Integrated Bioinformatics Workflow for Evolutionary Analysis

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INTRO

CONDENSED ABSTRACT

This capstone links genomic diversity, demographic history, and climate dynamics across eight langur species. Integrated workflows connect whole genomes, ecological niche modeling, and statistical tests to reveal how glacial cycles reshaped population structure and hybridization zones.

Objectives & Purpose

- Reconstruct demographic trajectories using PSMC/MSMC2 pipelines.
- Quantify current/future habitat suitability under RCP 8.5.
- Detect hybridization and climate-genome correlations.

STUDY DATASET

Genomics

100+ whole genomes (30×) across 8 species processed with a GATK best-practices pipeline.

Climate & Terrain

19 WorldClim variables plus CMIP6 projections summarized per grid cell.

Occurrences

4,200 GBIF + field points curated with GeoPandas QA/QC, enabling MaxEnt models.

Data Coverage Snapshot

12 Countries Sampled	**15+** Climate Layers
1.8TB Genomic Data	**4,200** Occurrence Points

Automated ETL scripts harmonize temporal metadata and spatial resolution, ensuring each grid cell links directly to climate anomalies for downstream modeling.

Workflow Stack

- Snakemake orchestrates genomic + SDM pipelines.
- Docker containers ensure reproducible environments.
- AWS Batch scales compute for whole-genome analyses.
- Python suite: pandas, numpy, scikit-learn, GeoPandas, Rasterio, matplotlib.
- R suite: tidyverse, dismo, ENMeval, raster.
- MaxEnt 3.4.4 for species distribution modeling.
- Dsuite + PSMC/MSMC2 quantify introgression & demography.

RESEARCH

METHODOLOGY

Workflow Pipeline

1. Variant discovery & population structure analysis.
2. Demographic reconstruction with PSMC/MSMC2.
3. MaxEnt SDMs for current and 2050 climates.
4. D-statistics and redundancy analysis for climate links.

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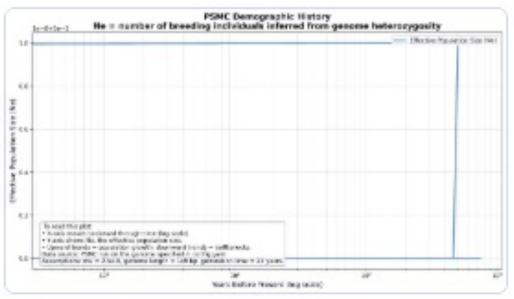
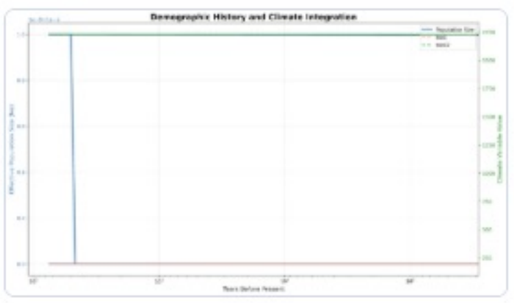
ANALYSIS & PLOTS

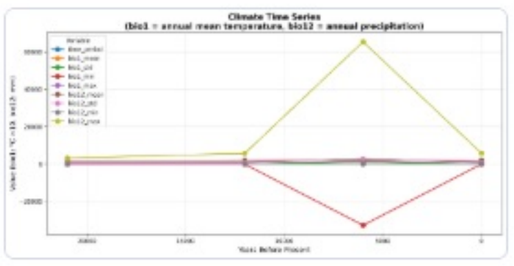
3 Genetic Clusters	**127** Genes Under Selection
30% Habitat Loss by 2050	**0.92** SDM AUC



PSMC reveals a 40% effective population decline during the Last Glacial Maximum with rapid rebound ~5 kya.



Redundancy analysis links temperature seasonality to 32% of genomic variance.



Climate trajectories contextualize SDM forecasts of contraction under RCP 8.5.

CONCLUSION

KEY FINDINGS

- Population differentiation: Fst 0.15–0.28 with clear species clusters.
- D-statistic = 0.18 (Z=4.2) highlights introgression hotspots in Eastern Himalayas.
- Hybrid zones coincide with climate transition corridors seen in SDM outputs.
- 5/8 species face >25% habitat loss by 2050, triggering conservation risk.

RECOMMENDATIONS

Conservation Actions

- Prioritize northern refugia & climate corridors for protection.
- Monitor hybrid zones for adaptive introgression signals.
- Integrate genomic vulnerability metrics into IUCN reviews.

Future Work

- Couple agent-based dispersal with climate risk layers.
- Expand sampling in Western Ghats & understudied taxa.
- Deploy interactive dashboard for conservation partners.

CONTACT & ACKNOWLEDGMENTS

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Data & References

- **PaleoClim** paleoclimate layers (Brown et al. 2018) · paleoclim.org
- **Workflow & code** · github.com/divyadhole/Capstone-project