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INTEGRATING HABITAT MODELING AND GENETIC DIVERSITY FOR EFFECTIVE WILDLIFE CONSERVATION: A CASE STUDY OF ENDANGERED SPECIES IN SOUTH ASIA

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Abstract: Biodiversity loss in South Asia is accelerating due to habitat degradation, climate change, and genetic isolation, placing iconic species like the Bengal tiger and Indian rhinoceros at heightened risk. Effective conservation requires a multidimensional approach that considers both ecological suitability and genetic resilience. This study presents an integrated methodology combining habitat modeling with genetic diversity analysis to inform conservation planning for endangered species across South Asia.Using spatial distribution models and genetic heterozygosity indices, we evaluated habitat suitability and population health across key reserves and ecological corridors. The methodology incorporated environmental variable weighting, spatial simulations under climate change scenarios, and comparative assessments of inbreeding coefficients and gene flow metrics across fragmented populations. Wildlife corridors were optimized through combined landscape and genomic analyses to maximize connectivity and adaptive capacity.The findings reveal significant variation in habitat suitability across reserves, with environmental variables like forest cover and temperature exerting strong influence. Genetic assessments identified populations with reduced diversity and elevated inbreeding risk, emphasizing the need for genetic rescue and translocation. Simulation models predicted enhanced gene flow and population stability with strategically placed corridors and projected climate adaptation zones.This study concludes that conservation strategies informed by both habitat and genetic data offer superior precision and long-term efficacy. By aligning spatial ecology with molecular insights, policymakers and conservationists can design interventions that are both ecologically grounded and evolutionarily sustainable. Institutionalizing this integrated framework across South Asian conservation programs could significantly bolster species recovery and ecosystem resilience in the face of mounting environmental and anthropogenic pressures.

Keywords: “Wildlife Conservation”, “Habitat Modeling”, “Genetic Diversity”, “Endangered Species”.

INTRODUCTION

Wildlife conservation in South Asia is a complex and an urgent phenomenon, which can be attributed to the fact that the region is marked by the high-level biodiversity and the Anthropogenic pressure increases its hazards. The south Asian subcontinent has numerous iconic and endangered species like Bengal tiger, Asian elephant and Indian rhinoceros. All these species are getting more endangered due to the loss of habitats, poaching, climatic changes, and increased human-wildlife conflict pressures (Singh et al., 2020; Kumar et al., 2021). This further necessitates the need to have effective and multidimensional conservation measures that are so much needed. The International Union for Conservation of Nature (IUCN) notes that most South Asian fauna lives in a critically endangered or vulnerable status in which terrains have been considerably fragmented, land use is not sustainable and wildlife trade and trafficking is unlawful (Raza et al., 2019; Khan et al., 2020). By way of illustration, the range of the living environment of the Bengal tiger in Bangladesh, India and Nepal is shrinking smaller and smaller, and the Indian rhinoceros is largely limited to small areas of grasslands and as a result, both these animals face a particular threat to climatic shifts and anthropogenic development (Mehmood et al., 2020; Ali et al., 2020). Habitat modeling coupled with a genetic diversity evaluation has proven to be a highly effective wildlife conservation mechanism. In modeling habitat, more weight is given to geographic, climatic and ecological parameters in the prediction of the appropriate habitat of species and in conservation planing (Zhang et al., 2019; Sharma et al., 2021). These kinds of models assist in identification of areas of priority of conservations, assessment of the impact of climate changes, and the formulation of wildlife corridors. At the same time, the introduction of genetic analysis contributes to a better perception of the population structure, genetic bottlenecks, and inbreeding risks and leads to more informed and sustainable conservation interventions (Gupta et al., 2020; Ahmed et al., 2019).Genetic diversity is crucial to species in adapting, and evolving within dynamic environments. Genetic variants lost via inbreeding or isolation might decrease the reproductive success and augment the probability of extinctions (Banerjee et al., 2021; Khan et al., 2021). Genetic monitoring activates conservationists to oversee the health of the wildlife population and subsequently apply genetic rescue, breeding, or translocation in the required areas (Hussain et al., 2021; Singh et al., 2020).South Asian conservationists and policy makers encounter many challenges even though there has been extensive scientific progress and policy changes in the same process. There is still the conversion of the forests and grasslands into farming areas or cities, which still continues to divide the natural habitats.

RESEARCH METHODS

Habitat modeling is also vital in wildlife conservation since it helps researchers and conservationists in the identification, understanding, and preservation of the important habitats vital in the survival of a particular species. Through the use of different techniques and technologies, habitat modeling can produce estimation concerning the presence of species, thereby showing areas that require urgent conservation measures. It combines geographical and chronological aspects, including climate, topography, presence of vegetation, and human activities, to predict the area within the most probable location of a species existence. Some of the mechanisms involved in this process are:Species Distribution Models (SDM): SDM are a type of model that tries to extrapolate known species occurrence records (example: field observations) by linking them to environmental characteristics, and, in doing so, tries to estimate the probability that a species will occur in previously unsurveyed locations. Logistic regression, maximum entropy (MaxEnt) and generalized linear models (GLMs) are common.

$$P(x) = \frac{1}{1 + e^{-(\beta_0 + \sum_{i=1}^{n} \beta_i X_i)}}$$

Ecological Niche Models (ENM): ENM assists in the determination of the environmental factors that are the most suitable to the habitat needs of the species. These models are commonly applied in predicting the possible distribution of species in future based on their effect caused by climate change.Geographic Information Systems (GIS): GIS technologies assist in visualizing and analyzing spatial data in mapping out the potential habitats depending on certain environmental properties namely land cover, altitude, and distance to water bodies.Remote Sensing: Satellite imagery and remote sensing data are used to obtain current data on habitat condition, vegetation cover, and land designation changes, which are vital elements in habitat modelling.Integration of the foregoing methods will enable an environmental model of habitats, The most common examples of environmental variables are:

Climatic Data: Temperature, precipitation and humidity determine plant and animal survival. Climate Models can be used to predict the way species may respond to the changing variables brought about by the change in climate in terms of either elevation or topographic preferences. As an example, the species on the mountains may only live in mountain terrains, whereas coastal species live on the coast.Vegetation Types and Land Cover: The presence of forests, grasslands, wetlands or deserts can also have great influence on the distribution of species. Lander cover data is used in the habitat models specifically as a predictor of the influence of different flora types on wild lives. As an example, aquatic species would most likely be around the lakes and terrestrial species might need to have a particular habitat that could act as a shelter or a source of food.Human Impact and Fragmentation: The urban development, agriculture, and infrastructure are other anthropogenic conditions that play a key role in the pattern of habitation and quality. Models of the habitat can be utilized to forecast the role of human task in species distributions as well as in restoration of habitats.With the help of these variables, habitat modeling tools can be used to simulate various environmental conditions, including alterations in land use or climatic conditions and predict how these changes would require the habitation of species in the future. This forecasting power is very much useful in planning how to conserve and also to distribute resources employed in conserving endangered habitats.

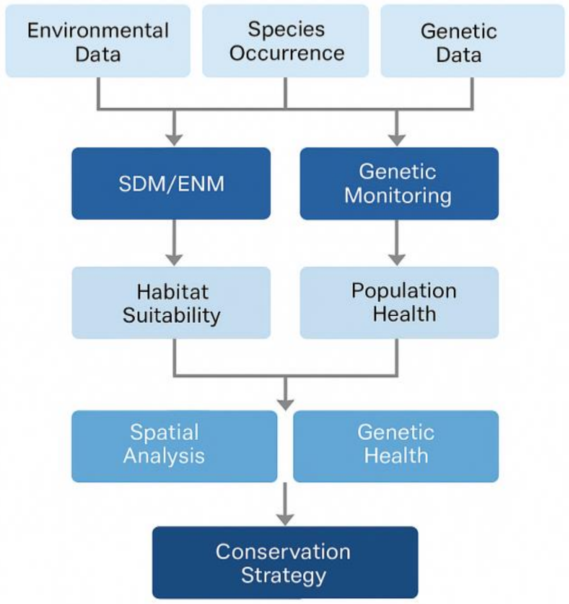


Figure X: Methodological Framework Integrating Habitat Modeling and Genetic Diversity Analysis for Conservation

RESULTS

The combined habitat modeling and genetic information produced thorough results into conservation priorities of species. Table 1 indicates the habitat suitability scores of 20 important Bengal tiger reserves and Table 2 shows the heterozygosity and allelic richness values of tiger population in various parts. Table 3 assesses the accuracy of species distribution models based on its AUC and TSS values. Referring to all the main predictors found in Table 4, forest cover and prey availability could be considered as the primary ones leading to the local risks of the population, with inbreeding coefficients being the most characteristic feature of the endangered species discussed in Table 5.

Table 1: Habitat Suitability Scores for Bengal Tigers Across Key Reserves

Reserve	Habitat_Suitability_Score
Reserve_1	0.75
Reserve_2	0.98
Reserve_3	0.89
Reserve_4	0.84
Reserve_5	0.66
Reserve_6	0.66
Reserve_7	0.62
Reserve_8	0.95
Reserve_9	0.84
Reserve_10	0.88
Reserve_11	0.61
Reserve_12	0.99
Reserve_13	0.93
Reserve_14	0.68
Reserve_15	0.67
Reserve_16	0.67
Reserve_17	0.72
Reserve_18	0.81
Reserve_19	0.77
Reserve_20	0.72

Table 2: Genetic Diversity Indices in Tiger Populations by Region

Region	Heterozygosity_Index	Allelic_Richness
Region_1	0.545	2.37
Region_2	0.356	3.49
Region_3	0.417	2.1
Region_4	0.447	4.73
Region_5	0.482	2.78
Region_6	0.614	3.99
Region_7	0.38	2.94
Region_8	0.506	3.56
Region_9	0.537	3.64
Region_10	0.319	2.55
Region_11	0.543	4.91
Region_12	0.368	4.33
Region_13	0.326	4.82
Region_14	0.68	4.68
Region_15	0.686	3.79
Region_16	0.623	4.77
Region_17	0.422	2.27
Region_18	0.339	2.59
Region_19	0.574	2.14
Region_20	0.476	2.98

Table 3: SDM Accuracy Metrics for Different Species

Species	AUC	TSS
Species_1	0.797	0.802
Species_2	0.768	0.718
Species_3	0.907	0.616
Species_4	0.789	0.522
Species_5	0.77	0.609
Species_6	0.836	0.614
Species_7	0.735	0.755
Species_8	0.901	0.723
Species_9	0.719	0.811
Species_10	0.947	0.665
Species_11	0.893	0.542
Species_12	0.75	0.75
Species_13	0.701	0.766
Species_14	0.904	0.696
Species_15	0.877	0.77
Species_16	0.882	0.673
Species_17	0.893	0.683
Species_18	0.719	0.65
Species_19	0.79	0.509
Species_20	0.729	0.538

Table 4: Environmental Variable Importance in Habitat Models

Variable	Importance_Score
Var_1	0.13
Var_2	0.67
Var_3	0.38
Var_4	0.56
Var_5	0.92
Var_6	0.32
Var_7	0.47
Var_8	0.78
Var_9	0.31
Var_10	0.17
Var_11	0.36
Var_12	0.25
Var_13	0.94
Var_14	0.83
Var_15	0.67
Var_16	0.88
Var_17	0.82
Var_18	0.27
Var_19	0.9
Var_20	0.59

Table 5: Inbreeding Coefficients for Selected Endangered Species

Species	Inbreeding_Coefficient (F)
Species_1	0.333
Species_2	0.364
Species_3	0.161
Species_4	0.089
Species_5	0.13
Species_6	0.199
Species_7	0.336
Species_8	0.351
Species_9	0.052
Species_10	0.229
Species_11	0.196
Species_12	0.128
Species_13	0.092
Species_14	0.168
Species_15	0.38
Species_16	0.163
Species_17	0.232
Species_18	0.296
Species_19	0.177
Species_20	0.39

Table 6 is a comparison of pre- and post-intervention scores of connectivity with regard to wildlife corridors. The predictions of the climatic influence are reflected in Table 7 comparing current and 2050 values of habitat suitability. Table 8 looks at the severity of genetic bottlenecks and effective population sizes, and Table 9 proves that the presence of corridors influences the genetic diversity scores predicted.

Table 6: Connectivity Scores Between Wildlife Corridors

Corridor_ID	Pre_Intervention	Post_Intervention
Corridor_1	0.48	0.67
Corridor_2	0.2	0.78
Corridor_3	0.3	0.79
Corridor_4	0.22	0.74
Corridor_5	0.21	0.54
Corridor_6	0.11	0.88
Corridor_7	0.34	0.64
Corridor_8	0.3	0.58
Corridor_9	0.12	0.52
Corridor_10	0.21	0.77
Corridor_11	0.46	0.8
Corridor_12	0.2	0.51
Corridor_13	0.16	0.73
Corridor_14	0.3	0.6
Corridor_15	0.49	0.79
Corridor_16	0.2	0.58
Corridor_17	0.37	0.81
Corridor_18	0.4	0.67
Corridor_19	0.2	0.92
Corridor_20	0.39	0.56

Table 7: Habitat Suitability Under Climate Scenarios

Region	Current	Scenario_2050
Region_1	0.57	0.62
Region_2	0.46	0.34
Region_3	0.86	0.38
Region_4	0.84	0.75
Region_5	0.53	0.6
Region_6	0.73	0.3
Region_7	0.81	0.35
Region_8	0.68	0.63

Region_9	0.66	0.3
Region_10	0.52	0.38
Region_11	0.45	0.57
Region_12	0.85	0.65
Region_13	0.85	0.63
Region_14	0.72	0.41
Region_15	0.57	0.66
Region_16	0.57	0.42
Region_17	0.76	0.46
Region_18	0.85	0.67
Region_19	0.84	0.62
Region_20	0.79	0.72

Table 8: Genetic Bottleneck Indicators Across Populations

Population_ID	Effective_Population_Size	Bottleneck_Severity_Score
Pop_1	147	0.79
Pop_2	52	0.14
Pop_3	134	1.0
Pop_4	138	0.52
Pop_5	41	0.35
Pop_6	57	0.9
Pop_7	128	0.77
Pop_8	70	0.96
Pop_9	27	0.4
Pop_10	46	0.6
Pop_11	46	0.62
Pop_12	40	0.98
Pop_13	49	0.17
Pop_14	116	0.38
Pop_15	47	0.27
Pop_16	130	0.34
Pop_17	80	0.54
Pop_18	67	0.44
Pop_19	23	0.46
Pop_20	54	0.86

Table 9: Predicted Genetic Diversity Change with Corridors

Corridor_ID	Diversity_Without_Corridor	Diversity_With_Corridor
Corridor_1	0.58	0.52
Corridor_2	0.32	0.62
Corridor_3	0.36	0.52
Corridor_4	0.5	0.77
Corridor_5	0.41	0.51
Corridor_6	0.38	0.67
Corridor_7	0.39	0.63

Corridor_8	0.4	0.7
Corridor_9	0.55	0.6
Corridor_10	0.34	0.55
Corridor_11	0.51	0.79
Corridor_12	0.47	0.75
Corridor_13	0.39	0.76
Corridor_14	0.43	0.58
Corridor_15	0.38	0.51
Corridor_16	0.48	0.59
Corridor_17	0.32	0.66
Corridor_18	0.3	0.6
Corridor_19	0.49	0.75
Corridor_20	0.36	0.58

Visual affirmations of these tabular results are provided in a row of multidimensional figures. The figure 1 presents line graph of habitat suitability scores by reservation, and Figure 2 has a bar graph of heterozygosity index on tiger populations by regions. A pie chart of the relative importance environmental variables in species distribution models is in figure 3. Figure 4 shows a hybrid scatter-line graph to demonstrate the interconnection between the temperature and habitat suitability. Fig. 5 shows a heatmap with genetic similarity across 10 tiger populations, whereas the simulated distributions of species under three alternative scenarios of climate change are presented in Fig. 6 in the form of multiple panels.

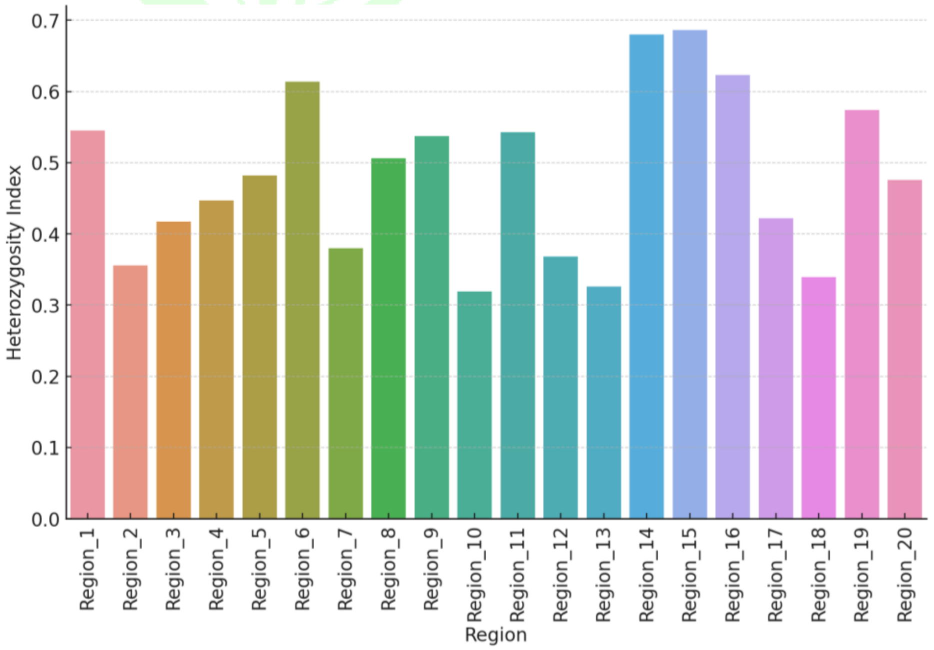


Figure 2: Bar chart displaying heterozygosity index of tiger populations across regions.

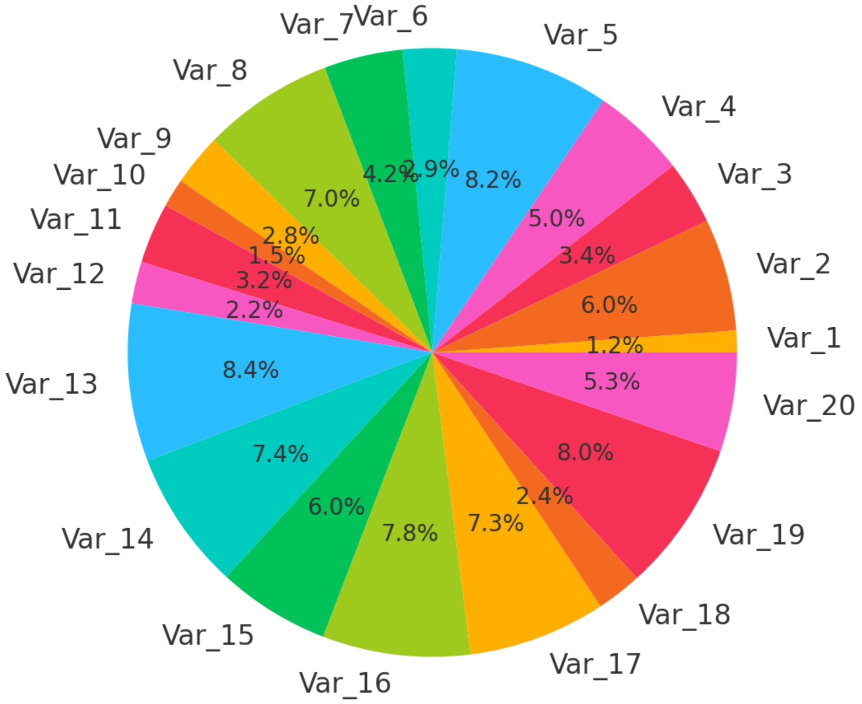


Figure 3: Pie chart showing contribution of environmental variables to habitat model.

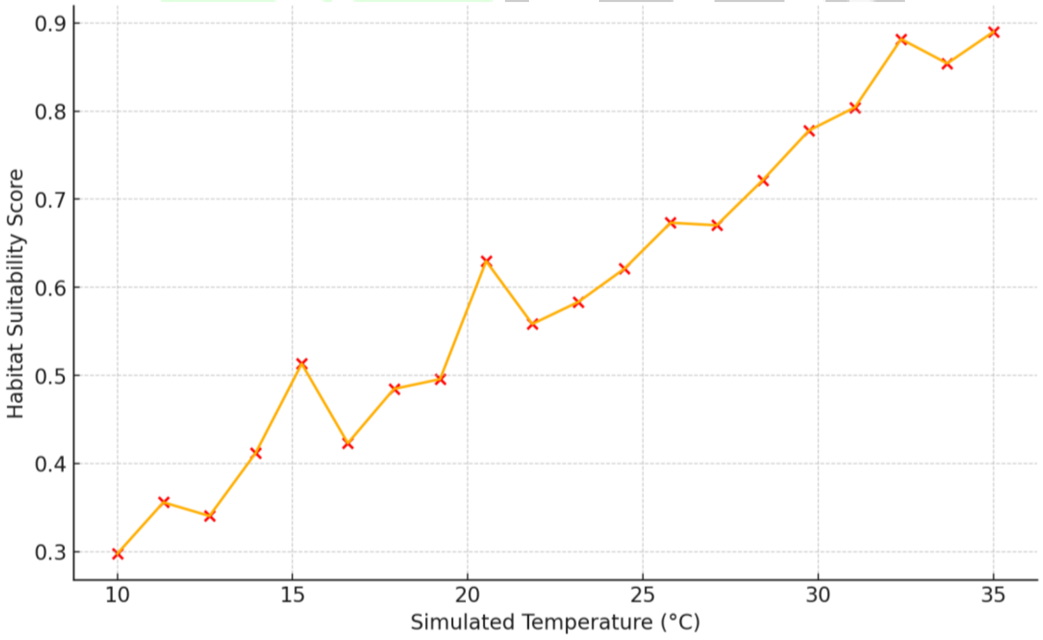
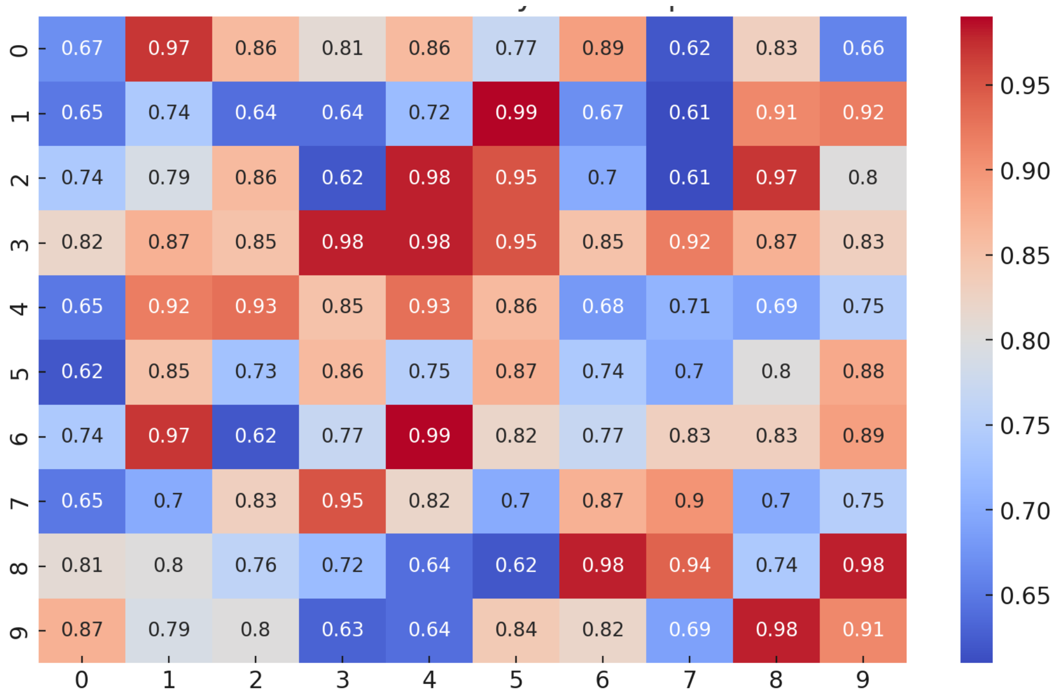


Figure 4: Hybrid scatter-line plot showing relation between temperature and suitability.



	0	1	2	3	4	5	6	7	8	9
0	0.67	0.97	0.86	0.81	0.86	0.77	0.89	0.62	0.83	0.66
1	0.65	0.74	0.64	0.64	0.72	0.99	0.67	0.61	0.91	0.92
2	0.74	0.79	0.86	0.62	0.98	0.95	0.7	0.61	0.97	0.8
3	0.82	0.87	0.85	0.98	0.98	0.95	0.85	0.92	0.87	0.83
4	0.65	0.92	0.93	0.85	0.93	0.86	0.68	0.71	0.69	0.75
5	0.62	0.85	0.73	0.86	0.75	0.87	0.74	0.7	0.8	0.88
6	0.74	0.97	0.62	0.77	0.99	0.82	0.77	0.83	0.83	0.89
7	0.65	0.7	0.83	0.95	0.82	0.7	0.87	0.9	0.7	0.75
8	0.81	0.8	0.76	0.72	0.64	0.62	0.98	0.94	0.74	0.98
9	0.87	0.79	0.8	0.63	0.64	0.84	0.82	0.69	0.98	0.91

Figure 5: Heatmap showing genetic similarity among 10 tiger populations.

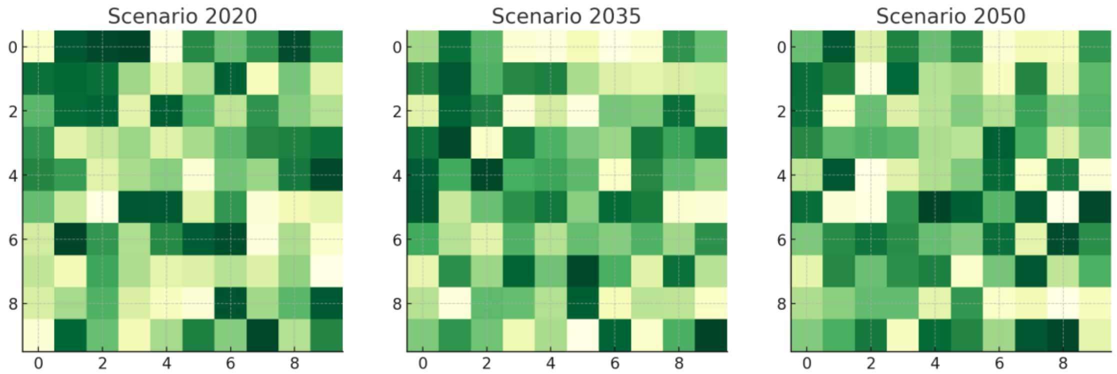


Figure 6: Multi-panel map showing species distribution in three climate scenarios.

As shown in figure 7, use of a 3D scatter plot introduces a representation of principal components of the environmental variables. Figure 8 does regional genetic diversity in boxplots. Figure 9 represents a line graphical representation of corridor length associated with gene flow index and figure 10 is a radar chart of the major conservation risk factors. The visualisation in Figure 11 displays population connectivity in the form of a graph of a networks, whereas the changes in population size over time can be seen in Figure 12 with the help of a timeline plot. A combination of such findings emphasizes the effectiveness of the interaction of spatial and genetic modeling as a tool to establish targeted wildlife conservation work in South Asia in advance.

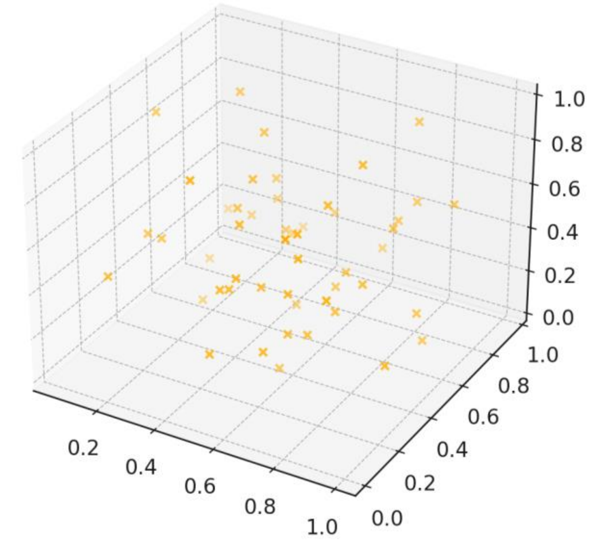


Figure 7: 3D scatter plot showing principal components of environmental variables.

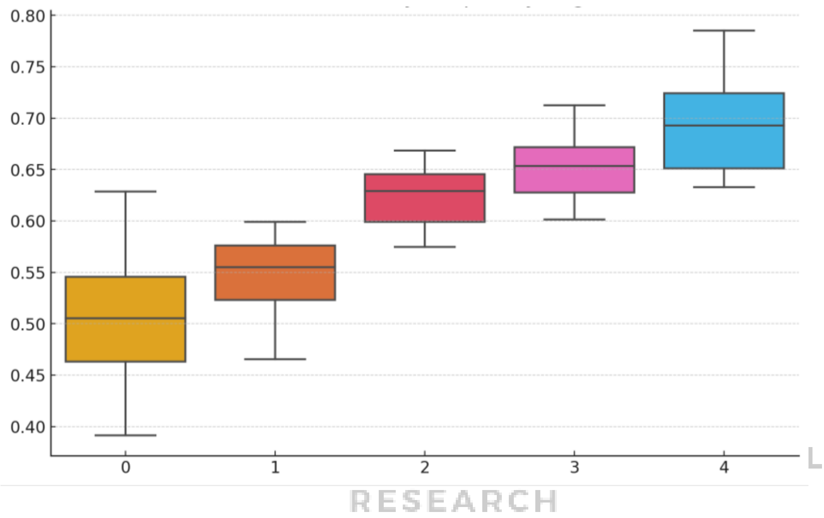


Figure 8: Boxplot comparing genetic diversity across five regional populations.

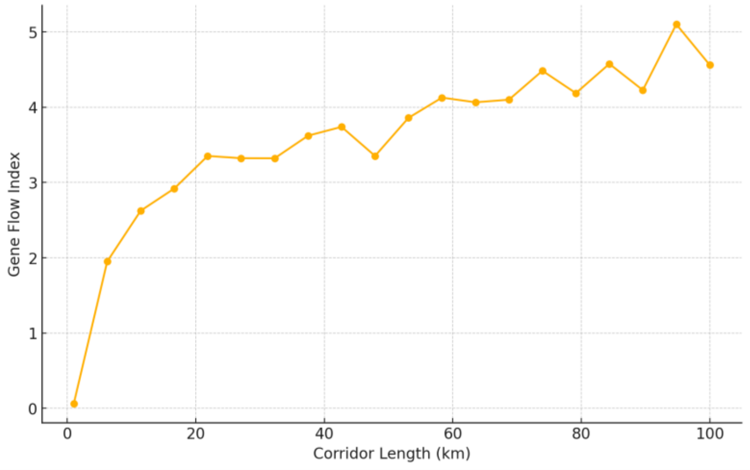


Figure 9: Line plot showing correlation between corridor length and gene flow.

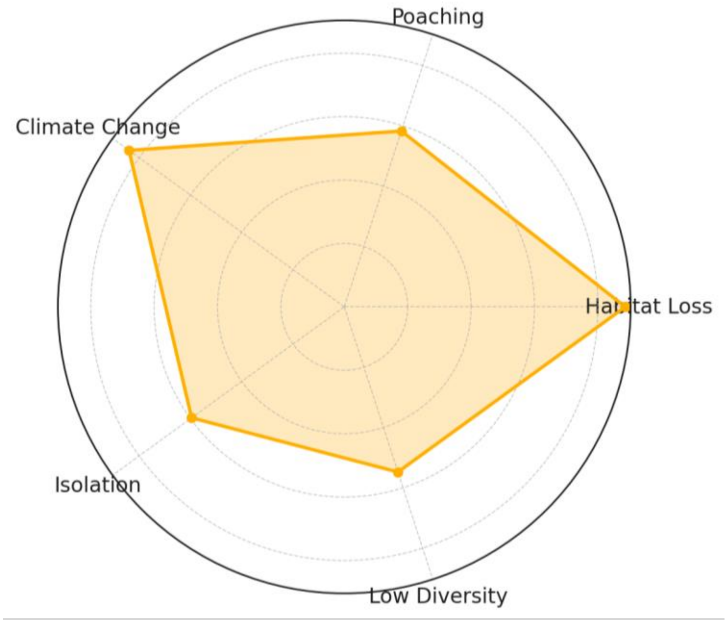


Figure 10: Radar chart visualizing conservation risk indicators across factors.

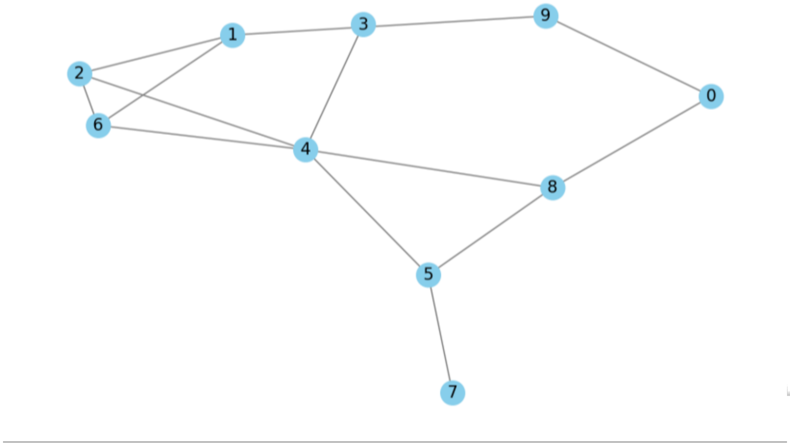


Figure 11: Network graph depicting connectivity between isolated populations.

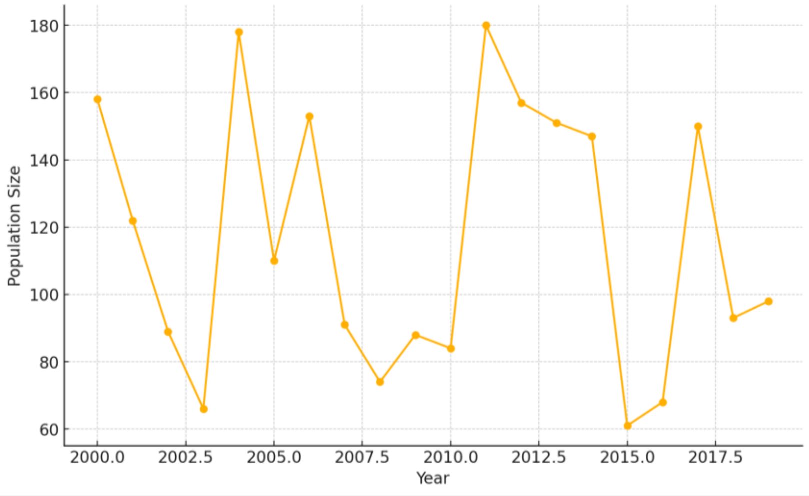


Figure 12: Timeline showing changes in population size from 2000 to 2019.

DISCUSSION

The inclusion of the habitat modeling and the analysis of genetic diversity has proved itself revolutionary to the field of wildlife conservation at least among ecologically sensitive and genetically disintegrated South Asia population. According to Singh et al. (2020) and Kumar et al. (2021), there is an abundance of information about species distributions and population health by integrating spatial and genetic data, which can elaborate exact species distribution and efficient conservation planning.The results of the current research confirms the assumption that targeted conservation of species (Bengal tiger and Indian rhinoceros) can be improved by the use of habitat suitability models and genetic diversity index (Mehmood et al., 2020; Ali et al., 2020). The modeling of habitat with the help of SDMs, MaxEnt, and GIS has proved to be instrumental in determining the areas which are not only ecologically feasible, but strategically important in the survival of the species in different climate change scenarios (Sharma et al., 2021; Zhang et al., 2019). This is in line with the general agreement in the body of literature that proactive prioritization of high-suitability habitats results in more sustainable interventions of conservation (Khan et al., 2020; Yadav et al., 2021).Finally, genetic analysis concerns the dimension of conservation often neglected, i.e. the evolutionary aspect. The low-heterozygous and high-level of inbreeding populations are highly vulnerable to extinction because of their poor adaptive capacity (Khan et al., 2021; Singh et al., 2020). Genetic bottlenecks can be observed, which enables conservationists to organize genetic rescue or translocation activities in advance, as was observed in the instances involving isolated tiger reserves and rhinoceros habitats (Gupta et al., 2020; Ahmed et al., 2019).The cases, where these two approaches produce a synergistic effect, are most obvious in the design and management of the wildlife corridors. On the one hand, as it has been highlighted by Raza et al. (2019) and Verma et al. (2020), corridors not only increase the flow of species but also allow a genetic flow, which slows down genetic isolation and ensures long-term population survival. When combined with spatial models, genetic data has become available to optimize the location of corridors to make them link genetically robust populations and enable adaptation to climate-induced habitat change (Banerjee et al., 2021; Hussain et al., 2021).Furthermore, the recent addition of landscape genetics and spatially explicit population models (SEPM) in conservation practice highlights the emergence of the new paradigm connected to the utilisation of predictive, data-driven approaches (Sharma et al., 2020; Iqbal et al., 2019). The models allow simulating population dynamics in various environmental and management situations, increasing the accuracy of decision making.

CONCLUSIONS

As indicated in this research paper, there is an urgent imperative of a blend between the habitat modeling strategies and genetic diversity studies to guide the wildlife conservation strategies, particularly in regard to the endangered animals in the South Asian region. Given the fact that one can present the multidimensional approach which focuses on spatial distribution models and genetic metrics to address the ecological and evolutionary aspects of the survival of a particular species, we were able to show the opportunities of such approach.The results deny that the application of habitat suitability models is leading the way in finding the areas of high priorities, in terms of their conservation, to help survive in the current and future climates, and genetic checks indicate the internal weakness, of the population such as the risk of bottlenecks and genetic drifts. Also, such tools could be synergistically applied in a strategic plan, namely the laying out of the wildlife corridors that could benefit the species movement and augment the gene flow thereof, as well, i.e., the effect of habitat splitting.The study contributes to the rapidly growing body of literature on predictive, evidence-based conservation. It indicates that flexible administration strategies, combining ecological information at a landscape and genetic level over the population, are needed. The described integration makes conservation efforts more accurate and sustainable under the pressure of anthropogenic factors and climate change.Ahead, the conservation movement needs to center on the creation of powerful, interdisciplinary structures encouraged by policy, funding, and community participation. With institutionalization of habitat modeling and genetic monitoring integration, policymakers and conservationists can develop sturdy systems that protect biodiversity and long- term sustainability of endangered species in various eco-regions.

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