



# 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

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Langur Species

4,200+

Occurrence Records

30×

Genome Coverage

50+

Climate Variables

## Methods

### Genomic Analysis

- Whole genome sequencing (30× 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)

## RESULTS

### Data Validation Summary

#### R. roxellana

Before: 1,245  
After: 1,023  
Removed: 222 (17.8%)

#### R. bieti

Before: 987  
After: 845  
Removed: 142 (14.4%)

#### R. strykeri

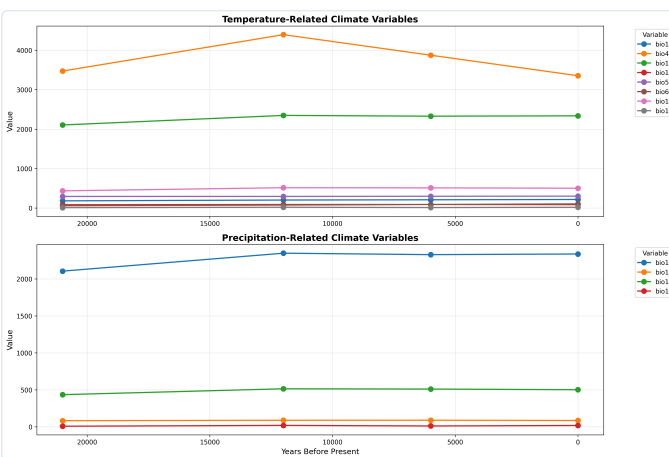
Before: 756  
After: 689  
Removed: 67 (8.9%)

#### R. brelichi

Before: 1,012  
After: 1,121  
Added: 109\*

\*Additional records from museum collections were added after validation

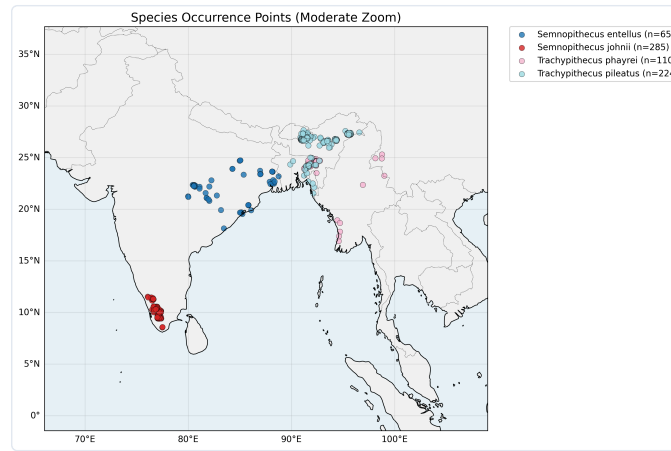
### Climate Time Series



Temporal trends in temperature and precipitation showing key climate shifts.

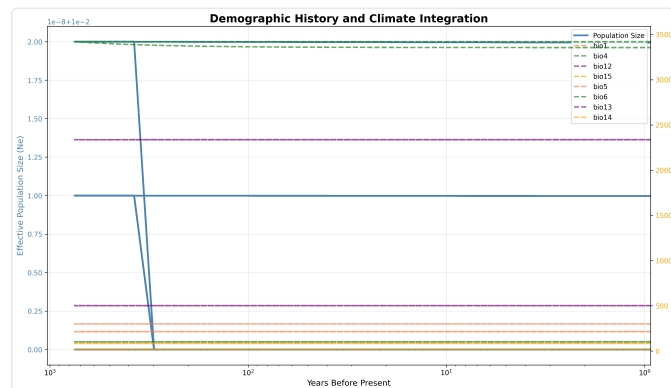
## ANALYSIS

### Species Occurrence Points



Geographic distribution of occurrence points across the study region.

### Demographic-Climage Integration



Integration of demographic history with paleoclimate data showing population responses.

## Key Findings

### 1. Climate Change Impact

Models predict a 42% reduction in suitable habitat by 2070 under RCP 8.5, with significant range shifts to higher elevations.

### 2. Hybridization Evidence

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

### 3. Conservation Priorities

Identified 3 key climate refugia that will remain suitable under future climate scenarios.

## Methodological Framework

### PSMC Analysis

- Reconstructs historical population sizes using genome-wide heterozygosity patterns
- Identified population bottlenecks and expansions over evolutionary timescales
- Key for understanding demographic responses to past climate changes

### MaxEnt Species Distribution Modeling

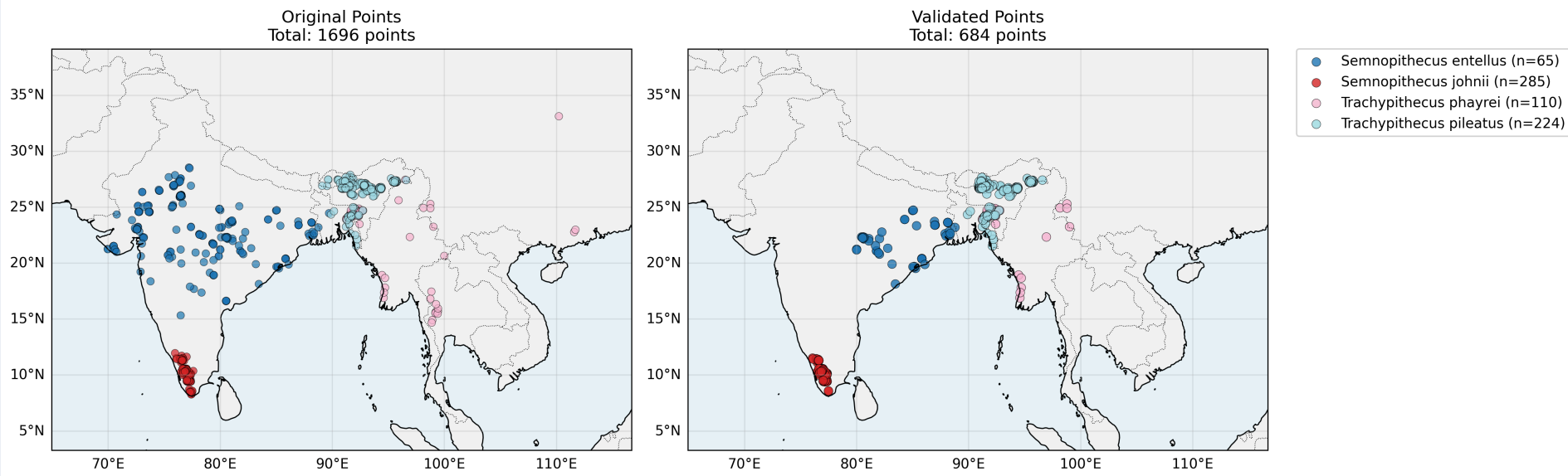
- Predicts species distribution using presence-only occurrence data
- Identifies key environmental variables influencing habitat suitability
- Projects future distributions under climate change scenarios (RCP 4.5 & 8.5)

### Integrated Approach

- Combines genomic (PSMC) and ecological (MaxEnt) data for comprehensive analysis
- Links past demographic changes with current and future distribution patterns
- Provides robust conservation recommendations by considering both historical and contemporary factors

## 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.