enables the estimation of survival and dispersal rates through mark-recapture analysis; and on-site nest monitoring, which yields direct measures of breeding success and productivity. Integrating these approaches allows for robust, multi-scale insights into population trends and demographic parameters (Zipkin et al., 2017; Reinke et al., 2019). Recent advances also emphasize the value of combining different data types—such as count data and detection-nondetection records—within unified analytical frameworks to improve inference about abundance and demographic rates, even when detection probabilities vary (Buckland et al., 2004; Hostetler and Chandler, 2015; Zipkin et al., 2017).

3.2 Demographic parameters

Key demographic parameters assessed through field observations include survival rates, breeding success rates, and juvenile survival. These metrics are critical for modeling population growth or decline and for identifying life stages most sensitive to environmental pressures. State-space models and integrated population models are increasingly used to estimate these parameters, accounting for both ecological process variation and observation error (Buckland et al., 2004; Hostetler and Chandler, 2015; Zipkin et al., 2017). Such models can incorporate data from marked and unmarked individuals, providing more accurate estimates of survival and reproduction over time (Buckland et al., 2004; Zipkin et al., 2017).

3.3 Population trends and threats

Long-term monitoring reveals that population trends are shaped by a combination of natural and anthropogenic factors. Habitat loss and fragmentation remain primary threats, reducing available nesting and foraging sites. Illegal trade, particularly in high-value raptor species, can cause significant population declines. Environmental pollution, including pesticides and heavy metals, further impacts survival and reproductive success. Field-based population viability analyses, especially when integrated with remote sensing and landscape data, help forecast the effects of these threats and guide conservation actions (Reinke et al., 2019; Giezendanner et al., 2020).

3.4 Influence of climatic and anthropogenic factors

Climatic variables such as temperature and precipitation directly influence demographic rates by affecting food availability, breeding timing, and survival (Giezendanner et al., 2020; Neta et al., 2021). Anthropogenic factors—including land use change, urbanization, and direct persecution—can exacerbate natural fluctuations, leading to increased extinction risk. Advanced modeling frameworks now incorporate both static (e.g., topography) and dynamic (e.g., climate, vegetation) variables to predict spatial and temporal trends in population occupancy and viability (Giezendanner et al., 2020; Neta et al., 2021). These approaches enable near-term ecological forecasting and support adaptive management in the face of rapid environmental change (Reinke et al., 2019; Giezendanner et al., 2020; Neta et al., 2021).

4 Genomic Approaches to Studying Adaptive Evolution

4.1 Genomic sequencing and assembly strategies

Advances in high-throughput sequencing technologies have enabled the generation of whole-genome assemblies for both model and non-model organisms, providing the foundation for comparative and population genomics studies of adaptive evolution (Bomblies and Peichel, 2022; Hu et al., 2023). These strategies include the use of next-generation sequencing to capture genome-wide variation, allowing for the identification of both single nucleotide polymorphisms (SNPs) and structural variants such as gene duplications, deletions, and transposable element insertions (Villanueva-Cañas et al., 2017; Bomblies and Peichel, 2022). The increasing accessibility of genomic data facilitates the detection of gene loss events and the construction of high-quality gene catalogs, which are crucial for understanding the molecular basis of adaptation (Villanueva-Cañas et al., 2017; Sharma et al., 2018).

4.2 Population genetic structure and gene flow

Population genomics enables the analysis of genetic structure and gene flow within and between populations, which is essential for understanding the evolutionary processes shaping adaptive traits (González-Martínez et al., 2006; Combrink et al., 2024). By sampling many individuals across the species' range, researchers can infer patterns of hybridization, introgression, and the re-use of standing genetic variation during adaptation (Combrink