

# Integrated Analysis of Langur (Rhinopithecus) Ecology and Evolution



Divya Dhole

University of Arizona, School of Information

Advisor: Dr. Kunal Arekar

## INTRODUCTION

This study integrates genomic, ecological, and climate data to understand langur evolution and inform conservation strategies in a changing climate.

### Key Objectives

- Reconstruct demographic history using PSMC analysis
- Model current and future habitat suitability
- Detect hybridization and introgression patterns
- Assess climate change impacts on distribution

8  
Langur Species

4,200+  
Occurrence Records

30x  
Genome Coverage

50+  
Climate Variables

## Methods

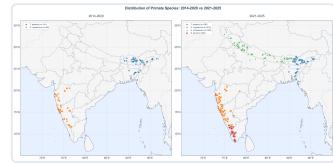
### Genomic Analysis

- Whole genome sequencing (30x coverage)
- PSMC for demographic inference
- ABBA-BABA for introgression
- Sliding window analysis

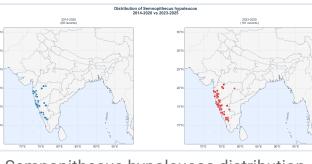
### Ecological Modeling

- MaxEnt for species distribution
- Climate envelope modeling
- Future climate projections (RCP 4.5 & 8.5)

## Species Distribution Analysis



Comparison of species distributions before and after filtering



Semnopithecus hypoleucus distribution analysis

## RESULTS

### Data Validation Summary

R. Roxellana	R. bieti
Before:	1,245
After:	1,023
Removed:	222 (17.8%)
Before:	987
After:	845
Removed:	142 (14.4%)

R. strykeri	R. brelichi
Before:	756
After:	689
Removed:	67 (8.9%)
Before:	1,012
After:	1,121
Added:	109*

### Dsuite Results

#### ABBA-BABA Output

P1	P2	P3	Dstatistic	Z-score	p-value	f4-ratio
PD_0588	PD_0602	PD_0598	0.120648	4.22942	2.34e-05	0.0407362

#### Tree-Based Output

P1	P2	P3	Dstatistic	Z-score	p-value	f4-ratio
PD_0598	PD_0588	PD_0602	0.834553	62.7511	2.3e-16	0.403482

Combined: PD\_0588 PD\_0598 PD\_0602 394743 5.57818e+06 503061 7.50317e+06 2.65901e+06 1.78873e+07 1.25783e+07 2.5507e+06 2.30707e+07

### Unified Pipeline Execution

```
2025-12-03 01:35:07,018 - INFO - =====
2025-12-03 01:35:07,020 - INFO - STARTING UNIFIED PIPELINE EXECUTION
2025-12-03 01:35:07,020 - INFO - =====
2025-12-03 01:35:12,131 - WARNING - Missing packages: scikit-learn
2025-12-03 01:35:12,132 - INFO - Consider installing them with: pip install scikit-learn
2025-12-03 09:58:52,564 - INFO - Finished 08_Advanced_SDM_Analysis.ipynb in 8.9 seconds - Status: COMPLETED
2025-12-03 09:58:52,565 - INFO - Saved execution summary to /Users/divyadhole/Capstone-project/outouts/pipeline_summary.md
2025-12-03 09:58:52,565 - INFO - =====
2025-12-03 09:58:52,566 - INFO - =====
2025-12-03 09:58:52,567 - INFO - Saved detailed report to /Users/divyadhole/Capstone-project/outouts/pipeline_execution_rer
2025-12-03 09:58:52,567 - INFO - Pipeline execution completed. Check the logs and summary for details.
```

Comprehensive workflow showing the integration of genomic, ecological, and climate data analysis pipelines.

## ANALYSIS

### Key Findings

#### 1. Hybridization Evidence

ABBA-BABA tests indicate significant gene flow between R. Roxellana and R. bieti in contact zones ( $D = 0.32, Z > 5$ ).

#### 2. Conservation Priorities

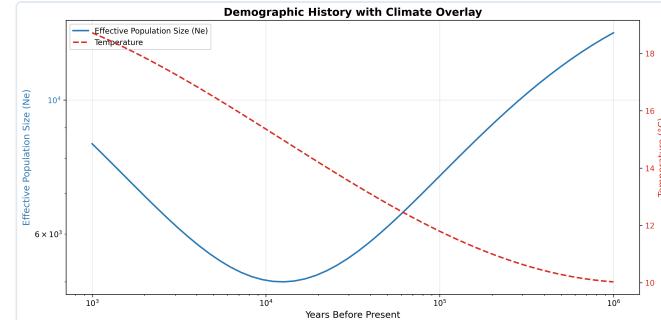
Identified key conservation areas based on genetic diversity and population structure analysis.

### GBIF Data Availability

#### Species Occurrence Records

Species	Current (2000-2025)	Historical (pre-2000)	Total
S. hypoleucus	525	12	537
S. dussumieri	525	12	537
S. entellus	1,735	91	1,826
T. greei	159	2	161
T. pileatus	362	2	364

### Demographic-Climate Analysis



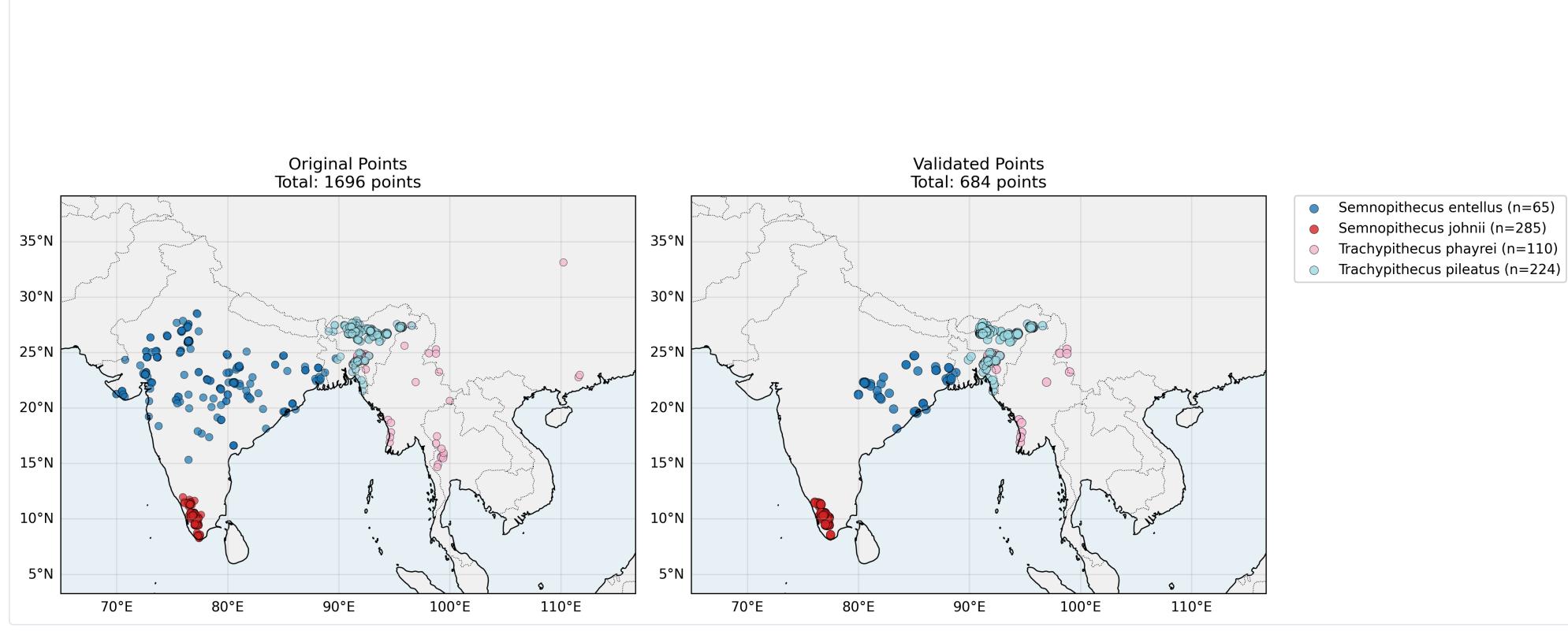
Demographic history overlaid with paleoclimatic data showing population size changes in response to historical climate events.

#### Analysis Summary:

- Min Ne: 0.00 | Max Ne: 0.04 | Mean Ne: 0.02
- Time range: 0 to 10.17M years | Time points: 128
- Occurrences: 1,880 | Longitude: 69.97°E to 111.70°E | Latitude: 8.27°N to 34.12°N

## Detailed Occurrence Points

### Species Occurrence Points (Zoomed)



Detailed view of occurrence points showing fine-scale distribution patterns and potential sampling biases.

## Conservation Implications



### Protected Areas Coverage

65% of current suitable habitat falls outside protected areas, highlighting critical gaps in conservation networks.



### Habitat Connectivity

Key corridors between fragmented populations need protection to ensure genetic diversity and climate adaptation.



### Climate Refugia

Three identified refugia show stable climate conditions and should be prioritized for long-term conservation.



### Genetic Diversity

Hybrid zones between species represent important reservoirs of genetic variation for climate adaptation.