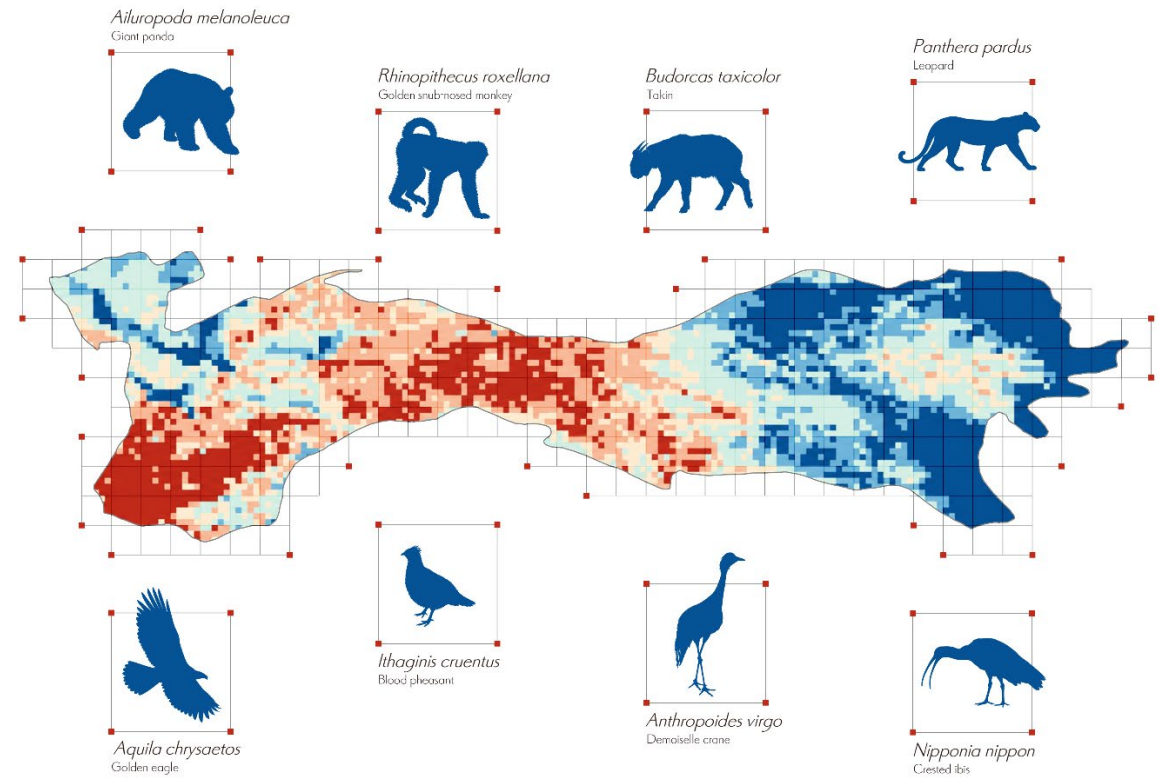
Spatial patterns, driving mechanisms, and priority areas for multidimensional biodiversity in the Qinling Mountains

MengHui Wei





S.T. Yau High School Science Award

Research Report

The Team

Name of team member: Menghui Wei
School: Princeton International School of Mathematics and Science
City, Country: Princeton, New Jersey, USA

Name of supervising teacher: Huizhong Fan
Job Title: Professor
School/Institution: Institute of Zoology, Chinese Academy of Sciences
City, Country: Beijing, China

Name of supervising teacher: Tong Mu
Job Title: Associate Research Scholar
School/Institution: Princeton School of Public and International Affairs, Princeton University
City, Country: Princeton, New Jersey, USA

Title of Research Report

Spatial patterns, driving mechanisms, and priority areas for multidimensional biodiversity in the Qinling Mountains

Date

September 10, 2026

Spatial patterns, driving mechanisms, and priority areas for multidimensional biodiversity in the Qinling Mountains

Menghui Wei

Abstract

The Qinling Mountains form a critical north–south climatic divide and a major faunal transition zone between the Palaearctic and Oriental realms, supporting rich terrestrial vertebrate diversity. Based on 470,025 occurrence records of 941 species, this study mapped the spatial patterns of taxonomic diversity (TD), phylogenetic diversity (PD), and genetic diversity (GD) at 5 km resolution across the Qinling Mountains and adjacent ecoregions. Results revealed a pronounced south-to-north declining gradient in multidimensional biodiversity. Within the mountain range, TD and PD decreased from west to east, while GD showed a distinct spatial decoupling. These patterns were primarily driven by annual mean precipitation (AMP), elevational range (DEM), and the Normalized Difference Vegetation Index (NDVI). To achieve the 50% protection target under the Kunming-Montreal Global Biodiversity Framework and the Half-Earth Concept, a systematic conservation planning framework was applied to jointly optimize multidimensional biodiversity representation while minimizing socioeconomic impacts. The identified priority areas avoid croplands and built-up land and form a spatially aggregated network adjoining existing protected areas, thereby increasing overall habitat protection for terrestrial vertebrates by 13.0% while affecting only an additional 1.9% of regional socioeconomic activity. This study provides a scalable blueprint for PA network expansion in the Qinling Mountains, offering a model that balances biodiversity conservation with socioeconomic development.

Keywords: Qinling Mountains, Multidimensional biodiversity, Protected areas, Driving mechanisms

Acknowledgement

This study was primarily motivated by my long-standing curiosity about the diverse forms of life on Earth. I still remember walking through the bamboo forests of the Qinling Mountains, looking carefully between the trees and hoping to catch a glimpse of a wild giant panda. I had first visited Foping Nature Reserve in 2015, but during my second trip in 2018, I finally saw one. For a child who had mostly known pandas from pictures and television, seeing one in its natural habitat was unforgettable.

Growing up, I often heard the ancient Chinese saying, “Oranges grown south of the Huai River become bitter trifoliate oranges when grown north of it (橘生淮南则为橘，生于淮北则为枳).” At first, it was simply an interesting saying. Later, when I learned in middle school that the Qinling Mountains and Huai River form an important geographical and climatic boundary between northern and southern China, I began to understand the science behind it. Why could the same country contain such different landscapes, plants, and animals? How did mountains and climate shape where species lived? These questions stayed with me.

As I took more field trips across the Qinling Mountains, those questions became more specific. I saw mountains, rivers and forests change as we traveled from one area to another. I participated in field surveys, set mouse traps and cages, talked with local villagers about wildlife, and gradually realized that biodiversity was something I could not only observe, but also study. These experiences eventually led to this research project.

However, curiosity alone was not enough to turn an idea into research. I am especially grateful to my advisor, Dr. Huizhong Fan, whom I met through the Beijing Youth Science and Technology Club. When I began working with him, many parts of scientific research were completely new to me. He taught me how to turn a broad question into something that could

actually be studied, how to collect and organize species data, and how to use R to analyze biodiversity.

I remember being particularly frustrated when some of my raster data simply would not work. I had tried different approaches but could not understand what was wrong. Instead of fixing the problem for me, Dr. Fan showed me how to examine the files carefully, one property at a time. Eventually, I discovered that the coordinate reference systems did not match. It was a small technical problem, but solving it taught me something much larger: research is often less about immediately knowing the answer than about learning how to find it.

I am also grateful to Dr. Tong Mu from Princeton University, whom I met when I entered ninth grade at the Princeton International School of Mathematics and Science. His lessons on biogeography and macroecology introduced me to ideas such as latitudinal diversity gradients and helped me see my observations from the Qinling Mountains in a much broader context. He later helped me improve my species distribution data and patiently pointed out problems in my figures and scientific terminology. Through his guidance, I began to understand how much precision matters in science.

My project also would not have reached this point without the teachers at the Research Club of the High School Affiliated to Renmin University of China and the Beijing Youth Science and Technology Club, especially Mr. Keke Fan. When I was in seventh and eighth grade, many of my “research questions” were really just things I happened to notice and wonder about. My teachers encouraged me to keep asking those questions, but they also challenged me to think about how I could test them. Slowly, my observations became hypotheses, and my curiosity became a research project.

Finally, I want to thank my parents. They supported my field trips, my research, and the many hours I spent working on something that began simply because I was curious about

mountains, animals, and an old Chinese saying. More importantly, they gave me the freedom to explore interests beyond what I learned in the classroom.

Looking back, this project has changed the way I think about science. I began with a simple question about why different environments support different forms of life. Along the way, I learned how to collect data, write code, solve unexpected problems, interpret results, and communicate what I found. But perhaps the most important lesson was learning that science begins with curiosity and grows through the patience and generosity of people willing to guide you.

I am grateful to everyone who helped turn my curiosity into something I could investigate for myself. Their support has made me want not only to continue exploring the natural world, but also, one day, to offer the same encouragement to someone else who begins with a question.

The study received no external funding. AI tools were used only for English grammar checking, language polishing and cover design during manuscript preparation. All academic guidance was provided voluntarily and without compensation. The Institute of Zoology, Chinese Academy of Sciences, provided computing resources free of charge.



My first field trip to Foping Nature Reserve, south of the Qinling Mountains in 2015



Searching the wild giant panda in the dense bamboo forest during my second field trip to Foping Nature Reserve, in southern Qinling Mountains in 2018



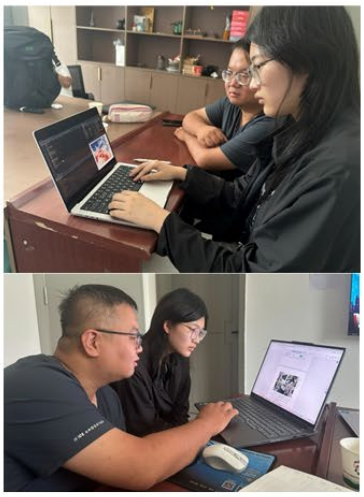
Field survey using mouse traps and cages in Zhouzhi Nature Reserve, in northern Qinling Mountains



Questionnaire survey of species distribution with local villagers during field survey in Zhouzhi Nature Reserve, in northern Qinling Mountains



Field survey with my supervisor Dr. Huizhong Fan in Changqing Nature Reserve, in southern Qinling Mountains



Discussion with my supervisor Dr. Huizhong Fan from the Institute of Zoology, Chinese Academy of Science



Field survey training with my supervisor Dr. Huizhong Fan in Foping Nature Reserve, in southern Qinling Mountains



Discussion with my supervisor Dr. Tong Mu from Princeton University

Commitments on Academic Honesty and Integrity

We hereby declare that we

1. are fully committed to the principle of honesty, integrity and fair play throughout the competition.
2. actually perform the research work ourselves and thus truly understand the content of the work.
3. observe the common standard of academic integrity adopted by most journals and degree theses.
4. have declared all the assistance and contribution we have received from any personnel, agency, institution, etc. for the research work.
5. undertake to avoid getting in touch with assessment panel members in a way that may lead to direct or indirect conflict of interest.
6. undertake to avoid any interaction with assessment panel members that would undermine the neutrality of the panel member and fairness of the assessment process.
7. observe the safety regulations of the laboratory(ies) where we conduct the experiment(s), if applicable.
8. observe all rules and regulations of the competition.
9. agree that the decision of YHSA is final in all matters related to the competition.

We understand and agree that failure to honour the above commitments may lead to disqualification from the competition and/or removal of reward, if applicable; that any unethical deeds, if found, will be disclosed to the school principal of team member(s) and relevant parties if deemed necessary; and that the decision of YHSA is final and no appeal will be accepted.

(Signatures of full team below)

X Menghui Wei

Name of team member: Menghui Wei

X Huizhong Fan

Name of supervising teacher: Huizhong Fan

X Tong Mu

Name of supervising teacher: Tong Mu

Table of Contents

1. Introduction 1

1.1 From Taxonomic Diversity to Multidimensional Biodiversity 2

1.2 Environmental Factors Associated with Biodiversity Patterns 2

1.3 Spatial Mismatch and Conservation Trade-offs 3

1.4 Study Design and Significance 3

1.5 Research Objectives 4

2. Materials and Methods 4

2.1 Species Distribution Modelling 4

2.1.1 Georeferenced Data Collection 4

2.1.2 Environmental Variables for ESMs 5

2.1.3 Mapping Species Distributions with ESMs 5

2.2 Multidimensional Biodiversity Mapping 7

2.2.1 Taxonomic Diversity 7

2.2.2 Phylogenetic Diversity 7

2.2.3 Genetic Data Acquisition and Estimation of Genetic Diversity 7

2.3 Driving Factors of Biodiversity Patterns 8

2.4 Systematic Conservation Planning for the Qinling Mountains 9

2.4.1 Current PA System and Socioeconomic Data Collection 9

2.4.2 Identification of Conservation Priority Gap 9

3. Results 10

3.1 Data Sources 10

3.2 Multidimensional Biodiversity Patterns in the Qinling Mountains and Adjacent Regions 10

3.3 The Qinling Mountains as a Biogeographic Transition Zone 12

3.4 Environmental Factors Related to Biodiversity Patterns 15

3.5 Optimizing the Protected Area Network 16

4. Discussion 18

4.1 Reassessing Spatial Biodiversity Patterns for Conservation in the Qinling Mountains: A Multidimensional Perspective 18

4.2 The Qinling Mountains as a Transition Zone 19

4.3 Improving Protected Areas in the Qinling Mountains 20

4.4 Limitations and Future Directions 21

Conflicts of Interest 22

References 23

Supplemental Figures 26

1. Introduction

The Qinling Mountains extend across central China from Gansu to Henan and form a major watershed between the Yangtze and Yellow River basins. They also mark an important climatic boundary between subtropical and warm-temperate China. Their steep elevational gradients, from low valleys to peaks above 3,000 m, create strong differences in temperature, precipitation, and vegetation (Meng et al., 2021; Xia et al., 2019). These environmental differences provide diverse habitats for many terrestrial vertebrates, including the giant panda (*Ailuropoda melanoleuca*), golden snub-nosed monkey (*Rhinopithecus roxellanae*), takin (*Budorcas taxicolor*), and crested ibis (*Nipponia nippon*). Because the Qinling Mountains lie between the Palaearctic and Oriental realms, they also provide a valuable natural system for studying how biodiversity changes across a major biogeographic transition.

The Qinling Mountains are widely recognized as an important conservation region. However, human activities such as infrastructure development, mining, pollution, and deforestation continue to cause habitat loss and fragmentation (Xie & Yao, 2024). Protected areas are therefore essential, but land and economic resources for conservation are limited. Previous conservation studies in the region have often focused on a small number of flagship species or on species richness alone (Zhang et al., 2017). Although these approaches are useful, they may overlook other important aspects of biodiversity, including evolutionary history and genetic variation.

This study therefore addresses three related questions: (1) how do different dimensions of terrestrial vertebrate biodiversity vary across the Qinling Mountains and surrounding regions; (2) which environmental factors are most strongly associated with these spatial patterns; and (3) can additional priority conservation areas be identified by combining multiple

biodiversity dimensions while also considering socioeconomic constraints?

1.1 From Taxonomic Diversity to Multidimensional Biodiversity

Taxonomic diversity (TD), usually measured as species richness, is widely used to identify biodiversity hotspots because it is simple and easy to interpret. However, species richness alone does not capture all aspects of biodiversity. Species differ in both their evolutionary history and their genetic variation. Phylogenetic diversity (PD) measures the amount of evolutionary history represented by a group of species (Faith, 1992), while genetic diversity (GD) reflects genetic variation within species and is related to their ability to respond to environmental change (Hu et al., 2021; Mastretta-Yanes et al., 2024).

PD and GD provide indispensable dimensions for comprehensive conservation planning. Indeed, an area with many species may not necessarily contain the greatest amount of evolutionary history or genetic variation. Therefore, integrating TD, PD, and GD provides a more complete picture of biodiversity and may identify important conservation areas that would be missed if only species richness were considered.

1.2 Environmental Factors Associated with Biodiversity Patterns

Climate, vegetation productivity, topography, and human activities influence biodiversity patterns (Liang et al., 2024). Temperature and precipitation affect physiological conditions and resource availability, while climatic stability may reduce environmental stress. Topographic complexity can increase habitat diversity, provide refuges, and separate populations (Jetz & Rahbek, 2001). In contrast, human activities can reduce biodiversity through habitat loss and fragmentation.

The Qinling Mountains contain strong climatic and elevational gradients over a relatively short geographic distance. This makes the region especially useful for comparing how different

environmental factors relate to taxonomic, phylogenetic, and genetic diversity.

1.3 Spatial Mismatch and Conservation Trade-offs

Different dimensions of biodiversity do not always reach their highest values in the same places. For example, an area with high species richness may not contain equally high phylogenetic or genetic diversity (Hu et al., 2021; Mazel et al., 2014). This spatial mismatch creates an important challenge for conservation planning.

Conservation decisions must also consider human land use and economic costs because protected areas cannot expand without limits. A practical conservation strategy should therefore protect complementary biodiversity features while reducing conflicts with agriculture, urban development, and other human activities. Integrating ecological value with socioeconomic constraints may help identify priority areas that are both biologically important and more feasible to protect.

1.4 Study Design and Significance

This study integrated taxonomic, phylogenetic, and genetic diversity for mammals, birds, reptiles, and amphibians across the Qinling Mountains and surrounding regions. First, the spatial patterns of these three biodiversity dimensions were mapped. Then, the environmental variables most strongly associated with each pattern were examined. Finally, a multi-objective conservation planning framework was used to identify additional priority areas while considering existing protected areas, land use, and socioeconomic constraints.

The main aim was to test whether a multidimensional approach could reveal conservation priorities that differ from those identified mainly by species richness or flagship species. By comparing several dimensions of biodiversity within the same spatial framework, this study provides a broader assessment of conservation value across the Qinling Mountains.

1.5 Research Objectives

The study had three main objectives: (i) to map the taxonomic, phylogenetic, and genetic diversity of terrestrial vertebrates; (ii) to identify the environmental variables most strongly associated with these spatial patterns; and (iii) to identify additional conservation priority areas that improve biodiversity coverage while limiting potential socioeconomic impacts.

For the conservation analysis, an aspirational scenario was examined in which 50% of the study area was included in the conservation network. This scenario was inspired by the Half-Earth Concept (Wilson, 2016) and was used as a planning exercise extending beyond the 30% conservation target of the Kunming-Montreal Global Biodiversity Framework.

2. Materials and Methods

2.1 Species Distribution Modelling

2.1.1 Georeferenced Data Collection

Georeferenced occurrence records for terrestrial vertebrates in the Qinling Mountains and adjacent regions were compiled from multiple repositories: the Global Biodiversity Information Facility (GBIF, https://www.gbif.org/; accessed November 2024), the National Animal Collection Resource Center (NACRC, http://museum.ioz.ac.cn/index.aspx), and citizen science data from iNaturalist (https://www.inaturalist.org/). To ensure data quality for subsequent biogeographic analyses, a rigorous quality control protocol was implemented. Records were excluded if they met any of the following criteria: (i) lacking valid taxonomic identifiers at the species level; (ii) were missing geospatial coordinates; (iii) with coordinates derived from unverified sources or those not validated by GRSciColl (Grosjean et al., 2022), (iv) with positional uncertainty exceeding 100 km; and (v) fossil specimens. For entries with fuzzy, small-scale georeferencing, locality names were standardized and converted into precise

geographic coordinates using the Baidu Geocoding API via the 'Remap' package (https://github.com/lchiffon/REmap).

All occurrence data were consolidated by removing duplicate records to produce a refined spatial dataset. Although inherent heterogeneity in sampling effort exists across regions and taxa, this integrated dataset represents the most comprehensive distribution data currently available for terrestrial vertebrates in the study area. To mitigate sampling bias, Ensembles of Small Models (ESMs) were employed to predict the potential distribution of each species (Breiner et al., 2015).

2.1.2 Environmental Variables for ESMs

A set of environmental variables recognized to influence terrestrial vertebrate distributions was selected (**Table S1**). The predictor set included 19 bioclimatic variables (BIO1–BIO19), growing degree days above 0°C, 5°C, and 10°C (gdd0, gdd5, gdd10), the number of growing degree days above these thresholds (ngd0, ngd5, ngd10), growing season length (gsl), mean temperature of the growing season (gst), and net primary productivity (npp). All data were sourced from CHELSA (version 2.1; https://chelsa-climate.org/) at a spatial resolution of 30 arc-seconds for the period 1981–2010. Environmental layers were resampled and projected onto a 5 km × 5 km equal-area grid covering the study region. To maintain administrative accuracy, the base map of China was obtained from the Standard Map Service of the Ministry of Natural Resources (http://bzdt.ch.mnr.gov.cn/). To avoid model overfitting and address multicollinearity, the variance inflation factor (VIF) was calculated for all predictors using the *vifstep* function in the R package 'usdm' (threshold VIF < 5) before running ESMs for each species (Naimi et al., 2014).

2.1.3 Mapping Species Distributions with ESMs

For each species with at least 20 spatially filtered occurrence records (maintaining one record per 5 km grid cell), potential distributions were predicted across China using an ESM framework (Breiner et al., 2015). For each species, numerous bivariate models were constructed using all possible pairs of predictor variables that passed the VIF screening. These were integrated across four modelling algorithms: generalized linear models (GLM), classification tree analysis (CTA), random forest (RF), and maximum entropy (MAXENT), balancing computational efficiency with predictive accuracy (Breiner et al., 2018). Algorithms were implemented through the R packages 'biomod2' and 'ecospat' (Di Cola et al., 2017; Thuiller et al., 2009). For each algorithm, 10,000 pseudo-absence points were randomly selected from the background environment, and key parameters were optimized using the *BIOMOD_Tuning* function of the 'biomod2' R package (Thuiller et al., 2009). Model training involved five-fold cross-validation, with occurrence data randomly partitioned into training (80%) and testing (20%) subsets.

A pooling procedure was adopted to validate ensemble models: predicted values of test data across all replicate runs were aggregated, and results for individual data points were averaged to generate an approximately independent prediction set. Ensemble performance was assessed based on this pooled set using the area under the receiver operating characteristic curve (AUC). This pooling strategy effectively overcomes the instability of model evaluation under small sample conditions and enhances the reliability of the assessment. Individual bivariate models with an AUC < 0.5 were excluded from the final ensemble. Continuous suitability maps were converted into binary presence-absence maps based on the maximum true skill statistic (MaxTSS) threshold for subsequent calculation of multidimensional biodiversity metrics (Di Cola et al., 2017).

2.2 Multidimensional Biodiversity Mapping

2.2.1 Taxonomic Diversity

The study area, defined as the Qinling Mountains and a 249-km buffer zone extending outward from their boundary (spanning over ~1,000 km from east to west, with a maximum north–south width of 249 km), was divided into 5 km × 5 km grid cells as the standardized spatial framework. All predicted species distribution maps were projected onto this grid. Taxonomic diversity (TD) for each cell was calculated as the total number of species present within that spatial unit.

2.2.2 Phylogenetic Diversity

Phylogenetic diversity (PD) for terrestrial vertebrates was characterized using established time-calibrated phylogenies (Hu et al., 2021). PD was quantified as Faith's phylogenetic diversity, representing the sum of branch lengths connecting all species present within a given grid cell (Faith, 1992).

2.2.3 Genetic Data Acquisition and Estimation of Genetic Diversity

The mitochondrial gene *COI* was used to estimate genetic diversity (GD). Coding sequences were retrieved from GenBank (www.ncbi.nlm.nih.gov/genbank) and the Barcode of Life Data System (BOLD; www.bold.systems.org). Comprehensive search strategies were implemented, encompassing all recognized synonyms and abbreviations for these molecular markers alongside species-specific taxonomic identifiers. For the BOLD database, sequences were accessed via the application programming interface to ensure maximal coverage. A stringent quality control protocol was applied: sequences shorter than 300 base pairs were excluded; at the species level, only taxa with at least four available sequences were retained. Multiple sequence alignment was conducted using MUSCLE with default parameters (Edgar,

2004). To maintain high data quality and mitigate the influence of sequencing artifacts, a stringent pairwise alignment filtering protocol was implemented. Pairwise alignments with <60% overlap or ≥10% divergence were filtered out. GD for each species was quantified using the equation proposed in a previous study (Miraldo et al., 2016) as follows:

$$\theta_{\pi} = \frac{1}{\binom{n}{2}} \sum_{i=1}^{n-1} \sum_{j}^{n} \frac{k_{ij}}{m_{ij}} \quad (Eq.1)$$

Where k_{ij} denotes the total number of nucleotide differences between sequence i and sequence j from a species, m_{ij} represents the length of the overlapping bases shared between these two sequences, The term $\binom{n}{2}$ signifies the total number of unique pairwise comparisons conducted for a given species. To assess spatial patterns, the community-wide GD for each individual grid cell was subsequently calculated by averaging the genetic diversity values of all species present within that cell as follows:

$$GD = \frac{\sum_{i=1}^{S_Q} \frac{\theta_{\pi i}}{Y_i}}{\sum_{i=1}^{S_Q} \frac{1}{Y_i}} \quad (Eq.2)$$

where S_Q is taxonomic diversity within each grid, Y_i was the number of grid cells occupied by the species, the overall genetic diversity $\theta_{\pi i}$ for a given species i was quantified by integrating all available genetic sequence data across its entire habitat distribution.

2.3 Driving Factors of Biodiversity Patterns

To identify primary determinants of spatial patterns of TD, PD, and GD, eight environmental variables were selected (**Table S2**). Zonal statistics were used to align environmental predictors with biodiversity metrics within each grid cell. Specifically, mean values for most variables were calculated using the 'exactextractr' package, while elevation

range (as a measure of topographic complexity) was computed from maximum and minimum elevation values (Baston, 2019). Independent contributions of these variables were quantified using Generalized Linear Mixed Models (GLMMs) combined with hierarchical partitioning, implemented in the R package 'glmm.hp' (Lai et al., 2022). This approach decomposes the marginal R^2 attributable to fixed effects in GLMMs, enabling estimation of independent and joint contributions of collinear variables. Longitude and latitude coordinates were incorporated as spatial covariates to account for potential spatial effects.

2.4 Systematic Conservation Planning for the Qinling Mountains

2.4.1 Current PA System and Socioeconomic Data Collection

The current protected area (PA) system was obtained from the Ministry of Ecology and Environment of the People's Republic of China (https://www.mee.gov.cn/) and the China Nature Reserve Specimen Resource Sharing Platform (http://www.papc.cn/), covering 2,729 nature reserves at national, provincial, municipal, and county levels. Land use data at 30-m resolution were obtained from the China land cover dataset (Yang & Huang, 2021). Gross Domestic Product (GDP) data for 2021 at 1-km resolution were sourced from the Resource and Environmental Science Data Platform (http://www.resdc.cn), spatialized from county-level statistics by integrating land-use type, nighttime light intensity, and settlement density.

2.4.2 Identification of Conservation Priority Gap

Systematic conservation planning was conducted using the R package 'prioritizr' (Hanson et al., 2025). Each 5 km × 5 km grid cell was characterized by multidimensional biodiversity features (TD, PD, GD) for different vertebrate groups. The corresponding spatial raster layers were projected, cropped, and masked to the study area, then normalized to a 0–1 range. GDP was used as a proxy for socioeconomic opportunity cost and was incorporated as the

planning-unit cost, enabling identification of priority areas covering 50% of the study area, a proportion aligned with the Kunming-Montreal Global Biodiversity Framework's long-term goal and the Half-Earth Concept, while minimizing socioeconomic impacts. Existing PAs were locked into the final network, while planning units dominated by cropland or urban land were excluded from new prioritization. To avoid overly fragmented conservation solutions, a boundary penalty was applied to promote spatial compactness and contiguity. Optimization was performed using the Gurobi solver with a 1% optimality gap termination criterion.

3. Results

3.1 Data Sources

The study covered the Qinling Mountains and ten nearby ecoregions, extending up to 249 km north and south of the main Qinling boundary (**Figure 1**). After data quality control, this study collected 470,025 occurrence records from 941 terrestrial vertebrate species. These included 129 mammals, 685 birds, 69 reptiles, and 58 amphibians (**Figure S1; Table S3**).

Species distribution models were built for species with at least 20 spatially independent records. All models used in the analysis had AUC values above 0.80, indicating good model performance (**Figure S3; Table S3**). For the other dimensions of biodiversity, PD was calculated for 858 species using a time-calibrated phylogenetic tree. GD was estimated using 9,317 mitochondrial *COI* sequences from 504 species (**Figure S4; Table S4**).

3.2 Multidimensional Biodiversity Patterns in the Qinling Mountains and Adjacent Regions

TD and PD showed similar geographic patterns across the study area. Both generally increased from north to south, while GD showed a different pattern (**Figure 1**).

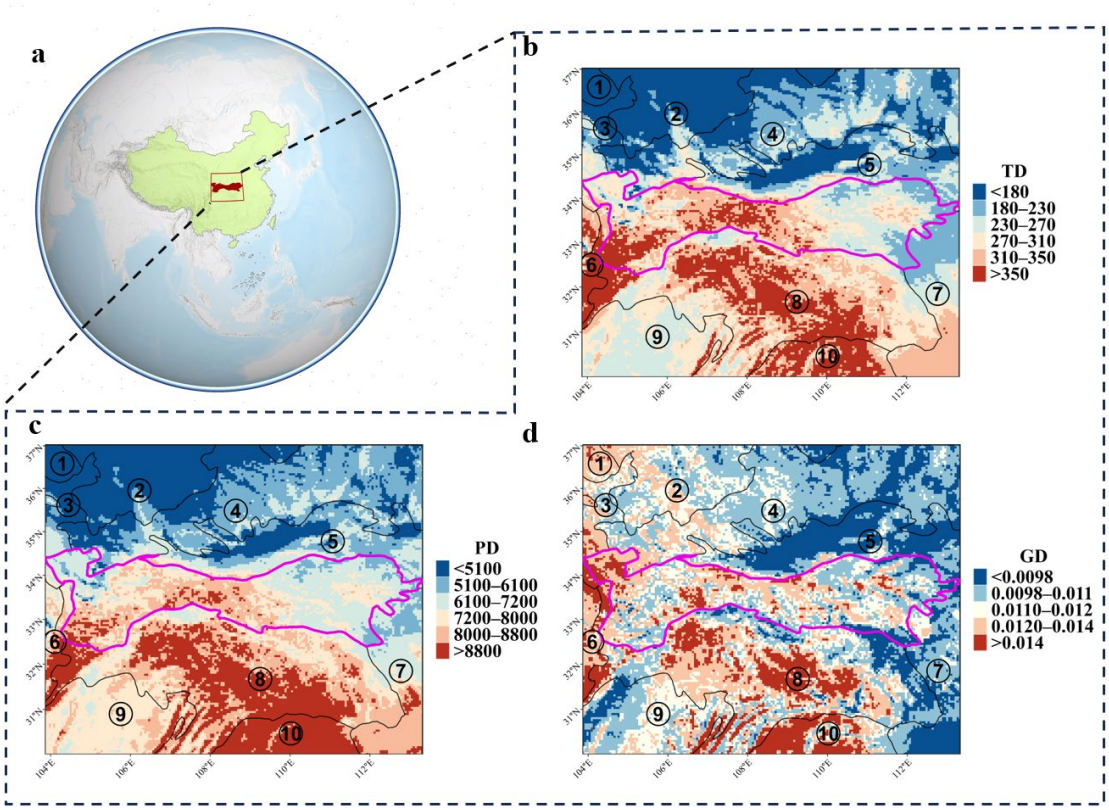


Figure 1. The geographical patterns of taxonomic diversity (TD), phylogenetic diversity (PD), and genetic diversity (GD) for terrestrial vertebrates in the Qinling Mountains and adjacent regions. (a) Geographic location of the study area in China. The red rectangle indicates the extent of the Qinling region, and the dashed lines indicate the zoomed-in spatial scope. (b) TD, (c) PD, and (d) GD for terrestrial vertebrates. The numbers on the map correspond to the names of the ecoregions (https://ecoregions.appspot.com/) as follows: 1, Alashan Plateau semi-desert; 2, Ordos Plateau steppe; 3, Southeast Tibet shrublands and meadows; 4, Central China Loess Plateau mixed forests; 5, Yellow River Plain mixed forests; 6, Qionglai-Minshan Mountains conifer forests; 7, Yangtze River Plain evergreen forests; 8, Daba Mountains evergreen forests; 9, Sichuan Basin evergreen broadleaf forests; 10, Guizhou Plateau broadleaf and mixed forests.

In the northern Qinling Mountains, TD and PD were particularly low in three ecoregions: the Alashan Plateau semi-desert, Central China Loess Plateau mixed forests, and Southeast Tibet shrublands and meadows (**Figure 1b, 1c**). However, GD was relatively high in some of these areas (**Figure 1d**). In contrast, some areas with relatively high TD and PD had lower GD. The Wei River Plain showed low values for all three dimensions of biodiversity (**Figure 1**).

The Qinling Mountains formed a clear boundary between the lower TD and PD in the north and the higher values in the south. Within the Qinling Mountains, TD and PD were generally higher in the western-central and southern areas and decreased toward the east. GD showed a less regular pattern, with high-diversity areas scattered across the northwestern, central, and eastern parts of the mountains. The Funiu, Xiong'er, and Xiaoshan Mountains in the east had relatively high levels of all three biodiversity dimensions (**Figure 1**).

In the southern Qinling Mountains, the Qionglai-Minshan Mountains forests showed high TD, PD, and GD. The Daba Mountains evergreen forests and Guizhou Plateau broadleaf and mixed forests also contained large areas with high TD and PD, although areas of high GD were more scattered. In contrast, the Yangtze River Plain evergreen forests had relatively low values for all three biodiversity dimensions. Similarly, the Sichuan Basin showed lower overall biodiversity than many surrounding southern mountain regions, even though its TD and PD were still generally higher than those of most regions north of the Qinling Mountains (**Figure 1**).

When mammals, birds, reptiles, and amphibians were analyzed separately, their overall patterns were generally similar to those observed for all terrestrial vertebrates, although some differences appeared at smaller spatial scales (**Figures S5–S7**). For example, reptiles showed relatively high TD and PD mainly in the western Qinling Mountains, while amphibian diversity was concentrated in several high-diversity patches in the western and central regions. For mammals and birds, GD was generally higher south of the Qinling Mountains. Within the Qinling range, however, GD tended to be lower in the west and higher in some central and eastern areas.

3.3 The Qinling Mountains as a Biogeographic Transition Zone

Biodiversity exhibited a distinct latitudinal gradient, peaking in the South, followed by the Qinling Mountains, and remaining lowest in the North (**Figure 2**).

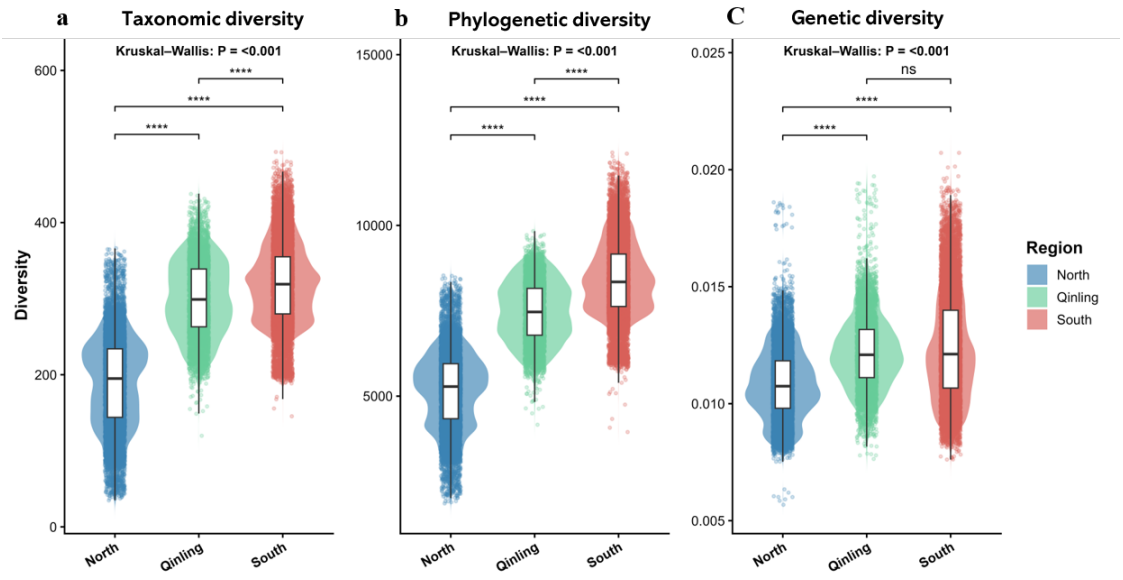


Figure 2. Variation in multidimensional biodiversity of terrestrial vertebrates among regions north of the Qinling Mountains (North), within the Qinling Mountains (Qinling), and south of the Qinling Mountains (South). (a) Taxonomic diversity (TD), (b) phylogenetic diversity (PD), and (c) genetic diversity (GD). Symbols denote statistical significance levels: ns, not significant; ****, $P \leq 0.001$.

Of the 941 species included in the study, 653 occurred in the North, 742 in the Qinling Mountains, and 902 in the South. A total of 605 species, or 64.29% of all species, were found in all three regions. These included 81 mammals, 500 birds, 11 amphibians, and 13 reptiles. Species found in only one region were most common in the South, where 157 species (16.68%) were unique to that region. In comparison, only 33 species (3.51%) were unique to the North, and no species were found only in the Qinling region (**Figure 3; Figure S8**).

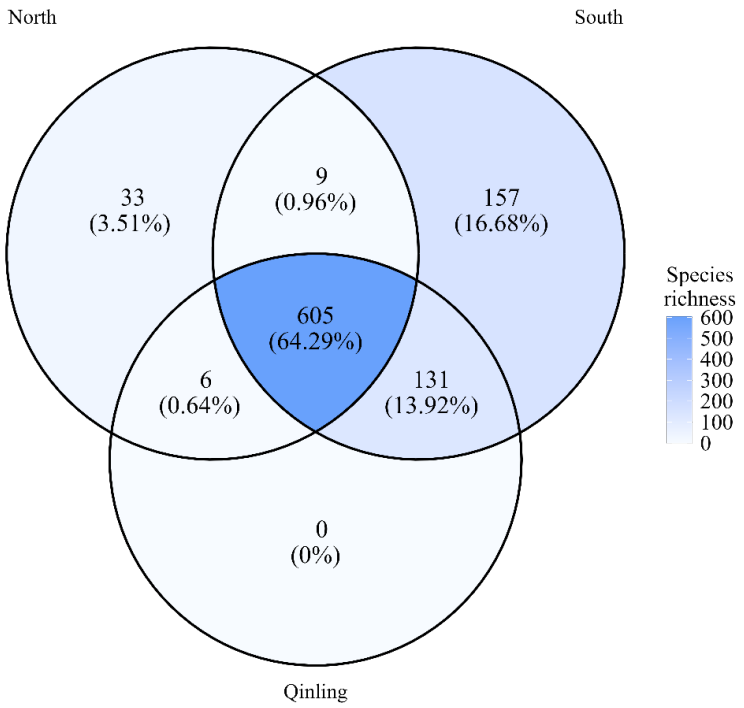


Figure 3. Venn diagram illustrating the species composition and distribution overlap of terrestrial vertebrates across the North, South, and Qinling regions. The three circles represent the respective geographical regions. Numbers indicate the number of species in each region or overlap section; percentages in parentheses denote proportions relative to the total number of terrestrial vertebrate species (N = 941). The blue gradient legend on the right represents species richness, with darker colors indicating higher species counts (0–605).

Comparison of species shared between the Qinling Mountains and neighboring regions revealed an interesting pattern. A total of 131 species (13.92%) were shared between the Qinling and South regions but were absent from the North. In contrast, only 6 species (0.64%) were shared between the Qinling and North regions but were absent from the South (**Figure 3**).

These results suggest that the Qinling Mountains act as a transition zone rather than an isolated region. The large number of species shared among all three regions shows strong connections between their animal communities. At the same time, the much larger number

of species shared between the Qinling and South regions (131 species) than between the Qinling and North regions (6 species) suggests that the Qinling fauna is more similar to the southern fauna.

3.4 Environmental Factors Related to Biodiversity Patterns

Next, the study examined how environmental conditions and human activities were related to the three dimensions of biodiversity. The statistical models explained 87.28% of the variation in TD, 91.14% in PD, and 64.82% in GD (**Figure 4**). This means that the environmental and human-related variables included in the analysis explained TD and PD particularly well, while GD was more difficult to explain. When the four vertebrate groups were analyzed separately, less than 50% of the variation in GD could be explained (**Table S5; Figure S9**).

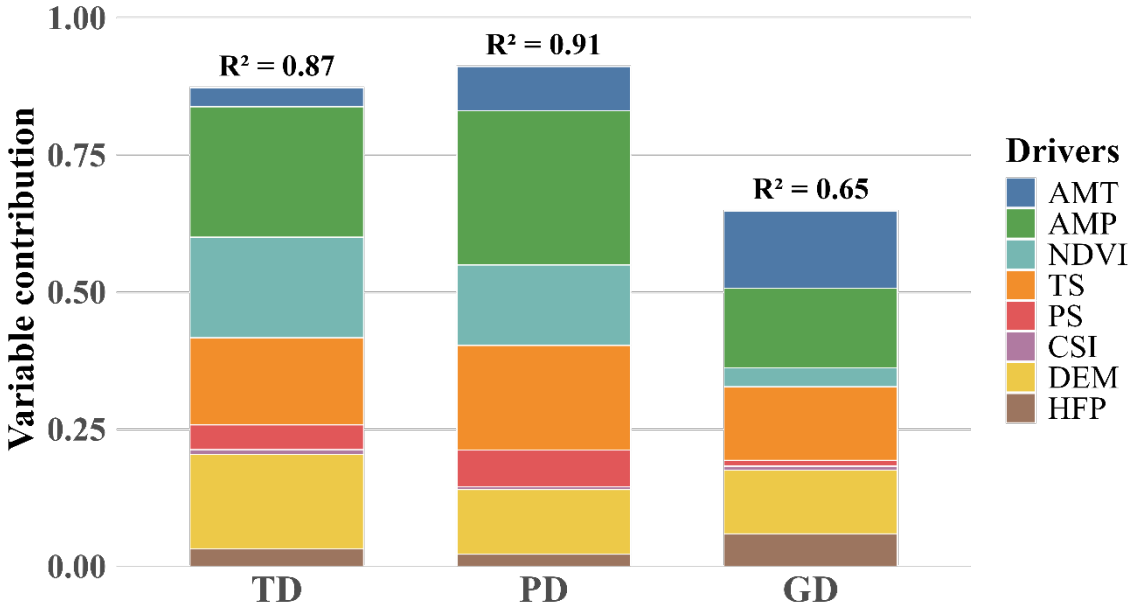


Figure 4. Relative individual contributions of environmental and anthropogenic drivers to multidimensional biodiversity of terrestrial vertebrates. Stacked bar charts illustrate the independent contributions of eight drivers to TD, PD, and GD across all terrestrial vertebrates. Total explained variance (R^2) for each biodiversity dimension is shown above the corresponding bar. The eight drivers were: AMT (Annual Mean Temperature), AMP (Annual Mean Precipitation), NDVI (Normalized Difference Vegetation

Index), TS (Temperature Seasonality), PS (Precipitation Seasonality), CSI (Historical Climatic Stability), DEM (Elevation Range), and HFP (Human Footprint).

Among the eight factors examined, annual mean precipitation (AMP), vegetation cover measured by NDVI, and elevation range (DEM) were the main positive factors associated with TD and PD. For TD, their contributions were 23.79%, 18.33%, and 17.20%, respectively. For PD, their contributions were 28.13%, 14.66%, and 11.79%, respectively. Temperature seasonality (TS), which describes how much temperature changes throughout the year, was the strongest negative factor, contributing 15.90% for TD and 19.07% for PD (**Table S5**).

However, different vertebrate groups responded differently to these environmental factors. For example, precipitation had a stronger positive relationship with TD in amphibians (32.07%) and reptiles (24.22%) than in mammals (17.21%) and birds (21.93%). NDVI was positively related to mammal and bird diversity but negatively related to amphibian and reptile diversity. Elevation range had a stronger positive effect on mammals and birds than on amphibians and reptiles. Similar differences among animal groups were also observed for PD (**Figure S9; Table S5**).

For GD, annual mean precipitation and elevation range were also the two largest positive contributors, accounting for 14.47% and 11.61%, respectively (**Figure 4; Table S5)**. However, their importance differed greatly among animal groups. For example, precipitation had a much stronger positive effect on mammal GD than on the other three groups. Historical climatic stability was especially important for amphibians, contributing 25.33% to their GD pattern. Overall, these results suggest that TD, PD, and GD are influenced by different combinations of environmental factors.

3.5 Optimizing the Protected Area Network

Finally, the study explored how the protected area network in the Qinling Mountains could be improved. The conservation analysis considered all three biodiversity dimensions (TD, PD, and GD), existing protected areas, land-use restrictions, and socioeconomic constraints based on GDP (**Figure 5**).

Under a scenario in which protected areas covered 50% of the Qinling Mountains, the main new priority areas were located in the northwestern mountain ranges, the southwestern Longmen region, and the south-central Qinling Mountains. These proposed areas were generally connected with existing protected areas, while cropland and urban areas were excluded.

Existing protected areas currently cover 39.6% of the Qinling Mountains and include an estimated 44.4% of terrestrial vertebrate distributions (**Figure 5**). Increasing protected-area coverage to 50% increased estimated habitat coverage from 44.4% to approximately 57.4%, an increase of 13.0 percentage points.

The improvement differed among vertebrate groups. Estimated habitat coverage increased by 13.0 percentage points for mammals, 12.6 for birds, 18.8 for amphibians, and 14.5 for reptiles. At the same time, the additional priority areas affected only an additional 1.9% of total regional socioeconomic activity.

Together, these results show that carefully expanding the protected area network could protect substantially more vertebrate habitat while keeping the increase in socioeconomic impacts relatively small.

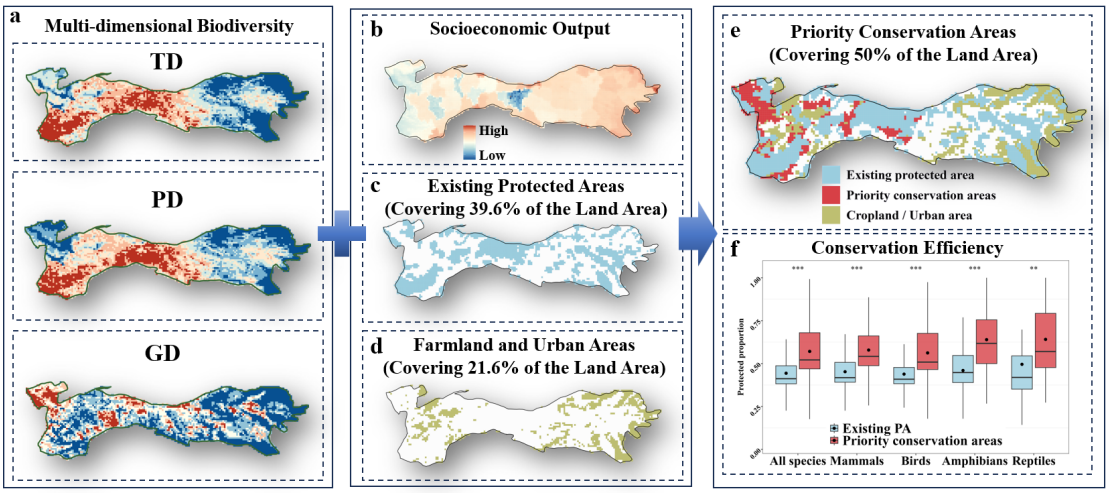


Figure 5. Schematic of the multi-objective optimization framework that accounts for socioeconomic constraints to identify priority areas. (a) Input layers for spatial prioritization encompassing three biodiversity dimensions (TD, PD, and GD for terrestrial vertebrates); (b) constraints including socioeconomic output; (c) binary layer of existing PAs (light blue); (d) land areas comprised of urban and agricultural land (olive green); (e) spatial distribution of existing PAs (light blue), newly identified priority conservation areas (red), and cropland/urban areas (olive green) in the Qinling Mountains; (f) comparison of habitat protection coverage before and after optimization. Points within the boxes represent mean values. Symbols denote statistical significance levels: **, $P \leq 0.01$; ***, $P \leq 0.001$.

4. Discussion

4.1 Reassessing Spatial Biodiversity Patterns for Conservation in the Qinling Mountains: A Multidimensional Perspective

Exploring biodiversity patterns is central to biogeography and provides an irreplaceable foundation for systematic conservation planning. This study provides a multidimensional biodiversity assessment across the Qinling Mountains and adjacent ecoregions. Contrary to Zhang et al. (2017), who reported higher taxonomic diversity (TD) concentrated in the eastern and central Qinling based on a limited subset of protected species, this analysis based on a substantially larger dataset reveals high TD in the western and central regions, consistent with Dang et al. (2025). These findings therefore provide a more complete view of biodiversity

patterns and underscore the critical need for broad-scale, multi-taxon inventories in regional conservation planning.

Although TD is a conventional conservation metric, phylogenetic diversity (PD) and genetic diversity (GD) capture evolutionary history and adaptive potential, revealing additional conservation value beyond species richness alone (Fletcher et al., 2025). Spatial congruence among dimensions was incomplete: TD and PD hotspots covaried in the central and southwestern Qinling, while GD hotspots were sparsely distributed across northwestern, central, and eastern areas. Future conservation in this globally significant ecoregion must therefore move beyond species-richness-based strategies to incorporate multidimensional biodiversity metrics, ensuring the long-term protection of not only species numbers but also evolutionary history and adaptive potential.

4.2 The Qinling Mountains as a Transition Zone

This study examines the spatial patterns of multidimensional biodiversity, encompassing taxonomic, phylogenetic, and genetic dimensions of terrestrial vertebrates across the Qinling Mountains and adjacent ecoregions (**Figures 1 and 2**). Biodiversity exhibits a sharp south-to-north decline, with species richness highest south of the Qinling, intermediate within the mountains, and lowest in the north (**Figure 3**). Despite serving as a major biogeographic divide, the Qinling does not constitute an isolated species pool; instead, it functions as a dynamic biogeographic melting pot where Palaearctic and Oriental faunas converge.

This gradient reflects asymmetrical dispersal. The southern Oriental realm contributes more species than the northern Palaearctic, with 131 species shared exclusively between the south and the Qinling but absent from the north. The absence of an endemic species pool suggests the region has primarily functioned as a species sink rather than a center of in situ

evolutionary diversification. Precipitation (AMP), NDVI, elevation (DEM), and temperature seasonality (TS) emerged as dominant drivers, with higher multidimensional biodiversity consistently associated with greater precipitation and lower temperature seasonality (**Figure 4**). The underlying mechanism is the historical uplift of the Qinling Mountains, which blocks cold, dry air masses from the northwest while forcing warm, moisture-laden southeast monsoon air to rise along the southern windward slopes (Dong et al., 2022). This orographic process generates abundant precipitation and stabilizes temperatures on the southern slopes, engineering a steep bioclimatic gradient that sustains the observed south-high, north-low biodiversity configuration. These findings highlight that conservation strategies in the Qinling Mountains must account for not only the spatial mismatch between TD and GD hotspots identified earlier, but also the asymmetric biogeographic processes and climatic gradients that sustain regional biodiversity.

4.3 Improving Protected Areas in the Qinling Mountains

In recent years, China's protected area (PA) network has expanded rapidly. However, its efficiency in conserving multidimensional biodiversity remains poorly evaluated. This study reveals that existing PAs in the Qinling Mountains effectively cover taxonomic diversity (TD) hotspots of terrestrial vertebrates but inadequately capture phylogenetic (PD) and genetic diversity (GD) hotspots concentrated in the western and central parts (**Figure 5**). Given that PD and GD safeguard evolutionary heritage and future adaptive potential, respectively, they represent indispensable pillars for maintaining long-term ecosystem resilience (Hu et al., 2021). To address these gaps, the PA network is proposed to be expanded to cover 50% of the study area—a target aligned with the Kunming-Montreal Global Biodiversity Framework and the Half-Earth Concept. The identified priority areas fill systematic conservation gaps across the northwestern mountains, the southwestern Longmen region, and the central-southern areas,

thereby substantially broadening the protection of multidimensional biodiversity.

These priority areas complement existing PAs in an aggregated and contiguous manner, achieving the 50% target while increasing terrestrial vertebrate habitat protection by 13.0% (from 44.4% to 57.4%) and affecting only 1.9% of regional socioeconomic activity. Crucially, these areas successfully avoid croplands and built-up land, enhancing conservation effectiveness while minimizing economic interference. By demonstrating that a 50% protection target can be achieved with minimal socioeconomic trade-offs, this study provides a replicable blueprint for PA expansion. These findings suggest that systematic conservation planning, which reconciles biogeographic patterns with socioeconomic constraints, promotes a more scientifically sound expansion of PA networks, not only in the Qinling Mountains but also globally, while minimizing potential negative socioeconomic impacts.

4.4 Limitations and Future Directions

This multidimensional framework successfully elucidates the spatial patterns of vertebrate biodiversity in the Qinling Mountains and provides a quantitative basis for identifying conservation priorities. However, the resolution of genetic diversity (GD) data remains limited, particularly for amphibians and reptiles. This limitation stems from labor-intensive field sampling and the sparse availability of genetic sequences in public repositories. Consequently, the GD model explained only 64.82% of the variation (**Figure 4**). Such data gaps may obscure population-level genetic differentiation and constrain a comprehensive assessment of evolutionary potential. Therefore, future studies should prioritize systematic genetic sampling across the Qinling Mountains and integrate advanced approaches such as genome-wide sequencing and environmental DNA (eDNA) metabarcoding. Enhanced genetic coverage will be essential for accurately capturing biodiversity patterns and improving future

conservation planning.

Conflicts of Interest

The author declares no conflicts of interest.

References

Baston, D. (2019). exactextractr: Fast extraction from raster datasets using polygons (Version 0.10.1) [R package]. https://doi.org/10.32614/CRAN.package.exactextractr

Breiner, F. T., Guisan, A., Bergamini, A., & Nobis, M. P. (2015). Overcoming limitations of modelling rare species by using ensembles of small models. Methods in Ecology and Evolution, 6(10), 1210–1218. https://doi.org/10.1111/2041-210X.12403

Breiner, F. T., Nobis, M. P., Bergamini, A., & Guisan, A. (2018). Optimizing ensembles of small models for predicting the distribution of species with few occurrences. Methods in Ecology and Evolution, 9(4), 802–808. https://doi.org/10.1111/2041-210X.12957

Dang, H., Lü, Y., Wang, X., Hao, Y., & Fu, B. (2025). Integrating species diversity, ecosystem services, climate and ecological stability helps to improve spatial representation of protected areas for quadruple win. Geography and Sustainability, 6(1), 100205. https://doi.org/10.1016/j.geosus.2024.06.005

Di Cola, V., Broennimann, O., Petitpierre, B., Breiner, F. T., D'Amen, M., Randin, C., Engler, R., Pottier, J., Pio, D., Dubuis, A., Pellissier, L., Mateo, R. G., Hordijk, W., Salamin, N., & Guisan, A. (2017). Ecospat: An R package to support spatial analyses and modeling of species niches and distributions. Ecography, 40(6), 774–787. https://doi.org/10.1111/ecog.02671

Dong, Y., Shi, X., Sun, S., Sun, J., Hui, B., He, D., Chong, F., & Yang, Z. (2022). Co-evolution of the Cenozoic tectonics, geomorphology, environment and ecosystem in the Qinling Mountains and adjacent areas, Central China. Geosystems and Geoenvironment, 1(2), 100032. https://doi.org/10.1016/j.geogeo.2022.100032

Edgar, R. C. (2004). MUSCLE: Multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research, 32(5), 1792–1797. https://doi.org/10.1093/nar/gkh340

Faith, D. P. (1992). Conservation evaluation and phylogenetic diversity. Biological Conservation, 61(1), 1–10. https://doi.org/10.1016/0006-3207(92)91201-3

Fletcher, R. J., Green, R. E., Bladon, E. K., Atkinson, P. W., Phalan, B. T., Williams, D., Visconti, P., & Balmford, A. (2025). Beyond species richness for biological conservation. Conservation Letters, 18(4), e13124. https://doi.org/10.1111/conl.13124

Grosjean, M., Høfft, M., Gonzalez, M., Hahn, A., & Robertson, T. (2022). GRSciColl: What is the global registry of scientific collections and how to contribute? Biodiversity Information Science and Standards, 6, e93875. https://doi.org/10.3897/biss.6.93875

Hanson, J. O., Schuster, R., Strimas-Mackey, M., Morrell, N., Edwards, B. P. M., Arcese, P., Bennett, J. R., & Possingham, H. P. (2025). Systematic conservation prioritization with the prioritizr R package. Conservation Biology, 39(1), e14376. https://doi.org/10.1111/cobi.14376

Hu, Y., Fan, H., Chen, Y., Chang, J., Zhan, X., Wu, H., Zhang, B., Wang, M., Zhang, W., Yang, L., Hou, X., Shen, X., Pan, T., Wu, W., Li, J., Hu, H., & Wei, F. (2021). Spatial patterns and conservation of genetic and phylogenetic diversity of wildlife in China. Science Advances, 7(4), eabd5725. https://doi.org/10.1126/sciadv.abd5725

Jetz, W., & Rahbek, C. (2001). Geometric constraints explain much of the species richness pattern in African birds. Proceedings of the National Academy of Sciences, 98(10), 5661–5666. https://doi.org/10.1073/pnas.091100998

Lai, J., Zou, Y., Zhang, S., Zhang, X., & Mao, L. (2022). glmm.hp: An R package for computing individual effect of predictors in generalized linear mixed models. Journal of Plant Ecology, 15(6), 1302–1307. https://doi.org/10.1093/jpe/rtac096

Liang, J., Ding, Z., Li, L., Hu, Y., Zhou, Z., Lie, G., Niu, X., Huang, W., Hu, H., & Si, X. (2024). Patterns and drivers of avian taxonomic and phylogenetic beta diversity in China vary across geographical backgrounds and dispersal abilities. Zoological Research, 45(1), 125–135. https://doi.org/10.24272/j.issn.2095-8137.2023.076

Mastretta-Yanes, A., Da Silva, J. M., Grueber, C. E., Castillo-Reina, L., Köppä, V., Forester, B. R., Funk, W. C., Heuertz, M., Ishihama, F., Jordan, R., Mergeay, J., Paz-Vinas, I., Rincon-Parra, V. J., Rodriguez-Morales, M. A., Arredondo-Amezcua, L., Brahy, G., DeSaix, M., Durkee, L., Hamilton, A., … Hoban, S. (2024). Multinational evaluation of genetic diversity indicators for the Kunming-Montreal Global Biodiversity Framework. Ecology Letters, 27(7), e14461. https://doi.org/10.1111/ele.14461

Mazel, F., Guilhaumon, F., Mouquet, N., Devictor, V., Gravel, D., Renaud, J., Cianciaruso, M. V., Loyola, R., Diniz-Filho, J. A. F., Mouillot, D., & Thuiller, W. (2014). Multifaceted diversity–area relationships

reveal global hotspots of mammalian species, trait and lineage diversity. Global Ecology and Biogeography, 23(8), 836–847. https://doi.org/10.1111/geb.12158

Meng, Q., Bai, H., Sarukkalige, R., Fu, G., Jia, W., & Zhang, C. (2021). Annual and seasonal precipitation trends and their attributions in the Qinling Mountains, a climate transitional zone in China. Theoretical and Applied Climatology, 144(1–2), 401–413. https://doi.org/10.1007/s00704-020-03482-z

Miraldo, A., Li, S., Borregaard, M. K., Flórez-Rodríguez, A., Gopalakrishnan, S., Rizvanovic, M., Wang, Z., Rahbek, C., Marske, K. A., & Nogués-Bravo, D. (2016). An Anthropocene map of genetic diversity. Science, 353(6307), 1532–1535. https://doi.org/10.1126/science.aaf4381

Naimi, B., Hamm, N. A. S., Groen, T. A., Skidmore, A. K., & Toxopeus, A. G. (2014). Where is positional uncertainty a problem for species distribution modelling? Ecography, 37(2), 191–203. https://doi.org/10.1111/j.1600-0587.2013.00205.x

Thuiller, W., Lafourcade, B., Engler, R., & Araújo, M. B. (2009). BIOMOD – a platform for ensemble forecasting of species distributions. Ecography, 32(3), 369–373. https://doi.org/10.1111/j.1600-0587.2008.05742.x

Wilson, E. O. (2016). Half-Earth: our planet's fight for life. WW Norton & Company.

Xia, H., Qin, Y., Feng, G., Meng, Q., Cui, Y., Song, H., Ouyang, Y., & Liu, G. (2019). Forest phenology dynamics to climate change and topography in a geographic and climate transition zone: The Qinling Mountains in central China. Forests, 10(11), 1007. https://doi.org/10.3390/f10111007

Xie, W., & Yao, Y. (2024). Quantifying human activity intensity in the Qinling-Daba Mountains. People and Nature, 6(4), 1486–1501. https://doi.org/10.1002/pan3.10649

Yang, J., & Huang, X. (2021). The 30 m annual land cover dataset and its dynamics in China from 1990 to 2019. Earth System Science Data, 13(8), 3907–3925. https://doi.org/10.5194/essd-13-3907-2021

Zhang, Y., Wang, Y., Phillips, N., Ma, K., Li, J., & Wang, W. (2017). Integrated maps of biodiversity in the Qinling Mountains of China for expanding protected areas. Biological Conservation, 210, 64–71. https://doi.org/10.1016/j.biocon.2016.04.022

Supplemental Figures

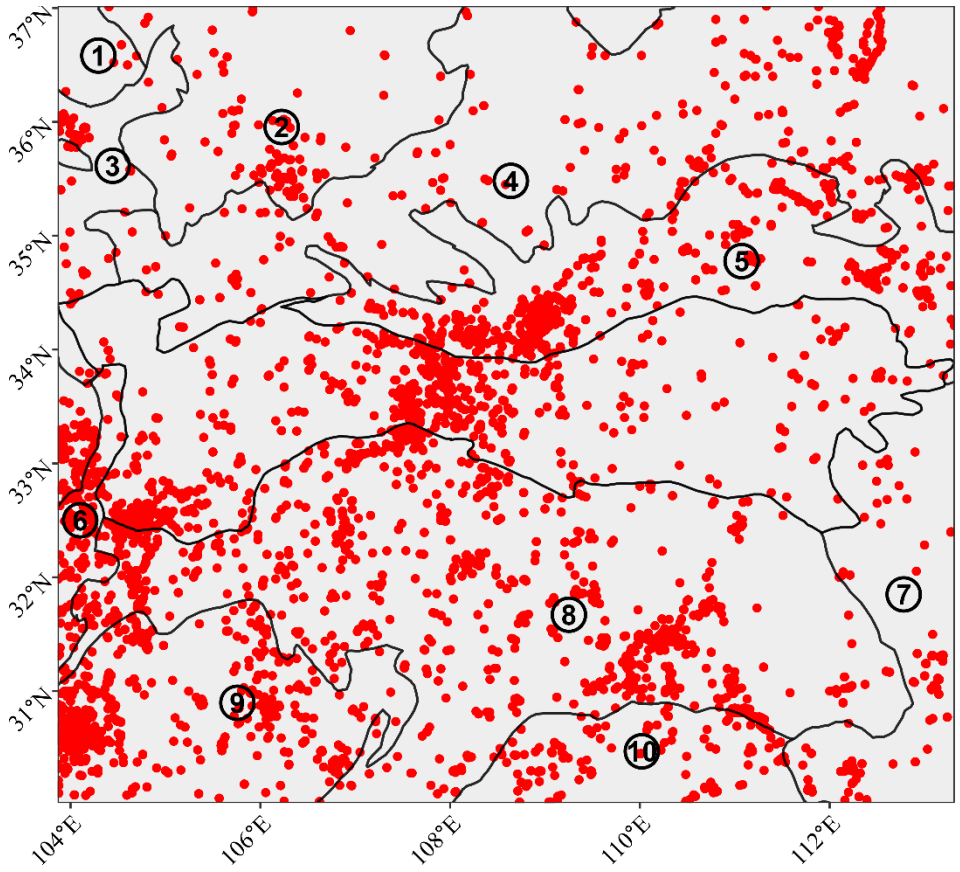


Figure S1. Spatial distribution of species occurrence records for terrestrial vertebrates in the Qinling Mountains and adjacent regions. Numbers on the map correspond to the names of the ecoregions (https://ecoregions.appspot.com/) as follows: 1, Alashan Plateau semi-desert; 2, Ordos Plateau steppe; 3, Southeast Tibet shrublands and meadows; 4, Central China Loess Plateau mixed forests; 5, Yellow River Plain mixed forests; 6, Qionglai-Minshan Mountains conifer forests; 7, Yangtze River Plain evergreen forests; 8, Daba Mountains evergreen forests; 9, Sichuan Basin evergreen broadleaf forests; 10, Guizhou Plateau broadleaf and mixed forests.

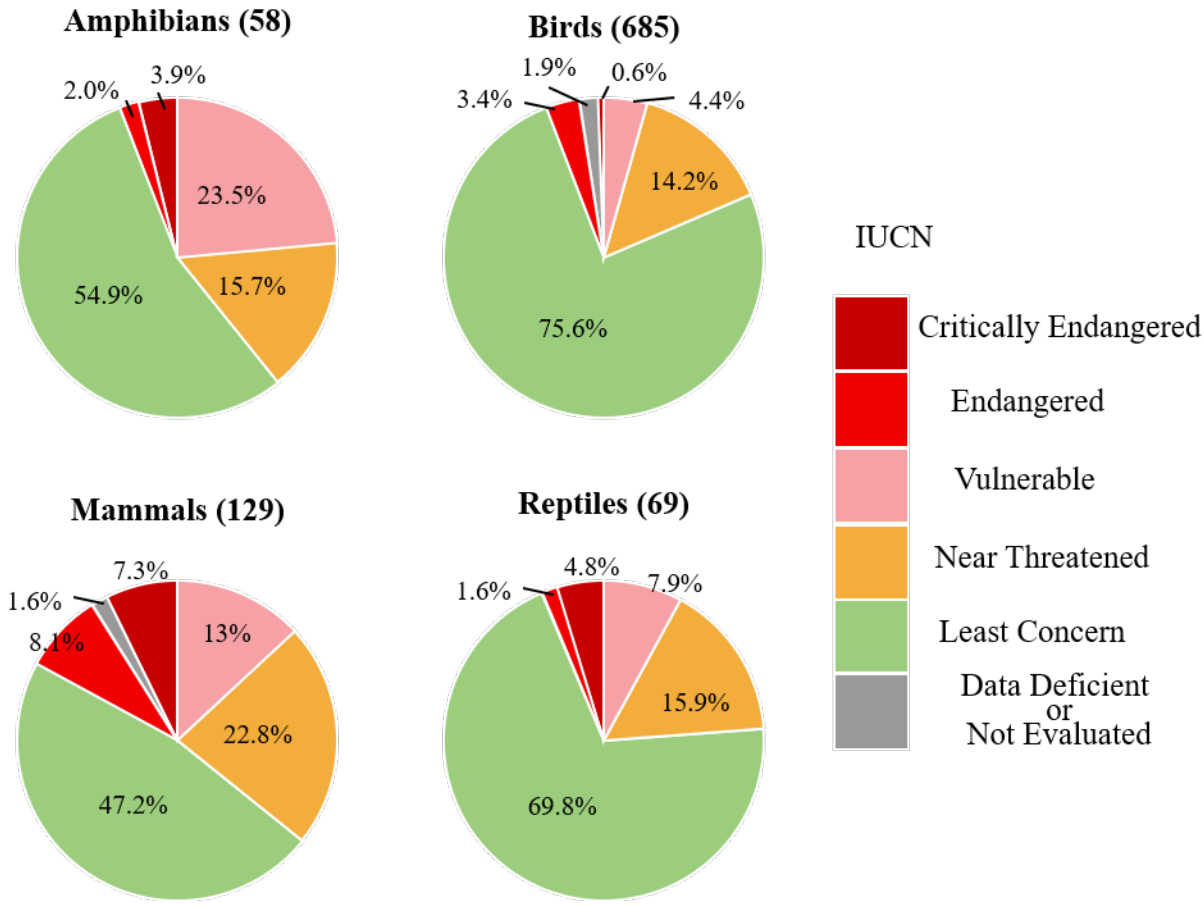


Figure S2. Taxonomic composition and IUCN Red List status of terrestrial vertebrate species in the Qinling Mountains and adjacent regions. Numbers in parentheses indicate the total number of species recorded for each taxonomic group (Amphibians, Birds, Mammals, and Reptiles). The pie charts show the proportion of species within each IUCN Red List category. The legend on the right corresponds to the six status categories displayed: Critically Endangered (dark red), Endangered (red), Vulnerable (pink), Near Threatened (orange), Least Concern (green), and Data Deficient or Not Evaluated (grey).

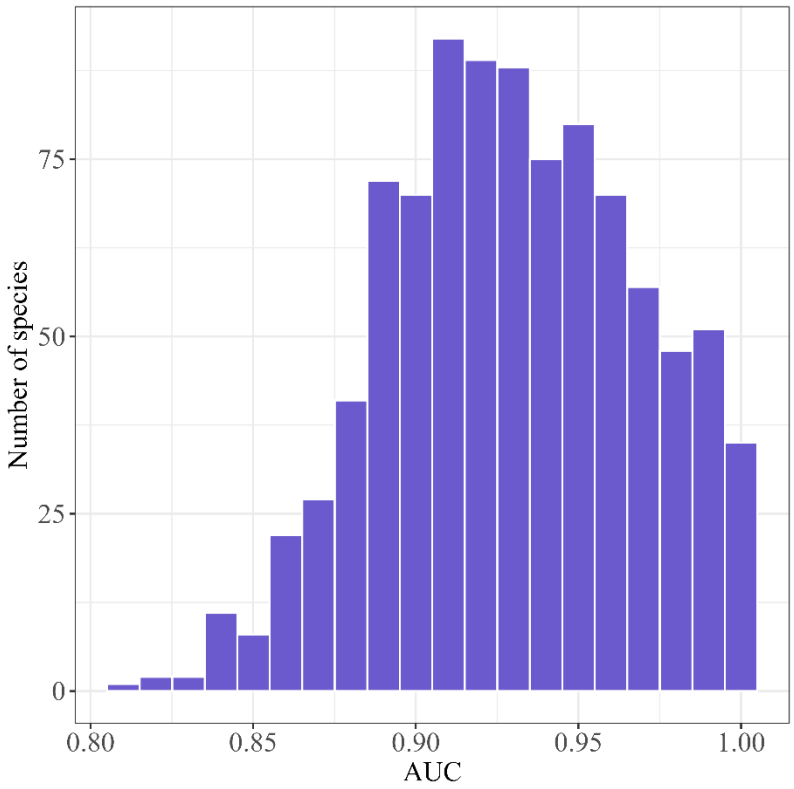


Figure S3. Frequency distribution of AUC values for ensembles of small models (ESMs) of terrestrial vertebrates in the Qinling Mountains and adjacent regions. The x-axis represents AUC (Area Under the Curve) values, reflecting the predictive accuracy of the ensembles of small models (ESMs), and the y-axis indicates the number of species within each AUC bin. Most species exhibit AUC values exceeding 0.86, with a prominent concentration between 0.90 and 0.95, indicating excellent predictive performance and high discriminatory ability.

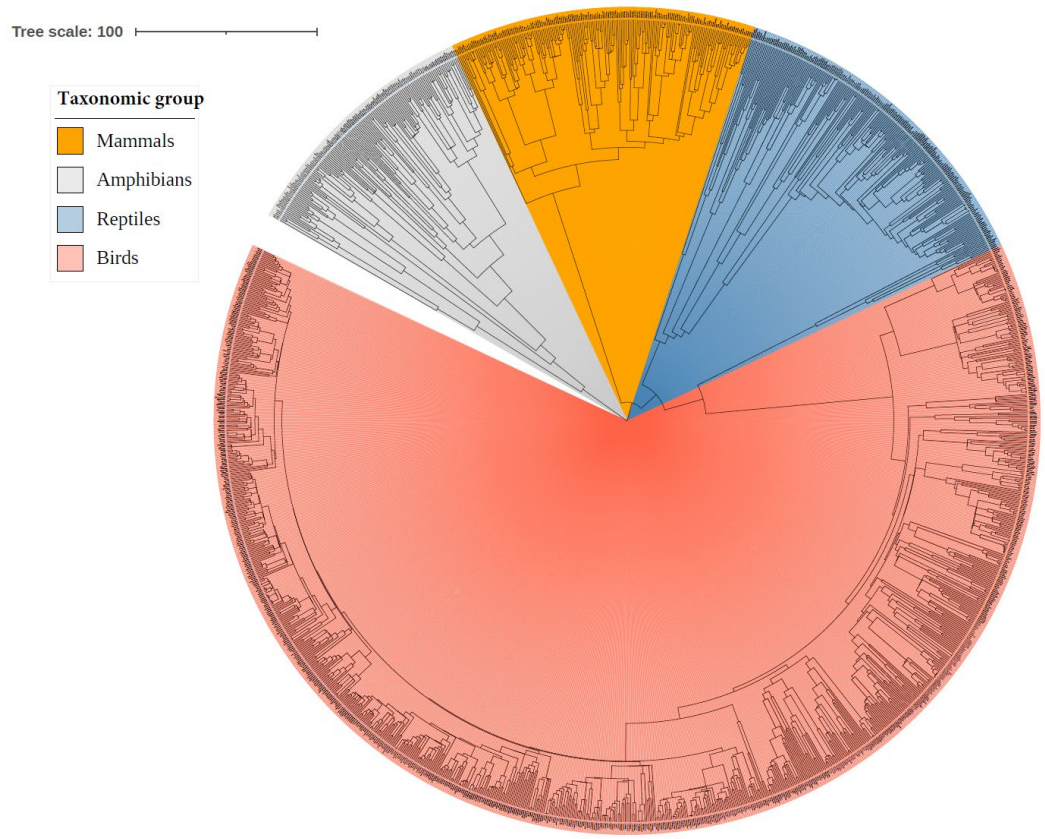


Figure S4. Circular phylogenetic tree of the 858 terrestrial vertebrate species analyzed in this study. The circular tree illustrates the evolutionary relationships among the terrestrial vertebrate species examined. The phylogeny is partitioned into four major taxonomic classes, with color-coded branches denoting Mammals, Amphibians, Reptiles, and Birds. This tree was derived from a time-calibrated phylogenetic framework and serves as the fundamental basis for quantifying multidimensional evolutionary facets, including phylogenetic diversity (PD). Branch lengths reflect divergence times and evolutionary distances among the diverse lineages of the study region's vertebrate fauna. A scale bar indicating relative evolutionary distance is provided in the top left corner.

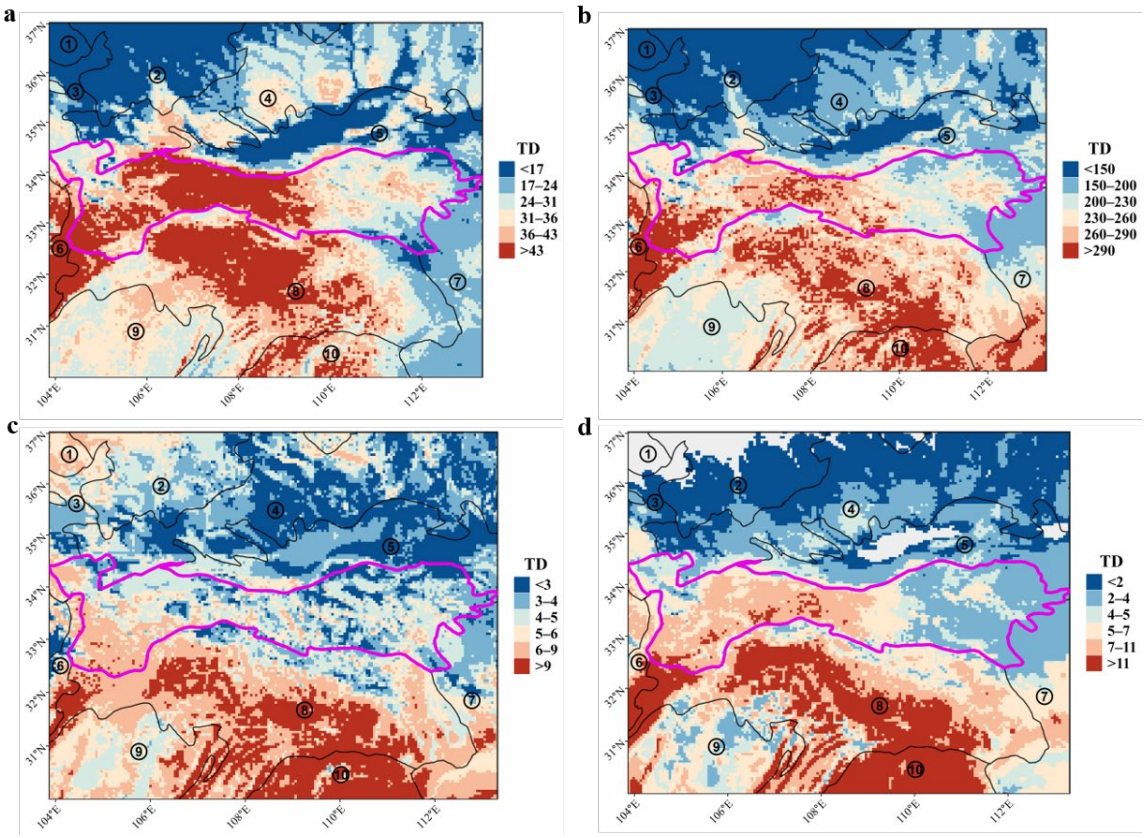


Figure S5. Spatial patterns of taxonomic diversity (TD) for terrestrial vertebrates in the Qinling Mountains and adjacent regions. (a) Mammals (129 species); (b) birds (685 species); (c) reptiles (69 species); (d) amphibians (58 species). Numbers on the maps indicate specific ecoregions, consistent with the numbering system defined in **Figure S1**.

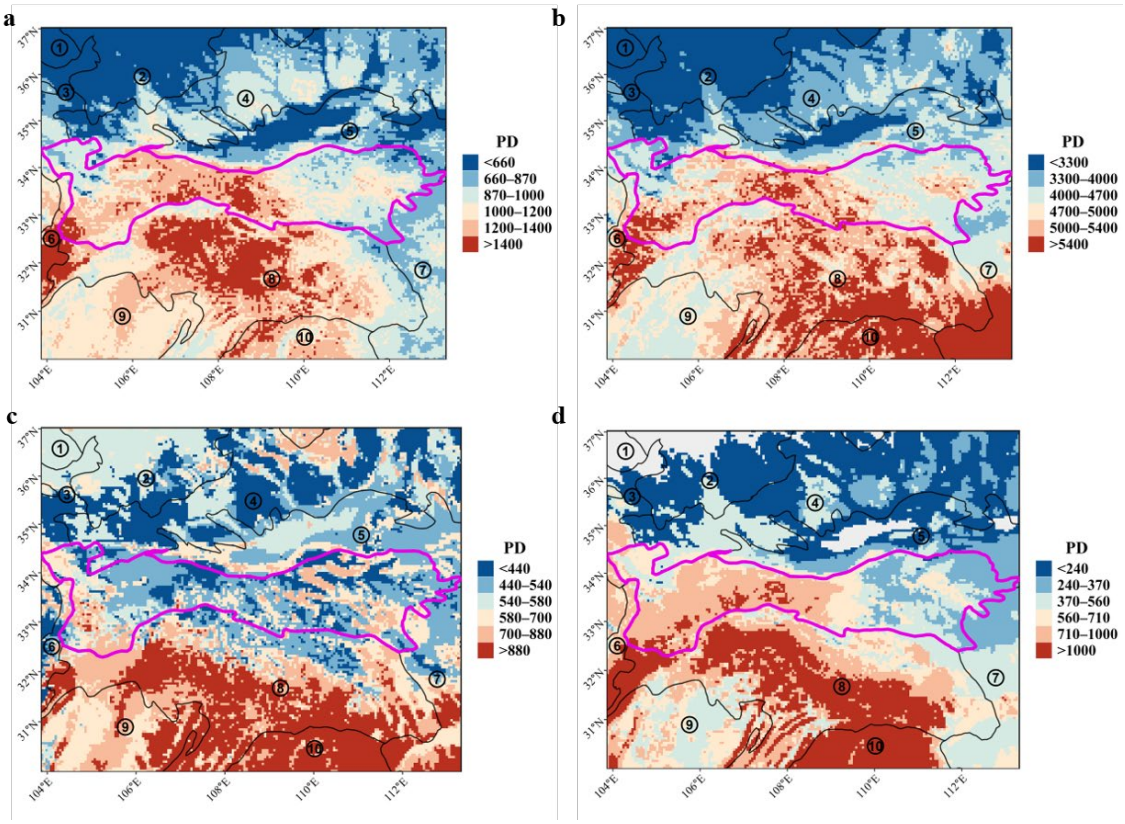


Figure S6. Spatial patterns of phylogenetic diversity (PD) for terrestrial vertebrates in the Qinling Mountains and adjacent regions. (a) Mammals (123 species); (b) Birds (617 species); (c) Reptiles (64 species); (d) Amphibians (54 species). Numerical annotations on the maps indicate specific ecoregions, the details of which are consistent with the numbering system defined in **Figure S1**.

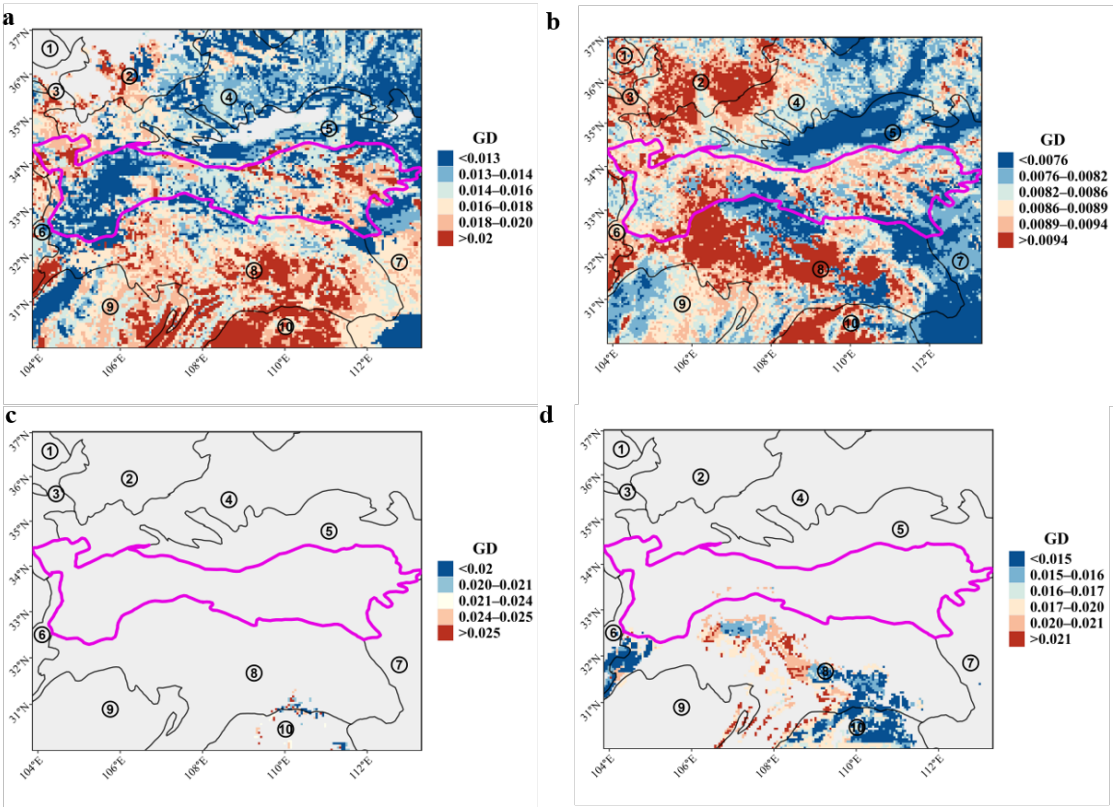


Figure S7. Spatial patterns of genetic diversity (GD) for terrestrial vertebrates in the Qinling Mountains and adjacent regions. (a) Mammals (93 species); (b) Birds (343 species); (c) Reptiles (36 species); (d) Amphibians (32 species); Numerical annotations on the maps indicate specific mountain systems and geographical regions, the details of which are consistent with the numbering system defined in **Figure S1**.

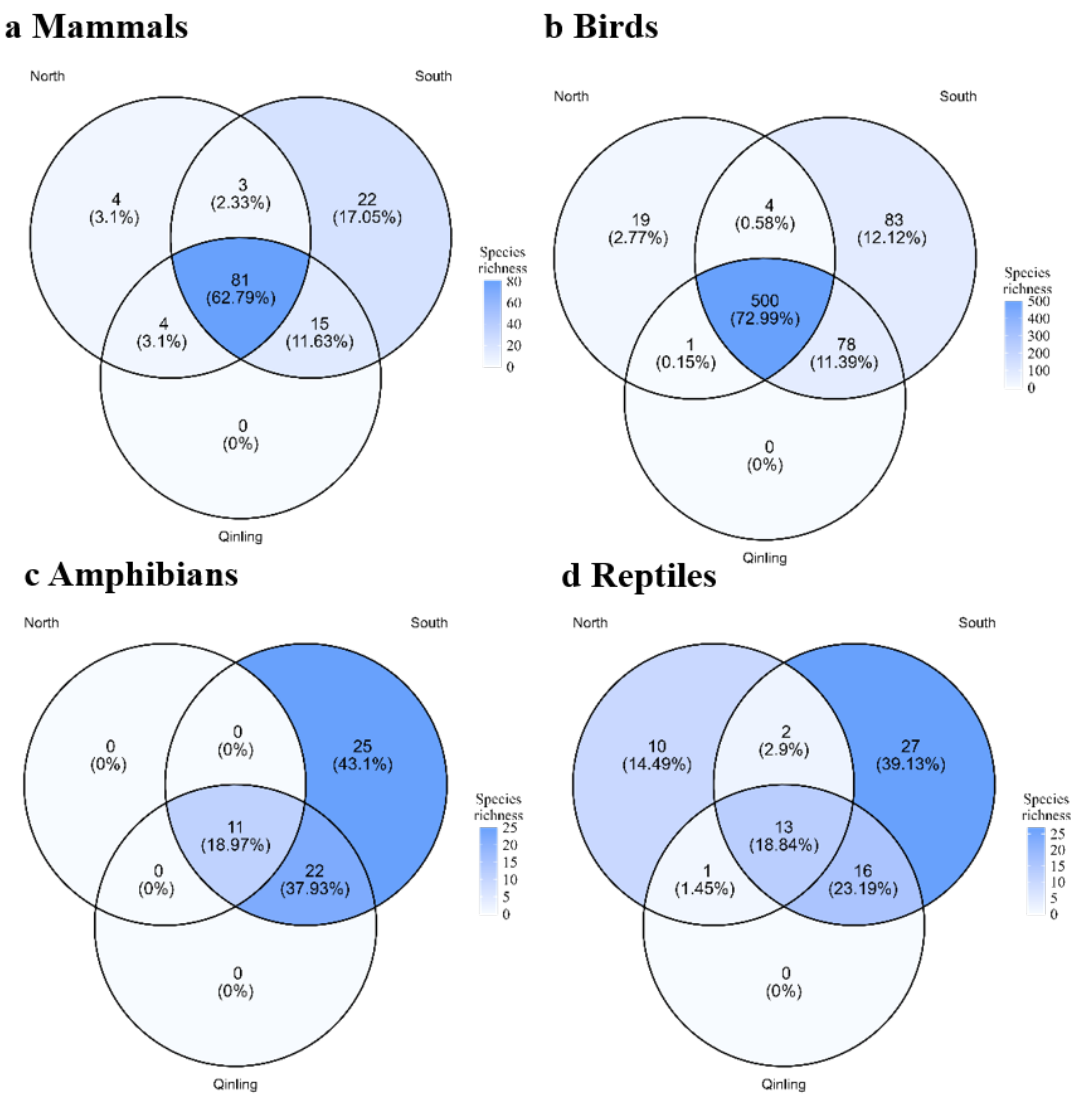


Figure S8. Venn diagrams illustrating the species composition and distribution overlap of four terrestrial vertebrate groups across the North, South, and Qinling regions. Panels show (a) Mammals, (b) Birds, (c) Amphibians, and (d) Reptiles. The three circles in each panel represent the North, South, and Qinling regions. Numbers indicate species counts, and percentages in parentheses denote the proportion of species in each overlap section relative to the total number of species in that taxonomic group. Blue gradient scales on the right indicate species richness levels.

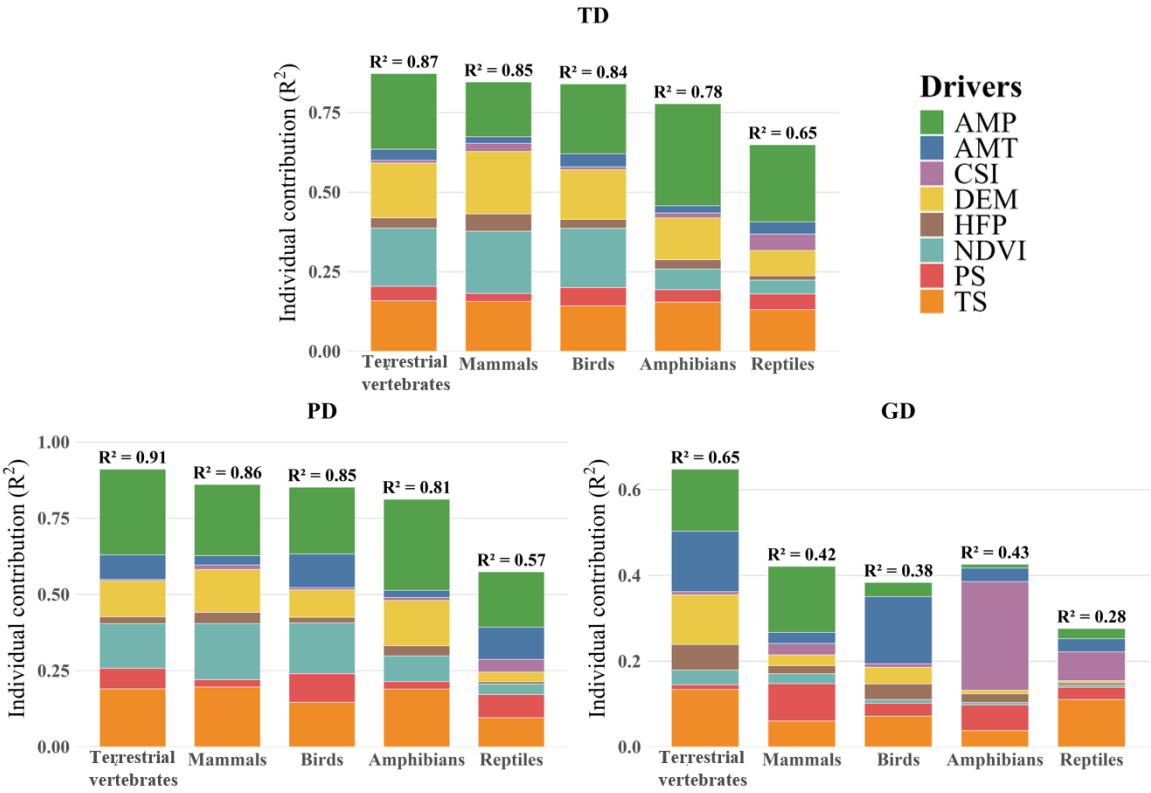


Figure S9. Relative individual contributions of environmental and anthropogenic drivers to multidimensional biodiversity across terrestrial vertebrate classes. The stacked bar charts illustrate the independent contributions (expressed as individual R^2 values) of eight drivers to taxonomic diversity (TD), phylogenetic diversity (PD), and genetic diversity (GD) for all terrestrial vertebrates combined and for mammals, birds, amphibians, and reptiles. The total explained variance (overall R^2) for each model is shown above the corresponding bar, representing the comprehensive explanatory power of the combined predictors. The eight drivers included in the analysis are AMT (Annual Mean Temperature), AMP (Annual Mean Precipitation), NDVI (Normalized Difference Vegetation Index), TS (Temperature Seasonality), PS (Precipitation Seasonality), CSI (Historical Climatic Stability), DEM (Elevation Range), and HFP (Human Footprint).