Leveraging Earth Observation to monitor genetic diversity from Space

Running title: EO to monitor genetic diversity

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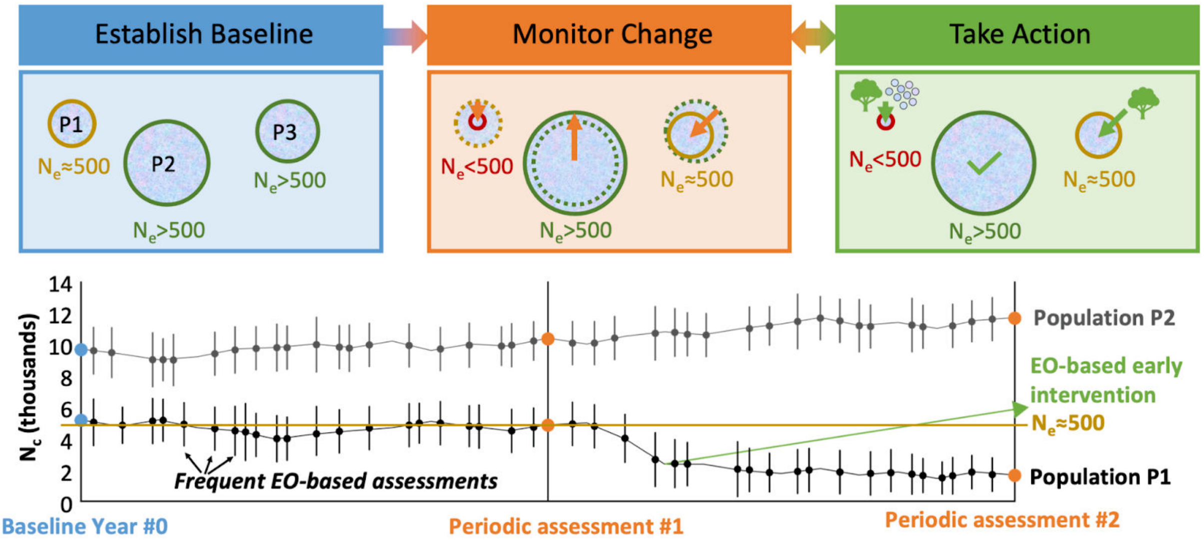
Abstract

Genetic diversity within and among populations is essential for species persistence. Despite the definition of key targets and pragmatic indicators in the Kunming-Montreal Global Biodiversity Framework (GBF), assessing genetic diversity across many species at national and regional scales remains challenging. Conservationists, ecosystem managers, and Parties to the Convention on Biological Diversity (CBD) still require accessible tools for reliable and efficient monitoring of genetic diversity, at multiple scales relevant for policy and decision-making. Building on examples, we describe how current Earth Observation (EO) missions make essential contributions to enable, accelerate, and improve genetic diversity monitoring. To illustrate this, we introduce a stepwise workflow for integrating EO into existing genetic diversity monitoring strategies. Specifically, we describe how available EO data can be made accessible in innovative ways to support calculation of the genetic diversity indicators for the GBF monitoring framework, and to inform management and monitoring decisions, especially for cases in which genetic sequence data are limited or absent. We then provide an outlook for integrating the forthcoming generation of EO data: Upcoming capabilities will provide unprecedented detail to characterize the changes to Earth's surface and their implications for biodiversity, and will support more direct assessments of genetic diversity from Space.

Keywords

essential biodiversity variables (EBVs) — remote sensing (RS) — Kunming-Montreal Global Biodiversity Framework (GBF) — Convention on Biological Diversity (CBD) — genetic diversity indicators — effective population size (N_e) — populations maintained (PM)

Graphical abstract



Publicly available Earth Observation (EO) data improve the establishment of baselines, effective regular monitoring, and targeted re-assessment and intervention to conserve the genetic diversity of natural populations. Examples are shown for three imaginary populations of the same species, P1, P2, and P3. P1 drifts below the threshold value for the genetically effective population size (N_e), as defined within the N_e > 500 Global Biodiversity Framework's Headline Indicator for genetic diversity monitoring. P2 is maintained above this threshold (N_e ~ 1000) while P3 drops close to the threshold. By the time of the second periodic assessment, the N_e > 500 indicator value for this example would be ⅔ and without intervention, is likely to drop to ⅓. Frequent EO-based assessments could support timely intervention. N_c is the census number of reproductively mature adults in a population and can be used to estimate N_e either with prior knowledge of typical N_e : N_c ratios for a species, or the default assumption, based on decades of population genetics studies, that N_e : N_c ~ 0.1 (Frankham, 1995, 2021; Hoban, da Silva, et al., 2024; Laikre et al., 2020, 2021; Mastretta-Yanes, da Silva, et al., 2024).

Introduction

Genetic diversity is an essential aspect of biodiversity protection

Genetic diversity is a foundational level of biodiversity below the species level, within and between populations (Allendorf, 2017): Genetically distinct groups of spatially aggregated, interbreeding individuals of a species (Waples & Gaggiotti, 2006). Genetic diversity underlies adaptive potential, which is material to the fitness of individuals and allows species to persist in the face of change (*i.e.*, resilience and resistance). Loss of genetic diversity leads to maladaptation, population decline, inbreeding and, eventually, extinction. Therefore, genetic diversity needs to be monitored as part of biodiversity assessments, conservation and restoration actions, and safeguarding nature's contributions to people – also called ecosystem services (Hoban, Bruford, et al., 2021; Hoban et al., 2020). Studies of multi-species genetic diversity trends have only recently become possible and indicate a net loss over time as a result of human activities (Exposito-Alonso et al., 2022; Leigh et al., 2019; Millette et al., 2020; Shaw et al., 2025). Revealing the specific, ongoing, local and global drivers of this trend, and doing so in a timely and constructive manner that supports mitigation, remains a grand and unmet challenge.

Yet efforts to monitor and conserve genetic diversity as a fundamental component of biodiversity build on a substantial body of policy. International treaties and national programs for the protection of biodiversity have required assessments of the state of nature since the 1970s, such as the 1971 Ramsar Convention on Wetlands, the US 1973 Endangered Species Act, the 1992 Convention on Biological Diversity (CBD); the 2010 Aichi Biodiversity Targets (Conference of the Parties to the CBD, 2010), and the 2015 Sustainable Development Goals[1]. The 2022 Kunming-Montreal Global Biodiversity Framework (GBF) is distinct from these previous efforts in that it incorporates specific indicators for genetic diversity including all species (wild and domestic). These indicators are aimed at measuring progress towards the GBF goal and target for genetic diversity (Conference of the Parties to the CBD, 2022a), and include a Headline Indicator for genetic diversity.

Measuring genetic diversity usually involves analyzing sequences of DNA extracted out of tissues sampled from individuals of a species (Hoban et al., 2022; Junker et al., 2023). Despite technological advances, this approach remains laborious and expensive – in the range of 10-1000 USD / sample depending on technique, genome size, and coverage, *not* including the cost to obtain the tissue samples in the first place or personnel time to analyze and interpret data, e.g. (Lou et al., 2021) – and thus difficult

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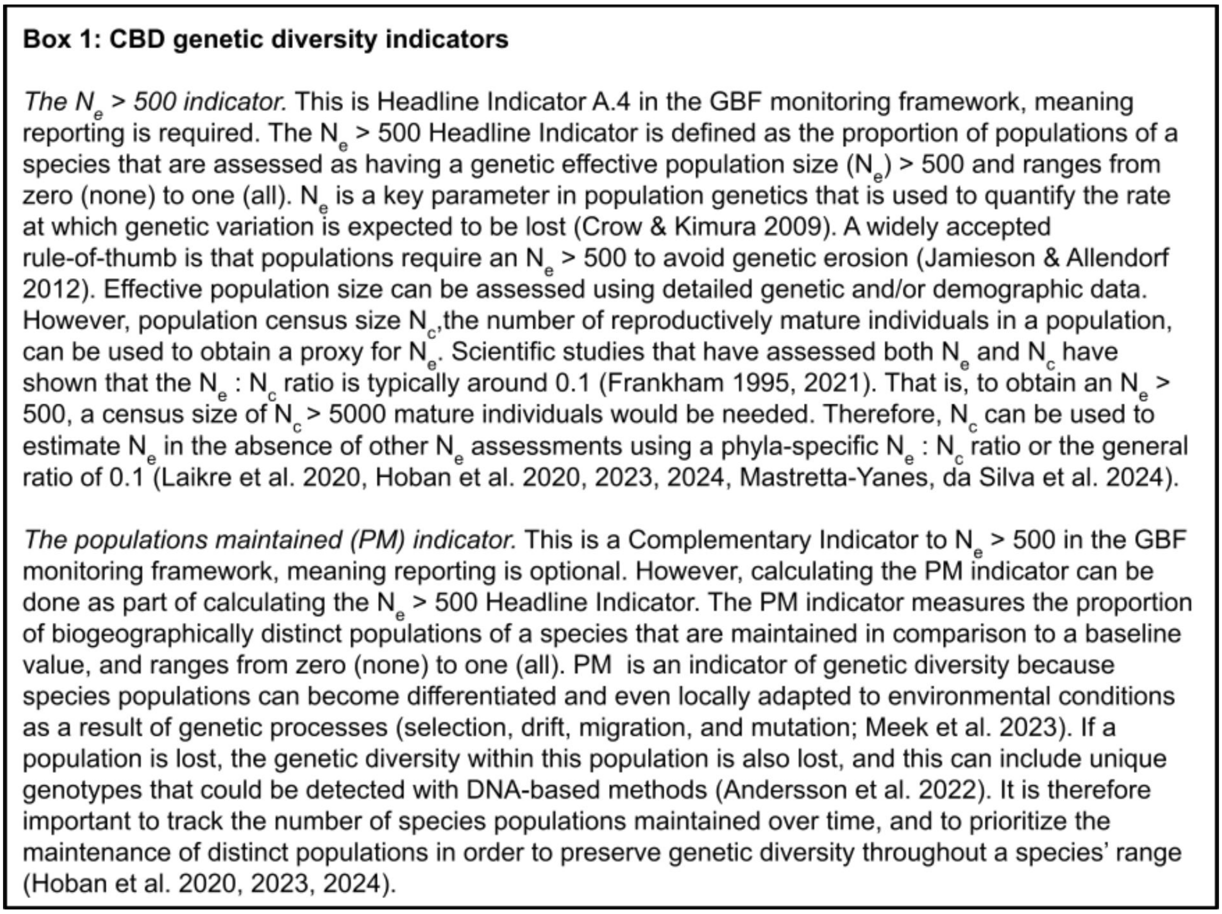
[1] https://sdgs.un.org/

to repeat across many species at national and global scales. To overcome this challenge, indicators for genetic diversity that can be assessed with or without DNA-based data (Hoban et al., 2020; Laikre et al., 2020; Mastretta-Yanes, da Silva, et al., 2024; Mastretta-Yanes, Suárez, et al., 2024; Thurfjell et al., 2022) have been developed for country- and global-scale genetic diversity assessments and monitoring (**Box 1**).



Box 1: CBD genetic diversity indicators

The N_e > 500 indicator. This is Headline Indicator A.4 in the GBF monitoring framework, meaning reporting is required. The N_e > 500 Headline Indicator is defined as the proportion of populations of a species that are assessed as having a genetic effective population size (N_e) > 500 and ranges from zero (none) to one (all). N_e is a key parameter in population genetics that is used to quantify the rate at which genetic variation is expected to be lost (Crow & Kimura 2009). A widely accepted rule-of-thumb is that populations require an N_e > 500 to avoid genetic erosion (Jamieson & Allendorf 2012). Effective population size can be assessed using detailed genetic and/or demographic data. However, population census size N_c,the number of reproductively mature individuals in a population, can be used to obtain a proxy for N_e. Scientific studies that have assessed both N_e and N_c have shown that the $N_e : N_c$ ratio is typically around 0.1 (Frankham 1995, 2021). That is, to obtain an N_e > 500, a census size of N_c > 5000 mature individuals would be needed. Therefore, N_c can be used to estimate N_e in the absence of other N_e assessments using a phyla-specific $N_e : N_c$ ratio or the general ratio of 0.1 (Laikre et al. 2020, Hoban et al. 2020, 2023, 2024, Mastretta-Yanes, da Silva et al. 2024).

The populations maintained (PM) indicator. This is a Complementary Indicator to N_e > 500 in the GBF monitoring framework, meaning reporting is optional. However, calculating the PM indicator can be done as part of calculating the N_e > 500 Headline Indicator. The PM indicator measures the proportion of biogeographically distinct populations of a species that are maintained in comparison to a baseline value, and ranges from zero (none) to one (all). PM is an indicator of genetic diversity because species populations can become differentiated and even locally adapted to environmental conditions as a result of genetic processes (selection, drift, migration, and mutation; Meek et al. 2023). If a population is lost, the genetic diversity within this population is also lost, and this can include unique genotypes that could be detected with DNA-based methods (Andersson et al. 2022). It is therefore important to track the number of species populations maintained over time, and to prioritize the maintenance of distinct populations in order to preserve genetic diversity throughout a species' range (Hoban et al. 2020, 2023, 2024).

The Headline Indicator A.4, which Parties to the CBD are required to report on, focuses on genetic diversity within populations. It is defined as the proportion of populations within a species having an effective population size (N_e) > 500 (hereafter, the "N_e > 500 indicator"). An N_e > 500 is an approximate, conservative, yet efficient, threshold to avoid the loss of genetic variation and adaptive potential over time (Crow & Kimura, 2009; Frankham, 1995, 2022; Franklin, 1980; Hoban, da Silva, et al., 2024; Hoban et al., 2020, 2023; Jamieson & Allendorf, 2012; Laikre et al., 2020) – although some studies indicate that an even larger N_e of 1000 is required to retain adaptive potential (Frankham et al., 2014). Importantly, N_e can be estimated based on DNA data, or it can be approximated as 10% of the number of reproductively mature individuals (census size, N_c), or another species-specific N_e:N_c ratio (Frankham, 2021; Frankham et al., 2017; Hoban, Paz-Vinas, et al., 2021). The second, Complementary Indicator – which is not required for reporting, but supports calculation of the Headline Indicator – focuses on conserving genetic diversity between populations and is estimated as the proportion of populations within species that are maintained over time in comparison to a baseline value, hereafter the “PM indicator” (Hoban, da Silva, et al., 2024; Hoban et al., 2020, 2023; Laikre et al., 2020; Mastretta-Yanes et al., 2023). The aim of the PM indicator is to avoid the loss of unique genetic diversity found in separate populations (Andersson et al., 2022; Meek et al., 2023). While DNA-based studies remain vital for quantifying genetic diversity and understanding how to conserve it, these indicators offer globally more affordable and accessible metrics to facilitate immediate monitoring (Hoban, Paz-Vinas, et al., 2024; Hunter et al., 2024). Yet, substantial information is still required to calculate these indicators, such as counts of numbers of individuals and evidence of population survival or loss, based on *in situ* surveys.

These two indicators were adopted by the United Nations Parties to the CBD at the fifteenth Conference of the Parties (COP15) in 2022, in the monitoring framework of the GBF (GBF, CBD/COP/DEC/15/5,2022b). Concretely, this means that signing Parties must monitor genetic diversity to prevent its loss and provide reports in 2026 and 2029 Thus it is urgent to implement existing genetic monitoring approaches for indicator assessments (Andersson et al., 2022; Hoban et al., 2023; Mastretta-Yanes, da Silva, et al., 2024; Mastretta-Yanes, Suárez, et al., 2024; Thurfjell et al., 2022) and to further develop scalable, globally accessible, and affordable methods for genetic diversity indicator calculation.

To facilitate reporting of the genetic diversity indicators, researchers and practitioners recently assessed these indicators in nine countries utilizing existing DNA studies, census population sizes, expert and local consultation, and georeferenced occurrence data (Mastretta-Yanes, da Silva, et al., 2024). Critical challenges identified in this assessment were the lack of any – even rough census size – data for particular taxonomic groups located in inaccessible regions (e.g., areas that are politically or geographically challenging to access) and a lack of historical data. Overall, the assessment highlighted the need for capacity-building and the development of ready-to-use tools to expedite and scale up monitoring (Hoban, da Silva, et al., 2024).

Contributions of Earth Observation satellites to biodiversity assessment

Earth Observation (EO) satellites and aircraft have become indispensable for understanding and monitoring global change. They are used for environmental assessments, disaster risk management, land and sea use, atmospheric and climate change, and to study changes in biodiversity (Mairota et al., 2015). While other technologies based on airborne and field-mobile platforms exist, here we focus on Space-based EO satellites such as the Copernicus Sentinel satellites and the NASA Earth Observing System (EOS) (**Table 1**), which make (global) data publicly available, in near real-time and free of charge (Malenovský et al., 2012).

EO data have unique attributes such as covering large geographic areas, providing non-intrusive global coverage, and providing uniform data sets over multiple decades (e.g., Landsat data since the 1970s[2]). These data are used to obtain information for environmental analyses and biodiversity assessment, often at the ecosystem level. Examples are land use and land cover (LULC) change; vegetation biochemical properties and conditions (e.g. Normalized difference vegetation index, NDVI) as well as structural information such as green leaf area index (LAI) and vegetation height (traits); land surface phenology; and photosynthetically active radiation (PAR) important for vegetation health and productivity (Verrelst et al., 2015). This information is then often used in models to infer species composition, traits, and other properties of ecosystems at the landscape scale (Mayor et al., 2024, 2025; Pasetto et al., 2018).

Uniquely and importantly, EO typically provide repeat measurements of the same area on a time scale of days to weeks, globally. For example, the Copernicus Sentinel-2 satellite monitors the entire globe in five days, with more frequent observations for some locations on Earth depending on the geographical latitude, but less frequent usable observations depending on cloud cover[3,4] (**Box 2**). The Sentinel family of satellites have observed the Earth’s surface with different instruments continually starting in 2014, detecting reflected radiation in the visible, infrared, microwave regions of the spectrum, at up to 10 m spatial resolution, depending on the sensor and satellite (Malenovský et al., 2012). Sentinel-2 provides multispectral images that can be used to assess, for example, vegetation structural properties such as LAI (Sebastiani et al., 2023) or vegetation conditions such as water content (Helfenstein et al., 2022; Sims & Gamon, 2003; Sturm et al., 2022). The European Copernicus Sentinel satellites and observations are complemented by long-term records obtained by the NASA Landsat and Earth observing satellites since the 1970’s. All ESA and NASA data are available openly and freely to all users, and are ideal for biodiversity assessment and monitoring from local to global scales, and annual to multi-decadal time frames (see available tools in **Table 1**).

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[2] https://landsat.gsfc.nasa.gov/

[3] https://sentiwiki.copernicus.eu/web/s2-applications

[4] https://esamultimedia.esa.int/docs/S2-Data_Sheet.pdf

Table 1*. EO platforms that lower or eliminate technical and financial barriers to application for genetic diversity monitoring and other uses by EO non-experts. For more technical details, see a recent comprehensive overview (Ustin & Middleton, 2021)***.

	EO Tool	Access	Brief description
Data browser / access to satellite data	Copernicus browser	https://dataspace.copernicus.eu/browser/	Easy visualization browser for Copernicus Sentinel data, download portal for archive of Sentinel data and products
	Earth Data	https://search.earthdata.nasa.gov/search	Discover and download NASA EO data; many different sensors available
	Earth Explorer	https://earthexplorer.usgs.gov/	Discover and download NASA (and Copernicus Sentinel) EO data; many different sensors available
	Sentinel Hub EO browser	https://www.sentinel-hub.com/	Browser for satellite data including options to display thematic topics and indices
	ESA third-party missions	https://earth.esa.int/eogateway/missions/third-party-missions	Browser for satellite data from commercial and other third-party sources shared with the public via ESA
	Google Earth Pro	https://www.google.com/intl/en/earth/about/versions/#earth-pro	Easy-to-use Earth software including (historical) high-resolution commercial images made freely available for visual inspection (irregularly)
	Google Earth Engine	https://earthengine.google.com/	Satellite EO data repository, cloud computing platform and API; free for academics & research
	Microsoft Planetary Computer	https://planetarycomputer.microsoft.com/	Global environmental data catalogue, cloud computing platform, and API
Process(ed) satellite data	Global Forest Watch	https://www.globalforestwatch.org/	Browse metrics of forest and biodiversity change from national and sub-national to global scales
	Global Mangrove Watch	https://www.globalmangrovewatch.org/	Remote sensing data and tools with near-real-time information for monitoring mangroves at global scale
	Sentinel Hub custom scripts	https://custom-scripts.sentinel-hub.com/	Scripts to calculate products from Sentinel data
Information repositories	Earth Observing Dashboard	https://eodashboard.org/explore	Tri-agency dashboard by NASA, ESA and JAXA for browsing EO data, with interactive features and simple analytics by drawing an area of interest
	Earth Online	https://earth.esa.int/eogateway/catalog	Catalog of data from ESA's EO missions
	Landsat Science	https://landsat.gsfc.nasa.gov/data/data-access/	Overview of access to NASA data products from Landsat and many other platforms
	SentiWiki	https://sentinels.copernicus.eu/web/sentinel/missions	Overview of the Copernicus Sentinel missions

For example, data from Sentinel-2 can be browsed via the Copernicus Browser. This cloud-based platform is easy to navigate for reviewing and visualizing the results from various combinations of different spectral bands (see **Glossary**) and satellites without the time-consuming, inefficient, and sometimes infeasible process of downloading a very large amount of data to a local computer for analysis. Alternatives include Google Earth Engine's web interface or Python API and Microsoft's Planetary Computer. This facilitates much-needed access to the resulting information, especially for areas with limited observations or that are difficult to access.

Box 2: Key concepts and considerations when using EO data

Key references are given in the main text referring to Box 2.

1. The smallest area observed by EO sensors – a pixel – always comprises a mixture of elements (different species, underlying ground cover, etc.) and there are techniques for "unmixing pixels". Uncertainties will be greater at transitions between different types of Earth surfaces (e.g., at the edges of ice floes or forests) due to pixel mixing.
2. Uncertainties are generally greater at the edges than at the centers of images – although well-established georectification algorithms are used to account for edge, terrain, and other possible distortions when mapping pixels to the Earth's surface.
3. Water strongly absorbs many wavelengths of electromagnetic radiation (signals measured by EO), and EO capabilities for aquatic species are best developed for species living at or near the water's surface.
4. Data are continuously available but not continuously usable: cloud cover can obstruct optical images, posing challenges especially for tropical regions. Active sensors like synthetic aperture radar (SAR), e.g. on Sentinel-1, provide information even in the presence of cloud cover. There are well-established procedures to correct for atmospheric effects of aerosols, water vapor, etc. For public data, these corrections are normally documented and attached to each dataset.
5. Generally, public data providers (e.g., space agencies like ESA and NASA) publish their algorithms so that the path from the acquisition of a signal to geophysical and biophysical products is transparent and traceable.
6. Public data products improve over time with improving knowledge and technology, and thus have a defined lifetime that is documented by different versions of products. Commercial EO data, which usually have the advantage of higher spatial resolution and can be "tasked" to acquire frequent observations for a given target area, may not have such detailed traceability and continuity as public EO data.
7. *In situ* calibration data is crucial for calibrating satellite data and essential for uncertainty and quality assessment and interpreting the signal in terms of Earth surface (target) properties. It is also important for training of classification algorithms using artificial intelligence (AI).
8. Assessment of uncertainty is more challenging for datasets leveraging AI or interpolation to improve spatial resolution or image aesthetics.

In a few cases, EO data has already been used to obtain information about species at the same (population) level at which genetic diversity is measured. Among the most outstanding of these applications is the identification and monitoring of emperor penguin (*Aptenodytes forsteri*) colonies in Antarctica. These penguins are upper-level predators and are considered a biomonitor of ecosystem change in the Southern Ocean (Barber-Meyer et al., 2007; Bargagli, 2005; Fretwell et al., 2012, 2023; Fretwell & Trathan, 2009, 2021; Kato et al., 2004; Kooyman & Mullins, 1990)2, 2023; Fretwell & Trathan, 2009, 2021) (Bargagli, 2005; Kato et al., 2004; Kooyman & Mullins, 1990). Given that their reproductive cycle is intimately linked to the integrity of the sea-ice coastline, they are sensitive to dynamic processes in the wider Antarctic ecosystem. Under current warming trends, over 80% of colonies are predicted to be almost extinct by the end of the century (Fretwell & Trathan, 2021). These colonies can be assigned to one of at least four metapopulations based on genetic data and corresponding to geographic regions (Younger et al., 2017). One of the major limitations on studying these populations is accessibility, given the remote and extreme conditions in which they live (e.g. -60 °C). Recently, researchers have applied machine learning approaches to publicly available Sentinel-2 satellite imagery to achieve a global census of this keystone species – approximately 600,000 individuals across 66 colonies (Fretwell et al., 2023). EO have thus become useful for monitoring penguin colonies and their habitat, taking advantage of the sharp contrast between penguins, their dark guano, and the background ice. Collectively, the emperor penguin studies indicate how EO provides cost-effective data to monitor species in an inaccessible location, giving access to fundamental information like changes in estimated population size and dramatic habitat modifications. The identification and monitoring of emperor penguin colonies in Antarctica by EO suggests that it is feasible to use EO to estimate the $N_e > 500$ and PM indicators.

Despite the demonstrations of its potential (Barber-Meyer et al., 2007; Fernández, 2013; Fretwell & Trathan, 2009; Schuman et al., 2023), EO data still have not been used for genetic diversity monitoring and assessment (Skidmore et al., 2021; Timmermans & Kissling, 2023) – although some initiatives connect landscape features to the conservation of populations (Cousins et al., 2022). Here, we describe how the current and forthcoming advances in EO capabilities, such as improved spatial and spectral resolution, can be used together with novel CBD genetic diversity indicators (**Box 1**) to facilitate the monitoring, assessment and conservation of genetic diversity in support of the GBF.

We demonstrate how currently available and accessible EO data can support assessment of the genetic diversity indicators for the monitoring framework of the Kunming-Montreal GBF. We propose an overarching workflow with descriptive steps to enable and accelerate genetic diversity monitoring using EO, and demonstrate the advantages of integrating EO in a set of examples with high priority for biodiversity assessment, monitoring and conservation. By discussing these examples, each with distinct challenges and opportunities, we show how available EO data can be embedded in innovative ways to support the calculation of genetic diversity indicators, especially in areas with limited research infrastructure or access, and why we can look forward to applications of EO for assessing genetic diversity more directly.

EO contributions to genetic diversity monitoring: A proposal

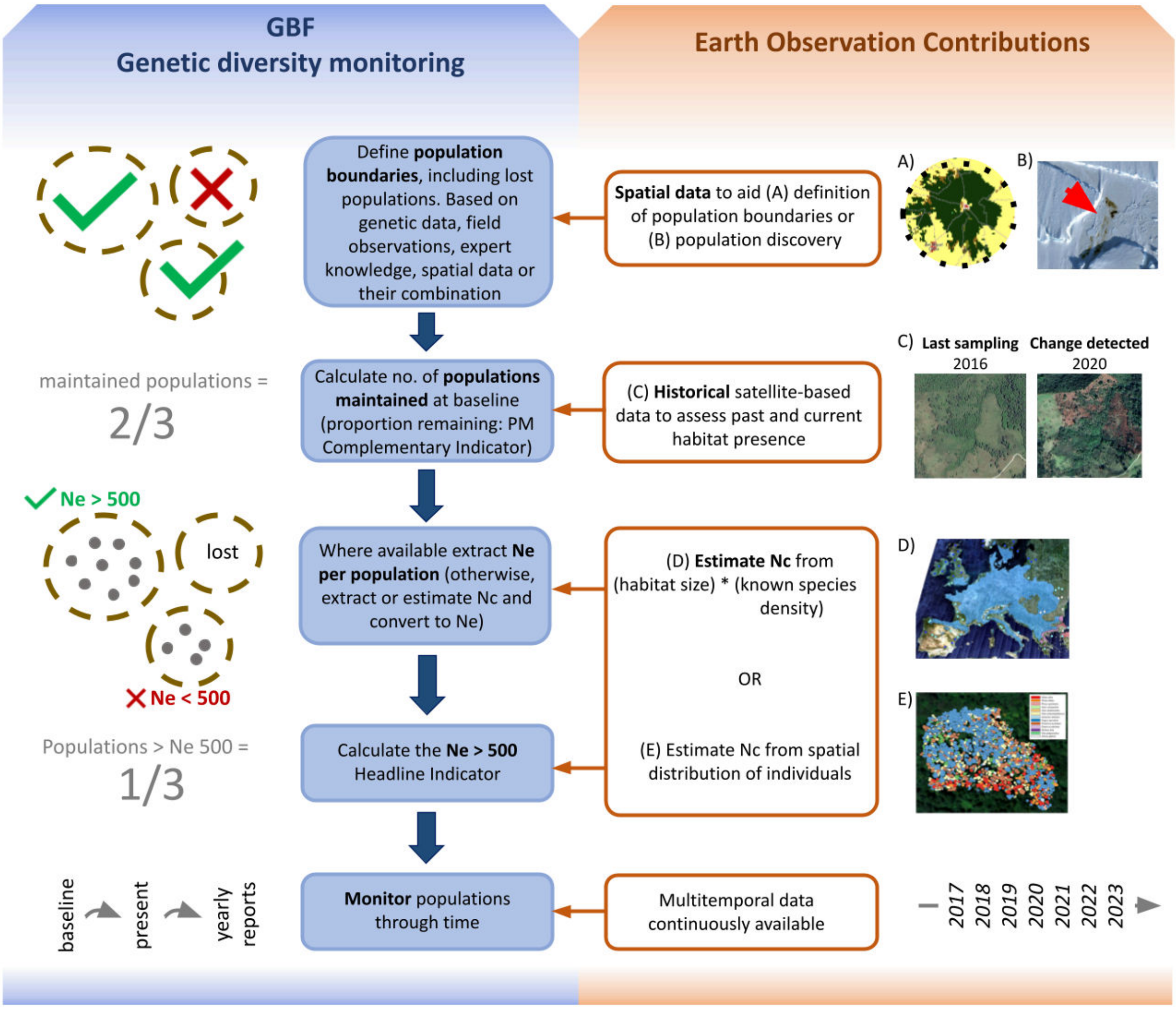

***Figure 1**. Overview of the proposed workflow for integrating EO data with genetic diversity monitoring and estimating the key GBF indicators proportion of populations within a species maintained (PM indicator) and proportion of populations within a species with a genetically effective population size (N_e) > 500 (N_e > 500 indicator) (see also **Box 1** and **Box 3**).*

In the indicator context, a ‘population’ is a group of spatially aggregated, interbreeding individuals, genetically distinct from other similar groups (Mastretta-Yanes, Suárez, et al., 2024; Waples & Gaggiotti, 2006). Spatially speaking, this translates into a subsection of the range that the species inhabits. Whether a population still exists, and whether it has grown, shrunk, migrated or maintained its size, is often linked to changes in its habitat extent (Mace et al., 2010). Habitat extent can change due to land use change, which can in turn be quantified and monitored with EO. Thus, EO can be used for observing and monitoring changes in habitat extent where populations occur, or in changing boundary conditions of habitats (such as long-term changes in land surface phenology (Garonna et al., 2018). We propose that this use can contribute to estimating, and monitoring change in GBF genetic diversity indicators (**Fig. 1**). This can be done in at least two ways: First, by assessing the likelihood of a given population’s continued existence for the PM indicator and second, by estimating a relationship between habitat size and the number of mature individuals of a species living in this habitat (density) to estimate N_c. In some cases (for large and immobile individuals such as trees), N_c may be more directly estimated from EO (see **Outlook**). In either case, EO data supports the assessment of the $N_e > 500$ indicator by providing a proxy for N_c data from which N_e can be estimated using the N_e:N_c ratio (**Box 3**, **Fig. 1**).

Box 3: A workflow to support genetic diversity monitoring with EO

We propose the following steps to include EO data for monitoring genetic diversity of species’ populations. We note that not all steps are feasible for all species.

1. Define population boundaries.
    a. Define populations that can be related to habitat area and size, where the area and size can be identified with support of EO.
    b. Pinpoint the contribution of EO (e.g. systematic land cover mapping or habitat assessment, systematic identification of population presence or activity) and identify what other information is needed.
2. Calculate the number of populations maintained (PM).
    a. Leverage current and historical EO data to assess recent trends in population presence and distribution.
    b. Use EO to support mapping population distribution, which can later help to guide *in situ* monitoring and conservation efforts.
3. Calculate the number of populations with $N_e > 500$.
    a. Define the relationship between area size and census size of each population to be monitored (e.g., validate N_c estimates from ground data).
    b. Use N_c estimates from EO area size or direct observations (e.g. for trees) to infer N_e with the ratio $N_e : N_c \sim 1 : 10$ for each population, and estimate the number which are above the $N_e > 500$ threshold.
4. Monitor the population areas for maintenance and size over time.
5. Targeted re-assessment.

Our proposed workflow relies on the following assumptions:

- That a habitat of a particular size does support a species population;

- That habitat quality can be sufficiently well assessed by EO; and
- That the relevant threats to populations are visible at the habitat scale (e.g., land-use change, but not poaching).
- The workflow furthermore requires information about the location of populations, population density (N_c per area), and N_e:N_c ratio.

In other words, the proposed approach would work for species where habitat changes such as land cover and land use change (see **Example: Monitoring habitat change to infer PM and N_e > 500 change in wild relatives of domesticated crops**), or landscape modification and fragmentation, can be detected and quantified using EO (**Box 3**, **Fig. 1**).

We propose that this approach will be most useful for cases in which there is still insufficient data to calculate the indicators but sufficient information about the location of species populations, habitat, dispersal distances, and approximate density (**Fig. 2A**). We furthermore expect that this approach can facilitate and accelerate indicator calculation even in cases where N_c estimates are available by making remote observation possible. In some cases, N_c estimates will be possible directly from EO data (**Fig. 1**, **Outlook**). Critically, we expect this approach to enable more frequent change monitoring in all cases (**Fig. 2B**).

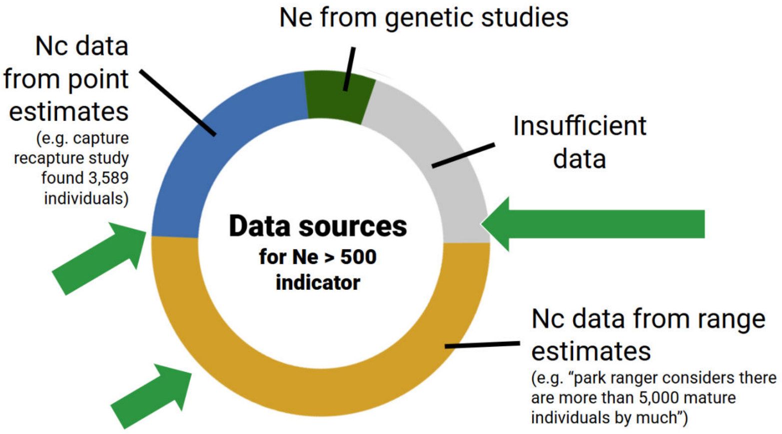

Figure 2. *EO enables estimation of key GBF indicators in cases where other data that could be used to calculate the indicators are unavailable (right side, large arrow), but can also complement assessments where ground data and expert knowledge are available (left side, smaller arrows). Made with data from Mastretta-Yanes et al (2024).*

The major challenge is to ensure the useability and accessibility of EO data for specific applications, such as biodiversity monitoring, as it requires expert knowledge to extract the needed information[5] (**Box 2**) (Pahlevan et al., 2021; Silva et al., 2008). The integration of EO data as an additional source of indirect (habitat extent, fragmentation, etc.) or direct information (N_c estimates, and see **Outlook**) about genetic diversity indicators for the assessment and monitoring of biodiversity requires the co-development and production of such information through collaboration among experts in population and conservation genetics and genomics, remote sensing, geography and geospatial information, ecology, conservation, and practitioners who will ultimately use this information routinely.

Example: Monitoring habitat change to estimate the N_e>500 and PM indicators in wild relatives of domesticated crops

The wild relatives of modern-day crops (e.g. crop wild relatives, CWRs) harbor an important proportion of crops' genetic diversity (Maxted et al., 2006). In Mexico, CWRs are threatened mainly by land use and land cover change (Goettsch et al., 2021). Several species (spp.) of wild avocados (*Persea* spp.) and teosintes (*Zea* spp., related to maize or corn) inhabit locations that are often dangerous or difficult to visit. Within these genera, several wild species are endangered or critically endangered (Goettsch et al., 2021). Populations of these species cannot be directly observed with EO due to the typical size of individuals and their habit of living under forest canopies, but critical aspects of their native habitat, such as proximity to and association with nearby forests, can be observed. In particular, tree-cover loss (land use or land cover change, and thus habitat loss) can be quantified to infer which populations may be experiencing greater decline. In terms of its impact on genetic diversity, habitat loss could mean population extinction (habitat annihilation in a given region, PM decline) or reduction of the effective population size (smaller habitat space, fewer individuals, N_e decline and thus elevated loss of genetic diversity through genetic drift, see **Glossary**).

EO are not yet used to monitor CWRs, but this could be achieved using publicly available EO data in a few straightforward steps. The first step is to define population boundaries (**Fig. 1**) based on occurrence points (combined with a rule for aggregating points to populations) or species distribution models, using methods including, for instance, geographic features (e.g., different mountains harbor different populations) or eco-biogeographic differences (e.g., different environmental zones harbor different populations) (Hoban et al., 2023; Tobón-Niedfeldt et al., 2022). The second step is to assess whether populations have been maintained since the last observation (PM indicator). In classical monitoring approaches, this would imply traveling to the locations on a regular basis. However, doing this for several species in megadiverse or large countries is challenging to impossible in terms of time and cost. EO data can be used in

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[5] And see https://www.ucgis.org/gis-t-body-of-knowledge

such situations to detect habitat loss using either visual inspection of satellite images or by analyzing satellite-derived time series of land use and land cover (LULC) change, such as tree-cover loss. The images and their derived products such as tree-cover change are publicly available free-of-charge from repositories such as the Sentinel Hub, Google Earth, and Global Forest Watch (**Table 1**). The third step is to estimate genetic diversity indicators from habitat size information. For the PM indicator, the procedure is straightforward: populations that have lost all of their habitat over time are expected to be lost, and the fraction of remaining populations corresponds to the PM indicator. For the Ne>500 indicator, two assumptions must be made. The first pertains to the population density of the species being studied: if we know the habitat size and population density, we can estimate the population's census size. The second assumption involves the Ne:Nc ratio: given the census size of a population, we can estimate the corresponding effective population size (N_e). Once the effective size of every population (N_e) is estimated, we can calculate how many populations are above the threshold value of 500.

Our first example is *Persea* (*P.*) *cinerascens*, a wild avocado growing among the tree species composing cloud forests, Mexico's most biodiverse terrestrial ecosystem type per unit area (Conabio, 2023; Rojas-Soto et al., 2012). *P. cinerascens* occupies less than 500 km^2 in a total of five populations separated by ca. 50-200 km in three geographic locations[6]. The species' presence was confirmed during the last visit to the known field localities in 2017, although no population size measurement was conducted. The second example is the teosinte species *Zea* (*Z.*) *perennis*. The location of a *Z. perennis* is only known from two areas, encompassing two genetically differentiated populations (Rivera-Rodríguez et al., 2023). These locations were last visited and populations observed in 2008, when conducting sampling for genetic studies (Rivera-Rodríguez et al., 2023). Based on those data, the N_e of both teosinte populations is below 500, so the $N_e > 500$ indicator value for the species is zero according to the first multinational assessment of genetic diversity indicators (Mastretta-Yanes et al., 2023). Unfortunately, although populations of both species were observed in the field relatively recently (2017 and 2008, respectively), their habitat is suspected to have decreased or disappeared due to rapid land use change.

EO data enable the monitoring of genetic diversity for these two species by assessing the persistence of their habitats in the locations where the species were last observed or sampled *in situ*, directly informing the PM indicator without the need for costly and dangerous field assessments. Direct inspection of true-color satellite images (**Fig. 3A and 3C**) allows a rapid assessment of vegetation, land use and land cover changes. By comparing satellite images taken before the last ground sampling (2016 for *P.*

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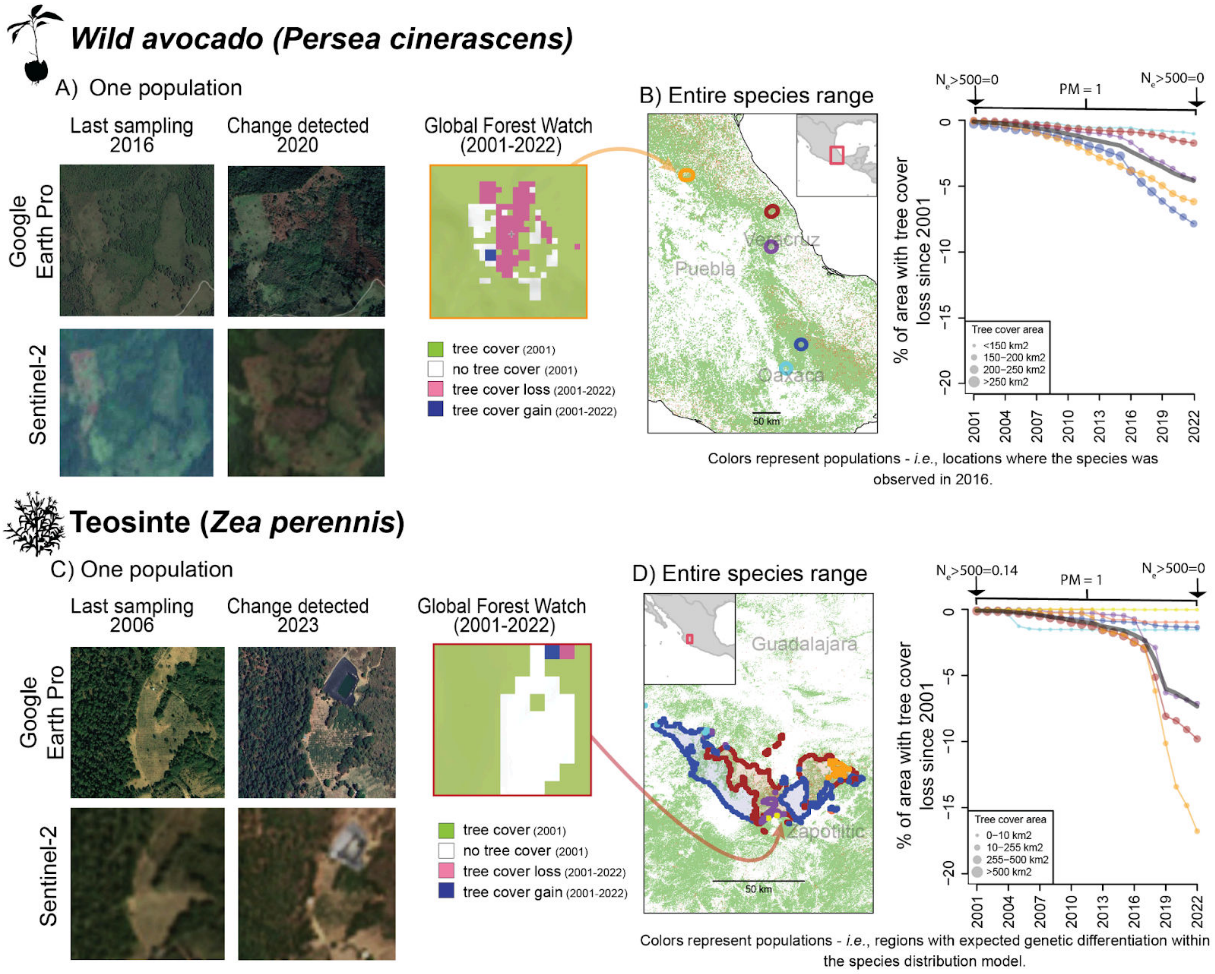
[6] https://www.iucnredlist.org/species/110067105/129767329

cinerascens and 2006 for *Z. perennis*) with more recent images, habitat change can be estimated. For instance, this method showed that for *P. cinerascens,* a controlled forest fire occurred in 2020 to clear land for agriculture, indicating a threat to the maintenance of this population. Conversely, for *Z. perennis*, the boundary of the avocado farm adjacent to the sampling location remained unchanged between 2007 and 2023.



Wild avocado (Persea cinerascens)

A) One population

B) Entire species range

Colors represent populations - *i.e.*, locations where the species was observed in 2016.

Teosinte (*Zea perennis*)

C) One population

D) Entire species range

Colors represent populations - *i.e.*, regions with expected genetic differentiation within the species distribution model.

***Figure 3**. Examples of habitat monitoring using EO for A-B) a wild avocado* (P. cinerascens) *and C-D) a teosinte* (Z. perennis)*. Shown in A) are the comparisons of imagery available from either Google Earth Pro (high spatial resolution) or Sentinel-2 showing habitat change for a wild avocado population, and the evaluation of tree cover change from Global Forest Watch. In B), the combination of Global Forest Watch data with ground data from 2017 (circles) indicates that the change took place between 2017 and 2020. In C), data from Google Earth Pro and Sentinel-2 for a different time frame indicate there has been no change in forest cover for the teosintes population which was last observed from the ground in 2008. In D), analysis of percentage tree cover*

change since 2001 and total tree cover used as an indicator for habitat change and size for distinct ecoregions (individual colors) of teosinte, and the black line shows the average over all populations. The PM indicator is estimated assuming that habitat maintenance indicates population maintenance, and the $N_e > 500$ *indicator is estimated assuming a low population density of* $N_c = 10$ *individuals / km*^{2} *and* $N_e : N_c = 0.1$.

Using the history function of Google Earth Pro often provides free access to high-resolution satellite images, although availability is by chance (i.e., different years and seasons), and automated processing is not possible with this platform. These limitations can be overcome using time-series analysis of publicly available EO data, such as Sentinel-2 images (10 m spatial resolution, 5-day temporal resolution since 2016), which can be combined with Landsat images (30 m spatial resolution, available since the 1970s). However, as a simple starting point, significant habitat changes can already be detected visually by selecting one high-quality image per year from the same season (e.g., dry season, as opposed to the rainy season) and examining such an annual time series. Additionally, products derived from EO data describing habitat and biodiversity changes are already accessible for non-EO-experts through platforms like Global Forest Watch, which provides assessments of tree cover loss (defined as removal or mortality of vegetation taller than 5 m) and tree cover gain derived through automated interpretation of 30 x 30 m EO data (Hansen et al., 2013; Potapov et al., 2022). Thus, this platform enables rapid assessments of tree cover loss over time (2001-2022) and might serve as an effective early alert system for habitat change detection (Schneider & Olman, 2020) (**Fig. 3B and D**).

These different tools and datasets can be applied to crop wild relatives, either for assessment of low-dispersal species or for landscape-scale assessments incorporating species distribution models (SDM), as commonly employed in systematic conservation planning and management (Tobón-Niedfeldt et al., 2022). For species with few occurrences – such as *P. cinerascens* – buffer zones around the specific areas can be used to assess whether the surrounding habitats crucial for their survival are adequately considered and protected. For more widely distributed species, such as *Z. perennis*, SDMs serve as a proxy for species distribution ranges (Villero et al., 2017). SDMs can be leveraged for genetic diversity monitoring by subdividing them into areas where some level of genetic differentiation is expected, for instance, due to environmental differences or historical isolation (Tobón-Niedfeldt et al., 2022; Villero et al., 2017). Once buffer zones around occurrence records, or SDMs, have been delimited and subdivided with proxies of genetic differentiation, they can be regarded as different populations for monitoring purposes. Subsequently, land use and cover change can be quantified and assessed in terms of habitat loss trends. For instance, in the case of wild avocado (**Fig. 3B**), the habitat surrounding the "purple population" (see colored circle) had a high percentage of tree-cover loss during the last two decades but remained large in absolute terms. Contrastingly, the “green” population already had minimal remaining natural vegetation, making subsequent losses more threatening to its survival. Similarly, in the teosinte example (**Fig. 3D**), the “red” population exhibited the most significant decline and is the second smallest, while it appears that the protection of the “yellow” population was successful. Note that the individual population trends differ from the species mean (dark black line), highlighting the importance of separately evaluating populations within a given species.

In both species, despite the clear decline in habitat size observed in some populations, no population experienced a complete loss of habitat. Therefore, the PM indicator for both species is estimated to be 1. However, populations of both species cover very small areas, often less than 200 km². Assuming a low population density of 10 individuals per km² and a conservative N_e:N_c ratio of 0.1, all populations remain below the critical effective population size threshold of 500. Therefore, while PM = 1, $N_e > 500$ is zero. This example shows how integrating habitat monitoring using EO within a population genetics framework can inform the assessment of the GBF indicators and the prioritization of *in situ* observations and future interventions.

Outlook: Genetic diversity assessments using EO

EO offers measurements at landscape level that are repeated in space and time. These observations are captured in wavelengths beyond the human-visible range of the electromagnetic spectrum and yield detailed and traceable information about processes that affect the composition and distribution of species at landscape scales. This information can be used directly to monitor and assess changes in habitats and, via proxies, change in genetic diversity within and between populations. Furthermore, it can help managers prioritize interventions and target them in space and time to areas where rapid changes are taking place, hence mitigating damage and maintaining or enhancing their resilience and protecting biodiversity (Langhammer et al., 2024). The cost-effectiveness of this approach is noteworthy as many biodiversity hotspots are located in economic resource-limited regions.

Available EO data and information, combined with ground-based methods, can be used for assessing and monitoring the quantity and quality of locally available habitat for geolocated populations, and can inform the PM and $N_e > 500$ indicators in several ways (**Table 2**): (1) Informing the PM indicator if habitat integrity or species vitality descends below a certain threshold, below which a species can be assumed to be locally lost; (2) informing the $N_e > 500$ indicator either (i) directly, if species density per unit area is known or if groups of mature individuals can be directly observed, or (ii) indirectly, where a baseline N_e value is known for a given population, the expected decline could be estimated as a function of habitat loss; and (3) supporting prioritization of *in situ* monitoring or conservation actions, or an early alert system, so that resources are directed to the regions where more change is occurring and ground-based observations are most needed.

Table 2. Proposed uses of EO data for genetic diversity monitoring.

Uses of EO data	Implementation for genetic diversity monitoring	Current limitations
Species range and habitat mapping *Accuracy increases with prior knowledge and in terrestrial habitats*	**Inference of census size** *from dispersal distance data, occupation density data, or occasionally counts of dominant individuals; supports* **assessment of N_e>500**	Cannot directly measure effective or census population sizes (N_e or N_c)
Estimate population size and number *Accuracy increases when combined with observational data*	*Inferred population locations can be combined with other data (e.g. biogeographical, traditional knowledge) to* **infer population boundaries** *or support the design of comprehensive DNA studies to confirm this*	Cannot independently identify genetically distinct populations
Detect habitat and ecosystem change *Requires a baseline and continued monitoring*	*Develop EO-based alert systems to support genetic diversity* **protection in real time** *and to* **monitor inferred PM or N_e>500 over time**	Cannot detect all on-the-ground threats to individuals (e.g., poaching)
Map variation or change in species visible from Space *e.g., trait variation, settlements, migration, breeding activities, species interactions*	*Currently still a focus of research: see* **Outlook**	Cannot directly estimate genetic diversity

Currently, the procedure outlined above is largely theoretical, but the examples above indicate its utility and potential importance. This potential for EO-based genetic diversity monitoring needs to be verified with ground-based data before large-scale deployment, although performing the necessary fieldwork is generally only possible “pointwise” for large countries and regions and may be restricted by limited operational resources. Thus, EO provides valuable global information, especially where no other data are available. Where local *in situ* monitoring, citizen science and other sources of ground data are, or become, available, EO data will be better complemented.

A window onto the future – mapping genetic diversity and resilience of an entire tree species using EO

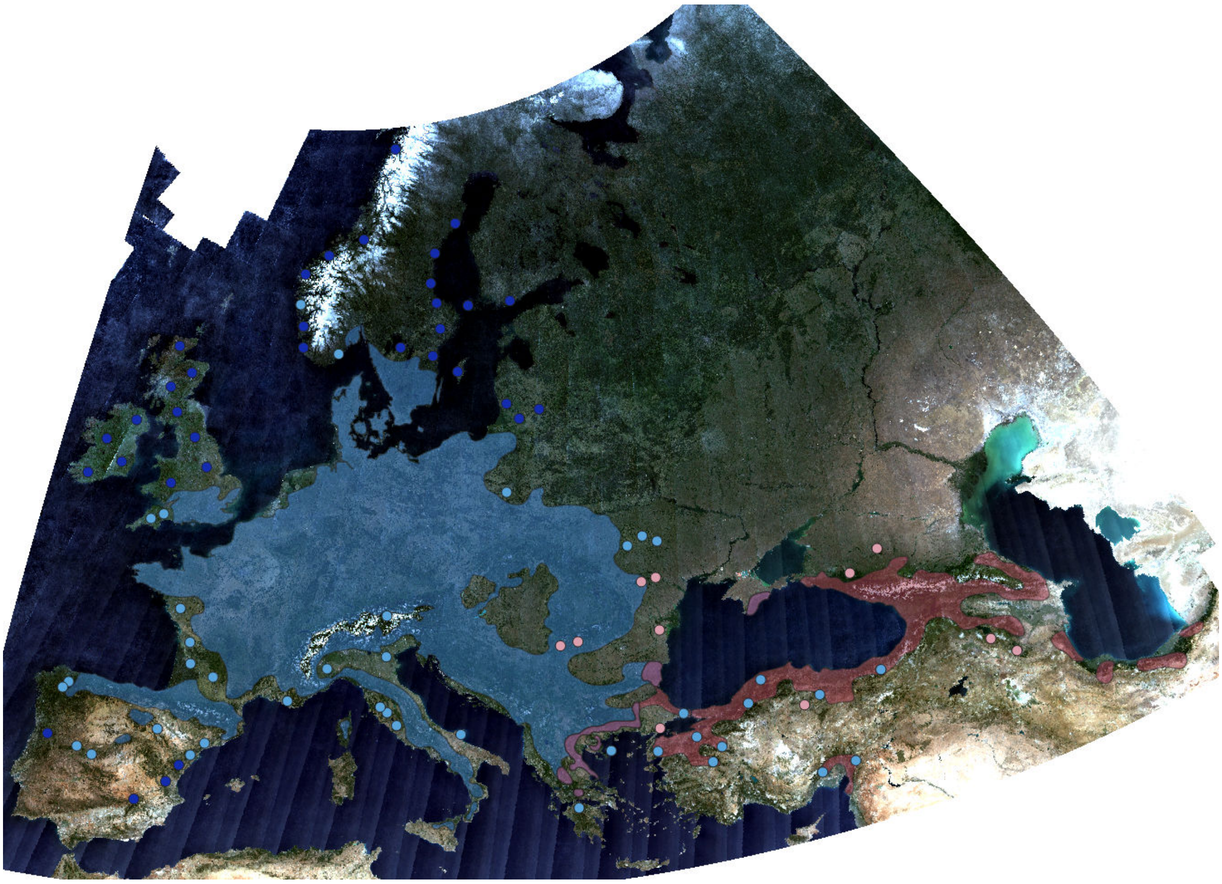


***Figure 4**. Layers of geospatial information on the distribution of Eurasian* Fagus*: Sentinel-2 mosaic from Google Earth Engine (Gorelick et al., 2017) for visualization purposes, overlaid with species distribution and isolated localities (dots) (Caudullo et al., 2017):* F. sylvatica *(blue) and the distributions of three closely related* Fagus *species (red) (Denk et al., 2024).*

A current research focus is to directly map variation or change in species visible from Space (**Table 2**), such as trees. EO can be used to assess important aspects of tree canopy structure, phenology and functions such as height and density, greening and browning, pigment concentration and water content, or to characterize tree species and even within-species variation. To illustrate the current state of research and development, we use the common beech, *Fagus* (*F.*) *sylvatica*, a keystone tree species that also has high economic importance in forests across Europe. *F. sylvatica* is closely related to, and likely able to hybridize with, three other species of *Fagus* found from the Balkans into the Arabian peninsula; in fact, these had all recently been considered to belong to *F. sylvatica* (Denk et al., 2024). We have overlaid distribution maps (Caudullo et al., 2017) with satellite imagery at continental scales: A Sentinel-2 mosaic produced with Google Earth Engine (Gorelick et al., 2017) (**Fig. 4**).

Beech species (*Fagus* spp.) pollen is spread both by insects and wind, and the species has relatively low genetic differentiation among different forest stands, so that divisions into populations are also challenging (Milesi et al., 2024). N_e estimates are likewise challenging: For example, genetic analysis of a stand in France with 167 individuals yielded N_e estimates ranging from two to 25 depending on the calculation method used (Gargiulo et al., 2024). This was of course below the threshold of 500 that would require ca. 5000 individuals to be analyzed; however, the results include the guideline ratio of $N_e : N_c = 0.1$ that would correspond to an N_e of 17 in this example. The weak, yet discernible genetic structure of *F. sylvatica* (European beech) – in other words, moderate isolation of populations by distance (Lazic et al., 2024; Milesi et al., 2024) – reveals its post-glacial migration history but also depends on management and planting decisions in forestry. Here, we discuss how recent developments in EO technologies can support the assessment of beech genetic diversity both in terms of the GBF indicators (**Box 1**), and in terms of essential biodiversity variables (EBVs) for genetic diversity (**Box 4**).

Decades of population genetics studies on *F. sylvatica* have produced hundreds of datasets on its genetic diversity and differentiation (Stefanini et al., 2023). However, these studies have used different molecular methods over time, and the advent of genomics has not resolved the issue. Older studies based on previously favored molecular markers remain valuable and are complemented, not replaced, by a newer generation of single nucleotide polymorphism (SNP)-based studies using genomic approaches (Stefanini et al., 2023). Furthermore, these SNP-based studies may in near future be overtaken by newer genomic markers such as kmers and structural variants (Roberts et al., 2024; Stefanini et al., 2023). As such, there is not a single common and agreed-upon way to measure the genetic EBVs (**Box 4**) for this species using DNA data, but rather several complimentary possibilities; and the situation is similar for many other species for which DNA-based population genetic data are available.

Box 4: Essential Biodiversity Variables (EBVs)

Essential variables have been developed to understand and measure climate, biodiversity, and other components of the Earth system (e.g. Essential Climate Variables, Essential Ocean Variables). The concept of Essential Biodiversity Variables (EBVs) was introduced to advance the collection, sharing, and use of biodiversity information (Pereira et al. 2013; Navarro et al. 2017), providing a way to integrate the many biodiversity observations collected through different methods such as *in situ* measurements or remote sensing (https://geobon.org/ebvs/what-are-ebvs/). EBVs are scalable, meaning the underlying observations can be used to represent different spatial or temporal resolutions required for the analysis of trends.

The EBVs for genetic composition include (Hoban et al. 2022; Junker et al. 2023):

1. Effective population size: Size of an ideal population that loses genetic variation at the same rate as the focal population. Related to the **N_e > 500 indicator** (see **Box 1**).
2. Inbreeding: Degree of relatedness between pairs of individuals, mating among relatives, or identity by descent. Not assessed by either the N_e > 500 indicator or the **PM indicator** (see **Box 1**).
3. Allelic richness and heterozygosity: Count of the number of alleles in a population or expected proportion of heterozygotes in a population at equilibrium. Not assessed by the N_e > 500 and PM indicators.
4. Genetic differentiation: Number of genetic units and degree of genetic differentiation among population units. Related to the PM indicator.

It is possible to infer the number of dominant (canopy-forming) *F. sylvatica* trees in EO images. To locate *F. sylvatica* (estimate the potential occurrence and coverage), distribution data over the species range (e.g., **Fig. 4**) can be divided into forested and non-forested areas (e.g., with land use land cover change or LULC products, or forest coverage products). Where more information is available, these can be classified as forests with known locations, percentages, or densities of beech trees using maps of land use, forest communities, or inventories, ideally combined with local and specialist knowledge. For application to larger scales or where less information is available, tree species classification using EO data has been demonstrated in beech habitats with simple machine learning approaches (Grabska-Szwagrzyk et al., 2020), neural networks (deep learning) on high spatial resolution data (Kaplan et al., 2024; Yao et al., 2021), or a combination of active and passive EO data from Sentinel-1 and Sentinel-2 in annual time series combined with forest inventory data (Blickensdörfer et al., 2024). In-field or aerial datasets with high resolution and accuracy are important for further refining tree species classification with EO (Fassnacht et al., 2016).

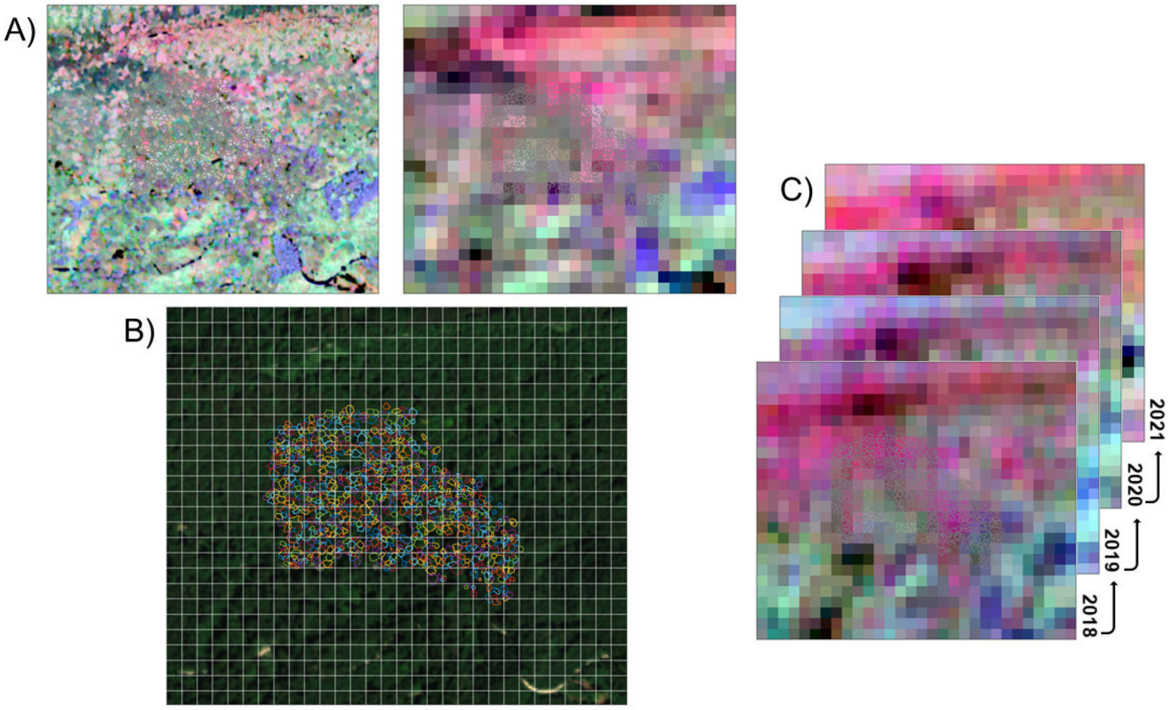


***Figure 5**. Components of change monitoring over forest canopies using EO. A) Spatial scaling of the canopy traits chlorophyll (green), carotenoids (red) and water content (blue) assessed using 2 m aerial imaging spectroscopy data (left), or 20 m EO data (right). B) 20 m Sentinel-2 pixels compared to the crown sizes at the Laegern forest. At 20 m pixels, multiple individuals contribute to the signal obtained for one pixel. C) Physiological traits mapped for the area of interest for four consecutive years using Sentinel-2 data to detect changes in canopy traits.*

Such data are available from the Laegern forest in Switzerland, a temperate mixed forest with a high proportion of *F. sylvatica*. Laegern is the subject of over a decade of remote sensing data collection by airborne imaging spectroscopy (continuous measurements covering most of the solar radiation spectrum with high resolution, i.e., 3-10 nm) several times per year, and complementary fieldwork has been conducted on the south-facing slope (Morsdorf et al., 2020) and in portions of the forest across a compositional gradient. Torabzadeh and colleagues achieved high binary classification accuracy of *F. sylvatica* versus all other trees in a beech-dominated stand at Laegern (**Figs. 5 and 6A**) based on pixels – in other words, without needing to define tree crowns (82% producer's accuracy / 92% user's accuracy) (Torabzadeh et al., 2019). It is important to note that binary classification of pixels as depicting beech vs. non-beech was more accurate than multiple classification of pixels as depicting one of several species present (Torabzadeh et al., 2019). At another well-documented test site in Allenwiller, France, where the closely related caucasian beech (*Fagus hohenackeriana*

Palibin) was co-planted with *F. sylvatica*, Kaplan and colleagues (2024) used a similar pixel-wise approach to distinguish these species with better than 90% accuracy (F1 score) using high-resolution (3 m) commercial multispectral EO data provided free of charge for research purposes by PlanetScope. Both of these approaches used signal characteristics overlapping with the detection ranges of current public EO instruments. Transferring these approaches to public data requires scaling from 3 m spatial resolution to ca. 10 to 20 m spatial resolution (**Fig. 5**).

A census number (N_c) of reproductively mature beech trees could be locally estimated directly from beech canopy pixels discernible from EO data via species classification. This could then be used to approximate the N_e > 500 indicator. This approach would likely yield an underestimate because N_c from EO would count dominant (canopy-forming) reproductively mature trees that are the easiest to detect from above, while reproductively mature but co-dominant, intermediate, and suppressed trees are difficult to assess. Inventory data, or data from *in situ* sources, could support the estimation of N_c via tree density and be used to upscale to larger areas. Changes in PM and N_e > 500 for known, monodominant populations of *F. sylvatica* could also be assessed by forest cover loss. Furthermore, the risk of losing individual trees from forest canopies could be predicted from changes in canopy vitality via changes in trait values. An approach to use EO to quantify the relationship of trait diversity to forest canopy drought responses has recently been demonstrated using public EO data at 20 m spatial resolution (Helfenstein et al., 2022, 2024; Sturm et al., 2022) (**Fig. 5**). European beech forests are increasingly threatened by drought, and individual trees vary in their susceptibility, in part due to genetic differences (Bolte et al., 2016; Braun et al., 2021; Pfenninger et al., 2021). Current efforts using high-spatial-resolution data from uncrewed aerial vehicles (UAVs) to document dead trees could help validate models predicting the dieback of individual trees[7].

Toward “Genes from Space”

So far, this paper has discussed using EO data to assess genetic change due primarily to habitat change or census count change. More advanced approaches get closer to achieving an ultimate aim of truly measuring genetic diversity from space. Data with higher spatial and spectral resolution data are also used to assess canopy traits and vitality (Asner & Martin, 2016; Helfenstein et al., 2022) instead of the number of individual trees and may furthermore help to predict the genetic distance among individual dominant trees. Czyż and colleagues used time series data from imaging spectroscopy (providing continuous spectra rather than distinct multispectral bands – see **Glossary**) with high spatial resolution (2 m) to generate a time series of differences

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[7] https://deadtrees.earth/

among spectra from center-of-canopy pixels for 69 dominant beech trees out of 260 dominant trees in a canopy (see **Fig. 6A**). They correlated these spectral differences, quantified as a conceptual distance with less similar spectra being more distant than more similar spectra, with the trees' genetic distance (a measure of how related the trees are), as determined by five nuclear microsatellite sequences (DNA sequences often used to quantify relatedness). The correlation strength between spectral distance and genetic distance reached a maximum of 60% for some parts of the spectrum at time points when trees were subject to drier conditions and later in the growing season (Czyż et al., 2023) (**Fig. 6B**). Interestingly, in humans, it is well known that microsatellite sequences, also called short tandem repeats (STRs), fine-tune individuals' genetically encoded responses to environmental pressures (Horton et al., 2023; Wright & Todd, 2023); these sequences evolve rapidly, which is why they are also useful to measure the relatedness of even very closely related individuals (Provatas et al., 2024). Thus, the prediction of genetic variation using EO data is sensitive to environmental conditions. Such studies help to investigate how predictable such effects may be and can inform models to predict genetic variation using EO.

For beech trees, EO from current multispectral and forthcoming imaging spectrometer sensors can thus support the assessment of genetic variation by providing information about forest canopy traits and spectral signatures using time series of observations (**Figs. 5 and 6**). Combined with a large and growing database of single-time-point genetic data for beech across its range, it may be feasible to develop models to predict genetic variation directly from EO data for *F. sylvatica*, and likely for other dominant forest tree species. Such predictors of genetic variation could improve genetic diversity indicators beyond population maintenance and size towards assessing genetic EBVs (**Box 4**). For example, several studies indicate that high-resolution spectroscopy (field and imaging spectroscopy) can reveal quantitative genetic differences and could thus help to scale up measurements of genetic differentiation (Cavender-Bares et al., 2016; Li et al., 2023; Meireles et al., 2020; Seeley, Stacy, et al., 2023; Stasinski et al., 2021).

These approaches are currently developed for "best-case scenarios" where aerial imaging spectroscopy or even individual leaf-level measurements provide high certainty for assigning spectral data to individual trees (Czyż et al., 2023; D'Odorico et al., 2023; Petibon et al., 2021). Scaling approaches for extending these measurements to landscape level are currently being established, starting with trait estimates such as canopy pigments and water content that are already possible with Space-based EO multispectral sensors (Helfenstein et al., 2022) (**Fig. 5**) or the delineation of closely related species based on spectral and trait differences from high-resolution EO data (Kaplan et al., 2024).

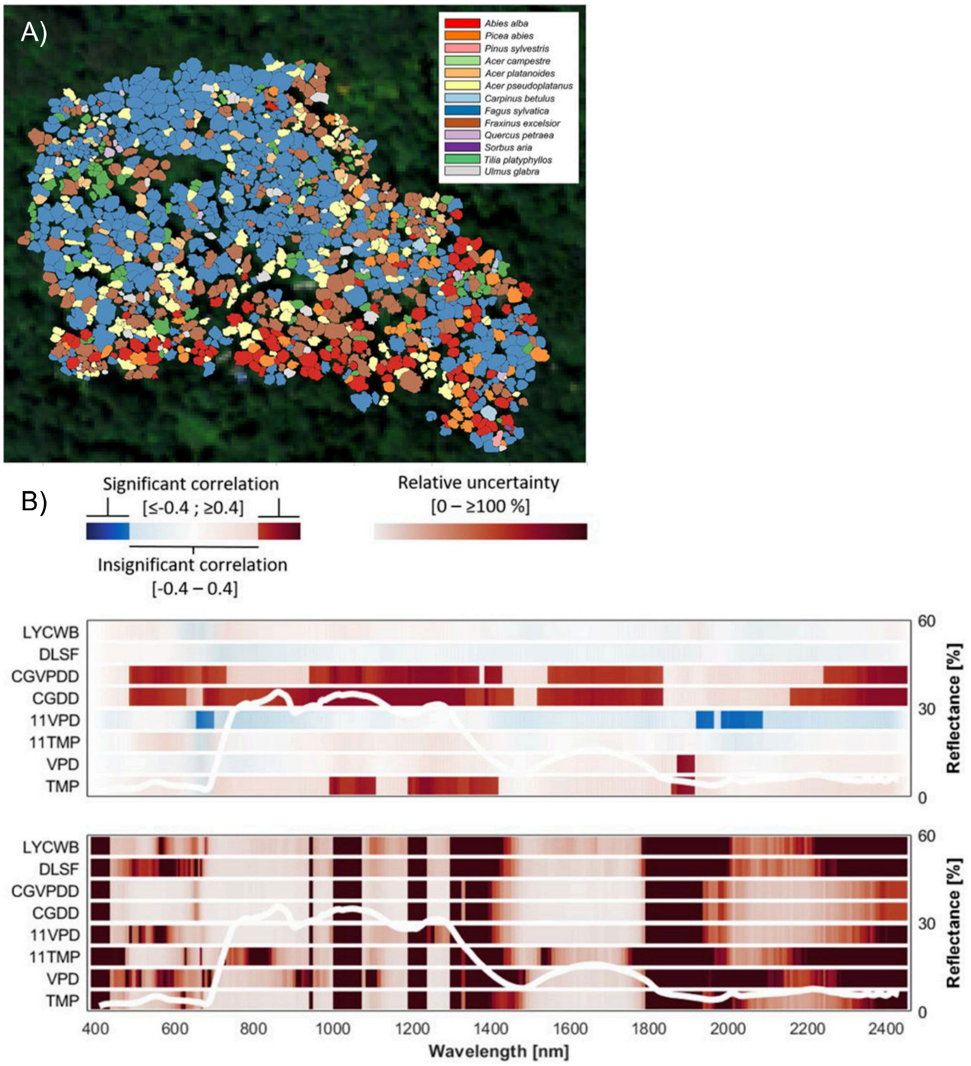

Figure 6. *Spectroscopy can help to distinguish species and assess genetic variation. A) Dominant tree crowns assigned to species by aligning forest inventory data with a 3D model of tree crowns and trunks made using LiDAR and photogrammetry; reproduced from (Guillén-Escribà et al., 2021), CC BY. B) Upper panel: Spectral similarity is correlated with a genetic relatedness measure (Nei's genetic distance) for 69 large dominant beech canopies in (A), with correlation strength related to environmental factors. Lower panel: Estimated relative uncertainties of correlations. White lines: mean canopy reflectance measured for focal trees (0-60% of incident sunlight). Environmental factors: temperature on day of acquisition [°C] (TMP), Vapor Pressure Deficit on day of acquisition [%] (VPD), Aggregated Temperature over 11 consecutive days [°C] (11TMP), Aggregated Vapor Pressure Deficit over 11 consecutive days [%] (11VPD), Cumulative Growing Degree Days [°C] (CGDD), Cumulative Growing Vapor Pressure Deficit Days [%] (CGVPDD), Day of Last Spring Frost (DLSF), or Last Year Climatic Water Balance*

(LYCWB). Pearson correlations are shown from -0.6 (dark blue) to 0.6 (dark red). Reproduced from (Czyż et al., 2023), CC BY.

When accounting for environmental variation, imaging spectroscopy observations with higher spectral resolution than current multispectral EO (Landsat, Sentinel-2) could even support the estimation of genetic distances across forest canopies. The improved spectral and radiometric capabilities of new EO imaging spectroscopy missions to be launched before the end of this decade by ESA (CHIME: Copernicus Hyperspectral Imaging Mission[8]) and NASA (SBG: Surface Biology and Geology[9]) will enhance the information content of EO measurements by two orders of magnitude compared with currently operating multispectral instruments such as those described so far in our examples. This opens up the possibility of using spectral fingerprints to better distinguish species using EO and even to estimate other components of genetic and trait variation beyond the genetic diversity indicators (Cavender-Bares et al., 2020; Czyż et al., 2023; Kaplan et al., 2024; Li et al., 2023; Meireles et al., 2020; Petibon et al., 2021; Seeley, Stacy, et al., 2023; Seeley, Vaughn, et al., 2023; Stasinski et al., 2021).

Conclusion

The incorporation of EO into assessments of genetic diversity represents a fundamental change in our ability to monitor, assess,and protect biodiversity at the national, regional, and global scales, especially in areas with limited accessibility. Our proposed workflow (**Figs. 1-2**, **Box 3**) could be developed from public EO and geolocation data as well as optional user-input data on platforms such as GEO BON's "BON-in-a-Box" (Griffith et al., 2024) to make it widely available and facilitate its use for biodiversity monitoring. To better understand and describe this proposed approach, we discuss three examples that each raise key considerations for the application of EO to monitor habitat change and study genetic diversity (**Tables 1-3**, **Box 2**). We consider the immediate goals of assessing genetic diversity indicators for biodiversity monitoring and providing early warning signs to support the protection of genetic diversity (**Figs. 3-4**, **Box 1**), as well as an outlook on approaches that may enable the assessment of essential biodiversity variables (EBVs) for genetic diversity from Space (**Figs. 5-6**, **Box 4**). We acknowledge many current limitations that are illustrated in the presented examples and summarized in **Tables 2** and **3**.

Table 3. A reflection on the applications of EO to monitor and study genetic diversity based on the examples discussed in this article.

Case	Aims	EO contributions	Challenges	Information for action

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[8] https://www.esa.int/ESA_Multimedia/Images/2020/11/CHIME

[9] https://sbg.jpl.nasa.gov/

Emperor penguins in the Antarctic	Infer PM and N_e	Inference from evidence of colony occurrence (guano) and patterns of ice cover Provides data for one of the least accessible locations on Earth for *in situ* assessment	• Colonies are not themselves genetically distinct populations, but can be assigned to populations • Difficult to estimate colony size from Space-based images of guano deposits	1. Temporal coverage → know when shelves break off (timing of major habitat change) 2. Spatial and temporal coverage → assessment of colony relocation versus loss
Crop wild relatives in Mexico	Infer PM Establish a warning trend	Inference based on habitat maintenance or change Provides data for locations that are too dangerous to visit *in situ* due to social conflicts or remoteness	• Habitat may persist although populations are lost • How does habitat change relate to changes in N_e?	1. Rate, extent, and timing of habitat change → timely intervention (alert) 2. Confluence of degree of habitat change with total habitat available for different ecotypes → prioritization
European beech forests	Infer PM and N_e Infer genetic EBVs	Inference based on forest coverage and biochemical and structural differences mapped across tree canopies	• Weak geographic separation of genotypes • Only dominant trees are directly accessible • Low accuracy for distinguishing multiple species (high accuracy for binary categories) • Statistical accounting for environmental effects	1. Combine information on stand-level vitality with genetic and trait variation across the species range → prioritize interventions 2. Information to support decisions about assisted migration or assisted gene flow interventions (see **Glossary**)

As EO data become increasingly available and accessible for non-experts, especially for use in genetic diversity monitoring and assessment, their use and interpretation still require some technical expertise (**Box 2**). This need for greater technical expertise becomes even more acute with the anticipated advances in EO such as existing EnMAP, and upcoming CHIME and SBG, imaging spectroscopy Space missions before the end of this decade. In combination with the needs of practitioners and the impetus provided by biodiversity monitoring mandates, this means that useful access requires the development of portals equipped with tools and interfaces that make key information provided by EO more widely and easily accessible. This implies a co-development approach incorporating the needs, workflows, and on-the-ground context of practitioners to ensure that the tools and resulting information are fit for purpose, thus building capacity for non-traditional users of EO (Jacobi et al., 2022; Speaker et al., 2022; Tabor & Holland, 2021). Such an approach provides motivation and opportunity for EO developers to understand the needs of practitioners and explore new methods and techniques for evaluating and validating the efficacy of EO products for genetic diversity monitoring. Thus, such toolboxes for genetic diversity monitoring and assessment will not only help democratize access to EO data, but also increasingly enable the archiving and distribution of detailed and well-documented information resulting from a combination of EO with other types of data for new and innovative applications.

Glossary

Population genetics and related terms

- **Assisted Migration** refers to the relocation of individuals within a species to different areas within the species range or new frontiers of a shifting range.
- **Assisted Gene Flow** refers to the introduction of individuals with novel genetic backgrounds (e.g., different provenances or subspecies) into existing populations to increase genetic diversity or otherwise alter population genetic properties.
- **Genetic diversity** (or genetic variation) comprises within-species differences in DNA sequences, as well as variation in the distribution of these differences within and among populations.
- **Genetic drift** refers to changes in allele frequencies within populations due to stochastic processes, specifically because some individuals reproduce more than others and some do not reproduce at all, leading to changes in genetic composition in the next generation. In small populations the process of genetic drift can decrease genetic diversity rapidly.
- **Genetics** is the study of heritable variation.
- **Genomics** (related to high-throughput sequencing, next-generation sequencing) refers to study of DNA sequences and associated molecular features across large parts of genomes, using for example thousands to millions of single-nucleotide polymorphisms (SNPs) per genome.
- **Habitat** is the geographical, environmental, and biotic space that a species can inhabit.
- **N_c** (census size) is an estimate of the number of reproductively mature individuals in a population.
- **N_e** (effective population size) is the size of an idealized population that has the same rate of genetic drift as an actual, “real-life” population. Several demographic factors affect the size of N_e, including number of reproducing individuals and the sex ratio among them, variation in offspring number,

non-random mating, and overlapping generations. N_e is typically much lower than N_c, with the ratio of $N_e : N_c$ around 0.1.

- **N_e > 500 Headline Indicator** is the proportion of populations of a species that are assessed as having a genetic effective population size (N_e) > 500 and ranges from zero (none) to one (all).
- **Nuclear microsatellites** are rapidly mutating, short tandem repeat sequences in the nuclear genome, often used to measure relatedness within populations. Also called short sequential repeats (SSRs) or short tandem repeats (STRs). Microsatellites are also found in organellar genomes and so the modifier “nuclear” is used to indicate the nuclear genome.
- **PM Complementary Indicator** measures the proportion of biogeographically distinct populations of a species that are maintained in comparison to a baseline value, and ranges from zero (none) to one (all).
- **Population**, in genetics, is a group of spatially aggregated, interbreeding individuals, genetically distinct from other similar groups. Populations occupy a geographical space, e.g., a subsection of the species distribution range.
- **Population genetics** is a field of research referring to theoretical and molecular study of genetic diversity within and among populations over space and time.
- **Species range** is the geographical area that encompasses all the remaining extant (i.e. not-extinct) populations of a species.
- **SNPs** (Single Nucleotide Polymorphisms) are single base pair differences in a DNA sequence. SNPs are often used to study genetic diversity within and among populations.
- **Traits** are heritable differences among organisms, meaning differences that result from the interaction of genetic and environmental factors, which can be observed.

Earth Observation and related terms

- **Atmospheric correction** of an image is the removal of scattering and absorption effects from the atmosphere - making an image look hazy - to obtain the surface properties of an observed area.
- **Change detection** refers to a sequence of EO data used to observe and detect change for an observed area over time.
- **Hyperspectral** is a term often used to describe sensors covering continously a wide range of electromagnetic spectrum from visible to mid-infrared (400-2500 nm) in discrete wavelength bands (usually 10 nm or less), which is significantly finer than current multispectral sensors onboard Sentinel and other Earth observing satellites. The use of such sensors to generate pixel-based images is also called **imaging spectroscopy**.
- **Imaging spectroscopy** is used to mean the imaging of light reflected from the Earth surface with continuous, narrow high-resolution spectral bands.

- **LiDAR** is an active sensor that uses light pulses to probe the vertical structure of trees and forests, either from an aircraft or satellite. Similar observations from LiDARs are used to make topographic maps of the surface.
- **LULC** refers to land use (i.e., how land is being used and for what purpose) and land cover (i.e., what type of vegetation/ecosystem covers the land surface), which is a product derived from various EO instruments. A common variation is LULCC which examines land use and land cover change.
- **Multispectral** sensors use a defined number of bands (more than two) to sample a part of the electromagnetic spectrum that may not be adjacent to each other along the spectrum and may comprise differently sized portions of the spectrum.
- **Spatial resolution** of an image is defined as the area on the ground represented in one pixel (Ground sampling distance). Sentinel-2 imagery, for instance, provides four bands available at 10 m, six bands at 20 m, and three bands at 60 m spatial resolution.
- **Spatial extent** defines the area that is imaged by the satellite during one overflight and depends on the field of view of the satellite (i.e., swath width). Often, this corresponds to the size of a delivered image; however, data platforms might provide images from multiple acquisitions that are stitched together.
- **Spectral bands** describe ranges of wavelengths within the electromagnetic spectrum in which reflected light is measured for imaging and analysis of an observed area in remote sensing.The position of these bands in the spectrum and the width of their range are defined by the spectral resolution.
- **Spectral resolution** is defined as the spectral bandwidth and the number of individual bands used to aggregate the reflected light from the observed area.
- **Temporal resolution** is defined by the revisit time of a satellite/sensor to observe the same area on Earth's surface. Depending on the satellite configuration, revisit time varies from hours to days. The temporal resolution determines the potential for monitoring, as it enables the temporal analysis of changes.
- **Multitemporal data** describes a dataset consisting of at least two images acquired at two different times. Multitemporal data is typically used for change detection and analysis.
- **Time series** are multi-temporal datasets, acquired in a sequence of observations obtained over a certain period of time. This can be several images within a short time frame to observe fast processes (e.g., volcanic eruption) or within a long time frame (one image per year to observe glacier retreat). In addition to change detection, time series are used to study the type, speed and sustainability of observed changes.

Data and Code Availability

Code for this study are provided with the input data necessary to analyze the examples: https://gitlab.issibern.ch/meredithchristine.schuman/eo4geneticdiversity-examples

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