Leveraging Earth Observation to monitor genetic diversity from Space

Running title: EO to monitor genetic diversity

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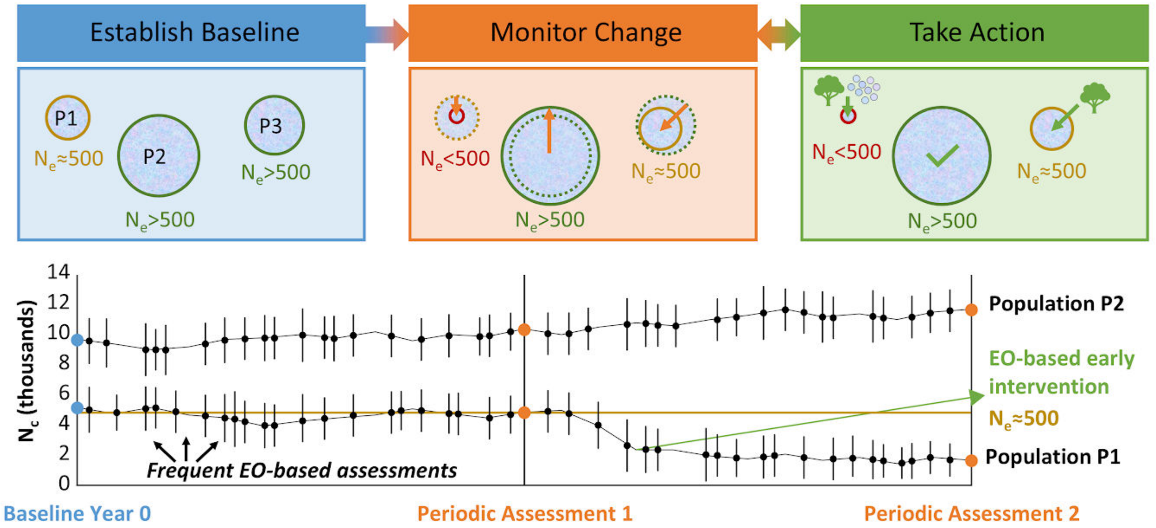
Abstract

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 the multiple scales relevant for policy and decision-making. Building on examples, we describe how Earth Observation (EO) makes 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 DNA sequence data are limited or absent. We then provide an outlook for integrating the forthcoming generation of EO data: Upcoming capabilities that will provide unprecedented detail to characterize changes to Earth's surface and their implications for biodiversity; and that will support more direct assessments of genetic diversity from Space.

Keywords

Earth Observation (EO) — 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) — essential biodiversity variables (EBVs)

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 ($N_e \sim 200$) 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 to be above this threshold ($N_e \sim 1000$) while P3 drops close to the threshold ($N_e \sim 500$). 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.

Here, 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). Here, populations refer to 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 – while 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, including 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 and thus difficult to repeat across many species at national and global scales. Costs are in the range of 10-1000 USD / sample depending on technique, genome size, and coverage – not including the cost to obtain the tissue samples or personnel and

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

computing time to analyze and interpret data (see *e.g.* Lou et al., 2021). 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 a 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). In population genetics, N_e is a key parameter 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). N_e can be assessed using detailed genetic and/or demographic data. However, the 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 reproductively 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 Headline Indicator A.4 in the GBF monitoring framework, meaning that reporting on the PM indicator 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).

We note that the values of these indicators reported for a country will be an average of each indicator's value per species for multiple monitored species.

The Headline Indicator A.4, which Parties to the CBD are required to report on, focuses on genetic diversity within populations. A.4 is defined as the proportion of populations within species having an effective population size (N_e)>500, hereafter the "N_e>500 indicator" (see **Box 1** and **Glossary**). N_e is the size of a theoretical population that has the same rate of genetic drift (see **Glossary**) as a real population and thus loses genetic diversity at the same rate. An N_e>500 is an approximate threshold to avoid the loss of genetic variation and adaptive potential over time that is accepted in literature (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). Nevertheless, some studies indicate that an even larger N_e of 1000 is required to retain adaptive potential (Frankham et al., 2014). For several reasons, the census size (N_c, see **Glossary**) – the number of reproductively mature individuals – of a real population is usually much larger than its genetically effective size N_e. This is because real populations include related individuals and migrants, and their mature members have different numbers of offspring, or do not reproduce at all, for example. Importantly, N_e can be estimated based on DNA data, or it can be approximated as 10% of N_c, or using another phyla-specific N_e:N_c ratio (Frankham, 2021; Frankham et al., 2017; Hoban, Paz-Vinas, et al., 2021). We note that the N_e>500 indicator reported for a country will be an average of the indicator's value per species for multiple monitored species.

The second, Complementary Indicator – which is not required for reporting, but supports calculation of the Headline Indicator – focuses on genetic diversity between populations. The Complementary Indicator to A.4 is the proportion of populations within species that are maintained over time in comparison to a baseline value, hereafter the "PM indicator" (see **Box 1** and **Glossary**) (Hoban, da Silva, et al., 2024; Hoban et al., 2020, 2023; Laikre et al., 2020; Mastretta-Yanes, da Silva, et al., 2024). The aim of the PM indicator is to monitor the maintenance of unique genetic diversity found in separate populations (Andersson et al., 2022; Meek et al., 2023). Here again, the value of the PM indicator reported for a country will be an average of the indicator's value per species for multiple monitored species.

DNA-based studies remain vital for quantifying genetic diversity and understanding how to conserve it; however, because the N_e>500 and PM indicators can also be calculated in the absence of DNA data, they represent a pragmatic compromise that is urgently needed to improve the affordability and accessibility of genetic diversity monitoring, thereby facilitating immediate action(Hoban, Paz-Vinas, et al., 2024; Hunter et al., 2024; Mastretta-Yanes, da Silva, 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. The 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 to calculate and monitor genetic diversity.

To facilitate reporting on the genetic diversity indicators, researchers and practitioners recently assessed these indicators in nine countries combining existing DNA studies, population census 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 N_c – data for particular taxonomic groups located in inaccessible regions (*e.g.,* areas that are politically or geographically challenging to access); or existing historical data that had not been updated in several years. 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) has become indispensable for understanding and monitoring global change. EO is used for environmental assessments and disaster risk management; to assess land and sea use and 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 from satellites such as the Copernicus Sentinels and the NASA Earth Observing System (**Table 1**), which make (global) data publicly available regularly, *i.e.*, every few days to weeks, and free of charge (Malenovský et al., 2012). Within this article, we use EO to refer to satellite-based observation systems unless explicitly stated otherwise.

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 or traits assessed using indices like the Normalized difference vegetation index (NDVI) as well as structural information such as green leaf area index (LAI) and vegetation height; 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, functional diversity, and other properties of ecosystems at the landscape scale (Mayor et al., 2024, 2025; Pasetto et al., 2018).

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

Table 1*. Selection of EO platforms that lower or eliminate technical and financial barriers to applications 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 and products and download portal for archived Sentinel data
	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
	ESA third-party missions	https://earth.esa.int/eogateway/missions/third-party-missions	Information on 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 (RGB, 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 and products, 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

Uniquely and importantly, EO typically provides repeated 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[3,4], but less frequent usable observations depending on cloud cover (**Box 2**). The Sentinel family of satellites have observed the Earth's surface with different instruments continuously starting in 2014, detecting reflected radiation in the visible, infrared, and 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**).

For example, data from the Copernicus Sentinels can be browsed via the Copernicus Browser. This cloud-based platform is easy to navigate for reviewing and visualizing the results from, *e.g.*, various combinations of different spectral bands of Sentinel-2 (see **Glossary**) and observation times 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 on the ground.

In a few cases, EO data have already been used to obtain information about species at the same (population) level at which genetic diversity is measured. An outstanding application 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). As 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

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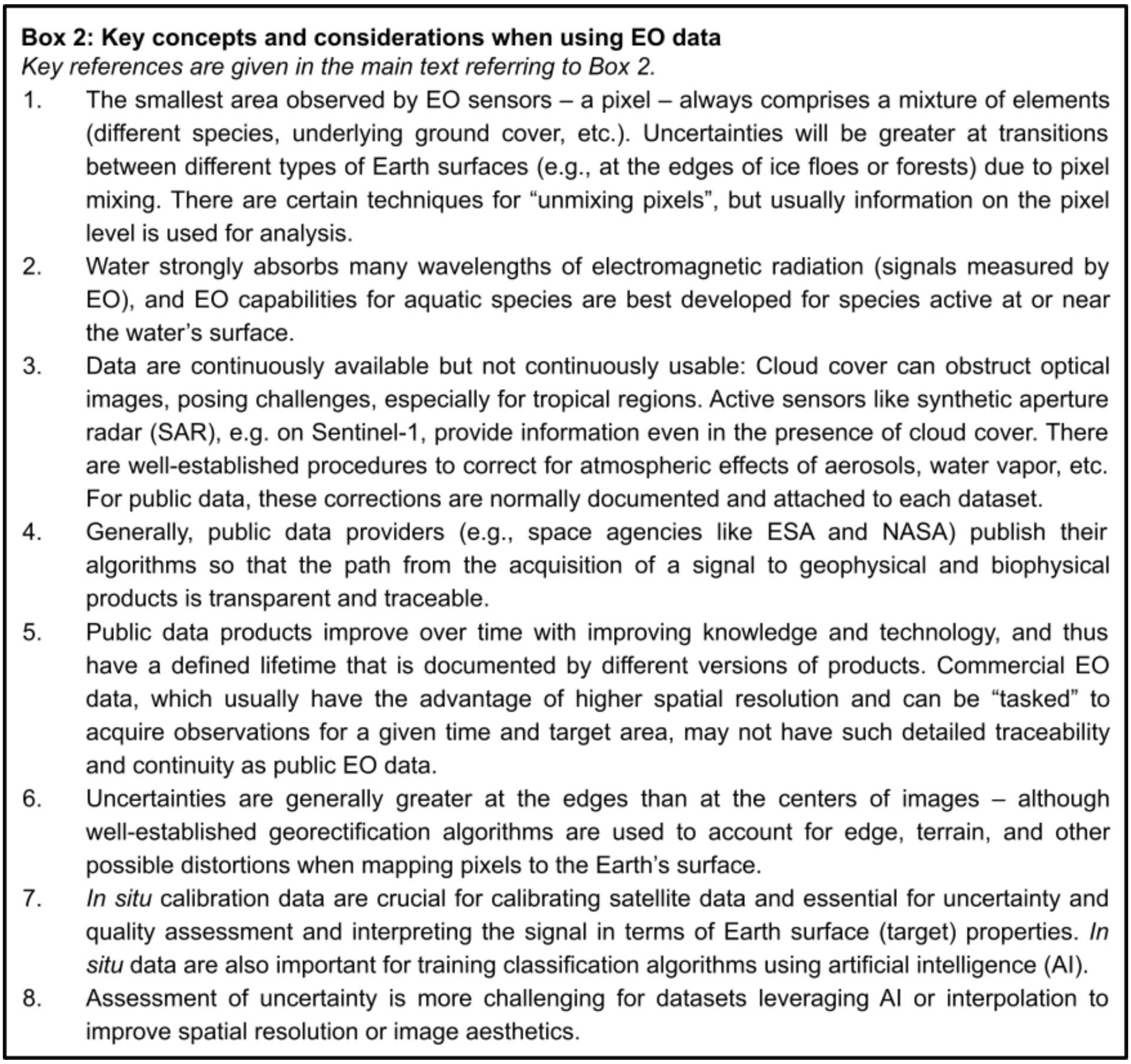
[3] https://sentiwiki.copernicus.eu/web/s2-applications

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

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 has thus become useful for monitoring penguin colonies and their habitat, taking advantage of the sharp contrast between penguins or, more often, their dark guano deposits, 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 based on signatures of population presence and habitat change.

Despite demonstrations of such potential (Barber-Meyer et al., 2007; Fernández, 2013; Fretwell & Trathan, 2009; Schuman, Roeoesli 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 recent initiatives connect landscape features to the conservation of populations (Cousins et al., 2022). Here, we describe how the current capacities of EO can be used together with the novel CBD genetic diversity indicators (**Box 1**) to facilitate the monitoring, assessment, and conservation of genetic diversity in support of the GBF goals and targets, and how forthcoming advances in EO capabilities, such as improved spatial and spectral resolution, will open new opportunities to monitor genetic diversity.

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: the Emperor penguins discussed above, crop wild relatives, and forest-forming trees. 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.



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.). 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. There are certain techniques for "unmixing pixels", but usually information on the pixel level is used for analysis.
2. Water strongly absorbs many wavelengths of electromagnetic radiation (signals measured by EO), and EO capabilities for aquatic species are best developed for species active at or near the water's surface.
3. 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.
4. 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.
5. 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 observations for a given time and target area, may not have such detailed traceability and continuity as public EO data.
6. 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.
7. *In situ* calibration data are crucial for calibrating satellite data and essential for uncertainty and quality assessment and interpreting the signal in terms of Earth surface (target) properties. *In situ* data are also important for training 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.

EO contributions to genetic diversity monitoring: A proposal

For purposes of genetic diversity indicators, 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, populations occupy 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 and land cover (LULC) 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), and can thus 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 even more directly estimated from EO (see **Outlook**). In either case, EO data supports the assessment of the N_e>500 indicator by providing an estimate for N_c from which N_e can be estimated using the N_e:N_c ratio (**Fig. 1**, **Box 3**).

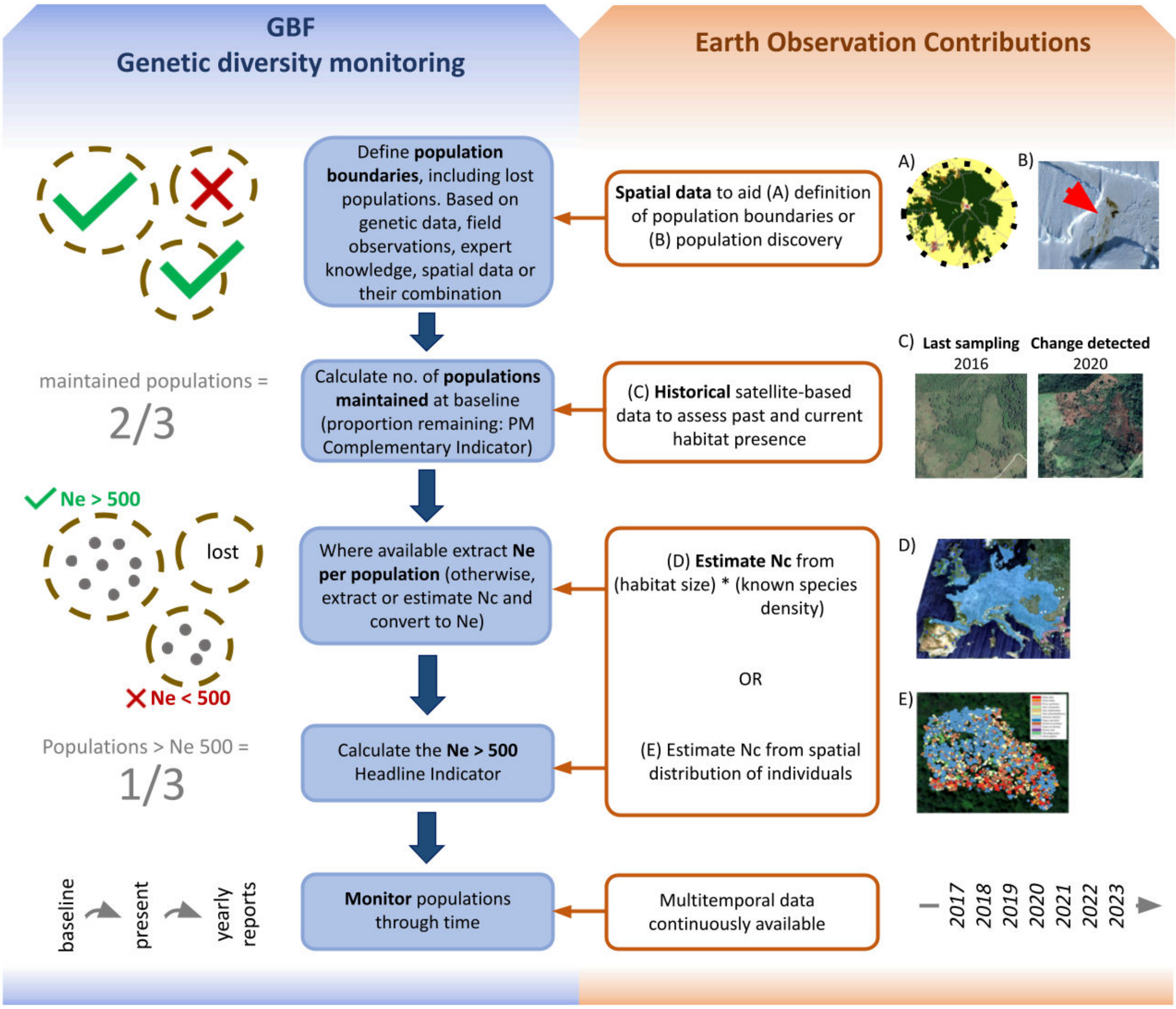


***Figure 1**. Overview of the proposed workflow for integrating EO data with genetic diversity monitoring and estimating the GBF indicators for genetic diversity: the Headline Indicator N_e>500 and Complementary Indicator PM (see **Box 1** and **Box 3**).*

Thumbnail images (A - E) show contributions of EO for obtaining information on the three examples discussed here. Furthermore, we propose that the complete workflow should be run for individual species, as elaborated in the rest of this article.

Our proposed workflow relies on the following assumptions:

- That a habitat of a particular size does support a species population;
- That habitat extent 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 expert knowledge about the location of populations, population density (N_c per area), and N_e:N_c ratio.

In sum, the proposed approach would work for species where habitat changes such as LULC change, or landscape modification and fragmentation, can be detected and quantified using EO (**Fig. 1**, **Box 3**).

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 (see main text).

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 proportion 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 proportion of populations with N_e>500 based on expert knowledge.
    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 ~ 1:10 for each population, or with a phyla-specific ratio, and estimate the number which are above the N_e>500 threshold.
4. Monitor the population areas for maintenance and size over time.
5. Leverage the features that can be detected with EO for regular remote re-assessments and to target further (e.g., ground-based) actions.

We propose that this approach will be most useful for cases in which there is still insufficient data to calculate the GBF genetic diversity indicators, but sufficient information about the location of species populations, habitat, approximate density, and dispersal distances (distance that individuals of a species or their germinative cells, like seeds, are able to move from an existing population – see **Glossary**) (**Fig. 2**). We furthermore expect that this approach can facilitate and accelerate indicator calculation even in cases where N_c estimates are available, by making repeated remote observation possible (**Box 3**). In some cases, N_c estimates will be possible directly from EO data (**Outlook**). Critically, we expect this approach to enable more frequent change monitoring in all cases (**Figs. 1** and **2**, **Box 3**).

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 (**Box 2**) (Pahlevan et al., 2021; Silva et al., 2008). The integration of EO data as an additional source of indirect information (habitat extent, fragmentation, etc.) or direct information about genetic diversity indicators (N_c estimates, and see **Outlook**) for the assessment and monitoring of biodiversity requires the co-development and production of such information. This can be achieved through collaboration among experts in population and conservation genetics and genomics; remote sensing, geography and geospatial information; ecology and conservation; and practitioners who will ultimately use this information routinely.

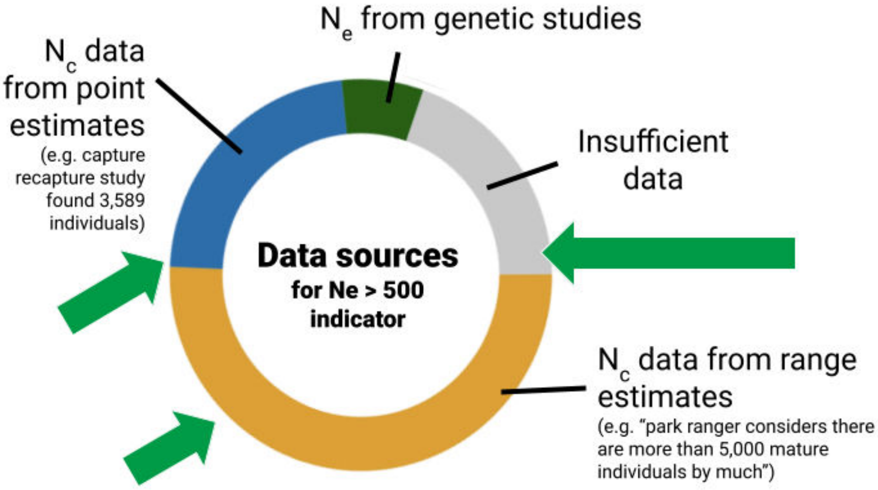


Figure 2. *EO enables estimation of key GBF genetic diversity indicators in cases where other data that could be used to calculate the indicators are unavailable (right side, large arrow), but can also complement assessments where ground data and expert knowledge are available (left side, smaller arrows) – especially by facilitating regular repeated assessments and prioritization of other actions, such as site visits or conservation measures. Made with data from Mastretta-Yanes, da Silva et al (2024).*

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) harbor an important proportion of crops' genetic diversity (Maxted et al., 2006). In Mexico, crop wild relatives are threatened mainly by LULC change (Goettsch et al., 2021). Several species (spp.) of wild avocados (*Persea* spp.) and teosintes (*Zea* spp., related to maize) 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 (LULC 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 loss of genetic diversity through genetic drift; see **Glossary**).

EO is not yet used to monitor indicators of genetic diversity for crop wild relatives, but this could be achieved using publicly available EO data in a few straightforward steps (**Fig. 1**). The first step is to define population boundaries based on occurrence points (combined with a rule for aggregating points to populations); or species distribution models on the level of populations, 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 – for example, teosintes populations in Mexico are distributed in an area the size of Western Europe). EO data can be used in such situations to detect habitat loss using either visual inspection of satellite images or by analyzing satellite-derived time series of 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 Copernicus Browser or 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 populations with remaining habitat is taken to correspond to the PM indicator. For the N_e>500 indicator, two assumptions based on expert knowledge 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 N_c. The second assumption involves the N_e:N_c ratio: For a given N_c, we can estimate the corresponding effective population size N_e. Once N_e is estimated for every population, we can calculate what proportion of populations are estimated to remain above the threshold value of N_e>500.

An 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[5]. The species' presence was confirmed during the last visit to the known field localities in 2017, although no population size measurement was conducted. A second example is the teosinte species *Zea* (*Z.*) *perennis*. This species has only been recorded to be present in two locations in Western Mexico (González et al., 2018) although species distribution models suggest it may occur in other localities within the region, where genetic differentiation is expected due to environmental and historical differences (Tobón-Niedfeldt et al., 2022). The two known locations were last visited and populations observed in 2008, when conducting sampling for genetic studies (Rivera-Rodríguez et al., 2023). Based on genetic data, the N_e of both documented *Z. perennis* 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, either of the specific locations that were visited, or from species distribution models, directly informing the PM indicator without the need for costly or dangerous field assessments. Direct inspection of true-color satellite images (**Fig. 3A and 3C**) allows a rapid assessment of vegetation and LULC change. By comparing satellite images taken before the last ground sampling (2016 for *P. cinerascens* and 2006 for *Z. perennis*) with more recent images, habitat change can be estimated. 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.

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

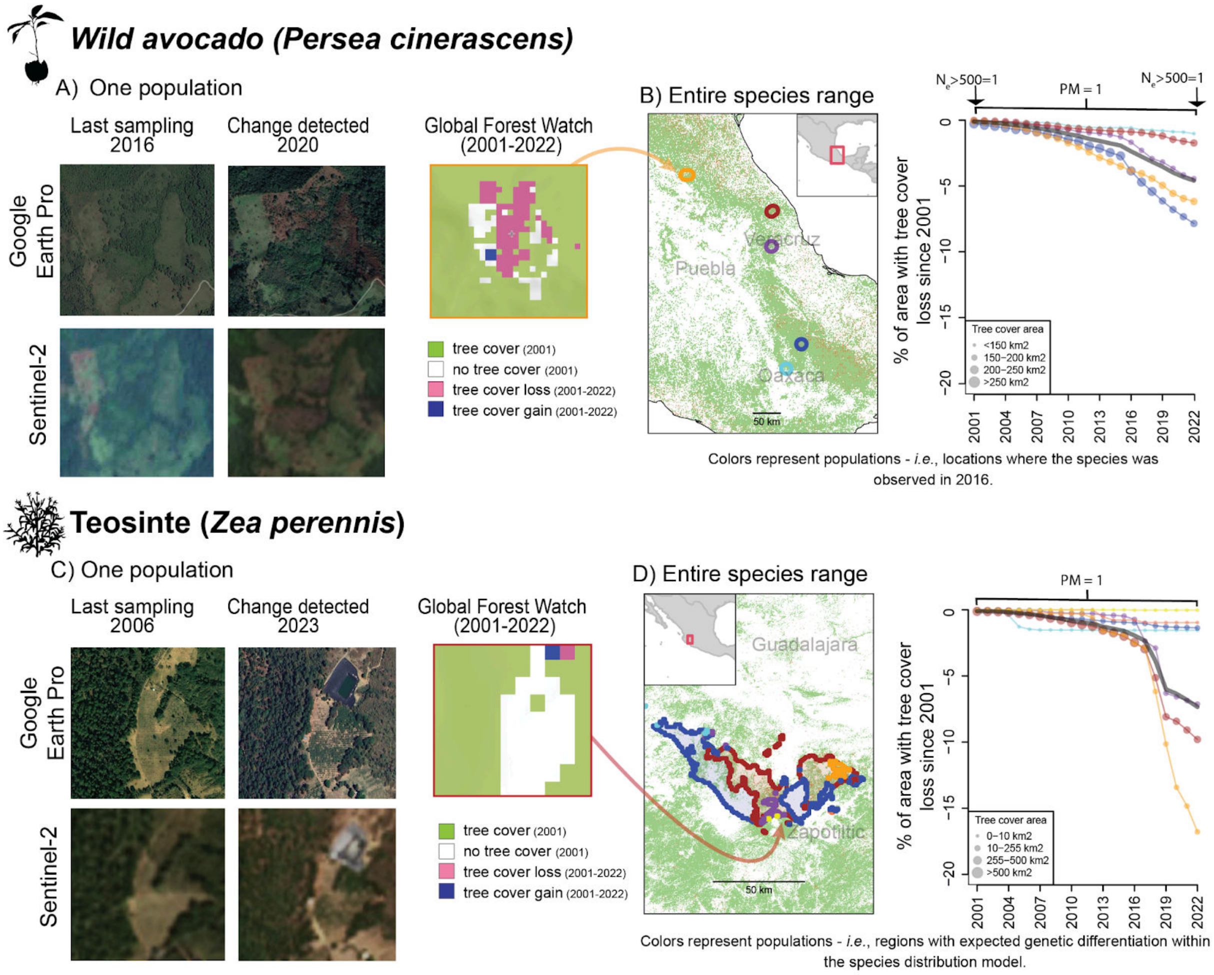

***Figure 3**. Examples of habitat monitoring using EO for A-B) a wild avocado* (P. cinerascens) *and C-D) a teosinte* (Z. perennis)*. Shown in A) are the comparisons of imagery available from either Google Earth Pro (better than 5 m spatial resolution) or Sentinel-2 (10 m spatial resolution) showing 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 observations from 2017 indicates that change took place between 2017 and 2020 (circles represent a potential habitat area of 10 km around the exact location where the species was sampled). 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 = 100 individuals / km^2 and N_e:N_c = 0.1. In C), data from Google Earth Pro and Sentinel-2 for a different time frame indicate there has been no change in forest cover in one of the teosinte's known populations, which was last observed on the ground in 2008. In D), analysis of percentage tree cover change since 2001 and total tree cover are used as an indicator for habitat change within the teosintes species distribution*

model. In this example, the species distribution was previously subdivided in six subregions where genetic differentiation is expected based on ecological and biogeographic data (Tobon et al 2022). In this case, N_e *is not estimated due to the very low number of observations, but it is possible to estimate the percentage of habitat loss within each region where the species potentially occurs in differentiated populations for conservation purposes (PM indicator).*

Using the history function of Google Earth, either the free Pro application or the web version, often provides free access to high-spatial-resolution satellite images free of charge, although the user does not control image availability (*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 change 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**).

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*, species distribution models (SDMs) serve as a proxy for species distribution ranges as commonly employed in systematic conservation planning and management (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 *P. cinerascens* (**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. In contrast, the “green” population already had minimal remaining natural vegetation, making subsequent losses more threatening to its survival. Similarly, in the *Z. perennis* 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. For *P. cinerascens*, assuming a population density of 100 mature trees per km^2 and a conservative N_e:N_c ratio of 0.1, all populations remain above the critical effective population size threshold of 500. Therefore, the N_e>500 is estimated to be 1. Notice that the assumed density is a critical parameter that can significantly affect the value of the indicator. For example, the indicator value will drop to zero if a density of 10 individuals per km^2 were assumed. In the *Z. perennis* example, habitat size is derived from an SDM, which represents areas where the species is likely to occur but does not necessarily reflect true occurrences. As a result, estimating the densities and sizes of individual populations is infeasible. However, it is notable that habitat size declined by an average of 7%, with two populations experiencing even steeper declines of up to 15%. 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. Importantly, the example furthermore shows ways in which EO-based LULC assessments enable the identification, characterization, and ranking of threats to populations, prior to indicator decline.

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 estimate 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 resilience and protecting biodiversity (Langhammer et al., 2024). The cost-effectiveness of such an EO-based approach is noteworthy, as many biodiversity hotspots are located in economic resource-limited regions.

***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 N_e** *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 for confirmation*	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

In summary, 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, and so 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.

Currently, the workflow laid out here (above and in **Figs. 1** and **3** and **Box 3**) is largely theoretical, but the examples we discuss indicate its utility and potential importance. This potential for EO-based genetic diversity monitoring needs to be co-developed with available ground-based data to understand its full potential and limitations (*i.e.*, in EO and the available ground-based data). 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 (**Fig. 2**).

Example: mapping genetic diversity of an entire tree species using EO

EO is increasingly used to directly map features of forests from Space, a focus of current research (**Table 2**). EO is used not only to estimate changes in tree cover as implemented in Global Forest Watch, but also to assess important aspects of tree canopy structure, phenology and functions including height and density, greening and browning, pigment concentration and water content; or to characterize tree species and even within-species variation. Here, we discuss how EO technologies can support the assessment of genetic diversity in terms of the GBF indicators (**Box 1**) for a dominant forest-forming tree.

To illustrate the current state of research and development, we use the European beech *Fagus* (*F.*) *sylvatica*, a dominant forest tree with high economic importance in forests across Europe. *F. sylvatica* is now threatened by increasingly severe droughts across much of its natural range, and the future of Europe's widespread beech forests is uncertain (*e.g.*, Arend et al., 2022; Eisenring et al., 2024; González de Andrés et al., 2021; Martinez del Castillo et al., 2022, 2022; Neycken et al., 2022; Pfenninger et al., 2021). *F. sylvatica* is closely related to, and likely able to hybridize with, three other *Fagus* species found from the Balkans into the Arabian peninsula that have been considered as possible sources to introduce new genetic diversity and perhaps mitigate beech forest decline (*e.g.* D'Odorico et al., 2023); in fact, these species were, until recently, considered to be a genetically diverse subspecies of *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 *F. sylvatica* has relatively low genetic differentiation among different forest stands, so that divisions into populations are challenging (Milesi et al., 2024). The weak, yet discernible genetic structure of *F. sylvatica* – 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. Genetic analysis of a stand in France with 167 individuals yielded N_e estimates ranging from 2 to 25 depending on the calculation method used, corresponding to an N_e:N_c ratio ranging from 0.01 to 0.15 (central value 0.08) (Gargiulo et al., 2024).

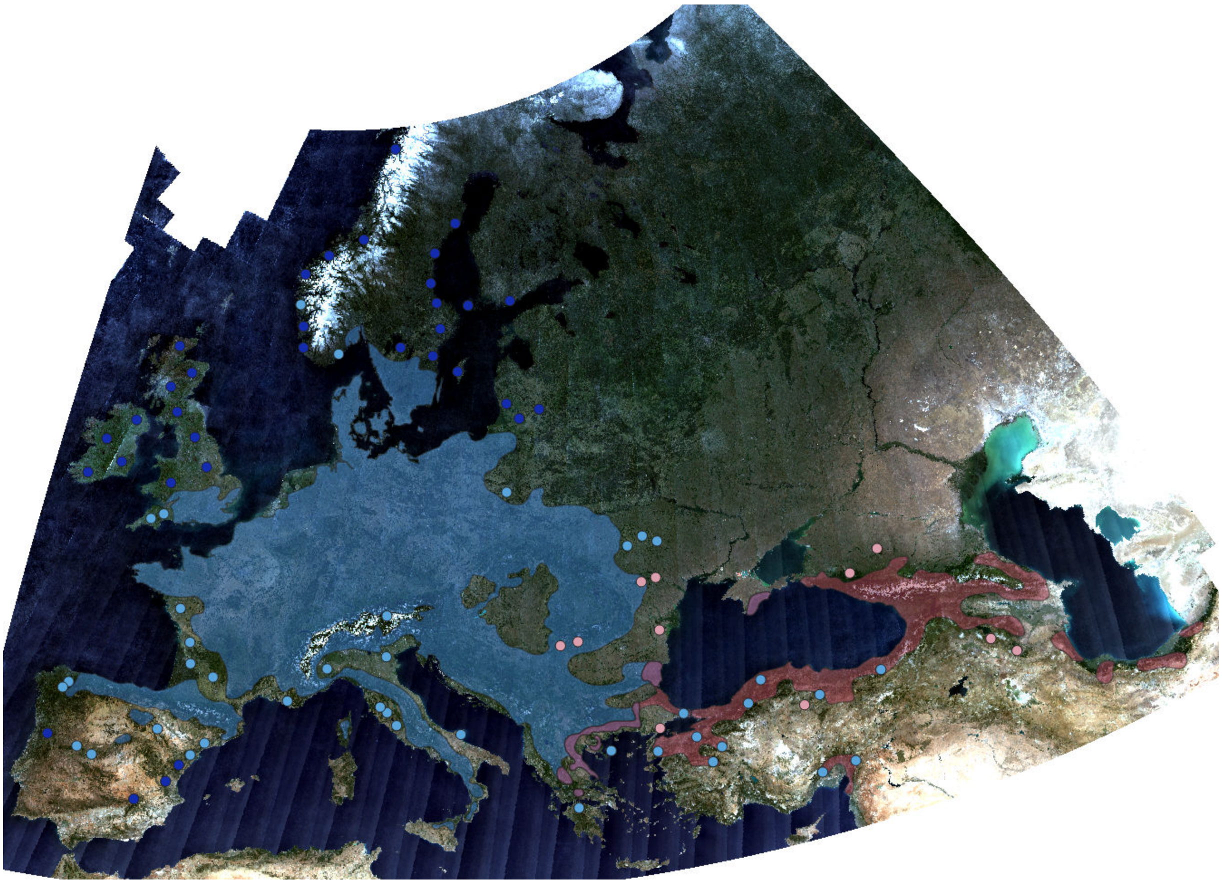

***Figure 4**. Layers of geospatial information on the distribution of Eurasian beech,* Fagus *(*F.*) species. Sentinel-2 mosaic from Google Earth Engine* (Gorelick et al., 2017) *for visualization purposes, overlaid with species distribution and isolated localities (dots)* (Caudullo et al., 2017)*:*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

It is possible to infer the number of dominant (canopy-forming) *F. sylvatica* trees in high-resolution (<10 m) EO images to estimate N_c. 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 LULC products – see **Glossary**, 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 expert 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 machine learning using 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). Using data with both high spatial (2-3 m) and spectral resolution (ca. 10 nm, continuous) from aerial imaging spectroscopy (see **Glossary**), Torabzadeh and colleagues achieved high binary classification accuracy of *F. sylvatica* versus all other trees in a beech-dominated stand based on pixels – in other words, without needing to define tree crowns (82% producer's accuracy / 92% user's accuracy) (Torabzadeh et al., 2019). Generally, binary classification (*e.g.*, beech or not-beech) is more accurate than multiple classification of pixels as depicting one of several species, which was also the case in this study (Torabzadeh et al., 2019). At another well-documented test site in Allenwiller, France, where the closely related caucasian beech *F. hohenackeriana* Palibin (among the Eurasian beeches, **Fig. 4**) 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 but with higher spatial resolution. Transferring these approaches to public data requires scaling from 3 m spatial resolution to ca. 10 to 20 m spatial resolution (see **Fig. 5**).

For *F. sylvatica*, N_c could thus be locally estimated directly from beech canopy pixels discernible from EO data via species classification, especially if the primary task is to distinguish beech from non-beech pixels. This would require either automated crown delineation, which is still best supported by laser scanning or dense photogrammetry data from drones or airplanes, or could be approximated by dividing the total pixel number by a number of average pixels per crown. 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 or other *in situ* data 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 then 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. Data from aerial imaging spectroscopy platforms are also used to assess canopy traits and vitality (Asner & Martin, 2016; Helfenstein et al., 2022) beyond counting mature trees. An approach has recently been demonstrated to relate differences in such canopy characteristics and their local diversity to the response of forest canopies to drought 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 individuals[6]. Furthermore, such trait maps suggest the possibility of more directly measuring genetic variation using EO.

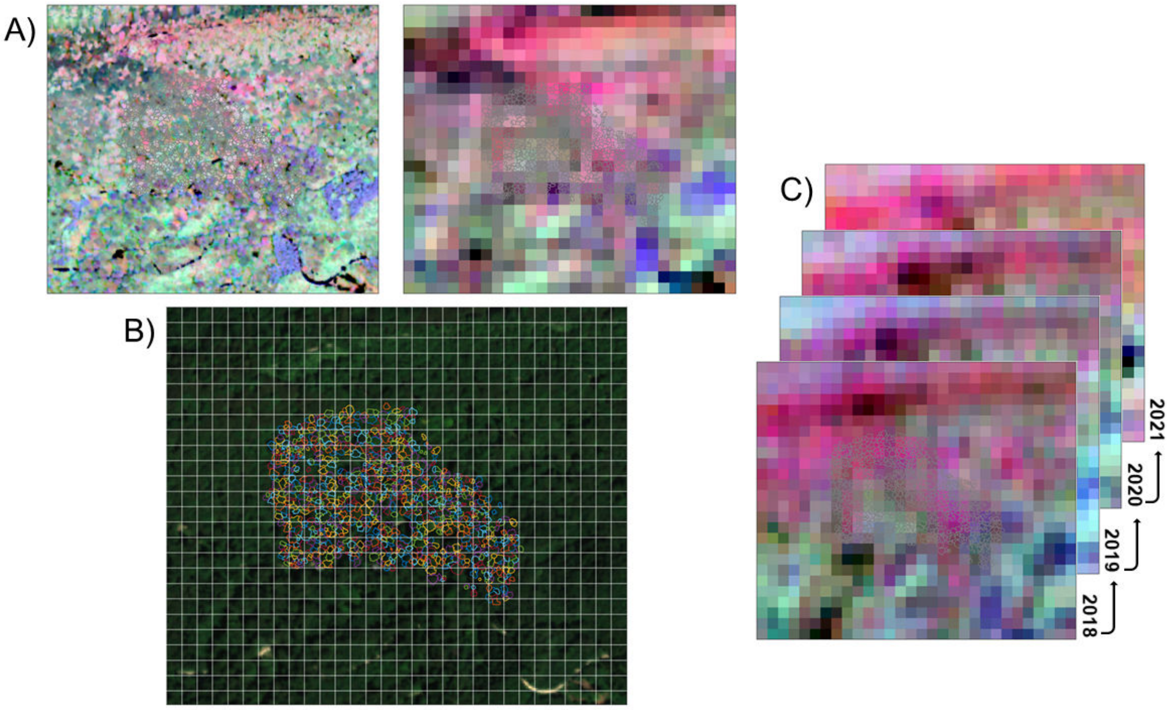

***Figure 5**. Mapping the diversity of forest canopy characteristics using EO. A) Impact of spatial resolution on the derived canopy traits chlorophyll, estimated using spectral indices from Sentinel-2 bands: Chlorophyll content, estimated using the red-edge chlorophyll index CIre (green); carotenoid:chlorophyll ratio, estimated using the chlorophyll carotenoid index CCI (red); and water content, estimated using the normalized differential infrared index NDII (blue) (Helfenstein et al., 2022). These were 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 Laegern forest. For 20 m pixels, multiple individuals contribute to the signal per pixel. C) Potential of EO data for monitoring: Canopy traits mapped for the area of interest for four consecutive years using Sentinel-2 data.*

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[6] https://deadtrees.earth/

Toward “Genes from Space”

So far, this paper has discussed using EO data to assess genetic change primarily via assessing habitat change or estimating N_c change. However, the capabilities of EO, and our ability to interpret EO data in terms of biological variation, are advancing toward an ultimate aim of truly measuring genetic diversity from space. To understand these advances and how they relate to monitoring genetic diversity, it is important to have an overview of the essential biodiversity variables (EBVs) for genetic composition, which provide an agreed-upon language for defining and measuring genetic diversity. In **BOX 4**, we explain the genetic EBVs and how they relate to the GBF indicators of genetic diversity.

Box 4: Essential Biodiversity Variables (EBVs) and their relationship to GBF indicators

Researchers have developed essential variables 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 either the N_e > 500 indicator or the PM indicator.
4. Genetic differentiation: Number of genetic units and degree of genetic differentiation among population units. Related to the PM indicator.

EBVs for genetic composition are commonly measured, although not necessarily defined, in terms of DNA sequence variation (**Box 4**). Importantly, DNA-based measures are not uniform. Taking *F. sylvatica* as an example, decades of population genetics studies have produced hundreds of datasets on genetic EBVs using different molecular methods over time; older marker-based studies remain valuable and are complemented but not replaced by a newer generation of genomic approaches using single nucleotide polymorphisms (SNPs, see **Glossary**) (Stefanini et al., 2023). SNP-based studies may in turn be overtaken by newer genomic approaches such as kmers and structural variants (Roberts et al., 2024; Stefanini et al., 2023). The situation is similar for other species where DNA-based population genetic data are available: There is no agreed-upon single way to measure EBVs for genetic composition using

DNA data. Furthermore, genetics fundamentally concerns heritable differences, *i.e.*, differences among individuals that are due in part to the genetic material inherited from their ancestors and not solely to environmental differences. Therefore, systematic measurements of individual differences, especially when combined with environmental information, are informative about genetic diversity.

Czyż and colleagues used imaging spectroscopy data with high spatial resolution (2 m) to generate a time series of differences 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 Euclidian 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 microsatellites from DNA sequencing (markers often used to quantify relatedness; see **Glossary**). The correlation strength between spectral distance and genetic distance reached a maximum of 60% across several 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 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). This study indicates that environmentally contingent differences among individuals that can be observed using EO may be predictive of genetic differences. Several other 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 (Petibon et al., 2021). Here again, to use public EO data from Space, such analyses and their interpretation must be scaled spatially from 2 m to 10-20 m pixels, thus potentially representing genetic composition on a patch-wise rather than an individual-by-individual basis.

Thus, when accounting for environmental variation, imaging spectroscopy observations with higher spectral resolution than current multispectral EO (*i.e.*, Landsat, Sentinel-2) could 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[7]) and NASA (SBG: Surface Biology and Geology[8]) 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.

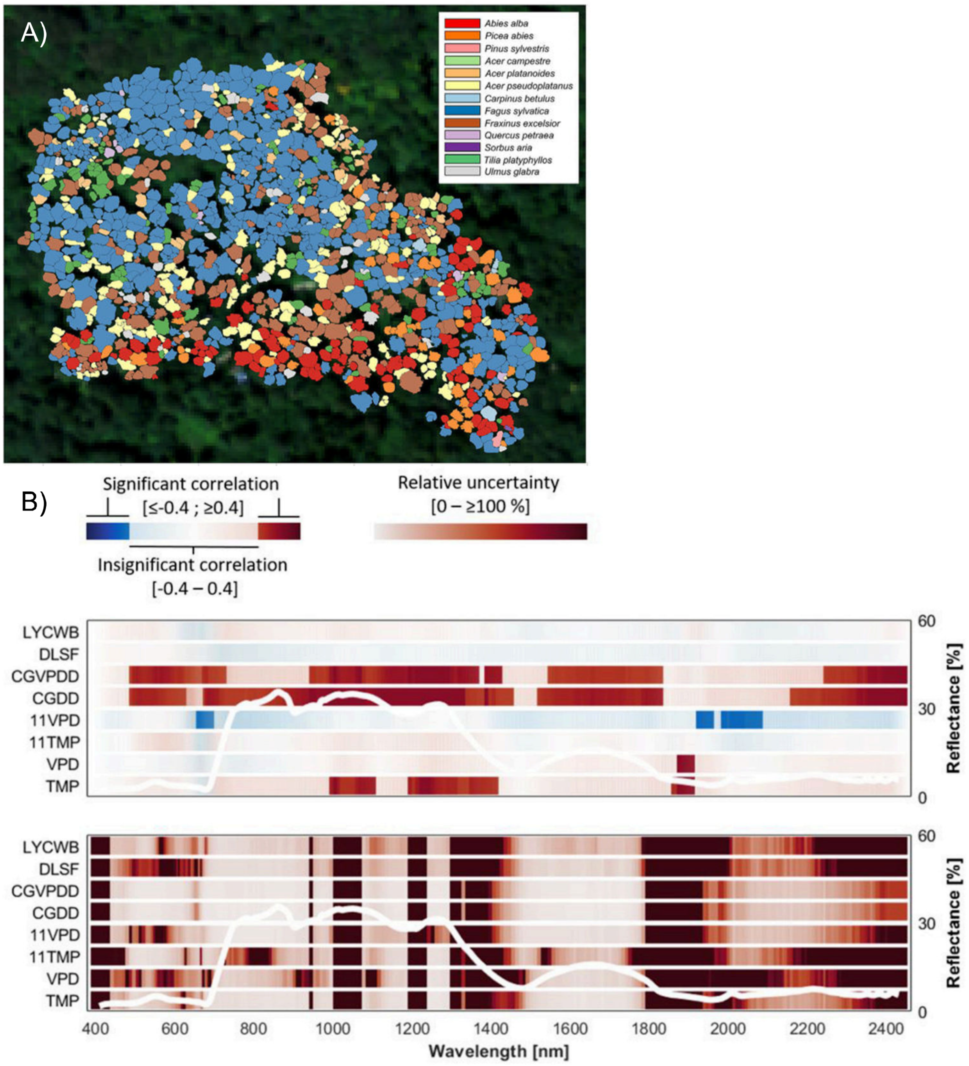

***Figure 6**. Imaging spectroscopy can help to distinguish species and assess genetic variation. A) Dominant tree crowns assigned to species by aligning forest inventory data with a 3D model of tree crowns and trunks made using LiDAR and photogrammetry; reproduced from (Guillén-Escribà et al., 2021), CC BY. B) Upper panel: Spectral*

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[7] https://www.esa.int/ESA_Multimedia/Images/2020/11/CHIME
[8] https://sbg.jpl.nasa.gov/

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.

In summary, for dominant *F. sylvatica* trees, EO from current multispectral missions can be used to map the variation of specific traits across canopies (**Fig. 5**) and, given sufficient spatial resolution, to distinguish (stands of) *F. sylvatica* trees from surrounding forest species. Data with higher spectral resolution from forthcoming imaging spectrometer sensors may support the assessment of genetic variation by providing information about forest canopy traits and spectral signatures using time series observations (**Fig. 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 EBVs for genetic composition directly from EO data for *F. sylvatica*, and likely for other dominant forest tree species, such as oaks and ʻŌhiʻa (Cavender-Bares et al., 2020; Czyż et al., 2023; Seeley, Stacy, et al., 2023; Seeley, Vaughn, et al., 2023).

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 resources or 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 discussed 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 further essential biodiversity variables (EBVs) for genetic diversity from Space (**Figs. 5-6**, **Box 4**). We acknowledge many current limitations that are illustrated and discussed 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**
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 ● Estimation of colony size from Space-based images of guano deposits instead of penguin counts	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? ● Density estimate challenging for very low 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 composition EBVs	Inference based on forest coverage and biochemical and structural differences mapped across tree canopies	● Weak geographic separation of genotypes ● Only dominant trees are visible from above and 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 the upcoming imaging spectroscopy Space missions this decade (see **Glossary**; *e.g.*, CHIME, and

SBG). 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 co-development, 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 human-assisted 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 by humans to increase genetic diversity or otherwise alter population genetic properties.
- **Dispersal distance** is the distance that individuals of a species or their germinative cells, like seeds, are able to move from an existing population.
- **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 or next-generation / third-generation sequencing) refers to the 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 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. The value of this indicator 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. These are also called short sequential repeats (SSRs) or short tandem repeats (STRs). Microsatellites are also found in organellar genomes (*i.e.*, genomes of mitochondria and plastids), and so the modifier “nuclear” is used to indicate the genome in the cell nucleus.
- **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, *i.e.*, a subsection of the species distribution range.
- **Population genetics** is a field of research focused on the 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.*, non-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 observable, heritable differences among organisms. In other words, these are differences that result from the interaction of genetic and environmental factors and that can be observed.

Earth Observation and related terms

- **Earth Observation EO** is the gathering of information about the physical, chemical, and biological processes of the Earth. In Europe, EO is often used with focus on satellite-based observations, however, EO often also includes airborne or in situ observations.
- **Remote Sensing RS** is used in the US context often connected with satellite observation, however, can be used for any measuring techniques without intervention with the object (*i.e.*, remote = without touching)
- **Atmospheric correction** of an image is the reduction 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 analysis of a sequence of EO data to observe and detect change for an observed area over time.
- **Hyperspectral** is a term often used to describe sensors covering continuously a wide range of the electromagnetic spectrum from visible to mid-infrared (400-2500 nm) in discrete, narrow wavelength bands (*e.g.*, 10 nm or less), which is significantly finer than current multispectral sensors onboard the Sentinel-2 satellites and other Earth observation 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 a target (*e.g.*, trees in forests and other features of and on the Earth's surface), either from an aircraft or satellite.
- **LULC** refers to land use (*i.e.*, how land is being used and for what purpose) and land cover (*i.e.*, what type of ecosystem covers the land surface), which is a product derived from various EO instruments. A common variation is LULCC, which refers to land use and land cover change.
- **Multispectral** sensors use a defined number of bands (more than two) to sample parts of the electromagnetic spectrum and may comprise differently sized portions of the spectrum. Each band represents a contiguous part of the spectrum, but the bands may not be adjacent along the spectrum.
- **Spatial resolution** of an image is defined as the area on the ground represented in one pixel (ground sampling distance, GSD). 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 several 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 (*e.g.*, one image per year to observe glacier retreat). In addition to change detection, time series are used to study the type, speed, and duration 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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WT-N; Supervision: MCS, CR; Visualization: AM-Y, CR, DML, ISH, MCS, OS, WT-N; Writing - original draft: MCS, CV, AM-Y, GRA, KLM, LL, CR, OS; Writing - review & editing: All

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