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Conservation Genomics and Artificial Intelligence in the Recovery of Critically Endangered Species

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ABSTRACT: Critically endangered species are managed at the limits of both biological and informational constraints: populations of tens to hundreds of individuals, fragmented habitat, and decisions taken before the evidence is complete. Two technological shifts have changed that evidence. Genome-wide data have replaced sparse neutral markers, allowing inbreeding to be measured directly from runs of homozygosity, genetic load to be quantified, conservation units to be delimited, pedigrees to be reconstructed and adaptive potential to be assessed. More recently, artificial intelligence (AI) has entered the same workflow, processing camera-trap and acoustic archives, performing variant calling and sequence annotation, inferring demographic history from simulated training data, and prioritising protected areas under budget constraints. This review synthesises literature published mainly between 2010 and 2025 on conservation genomic approaches for critically endangered taxa and integrates it with work on AI in biodiversity conservation. We summarise the genomic data types now available, the population-genomic metrics that translate most directly into management, and the interventions they inform, including genetic rescue, genetically guided captive breeding, biobanking and wildlife forensics. AI applications are then reviewed across the same pipeline and four points of convergence between the two fields are identified. Case studies of the kākāpō, vaquita, Florida panther and black-footed ferret indicate that low genetic diversity alone is a poor predictor of extinction risk, and that demographic history determines whether inbreeding constitutes an emergency. We conclude that genomics and AI sharpen conservation decisions rather than substituting for habitat protection and threat reduction, and identify the barriers limiting their use.

1. INTRODUCTION

Extinction has become an immediate conservation concern. Vertebrate populations are disappearing far faster than the historical background rate inferred from fossils, and the species in the highest IUCN threat category, Critically Endangered, are those for which the opportunity for effective intervention is especially limited (Ceballos et al., 2020). For such taxa, protection seldom consists simply of reserving habitat and waiting for recovery. Management commonly requires active

demographic intervention, translocation, captive propagation, disease control, predator exclusion and enforcement, frequently in parallel, while decisions must be made with limited time, funding and evidence.

Genetic information has supported this toolkit since the 1980s, when concerns about inbreeding depression and the loss of evolutionary potential in limited populations became established in conservation biology. For much of that period, the available empirical evidence was limited: limited microsatellite panels or short mitochondrial sequences, which were used to approximate heterozygosity, population differentiation and parentage. Although informative, these markers had substantial sampling limitations, and they represented only a very limited portion of the genome. The transition to genome-wide datasets changed the situation qualitatively rather than merely quantitatively (Allendorf et al., 2010; Supple and Shapiro, 2018). With thousands to millions of loci, and with increasing frequency with chromosome-level reference assemblies, researchers could estimate realised individual inbreeding, to examine deleterious variants associated with inbreeding depression, to reconstruct the timing of historical bottlenecks, and and to separate recent human-driven contraction from long-term natural rarity.

A further transformation is occurring. Ecological conservation now generates datasets volumes that are difficult to process manually: camera networks generating millions of images during a season, passive acoustic sensors operating continuously for extended periods, high-resolution satellite and drone imagery, GPS telemetry streams, and sequencing output measured in terabases. Machine-learning methodological approaches, especially deep neural approaches, have progressed from demonstrations toward routine applications across these datasets streams (Kwok, 2019; Tuia et al., 2022; Christin et al., 2019). Within genomic analysis, neural networks now perform variant calling at or above the accuracy of hand-engineered statistical callers (Poplin et al., 2018), predict protein structure from sequence (Jumper et al., 2021), and infer demographic history from simulated training datasets (Schrider and Kern, 2018; Sanchez et al., 2021). At the management-decision stage, reinforcement learning has been applied to spatial conservation prioritisation under explicit budget constraints (Silvestro et al., 2022).

2. SCOPE, APPROACH AND SOURCE VERIFICATION

This paper is a narrative synthesis and was not conducted as a PRISMA systematic review; it does not use a preregistered, fixed search protocol with a reproducible date range, and readers seeking a systematic evidence synthesis should treat it accordingly. Relevant literature was located through an iterative process using topic-based searches of the genomic and machine-learning conservation literature (indicative terms included “conservation genomics”, “runs of homozygosity”, “genetic rescue”, “genetic load”, “deep learning” and “artificial intelligence” in combination with “critically endangered” and “threatened species”), with additional backward citation tracing from influential investigations and by and targeted checks of bibliographic information, publication venue and factual claims for every cited source against the original publication or an indexing record. Primary research was prioritised in high-visibility journals, to methodological papers with demonstrated application beyond model organisms, and to the most recent synthesis available for each topic.

investigations were considered when they addressed IUCN-listed Critically Endangered or Endangered taxa, or presented a method with demonstrated application to non-model organisms, and provided that the findings had a plausible link to conservation or management action. investigations concerned solely with model or domesticated organisms, work centred on de-extinction, and non-English-language sources were generally excluded. Because the selection process was iterative rather than strictly protocol based, the resulting coverage reflects the authors' judgement of what is representative and load-bearing for the argument rather than a complete inventory of published work; readers requiring a comprehensive, auditable evidence base should consult the systematic reviews cited within specific sections.

Three additional scope limitations should be noted. First, plants, invertebrates and marine taxa receive less extensive treatment than terrestrial vertebrates, consistent with the uneven distribution of published investigations rather than a judgement about importance. Second, de-extinction is outside the detailed scope of this review, since it raises distinct scientific and ethical questions, though cloning and biobanking are covered where they facilitate extant populations. Third, the term artificial intelligence is used here in its standard technical sense of statistical learning from datasets, encompassing supervised and unsupervised machine learning, deep neural networks and reinforcement learning, and does not refer to artificial general intelligence.

Figure 1 summarises the framework used to organise what follows: a pipeline running from sampling and monitoring, through genomic data generation and population-genomic inference, to the management decisions those inferences support, with artificial intelligence entering at every stage rather than at any single point.

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3. GENOMIC APPROACHES: DATA TYPES AND PLATFORMS

3.1 From markers to genomes

Early conservation genetics progressed from allozyme markers to mitochondrial sequences and later to microsatellite panels. Each successive marker system increased analytical resolution, but all shared a limitation: they covered only a limited and sometimes non-representative part of the genome, and they could not distinguish the genomic regions that matter for fitness from those that do not. High-throughput sequencing substantially reduced this limitation. The practical consequence for limited populations is that estimates which were previously imprecise, individual inbreeding coefficients, effective population size, relatedness among captive founders, became precise enough to act on (Hohenlohe et al., 2021).

Genome-scale analysis in addition expanded the range of biological questions that could be examined. Marker investigations mainly characterised contemporary genetic diversity. Genome-scale datasets in addition permit reconstruction of population history: the timing and depth of bottlenecks, the age of inbreeding events recorded in the length distribution of homozygous tracts, the accumulation or purging of deleterious alleles, and signatures of selection associated with environmental gradients or disease. For critically endangered taxa, these historical inferences have direct management relevance; they determine whether low diversity is an emergency or a long-standing condition the species has already survived.

3.2 Reference genomes and global sequencing initiatives

A well assembled reference genome greatly expands the analyses possible with population samples. It facilitates more reliable variant identification and phasing, annotation of coding regions so that variants can be classified by predicted effect, detection of structural variation, and comparative analyses across related taxa. Chromosome-level assemblies produced with long-read and long-range scaffolding technologies have become the standard target (Rhie et al., 2021), and consortia including the Vertebrate Genomes Project and the broader Earth BioGenome Project have made reference genomes available for a rapidly growing number of threatened species (Lewin et al., 2022). The kākāpō assembly, generated within the Vertebrate Genomes Project and used directly in the analysis of the surviving population, is a clear example of a reference genome built with a conservation programme rather than merely for one (Dussex et al., 2021).

3.3 Reduced-representation and low-coverage strategies

Sequencing many individuals at whole-genome scale can still be costly for programmes operating on typical conservation budgets, and so several intermediate approaches are commonly adopted. Restriction-site-associated approaches, including RADseq and double-digest variants, and genotyping-by-sequencing produce thousands to tens of thousands of markers without a reference genome, and remain appropriate for questions of population structure, parentage and coarse diversity. Targeted capture of exomes or curated panels concentrates sequencing effort on functionally annotated regions, which suits disease-related or adaptive questions and works comparatively well on degraded DNA. Low-coverage whole-genome sequencing combined with genotype-likelihood methodological approaches has become an attractive compromise, delivering genome-wide inference from shallow datasets across many individuals.

Table 1. Principal genomic approaches used in the conservation of critically endangered species

method	Typical datasets yield	principal conservation uses	Key limitations
Whole-genome sequencing (medium to high coverage)	Genome-wide variants	Runs of homozygosity, genetic load, demographic history, structural variants	Cost per sample; requires reference assembly; computational demand
Low-coverage WGS with genotype likelihoods	Genome-wide, probabilistic genotypes	Diversity, structure, relatedness across many individuals	Uncertainty at individual genotypes; reference needed
Reduced-representation (RADseq, ddRAD,	Many genome-wide markers	Population structure, parentage, conservation unit delimitation	Allele dropout; poor for ROH and load estimation

method	Typical datasets yield	principal conservation uses	Key limitations
GBS)			
Targeted capture and amplicon panels	Curated loci or exome	Immunogenetic and disease loci; degraded and museum DNA	Ascertainment bias; panel design cost
Reference genome assembly	Chromosome-scale assembly	Foundation for all of the above; comparative and functional inference	Requires high-molecular-weight DNA; assembly and annotation effort
Non-invasive and environmental DNA	Trace environmental DNA	Detection, census, individual identification, diet, pathogens	Contamination, degradation, incomplete reference databases
Historical and museum DNA	Degraded historical DNA	Temporal comparison of diversity; extinct source populations	Post-mortem damage; specialised laboratory facilities

3.4 Non-invasive, historical and environmental DNA

When a species has been reduced to a very limited population, capture or handling may be impractical or undesirable. DNA collected from faeces, hair, feathers, shed skin or saliva can supply genetic information without capturing animals, and improvements in library preparation and target enrichment have made genome-scale work feasible from such material, though allelic dropout and contamination remain persistent issues. Environmental DNA from water, soil or air extends non-invasive surveillance even further by removing the need to encounter the organism at all (Taberlet et al., 2012; Deiner et al., 2017). For rare aquatic species in particular, eDNA surveys frequently detect presence where conventional survey effort fails, and metabarcoding of the same samples characterises the surrounding community.

Museum skins, bones and archived tissues add a historical dimension that contemporary sampling cannot. Comparison of genomes sampled before and after population decline quantifies exactly how much diversity has been lost and over what period, identifies source populations for restoration, and in some cases identifies that the current population is not representative of the historical species. The kākāpō investigation, which included fourteen genomes from the extinct mainland population alongside thirty-five modern island birds, illustrates the interpretive power of this design (Dussex et al., 2021).

4. GENOMIC METRICS THAT INFORM MANAGEMENT

Table 2. Population-genomic metrics and their management interpretation

Metric	What it measures	Management interpretation
Genome-wide heterozygosity	Standing genetic variation	Compare diversity
Runs of homozygosity	Realised individual inbreeding and its age	Guide breeding; infer inbreeding history
Effective population size (Ne)	Rate of drift and inbreeding accumulation	Assess drift and gene-flow needs

Metric	What it measures	Management interpretation
Genetic load and masked load	Burden of deleterious variation	Assess deleterious burden
Population structure and admixture	Differentiation and gene flow	Define units; detect admixture
Relatedness and reconstructed pedigree	Kinship among individuals	Support breeding pairs
Genotype-environment associations	Candidate adaptive variation	Guide source selection

4.1 Diversity and effective population size

Effective population size influences the rate at which drift erodes variation and inbreeding accumulates, and is often substantially smaller than the census count in species with skewed reproductive success, overlapping generations or fluctuating abundance. Genomic estimators based on linkage disequilibrium or on the coalescent allow Ne to be estimated over distinct time horizons from a single sample, which is valuable when historical monitoring datasets are absent. The appropriate thresholds remain debated for short-term and long-term viability, but the general conclusion is robust: maintaining genome-wide variation is the most reliable general strategy for avoiding inbreeding depression and preserving adaptive capacity, and attempts to substitute management of a limited set of putatively functional loci are usually infeasible and sometimes counterproductive (Kardos et al., 2021).

4.2 Inbreeding and runs of homozygosity

Pedigree-derived inbreeding coefficients represent expected relatedness; whereas ROH-based genomic inbreeding reflects realised homozygosity, and the two can diverge substantially for individuals with identical pedigrees. Because recombination progressively fragments long homozygous segments, the length distribution of these runs carries temporal information: long tracts generally point to recent shared ancestry, shorter ones an older history of limited population size. For a captive programme this permits pairing decisions that minimise realised inbreeding in offspring rather than its expectation, and for a wild population it distinguishes an incipient inbreeding problem from a long-standing equilibrium (Figure 2).

4.3 Genetic load, purging and the reinterpretation of low diversity

One of the relevant recent developments in conservation genomics is the analysis of genetic load. Deleterious recessive alleles that are effectively hidden in substantial outbred populations become exposed as homozygotes when populations shrink. The biological consequence depends strongly on the demographic history of decline. Populations that have been limited for a long time may have purged much of their highly deleterious recessive variation through purifying selection, at a demographic cost, and accordingly carry a lighter masked load than their heterozygosity alone would suggest (Hedrick and Garcia-Dorado, 2016).

4.4 Structure, hybridisation and conservation units

Identifying the appropriate conservation unit is a prerequisite for almost every management decision, and genomic datasets have both sharpened and complicated this task. Higher-resolution genomic datasets can reveal structure that smaller marker sets miss, sometimes identifying cryptic lineages that warrant separate management, sometimes showing that populations previously treated as distinct are not. Genomics has in addition identified how widespread hybridisation and introgression are, including among threatened taxa, raising legal and practical questions about the status of admixed individuals that conservation policy in many jurisdictions is still poorly equipped to answer (Wayne and Shaffer, 2016). The pragmatic position emerging from the literature is that admixture should be evaluated by its consequences for population persistence and adaptive capacity rather than by an abstract standard of genetic purity.

4.5 Adaptive potential and landscape genomics

Detecting genetic variation correlated with environmental gradients, through genotype-environment association methodological approaches and ordination-based approaches such as redundancy analysis (Capblancq and Forester, 2021), facilitates source selection for translocation and assisted gene flow, especially where climate change will shift the conditions a restored population must tolerate. Such associations are correlational, and in very limited populations the statistical power to detect selection is limited, so candidate adaptive loci are best treated as hypotheses supplementing, not replacing, genome-wide management (Kardos et al., 2021).

5. FROM GENOMIC DATA TO CONSERVATION ACTION

5.1 Genetic rescue and assisted gene flow

Genetic rescue involves introducing individuals from a genetically differentiated population to improve the fitness of an inbred population, is the intervention with the clearest genomic rationale and the strongest empirical facilitate. Meta-analytic evidence reports recurring fitness benefits of gene flow into limited inbred populations, and that the risk of outbreeding depression has generally been overestimated relative to the risk of continued inbreeding (Frankham, 2015; Whiteley et al., 2015). The Florida panther remains the reference case: eight female Texas pumas released in 1995 into a population showing multiple correlates of inbreeding depression were followed by a threefold increase in numbers, a doubling of heterozygosity, improved survival and fitness measures, and a decline in inbreeding correlates (Johnson et al., 2010).

5.2 Genetically guided captive breeding

Captive breeding programmes have traditionally relied on studbooks and pedigree-derived kinship to maximise retained diversity. Genomic information can extend this method in several ways. Where pedigrees are incomplete, wild-caught founders of unknown relationship, uncertain paternity, they can be reconstructed from genotypes. Where pedigrees are complete, realised relatedness replaces expected relatedness, thereby enabling finer pairing decisions. And where load has been characterised, breeding can be managed with explicit attention to known deleterious variants, as has been done for chondrodystrophy in the California condor and for several inherited disorders in captive ungulate populations. The kākāpō programme, in which every living individual has been sequenced, represents the current upper bound of this method: management decisions for an entire species informed by complete genomic coverage of its population (Dussex et al., 2021).

5.3 Biobanking, cloning and assisted reproduction

Frozen cell lines and gametes can retain genetic variation that would otherwise be lost as founders die, and have moved from insurance policy to active management tool. Somatic cell nuclear transfer has produced viable offspring from long-cryopreserved cells in the black-footed ferret and Przewalski's horse, reintroducing founder lineages absent from the living population for decades. These methodological approaches remain costly, technically specialised and relevant to only a limited number of species, and they do not address the causes of decline. Their appropriate role is narrow but real: restoring specific lost variation to a managed population whose habitat and threat situation is otherwise being addressed.

5.4 Wildlife forensics and trade enforcement

Genomic methodological approaches can strengthen wildlife-law enforcement by assigning seized material to geographic origin, identifying species from processed products, and matching individuals to poaching events. Assignment of substantial ivory seizures to source populations has identified the major African poaching hotspots and supported transnational investigations (Wasser et al., 2015), and standardised forensic genetic methodological approaches now underpin admissible evidence in several jurisdictions (Ogden and Linacre, 2015). For critically endangered species subject to targeted harvest, this application often has more immediate demographic consequence than any diversity metric.

6. ARTIFICIAL INTELLIGENCE IN THE CONSERVATION OF THREATENED SPECIES

6.1 Why machine learning entered conservation

6.2 Monitoring: computer vision, bioacoustics and remote sensing

Deep convolutional models trained with extensive camera-trap datasets now detect, identify and count animals with accuracy approaching that of human annotators on common species, eliminating most manual labour in the process (Norouzzadeh et

al., 2018). Generic detectors that separate animal from empty frames transfer well across regions and have become standard preprocessing. In bioacoustics, models such as BirdNET identify species from continuous audio at scale, enabling monitoring of cryptic and nocturnal taxa over long periods (Kahl et al., 2021). Applied to remote sensing, learned models detect deforestation, map habitat and count substantial animals in aerial and satellite imagery. Individual re-identification from natural markings facilitates mark-recapture estimation without physical capture, which for a critically endangered species may be the only acceptable method.

6.3 Machine learning inside the genomic pipeline

6.4 Deep learning for population-genomic inference

6.5 Functional prediction and structural biology

Table 3. Artificial intelligence methods across the conservation workflow

Stage	AI method	Representative application
Field monitoring	Convolutional and transformer vision models	Species identification and counting in camera-trap and aerial imagery
Acoustic monitoring	Deep audio classifiers	Automated species detection in continuous passive recordings
Individual identification	Metric learning and re-identification networks	Non-invasive mark-recapture from natural markings
Sequence processing	Neural basecalling and variant calling	Genotyping from short- and long-read datasets in non-model species
Variant interpretation	Supervised deleteriousness prediction; structure prediction	Estimation of genetic load; functional triage of candidate variants
Evolutionary inference	Simulation-trained supervised learning	Demographic history, selection scans, introgression detection
Risk and distribution modelling	Ensemble and deep species distribution models	Habitat suitability, range shifts under climate scenarios
Prioritisation and enforcement	Reinforcement learning; game-theoretic models	Protected area selection under budget; predictive patrol planning

6.6 Prediction, prioritisation and enforcement

At the management stage, learning algorithms can help allocate limited conservation resources. Reinforcement learning frameworks for spatial conservation prioritisation optimise the choice of protected areas against explicit budgets, human pressure and climate projections, outperforming established prioritisation software on simulated and empirical datasets (Silvestro et al., 2022). Predictive models trained on historical patrol and poaching records guide ranger deployment in protected areas, with field trials reporting increased detection of snares and illegal activity (Fang et al., 2016). Real-time analysis of telemetry datasets can trigger alerts when individuals leave protected boundaries or indicate movement patterns consistent with distress (Wall et al., 2014). Machine learning is in addition used to extend IUCN-style extinction risk assessment to the many species that remain unassessed, by learning from the relationships between assessed status and available occurrence, trait and environmental datasets.

6.7 Where genomics and AI converge

7. CASE STUDIES

Table 4 summarises programmes in which genomic data, and in several cases computational modelling, materially changed management. They are selected to illustrate different relationships between genetic information and outcome rather than to represent the field exhaustively.

Table 4. Representative applications of genomic and computational approaches in threatened species

Species	method	Principal finding or outcome
Florida panther (Puma concolor coryi)	Pedigree and marker-based genetic restoration	Translocation of eight Texas pumas tripled numbers and doubled heterozygosity; inbreeding correlates declined
Kākāpō (Strigops habroptilus)	Whole-genome sequencing of the entire living population plus historical genomes	Reduced mutational load in the long-isolated island population; genome-informed breeding management
Vaquita (Phocoena sinus)	Whole-genome sequencing with individual-based simulation	Low deleterious burden from historical rarity; recovery predicted if bycatch mortality ceases
Black-footed ferret (Mustela nigripes)	Biobanking and somatic cell nuclear transfer	Restoration of founder lineages absent from the living population
California condor (Gymnogyps californianus)	Genomic screening within a managed pedigree	Management of a lethal recessive disorder; detection of facultative parthenogenesis
Tasmanian devil (Sarcophilus harrisii)	Population genomics of host and transmissible tumour	Evidence of rapid selection at immune-related loci in response to devil facial tumour disease
African elephants (Loxodonta spp.)	Forensic genetic assignment of seizures	Identification of major poaching hotspots supporting transnational enforcement

8. CHALLENGES AND LIMITATIONS

8.1 Data, taxonomic and geographic bias

8.2 Sample quality and analytical pitfalls

Critically endangered taxa often supply the most challenging biological samples: limited numbers, non-invasive material, degraded museum specimens. Low-quality DNA produces allelic dropout, reference bias and artefactual homozygosity that can be mistaken for inbreeding. limited sample sizes limit power for selection scans and association analyses. Predictions of variant deleteriousness rest on annotation transferred from distant model organisms and are noisy for any individual variant, so aggregate measures of load should be preferred to claims about specific alleles.

8.3 Opacity, validation and misplaced confidence in models

8.4 Governance, equity and the research-implementation gap

9. FUTURE DIRECTIONS

10. CONCLUSION

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AUTHOR CONTRIBUTIONS

R.K. Sahu: Conception and design, literature search and screening, interpretation, writing — original draft.

R. Bhan: Literature search and screening, datasets curation, preparation of figures and tables.

G.K. Mahato: Methodology, interpretation, supervision, writing — review and editing. All authors read and approved the final manuscript.

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CONFLICT OF INTEREST

The authors report no competing interests.

ETHICS STATEMENT

This work synthesises published studies only; no new animal or human research was undertaken.

DATA AVAILABILITY STATEMENT

The review generated no new dataset. Source studies are cited, and the figures are author-prepared schematics.

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FIGURE LEGENDS

Figure 1. Framework for genome-informed conservation of critically endangered species. Each column represents a stage of the pipeline, from field sampling to management action; the lower panel indicates where artificial intelligence methods are currently applied.

Figure 2. Runs of homozygosity as a record of inbreeding history. (a) Recent common ancestry produces few long homozygous tracts, whereas inbreeding many generations in the past leaves numerous short tracts after recombination. (b) The resulting difference in tract length distributions. Schematic illustration of a conceptual pattern, not measurements from a specific dataset.

Figure 3. Demographic history and genetic load. (a) A population collapsing rapidly from a large historical size retains deleterious recessive variation that was previously masked, whereas a population small over long evolutionary time is exposed to sustained purifying selection. (b) Expected consequences for masked load and for the severity of inbreeding depression under further inbreeding. Schematic illustration of a conceptual relationship, not measurements from a specific dataset.

Figure 4. Artificial intelligence across the conservation workflow, showing the principal method families applied at each stage and the operational outputs they produce.

FIGURES

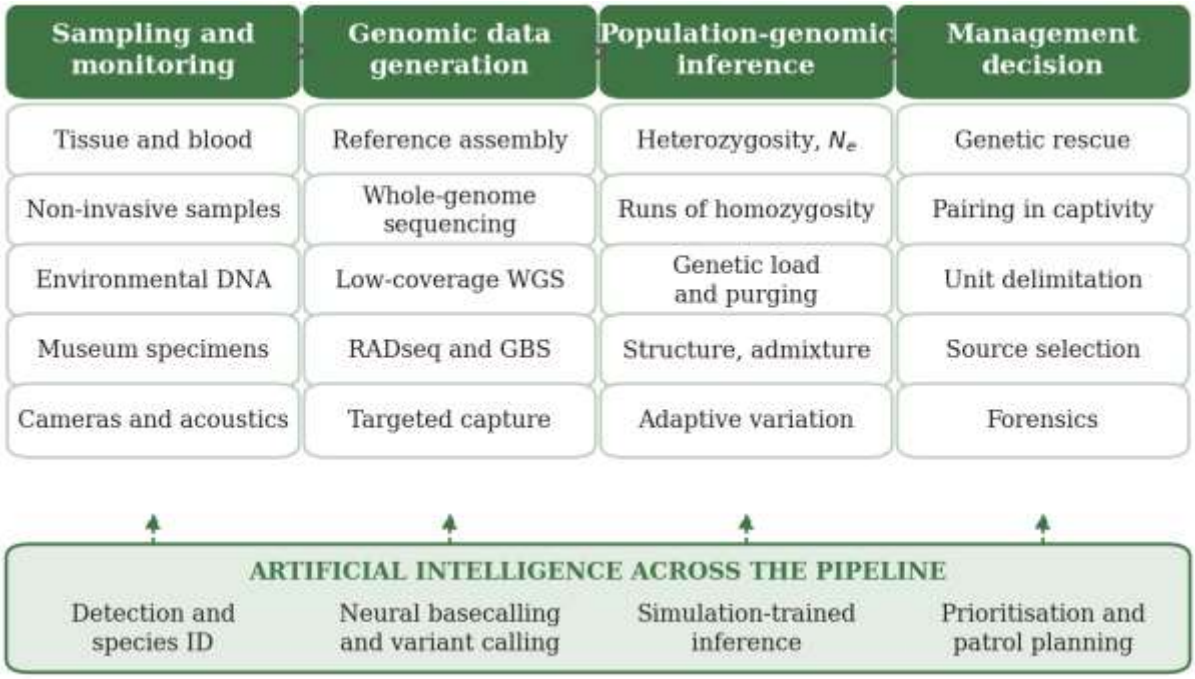

Figure 1

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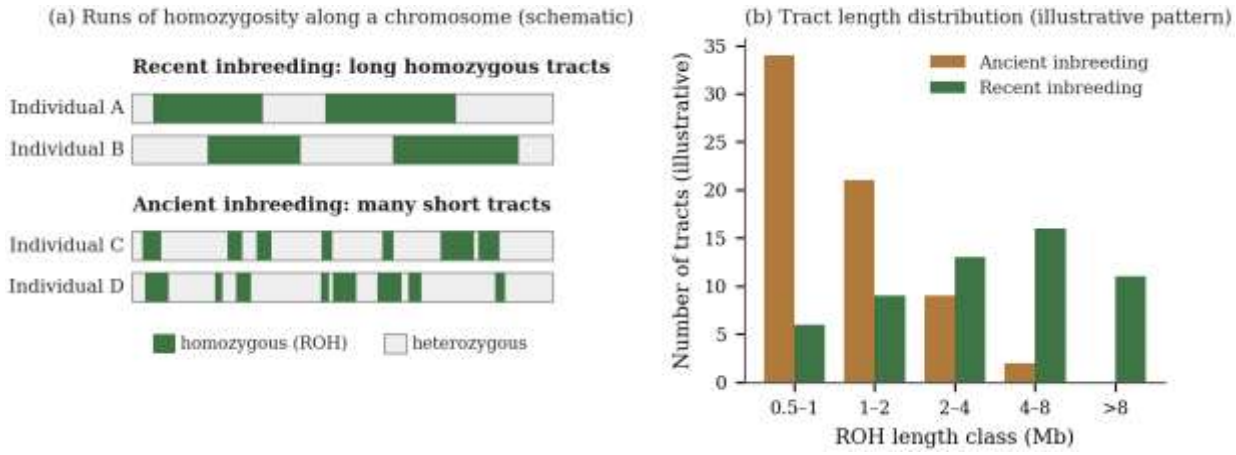

Figure 2

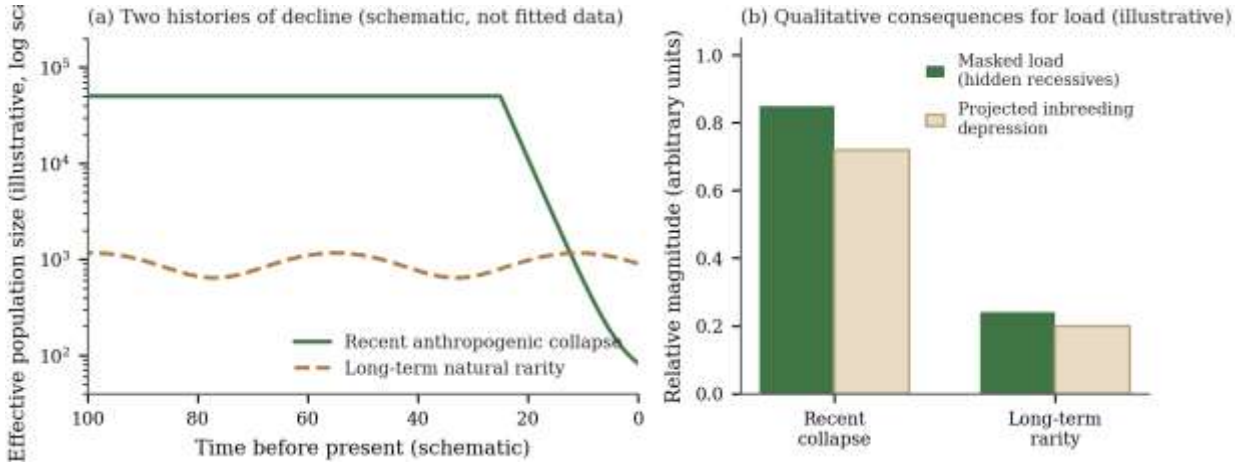

Figure 3

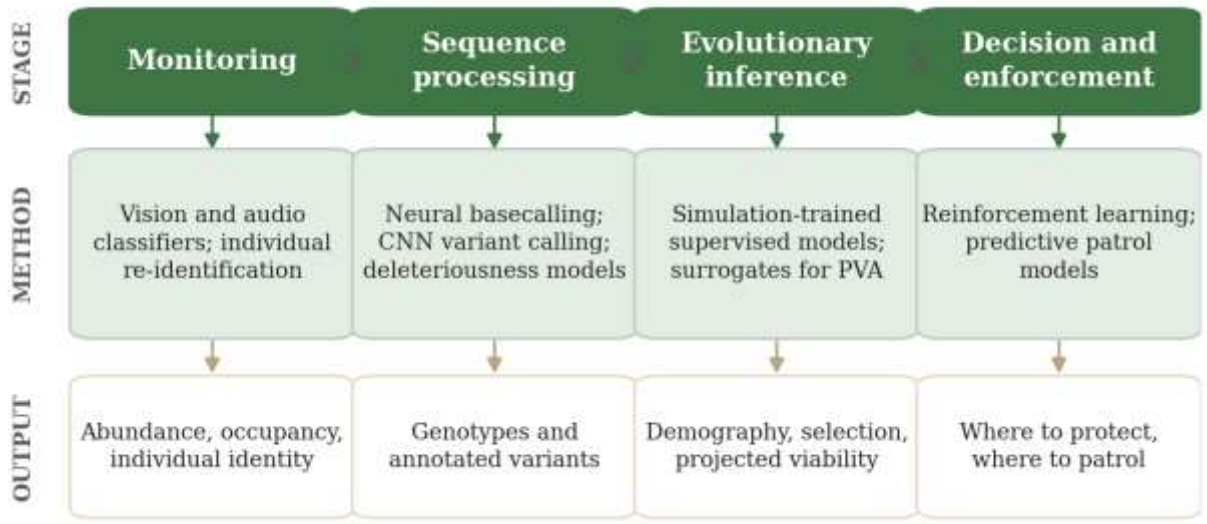

Figure 4