



Research Report

Open Access

Integrating Genomics and Remote Sensing Technologies for Wildlife Monitoring

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Animal Molecular Breeding, 2024, Vol.14, No.1 doi: [10.5376/amb.2024.14.0015](https://doi.org/10.5376/amb.2024.14.0015)

Received: 08 Jan., 2024

Accepted: 18 Feb., 2024

Published: 29 Feb., 2024

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Preferred citation for this article:

Zhu X., 2024, Integrating genomics and remote sensing technologies for wildlife monitoring, Animal Molecular Breeding, 14(1): 130-140 (doi: [10.5376/amb.2024.14.0015](https://doi.org/10.5376/amb.2024.14.0015))

Abstract This study outlines the integration of genomic and remote sensing technologies to enhance wildlife monitoring efforts. By combining these advanced methodologies, the study aims to foster a comprehensive understanding of wildlife populations and their dynamics in the face of global environmental challenges. We explore a range of genomic techniques, including DNA sequencing and CRISPR, alongside various remote sensing tools such as satellite imagery, drones, and camera traps. The study synthesizes data from diverse case studies and research findings to evaluate the efficacy and scope of these integrated technologies in real-world applications. The findings reveal significant advancements in wildlife monitoring, including improved accuracy in species identification, better understanding of genetic diversity, and enhanced capability for tracking habitat changes and animal movements over large spatial scales. Case studies demonstrate the practical benefits of technology integration in addressing conservation and management issues. Integrating genomics with remote sensing technologies offers transformative potential for wildlife conservation and management. This synergy enhances our ability to monitor ecosystem health, predict biodiversity changes, and implement effective conservation strategies, thereby supporting sustainable management of natural resources.

Keywords Wildlife monitoring; Genomics; Remote sensing; Conservation technology; Biodiversity management

Wildlife monitoring is a critical component of conservation biology, ecology, and environmental management. It involves the systematic collection of data on wildlife populations, their habitats, and the ecological processes that sustain them. Effective monitoring is essential for understanding biodiversity trends, assessing the health of ecosystems, and implementing conservation strategies to mitigate the impacts of human activities and environmental changes. The integration of advanced technologies, such as genomics and remote sensing, has the potential to revolutionize wildlife monitoring by providing more precise, comprehensive, and timely data. The field of wildlife monitoring has evolved significantly over the past few decades. Traditional methods, such as direct observation and manual tracking, have been supplemented and, in some cases, replaced by more sophisticated techniques. Genomics, for instance, has emerged as a powerful tool for understanding the genetic diversity, population structure, and adaptive potential of wildlife species. Advances in next-generation sequencing (NGS) technologies have enabled researchers to conduct genome-wide studies, providing insights into evolutionary processes and conservation genetics (Cruz et al., 2012; Hohenlohe et al., 2020; Storfer et al., 2020).

Simultaneously, remote sensing technologies have transformed the way we monitor wildlife and their habitats. High-resolution satellite imagery, aerial photography, and unmanned aerial vehicles (UAVs) offer unprecedented capabilities for mapping and monitoring large and inaccessible areas. These technologies facilitate the detection of habitat changes, the tracking of animal movements, and the assessment of environmental variables that influence wildlife populations (Shafer et al., 2016; Yamasaki et al., 2017; Drakshayini et al., 2023).

The integration of genomics and remote sensing technologies holds great promise for advancing wildlife monitoring. By combining genetic data with spatial and environmental information, researchers can gain a more holistic understanding of the factors driving biodiversity patterns and population dynamics. For example, population genomics can provide detailed insights into the demographic history, genetic diversity, and adaptive capacity of wildlife populations, which are crucial for effective conservation management (Forester et al., 2018; Hohenlohe et al., 2020; Hohenlohe and Rajora, 2021). Remote sensing, on the other hand, can offer real-time monitoring of habitat conditions and landscape changes, enabling the timely detection of threats such as habitat destruction, climate change, and human encroachment (Bourlat et al., 2013; Drakshayini et al., 2023). The synergy

between these technologies can enhance our ability to predict and mitigate the impacts of environmental changes on wildlife, ultimately contributing to more informed and effective conservation strategies.

This study will explore the current state of research on the integration of genomics and remote sensing technologies for wildlife monitoring. We will examine the methodologies, applications, and case studies that demonstrate the potential of these technologies to improve our understanding and management of wildlife populations. By highlighting the advancements and challenges in this field, we aim to provide a comprehensive overview of the prospects for integrating genomics and remote sensing in wildlife conservation.

1 Overview of Genomic Technologies

Genomic technologies have revolutionized the field of wildlife monitoring and conservation, providing unprecedented insights into genetic diversity, population structure, and disease dynamics. These advancements are crucial for developing effective conservation strategies and managing wildlife populations in the face of environmental changes and anthropogenic pressures.

1.1 Key genomic tools and techniques

The advent of next-generation sequencing (NGS) has been a game-changer in genomics, enabling the collection of genome-wide data across a broad range of taxa. Techniques such as reduced single nucleotide polymorphism (SNP) panels, microfluidic genotyping, and deep sequencing platforms have become essential tools in wildlife genomics (Ogden, 2011; Steiner et al., 2013; Thaden et al., 2020). These methods allow for the precise identification of genetic markers, which are critical for various applications, including individual identification, hybridization assessment, and population structure analysis (Ogden, 2011; Thaden et al., 2020).

1.2 Applications in genetic diversity and population structure analysis

Genomic tools provide detailed insights into the genetic diversity and population structure of wildlife species, which are vital for conservation efforts. For instance, population genomics can estimate effective population size, inbreeding levels, and demographic history, all of which are crucial for understanding the evolutionary potential of populations (Steiner et al., 2013; Hohenlohe et al., 2020). These analyses help identify genetic loci responsible for adaptation to changing environments, thereby informing strategies to manage adaptive variation and enhance the resilience of wildlife populations (Steiner et al., 2013; Hohenlohe et al., 2020; Wambugu and Henry, 2022).

1.3 Implications for disease surveillance and management in wildlife

Genomic methodologies are also pivotal in wildlife disease surveillance and management. They enable the detection and characterization of pathogens, uncover routes of disease transmission, and elucidate the interactions between hosts and pathogens (Blanchong et al., 2016). For example, genetic and genomic tools can identify loci associated with disease susceptibility and inbreeding depression, which are critical for predicting and mitigating the impacts of diseases on wildlife populations (Steiner et al., 2013; Blanchong et al., 2016). These insights are essential for developing targeted interventions to control wildlife diseases and protect both wildlife and human health (Blanchong et al., 2016).

In summary, the integration of genomic technologies into wildlife monitoring provides a robust framework for understanding genetic diversity, population dynamics, and disease ecology. These advancements are instrumental in shaping effective conservation strategies and ensuring the long-term sustainability of wildlife populations.

2 Overview of Remote Sensing Technologies

Remote sensing technologies have revolutionized wildlife monitoring by providing non-invasive, efficient, and comprehensive methods for tracking and studying wildlife populations and their habitats. These technologies encompass a wide range of tools and techniques that leverage satellite imagery, aerial photography, and ground-based sensors to collect data over large spatial and temporal scales.

2.1 Spectrum of remote sensing tools

Remote sensing tools vary widely in their capabilities and applications. Satellite imagery and aerial photography are commonly used for large-scale habitat mapping and monitoring, while ground-based sensors, such as camera

traps and acoustic sensors, provide detailed data on animal movements and behaviors. The integration of machine learning algorithms with remote sensing data has further enhanced the ability to automate species identification and habitat monitoring, making these tools indispensable for wildlife conservation efforts (Drakshayini et al., 2023).

2.2 Use of remote sensing in habitat mapping and change detection

Remote sensing technologies are particularly valuable for habitat mapping and change detection. By analyzing satellite images and aerial photographs, researchers can monitor changes in land cover, vegetation, and other habitat features over time. This information is crucial for understanding the impacts of environmental changes, such as deforestation and climate change, on wildlife habitats. The use of remote sensing data allows for the detection of habitat degradation and fragmentation, enabling conservationists to take timely actions to mitigate these threats (Drakshayini et al., 2023).

2.3 Monitoring animal movements and behavior

Monitoring animal movements and behavior is another critical application of remote sensing technologies. Camera traps and acoustic sensors are widely used to track the movements of individual animals and to study their behaviors in their natural habitats. These tools provide non-invasive methods for collecting data on animal density, migration patterns, and social interactions. For example, camera trap images combined with acoustic analysis have been used to monitor endangered species such as tigers, cheetahs, and sea turtles, providing valuable insights into their population dynamics and habitat use (Drakshayini et al., 2023). The analysis of animal vocalizations using machine learning techniques has also revealed important information about species behavior and habitat quality, further highlighting the potential of remote sensing technologies in wildlife monitoring (Drakshayini et al., 2023).

In conclusion, the integration of remote sensing technologies with machine learning and other advanced analytical tools offers significant advantages for wildlife monitoring and conservation. These technologies provide efficient, non-invasive methods for tracking and studying wildlife populations and their habitats, enabling conservationists to make informed decisions and take targeted actions to protect and preserve endangered species and their ecosystems.

3 Synergistic Integration of Genomics and Remote Sensing

The integration of genomics and remote sensing technologies offers a powerful approach to wildlife monitoring, providing comprehensive insights into species populations, genetic diversity, and environmental changes. This section explores the methodological integration, successful case studies, and the challenges associated with combining these technologies.

3.1 Methodological integration for comprehensive monitoring

The methodological integration of genomics and remote sensing involves combining genetic data with spatial and environmental information to enhance wildlife monitoring. Genomics provides detailed insights into population genetics, such as effective population size, inbreeding, and genetic diversity, which are critical for conservation efforts (Hohenlohe et al., 2020; Thaden et al., 2020). Remote sensing, on the other hand, offers large-scale and long-term environmental data, enabling the monitoring of habitat changes and species distributions (Stephenson, 2019; Thackeray and Hampton, 2020).

For instance, the use of reduced single nucleotide polymorphism (SNP) panels allows for the genotyping of degraded DNA samples collected noninvasively, such as from faeces or hair, which can be integrated with remote sensing data to monitor population structure and hybridization (Thaden et al., 2020). Additionally, genomic methods like DNA barcoding and metagenomics can be mapped to remote sensing indicators to provide a comprehensive assessment of environmental status and biodiversity (Bourlat et al., 2013; Yamasaki et al., 2017).

3.2 Case studies of successful integration

Several case studies highlight the successful integration of genomics and remote sensing in wildlife monitoring. For example, genomic tools have been used to monitor European wildcat populations by optimizing microfluidic SNP panels for individual identification and population structure assessment, which can be complemented with remote sensing data on habitat changes (Thaden et al., 2020) (Figure 1). In marine environments, genomic methods such as qPCR and DNA barcoding have been integrated with remote sensing to provide rapid and accurate assessments of marine health status, demonstrating the added value of combining these technologies (Bourlat et al., 2013).

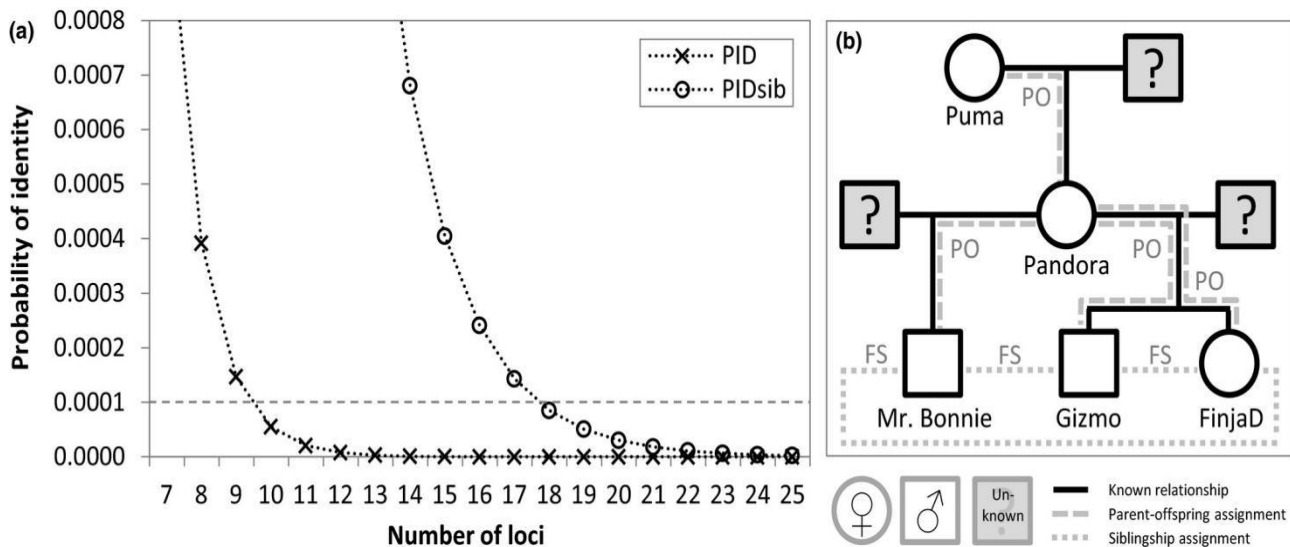


Figure 1 Power of the ID SNP panel to distinguish individuals (a) and reconstruct kinships (b) (Adopted from Thaden et al., 2020)
 Image caption: (a) Relationship between the number of genotyped SNP loci and probability of identity (PID) and probability of identity between siblings (PIDsib). Loci were ranked according to highest heterozygosity (HE). A cut-off of 0.0001 was used because it is considered as sufficiently low for most applications involving natural populations (Waits et al., 2001). (b) Assignments of parentage or sibship as calculated with ml-relate (Kalinowski et al., 2006) compared to known pedigrees of a domestic cat family. Circles represent females and squares represent males. Shaded symbols represent individuals not known or sampled. Assignments for single parent–offspring relationships are highlighted with grey dashed lines, and sibling relationships with dotted lines. PO, parent–offspring; FS, full siblingship (Adopted from Thaden et al., 2020)

The research results of Thaden et al. (2020) provide insights into the efficacy of single nucleotide polymorphism (SNP) panels in distinguishing individual identities and reconstructing kinships in a domestic cat family. The graph in panel (a) shows that as the number of genotyped SNP loci increases, the probability of identity (PID) and the probability of identity between siblings (PIDsib) decreases sharply, indicating the effectiveness of using a higher number of loci for accurate genetic differentiation. A cut-off of 0.0001 for PID is deemed sufficiently low for most natural population applications, ensuring reliable individual identification. Panel (b) illustrates the application of these genetic markers in assigning parentage and sibling relationships within a known cat pedigree. The use of the software ml-relate for genetic analysis aligns well with the known pedigrees, validating its utility in accurately determining familial relationships. This approach highlights the robustness of SNP panels in genetic studies involving natural populations and domestic animals.

Another notable example is the integration of genomic and remote sensing data to study the phenology and evolution of plant species under global change. Genome-wide RNA sequencing and DNA metabarcoding have been used alongside remote sensing to monitor functional traits and predict biodiversity changes, showcasing the potential of this synergistic approach (Yamasaki et al., 2017).

3.3 Technological and data integration challenges

Despite the promising potential, integrating genomics and remote sensing technologies presents several challenges. One major challenge is the need for standardized methodologies and data formats to ensure compatibility and

effective data sharing between genomic and remote sensing platforms (Bourlat et al., 2013; Stephenson, 2019). Additionally, the high cost and technical complexity of genomic technologies can be a barrier to their widespread adoption in wildlife monitoring (Carroll et al., 2018).

Another challenge is the need for interdisciplinary collaboration and training to bridge the gap between genomics and remote sensing experts. Many researchers may lack the expertise required to use these computationally intensive methodologies, highlighting the importance of workshops and training programs to build capacity in this area (Fitak et al., 2019). Furthermore, the integration of these technologies requires addressing issues related to data quality and resolution. For example, genomic data from minimally invasive sampling methods often yield low-quality DNA, which can limit the type of molecular methods used. Developing robust protocols and error-correction techniques is essential to overcome these limitations (Carroll et al., 2018).

In conclusion, while the integration of genomics and remote sensing technologies holds great promise for wildlife monitoring, addressing the methodological, technological, and collaborative challenges is crucial for realizing their full potential in conservation efforts.

4 Advances in Data Analysis and Modeling

4.1 Bioinformatics and spatial analysis techniques

The integration of bioinformatics and spatial analysis techniques has significantly advanced the field of wildlife monitoring. Genomic data, which have become increasingly affordable and accessible, are now being utilized to provide precise estimates of wildlife population features such as effective population size, inbreeding, demographic history, and population structure. These estimates are critical for conservation efforts, as they help in understanding the genetic health and adaptive capacity of wildlife populations (Hohenlohe et al., 2020; Schmidt et al., 2023).

Moreover, the development of standardized methods for assessing genetic variation and inbreeding, as well as identifying genetic interchange patterns between populations, has been emphasized. These methods require robust bioinformatic support to handle the complex data and analyses involved (Schmidt et al., 2023). The application of these genomic tools in conservation biology is still evolving, but the potential for these techniques to inform and improve conservation strategies is substantial (Hohenlohe et al., 2020; Schmidt et al., 2023).

4.2 Predictive modeling and its applications

Predictive modeling, particularly through the use of species distribution models (SDMs), has seen significant advancements with the incorporation of remote sensing technologies. Traditional SDMs often faced limitations due to spatial biases in occurrence data and a lack of spatially explicit predictor variables. However, modern remote sensing technologies, including multispectral and hyperspectral sensors, LiDAR, and RADAR, are revolutionizing the way habitat characteristics are captured and integrated into these models (He et al., 2015).

These advanced sensors, deployed on satellites, planes, and unmanned aerial vehicles, provide high-resolution data that enhance the accuracy and predictive power of SDMs. This allows for better detection and monitoring of both plant and animal species across various ecosystems (Kerr and Ostrovsky, 2003; He et al., 2015). Additionally, the integration of machine learning algorithms with remote sensing data has enabled automated species identification, habitat mapping, and population monitoring (Figure 2), further enhancing the effectiveness of predictive models in wildlife conservation (Drakshayini et al., 2023).

The research results of Toro et al. (2023) evaluate the suitability of different remote sensing methods for classifying land use and land cover (LULC) in integrated crop-livestock systems (ICLS). Two study sites (SS1 and SS2) are analyzed using Sentinel-2 data, with different algorithm and time window specifications. In the SS1 map, the classification accuracy for various LULC classes such as eucalyptus, native forest, and pasture shows a high degree of precision and recall, indicating robust model performance. The confusion matrix for SS1 reveals minor misclassifications between classes, with overall high F1-scores, especially for pasture and eucalyptus. The SS2 map demonstrates the capability of Sentinel-2 data in a more heterogeneous landscape. Despite the complexity,

the model achieves high precision, recall, and F1-scores for double crop and pasture. The confusion matrix for SS2 highlights effective discrimination between these classes, although minor overlaps exist. Overall, the research underscores the effectiveness of remote sensing techniques in accurately mapping LULC, crucial for monitoring and managing ICLS.

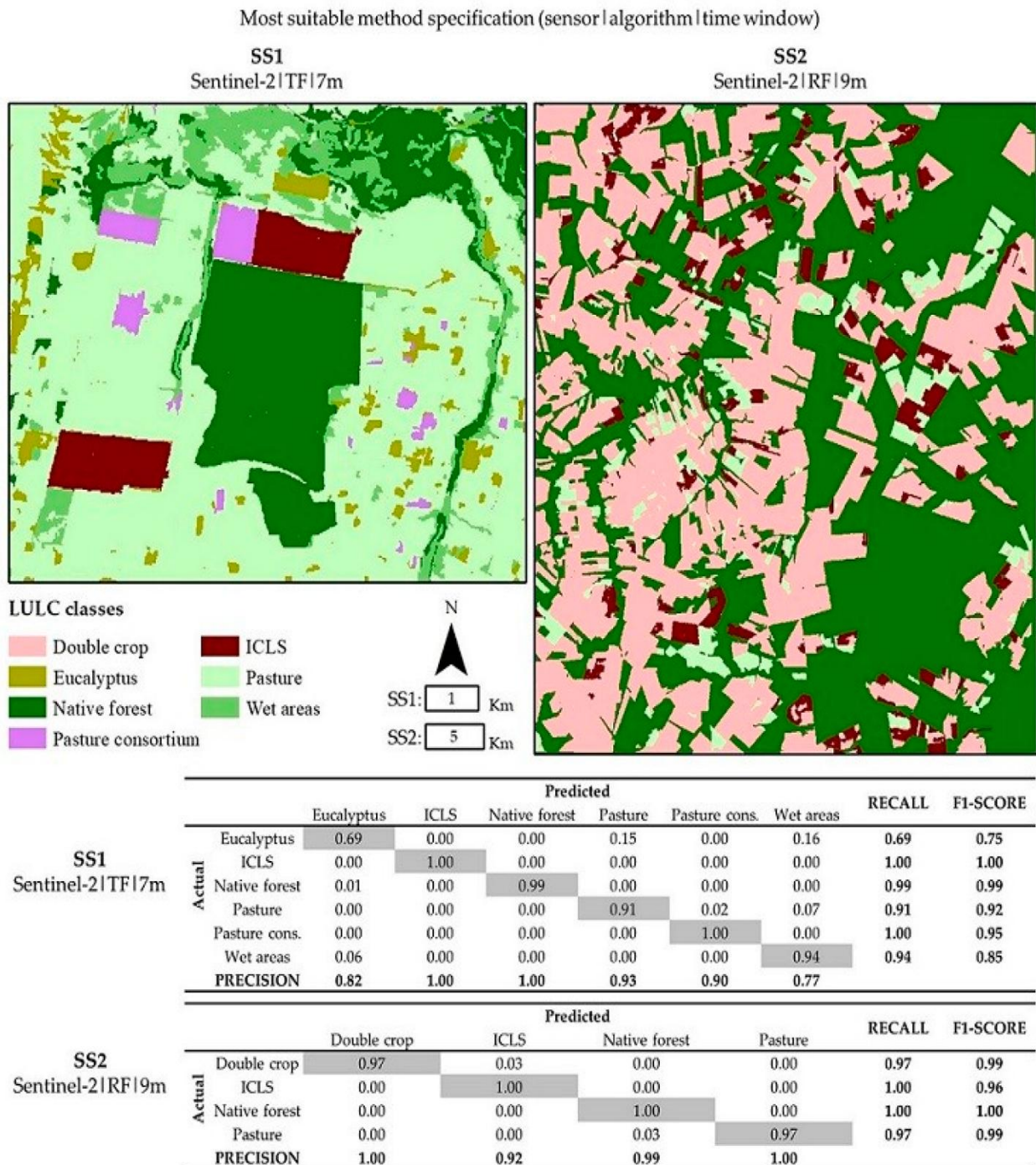


Figure 2 More suitable method specifications for ICLS (sensor, algorithm, and time window) for each study site, confusion matrices, and the respective values of precision, recall, and the F1 score for all classes (Adopted from Toro et al., 2023)

The combination of genomic data and remote sensing technologies holds great promise for the future of wildlife monitoring. By leveraging these advanced data analysis and modeling techniques, conservationists can develop more informed and targeted strategies to protect and preserve endangered species and their habitats (Kerr and Ostrovsky, 2003; Marvin et al., 2016; Drakshayini et al., 2023).

5 Ethical, Legal, and Social Implications

5.1 Ethical concerns in wildlife monitoring

The integration of genomics and remote sensing technologies in wildlife monitoring raises several ethical concerns. One primary issue is the potential for genetic data misuse. The collection and storage of genetic information from wildlife populations must be handled with strict confidentiality to prevent exploitation or harm to the species being studied (Hohenlohe et al., 2020). Additionally, there is a risk of prioritizing certain species over others based on their genetic information, which could lead to biased conservation efforts and neglect of less genetically diverse species (Hohenlohe et al., 2020).

Another ethical concern is the impact of invasive sampling methods on wildlife. While genomics can provide valuable insights into population health and dynamics, the methods used to collect genetic samples, such as blood or tissue sampling, can be stressful or harmful to the animals (Hohenlohe et al., 2020). Researchers must balance the need for accurate data with the welfare of the animals being studied.

Furthermore, the use of remote sensing technologies, such as drones, can disturb wildlife and their habitats. The presence of drones can cause stress and behavioral changes in animals, potentially affecting the data collected and the well-being of the species (Cordier et al., 2020). Ethical guidelines must be established to minimize the impact of these technologies on wildlife.

5.2 Legal frameworks and compliance

The application of genomics and remote sensing in wildlife monitoring is subject to various legal frameworks and compliance requirements. One significant challenge is the lack of standardized regulations governing the use of these technologies in different regions. This can lead to inconsistencies in data collection, analysis, and reporting, making it difficult to compare results across studies and implement effective conservation strategies (Cordier et al., 2020).

Moreover, the integration of genomics into wildlife monitoring requires adherence to international agreements and conventions, such as the Convention on Biological Diversity (CBD) and the Nagoya Protocol, which regulate access to genetic resources and the fair and equitable sharing of benefits arising from their use (Hohenlohe et al., 2020). Researchers must navigate these legal frameworks to ensure that their work complies with international standards and respects the rights of indigenous communities and local stakeholders.

In addition, the use of remote sensing technologies is subject to aviation and privacy laws. For instance, the operation of drones for wildlife monitoring must comply with national and international aviation regulations to ensure safety and avoid conflicts with other airspace users (Cordier et al., 2020). Privacy laws also need to be considered, particularly when monitoring wildlife in areas close to human settlements, to prevent unintentional surveillance of people.

The implementation of genomics-based monitoring programs requires collaboration with regulatory bodies to develop guidelines and standards for data collection, storage, and sharing. This includes establishing protocols for obtaining permits and ensuring that research activities are conducted ethically and legally (Ward et al., 2019; Cordier et al., 2020). By working closely with regulators, researchers can help to create a robust legal framework that supports the responsible use of genomics and remote sensing technologies in wildlife conservation.

6 Future Directions and Innovations

6.1 Emerging technologies on the horizon

The integration of genomics and remote sensing technologies in wildlife monitoring is poised to benefit significantly from several emerging technologies. One promising area is the development of genome-editing technologies such as CRISPR-Cas9, which can be used to manage genetic diversity and combat invasive species (Johnson et al., 2016). Additionally, the use of environmental DNA (eDNA) and metabarcoding approaches are becoming increasingly important for mapping species occurrence and interaction networks (Johnson et al., 2016). These technologies offer non-invasive methods to monitor wildlife populations and their habitats, providing critical data for conservation efforts.

Another emerging technology is the application of reduced single nucleotide polymorphism (SNP) panels for genotyping degraded DNA samples, such as faeces or hairs. This approach allows for the efficient monitoring of wildlife populations, even with non-invasively collected samples, and can be tailored to address specific population genetics questions (Thaden et al., 2020). Furthermore, real-time telemetry and algorithm-based analytical capabilities are revolutionizing wildlife monitoring by enabling continuous tracking and analysis of animal movements and behaviors (Wall et al., 2014). These advancements facilitate more responsive and adaptive conservation strategies.

6.2 Role of artificial intelligence and machine learning

Artificial Intelligence (AI) and Machine Learning (ML) are playing increasingly pivotal roles in wildlife monitoring and conservation. These technologies are being used to automate species identification, map and monitor habitats, and track population dynamics. For instance, machine learning algorithms have been developed to classify bird and amphibian calls, differentiate fish species, and identify plant species, making automated species identification possible (Drakshayini et al., 2023). The integration of AI with remote sensing techniques provides significant advantages for habitat mapping and monitoring, enabling more efficient and effective conservation strategies (Drakshayini et al., 2023).

Deep learning, a subset of machine learning, has significantly advanced automatic wildlife recognition through camera trapping. However, current methods often rely on large static datasets, which can be limiting. A hybrid approach that combines machine learning with human input has been proposed to overcome these limitations, achieving high accuracy with reduced human annotation effort (Miao et al., 2021). This iterative human and automated identification approach enhances the efficiency and accuracy of wildlife monitoring.

AI and ML are also being utilized in precision livestock farming, where sensing technologies supported by these algorithms monitor animal growth dynamics and activity status. Computer vision and wearable sensor systems are particularly effective in providing non-intrusive measurements of animals, accelerating phenotyping efforts and improving the quality of data collected (Morota et al., 2022). These advancements in AI and ML are transforming the field of wildlife monitoring, offering new tools and methodologies to support conservation efforts.

In summary, the future of wildlife monitoring lies in the continued development and integration of emerging genomic technologies and AI-driven approaches. These innovations promise to enhance our ability to monitor, understand, and protect wildlife populations and their habitats.

7 Concluding Remarks

The integration of genomics and remote sensing technologies has shown significant promise in advancing wildlife monitoring and conservation efforts. Genomics tools have provided precise estimates of critical population parameters such as effective population size, inbreeding, demographic history, and population structure, which are essential for conservation strategies. These tools have also enabled the identification of genetic loci responsible for inbreeding depression and adaptation to changing environments, thereby aiding in the management of adaptive variation. Remote sensing technologies, particularly when combined with machine learning, have revolutionized wildlife monitoring by automating species identification, mapping habitats, tracking population dynamics, and detecting wildlife crime. These technologies offer non-invasive methods to monitor and manage animal populations, providing significant advantages over traditional monitoring systems. Moreover, the application of genomics in marine environments has demonstrated the potential for rapid and cost-efficient monitoring, enhancing the assessment of marine health status and aiding in the implementation of marine legislation. The use of portable sequencing technologies in remote areas has also democratized scientific research, making it accessible to a broader network of conservation scientists.

To further harness the potential of genomics and remote sensing technologies in wildlife monitoring, several steps need to be taken. First, there is a need for standardized guidelines and protocols to integrate these technologies into existing monitoring programs effectively. This includes developing comprehensive workflows for adaptive landscape genomics studies, which encompass sampling design, data production, and analysis. Second, addressing

the computational and sampling constraints associated with genomic tools in wild species is crucial. This involves investing in infrastructure and training to build capacity for genomic research in biodiverse regions. Educational initiatives, such as field courses that provide hands-on training in molecular biology and real-time DNA sequencing, are essential for empowering local scientists and conservationists. Third, continued development and refinement of machine learning algorithms and remote sensing techniques are necessary to enhance the accuracy and efficiency of wildlife monitoring. This includes improving the integration of acoustic analysis with camera trap images to monitor population dynamics and track endangered species. Finally, fostering collaborations between researchers, conservationists, and policymakers is vital to ensure that the insights gained from genomics and remote sensing technologies are translated into effective conservation actions. By leveraging these advanced technologies, we can make informed decisions and take targeted actions to protect and preserve wildlife and their habitats for future generations.

In conclusion, the integration of genomics and remote sensing technologies holds great promise for the future of wildlife monitoring and conservation. By addressing current challenges and building on the progress made, we can enhance our ability to monitor, manage, and protect wildlife populations in an ever-changing world.

Acknowledgements

Author would like to express our gratitude to the two anonymous peer reviewers for their critical assessment and constructive suggestions on our manuscript.

Conflict of Interest Disclosure

Author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

- Blanchong J., Robinson S., Samuel M., and Foster J., 2016, Application of genetics and genomics to wildlife epidemiology, *The Journal of Wildlife Management*, 80(4): 593-608.
<https://doi.org/10.1002/jwmg.1064>
- Bourlat S., Borja Á., Gilbert J., Taylor M., Davies N., Weisberg S., Griffith J., Lettieri T., Field D., Benzie J., Glöckner F., Rodríguez-Ezpeleta N., Faith D., Bean T., and Obst M., 2013, Genomics in marine monitoring: new opportunities for assessing marine health status, *Marine Pollution Bulletin*, 74(1): 19-31.
<https://doi.org/10.1016/j.marpolbul.2013.05.042>
PMid:23806673
- Carroll E., Bruford M., Dewoody J., Leroy G., Strand A., Waits L., and Wang J., 2018, Genetic and genomic monitoring with minimally invasive sampling methods, *Evolutionary Applications*, 11(7): 1094-1119.
<https://doi.org/10.1111/eva.12600>
PMid:30026800 PMCID:PMC6050181
- Cordier T., Alonso-Sáez L., ApothéLoz-Perret-Gentil L., Aylagas E., Bohan D., Bouchez A., Chariton A., Creer S., Frühe L., Keck F., Keeley N., Laroche O., Leese F., Pochon X., Stoeck T., Pawłowski J., and Lanzén A., 2020, Ecosystems monitoring powered by environmental genomics: a review of current strategies with an implementation roadmap, *Molecular Ecology*, 30(13): 2937-2958.
<https://doi.org/10.1111/mec.15472>
PMid:32416615 PMCID:PMC8358956
- Cruz F., Brennan A., Gonzalez-Voyer A., Muñoz-Fuentes V., Eaaswarkhanth M., Roques S., and Picó F., 2012, Genetics and genomics in wildlife studies: implications for ecology, evolution, and conservation biology, *BioEssays*, 34(3):245-246.
<https://doi.org/10.1002/bies.201100171>
PMid:22223439
- Drakshayini A., Mohan S.T, Swathi M, and Nanjundeshwara K., 2023, Leveraging machine learning and remote sensing for wildlife conservation: a comprehensive review, *International Journal of Advanced Research*, 11: 636-647.
<https://doi.org/10.21474/IJAR01/17110>
- Fitak R., Antonides J., Baitchman E., Bonaccorso E., Braun J., Kubiski S., Chiu E., Fagre A., Gagne R., Lee J., Malmberg J., Stenglein M., Dusek R., Forgacs D., Fountain-Jones N., Gilbertson M., Worsley-Tonks K., Funk W., Trumbo D., Ghersi B., Grimaldi W., Heisel S., Jardine C., Kamath P., Karmacharya D., Kozakiewicz C., Kraberger S., Loisel D., McDonald C., Miller S., O'Rourke D., Ott-Conn C., Páez-Vacas M., Peel A., Turner W., VanAcker M., Vandewoude S., and Pecon-Slattery J., 2019, The expectations and challenges of wildlife disease research in the era of genomics: forecasting with a horizon scan-like exercise, *The Journal of Heredity*, 110(3): 261-274.
<https://doi.org/10.1093/jhered/esz001>
PMid:31067326

- Forester B., Landguth E., Hand B., and Balkenhol N., 2018, Landscape Genomics for Wildlife Research, In: Population Genomics: Wildlife, pp.1-40.
https://doi.org/10.1007/13836_2018_56
- He K., Bradley B., Cord A., Rocchini D., Tuanmu M., Schmidlein S., Turner W., Wegmann M., and Pettorelli N., 2015, Will remote sensing shape the next generation of species distribution models, *Remote Sensing in Ecology and Conservation*, 1(1): 4-18.
<https://doi.org/10.1002/rse2.7>
- Hohenlohe P., Funk W., and Rajora O., 2020, Population genomics for wildlife conservation and management, *Molecular Ecology*, 30(1): 62-82.
<https://doi.org/10.1111/mec.15720>
PMid:33145846 PMCID:PMC7894518
- Hohenlohe P.A., and Rajora O.P., (eds.), 2021, Population Genomics: Wildlife, pp.41-55.
<https://doi.org/10.1007/978-3-030-63489-6>
- Johnson J., Altwegg R., Evans D., Ewen J., Gordon I., Pettorelli N., and Young J., 2016, Is there a future for genome-editing technologies in conservation, *Animal Conservation*, 19: 97-101.
<https://doi.org/10.1111/acv.12273>
- Kerr J., and Ostrovsky M., 2003, From space to species: ecological applications for remote sensing, *Trends in Ecology and Evolution*, 18(6): 299-305.
[https://doi.org/10.1016/S0169-5347\(03\)00071-5](https://doi.org/10.1016/S0169-5347(03)00071-5)
- Marvin D., Koh L., Lynam A., Wich S., Davies A., Krishnamurthy R., Stokes E., Starkey R., and Asner G., 2016, Integrating technologies for scalable ecology and conservation, *Global Ecology and Conservation*, 7: 262-275.
<https://doi.org/10.1016/j.gecco.2016.07.002>
- Miao Z., Liu Z., Gaynor K., Palmer M., Yu S., and Getz W., 2021, Iterative human and automated identification of wildlife images, *Nature Machine Intelligence*, 3(10): 885-895.
<https://doi.org/10.1038/s42256-021-00393-0>
- Morota G., Ha D., and Chen J., 2022, 19 how can artificial intelligence accelerate phenotyping efforts in animal breeding, *Journal of Animal Science*, 100(Suppl 3): 11.
<https://doi.org/10.1093/jas/skac247.020>
PMCID:PMC9493747
- Ogden R., 2011, Unlocking the potential of genomic technologies for wildlife forensics, *Molecular Ecology Resources*, 11: 109-116.
<https://doi.org/10.1111/j.1755-0998.2010.02954.x>
PMid:21429167
- Schmidt T., Thia J., and Hoffmann A., 2023, How can genomics help or hinder wildlife conservation, *Annual Review of Animal Biosciences*, 12(1): 45-68.
<https://doi.org/10.1146/annurev-animal-021022-051810>
PMid:37788416
- Shafer A., Northrup J., Wikelski M., Wittemyer G., and Wolf J., 2016, Forecasting ecological genomics: high-tech animal instrumentation meets high-throughput sequencing, *PLoS Biology*, 14(1): e1002350.
<https://doi.org/10.1371/journal.pbio.1002350>
PMid:26745372 PMCID:PMC4712824
- Steiner C., Putnam A., Hoeck P., and Ryder O., 2013, Conservation genomics of threatened animal species, *Annual Review of Animal Biosciences*, 1(1): 261-281.
<https://doi.org/10.1146/annurev-animal-031412-103636>
PMid:25387020
- Stephenson P., 2019, Integrating remote sensing into wildlife monitoring for conservation, *Environmental Conservation*, 46(3): 181-183.
<https://doi.org/10.1017/S0376892919000092>
- Storfer A., Kozakiewicz C., Beer M., and Savage A., 2020, Applications of population genomics for understanding and mitigating wildlife disease, In: *Population Genomics: Wildlife*, pp.357-383.
https://doi.org/10.1007/13836_2020_73
- Thackeray S., and Hampton S., 2020, The case for research integration, from genomics to remote sensing, to understand biodiversity change and functional dynamics in the world's lakes, *Global Change Biology*, 26(6): 3230-3240.
<https://doi.org/10.1111/gcb.15045>
PMid:32077186
- Thaden A., Nowak C., Tiesmeyer A., Reiners T., Alves P., Lyons L., Mattucci F., Randi E., Cragnolini M., Galián J., Hegyeli Z., Kitchener A., Lambinet C., Lucas J., Mölich T., Ramos L., Schockert V., and Cocchiararo B., 2020, Applying genomic data in wildlife monitoring: Development guidelines for genotyping degraded samples with reduced single nucleotide polymorphism panels, *Molecular Ecology Resources*, 20(3): 662-680.
<https://doi.org/10.1111/1755-0998.13136>
PMid:31925943 PMCID:PMC7199164
- Toro A.P., Bueno I.T., Werner J.P., Antunes J.F., Lamparelli R.A., Coutinho A.C., Esquerdo J.C., Magalhães P.S., and Figueiredo G. K., 2023, SAR and optical data applied to early-season mapping of integrated crop–livestock systems using deep and machine learning algorithms, *Remote Sensing*, 15(4): 1130.
<https://doi.org/10.3390/rs15041130>

- Wambugu P., and Henry R., 2022, Supporting in situ conservation of the genetic diversity of crop wild relatives using genomic technologies, *Molecular Ecology*, 31(8): 2207-2222.
<https://doi.org/10.1111/mec.16402>
PMid:35170117 PMCID:PMC9303585
- Wall J., Wittemyer G., Klinkenberg B., and Douglas-Hamilton I., 2014, Novel opportunities for wildlife conservation and research with real-time monitoring, *Ecological Applications*, 24(4): 593-601.
<https://doi.org/10.1890/13-1971.1>
PMid:24988762
- Ward E., Kostick K., and Lázaro-Muñoz G., 2019, Integrating genomics into psychiatric practice: ethical and legal challenges for clinicians, *Harvard Review of Psychiatry*, 27(1): 53-64.
<https://doi.org/10.1097/HRP.000000000000203>
PMid:30614887 PMCID:PMC6326091
- Yamasaki E., Altermatt F., Cavender-Bares J., Schuman M., Zuppinge-Dingley D., Garonna I., Schneider F., Guillén-Escribà C., Moorsel S., Hahl T., Schmid B., Schaepman-Strub G., Schaepman M., and Shimizu K., 2017, Genomics meets remote sensing in global change studies: monitoring and predicting phenology, evolution and biodiversity, *Current Opinion in Environmental Sustainability*, 29: 177-186.
<https://doi.org/10.1016/j.cosust.2018.03.005>

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