belonged.

## 3. Results

### 3.1. Species clustering

The ordination of the species with PCA and NMDS, with respect to the selected variables, reveals species assemblages and environmental associations resulted in the formulation of three groups. The ordination and clustering methods revealed similar group affiliations among the Galliformes species (Fig. 2a and b; Table 2; Appendix Fig. S4.3 – S4.7, Appendix Table S4.3 and Appendix Text S4.5). However, according to the SAM framework, 4 archetype groups were formed, and Hill Partridge could not be allotted any archetype group (Appendix Text S4.3) and had very low π value (Appendix Text S4.9). Interestingly, two of the groups suggested by the ordination and clustering algorithms remained consistent with the SAM results, but one of the groups were split into two. Since, SAM is known for its robust approach to species archetype formation (Galanidi et al., 2016; Murillo et al., 2018), the latter suggested 4 archetype groups were used for the clustered modelling of SDM and BEM (Table 2). Henceforth, we refer to these three groups as Wide-ranging, all Vegetation type Galliformes (WRVG); Eastern Himalayas, Dense Vegetation, mid-altitude Galliformes (EMA); Eastern Himalayas, Dense Vegetation affinity Galliformes (EHDVG); and West Himalayas, Sparse to moderate Vegetation Galliformes (WHSVG), (Table 2).

The WRVG group consists of Black Francolin, Kalij Pheasant and White-cheeked Partridge. Both Black Francolin and Kalij Pheasant have a wide distribution along the Himalayan arc, and the White-cheeked Partridge has distribution in the North-east Himalayas (Table 2). Grey Peacock, Hume's Pheasant, Mountain-bamboo Partridge and Rufous-throated Partridge together form the group EMA that inhabits low to mid altitudinal ranges of the East Himalayas having dense forests (Table 2). Blood Pheasant, Blyth's Tragopan, Chestnut-breasted Partridge, Satyr Tragopan, Sclater's Monal, Temnick's Tragopan and Tibetan Partridge characterized by dense vegetation and Rhododendron dominated forests in the mid to high elevational ranges of the East and North-east Himalayas form the EHDVG group (Table 2). Himalayan Snowcock, Cheer Pheasant, Koklass Pheasant, Himalayan Monal Pheasant, Snow Partridge and Western Tragopan in the Western Himalayas, inhabiting sparse to moderately dense vegetation at the mid to high elevational ranges were grouped as WHSVG (Table 2). Other than the group WRVG which had wide-spaced distribution along the longitudinal gradient of the Himalayas, all the other groups confined to the Western and Eastern Himalayas. The West Himalayan boundary as defined by Rodgers and Panwar (1988) extends from Jammu & Kashmir (except Ladakh), Himachal Pradesh (except Lahaul & Spiti) to Garhwal

**Table 2**
Cluster allocations of the Galliformes species based on the different clustering algorithms. Distribution, vegetation and elevation information adapted from Sathyakumar and Sivakumar (2007).

| Species | Distribution | Vegetation | Elevation (m) | hc | agnes | pam | k-means | SAM | Cluster named as |
|---|---|---|---|---|---|---|---|---|---|
| Black Francolin | Wide | Sparse | 2500–5000 | 1 | 1 | 1 | 1 | 1 | WRVG |
| Kalij Pheasant | Wide | All vegetation type | 245–3050 | 1 | 1 | 1 | 1 | 1 | WRVG |
| Wihte-cheeked Partridge | East | Moderately Dense | 1500–5000 | 1 | 1 | 1 | 1 | 1 | WRVG |
| Grey Peacock | East | Dense | 1200–5000 | 1 | 1 | 1 | 1 | 2 | EMA |
| Hume's Pheasant | East | Sparse | 1200–3000 | 1 | 1 | 1 | 1 | 2 | EMA |
| Mountain-bamboo Partridge | East | Dense | 2000–5000 | 1 | 1 | 1 | 1 | 2 | EMA |
| Rufous-throated Partridge | East-Central | Dense | 460–2500 | 1 | 1 | 1 | 1 | 2 | EMA |
| Hill Partridge | Wide | Dense | 400–4000 | 1 | 1 | 1 | 2 | 3 | – |
| Blood Pheasant | East-Central | Rhododendron dominated | 1500–4700 | 1 | 1 | 1 | 2 | 4 | EHDVG |
| Blyth's Tragopan | East | Dense | 1800–3500 | 2 | 2 | 2 | 2 | 4 | EHDVG |
| Chestnut-breasted Partridge | East | Dense | 350–2500 | 2 | 2 | 2 | 2 | 4 | EHDVG |
| Satyr Tragopan | Central | Dense | 2000–3800 | 2 | 2 | 2 | 2 | 4 | EHDVG |
| Sclater's Monal | East | Rhododendron dominated | 3000–4000 | 2 | 2 | 2 | 2 | 4 | EHDVG |
| Temnick's Tragopan | East | Dense | 2100–3600 | 2 | 2 | 2 | 2 | 4 | EHDVG |
| Tibetan Partridge | East | Sparse | 2800–5200 | 2 | 2 | 2 | 2 | 4 | EHDVG |
| Himalayan Snowcock | West-Central | Sparse | 3000–5800 | 2 | 2 | 3 | 1 | 5 | WHSVG |
| Cheer Pheasant | West | Sparse | 1500–3050 | 3 | 3 | 3 | 3 | 5 | WHSVG |
| Koklass Pheasant | West-Central | Moderately Dense | 2100–3300 | 3 | 3 | 3 | 3 | 5 | WHSVG |
| Himalayan Monal Pheasant | Wide | Moderately Dense | 2000–4875 | 3 | 3 | 3 | 3 | 5 | WHSVG |
| Snow Partridge | West-Central | Rhododendron dominated | 3000–3500 | 3 | 3 | 3 | 3 | 5 | WHSVG |
| Western Tragopan | West | Dense | 2000–2800 | 3 | 3 | 3 | 3 | 5 | WHSVG |

*Note*: hc – Hierarchical clustering, agnes – Agnes clustering, pam – Partitioning Around Medoids, k-means – K-means clustering, SAM – Species Archetype Modelling.

and Kumaon (Uttarakhand). These mountains are characterized by tropical, subtropical, temperate, subalpine, alpine vegetation (Raju et al., 2010). The East Himalayan mountains extend from Sikkim, Darjeeling (West Bengal) to Arunachal Pradesh (Rodgers and Panwar, 1988) and are characterized by tropical, subtropical, temperate and subalpine vegetation (Raju et al., 2010). The species in the EMA and EHDVG clusters also cut across the North-east Himalayas which according to Rodgers and Panwar (1988) is a biogeographic zone extending from Assam, Manipur, Meghalaya, Mizoram, Nagaland to Tripura and are characterized by tropical, subtropical, temperate, subalpine vegetation (Raju et al., 2010).

### 3.2. Species distribution models and bioclimatic Envelope models

The SDMs and BEMs for the identified clusters WRVG, EMA, EHDVG and WHSVG were developed using ensembles of selected models for each group, variable importance was assessed, the accuracy of modelled outputs in each cluster were evaluated, and threshold values for the conversion of probability surfaces (Fig. S4.10) to binary maps were calculated (Appendix Text S4.6). The ROC based accuracies for all groups varied between 0.701 and 0.988 (Table 3). BEM results for the individual species (Appendix 2 Figs. 2–9) also show overlap with the suitable areas predicted under the clustered models (Fig. 3). However, we advise precaution in using the individual species models due to their low accuracies and few model failures while attempting the ensemble models (Appendix 2 Table 1).

### 3.3. Area of predicted habitat according to SDM and BEM

The probability surfaces of the current (SDM and BEM) and future (BEM) distributions were converted into binary maps (Fig. 3) of presence and absence using the respective threshold values (Appendix Text S4.6). The SDMs predicted 13.11% (120851.1 km$^2$), 5.74%

**Table 3**
Model evaluation scores on test data for the clusters and respective models selected for each cluster for the SDMs and BEMs.

| SDM | | | | BEM | | | |
|---|---|---|---|---|---|---|---|
| Model | ROC | KAPPA | TSS | Model | ROC | KAPPA | TSS |
| WRVG | | | | | | | |
| RF | 0.873 | 0.582 | 0.568 | GLM | 0.903 | 0.627 | 0.643 |
| GBM | 0.865 | 0.549 | 0.523 | GAM | 0.923 | 0.727 | 0.718 |
| GAM | 0.854 | 0.544 | 0.543 | GBM | 0.937 | 0.739 | 0.743 |
| FDA | 0.845 | 0.563 | 0.563 | | | | |
| MARS | 0.822 | 0.501 | 0.497 | | | | |
| CTA | 0.778 | 0.542 | 0.545 | | | | |
| GLM | 0.771 | 0.382 | 0.362 | | | | |
| Mean | 0.829 | 0.523 | 0.515 | Mean | 0.902 | 0.698 | 0.702 |
| Ensemble | 0.803 | 0.516 | 0.501 | Ensemble | 0.891 | 0.569 | 0.611 |
| EMA | | | | | | | |
| GAM | 0.722 | 0.288 | 0.283 | RF | 0.814 | 0.444 | 0.447 |
| GBM | 0.712 | 0.284 | 0.287 | FDA | 0.774 | 0.399 | 0.402 |
| MARS | 0.713 | 0.273 | 0.274 | | | | |
| RF | 0.719 | 0.296 | 0.298 | | | | |
| Mean | 0.717 | 0.285 | 0.286 | Mean | 0.794 | 0.422 | 0.423 |
| Ensemble | 0.704 | 0.324 | 0.324 | Ensemble | 0.717 | 0.465 | 0.451 |
| EHDVG | | | | | | | |
| | | | | ANN | 0.765 | 0.517 | 0.246 |
| | | | | SRE | 0.776 | 0.552 | 0.451 |
| | | | | CTA | 0.801 | 0.570 | 0.443 |
| FDA | 0.807 | 0.474 | 0.552 | GAM | 0.830 | 0.601 | 0.427 |
| GAM | 0.833 | 0.515 | 0.546 | MARS | 0.839 | 0.585 | 0.469 |
| GBM | 0.899 | 0.639 | 0.689 | FDA | 0.840 | 0.596 | 0.441 |
| MARS | 0.829 | 0.494 | 0.551 | GBM | 0.902 | 0.732 | 0.517 |
| RF | 0.927 | 0.712 | 0.771 | RF | 0.907 | 0.793 | 0.524 |
| Mean | 0.859 | 0.567 | 0.622 | Mean | 0.833 | 0.618 | 0.440 |
| Ensemble | 0.951 | 0.726 | 0.783 | Ensemble | 0.955 | 0.75 | 0.828 |
| WHSVG | | | | | | | |
| | | | | GBM | 0.676 | 0.363 | 0.384 |
| GBM | 0.702 | 0.364 | 0.425 | RF | 0.700 | 0.375 | 0.406 |
| RF | 0.733 | 0.401 | 0.476 | SRE | 0.686 | 0.319 | 0.372 |
| Mean | 0.717 | 0.382 | 0.451 | Mean | 0.687 | 0.353 | 0.387 |
| Ensemble | 0.988 | 0.907 | 0.92 | Ensemble | 0.902 | 0.609 | 0.611 |

*Note*: GAM – Generalised Additive Models; GBM - Gradient Boosted Models; RF – Random Forests; GLM – Generalised Linear Model; ANN – Artificial Neural Networks; SRE – Surface Range Envelope; CTA – Classification Tree Analysis; FDA – Flexible Discriminant Analysis; MARS – Multiple Adaptive Regression Splines; WRVG - Wide ranging, all Vegetation type Galliformes; EMA – Eastern Himalayas, Dense Vegetation, mid altitude Galliformes; EHDVG - Eastern Himalaya, Dense Vegetation affinity Galliformes; WHSVG - West Himalaya, Sparse to moderate Vegetation Galliformes.

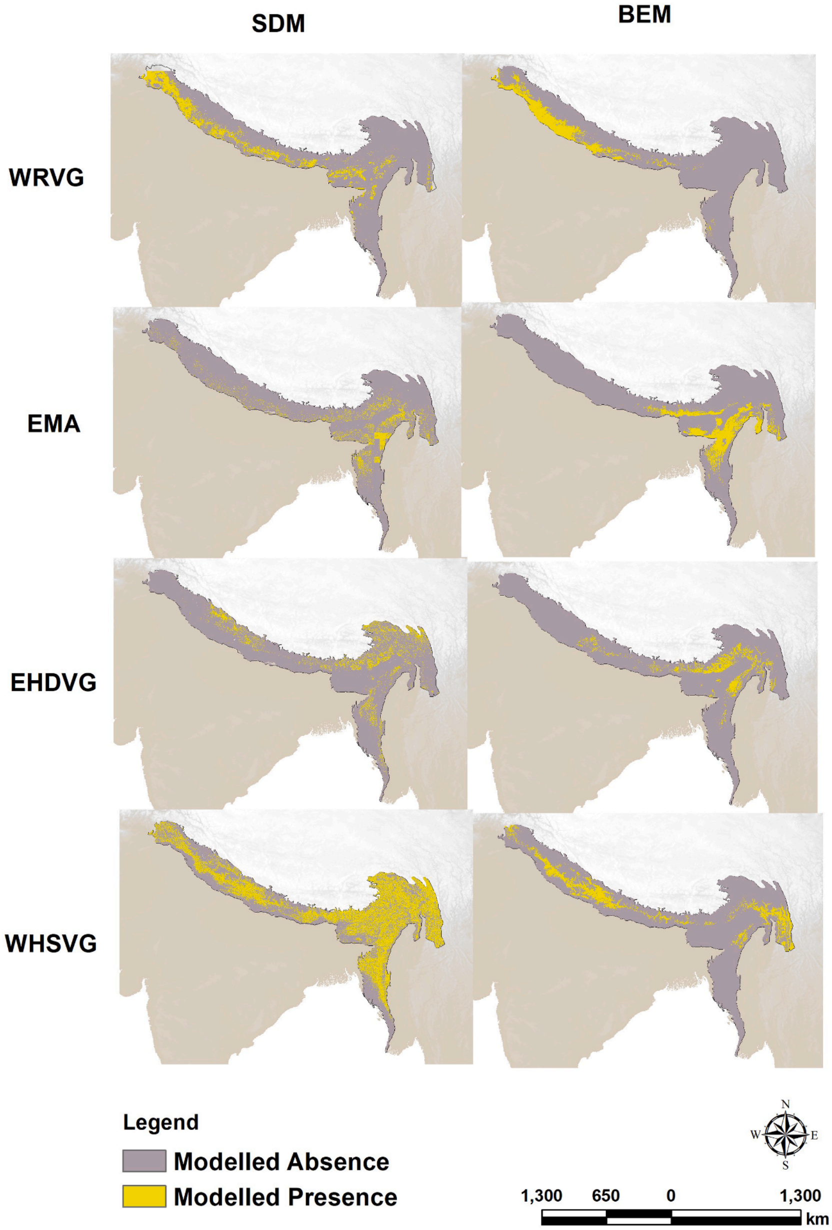


**Fig. 3.** Distributions predicted by the SDM and BEM (current) frameworks, for the four Galliformes clusters. Note: WRVG - Wide ranging, all Vegetation type Galliformes; EMA – Eastern Himalayas, Dense Vegetation, mid altitude Galliformes; EHDVG - Eastern Himalaya, Dense Vegetation affinity Galliformes; WHSVG - West Himalaya, Sparse to moderate Vegetation Galliformes; SDM – Species Distribution Model; BEM – Bioclimatic Envelope Model. The base map is a Digital Elevation Model (DEM) from Shuttle Radar Topographic Mission (SRTM), NASA.

(52937.71 km$^2$), 8.663% (79851.97 km$^2$) and 55.29% (509608.88 km$^2$) of the area of the entire landscape to be suitable for WRVG, EMA, EHDVG and WHSVG, respectively. On the other hand, according to the BEMs, the projected percentage of climatically suitable habitat in the landscape was 10.68% (WRVG, 98401.12 km$^2$), 11.63% (EMA, 107204.9 km$^2$), 7.17% (EHDVG, 66043.69 km$^2$) and 15.56% (WHSVG, 143453.24 km$^2$) for the respective clusters of Galliformes (Appendix Text S4.6).

### 3.4. Climate driven predicted changes

The binary maps of the current and future (2070, Fig. S3.11) climate projections were used for estimating the gain, and loss in the bioclimatic envelopes of the four Galliformes clusters (Table 4, Fig. 4). The cluster WRVG (Fig. 4) was predicted to lose about 81.44% of its climatically suitable habitat by 2070 at RCP 4.5, and 79.27% at RCP 8.5 (Table 4). The habitat gain or range shifts were minimal (0.44% at RCP 4.5 and 0.41% at RCP 8.5), indicating range contraction in both the scenarios. Habitat retention was estimated at about

18.62% at RCP 4.5, and 20.81% at the higher emission scenario of RCP 8.5. In the cluster EMA, habitat losses were estimated at 67.14% (4.5) and 91.65% (8.5) in the respective RCP scenarios, with small gains of 6.26% in RCP 4.5, but negligible gains (0.62%) in RCP 8.5 scenario. Retention of habitat was estimated at 32.92% (RCP 4.5) and 8.39% (RCP 8.5).

The cluster EHDVG (Fig. 4) was predicted to suffer significant losses in both the scenarios (91.88%, RCP 4.5 and 96.90%, RCP 8.5). Estimated percentages of retained habitat were also the least for the EHDVG cluster (8.18% in RCP 4.5 and 3.24% in RCP 8.5), indicating significant range contraction (Table 4). However, in case of cluster WHSVG (Fig. 4), about one-third of its climatic envelope is expected to be retained in both the RCP scenarios (31.64%, RCP 4.5 and 28.08%, RCP 8.5), while two-thirds is expected to be lost; along with gains of 3.3% (RCP 4.5) and 4.58% (RCP 8.5) (Table 4). Overall, species under the EHDVG group are predicted to be the worst-hit group in the event of future climate change. Change predictions in BEM based suitable areas for the individual species have also been estimated (Appendix 2 Table 2). Though overall spatial overlap (Appendix 2 Figs. 2–9) is seen between the clusters and their species, we use the individual species modelling results with caution, due to their low accuracies and poor convergence in models (Appendix 2 Table 1). Based on individual species modelling, Kalij Pheasant and White-cheeked Partridge (WRVG, both RCP 4.5 and 8.5), all species of EMA group (both RCP 4.5 and 8.5), Chestnut-breasted Partridge (EHDVG, RCP 8.5) and Himalayan Monal Pheasant (WHSVG, RCP 8.5) are expected to register habitat losses of more than 80% in the respective RCP scenarios by 2070 (Appendix 2 Table 2).

## 4. Discussion

The present study highlighted that the spatial distributions of species occupying similar habitat are also statistically proven to have similar habitat associations (Fig. 2, Table 2, Appendix Text S4.5). The environmental niche of one species can be pedagogic about another species (Thorson et al., 2015). The grouping of multiple species to generate a single SDM or BEM may help to develop a spatial understanding of the distributions and occurrence probabilities of rare species (Zipkin et al., 2010), as they can borrow strength from data abundant species (Dunstan et al., 2011). It has been established that multiple species can be clustered together based on their responses to the environmental gradients, and be further used as single entities for the prediction of spatial distributions (Dunstan et al., 2011; Burton et al., 2012; Thorson et al., 2015). The formation of Galliformes species clusters based on their environmental niche has allowed the possibility to include rare and elusive species (e.g., Blood Pheasant and Snow Partridge) with other species that had similar environmental affiliations.

However, a limitation and uncertainty in inferring ecological relationships of rare species will always exist and be limited by their small sample size. Another anticipated source of uncertainty in clustering species together lies in the aggregation of species responses to environmental variables, an issue also faced by other authors (Burton et al., 2012). Nevertheless, from a broader perspective, multi-species clustered modelling results are indicative of their usefulness in the estimation of area identification for intensive surveys in future. The SAM framework for species archetype formation was found to be a robust technique for species clustering. Nevertheless, the inability of SAM to allow a group to Hill Partridge (Appendix Table S4.3) may indicate habitat specificity in the species.

Among the algorithms in the ensemble modelling, Random Forest (RF) was found to be the overall highest performing model for all the clusters (Table 3). RF is a classification algorithm introduced by Breiman (1999) that selects features randomly and creates a tree of bootstrapped samples of the training data. A large number of such trees is generated and unweighted voting is assigned to them, finally leading to classified data. Our results indicate a considerable difference between the suitable area estimates from the SDMs and BEMs for WHSVG (Table 4). The area estimates under the BEM framework indicate that the bioclimatic envelopes present a conservative approach towards modelling of species distributions and are representative only of the climatic niche of species (Peterson, 2003). At the same time, it must be noted that the change predictions made with the use of BEMs, strictly present the bioclimatic restrictions that the species might face in the future climate, while still being able to survive in topographically hospitable areas.

**Table 4**
Predicted changes in the climatically suitable area (km$^2$) for the Galliformes clusters in 2070 under RCP scenarios 4.5 and 8.5.

| | WRVG | | EMA | | EHDVG | | WHSVG | |
|---|---|---|---|---|---|---|---|---|
| Current status of suitable habitat (km$^2$) | | | | | | | | |
| SDM | 120851.1 | 13.11% | 52937.71 | 5.74% | 79851.97 | 8.663% | 509608.88 | 55.290% |
| BEM | 98401.12 | 10.68% | 107204.9 | 11.63% | 66043.69 | 7.165% | 143453.24 | 15.564% |
| Predicted change in area (km$^2$) 2070 under RCP 4.5 | | | | | | | | |
| Absence | 819098.4 | 88.86% | 756672.5 | 82.09% | 845420.40 | 91.72% | 747774.18 | 81.13% |
| Habitat gain | 4126.536 | 0.44% | 57758.7 | 6.26% | 10243.01 | 1.11% | 30416.06 | 3.30% |
| Habitat loss | 80144.43 | 81.44% | 71973.94 | 67.14% | 60634.22 | 91.88% | 98147.72 | 68.47% |
| Retained habitat | 18328.17 | 18.62% | 35292.38 | 32.92% | 5399.92 | 8.18% | 45359.60 | 31.64% |
| Predicted change in area (km$^2$) 2070 under RCP 8.5 | | | | | | | | |
| Absence | 819399.8 | 88.9% | 808693.7 | 87.74% | 851625.23 | 92.40% | 735878.16 | 79.84% |
| Habitat gain | 3804.435 | 0.41% | 5745.454 | 0.62% | 3984.09 | 0.43% | 42206.46 | 4.58% |
| Habitat loss | 78009.74 | 79.27% | 98257.81 | 91.65% | 63947.57 | 96.90% | 103359.40 | 72.11% |
| Retained habitat | 20483.62 | 20.81% | 9000.584 | 8.39% | 2140.56 | 3.24% | 40253.52 | 28.08% |

*Note*: Percentages of suitable areas according to the SDM and BEM models with respect to the total area of the landscape (921697 km$^2$). Percentage of retained habitat and habitat loss were calculated with respect to the respective areas of climatically suitable habitat of each cluster under the current climate. Percentages of absence and habitat gain were calculated with respect to the total area of the landscape.

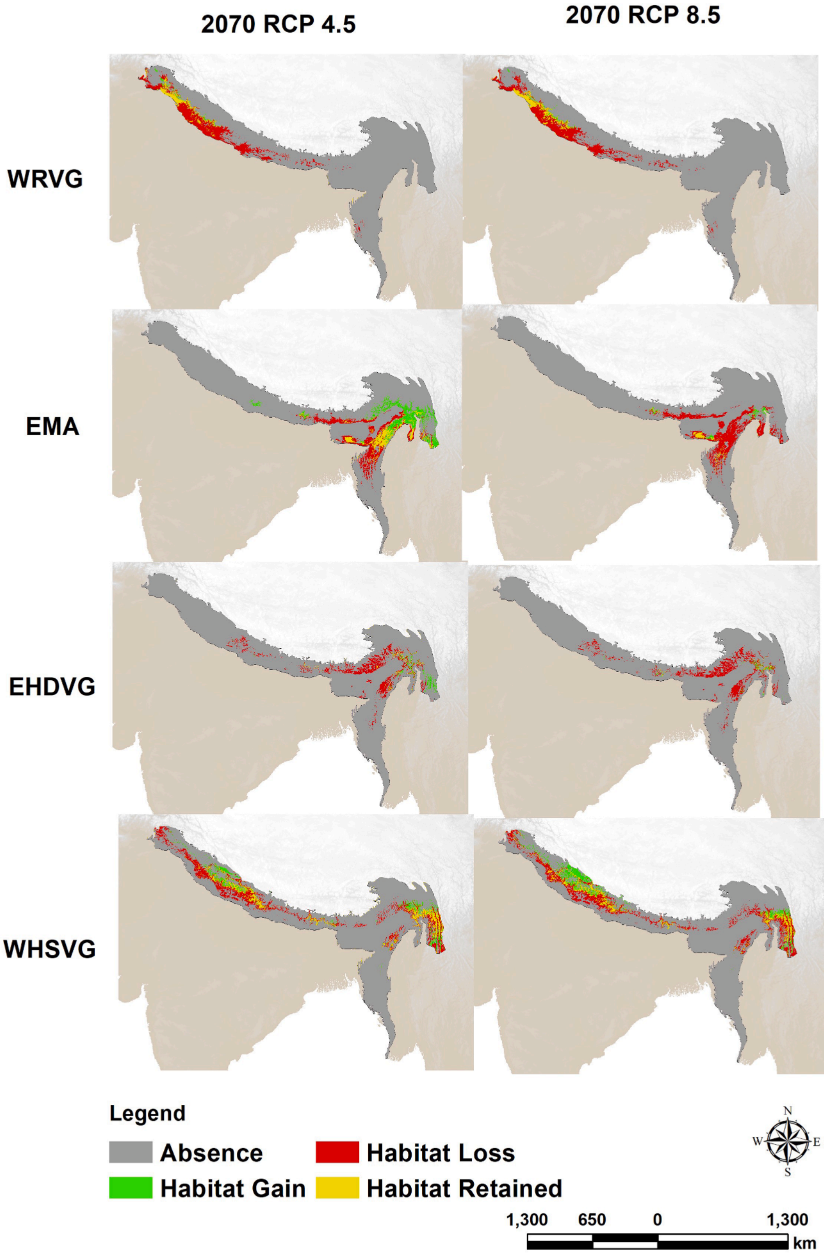


**Fig. 4.** Predicted gains, losses and habitat retentions of the bioclimatic envelopes. Predictions of changes in bioclimatic envelopes among the four clusters, in the face of predicted climate change for the year 2070 (RCP 4.5 and RCP 8.5). Note: WRVG - Wide ranging, all Vegetation type Galliformes; EMA – Eastern Himalayas, Dense Vegetation, mid altitude Galliformes; EHDVG - Eastern Himalaya, Dense Vegetation affinity Galliformes; WHSVG - West Himalaya, Sparse to moderate Vegetation Galliformes. The base map is a Digital Elevation Model (DEM) from Shuttle Radar Topographic Mission (SRTM), NASA.

Nevertheless, the BEM based estimate of the impacts of climate change presents a conservative approximation of the potential habitat losses that can be caused in the future climate (Carroll, 2010). These models also address the question of whether the protected area boundaries will remain relevant in the face of climate change (Hannah et al., 2007). Such quantification and visualization of modelled predictions through maps has been helpful in initializing discussions on the severe impacts of climate change (Jeschke and Strayer, 2008). All the more, the first step towards conservation of rare species is approximating their geographic boundaries (Hoffmann et al., 2008), and they can be easily estimated through bioclimatic models (Sérgio et al., 2007). In the BEM outcomes for the Galliformes, precipitation variables were found to have a significant influence on the models (Fig. S4.12 – S4.13), indicating that precipitation plays an essential role in guiding the distribution and presence of the Galliformes in the Himalayan region. As noted in (Schickhoff et al., 2015), the pre-monsoon future climate may become an essential determinant for forest growth, thereby having indirect effects on faunal diversity as well. Bio_15 had emerged as the most crucial variable among the initial set of 36 variables, and bio_14 and bio_17 were among the top five essential variables; indicating the significance of precipitation for the distribution of Galliformes. The cluster WHSVG had positive correlations with the variables related to precipitation (Fig. 2a, bio_14 and bio_17), while the cluster EHDVG showed negative relations.

Whereas, the WRVG and EMA clusters showed stronger correlations with other parameters such as vegetation, human presence, slope and aspect (Fig. 2a). The SDM and BEM models showed similar proportions of suitable habitat for the clusters WRVG and EHDVH (Table 4). At the same time, the variable importance scores for both these clusters have shown significant responses for NDVI of pre-monsoon and monsoon months (Appendix Text S4.6). Both the WRVG and EHDVG groups occupy the low to the mid altitudinal range (500–2500 m asl) characterized by tropical moist deciduous and sub-tropical forests, which themselves are influenced by precipitation and climate (Rawat, 2017). Hence, it can be said that bioclimatic variables have a significant role in habitat selection for the species in WRVG and EHDVG clusters. In the EMA cluster, the suitable habitat estimated via SDM (5.74%) was lower in proportion than BEM (11.63%) estimated suitable area (Table 4). The EMA SDM has shown NDVI for pre-monsoon months, precipitation and slope as important variables in the model (Appendix Text S4.6). The slope has been known to control vegetation and microclimate at mid-altitudes (1000–2000 m asl) (Sharma et al., 2010). In general, species richness is known to decline with elevational gradient and slope (Pandita et al., 2019). This influence of slope in the Eastern Himalayas could be the reason for a conservative model outcome in SDM for EMA. On the other hand, WHSVG cluster showed a major difference between the suitable habitat proportions via SDM (55%) and BEM (15%). It has been earlier found that, SDMs predict larger areas as suitable habitat in comparison to the BEMs, as the latter takes only the climate under consideration and estimates only climatically suitable areas (Peterson, 2003). The additional areas estimated as suitable habitat in an SDM, may be a cumulative effect from other biophysical and topographical variables; NDVI for pre-monsoon months and aspect in the case of WHSVG. Aspect has a role in forming microclimates due to the differences in insolation periods at each aspect (Sharma et al., 2010), and hence, vegetation distribution is strongly affected by aspect (Zhou et al., 2013).

Overall, we find that the SDMs for the clusters which were influenced by vegetation (pre-monsoon and monsoon NDVI) and population density, showed closer agreement with BEMs in the proportion of modelled suitable area. On the other hand, slope and aspect influenced SDMs, EMA and WHSVG respectively, show contrasting proportions of modelled suitable areas through the SDM and BEM models. Slope influenced SDM (for EMA in this study), defined a more conservative area than BEM. However, it must be noted that spatially, the geographic bounds for both the SDM and BEM in EMA show similar extents, and SDM pixels are widely spaced within the same extent (Fig. 3). And aspect influenced SDM (for WHSVG in this study), defined a larger suitable area than BEM. This emphasizes that the role of aspect in defining the microclimate and vegetation is more pronounced than the effect of the slope. Aspect, in fact, can also cause differences in the soil, climate and vegetation properties of the same slope having different aspects (Selvakumar et al., 2009).

The future climate model for the WRVG cluster suggests that the species under this cluster may be able to retain almost 20% of their current climatically suitable area under both the RCP scenarios, 4.5 and 8.5, but lose almost 80% of the BEMs (Table 4). The regional projections of temperature and precipitation changes based on ensemble mean of CMIP5 GCMs deduced prediction of an overall rise in temperature by 2.5 °C (RCP 4.5) and 5.5 °C (RCP 8.5); and an overall rise in precipitation by 8% (RCP 4.5) and 14% (RCP 8.5) in the Himalayan region (Wester, Mishra, Mukherji & Shreshtha, 2019). It is quite evident from the predictions that climatically, the region is expected to become unfavourable for most of the species in the region. Such enormous warming of climate specifically to the east and west region of Himalayas may result in severe consequences for many species. It has been hypothesized that every degree of warming of the globe, can lead to 100–150 extinctions in birds (Sekercioglu et al., 2008).

For the species under both EMA and EHDVG clusters, range contraction is predicted, since entire bioclimatic umbrella is expected to become unsuitable under both the RCP assumptions by 2070, with slightly better situation for EMA under RCP 4.5. The BEM for EMA Galliformes which has shown higher dependence on the temperature variables (Appendix Fig. S4.13), might have to experience rising temperatures as the Eastern Himalayas are expected to see a rise in summer temperature by 2.5 °C and winter temperature by 3.3 °C (RCP 4.5), while 4.4 °C and 5.4 °C rises respectively for summer and winter in RCP 8.5 scenario (Wester et al., 2019). At the same time, the EHDVG cluster which showed a negative correlation with precipitation (Fig. 2a) may also have to experience the predicted rise in precipitation by 7.3% (summer) and 5.5% (winter) in RCP 4.5 and 9.7% (summer) and 6% (winter) in RCP 8.5 (Wester et al., 2019). The predicted rise in precipitation, a limiting factor for the distribution of EHDVG, is almost doubled in RCP 8.5 in comparison to RCP 4.5. Such predicted rise in temperature and precipitation will result in creating a unique climate and change in isotherm in both emission scenarios. Conclusively, the clusters EMA and EHDVG which dominate the Eastern Himalayas are predicted to experience maximum climatic resistance in the future climate. Moreover, the SDM and BEM for the EHDVG cluster had the smallest difference in terms of modelled suitable area, and this indicates that the suitable areas for EHDVG species are greatly pronounced by climatic isotherm. The area of suitable habitat for the EMA and EHDVG species based on SDM and BEM models is relatively minimal (Table 4) with respect to the total geographic area of the Himalayan arc. This makes the EMA and EHDVG clusters most vulnerable among the studied clusters, as species with smaller ranges are highly susceptible to environmental changes (Sekercioglu et al., 2008). Our findings are in line with the study published on Satyr Tragopan (Chhetri et al., 2018), which is one of the species under the EHDVG cluster.

The species cluster WHSVG is predicted to face similar losses and habitat retentions in both the RCP scenarios. In the Western Himalayan region, higher warming during summer and lower warming during winter have been predicted in both the RCP scenarios. The species under this cluster has shown a positive correlation with precipitation (Fig. 2a). The Western Himalayan region, being drier than the Eastern Himalayas, will respond to an increase in precipitation, as this region typically receives lesser precipitation (Singh & Singh, 1987). Furthermore, the regional projections for this region predict a rise in summer temperature by 3.3 °C (RCP 4.5) and 5.7 °C (RCP 8.5) and rise in winter temperature by 3 °C (RCP 4.5) and 5.1 °C (RCP 8.5) (Wester et al., 2019). Climatically, these changes will render the loss of about two-thirds of the current habitat, making it not suitable for WHSVG in the future. This cluster consists of species that have some of the highest elevation niches among the Galliformes in the Himalayas (Table 2). The Himalayan Snowcock, Snow Partridge and Himalayan Monal Pheasant already occupy high elevations, which may become a factor for their limited dispersal capability in the face of climate change (Hof & Allen, 2019). The Himalayan Quail *Ophrysia superciliosa* a species which has not been recorded since 1826 and thus, not included in this study, shares similar habitat traits as Cheer Pheasant and Himalayan Monal Pheasant (Dunn et al., 2015). Hence, the predicted SDM and BEM for the WHSVG cluster may be useful in conducting surveys for the rediscovery of Himalayan Quail. The results achieved for this cluster may also apply to the elusive Himalayan Quail.

The impact of climate change on the Galliformes order, estimated in parts of the Himalayas and other parts of the world has shown range shifts in Satyr Tragopan (Chhetri et al., 2018), range expansion for White-breasted Guineafowl *Agelastes meleagrides* in west Africa (Freeman et al., 2019), range contraction for Caucasian Snowcock *Tetraogallus caucasicus* and Caucasian Grouse *Tetrao mlokosiewiczi* in the Caucasus mountains of Europe (Hof and Allen, 2019), in a few examples. The losses in the bioclimatic isotherm for the three clusters in this study are in accordance with the species-climate relationships. Nonetheless, these predictions are made with consideration of the climatic variables only, to assess the impact of climate change on the habitats of these species. The SDMs built with the use of a combination of topographic, anthropogenic and bioclimatic factors, had scope for inclusion of only one bioclimatic factor (bio_15), due to collinearity. Building climate change models with the SDM dataset, may not have allowed the use of other climate variables, leaving a gap for understanding the climate suitability for the Galliformes clusters. Since the change predictions are conservative, they may be used as a climate change warning, while not necessarily, their realized habitats in future.

Climate-driven shifts in treeline have already become a visible phenomenon, evident from a recent study (Singh et al., 2019), which reported an increasing trend in the treeline elevation from the North-west to the South-east along the Himalayan arc, and revealed significant longitudinal shifts among the major ecotone species - *Juniperus* spp (28.5 m/degree longitude), *Picea* spp (27.2 m/degree longitude), *Betula* spp (13.9 m/degree longitude), *Rhododendron* spp (15.1 m/degree longitude) and *Salix* spp (22.4 m/degree longitude). Apart from the possibilities of the future climate, the Himalayas has already been experiencing fluctuations in its precipitation regime (Wester et al., 2019). Species can adapt to climate change either by shifting habitats according to the biophysical requirements or by evolving physiological and behavioral adaptations (Menzel et al., 2020). However, the physiographic conditions of the Himalayas may present geographic barriers to species for shifting ranges (Xu et al., 2009), more so with Galliformes which have high site fidelity and low dispersal ability (WPA, 2009). Studies on the ecology and distribution of Galliformes species included in this study speak of habitat destruction due to human encroachment or poaching as one of the threats to the Galliformes habitat, besides the looming threat of climatically challenging future ahead.

In pheasant surveys on Blyth's Tragopan, Sclater's Monal, Satyr Tragopan, Blood Pheasant (grouped under EHDVG in this study), and Grey Peacock (grouped under EMA in this study), it was observed that the practice of shifting cultivation in Arunachal Pradesh, caused disturbances to pheasant habitats (Kaul et al., 1995). Chestnut-breasted Partridge (EHDVG) which is known to inhabit broadleaved evergreen forests in the East Himalayas, was found to restrict its range due to disturbances from socio-economic activities near the Thrumshingla National Park in Bhutan (Dhendup, 2015). Hume's Pheasant (EMA) which prefers successional mixed-coniferous broadleaved forests on hillsides is easy bait for hunting (Fuller et al., 2000). Hunting, along with habitat destruction in Mizoram forests of North-east India, makes the populations of Hume's Pheasant very vulnerable (Katju, 1996). The Mountain-bamboo Partridge (EMA) which inhabits the North-east Himalayan moist tropical forests has a low detection probability, but still may be under pressures of hunting in the Nongkhyllem Wildlife Sanctuary, Meghalaya (Dohling and Sathyakumar, 2011). A study in the Kumaon region of Uttarakhand (West Himalayas), revealed that the prime threat to Kalij Pheasant (WRVG) and Koklass Pheasant (WHSVG) in the Kumaon Himalayas was deforestation (Hussain et al., 2001). Ramesh et al., (1999) also pointed out that habitat degradation, lopping of Kharsu Oak *Quercus semecarpifolia* and Pine tree *Pinus wallichiana*, grazing, hunting etc. were causes for the decline of Western Tragopan, Himalayan Monal and Koklass Pheasant (under cluster WHSVG in this study), in the Great Himalayan National Park in Himachal Pradesh were the major threats to these species. Back in 1981, too, habitat destruction was a cause of concern for the habitat loss of these species (Gaston et al., 1981). Another study on Himalayan Monal, Koklass Pheasant, Himalayan Snowcock and Snow Partridge (WHSVG) in the meadows of the Nanda Devi Biosphere Reserve in Uttarakhand (Central Himalayas), pointed out the problem of habitat disturbance due to extraction of non-timber forest product (NTFP), grazing and *Cordyceps sinensis* collection (Bhattacharya et al., 2007). Findings from the present study highlighting climate-induced habitat losses, add to the existing concerns raised by these previous studies. Overall, the BEM change maps (Fig. 4), and percentages of loss in the climatically suitable area (Table 4), do speak about the Galliformes habitats in the Himalayan arc becoming climatically unsuitable under the predicted warming and fluctuating precipitation. Strengthening of the protected area networks for the conservation of Galliformes and other fauna reverberates as a key recommendation throughout the Galliformes literature (Kaul et al., 1995; Ramesh et al., 1999; Fuller et al., 2000; Hussain et al., 2001; Jayapal et al., 2007).

## 5. Conclusion

The SDMs function as informative maps for management purposes and act as precursors for developing wildlife protection strategies. Using multiple SDMs maps of many species may be a cumbersome and exhaustive task for planners. In this light, clustered SDMs highlighting the spatial distributions of multiple species in a single SDM map may bring ease into the decision-making process. Cluster-based distribution modelling approach may work as a key to understanding the distribution patterns of data deficient, rare and elusive species. In this study, clustering of the Galliformes species in the Himalayan arc could be achieved, and both SDMs and BEMs were generated that would prove useful for taking early action in species conservation and management. To the best of our knowledge, no researcher has tested the efficiency of the multispecies model for Galliformes, and this is the first attempt to model distributions of Himalayan Galliformes at a pan Himalayan scale, with use of proxy data borrowed from archetypal cohorts of similar species-environment relationships. The findings of the present study will help in advancing the understanding of Galliformes of the Himalayas and thereby, aid in formulating future conservation strategies.

## 6. Data Accessibility Statement

The occurrences and habitat variables used in this study which were sourced from open databases, have been cited with their download links. Field data generated by the authors of this study may be available upon request.

## Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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## Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.crm.2020.100264.

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